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Kumar Singh, Dhiraj, dksingh@zh.du.ac.in, Department of Mathematics, Zakir Husain Delhi College, University of Delhi, Delhi, India.

Kumar Singh, Karunesh, kksingh@ietlucknow.ac.in, Institute of Engineering & Technology, Lucknow, India.

Manoj, Kumar, manojkumar@ietlucknow.ac.in, Institute of Engineering & Technology, Lucknow, India.

Jain, Manish, jainmanish26128301@gmail.com, Ahir College, Rewari, India, Rewari, India.

Mari, Carlo, carlo.mari@unich.it, Department of Economics, University of Chieti-Pescara, Chieti, Italy.

Martire, Antonio Luciano, antonioluciano.martire@uniroma3.it, Università Roma Tre, Rome, Italy.

Mohamed, Ali, mohamedali.maths@gtartscollege.ac.in, Department of Mathematics, G.T.N Arts College (Autonomous), Dindigul, India.

Mohamed S., Yahya, yahya_md@yahoo.com, Department of Mathematics, Government Arts College, Tiruchirappalli, Tamil Nadu, India.

Rackova, Pavlina, pavlina.rackova@unob.cz, Department of Mathematics and Physics, University of Defence, Brno, Czech Republic.

Rajeshwari, S, rajeshwaripreetham@gmail.com, Department of Mathematics, Bangalore Institute of Technology, Bangalore, India.

Ram, Madhu, madhuras0502@gmail.com, University of Jammu, Jammu, India.

Rahman, Bootan, bootan.rahman@ukh.edu.krd, Mathematics Unit, School of Science and Engineering, University of Kurdistan Hewlêr (UKH), Erbil Iraq.

Rosenberg, Ivo, rosenb@dms.umontreal.ca, Université de Montreal, Montreal, Canada.

Sakonidis, Haralambos, xsakonid@eled.duth.gr, Democritus University of Thrace, Komotini (DUTH), Alexandroupolis, Greece.

Scognamiglio, Salvatore, salvatore.scognamiglio@uniparthenope.it, Department of Management and Quantitative Sciences, University of Naples Parthenope, Naples, Italy.

Sessa, Salvatore, sessa@unina.it, Department of Architecture, University of Naples Federico II, Naples, Italy.

Simonetti, Biagio, simonetti@unisannio.it, Department of Law, Economics, Management and Quantitative Methods (D.E.M.M.), University of Sannio, Benevento, Italy.

Squillante, Massimo, proretore@unisannio.it, Department of Law, Economics, Management and Quantitative Methods (D.E.M.M.), University of Sannio, Benevento, Italy.

Sunday, Fadugba, sunday.fadugba@eksu.edu.ng, Department of Mathematics, Ekiti State University, Ado Ekiti, Nigeria.

Padiyar, Surendra Vikram Singh, Surendrapadiyar4791@gmail.com, Department of Mathematics, Govt. Degree College Haldwani City, Nainital, Uttarakhand, India.

Syed Ali, Muhammad, syedgru@gmail.com, Department of Mathematics, Thiruvalluvar University, Vellore, India.

Tallini, Maria Scafati, tallini@mat.uniroma1.it, Department of Mathematics "Guido Catelnuovo", University of Rome La Sapienza, Rome, Italy.

Tallini, Luca, ltallini@unite.it, Faculty of Communication Sciences, University of Teramo, Teramo, Italy.

Tofan, Ioan, ioantofan@yahoo.it, Faculty of Mathematics, Alexandru I. Cuza University, Iasi, Romania.

Tonin, Simone, simone.tonin@uniud.it, Department of Economics and Statistics, University of Udine, Udine, Italy.

Udhayakumar, R., udhayakumar.r@vit.ac.in, Dept of Mathematics, School of Advanced Science, Vellore Institute of Technology (VIT), Tamil Nadu, India.

Vagaska, Alena, alena.vagaska@tuke.sk, Technical University of Kosice - Technicka univerzita v Kosiciach, Košice, Slovakia.

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The Bayesian Hidden Markov Chain Modeling of the Ghana COVID-19 Blood Type Infection Distribution

Joseph Johnson Kwabina Arhinful*
Emmanuel deGraft Johnson Owusu-Ansah[†]
Adebanji Atinuke[‡]
Accam Bennet[§]

Abstract

This study uses Hidden Markov Chain (HMC) analysis to explore how blood type influences infection progression and recovery probabilities. The results show significant differences between blood types. Individuals with blood type O^+ have higher transition probabilities from severe to milder infection states, especially from state $[5, 1]$ to $[1, 1]$ with a probability of 0.3634, indicating a better likelihood of recovery. In contrast, O^- individuals are more likely to remain in severe states, with a transition probability of 0.5132 from state $[1, 1]$ to itself, suggesting prolonged illness. Blood types A^+ and A^- generally show stability, with higher recovery probabilities for A^+ . For B^+ and B^- , early intervention is crucial, with favorable outcomes suggested by transition probabilities. AB^+ and AB^- were more stable and less infectious group. Overall, blood type influences disease progression, highlighting the need for personalized treatment strategies.

Keywords: Hidden Markov Chain; Bayesian-Poisson Hidden Markov; COVID-19; Transition Probabilities

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*Statistics and Actuarial Science, Kwame Nkrumah Univ. of Sci. & Tech. (KNUST) Ghana, Takoradi Technical University, Ghana; johnsonjoseph83@yahoo.com.

[†]Statistics & Actuarial Science, KNUST Ghana; edjowusu-ansah.cos@knust.edu.gh.

[‡]Statistics & Actuarial Science, KNUST Ghana, aoadebanji.cos@knust.edu.gh

[§]Statistics & Actuarial Science, KNUST Ghana, barneytotos@hotmail.com

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1 Background

The rapid spread and varying clinical outcomes of COVID-19 are continuing to highlight the importance of identifying factors that are influencing disease susceptibility, progression, and recovery. Among these factors, blood types are attracting attention for their potential role in modulating the risk and severity of infection. Researchers are currently suggesting associations between specific blood types and susceptibility to COVID-19, yet the mechanisms underlying these associations are remaining unclear. This is opening an opportunity for advanced modeling techniques to explore these relationships and provide robust, data-driven insights (Mielke N [2024]).

Hidden Markov Models (HMMs) are offering a powerful framework for studying the progression of infectious diseases, particularly when direct observations of health states are remaining challenging. HMMs are being used to capture temporal dynamics and stochastic transitions between latent states—such as susceptibility, infection, and recovery—that are playing a crucial role in disease progression. By incorporating observable markers such as blood types, HMMs are quantifying their influence on these transitions and are providing a probabilistic understanding of the disease’s underlying processes (Sarode Rekha [2023]).

Hidden Markov Chains (HMCs) are strong probabilistic models that explain sequences of observable events by assigning each event to an underlying unobservable state (Raffa [2012], Nam et al. [2014], Koerniawan et al. [2020]). These models have a wide range of applications, including voice recognition, bioinformatics, natural language processing, finance, and other areas of importance to researchers (Luo et al. [2014]). In a Hidden Markov Chain, the underlying process progresses through a series of states, but the states themselves are not readily visible (Song et al. [2018]). Instead, an observation or measurement is performed at each time step based on the probability of the present underlying condition. The sequence of observations gives indirect information on the sequence of underlying states, and the purpose is to determine the most probable sequence of states based on the observed data (Castillo-Riquelme et al. [2008]). One of the main components of HMC is the Markov property, which asserts that the likelihood of transitioning to a certain state is determined only by the present state and not by the sequence of events that preceded it. This trait simplifies the modeling process and enables the efficient calculation of probabilities inside the model (Ackermann et al. [2019]). The HMC generally has three sets of parameters: starting state probabilities, state transition probabilities, and emission probabilities. The starting state probabilities reflect the probability distribution of the concealed states

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at the start of the series (Alafchi et al. [2018]). The state transition probabilities indicate the chance of moving from one concealed state to another. Finally, emission probabilities indicate the chances of seeing a certain event given a concealed state.

A Bayesian method for modeling HMMs uses a probabilistic framework to estimate model parameters and make predictions. Bayesian approaches provide more robust inference by including previous information about the parameters into the model, which is especially useful when data is limited or noisy (King et al. [2016]). The Bayesian Poisson Markov Chain (BPMC) is a special variation of the Hidden Markov Chain. In BPMCs, observations are assumed to follow a Poisson distribution, while underlying states change using a Markovian process. BPMCs are especially effective for modeling count data, which is concerned with the number of occurrences of an event over a certain time or space period (Su and Wang [2020]). Prior distributions are allocated to model parameters in BPMC based on known or perceived values. These priors are subsequently updated with observed data, yielding posterior distributions that include both prior knowledge and empirical evidence (Rojas-Salazar et al. [2020]). In comparison to standard frequentist approaches, this Bayesian approach enables more robust and flexible modeling.

In this study, HMMs is used to investigate the role of blood types in the progression of COVID-19. Specifically, HMMs are enabling the integration of multivariate data, including blood types and clinical indicators, to infer latent health states and transition probabilities. By doing so, this approach is enhancing our understanding of the relationship between blood types and COVID-19 outcomes while demonstrating the broader applicability of HMMs in personalized diagnostics and disease modeling. Specifically, the study seeks to estimate the transmission and infection rates among the blood types and go into the complexities of the transition probability estimation process, explaining the approaches used and the insights gained. Moreover, to uncover the latent dynamics contained inside the hidden Markov model using actual data and robust statistical approaches and understand the transitions within the stages to explain the stages of the infection. The study's investigation into Hidden Markov Chains goes beyond theoretical abstractions, attempting to bridge the gap between seen data and underlying processes, helping to reveal the underlying transitions of COVID-19 infection in the face of blood types and rhesus factors, by revealing the estimated transition probabilities inside the hidden Markov model, hence, the study intends to provide a thorough knowledge of the blood system's behavior, opening the way for informed decision-making and predictive modeling in dealing with pandemics.

2 Related Works

2.1 The Hidden Markov Chain and Models

The Hidden Markov Chain (HMC) model has been widely explored and implemented in many domains, including voice recognition, bioinformatics, and finance. Baum and colleagues introduced the HMC in the 1960s (Sarode Rekha [2023], Baum L. E. [1966]), a probabilistic model used to study sequences of observable data. The model assumes that the underlying Markov process has unobservable states. The model is made up of two primary components: the hidden states, which develop via a Markov process, and the observable emissions, which are dependent on the underlying hidden states. R. [1989] pioneered the use of HMC for voice recognition problems. Rabiner proved the HMC's usefulness in modeling sequential data, notably voice signals, by taking advantage of the data's intrinsic temporal relationships. In bioinformatics, HMC has been used to solve a variety of issues, including gene prediction, protein structure prediction, and sequence alignment (Gang Q [2024], Johnson and Willsky [2013]). Other works, which has seen the HMM applications include financial time series (Zhang Y. [2019]), voice and hand writing recognitions(Li Y. [2016]). It has been established that, the utility of HMMs in modeling continuous physiological signals, such as EEG, ECG and MRI data has been highlighted, demonstrating their relevance in personalized medicine and disease progression modeling, evaluation of metrics, including accuracy, sensitivity and specificity in the model's clinical applicability and predictive power are highly accountable (Gang Q [2024]).

Notwithstanding the earlier application of HHM, recent works by (Mielke N [2024])has shown that, existing evidence suggests a link between ABO blood type and severe outcomes in coronavirus disease 2019 (COVID-19), hence assessing the relationship between blood type and severe outcomes across variant strains throughout the pandemic presents itself as a classical case for the application of HMM. In a recent study (Wei Zhang [2021]) utilizing Markov models is reporting that the expected duration of stay for patients infected with COVID-19 is approximately 14 days. Significant differences were observed between patient groups in terms of complications, with factors such as gender, age, hypertension, coronary heart disease, shortness of breath, myocardial damage, and thrombocytopenia showing statistically significant variations. Additionally, logistic multivariate regression analyses are identifying key clinical risk factors for COVID-19 patients. These factors primarily include gender, age, and the presence of comorbidities such as hypertension, coronary heart disease, shortness of breath, myocardial damage, and thrombocytopenia.

Moreover, another study (Soper BC [2022]) investigating the disease state-dependent risk profiles of patient demographics and medical comorbidities asso-

ciated with adverse outcomes of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections. A covariate-dependent, continuous-time hidden Markov model with four states (moderate, severe, discharged, and deceased) is being utilized to model the dynamic progression of COVID-19 during hospitalization. The findings are revealed that the association between patient-level covariates and the risk of progression is disease state-dependent. Notably, factors such as being male, being Black, or having a medical comorbidity are associated with an increased risk of progressing from the moderate to the severe disease state. However, these same factors are correlating with a decreased risk of transitioning from the severe disease state to the deceased state.

2.2 Bayesian Hidden Markov Models (BHMM)

Bayesian Hidden Markov Models (BHMMs) build on the standard HMC framework, including Bayesian inference methods for model estimation and parameter learning. BHMMs have received a lot of interest because of their capacity to manage uncertainty, integrate previous information, and give principled approaches for model selection. The paper of Beal M. J. [2002] presented the Bayesian framework for training HMMs, which significantly impacted the development of BHMMs. Beal and colleagues solved the overfitting problems and model complexity inherent in standard maximum likelihood estimate techniques by using Bayesian inference. Their study highlighted the benefits of Bayesian approaches for capturing uncertainty and giving strong estimates, even in settings with little data. In recent years (Rojas-Salazar et al. [2020] Shaochuan [2019] Murakami [2009]), BHMMs have found applications in a variety of domains. For example, Ghahramani Z. [1997] suggested a variational Bayesian strategy for learning BHMMs and used it to the problem of voice recognition, attaining comparable performance to standard approaches. Despite the computing limitations of Bayesian inference, BHMMs remain an active field of study, with continuous efforts aimed at creating efficient algorithms, scalable methodologies, and real-world applications. One frequent use of BPMC is to model count data, in which the number of occurrences of an event is represented by a Poisson distribution using Bayesian inference for parameter estimate. By adding previous knowledge into the modeling process, BPMC may provide more accurate estimates and better reflect uncertainty in parameter estimations. . In the natural language processing sector, Tran T. [2016] suggested a Bayesian non-parametric strategy for modeling sequential data using Dirichlet process-based BHMMs. Their findings revealed the effectiveness of Bayesian nonparametrics in automatically establishing the right model complexity and capturing the underlying structure of sequential data. In computational biology, Liao Y. [2018] proposed a Bayesian hierarchical strategy for interpreting single-cell RNA sequencing data using BHMMs. Their findings demonstrated the

efficacy of BHMMs in simulating the variability seen in single-cell gene expression patterns and recognizing various cell types. In time-series analysis, Fox E. B. [2015] created a Bayesian framework for inferring latent states and dynamics in complex systems using BHMMs. Their findings demonstrated the effectiveness of BHMMs in detecting hidden patterns and dynamics in noisy observational data.

3 Methodology

3.1 BP-HMM to ABO blood type distribution

Suppose

$$N_c^{O^+} = (n_1^{O^+}, n_2^{O^+}, \dots, n_m^{O^+}), N_c^{A^+} = (n_1^{A^+}, n_2^{A^+}, \dots, n_m^{A^+}), \dots, N_c^{AB^+} \quad (1)$$

$$= (n_1^{AB^+}, n_2^{AB^+}, \dots, n_m^{AB^+}) \quad (2)$$

are counts of number of cases of COVID-19 for blood types, while $O^+, A^+, \dots, AB^-$ while $c = 1, 2, \dots, m$ specify a particular country with COVID-19 infection cases. This can be simplified in contingency table form as in Table 1

Table 1: Description of COVID-19 cases per blood type are distributed

Country(c)	O^+	A^+	B^+	AB^+	O^-	A^-	B^-	AB^-	Total
1	$n_1^{O^+}$	$n_1^{A^+}$	.	.	.	.	.	$n_1^{AB^-}$	N_1
2	$n_2^{O^+}$	$n_2^{A^+}$	.	.	.	.	.	$n_2^{AB^-}$	N_2
.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.
m	$n_m^{O^+}$	$n_m^{A^+}$	.	.	.	.	.	$n_m^{AB^-}$	N_c
Total	$N_{mc}^{O^+}$	$N_{mc}^{A^+}$	.	.	.	.	.	$N_{mc}^{AB^+}$	N

Assuming the number of cases for each blood type

$N_c^{O^+}, N_c^{A^+}, \dots, N_c^{AB^-}$ is governed by an unobserved(latent) process, $Y_c^{O^+} = \{y_1^{O^+}, y_2^{O^+}, \dots, y_m^{O^+}\}, Y_c^{A^+} = \{y_1^{A^+}, y_2^{A^+}, \dots, y_m^{A^+}\}, \dots, Y_c^{AB^-} = \{y_1^{AB^-}, y_2^{AB^-}, \dots, y_m^{AB^-}\}$ respectively. Further, assume the number of cases is independent. Then the model for each of the number of cases $\{N_c^{O^+}, N_c^{A^+}, \dots, N_c^{AB^-}\}$ is assumed Poisson distribution with mean, $\theta_E^{O^+} = \{\theta_1^{O^+}, \theta_2^{O^+}, \dots, \theta_K^{O^+}\}, \theta_E^{A^+} = \{\theta_1^{A^+}, \theta_2^{A^+}, \dots, \theta_K^{A^+}\}, \dots, \theta_E^{AB^-} = \{\theta_1^{AB^-}, \theta_2^{AB^-}, \dots, \theta_K^{AB^-}\}$ on a finite state space

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$E = (1, \dots, K)$ i.e.,

$$\omega(N_c^{O^+} | Y_c^{O^+}) = E \sim \text{Poisson}(\theta_K^{O^+}) \quad (3)$$

$$\omega(N_c^{A^+} | Y_c^{A^+}) = E \sim \text{Poisson}(\theta_K^{A^+}) \quad (4)$$

$\vdots$

$$\omega(N_c^{AB^-} | Y_c^{AB^-}) = E \sim \text{Poisson}(\theta_K^{AB^-}) \quad (5)$$

Meaning the number of COVID-19 infection count for each blood type $\{N_c^{O^+}, N_c^{A^+}, \dots, N_c^{AB^-}\}$ depends on unobserved $\{Y_c^{O^+}, Y_c^{A^+}, \dots, Y_c^{AB^-}\}$ process where $\{\theta_E^{O^+}, \theta_E^{A^+}, \dots, \theta_E^{AB^-}\}_{E=(1, \dots, K)}$ are state-dependent means of COVID-19 cases for each blood type in the finite state space.

Therefore, assuming a Poisson-Hidden Markov Model $\{N_c^{O^+}, N_c^{A^+}, \dots, N_c^{AB^-}\}$ on a finite state space $E = (1, \dots, K)$, where the unobserved (latent) $\{Y_c^{O^+}, Y_c^{A^+}, \dots, Y_c^{AB^-}\}$ processes is the Markov Chain with Transition Probability for each blood types denoted by $\{P^{O^+}, P^{A^+}, \dots, P^{AB^-}\}$. The initial state is assumed to have a uniform distribution on $E = (1, \dots, K)$ which is the least informative choice and with a large number of iterations, the choice of the prior on the initial state has less influence on the inference.

In Bayesian structure the transition probabilities, $\{P_i^{O^+}, P_i^{A^+}, \dots, P_i^{AB^-}\}$ and each mean of COVID-19 infection cases $\theta_i^{O^+}, \theta_i^{A^+}, \dots, \theta_i^{AB^-}, i = (1, \dots, K)$ are all unknown parameters. In the transition probability matrix component, it is assumed that each, $P_i^{O^+} = \{P_{i1}^{O^+}, P_{i2}^{O^+}, \dots, P_{iK}^{O^+}\}$, $P_i^{A^+} = \{P_{i1}^{A^+}, P_{i2}^{A^+}, \dots, P_{iK}^{A^+}\}$, $\dots$, $P_i^{AB^-} = \{P_{i1}^{AB^-}, P_{i2}^{AB^-}, \dots, P_{iK}^{AB^-}\}$, i.e., the i^{th} row of each transition probability follows a Dirichlet distribution, $P_i^{O^+} \sim \text{Dir}(\mu_{i1}^{O^+}, \mu_{i2}^{O^+}, \dots, \mu_{iK}^{O^+})$, $P_i^{A^+} \sim \text{Dir}(\mu_{i1}^{A^+}, \mu_{i2}^{A^+}, \dots, \mu_{iK}^{A^+})$, $\dots$, $P_i^{AB^-} \sim \text{Dir}(\mu_{i1}^{AB^-}, \mu_{i2}^{AB^-}, \dots, \mu_{iK}^{AB^-})$ which can be expressed in probability density function as:

$$\omega(P_i^{O^+}) \sim \prod_{j=1}^K P_{ij}^{(O^+)\mu_{ij}-1} \quad (6)$$

$$\omega(P_i^{A^+}) \sim \prod_{j=1}^K P_{ij}^{(A^+)\mu_{ij}-1} \quad (7)$$

$\vdots$

$$\omega(P_i^{AB^-}) \sim \prod_{j=1}^K P_{ij}^{(AB^-)\mu_{ij}-1} \quad (8)$$

Where μ_{ij} is the parameter vector and $i, j = 1, \dots, K$. This implies P'_i s are here independent of each other. Where $\mu_{ij} \geq 0$ and $P_{ij} \geq 0$ and $\sum P_{ij} = 1$ Assuming

Gamma prior for each of the state-dependent means $\{\theta_i^{O+}, \theta_i^{A+}, \dots, \theta_i^{AB-}\}$ for a given state $i = (1, \dots, K)$. i.e.,

$$\theta_i^{O+} \sim \gamma(\alpha_i^{O+}, \beta_i^{O+}) \quad (9)$$

$$\theta_i^{A+} \sim \gamma(\alpha_i^{A+}, \beta_i^{A+}) \quad (10)$$

$\vdots$

$$\theta_i^{AB+} \sim \gamma(\alpha_i^{AB+}, \beta_i^{AB+}) \quad (11)$$

Here, $\theta_i^{O+}, \theta_i^{A+}, \dots, \theta_i^{AB-}$ are independent of each other. The independence of prior distribution is a result of no association of information between states. Therefore, given number of COVID-19 cases by each country according to their blood type distributions as: $N_c^{O+} = (n_1^{O+}, n_2^{O+}, \dots, n_m^{O+})$, $N_c^{A+} = (n_1^{A+}, n_2^{A+}, \dots, n_m^{A+})$, $\dots$, $N_c^{AB+} = (n_1^{AB+}, n_2^{AB+}, \dots, n_m^{AB+})$, we are interested in the joint posterior distribution of unknown parameters of each blood type $\pi^{O+} = (\theta_i^{O+}, P_i^{O+}), \dots, \pi^{AB-} = (\theta_i^{AB-}, P_i^{AB-})$. With the help of Gibbs sampler, we can draw samples from the joint posterior distribution since evaluating the joint posterior distribution of π computationally is not possible in close form.

Given the Markov chain, $(Y_j^{O+}, Y_j^{A+}, \dots, Y_j^{AB-})$ where, $j = 1, \dots, K$ we estimate the full conditional distribution of the elements of $(P_i^{O+}, P_j^{A+}, \dots, P_j^{AB-})$ which is proportional to the prior probability distribution in equations 6 and its likelihood functions which is the multinomial distribution function as:

$$\omega(P_i^{O+}, P_j^{A+}, \dots, P_j^{AB-} | Y_j^{O+}, Y_{i,j}^{A+}, \dots, Y_{i,j}^{AB-}) \propto \omega(P_j^{O+}, P_j^{A+}, \dots, P_j^{AB-}) \omega(Y_j^{O+}, Y_j^{A+}, \dots, Y_j^{AB-} | P_i^{O+}, P_j^{A+}, \dots, P_j^{AB-}) \quad (12)$$

$$\begin{aligned} \omega(P_j^{O+}) \omega(Y_j^{O+} | P_j^{O+}) &= \omega(P_j^{O+} | \mu_{i,1}^{O+}, \dots, \mu_{i,j}^{O+}) \prod_j^K \omega(Y_j^{O+} | P_j^{O+}) \\ &= \left(\frac{\prod_j^K \Gamma \mu_K}{\Gamma(\sum_j^K \mu_K)} \prod_{j=1}^K (P_j^{O+})^{\mu_{ij}-1} \right) \times \\ &\quad \left(\frac{m!}{y_1^{O+}! \dots y_j^{O+}!} (P_1^{O+})^{y_1^{O+}}, \dots, (P_j^{O+})^{y_j^{O+}} \right) \\ &\propto \prod_{j=1}^K (P_j^{O+})^{\mu_{ij}-1} \prod_{j=1}^K (P_j^{O+})^{\mathbf{1}\{y_c^{O+}=j\}} \\ \omega(P_j^{O+} | Y_j^{O+}) &\propto \prod_{j=1}^K (P_j^{O+})^{\mu_{ij}-1 + \sum \mathbf{1}\{y_c^{O+}=j\}} \end{aligned} \quad (13)$$

Bayesian Hidden Markov Model for Blood Type Distribution

Therefore, with the Gibb's sampler while given $(Y_j^{O+}, Y_j^{A+}, \dots, Y_j^{AB-})$ the full conditional distribution of each of $P_j^{O+}, P_j^{A+}, \dots, P_j^{AB-}$ is derived as

$$\omega(P_j^{O+} | Y_j^{O+}) \sim \text{Dirichlet} \left(\mu_{ij}^{O+} + \sum \mathbf{1}\{Y_c^{O+} = j\} \right) \quad (14)$$

$$\omega(P_j^{A+} | Y_j^{A+}) \sim \text{Dirichlet} \left(\mu_{ij}^{A+} + \sum \mathbf{1}\{Y_c^{A+} = j\} \right) \quad (15)$$

$\vdots$

$$\omega(P_j^{AB-} | Y_j^{AB-}) \sim \text{Dirichlet} \left(\mu_{ij}^{AB-} + \sum \mathbf{1}\{Y_c^{AB-} = j\}; i, j = (1, 2, \dots, K) \right) \quad (16)$$

Where each of $\sum \mathbf{1}\{Y_c' = j\}$ is an indicator function that represents the counts of instances $\{Y_c' = j\}$ in the simulated sample path of the Markov chain. Here, the P_j 's are also obtained as independent Dirichlet vectors.

Next is the derivation of the posterior distribution $(\theta_j^{O+}, \theta_j^{A+}, \dots, \theta_j^{AB-})$ which has Gamma prior with Poisson distribution function as its likelihood. Given the State-dependent means $\theta_i^{O+}, \theta_i^{A+}, \dots, \theta_i^{AB-}$ and the Transition Probability $(P_i^{O+}, P_i^{A+}, \dots, P_i^{AB-})$ the joint likelihood function for the observations and the Markov-Chain is given as:

$$\begin{aligned} \omega(N_c^{O+}, Y_j^{O+} | \theta_i^{O+}, P_i^{O+}) &= \omega(n_1^{O+} | y_1^{O+}, \theta_1^{O+}), \dots, \omega(n_m^{O+} | y_m^{O+}, \theta_m^{O+}) \\ &\times \omega(y_1^{O+} | P_1^{O+}, \dots, y_m^{O+} | P_k^{O+}) \end{aligned} \quad (17)$$

$$\begin{aligned} \omega(N_c^{O+} | Y_j^{O+} \theta_i^{O+}, P_i^{O+}) &= \prod_{i=1}^K \left\{ \prod_{c=1}^m P_{y_c, y_{c+1}}^{O+} \frac{(\theta_i^{O+})^{n_c^{O+}}}{n_c^{O+}!} e^{-\theta_i^{O+}} \right\} \\ \omega(N_c^{O+} | Y_j^{O+} \theta_i^{O+}, P_i^{O+}) &= \prod_{i=1}^K \left\{ [\theta_i^{O+}]^{\sum_c^m \mathbf{1}(Y_c^{O+}=i) n_c^{O+}} e^{-\theta_i^{O+} \cdot \sum_c^m \mathbf{1}(Y_c^{O+}=i)} \right\} \end{aligned} \quad (18)$$

Next, we derive the posterior distribution which has Gamma prior from equation (3.38-3.40) with its likelihood function in equation (3.47) as

$$\omega(\theta_j^{O+} | N_c^{O+}, Y_j^{O+}, \theta_j^{O+}) = \theta_j^{O+} \sim \gamma(\alpha_j^{O+}, \beta_j^{O+}) \times \omega(N_c^{O+} | Y_j^{O+}, \theta_j^{O+}, P_j^{O+}) \quad (19)$$

$$\begin{aligned} \omega(\theta_j^{O+} | N_c^{O+}, Y_j^{O+}, \theta_j^{O+}) &\propto \\ \prod_j^k [\theta_i^{O+}]^{\alpha_j^{O+}-1} e^{-\beta_j^{O+} \theta_j^{O+}} &\times \prod_{j=1}^K \left\{ [\theta_j^{O+}]^{\sum_c^m \mathbf{1}(Y_c^{O+}=j) n_c^{O+}} e^{-\theta_j^{O+} \cdot \sum_c^m \mathbf{1}(Y_c^{O+}=j)} \right\} \end{aligned} \quad (20)$$

$$\omega(\theta_j^{O+} | N_c^{O+}, Y_j^{O+}, \theta_j^{O+}) \propto \prod_{j=1}^K \left\{ [\theta_j^{O+}]^{\alpha_j^{O+} - 1 + (\sum_c^m \mathbf{1}(Y_c^{O+} = \mathbf{j}) n_{jc}^{O+})} \times e^{-\beta_j^{O+} \theta_j^{O+} + (-\theta_j^{O+} \cdot \sum_c^m \mathbf{1}(Y_c^{O+} = \mathbf{j}))} \right\} \quad (21)$$

$$\omega(\theta_j^{O+} | N_c^{O+}, Y_j^{O+}, \theta_j^{O+}) \propto \prod_{j=1}^K \left\{ [\theta_j^{O+}]^{\alpha_j^{O+} - 1 + \sum_c^m \mathbf{1}(Y_c^{O+} = \mathbf{j}) n_{jc}^{O+}} e^{-\theta_j^{O+} (\beta_j^{O+} + \sum_c^m \mathbf{1}(Y_c^{O+} = \mathbf{j}))} \right\} \quad (22)$$

The full conditional posterior distribution of the mean of each blood type, $\theta_j^{O+}, \theta_j^{A+}, \dots, \theta_j^{AB-}$ is obtained as

$$\theta_j^{O+} | N_c^{O+}, Y_j^{O+} \sim \gamma \left(\alpha_j^{O+} - 1 + \sum_c^m \mathbf{1}(Y_c^{O+} = \mathbf{j}) n_{jc}^{O+}, \quad \beta_j^{O+} + \sum_c^m \mathbf{1}(Y_c^{O+} = \mathbf{j}) \right) \quad (23)$$

$$(24)$$

$$\theta_j^{A+} | N_c^{A+}, Y_j^{A+} \sim \gamma \left(\alpha_j^{A+} - 1 + \sum_c^m \mathbf{1}(Y_c^{A+} = \mathbf{j}) n_{jc}^{A+}, \quad \beta_j^{A+} + \sum_c^m \mathbf{1}(Y_c^{A+} = \mathbf{j}) \right) \quad (25)$$

$\vdots$

$$\theta_j^{AB-} | N_c^{AB-}, Y_j^{AB-} \quad (26)$$

$$\sim \gamma \left(\alpha_j^{AB-} - 1 + \sum_c^m \mathbf{1}(Y_c^{AB-} = \mathbf{j}) n_{jc}^{AB-}, \quad \beta_j^{AB-} + \sum_c^m \mathbf{1}(Y_c^{AB-} = \mathbf{j}) \right)$$

$; j = (1, 2, \dots, K)$

Where, $\{\alpha_j^{O+}, \alpha_j^{A+}, \dots, \alpha_j^{AB-}\}$ and $\{\beta_j^{O+}, \beta_j^{A+}, \dots, \beta_j^{AB-}\}$ the prior shape and rate parameters for each blood type respectively. $\{\mathbf{1}(Y_c' = j)\}$ is an indicator function representing each count of instances in the simulated sample path of the Markov chain. $\{\sum_{c=1}^n \mathbf{1}(Y_c' = j) N_{jc}'\}$ is the contribution of regime j to each of the observed values of $\{N_c^{O+}, N_c^{A+}, \dots, N_c^{AB-}\}$. In the Gibbs Sampler, the model will first generate a sample path of the Markov chain (MC). The model then uses this

sample path to decompose the observed counts into (simulated) regime contributions. Finally, with the availability of the Markov chain sample path, and the regime contributions, the developed model can now update $P_j^{O^+}, P_j^{A^+}, \dots, P_j^{AB^-}$ and $\theta_j^{O^+}, \theta_j^{A^+}, \dots, \theta_j^{AB^-}$.

If the steps above are repeated for a large number of times, the resulting samples of values of $\hat{P}_j^{O^+}, \hat{P}_j^{A^+}, \dots, \hat{P}_j^{AB^-}$ and $\hat{\theta}_j^{O^+}, \hat{\theta}_j^{A^+}, \dots, \hat{\theta}_j^{AB}$ provide the required estimates of their posterior distributions. In the posterior, the hidden states are ranked according to the state-dependent mean of infection occurrence respecting each blood type, i.e. $\hat{\theta}_j^{O^+} = \{\hat{\theta}_1^{O^+}, \hat{\theta}_2^{O^+}, \dots, \hat{\theta}_K^{O^+}\}, \theta_j^{A^+} = \{\hat{\theta}_1^{A^+}, \hat{\theta}_2^{A^+}, \dots, \hat{\theta}_K^{A^+}\}, \dots, \hat{\theta}_j^{AB^-} = \{\theta_1^{AB^-}, \theta_2^{AB^-}, \dots, \hat{\theta}_K^{AB^-}\}$ for a given state $j = 1, \dots, K$. Given this, a smaller rate of infection occurring in a state is an indication of a lesser probability of getting that infection of that particular blood type.

The deviance information criterion (DIC) is used as a measure of model comparison and adequacy. Mathematically is given as $DIC(K) = D(\hat{\theta}_K^{A^+}, K) + 2\tau$, where, is the deviance measure which is equal to minus twice the log-likelihood, is the posterior mean of the model for blood type and is the number of effective parameters for the model. Smaller DIC values indicate a better-fitting model.

In this study, using OpenBugs as a statistical tool, the Monte Carlo error, traceplot, and autocorrelations were monitored to check the convergence of the analyses. The Monte Carlo errors measure the variation of the mean of the parameter of interest due to the simulation. Therefore, a lower MC error in the comparison with the corresponding estimated posterior standard deviation is an indication that the posterior mean was estimated with high precision. The trace plot gives a plot of the generated values versus each iteration number. When there is an indication of no patterns or irregularities then we assumed convergence of the algorithm. The autocorrelation plots the chain of each parameter of interest. In this study, the plot was done using lag from 1 to 50 to monitor the autocorrelations. When a lower autocorrelation is observed for all parameters at a certain lag then that would imply that an independent sample can be obtained by re-running the algorithm with a *thin*-set equal to that lag as an update.

In the Bayesian paradigm, the choice of the prior distribution is driven by mathematical convenience rather than prior information [Zucchini et al., 2018].

4 Data Assimilation, Analysis and Results

The Bayesian Poisson Hidden Markov Model (BP-HMM) was used to analyze COVID-19 incidence counts by blood type distribution in sixteen (16) Ghanaian

areas. The study data comes from the Ghana Health Service's COVID-19 dashboard as of September 1st, 2021. These data sets were used in this study for two purposes: first, to determine whether the model would select the same hidden states for each blood type distribution across Ghana's sixteen (16) regions, and second, to compare the rate of infection across blood type distributions. This comparison is feasible since the research used the MCMC sampling technique, which includes 98,000 iterations and 2000 burn-ins.

For the avoidance of doubt For the avoidance of doubt, the blood types with hidden states are classified as shown in Table 2 with stage 1 being the severe condition stage and stage 5 being the early infection state. For a four-state transition hidden states, state 4 is the earliest of infection, with stage 1 being the detection stage of the transmission.

Table 2: Hidden States of Blood Type COVID-19 Infections

	5 States	4 States
State 1	Catastrophe	Detected
State 2	Detected	Symptomatic
State 3	Symptomatic	Asymptomatic
State 4	Asymptomatic	Healthy
State 5	Healthy	

4.1 Selection of Hidden States Associated with the Blood Type Distribution in COVID-19 Patients in Ghana

The Deviance Information Criterion (DIC) is used to determine how many concealed states are present. The figures show the lower DIC for each blood type distribution within a certain number of states, as well as the connected states. Table 3 provides a crucial model comparison for model selection. In the table, τ represents the number of parameters, whereas i represents the number of hidden states. For BP-HMM, $i = \tau^2$. In this scenario, the model evaluates the lower DIC and selects the optimal choice. Table 3 shows that blood types O^+ , O^- , A^+ , A^- , B^+ , B^- , AB^+ selected five [5] states for the Ghana COVID-19 datasets, whereas blood type AB^- picked four [4]. Consistent hidden states of five (5) were found for seven blood and rhesus types, with only blood mixed with the rhesus factor having a hidden state of four.

Table 3: Summary results of model selection for COVID-19 cases of blood type

Blood Type	(BP-HMM) Selected State (K)	τ	Deviance	DIC
O^+	5	25	1541.58	1591.58
A^+	5	25	584.6	634.6
B^+	5	25	603.58	653.58
AB^+	5	25	176.44	226.44
O^-	5	25	226.61	276.61
A^-	5	25	126.13	176.13
B^-	5	25	124.53	174.53
AB^-	4	16	79.24	129.24

4.2 Estimated Average Transition Probabilities and Convergence

The estimated posterior mean for the different blood type distributions is correct since the MC error relative to each associated estimated posterior standard deviation (MC error%) is small in all cases. Tables 4 to 7 show that for a sample of 98000 iterations after deleting 2000 as a burn-in, each MC error is smaller than the corresponding standard deviation provided a lower MC error% in the range 0.2971% - 1.5236%. The approach is assumed to be convergent since there are no patterns or abnormalities in trace plot data (Figure 1). The posterior summaries provide detailed insights into the distribution of blood types, highlighting significant variations in prevalence and precision across groups. Blood type O^+ demonstrates the highest mean distribution, indicating its predominance in the studied population, while O^- , A^- , B^- , and AB^- exhibit lower means, reflecting their rarity and critical importance in medical emergencies. Blood types A^+ and B^+ show moderately high mean values, aligning with global trends of their commonality. In contrast, AB^+ and AB^- are the least represented, underscoring the need for targeted donor recruitment and resource planning. The low Monte Carlo (MC) error percentages across all groups validate the robustness of the Bayesian model, ensuring reliable estimates for healthcare planning, policy formulation, and epidemiological studies.

Table 4: Posterior summary of the estimated mean for blood type O^+

	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
O^+									
[1]	334	7.438	0.0287	0.3858	319.5	348.7	348.7	2001	98000
[2]	1005.1	15.76	0.069	0.4378	974.6	1005	1037	2001	98000
[3]	2878.4	26.77	0.0996	0.372	2826	2879	2931	2001	98000
[4]	10774.5	103.9	0.4616	0.4442	10570	10770	10980	2001	98000
[5]	31968.4	173.4	0.5628	0.3245	31630	31970	32310	2001	98000
O^-									
[1]	27.1	3.136	0.0463	1.4764	18.8	27.54	32.27	2001	98000
[2]	83	5.919	0.0804	1.3583	69.39	83.58	93.42	2001	98000
[3]	241.2	7.737	0.0279	0.3606	226.3	241.1	256.6	2001	98000
[4]	901.8	29.97	0.119	0.397	843.7	901.6	961.4	2001	98000
[5]	2674.1	49.73	0.1601	0.3219	2578	2674	2772	2001	98000

4.3 Hidden -States Infection Rates with COVID-19 Infection Stages (Number of Hidden States)

The study reveals that the incidence of infection is directly linked to the number of states, as shown in Table 8. This means that as the number of states increases for each blood type, the infection rate also rises, leading to a higher estimated number of infected individuals. Specifically, blood type O^+ has the highest total estimated infections (approximately 46,961), while blood types AB^- has the lowest (around 261). In general, the estimated infection rates follow a pattern where more common blood types like O^+ , B^+ , and A^+ have higher infection numbers, whereas rarer types like AB^- have fewer. This suggests that the spread of infection increases with the number of states, which could imply the importance of broader surveillance and control measures across multiple regions.

Table 9 displays the estimated percentage rate of infection per state for blood types and associated rhesus factors among Ghana COVID-19 participants. The results demonstrate that in state [1], the infection rate differs by blood type, with positive rhesus factors infected more often than negative rhesus factors. Except for blood type AB^+ , the infection rate for positive rhesus factors in the state [1]

Table 5: Posterior summary of the estimated mean for blood type A^+

	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
A^+									
[1]	109.3	4.28	0.017	0.3971	101.1	109.3	117.8	2001	98000
[2]	328.7	9.085	0.0358	0.394	311.3	328.6	346.9	2001	98000
[3]	942.3	15.4	0.0551	0.3577	912.6	942.2	972.7	2001	98000
[4]	3525.5	59.5	0.2609	0.4384	3410	3525	3642	2001	98000
[5]	10458.6	98.5	0.2969	0.3014	10270	10460	106550	2001	98000
A^-									
[1]	8.14	1.714	0.0184	1.0735	4.544	8.207	11.45	2001	98000
[2]	25.3	3.32	0.0342	1.0301	19.36	25.23	32.15	2001	98000
[3]	75.28	4.37	0.0147	0.3363	66.96	75.16	84.08	2001	98000
[4]	281.03	16.77	0.0677	0.4036	249.1	280.8	314.8	2001	98000
[5]	832.4	27.82	0.0851	0.3058	779	832	887.9	2001	98000

seems to be around 0.7. Insights across the states show that a substantially larger proportion of rates happened in state [5], followed by state [4]. This trend appears to be accepted due to the transition requirements from one state to another, with state [5] being an early stage of infection and state [1] being the worst state of infection. Thus, more infected individuals are expected to be within the early stages of infection, with few individuals being in the compartment of worse case stages due to the low fatality recorded in Ghana for COVID-19. Table 10 shows that state transition percentages are highest in the early stages for all blood types and lowest in the worst stage. However, blood types with a positive rhesus factor had a higher risk of developing a severe COVID-19 infection.

4.4 Analysis of Hidden Markov Chain for Blood Types

In this section, Hidden Markov Chains (HMMs), as a valuable tool for modeling systems with hidden states whose behavior can only be deduced from observable outcomes, are presented. This is a critical step in understanding the dynamics of complex systems and extracting relevant insights. In this section, the study looks at the estimate of transition probabilities inside the hidden Markov model, which is an important feature that offers insight into the underlying structure and development of COVID-19 infection graduating states within the blood types and corresponding rhesus factors. The goal is to uncover the complicated linkages between hidden states that can only be detected via seen data sequences. By methodically predicting the transition probabilities between these latent states, we hope to discover and understand patterns, trends, and dependencies that regulate the stages of the infection amid the blood types.

Table 6: Posterior summary of the estimated mean for blood type B^+

	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
B^+									
[1]	113.7	4.371	0.0179	0.4095	105.4	113.8	122.6	2001	98000
[2]	342.2	9.289	0.0404	0.4349	324.2	342.2	360.7	2001	98000
[3]	979.4	15.68	0.0518	0.3303	949.3	979.6	1010	2001	98000
[4]	3665.9	60.83	0.2488	0.409	3548	3666	3786	2001	98000
[5]	10875.4	100.7	0.2992	0.2971	10680	10870	11070	2001	98000
B^-									
[1]	7.29	1.782	0.0225	1.2626	3.359	7.412	10.58	2001	98000
[2]	23.33	3.238	0.0375	1.1581	17.52	23.22	29.89	2001	98000
[3]	70.01	4.19	0.0148	0.3532	62.05	69.94	78.45	2001	98000
[4]	260.9	16.06	0.0674	0.4196	230.6	260.7	293.6	2001	98000
[5]	773.1	26.68	0.0901	0.3377	721.8	772.9	826.2	2001	98000

Table 7: Posterior summary of the estimated mean for blood type AB^+

	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
AB^+									
[1]	15.5	3.019	0.046	1.5236	9.352	15.97	20.56	2001	98000
[2]	49.26	5.063	0.07	1.3825	40.06	49.27	58.92	2001	98000
[3]	149.9	6.121	0.02	0.3267	138.3	149.9	162.2	2001	98000
[4]	562	23.76	0.097	0.4082	516.4	561.8	609.9	2001	98000
[5]	1664.7	39.3	0.12	0.3053	1589	1589	1742	2001	98000
AB^-									
[1]	3.73	0.651	0.001	0.1536	3.293	3.293	5.099	2001	98000
[2]	16.09	2.217	0.013	0.5863	14.57	16.03	20.61	2001	98000
[3]	62.02	7.856	0.041	0.5218	56.54	61.72	78.38	2001	98000
[4]	179.59	12.88	0.09	0.6987	170.7	179.3	188.1	2001	98000

4.4.1 Analysis of the Blood Type O^+ and O^-

The Hidden Markov Chain (HMC) analysis reveals significant differences in the infection progression and recovery probabilities between individuals with blood types O^+ and O^- . By examining the transition probabilities between infection states, the findings offer key insights into how blood type may influence disease outcomes.

For individuals with the O^+ blood type, the transition from severe infection states to milder ones is notably higher. The transition probability from state [5, 1] (most severe phase) to state [1, 1] (least severe phase) is 0.3634, the highest among all transitions for O^+ individuals (Table 11). This suggests that individuals with this blood type are more likely to recover from the most severe stages of infection. Additionally, the transition probabilities from state [1, 2] (mild to moderate)

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Table 8: Summary Statistic of Blood Types by States for Ghana (GH)

Blood Type	State [1]	State [2]	State [3]	State [4]	State [5]	Total
$\hat{\theta}_i^{GH-O^+}$	334.08	1005.18	2878.40	10774.59	31968.48	46,960.73
$\hat{\theta}_i^{GH-O^-}$	27.15	83.00	241.28	901.83	2674.17	3927.43
$\hat{\theta}_i^{GH-A^+}$	109.32	328.75	942.30	3,525.52	10,458.68	15,364.57
$\hat{\theta}_i^{AF-A^-}$	8.14	25.30	75.28	281.03	832.43	1222.18
$\hat{\theta}_i^{GH-B^+}$	113.77	342.28	979.48	3,665.93	10,875.47	15,976.93
$\hat{\theta}_i^{GH-B^-}$	7.29	23.33	70.01	260.95	773.19	1134.77
$\hat{\theta}_i^{GH-AB^+}$	15.50	49.26	149.99	562.01	1664.76	2441.52
$\hat{\theta}_i^{GH-AB^-}$	3.73	16.09	62.02	179.59	-	261.43

Table 9: Estimated percentage rate of infection per state of blood types and Rhesus for Ghana COVID-19

Blood Type	State [1]	State [2]	State [3]	State [4]	State [5]
O+	0.71	2.15	6.13	22.94	68.07
O-	0.69	2.11	6.14	22.96	68.08
A+	0.71	2.13	6.14	22.95	68.08
A-	0.66	2.07	6.2	23	68.07
B+	0.71	2.14	6.13	22.94	68.06
B-	0.64	2.05	6.17	22.99	68.13
AB+	0.63	2.01	6.14	23.01	68.21

Table 10: Estimated percentage rate of infection per state of blood types for Ghana COVID-19

Blood Type	State [1]	State [2]	State [3]	State [4]	State [5]
O	0.7	2.13	6.14	22.95	68.07
A	0.68	2.1	6.17	22.98	68.07
B	0.67	2.1	6.15	22.97	68.17
AB	0.32	4.08	14.93	46.57	34.11

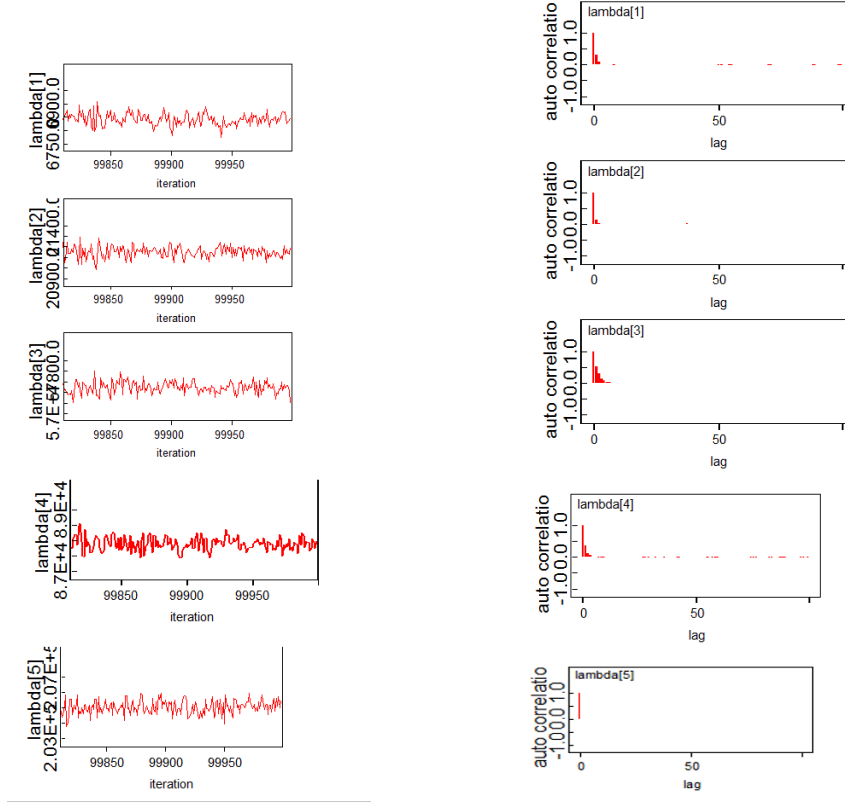


Figure 1: Patterns and Anomalies

and state $[4, 2]$ (severe to moderate) are also significant, with values of 0.3272 and 0.3313, respectively. These findings suggest a higher likelihood of recovery and stabilization for O^+ individuals compared to other blood types. The higher transition probabilities from severe to milder states indicate that individuals with blood type O^+ may have a more favorable prognosis in terms of recovery. This suggests that O^+ individuals are less likely to experience a worsening of their condition and may require less intensive medical intervention during the course of the infection (Table 11). In contrast, individuals with blood type O^- appear to face a more challenging course of infection. The transition probability from state $[1, 1]$ (severe) to the same state, 0.5132, is the highest among all transitions for O^- individuals (Table 12). This suggests that O^- individuals are more likely to remain in severe stages of infection and are less likely to progress to milder states. Further, the transition probabilities from state $[1, 2]$ (mild to moderate) and state $[2, 1]$ (moderate to mild) are comparatively low at 0.1634 and 0.1568, respectively, indicating a reduced likelihood of improvement for O^- individuals once they have reached a severe phase (Table 12). The findings imply that individuals

with blood type O^- may have a higher risk of prolonged illness or deterioration, which could warrant more intensive monitoring and medical care. Their lower transition probabilities to less severe states suggest that early intervention may be critical to prevent further complications. These results underscore the potential role of blood type in influencing the course of infectious diseases. For blood type O^+ individuals, the higher transition probabilities from severe to milder infection stages indicate a greater likelihood of recovery, which could inform more lenient management strategies for this group. On the other hand, individuals with blood type O^- face a higher risk of remaining in or deteriorating into severe stages of infection. This suggests the need for targeted and possibly more aggressive treatment and monitoring for O^- individuals.

4.4.2 Analysis of the Blood Type A^+ and A^-

Blood groups A^+ and A^- type did not see worse transitions comparatively to the O^- blood group type. As shown in Table 13 and Table 14, transitions from state 1 and state 2 to other states were all lower than 0.3, except in the state [1,2] in the A^- which recorded a transition probability of 0.3764, however since the transition is from state 1 to state 2, such a high probability of transition is for improvement of health condition, and positive results for the management of the infection.

For individuals with the A^+ blood type, the transition probabilities generally indicate stable health states across the five defined health states. The most notable transition occurs from state 1 (initial state) to state 2, with a probability of 0.3961. This suggests that individuals with A^+ blood type are relatively more likely to improve or recover during the infection period. Importantly, the probabilities of transitioning to more negative health states (such as state 3, state 4, and state 5) are lower, reflecting the possibility that individuals with A^+ blood type may be more resilient to deterioration. Overall, the distribution of transition probabilities for the A^+ group suggests a trend towards health stability, with positive outcomes being more probable than negative ones. The relatively lower transition probabilities to worse health states indicate that this group may have better baseline resilience against infection and related health challenges. In conclusion, individuals with A^+ blood type tend to experience fewer dramatic fluctuations in their health status and are more likely to show improvement with treatment. Individuals with A^- blood type exhibit a higher probability of transitioning from state 1 to state 2 (0.3764). This is a significant finding, as it suggests that individuals with A^- blood type are more likely to experience positive health outcomes and recovery during the infection period. However, the transition probabilities for other states are more scattered, particularly for the negative health states (states 4 and 5), indicating a

greater range of health outcomes for this group. The higher variability in transitions, coupled with the relatively high transition probability to state 2, suggests that individuals with A^- blood type may show a broader spectrum of responses to infection and management interventions. While some may experience recovery, others could face deterioration in health. This variability may indicate that people with A^- blood type could benefit from more tailored or personalized treatment strategies to address the different health outcomes they may experience.

Table 11: Estimated Posterior Hidden Transition Probability for Ghana Blood Type O^+

GH O^+	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.2429	0.1414	0.004653	0.03439	0.2211	0.5619
State[1,2]	0.3272	0.1478	0.004288	0.08465	0.3128	0.64
State[1,3]	0.1071	0.09678	0.00265	0.002887	0.07928	0.3607
State[1,4]	0.2115	0.1285	0.003486	0.0307	0.1899	0.5147
State[1,5]	0.1112	0.1012	0.002989	0.002996	0.08189	0.375
State[2,1]	0.2801	0.153	0.004797	0.04207	0.2595	0.6219
State[2,2]	0.2404	0.1376	0.003791	0.03409	0.2202	0.5579
State[2,3]	0.2388	0.1384	0.0041	0.03604	0.2169	0.5561
State[2,4]	0.121	0.1049	0.002867	0.003249	0.09169	0.3897
State[2,5]	0.1196	0.1076	0.003239	0.003466	0.09003	0.4024
State[3,1]	0.1603	0.1321	0.004053	0.005553	0.1284	0.4919
State[3,2]	0.1386	0.1202	0.002826	0.004254	0.106	0.4489
State[3,3]	0.2769	0.1545	0.005266	0.04239	0.2568	0.6163
State[3,4]	0.1402	0.1215	0.003276	0.004429	0.1071	0.4526
State[3,5]	0.284	0.1597	0.004911	0.04357	0.2617	0.6351
State[4,1]	0.1805	0.1475	0.003959	0.004709	0.1441	0.541
State[4,2]	0.3313	0.1796	0.00561	0.05042	0.3108	0.7151
State[4,3]	0.1603	0.1365	0.003443	0.004793	0.1246	0.5029
State[4,4]	0.1639	0.1383	0.004621	0.004647	0.1278	0.5112
State[4,5]	0.164	0.1383	0.00345	0.00553	0.1269	0.5141
State[5,1]	0.3634	0.1807	0.005465	0.06206	0.3501	0.7409
State[5,2]	0.1597	0.1335	0.003279	0.005148	0.1233	0.4948
State[5,3]	0.1579	0.1355	0.003856	0.004864	0.122	0.5086
State[5,4]	0.1506	0.1339	0.003478	0.004257	0.1138	0.4962
State[5,5]	0.1684	0.1421	0.004532	0.005209	0.1318	0.5284

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Table 12: Estimated Posterior Hidden Transition Probability for Ghana Blood Type O^-

GHO-	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.5132	0.1458	0.007044	0.2199	0.5195	0.7816
State[1,2]	0.1634	0.1107	0.004899	0.02131	0.1412	0.4356
State[1,3]	0.1531	0.1048	0.003619	0.0132	0.1315	0.4089
State[1,4]	0.08815	0.08149	0.003263	0.002587	0.06348	0.3012
State[1,5]	0.08217	0.0743	0.001991	0.002257	0.06134	0.2802
State[2,1]	0.1568	0.1307	0.003577	0.004847	0.1235	0.4811
State[2,2]	0.263	0.1445	0.00399	0.04195	0.2448	0.5785
State[2,3]	0.1492	0.1291	0.003443	0.004706	0.1132	0.4812
State[2,4]	0.1473	0.1255	0.003446	0.004695	0.114	0.4621
State[2,5]	0.2837	0.1641	0.005388	0.04043	0.2597	0.6475
State[3,1]	0.3376	0.1898	0.007315	0.03205	0.3212	0.7273
State[3,2]	0.1634	0.1418	0.003981	0.005102	0.1254	0.5246
State[3,3]	0.1682	0.1392	0.003911	0.005787	0.1313	0.509
State[3,4]	0.1657	0.1393	0.004025	0.005116	0.1299	0.5201
State[3,5]	0.1651	0.1427	0.004628	0.004414	0.1267	0.5265
State[4,1]	0.2413	0.1788	0.006502	0.009001	0.2048	0.6472
State[4,2]	0.1967	0.1647	0.005662	0.005673	0.1515	0.6059
State[4,3]	0.1949	0.1626	0.004479	0.005891	0.1515	0.5959
State[4,4]	0.1784	0.1491	0.00453	0.005618	0.1389	0.5544
State[4,5]	0.1887	0.1555	0.00391	0.005836	0.1511	0.571
State[5,1]	0.3518	0.1774	0.00511	0.06166	0.3358	0.7349
State[5,2]	0.155	0.1339	0.003921	0.004474	0.1167	0.4928
State[5,3]	0.1621	0.1395	0.003598	0.004791	0.1243	0.5176
State[5,4]	0.1633	0.1385	0.003834	0.004922	0.1263	0.5136
State[5,5]	0.1678	0.1359	0.003581	0.005245	0.1327	0.4962

4.4.3 Analysis of the Blood Type B^+ and B^-

Individuals with B^+ and B^- blood types have lower transition probabilities in state 5, indicating individuals with this blood group are unlikely to transition to other states. However, when it happens, state [5,1] indicates a transition probability of 0.3 to get worse; thus, once infected, their infection has a 30% chance of deteriorating into a worse form. Despite this, state [1,2] exhibited dominance transitions with a probability of 0.4009 for B^+ and 0.383 for B^- , suggesting that there are roughly 40.08 % and 38.9 % possibilities, respectively, to ameliorate the infection situation to gain a better or improved infection condition. The Hidden Markov Chain (HMC) model for blood types B^+ and B^- reveals important insights into disease progression. For both blood types, the probability of tran-

sitioning to state 5 is relatively low, indicating that once individuals reach this severe state, their likelihood of moving to other states decreases. This suggests a level of less stability but a prolong period of getting better, however, there remains a 0.30 probability of further deterioration into state [5,1], which highlights the risk of worsening conditions if not managed appropriately. Additionally, both blood types exhibit dominant transitions to state [1,2], with approximately 0.40 probability for B^+ and 0.38 for B^- . This suggests that, for the majority of individuals, improvement or stabilization is more likely than deterioration, pointing to a generally favorable prognosis.

Table 13: Estimated Posterior Hidden Transition Probability for Ghana Blood Type A^+

GHA+	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.2421	0.1394	0.003923	0.03546	0.223	0.5548
State[1,2]	0.3961	0.1624	0.005033	0.11	0.3879	0.7267
State[1,3]	0.1179	0.1041	0.00262	0.003391	0.08887	0.3907
State[1,4]	0.123	0.1082	0.003158	0.003873	0.0933	0.405
State[1,5]	0.121	0.1076	0.003119	0.003547	0.09116	0.3997
State[2,1]	0.2156	0.1265	0.003614	0.03408	0.1951	0.5077
State[2,2]	0.2417	0.1395	0.004422	0.03402	0.2194	0.5592
State[2,3]	0.2126	0.1279	0.003567	0.03021	0.1926	0.5073
State[2,4]	0.2174	0.1301	0.004471	0.02986	0.1973	0.5184
State[2,5]	0.1127	0.09658	0.002999	0.00337	0.08716	0.3593
State[3,1]	0.1464	0.1273	0.003588	0.00426	0.1115	0.4735
State[3,2]	0.152	0.1287	0.003275	0.004525	0.1197	0.4755
State[3,3]	0.2691	0.1491	0.004478	0.04114	0.2479	0.6022
State[3,4]	0.145	0.1264	0.003151	0.004001	0.1088	0.4696
State[3,5]	0.2875	0.1626	0.004286	0.04315	0.2646	0.6503
State[4,1]	0.1641	0.138	0.003616	0.00497	0.128	0.5127
State[4,2]	0.3579	0.1822	0.004922	0.06061	0.3412	0.7432
State[4,3]	0.1514	0.1313	0.003136	0.003841	0.1145	0.4865
State[4,4]	0.1679	0.1406	0.004054	0.005043	0.1314	0.5124
State[4,5]	0.1587	0.134	0.003192	0.005282	0.1236	0.4965
State[5,1]	0.3404	0.1809	0.005663	0.05331	0.3241	0.7265
State[5,2]	0.18	0.1487	0.004025	0.005845	0.1425	0.5555
State[5,3]	0.162	0.1392	0.003728	0.004607	0.1245	0.5116
State[5,4]	0.159	0.1358	0.003385	0.004683	0.121	0.5019
State[5,5]	0.1586	0.1323	0.004271	0.004981	0.1246	0.4946

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Table 14: Estimated Posterior Hidden Transition Probability for Ghana Blood Type A^-

GHA-	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.2323	0.1457	0.004861	0.02087	0.2106	0.5627
State[1,2]	0.3764	0.1666	0.005638	0.09192	0.3649	0.7226
State[1,3]	0.118	0.1049	0.002824	0.003461	0.08834	0.3823
State[1,4]	0.1553	0.1252	0.003955	0.005026	0.1261	0.464
State[1,5]	0.118	0.1052	0.002584	0.003616	0.08832	0.3932
State[2,1]	0.2362	0.1401	0.00408	0.03474	0.2129	0.5585
State[2,2]	0.253	0.1442	0.004632	0.03833	0.2318	0.5768
State[2,3]	0.2172	0.1317	0.004216	0.03058	0.1954	0.5299
State[2,4]	0.1804	0.1295	0.004232	0.008837	0.1554	0.4921
State[2,5]	0.1131	0.103	0.003084	0.003112	0.08376	0.3801
State[3,1]	0.1478	0.1294	0.003525	0.004339	0.1125	0.4866
State[3,2]	0.1513	0.1269	0.003294	0.004653	0.1184	0.4703
State[3,3]	0.2804	0.1584	0.006055	0.04256	0.2549	0.6431
State[3,4]	0.1403	0.1253	0.003516	0.003791	0.1036	0.4585
State[3,5]	0.2802	0.1572	0.004279	0.03947	0.2602	0.6274
State[4,1]	0.1746	0.1426	0.00372	0.005311	0.1413	0.5373
State[4,2]	0.3483	0.1792	0.004871	0.05624	0.335	0.7222
State[4,3]	0.1652	0.1387	0.00353	0.004827	0.1292	0.5197
State[4,4]	0.1547	0.1274	0.003102	0.005019	0.1241	0.4707
State[4,5]	0.1571	0.1348	0.003533	0.004224	0.1205	0.502
State[5,1]	0.3415	0.1804	0.00537	0.05563	0.323	0.7253
State[5,2]	0.1781	0.1464	0.003883	0.006169	0.1403	0.5447
State[5,3]	0.1643	0.1382	0.003811	0.005612	0.1304	0.5145
State[5,4]	0.1631	0.1368	0.003856	0.005166	0.1283	0.5109
State[5,5]	0.153	0.1285	0.003557	0.004937	0.1195	0.4789

The findings imply that early intervention is key to capitalizing on these positive transitions, ensuring that individuals have a greater chance of recovery or stabilization rather than progressing to more severe states. The statistical uncertainty in the model is also noteworthy. For B^+ , the probability of transitioning to state [1,2] is 0.4009 with a standard deviation of 0.1586, indicating variability in outcomes, with a confidence interval ranging from 0.1193 to 0.728. For B^- , the probability is 0.383, with a standard deviation of 0.1701, and a confidence interval of 0.08977 to 0.7314. This suggests that while improvement is likely for a significant portion of both groups, there is still some uncertainty in predicting individual outcomes. This result underscores the importance of timely medical in-

tervention to prevent deterioration, particularly in individuals who is yet to reach state 5, while also highlighting the relatively high probability of improvement for individuals with either blood type. Early clinical care can help mitigate risks and improve overall health outcomes, as a substantial proportion of individuals with B^+ and B^- blood types are likely to experience stabilization or recovery.

Table 15: Estimated Posterior Hidden Transition Probability for Ghana Blood Type B^+

GHB+	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.2378	0.1374	0.003875	0.03467	0.2184	0.551
State[1,2]	0.4009	0.1586	0.003824	0.1193	0.3947	0.728
State[1,3]	0.12	0.1065	0.002605	0.003502	0.08955	0.4016
State[1,4]	0.1194	0.107	0.003032	0.003397	0.08938	0.3949
State[1,5]	0.1219	0.1071	0.002821	0.00354	0.09208	0.3995
State[2,1]	0.2218	0.1314	0.004021	0.02913	0.2008	0.519
State[2,2]	0.2462	0.141	0.004249	0.03699	0.2266	0.5601
State[2,3]	0.2092	0.1296	0.004182	0.02862	0.1875	0.5229
State[2,4]	0.2158	0.1307	0.004113	0.03059	0.1933	0.5242
State[2,5]	0.107	0.09558	0.002577	0.002995	0.08008	0.3592
State[3,1]	0.1447	0.1252	0.003553	0.003974	0.1105	0.4654
State[3,2]	0.1592	0.1346	0.004235	0.00481	0.1233	0.5054
State[3,3]	0.2842	0.159	0.0053	0.04268	0.2615	0.6469
State[3,4]	0.1408	0.1229	0.003055	0.004068	0.107	0.4532
State[3,5]	0.2711	0.1582	0.005239	0.03591	0.2467	0.6273
State[4,1]	0.1597	0.1352	0.003625	0.004829	0.1227	0.506
State[4,2]	0.3517	0.181	0.004714	0.06179	0.3354	0.7292
State[4,3]	0.1663	0.1394	0.003653	0.004975	0.1285	0.5126
State[4,4]	0.1626	0.1366	0.004342	0.005057	0.1257	0.5113
State[4,5]	0.1598	0.1331	0.003219	0.005932	0.1263	0.4939
State[5,1]	0.3277	0.1744	0.004904	0.05391	0.3118	0.7027
State[5,2]	0.1839	0.1491	0.003809	0.006688	0.1473	0.5601
State[5,3]	0.1702	0.1423	0.003768	0.00486	0.1339	0.5251
State[5,4]	0.1629	0.1386	0.003247	0.004693	0.1261	0.52
State[5,5]	0.1554	0.1308	0.003539	0.00477	0.1198	0.4834

4.4.4 Analysis of the Blood Type AB^+ and AB^-

The AB^+ and AB^- blood groups showed comparable transitions to the B^+ and B^- blood groups (Tables 17 and 18). State [1,2] has a transition probability

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of 0.3601, suggesting a 36.01% possibility of improvement for the AB^+ group, moving from a poorer stage to a better one.

Table 16: Estimated Posterior Hidden Transition Probability for Ghana Blood Type B^-

GHB-	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.2048	0.1411	0.004479	0.01122	0.1817	0.5298
State[1,2]	0.383	0.1701	0.005711	0.08977	0.3738	0.7314
State[1,3]	0.1247	0.1085	0.00279	0.003519	0.09511	0.3953
State[1,4]	0.1621	0.1324	0.00429	0.005402	0.1292	0.4922
State[1,5]	0.1254	0.1127	0.003581	0.003705	0.0937	0.4261
State[2,1]	0.225	0.1326	0.004298	0.03206	0.2036	0.5301
State[2,2]	0.2726	0.1448	0.004598	0.04295	0.2578	0.587
State[2,3]	0.2154	0.1308	0.004237	0.03243	0.1932	0.5231
State[2,4]	0.1814	0.1283	0.004537	0.01004	0.155	0.4931
State[2,5]	0.1056	0.09585	0.002449	0.003057	0.07852	0.3628
State[3,1]	0.15	0.127	0.003516	0.004802	0.1156	0.4635
State[3,2]	0.1428	0.1233	0.003279	0.004322	0.1097	0.4584
State[3,3]	0.2818	0.1575	0.005301	0.04286	0.2597	0.6368
State[3,4]	0.1442	0.1231	0.002993	0.00431	0.1109	0.4534
State[3,5]	0.2812	0.1553	0.004141	0.047	0.2596	0.6309
State[4,1]	0.1652	0.1391	0.00384	0.005018	0.1277	0.5142
State[4,2]	0.3444	0.1795	0.004538	0.05596	0.3272	0.7286
State[4,3]	0.1635	0.1377	0.003239	0.004175	0.1272	0.5099
State[4,4]	0.1634	0.1386	0.003918	0.00544	0.1257	0.513
State[4,5]	0.1635	0.141	0.004169	0.004556	0.1257	0.5242
State[5,1]	0.3374	0.18	0.005048	0.05555	0.3163	0.7191
State[5,2]	0.1751	0.1487	0.00424	0.005745	0.1357	0.5534
State[5,3]	0.1633	0.1401	0.003773	0.00469	0.1251	0.5187
State[5,4]	0.1624	0.1378	0.003817	0.005154	0.1273	0.514
State[5,5]	0.1619	0.1376	0.00397	0.004513	0.1261	0.5056

In general, transitions between states were smaller, ranging at 0.20 or less for AB^+ and AB^- blood types. Nonetheless, states [1,1], [2,2], and [3,3] all revealed a possibility of an infected person continuing in the same condition for people with this blood type (0.20). The analysis indicates that residents of states [4,4] and [5,5] have a lower than 0.18 probability likelihood of remaining in their respective states. these results show that this blood type exhibits the lower infection rates and movement among the various states. The transition probabilities between various states for the AB^+ and AB^- blood groups were analyzed, revealing interesting

patterns. For the AB^+ blood group, the transition from state [1,2] had the highest probability at 0.3601 (0.36), indicating a moderate chance of improving from a worse state to a better one. In contrast, transitions for this group generally ranged at or below 0.20, suggesting smaller shifts between states. Notably, states [1,1], [2,2], and [3,3] exhibited a 0.20 probability of individuals staying in the same state, while states [4,4] and [5,5] showed a less than 0.18 probability of remaining unchanged, indicating lower movement and lower infection rates in these categories. For the AB^- blood group, the transition from state [1,1] showed a higher probability of 0.4565 (0.4565), suggesting a stronger likelihood of remaining in the same state. Meanwhile, the transitions for other states were generally lower, with probabilities under 0.20. In particular, state [1,5] had the lowest probability (0.0961), and state [5,5] had a transition probability of 0.1654, showing that individuals in the AB^- group were more likely to remain in a stable state, similar to the AB^+ group. However, the analysis indicates that the AB^+ group experiences slightly more movement compared to the AB^- group, with both blood types showing relatively lower infection rates.

5 Discussion

The results from this study, based on Hidden Markov Chain (HMC) analysis, provide compelling evidence that blood type significantly influences the progression and recovery of infections. This has important clinical implications, particularly in how different blood types may respond to infectious diseases, potentially informing treatment strategies and intervention approaches.

Blood Type O^+ and O^-

Individuals with blood type O^+ show a favorable infection progression, as indicated by their higher transition probabilities from severe infection states to milder ones. Notably, the probability of transitioning from state [5, 1] (most severe) to [1, 1] (least severe) is 0.3634, the highest among all blood types. This suggests that O^+ individuals are more likely to recover from severe stages of infection and may experience a faster and more efficient healing process. The transition probabilities from states [1, 2] (mild to moderate) and [4, 2] (severe to moderate) also support this notion, suggesting that individuals with this blood type tend to stabilize and recover more easily compared to those with other blood types. Clinically, this may indicate that O^+ individuals require less intensive medical intervention, as they are more likely to improve on their own.

Bayesian Hidden Markov Model for Blood Type Distribution

Table 17: Estimated Posterior Hidden Transition Probability for Ghana Blood Type AB^+

GHAB+	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.2724	0.1819	0.01244	0.01668	0.2387	0.6618
State[1,2]	0.3601	0.1815	0.01071	0.05732	0.3507	0.7241
State[1,3]	0.1297	0.1103	0.003136	0.004129	0.1008	0.4083
State[1,4]	0.1277	0.113	0.003514	0.004046	0.09585	0.4198
State[1,5]	0.1101	0.1006	0.003097	0.002657	0.08231	0.3651
State[2,1]	0.2061	0.1327	0.005053	0.01719	0.1823	0.5132
State[2,2]	0.2589	0.1481	0.005294	0.03718	0.2369	0.5923
State[2,3]	0.1938	0.128	0.00462	0.01464	0.1724	0.4972
State[2,4]	0.1987	0.1334	0.004583	0.01386	0.1749	0.5056
State[2,5]	0.1425	0.1347	0.008162	0.003556	0.1015	0.5099
State[3,1]	0.1766	0.1571	0.008396	0.005219	0.1306	0.5891
State[3,2]	0.1567	0.1305	0.002856	0.004712	0.1233	0.4857
State[3,3]	0.2591	0.1601	0.006837	0.02095	0.2386	0.6209
State[3,4]	0.1452	0.127	0.003284	0.004155	0.1085	0.4748
State[3,5]	0.2623	0.1644	0.006141	0.02058	0.2378	0.6301
State[4,1]	0.174	0.1518	0.005546	0.004444	0.1312	0.5617
State[4,2]	0.3264	0.1876	0.007818	0.0299	0.3117	0.7149
State[4,3]	0.1634	0.1425	0.003735	0.004691	0.1235	0.5328
State[4,4]	0.1664	0.1405	0.00453	0.005326	0.1296	0.5174
State[4,5]	0.1697	0.1426	0.004171	0.005417	0.1318	0.5296
State[5,1]	0.3432	0.1804	0.004899	0.05494	0.3263	0.7222
State[5,2]	0.1704	0.1424	0.003399	0.00535	0.1327	0.5222
State[5,3]	0.1577	0.134	0.003464	0.004972	0.1211	0.4933
State[5,4]	0.1638	0.1397	0.003546	0.004949	0.1264	0.5127
State[5,5]	0.1649	0.1388	0.004525	0.004569	0.128	0.5164

In stark contrast, individuals with blood type O^- have lower probabilities of transitioning to milder infection states, with a transition probability of 0.5132 from state [1, 1] (severe) to the same state, suggesting a higher likelihood of remaining in severe stages of infection. This is indicative of a more challenging disease course for O^- individuals, who may face prolonged illness and a greater risk of deterioration. These individuals may require more intensive and proactive medical management to prevent complications. The findings imply that early intervention and close monitoring are crucial for this group, as their transition probabilities suggest a reduced likelihood of spontaneous recovery.

Table 18: Estimated Posterior Hidden Transition Probability for Ghana Blood Type AB^-

GHAB-	Average	StanDev	MC_error	2.5Percent	Median	97.5 Percent
State[1,1]	0.4565	0.1913	0.01119	0.04896	0.4747	0.7834
State[1,2]	0.1692	0.1364	0.006112	0.007977	0.134	0.5246
State[1,3]	0.1349	0.1096	0.004052	0.005732	0.1098	0.4127
State[1,4]	0.1434	0.1183	0.005767	0.005092	0.1144	0.4429
State[1,5]	0.09609	0.08981	0.002818	0.00259	0.06915	0.3344
State[2,1]	0.1837	0.1528	0.005676	0.006159	0.1428	0.5733
State[2,2]	0.2753	0.1719	0.007237	0.01772	0.254	0.6554
State[2,3]	0.1913	0.1506	0.006208	0.006659	0.1552	0.5571
State[2,4]	0.1539	0.1336	0.004569	0.004862	0.1173	0.4994
State[2,5]	0.1958	0.1571	0.007056	0.006017	0.1579	0.5788
State[3,1]	0.2301	0.1817	0.009346	0.007574	0.1848	0.6637
State[3,2]	0.1718	0.1464	0.004509	0.005039	0.1327	0.5434
State[3,3]	0.2142	0.1596	0.006764	0.008129	0.1818	0.581
State[3,4]	0.1609	0.1411	0.003637	0.004101	0.1233	0.5246
State[3,5]	0.223	0.164	0.007258	0.008772	0.1923	0.6185
State[4,1]	0.2455	0.1821	0.006718	0.008622	0.2118	0.6646
State[4,2]	0.2381	0.1791	0.00625	0.007577	0.2031	0.6552
State[4,3]	0.1801	0.1493	0.00415	0.004795	0.1414	0.5458
State[4,4]	0.1654	0.1373	0.003879	0.00523	0.1301	0.515
State[4,5]	0.171	0.1467	0.004202	0.005473	0.1314	0.5444
State[5,1]	0.3354	0.1841	0.00503	0.0391	0.3167	0.7206
State[5,2]	0.1753	0.152	0.004673	0.004829	0.1322	0.5658
State[5,3]	0.1647	0.1392	0.003445	0.005226	0.1279	0.5158
State[5,4]	0.1591	0.1367	0.003345	0.004613	0.1208	0.5075
State[5,5]	0.1654	0.14	0.004374	0.004893	0.1291	0.518

Blood Type A^+ and A^- :

Blood types A^+ and A^- show a general tendency toward stable infection states, with transition probabilities indicating more favorable outcomes for A^+ . The transition from state $[1, 1]$ (severe) to $[1, 2]$ (mild to moderate) for A^+ individuals, with a probability of 0.3961, is notably higher than for other blood types, suggesting that they are more likely to recover or stabilize during the infection. The relatively lower probabilities of deterioration to more severe states imply that individuals with blood type A^+ may exhibit a higher baseline resilience, making them more resistant to deterioration during an infection. In contrast, A^- individuals show some variability in health outcomes, with a greater range of transition

probabilities. While the transition from state $[1, 1]$ to $[1, 2]$ is relatively high at 0.3764, there is greater uncertainty in the recovery process, suggesting that individuals with A^- may experience a broader spectrum of responses, ranging from recovery to deterioration. As a result, treatment for A^- individuals may need to be more tailored, considering the variability in their response to infection.

Blood Type B^+ and B^- :

For individuals with blood types B^+ and B^- , the study finds that early intervention plays a crucial role in improving health outcomes. While the probability of transitioning to state 5 (the most severe state) is relatively low, individuals in these blood groups may still face a 30% chance of deterioration into worse conditions if not properly managed. However, there is a strong probability of improvement for most individuals, with dominant transitions to state $[1, 2]$ (mild to moderate), with transition probabilities of 0.4009 for B^+ and 0.3830 for B^- . This suggests that with timely medical intervention, individuals with these blood types are more likely to recover or stabilize. The observed statistical uncertainty in the model indicates that while improvement is likely for a majority of B^+ and B^- individuals, some level of variability in outcomes exists. This uncertainty highlights the importance of monitoring patients closely and adjusting treatment plans as necessary.

Blood Type AB^+ and AB^- :

Individuals with AB^+ and AB^- blood types exhibit lower probabilities of deterioration, indicating more stable infection states. For example, the highest transition probability for the AB^+ group is 0.3601, transitioning from state $[1, 2]$ to a better condition, suggesting that these individuals have a moderate chance of improving. However, the overall probabilities of movement between states are lower for AB^+ and AB^- , indicating that these individuals are less likely to experience severe fluctuations in their health state. This stability may reflect lower infection rates and less aggressive progression of the disease in these groups. Moreover, both blood types show a reduced likelihood of remaining in the most severe states, with transition probabilities of less than 0.18 for states $[4, 4]$ and $[5, 5]$, highlighting a relatively more favorable prognosis.

Implications for Clinical Practice

The findings from this study suggest that blood type plays a significant role in influencing infection outcomes, underscoring the need for personalized treatment strategies. For blood type O^+ individuals, less intensive treatment may be

warranted due to their higher likelihood of recovery. In contrast, individuals with blood type O^- require closer monitoring and more aggressive treatment to prevent deterioration. Blood types A^+ and B^+ , as well as their negative counterparts, demonstrate varied yet significant responses, suggesting that treatment strategies should be flexible and adaptive. Personalized care, based on blood type, can therefore optimize recovery rates and reduce complications.

5.1 Conclusion and Future Directions

The study found that blood types A^+ , A^- , B^+ , B^- , AB^+ , O^+ , and O^- may be classified into five (5) states, with the exception of $AB-$, which is classified into four states. The findings also highlight the need to consider blood type alongside other known risk factors, such as age, pre-existing conditions, and vaccination status, in predicting infection outcomes. Incorporating blood type into predictive models could improve disease management and outcome predictions, facilitating more personalized care approaches. This study highlights the importance of blood type in infection progression and recovery. The variability in transition probabilities between blood types provides valuable insights into how individuals may respond to infection, allowing for more targeted treatment strategies. As such, blood type should be considered a key factor when managing infectious diseases, guiding healthcare providers in making more informed decisions about patient care and treatment plans. While the results provide important insights into the potential influence of blood type on infection progression, further studies are needed to validate these findings across different populations. Additionally, research into the biological mechanisms underlying the observed differences between blood types could provide deeper understanding into the immune responses that influence disease severity and recovery. Future work should also explore how blood type interacts with other factors to offer more comprehensive predictions for individual disease outcomes.

While the results provide important insights into the potential influence of blood type on infection progression, further studies are needed to validate these findings across different populations. Additionally, research into the biological mechanisms underlying the observed differences between blood types could provide deeper understanding into the immune responses that influence disease severity and recovery. Future work should also explore how blood type interacts with other factors to offer more comprehensive predictions for individual disease outcomes.

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η -Ricci solitons in a LP-Sasakian manifolds admitting quarter-symmetric metric connection

Abhishek Singh^{*}

Sangeeta Gautam[†]

Lalit Kumar[‡]

Abstract

The objective of this paper is to investigate the η -Ricci solitons in a LP-Sasakian manifolds admitting quarter-symmetric metric connection satisfying certain curvature conditions. We study the Ricci solitons in a LP-Sasakian manifolds admitting quarter-symmetric metric connection satisfying certain conditions. Finally, we have given an example of 3-dimensional η -Ricci solitons in a LP-Sasakian manifolds with respect to quarter-symmetric metric connection.

Keywords: LP-Sasakian manifolds; quarter-symmetric metric connection; η -Ricci solitons; η -Einstein manifold

2020 AMS subject classifications: 53C05, 53C15, 53C25, 53D10, 53D15. ¹

^{*}Department of Mathematics and Statistics (Dr. Rammanohar Lohia Avadh University, Ayodhya-224001 (U.P.), India); abhi.rmlau@gmail.com.

[†]Department of Mathematics and Statistics (Dr. Rammanohar Lohia Avadh University, Ayodhya-224001 (U.P.), India); sangeeta.ssd@gmail.com.

[‡]Department of Mathematics and Statistics (Dr. Rammanohar Lohia Avadh University, Ayodhya-224001 (U.P.), India); lalitkumargautamjrf@gmail.com

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1 Introduction

In 1989, K. Matsumoto (18) introduced the notion of Lorentzian Para-Sasakian manifold (LP-Sasakian manifold). In 1992, the same notion was independently studied by I. Mihai and R. Rosca (19) and they obtained several results on this manifold. LP-Sasakian manifold have been also studied by various authors (2; 27; 28; 16). The quarter-symmetric connection generalizes the semi-symmetric connection. In 1975, Golab (13) defined and studied quarter-symmetric connection in a differentiable manifold. After Golab (13), Rastogi (25) continued the systematic study of quarter-symmetric metric connection. In 1980, Mishra and Pandey (20) studied quarter-symmetric metric connection in a Riemannian, Kaehlerian and Sasakian manifold. In 1982, Yano and Imai (32) studied quarter-symmetric metric connection in Hermitian and Kaehlerian manifold. A quarter-symmetric metric connection have been studied by many authors (21; 24; 29; 12) in several ways to a different extent.

Ricci solitons in contact metric manifolds have been studied by Bagewadi et al. (1; 4; 5), Bejan and Crasmareanu (6), Chandra et al. (9), Chen and Deshmukh (10), Chenxu and Meng (14) and Nagaraja and Premalatha (22). Later on, η -Ricci soliton have been studied by various authors (23; 31; 7; 8) and many others. The Ricci flow is an evolution equation for metrics on a Riemannian manifold defined as follows:

$$\frac{\partial}{\partial t} g^{ij}(t) = -2R_{ij}.$$

A Ricci soliton (g, V, λ) on a Riemannian manifold (M, g) is generalization of an Einstein metric such that it satisfies the following condition (15)

$$(L_V g)(X, Y) + 2S(X, Y) + 2\lambda g(X, Y) = 0, \quad (1)$$

where S is the Ricci tensor, L_V is the Lie derivative operator along the vector field V on M and λ is a real number. The Ricci soliton is said to be shrinking, steady, or expanding according as λ is negative, zero or positive.

Ricci solitons, in the context of general relativity, have been studied by M. Ali and Z. Ahsan (3). As a generalization of Ricci soliton, the notion of η -Ricci soliton was introduced by J. T. Cho and M. Kimura (11). They have studied Ricci soliton of real hypersurfaces in a non-flat complex space form and defined η -Ricci soliton, which satisfies the equation

$$(L_V g)(X, Y) + 2S(X, Y) + 2\lambda g(X, Y) + 2\mu \eta(X)\eta(Y) = 0, \quad (2)$$

where λ and μ are real numbers. In particular, $\mu = 0$, then the notion of η -Ricci soliton (g, V, λ, μ) reduce to the notion of (g, V, λ) . Recently η -Ricci solitons have been studied by various authors such as A. Singh and S. Kishor (30), A. M. Blaga (8), D. G. Prakasha and B. S. Hadimani (23) and many others.

The present work is organized as follows: After introduction, in section-2, we recall basic formulas and results of LP-Sasakian manifold. Section-3 deals with curvature tensor in a LP-Sasakian manifolds admitting quarter-symmetric metric connection ($QSMC$). Section-4 is concerned with the study of η -Ricci solitons on LP-Sasakian manifolds admitting quarter-symmetric metric connection ($QSMC$) with example. In section-5, we study η -Ricci soliton on LP-Sasakian manifold admitting quarter-symmetric metric connection ($QSMC$) satisfying $\tilde{R}(X, Y) \cdot \tilde{S} = 0$. Section-6 Example of 3-dimensional LP-Sasakian manifold admitting quarter-symmetric metric connection ($QSMC$).

2 Preliminaries

An n -dimensional smooth manifold M together with a $(1, 1)$ -tensor field ϕ , a contravariant vector field ξ , η is 1-form and Lorentzian like metric g is called a LP-Sasakian manifold if

$$\phi^2 X = X + \eta(X)\xi, \quad \eta(\xi) = -1, \quad (3)$$

$$g(X, \xi) = \eta(X), \quad \phi(\xi) = 0, \quad \eta(\phi X) = 0, \quad (4)$$

$$g(\phi X, \phi Y) = g(X, Y) + \eta(X)\eta(Y) \quad (5)$$

$$(\nabla_X \phi)Y = g(X, Y)\xi + \eta(Y)X + 2\eta(X)\eta(Y)\xi, \quad (6)$$

$$\nabla_X \xi = \phi(X), \quad (7)$$

$\forall X, Y \in \chi(M)$, where $\chi(M)$ is a set of all smooth vector fields on M and ∇ is the Levi-Civita connection with respect to g . If we put

$$\phi(X, Y) = g(\phi X, Y), \quad (8)$$

$\forall X, Y \in M$, then $\phi(X, Y)$ is a symmetric $(0, 2)$ tensor field. Since the 1-form η is closed in a LP-Sasakian manifold, so we have

$$(\nabla_X \eta)Y = \phi(X, Y), \quad \phi(X, \xi) = 0 \quad (9)$$

$\forall X, Y \in \chi(M)$. In a LP-Sasakian manifold M the following relations holds

$$R(X, Y)\xi = \eta(Y)X - \eta(X)Y, \quad (10)$$

$$R(\xi, X)Y = g(X, Y)\xi - \eta(Y)X, \quad (11)$$

$$R(\xi, X)\xi = -R(X, \xi)\xi = X + \eta(X)\xi, \quad (12)$$

$$\eta(R(X, Y)Z) = [g(Y, Z)\eta(X) - g(X, Z)\eta(Y)], \quad (13)$$

$$S(X, \xi) = (n - 1)\eta(X), \quad Q\xi = (n - 1)\xi, \quad (14)$$

$\forall X, Y, Z \in \chi(M)$, $g(QX, Y) = S(X, Y)$ and R is the curvature tensor, S is the Ricci tensor, Q is the Ricci operator in a LP-Sasakian manifold with the Levi-Civita connection ∇ .

Definition 2.1. A LP-Sasakian manifold is said to be a generalized η -Einstein manifold if its Ricci tensor S of type $(0, 2)$ satisfies the following condition

$$S(Y, Z) = ag(Y, Z) + b\eta(Y)\eta(Z) + cg(\phi Y, Z). \quad (15)$$

on M , where a, b and c are smooth functions on M . If $c = 0$, then the manifold is called an η -Einstein manifold.

3 Curvature tensor in a LP-Sasakian manifolds admitting quarter-symmetric metric connection (QSMC)

Let M be a LP-Sasakian manifold with Levi-Civita connection ∇ , A quarter-symmetric metric connection $\tilde{\nabla}$ in a LP-Sasakian manifold (17) is given by

$$\tilde{\nabla}_X Y = \nabla_X Y + \eta(Y)\phi X - g(\phi X, Y)\xi. \quad (16)$$

A linear connection $\tilde{\nabla}$ in a Riemannian manifold M is said to be a quarter symmetric metric connection if the torsion tensor $\tilde{T}$ with respect to connection $\tilde{\nabla}$ satisfies

$$\tilde{T}(X, Y) = \eta(Y)\phi X - \eta(X)\phi Y = \tilde{\nabla}_X Y - \tilde{\nabla}_Y X - [X, Y], \quad (17)$$

where η is a 1-form and ϕ is $(1, 1)$ tensor field. A linear connection $\tilde{\nabla}$ is said to be a metric connection. if $\tilde{\nabla}_g = 0$. i.e.,

$$(\tilde{\nabla}_X g)(Y, Z) = 0. \quad (18)$$

$\forall X, Y, Z \in \chi(M)$, where $\chi(M)$ is the Lie algebra of vector fields on M , then $\tilde{\nabla}$ is said to be a quarter-symmetric metric connection, otherwise it is said to be a quarter-symmetric non-metric connection.

The curvature tensor $\tilde{R}$ of LP-Sasakian manifold with a quarter-symmetric metric connection $\tilde{\nabla}$ is defined by

$$\tilde{R}(X, Y)Z = \tilde{\nabla}_X \tilde{\nabla}_Y Z - \tilde{\nabla}_Y \tilde{\nabla}_X Z - \tilde{\nabla}_{[X, Y]}Z. \quad (19)$$

Using (3), (7), (9), (16) and (19), we have

$$\begin{aligned} \tilde{R}(X, Y)Z &= R(X, Y)Z + [g(\phi X, Z)\phi Y - g(\phi Y, Z)\phi X] \\ &\quad + \eta(Z)[\eta(Y)X - \eta(X)Y] + [\eta(X)g(Y, Z) \\ &\quad - \eta(Y)g(X, Z)]\xi. \end{aligned} \quad (20)$$

$\forall X, Y, Z \in \chi(M)$ and $R(X, Y)Z = \nabla_X \nabla_Y Z - \nabla_Y \nabla_X Z - \nabla_{[X, Y]}Z$ is the Riemannian curvature tensor of the Levi-Civita connection ∇ .

Contracting above equation (20), we have

$$\tilde{S}(Y, Z) = S(Y, Z) + (n-1)\eta(Y)\eta(Z) - g(\phi Y, Z)\psi. \quad (21)$$

where $\psi = \text{trace}\phi$ and is defined by $\psi = \sum_{i=1}^n g(\phi e_i, e_i)$.

Again contracting (21), we have

$$\tilde{r} = r - (n-1) - \psi^2, \quad (22)$$

where r is the scalar curvature of the connection ∇ .

Replacing Z by ξ in (20) and using (3), (4), we have

$$\tilde{R}(X, Y)\xi = 0. \quad (23)$$

Replacing X by ξ , Y by X and Z by Y in (21) and using (3), (4), (11), we have

$$\tilde{R}(\xi, X)Y = 0. \quad (24)$$

Putting $Y = \xi$ in (24) and using (3), we have

$$\tilde{R}(\xi, X)\xi = 0. \quad (25)$$

Putting $Y = X$ and $Z = \xi$ in (21) and using (3), (4), we have

$$\tilde{S}(X, \xi) = 0. \quad (26)$$

Replacing Y by ξ in (16) and using (3), (4), (7), we have

$$\tilde{\nabla}_X \xi = 0. \quad (27)$$

$\forall X, Y \in \chi(M)$.

Now, we express the Lie derivative along ξ on M with a quarter-symmetric metric connection as follows:

$$(\tilde{L}_\xi g)(Y, Z) = \tilde{L}_\xi g(Y, Z) - g(\tilde{L}_\xi Y, Z) - g(Y, \tilde{L}_\xi Z). \quad (28)$$

By virtue of (17), (28) takes the form

$$\begin{aligned} (\tilde{L}_\xi g)(Y, Z) &= \tilde{\nabla}_\xi g(Y, Z) - g(\tilde{\nabla}_\xi Y - \tilde{\nabla}_Y \xi - \phi Y, Z) \\ &\quad - g(Y, \tilde{\nabla}_\xi Z - \tilde{\nabla}_Z \xi - \phi Z). \end{aligned} \quad (29)$$

which after computation gives

$$(\tilde{L}_\xi g)(Y, Z) = 2g(\phi Y, Z). \quad (30)$$

$\forall Y, Z \in \chi(M)$.

Hence, we have the following:

Theorem 3.1. *Every n -dimensional η -Ricci soliton LP-Sasakian manifold admitting quarter-symmetric metric connection is irregular.*

Theorem 3.2. *In a η -Ricci soliton LP-Sasakian manifold, ξ and g are parallel with respect to the connection $\tilde{\nabla}$.*

Theorem 3.3. *In a η -Ricci soliton LP-Sasakian manifold, the integral curves of the vector field ξ are geodesic with respect to the connection $\tilde{\nabla}$.*

4 η -Ricci solitons on LP-Sasakian manifolds admitting quarter-symmetric metric connection (QSMC)

Suppose that a LP-Sasakian manifolds with quarter-symmetric metric connection admits an η -Ricci solitons (g, ξ, λ, μ) , then it holds (2) and we have

$$(\tilde{L}_\xi g)(Y, Z) + 2\tilde{S}(Y, Z) + 2\lambda g(Y, Z) + 2\mu\eta(Y)\eta(Z) = 0. \quad (31)$$

By virtue of (30), (31) takes the form

$$\tilde{S}(Y, Z) = -g(\phi Y, Z) - \lambda g(Y, Z) - \mu\eta(Y)\eta(Z). \quad (32)$$

Replacing Y by ξ and Z by ξ in (32) and using (3), (4), (26), we have

$$\lambda = \mu = 0. \quad (33)$$

Hence, we have the following:

Theorem 4.1. *If (g, ξ, λ, μ) is an η -Ricci soliton in a LP-Sasakian manifolds with quarter-symmetric metric connection, then the scalars λ and μ are equal.*

Example 4.1. *Let $M = \{(x, y, z) \in \mathcal{R}^3 : z > 0\}$ be a 3-dimensional manifold, where (x, y, z) are the standard coordinates in $\mathcal{R}^3$. The vector fields (17)*

$$e_1 = e^z \frac{\partial}{\partial y}, \quad e_2 = e^z \left(\frac{\partial}{\partial x} + \frac{\partial}{\partial y} \right), \quad e_3 = \frac{\partial}{\partial z} = \xi,$$

are linearly independent at every point of M and hence form a basis of $T_p M$.

The Lorentzian like (semi-Riemannian) metric g on M is defined by

$$\begin{aligned} g(e_1, e_1) &= 1, & g(e_2, e_2) &= 1, & g(e_3, e_3) &= -1, \\ g(e_1, e_2) &= 0, & g(e_2, e_3) &= 0, & g(e_1, e_3) &= 0, \end{aligned} \quad (34)$$

Suppose η be the 1-form defined as $\eta(X) = g(X, e_3) = g(X, \xi)$, $\forall X \in \chi(M)$. Let ϕ be the $(1, 1)$ -tensor field defined by

$$\phi(e_1) = -e_1, \quad \phi(e_2) = -e_2, \quad \phi(e_3) = 0. \quad (35)$$

By linearity property of ϕ and g , we have

$$\eta(e_3) = -1, \quad \phi^2 X = X + \eta(X)\xi, \quad g(\phi X, \phi Y) = g(X, Y) + \eta(X)\eta(Y),$$

$\forall X, Y \in \chi(M)$.

Now by direct computations, we obtain

$$[e_1, e_2] = 0, \quad [e_2, e_3] = -e_2, \quad [e_3, e_1] = e_1. \quad (36)$$

Koszul's formula is given as

$$\begin{aligned} 2g(\nabla_X Y, Z) &= Xg(Y, Z) + Yg(Z, X) - Zg(X, Y) \\ &\quad - g([Y, Z], X) + g([Z, X], Y) + g([X, Y], Z), \end{aligned}$$

for arbitrary vector fields $X, Y, Z \in \chi(M)$.

Using Koszul's formula, we can easily calculate

$$\begin{aligned} \nabla_{e_1} e_1 &= -e_3, & \nabla_{e_1} e_2 &= 0, & \nabla_{e_1} e_3 &= -e_1, \\ \nabla_{e_2} e_1 &= 0, & \nabla_{e_2} e_2 &= -e_3, & \nabla_{e_2} e_3 &= -e_2, \\ \nabla_{e_3} e_1 &= 0, & \nabla_{e_3} e_2 &= 0, & \nabla_{e_3} e_3 &= 0. \end{aligned} \quad (37)$$

Let $X = \sum_{i=1}^3 X^i e_i = X^1 e_1 + X^2 e_2 + X^3 e_3 \in \chi(M)$.

Also one can easily verify that $\nabla_X \xi = \phi X$, and $(\nabla_X \phi)Y = g(X, Y)\xi + \eta(Y)X + 2\eta(X)\eta(Y)\xi$.

Thus, the manifold M is a LP-Sasakian manifold. From (16) and (37), we find

$$\begin{aligned}\tilde{\nabla}_{e_1} e_1 &= 0, & \tilde{\nabla}_{e_1} e_2 &= 0, & \tilde{\nabla}_{e_1} e_3 &= 0, \\ \tilde{\nabla}_{e_2} e_1 &= 0, & \tilde{\nabla}_{e_2} e_2 &= 0, & \tilde{\nabla}_{e_2} e_3 &= 0, \\ \tilde{\nabla}_{e_3} e_1 &= 0, & \tilde{\nabla}_{e_3} e_2 &= 0, & \tilde{\nabla}_{e_3} e_3 &= 0.\end{aligned}\tag{38}$$

It is known that

$$R(X, Y)Z = \nabla_X \nabla_Y Z - \nabla_Y \nabla_X Z - \nabla_{[X, Y]} Z.$$

By using the above results, we easily calculate the components of the curvature tensors $R(e_i, e_j)e_k$; $i, j, k = 1, 2, 3$ of ∇ as follows:

$$\begin{aligned}R(e_1, e_2)e_1 &= -e_2, & R(e_1, e_2)e_2 &= e_1, & R(e_1, e_2)e_3 &= 0, \\ R(e_2, e_3)e_1 &= 0, & R(e_2, e_3)e_2 &= -e_3, & R(e_2, e_3)e_3 &= -e_2, \\ R(e_1, e_3)e_1 &= -e_3, & R(e_1, e_3)e_2 &= 0, & R(e_1, e_3)e_3 &= -e_1,\end{aligned}\tag{39}$$

The curvature tensor $\tilde{\nabla}$ can be calculated by using (19), (36) and (38), we have

$$\tilde{R}(e_i, e_j)e_k = 0; \forall i, j, k = 1, 2, 3.\tag{40}$$

From these curvatures tensors, we obtain

$$S(e_1, e_1) = S(e_2, e_2) = 2, \quad S(e_3, e_3) = -2.\tag{41}$$

$$\tilde{S}(e_1, e_1) = \tilde{S}(e_2, e_2) = \tilde{S}(e_3, e_3) = 0.\tag{42}$$

Therefore from (41) and (42) we get $r = 6$ and $\tilde{r} = 0$, respectively. Thus it can be seen that the equation (22) is satisfied, where $\psi = \sum_{i=1}^3 g(\phi e_i, e_i) = -2$. Now from equations (8), (17) and (18), we find

$$\phi(e_1, e_1) = \phi(e_2, e_2) = -1, \quad \phi(e_3, e_3) = 0.\tag{43}$$

In view of (17), the torsion tensor $\tilde{T}$ with respect to $\tilde{\nabla}$ as follows:

$$\begin{aligned}\tilde{T}(e_1, e_1) &= 0, & \tilde{T}(e_2, e_2) &= 0, & \tilde{T}(e_3, e_3) &= 0, \\ \tilde{T}(e_1, e_2) &= 0, & \tilde{T}(e_1, e_3) &= e_1, & \tilde{T}(e_2, e_3) &= e_2,\end{aligned}\tag{44}$$

and also

$$(\tilde{\nabla}_X g)(Y, Z) = 0. \quad (45)$$

for any vector fields $X, Y, Z \in \chi(M)$ respectively. Thus the connection $\tilde{\nabla}$ defined on M is a quarter-symmetric metric connection.

Now from (32), we find $\tilde{S}(e_1, e_1) = 1 - \lambda$ and $\tilde{S}(e_3, e_3) = \lambda - \mu$, therefore from equation (42) it follows that $\lambda = 1$ and $\mu = 1$. Thus (g, ξ, λ, μ) for $\lambda = 1$ and $\mu = 1$ defines an η -Ricci soliton in a LP-Sasakian manifold admitting quarter-symmetric metric connection.

By using the values of λ and μ in (32), we get

$$\tilde{S}(Y, Z) = -g(\phi Y, Z) - g(Y, Z) - \eta(Y)\eta(Z). \quad (46)$$

Thus the manifold M (defined in example 4.1) admitting an η -Ricci soliton (g, ξ, λ, μ) with a quarter-symmetric metric connection is a generalized η -Einstein manifold of the form (46).

Let (g, V, λ, μ) be an η -Ricci soliton in a LP-Sasakian manifold with quarter-symmetric metric connection, then we have

$$(\tilde{L}_V g)(Y, Z) + 2\tilde{S}(Y, Z) + 2\lambda g(Y, Z) + 2\mu\eta(Y)\eta(Z) = 0, \quad (47)$$

where $\tilde{L}_V$ is the Lie derivative along the vector field V on M with a $QSMC$. Now, let (g, V, λ, μ) be an η -Ricci soliton in a LP-Sasakian manifold with a quarter-symmetric metric connection such that V is pointwise collinear with ξ , i.e., $V = b\xi$, where b is a function. Then (47) holds and we have

$$\begin{aligned} &bg(\tilde{\nabla}_V \xi, Z) + (Yb)\eta(Z) + bg(Y, \tilde{\nabla}_Z \xi) + 2bg(\phi Y, Z) \\ &+ (Zb)\eta(Y) + 2\tilde{S}(Y, Z) + 2\lambda g(Y, Z) + 2\mu\eta(Y)\eta(Z) = 0. \end{aligned} \quad (48)$$

which in view of (27) takes the form

$$\begin{aligned} &(Yb)\eta(Z) + 2bg(\phi Y, Z) + (Zb)\eta(Y) \\ &+ 2\tilde{S}(Y, Z) + 2\lambda g(Y, Z) + 2\mu\eta(Y)\eta(Z) = 0. \end{aligned} \quad (49)$$

Putting $Z = \xi$ in (49) and using (3), (4) and (26), we have

$$-(Yb) + (\xi b)\eta(Y) + 2\lambda\eta(Y) - 2\mu\eta(Y) = 0. \quad (50)$$

Again putting $Y = \xi$ in (50) and using (3), we get

$$(\xi b) + \lambda - \mu = 0. \quad (51)$$

Combinning the equations (50) and (51), we get

$$db = (\lambda - \mu)\eta. \quad (52)$$

Now applying d on (52), we find

$$(\lambda - \mu)d\eta = 0. \quad (53)$$

i.e.,

$$\lambda = \mu, \quad d\eta \neq 0. \quad (54)$$

Using (54) in (52), we find $db = 0$, i.e., b is constant. Therefore (49) reduce to

$$\tilde{S}(Y, Z) = -\lambda g(Y, Z) - bg(\phi Y, Z) - \mu\eta(Y)\eta(Z). \quad (55)$$

In view of (21), (55) takes the form

$$S(Y, Z) = -\lambda g(Y, Z) - (n - 1 + \mu)\eta(Y)\eta(Z) - (\psi - b)g(\phi Y, Z). \quad (56)$$

Hence, we have the following theorem:

Theorem 4.2. *If (g, V, λ, μ) is an η -Ricci soliton in a LP-Sasakian manifold with a quarter-symmetric metric connection such that V is pointwise collinear with ξ , then V is a constant multiple of ξ and the manifold is a generalized η -Einstein manifold.*

Corollary 4.1. *If (g, V, λ, μ) is an η -Ricci soliton in a LP-Sasakian manifold with a quarter-symmetric metric connection such that V is pointwise collinear with ξ , then the Ricci soliton on M is steady, shrinking and expanding according as $\mu = 0$, $\mu < 0$ and $\mu > 0$, respectively.*

5 η -Ricci solitons on LP-Sasakian manifold admitting quarter-symmetric metric connection (QSMC) satisfying $\tilde{R}(X, Y).\tilde{S} = 0$.

Let M be an n -dimensional LP-Sasakian manifolds with quarter-symmetric metric connection admits an η -Ricci soliton. Now we have

$$\tilde{S}(\tilde{R}(X, Y)U, V) + \tilde{S}(U, \tilde{R}(X, Y)V) = 0. \quad (57)$$

$\forall X, Y, U, V \in \chi(M)$.

Replacing X by ξ in (57), we get

$$\tilde{S}(\tilde{R}(\xi, Y)U, V) + \tilde{S}(U, \tilde{R}(\xi, Y)V) = 0. \quad (58)$$

In view of (24), (58) becomes

$$g(Y, U)\tilde{S}(\xi, V) + \eta(U)\tilde{S}(Y, V) + g(Y, V)\tilde{S}(U, \xi) + \eta(V)\tilde{S}(U, Y) = 0. \quad (59)$$

Replacing U by ξ and using (3), (25) reduces to

$$\tilde{S}(Y, V) = 0. \quad (60)$$

In view of (21), (60) takes the form

$$S(Y, V) = -(n-1)\eta(Y)\eta(V) + g(\phi Y, V)\psi. \quad (61)$$

From (30), (31) and (60), we find

$$g(\phi Y, V) + \lambda g(Y, V) + \mu \eta(Y)\eta(V) = 0. \quad (62)$$

Putting $V = Y = \xi$ in (62) and using (3) and (4), it follows that

$$\lambda = \mu. \quad (63)$$

Hence, we have the following theorem:

Theorem 5.1. *If (g, ξ, λ, μ) is an η -Ricci soliton in a LP-Sasakian manifold with a quarter-symmetric metric connection satisfying $\tilde{R}(X, Y).\tilde{S} = 0$, then the manifold is a class of generalized η -Einstein manifold and the scalars λ and μ are equal.*

Corollary 5.1. *If (g, ξ, λ, μ) is an η -Ricci soliton in a LP-Sasakian manifold with a quarter-symmetric metric connection satisfying $\tilde{R}(X, Y).\tilde{S} = 0$, then the Ricci soliton on M is steady, shrinking and expanding according as $\mu = 0$, $\mu < 0$ and $\mu > 0$, respectively.*

6 Example of 3-dimensional LP-Sasakian manifold with a quarter-symmetric metric connection

Example 6.1. *Let $M = \{(x_1, y_1, z_1) \in \mathcal{R}^3 : z_1 > 0\}$ be a 3-dimensional manifold, where (x_1, y_1, z_1) are the standard coordinates in $\mathcal{R}^3$. The vector fields (17)*

$$e_1 = \cosh z_1 \frac{\partial}{\partial x_1} + \sinh z_1 \frac{\partial}{\partial y_1}, \quad e_2 = \sinh z_1 \frac{\partial}{\partial x_1} + \cosh z_1 \frac{\partial}{\partial y_1}, \quad e_3 = \frac{\partial}{\partial z_1} = \xi,$$

are linearly independent at every point of M and hence form a basis of $T_p M$.

The Lorentzian like (semi-Riemannian) metric g on M is defined by

$$\begin{aligned} g(e_1, e_1) &= 1, & g(e_2, e_2) &= 1, & g(e_3, e_3) &= -1, \\ g(e_1, e_2) &= 0, & g(e_2, e_3) &= 0, & g(e_1, e_3) &= 0, \end{aligned} \quad (64)$$

Suppose η be the 1-form defined as $\eta(X)=g(X, e_3)=g(X, \xi), \forall X \in \chi(M)$. Let ϕ be the $(1, 1)$ -tensor field defined by

$$\phi(e_1) = -e_2, \quad \phi(e_2) = -e_1, \quad \phi(e_3) = 0. \quad (65)$$

By linearity property of ϕ and g , we have

$$\eta(e_3) = -1, \quad \phi^2 X = X + \eta(X)\xi, \quad g(\phi X, \phi Y) = g(X, Y) + \eta(X)\eta(Y),$$

$\forall X, Y \in \chi(M)$.

Now by direct computations, we obtain

$$[e_1, e_2] = 0, \quad [e_2, e_3] = -e_1, \quad [e_3, e_1] = e_2. \quad (66)$$

Using Koszul's formula, we can easily calculate

$$\begin{aligned} \nabla_{e_1} e_1 &= 0, & \nabla_{e_1} e_2 &= -e_3, & \nabla_{e_1} e_3 &= -e_2, \\ \nabla_{e_2} e_1 &= -e_3, & \nabla_{e_2} e_2 &= 0, & \nabla_{e_2} e_3 &= -e_1, \\ \nabla_{e_3} e_1 &= 0, & \nabla_{e_3} e_2 &= 0, & \nabla_{e_3} e_3 &= 0. \end{aligned} \quad (67)$$

Also one can easily verify that $\nabla_X \xi = \phi X$, and $(\nabla_X \phi)Y = g(X, Y)\xi + \eta(Y)X + 2\eta(X)\eta(Y)\xi$.

Thus, the manifold M is a LP-Sasakian manifold. From (16) and (67), we find

$$\begin{aligned} \tilde{\nabla}_{e_1} e_1 &= 0, & \tilde{\nabla}_{e_1} e_2 &= 0, & \tilde{\nabla}_{e_1} e_3 &= 0, \\ \tilde{\nabla}_{e_2} e_1 &= 0, & \tilde{\nabla}_{e_2} e_2 &= 0, & \tilde{\nabla}_{e_2} e_3 &= 0, \\ \tilde{\nabla}_{e_3} e_1 &= 0, & \tilde{\nabla}_{e_3} e_2 &= 0, & \tilde{\nabla}_{e_3} e_3 &= 0. \end{aligned} \quad (68)$$

It is known that

$$R(X, Y)Z = \nabla_X \nabla_Y Z - \nabla_Y \nabla_X Z - \nabla_{[X, Y]} Z.$$

By using the above results, we easily calculate the components of the curvature tensors $R(e_i, e_j)e_k ; i, j, k = 1, 2, 3$ of ∇ as follows:

$$\begin{aligned} R(e_1, e_2)e_1 &= e_2, & R(e_1, e_2)e_2 &= -e_1, & R(e_1, e_2)e_3 &= 0, \\ R(e_2, e_3)e_1 &= 0, & R(e_2, e_3)e_2 &= -e_3, & R(e_2, e_3)e_3 &= -e_2, \\ R(e_1, e_3)e_1 &= -e_3, & R(e_1, e_3)e_2 &= 0, & R(e_1, e_3)e_3 &= -e_1, \end{aligned} \quad (69)$$

$\tilde{R}(e_i, e_j)e_k$; $i, j, k = 1, 2, 3$ of $\tilde{\nabla}$ can be calculated by using (19), (66) and (68). Thus, we have

$$\begin{aligned}\tilde{R}(e_1, e_2)e_1 &= e_2, & \tilde{R}(e_1, e_2)e_2 &= 0, & \tilde{R}(e_1, e_2)e_3 &= 0, \\ \tilde{R}(e_2, e_3)e_1 &= 0, & \tilde{R}(e_2, e_3)e_2 &= 0, & \tilde{R}(e_2, e_3)e_3 &= 0, \\ \tilde{R}(e_1, e_3)e_1 &= 0, & \tilde{R}(e_1, e_3)e_2 &= 0, & \tilde{R}(e_1, e_3)e_3 &= 0,\end{aligned}\tag{70}$$

From these curvature tensors, we obtain

$$S(e_1, e_1) = S(e_2, e_2) = 0, \quad S(e_3, e_3) = -2.\tag{71}$$

$$\tilde{S}(e_1, e_1) = \tilde{S}(e_2, e_2) = \tilde{S}(e_3, e_3) = 0.\tag{72}$$

Therefore from (71) and (72) we get $r = 2$ and $\tilde{r} = 0$, respectively. Thus it can be seen that the equation (22) is satisfied, where $\psi = \sum_{i=1}^3 g(\phi e_i, e_i) = 0$.

Now from equation (32), we have

$$\tilde{S}(e_1, e_1) = -\lambda, \quad \tilde{S}(e_3, e_3) = \lambda - \mu.\tag{73}$$

Therefore from (72) it follows that $\lambda = \mu = 0$. Hence, Ricci soliton (g, ξ, λ, μ) in a LP-Sasakian manifold admitting a quarter-symmetric metric connection $\tilde{\nabla}$ is steady, which verifies corollaries (4.1) and (5.1).

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Thinking over the Goldbach conjecture solution from a probabilistic point of view

Rosario D'Amico*

Abstract

This paper aims to provide a set of considerations that allow us to see a possible solution to the problematic issue of Goldbach's "strong" conjecture, which amounts to asserting that *any even natural number greater than 2 can be written as the sum of two prime numbers that are not necessarily distinct*. Specifically, we will show mathematically that a hypothetical scenario in which no even composite number exists as a sum of two primes is impossible. This will be done by adopting a probabilistic method much simpler than the arithmetical attempts already present in literature.

Keywords: Goldbach's conjecture; Prime number; Probability.¹

* Mps Bank, Messina, Italy; damros978@gmail.com.

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1. Introduction

Goldbach's conjecture is one of the oldest and most unsolved problems in that branch of mathematics that studies the properties of integers. In its formulation treated here and called “strong”, it states that every even natural number greater than 2 can be written as the sum of two prime numbers that are not necessarily distinct and is therefore a hypothesis on the properties of primes and, particularly, on their distribution among positive integers.

Is this statement, which seems true, doomed to be unable to be demonstrated using existing axiomatic foundations? (See [5] pp. 330-334).

When considering whether every even integer can be expressed as the sum of two primes, it is tempting to view the puzzle as a matter of arithmetic, of number theory, while the answer might also lie in a pattern of probability. Indeed, like any conjecture, it is an assumption based on clues and probable appearances, and some mathematicians believe that this assertion is true based on probabilistic/statistical considerations².

This will also be done below to ensure it is easily understood even by those without high mathematical skills.

But what exactly is to be understood by a prime number? There are basically two definitions of prime number: one counts 1 among the prime numbers, the other – and it is the one most widely accepted by mathematicians – excludes it only for mere reasons of convenience and expediency [3]. We are in doubt regarding this question. Take advantage of this ambiguity as a possible lever to try to confirm Goldbach's strong conjecture is the goal of this work.

It will be achieved in the second of the next two paragraphs that make up this paper. In the first we will preliminarily present seven definitions and four useful lemmas for the purpose of establishing the basic conditions of the reasoning that will be proposed and developed in the following. In the second we will construct a particular random experiment so that we can bring the problem of verifying Goldbach's strong conjecture back into the framework of probability theory and to seek its solution by the exclusive use of probabilistic methods.

2. Definitions and preliminary results

The discussion is focused principally on the natural numbers expressed in base 10, that are the elements of the set $\mathbf{N} = \{0, 1, 2, \dots, v, \dots\}$, and

² In 2003, for example, it has been obtained the probability that Goldbach's conjecture fails as roughly $10^{-150.000.000.000}$ for any $n > 4 \cdot 10^{14}$, SHELDON [7].

algebraic operations with such numbers.

Preliminarily, it is necessary to introduce seven basic concepts, to define both a terminology and a particular mathematical sequence and to present four fundamental results.

Definition 2.1: A natural number is called a *positive integer number*, or simply a *positive integer*, if and only if it is an element of the infinite set $\{1, 2, 3, \dots, v, \dots\} = \mathbb{N} - \{0\}$.

Definition 2.2: Let $n \in \mathbb{N} - \{0\}$. A *positive factor* of the given number n is any positive integer that divides n completely, leaving no remainder.

Definition 2.3: A *prime number*, or simply a *prime*, is any positive integer that has no positive factors other than 1 and itself. According to this definition, 1 is considered a prime number.

Definition 2.4: A *prime number* (or a *prime*) is any positive integer that has exactly two distinct positive factors: itself and the number 1. According to this definition, 1 is not a prime number.

Remark 2.1: If only positive integers greater than 1 are considered, the definitions 2.3 and 2.4 are equivalent, as it is possible to easily verify.

Definition 2.5: Let $n \in \mathbb{N} - \{0, 1\}$. A *pair of $2n$* is any pair $(n-k, n+k)$, with $k \in \{0, \dots, n-2\}$, formed by two positive integers that sum $2n$. Hence, we have $n-1$ pairs of $2n$.

Definition 2.6: Let $n \in \mathbb{N} - \{0, 1\}$. A *non-prime pair of $2n$* is any pair of $2n$ such that at least one of its two positive integers is not a prime number. E.g., $(9, 13)$ and $(10, 12)$ are two non-prime pairs of 22.

Definition 2.7: Let $n \in \mathbb{N} - \{0, 1\}$. A *prime pair of $2n$* is any pair of $2n$ such that both its positive integers are primes. E.g., $(3, 19)$ and $(5, 17)$.

Notation 2.1: Let $n \in \mathbb{N} - \{0\}$. Assuming the definition 2.3 to be true, ${}_1\Pi(n)$ indicates the quantity of primes that are less than or equal to n .

Notation 2.2: Let $n \in \mathbb{N} - \{0\}$. Assuming the definition 2.4 to be true, ${}_{bis}\Pi(n)$ indicates the quantity of primes that are less than or equal to n .

Notation 2.3: Let $n, \eta \in \mathbb{N} - \{0\}$, with $n \geq \eta$. Let η_n also be the positive integer η corresponding to the natural number (index) n . $\Pi(\eta_n)$ indicates the

quantity of primes in the first η of n natural numbers, i.e., fixed n , the quantity of positive integers $\eta_n = \eta$ – related to the index n – of the tuple $(1_n, \dots, n_n)$ that are primes and equal to or less than η . Precisely, $\Pi(\eta_n)$ is randomly and definitively identified by one of the two terms: ${}_i\Pi(\eta)$ and ${}_{bis}\Pi(\eta)$.³ If $\eta > 1$, we also can write $\eta_n \equiv \eta_n$ ⁴ and $\Pi(\eta_n) = \Pi(\eta) > 0$. For any $n \in \mathbf{N}-\{0,1\}$, $\Pi(1_n)$ was thus randomly and definitively selected between the two different values: $\Pi(1_n) = {}_i\Pi(1) = 1$, iff $\Pi(n) = {}_i\Pi(n)$; otherwise, i.e., iff $\Pi(n) = {}_{bis}\Pi(n)$, we have $\Pi(1_n) = {}_{bis}\Pi(1) = 0$.

Remark 2.2: Let $n \in \mathbf{N}-\{0,1\}$. It follows from the above that

$${}_i\Pi(n) \leq n, \quad {}_i\Pi(n) = {}_{bis}\Pi(n) + 1 \text{ and } 0 < {}_{bis}\Pi(n) \leq \Pi(n) \leq {}_i\Pi(n).$$

Notation 2.4: Let $n \in \mathbf{N}-\{0\}$. Later, we will use the symbol “ $\log(n)$ ”, instead of “ $\log_e n$ ”, as an abbreviation of “logarithm of n to the base e (Euler’s number)”, or “natural logarithm of n ”.

Finally, let $n \in \mathbf{N}-\{0,1\}$ and $k \in \{0, 1, \dots, n-2\}$. Based on remark 2.2, we introduce the following sequence of positive numbers:

$$\begin{aligned} (n)S_k &= [\Pi(n-k)/(n-k)] * [\Pi(n+k)-1/(n-1)] \text{ if } n > 2 \text{ and } k \in \{1, \dots, n-2\}; \\ (n)S_k &= (n)S_0 = \Pi(n)/n \leq 1 \text{ if } n = 2 \text{ or } k = 0. \end{aligned} \quad (2.1)$$

From the Rosser-Schoenfeld theorem – according to which, for any $n \in \mathbf{N}$ and $n \geq 67$, $1/(\log(n) - 0,5) < {}_{bis}\Pi(n)/n < 1/(\log(n) - 1,5)$ BANESCU [1] – and (2.1), the following four lemmas are derived:

Lemma 2.1: Let $n \in \mathbf{N}$, $n \geq 4*10^7$ and $k \in \{1, \dots, n-2\}$.⁵

Then, $(n)S_k < 2/[\log(n) - 1,5]$.

Proof. By (2.1) and remark 2.2, we can write

$$\begin{aligned} (n)S_k &= [\Pi(n-k)/(n-k)] * [\Pi(n+k) - 1/(n-1)] \leq {}_{bis}\Pi(n+k)/(n-1), \text{ from which} \\ (n)S_k &\leq [(n+k)/(n-1)] * [{}_{bis}\Pi(n+k)/(n+k)] < [(2n-2)/(n-1)] / [\log(n+k) - 1,5] \leq \\ &\leq 2/[\log(n) - 1,5], \text{ being } k \leq n-2. \end{aligned}$$

³ Let us consider $\Pi(\eta_n)$ as a key on a computer keyboard. As soon as any two numbers $\eta, n \in \mathbf{N}-\{0\}$ are entered and the key $\Pi(\eta_n)$ is pressed, the computer always provides the same result: the random value between ${}_i\Pi(\eta)$ and ${}_{bis}\Pi(\eta)$.

⁴ Then this implies here that, if $\eta > 1$, both or neither of the terms η_n and η_n are prime numbers.

⁵ From now on, to choose to place $n \geq 4*10^7$ is only due to the need to have a sufficiently high integer to validate the reasoning that is conducted in this section and in the next one.

Lemma 2.2: Let $n \in \mathbf{N}$, $n \geq 4 \cdot 10^7$ and $k \in \{1, \dots, n-2\}$.

Then, ${}_{\text{bis}}\Pi(n) - 1 > n/\log(n)$.

Proof. It is sufficient to prove that

$$\{n/[\log(n) - 0,5] - n/\log(n)\} > 1 \quad (2.2)$$

since ${}_{\text{bis}}\Pi(n) > n/[\log(n) - 0,5]$, for any $n \in \mathbf{N}$ and $n \geq 67$.

It is no difficult to rewrite (2.2) in the form $n > [2\log(n) - 1] \cdot \log(n)$. But this inequality is satisfied, because, if $n \in \mathbf{N}$ and $n \geq 67$, $f(n) = n / [2\log^2(n)]$ is a function of n greater than 1 and increasing.

Lemma 2.3: Let $n \in \mathbf{N}$, $n \geq 4 \cdot 10^7$ and $k \in \{1, \dots, n-2\}$.

Then, ${}_{(n)}S_k > 1/\log^2(n+92)$.

Proof. For remark 2.2, $\Pi(n) > {}_{\text{bis}}\Pi(n) - 1$ and, for lemma 2.2, we have ${}_{\text{bis}}\Pi(n) - 1 > n/\log(n)$. Moreover, for direct verification, we obtain

$$\Pi(68-t)/(68-t) > \Pi(94)/(94), \text{ for any } t \in \{0, 1, \dots, 66\}.$$

Applying (2.1), we find that

${}_{(n)}S_k = [\Pi(n-k)/(n-k)] \cdot [\Pi(n+k)-1/(n-1)] > 1/[\log(n+92-k) \cdot \log(n+k)]$, from which we get ${}_{(n)}S_k > \{1/[\log(n+92-k) \cdot \log(n+92+k)] \geq 1/\log^2(n+92)\}^6$.

Lemma 2.4: Let $n \in \mathbf{N}$ and $n \geq 4 \cdot 10^7$. Let $P(2n)$ be the real function of variable n , so defined:

$$P(2n) = {}_{(n)}S_0 + (1 - {}_{(n)}S_0) \cdot {}_{(n)}S_1 + (1 - {}_{(n)}S_0) \cdot (1 - {}_{(n)}S_1) \cdot {}_{(n)}S_2 + \dots + (1 - {}_{(n)}S_0) \cdot (1 - {}_{(n)}S_1) \cdot (1 - {}_{(n)}S_2) \cdot \dots \cdot (1 - {}_{(n)}S_{n-3}) \cdot {}_{(n)}S_{n-2}. \quad (2.4)$$

Then, $P(2n)$ assumes increasing(decreasing) values as at least one of its constituent parameters increases (decreases): ${}_{(n)}S_0, {}_{(n)}S_1, {}_{(n)}S_2, \dots, {}_{(n)}S_{n-2}$.

Proof. From (2.4), it follows that:

⁶ For this purpose, it is sufficient to show that

$$\log(n-k) \cdot \log(n+k) \leq \log^2(n). \quad (2.3)$$

Since $\log(n-k) = \{\log[(n-k)/n] + \log(n)\}$ and $\{\log(n+k) = \log[(n+k)/n] + \log(n)\}$, the inequality (2.3) can be written as $\{\log[(n-k)/n] + \log(n)\} \cdot \{\log[(n+k)/n] + \log(n)\} \leq \log^2(n)$,

$$\{\log(n) \cdot \log[(n-k)/n] + \log(n) \cdot \log[(n+k)/n] + \log[(n+k)/n] \cdot \log[(n-k)/n]\} \leq 0,$$

$$\{\log(n) \cdot \log[(n^2-k^2)/n^2] + \log[(n+k)/n] \cdot \log[(n-k)/n]\} \leq 0.$$

The first term of the latter inequality is less than or equal to zero, because it is the sum of two products either negative or zero, being $0 \leq k < n$ and, consequently, $[(n-k)/n] \leq 1$; so that (2.3) is verified.

$1 - P(2n) = 1 - {}_{(n)}S_0 - (1 - {}_{(n)}S_0) * {}_{(n)}S_1 - (1 - {}_{(n)}S_0) * (1 - {}_{(n)}S_1) * {}_{(n)}S_2 - \dots - (1 - {}_{(n)}S_0) * (1 - {}_{(n)}S_1) * (1 - {}_{(n)}S_2) * \dots * (1 - {}_{(n)}S_{n-3}) * {}_{(n)}S_{n-2}$, from which we have

$$1 - P(2n) = (1 - {}_{(n)}S_0) * [(1 - {}_{(n)}S_1) - (1 - {}_{(n)}S_1) * {}_{(n)}S_2 - \dots - (1 - {}_{(n)}S_1) * (1 - {}_{(n)}S_2) * \dots * (1 - {}_{(n)}S_{n-3}) * {}_{(n)}S_{n-2}],$$

$$P(2n) = 1 - [(1 - {}_{(n)}S_0) * (1 - {}_{(n)}S_1) * (1 - {}_{(n)}S_2) * \dots * (1 - {}_{(n)}S_{n-3}) * (1 - {}_{(n)}S_{n-2})].$$

By increasing (decreasing) at least one of the parameters ${}_{(n)}S_0, {}_{(n)}S_1, {}_{(n)}S_2, \dots, {}_{(n)}S_{n-2}$ the product $(1 - {}_{(n)}S_0) * (1 - {}_{(n)}S_1) * (1 - {}_{(n)}S_2) * \dots * (1 - {}_{(n)}S_{n-3}) * (1 - {}_{(n)}S_{n-2})$ decreases (increases) and, as a consequence, $P(2n)$ increases (decreases), since, by (2.1) and lemmas 2.1 and 2.3, $0 < {}_{(n)}S_k \leq 1$ for any $k \in \{0, \dots, n-2\}$.

Remark 2.3: By lemma 2.4, if $n \in \mathbb{N}$ and $n \geq 4 \cdot 10^7$, there exists an appropriate real number, let us call it ${}_{(n)}S$, such that

$P(2n) = {}_{(n)}S_0 + (1 - {}_{(n)}S_0) * {}_{(n)}S + (1 - {}_{(n)}S_0) * (1 - {}_{(n)}S) * {}_{(n)}S + (1 - {}_{(n)}S_0) * (1 - {}_{(n)}S) * (1 - {}_{(n)}S) * {}_{(n)}S + \dots + (1 - {}_{(n)}S_0) * (1 - {}_{(n)}S) * (1 - {}_{(n)}S) * \dots * (1 - {}_{(n)}S) * {}_{(n)}S$ – with $1/\log^2(n+92) < {}_{(n)}S < 2/[\log(n) - 1, 5]$ –, from which, putting $1 - {}_{(n)}S = {}_nq$, we get $P(2n) = {}_{(n)}S_0 + (1 - {}_{(n)}S_0) * \{ {}_{(n)}S * [(1 - {}_nq^{n-2}) / (1 - {}_nq)] \}$ and, thus,

$P(2n) = {}_{(n)}S_0 + (1 - {}_{(n)}S_0) * (1 - {}_nq^{n-2})$, since ${}_{(n)}S * [(1 - {}_nq^{n-2}) / (1 - {}_nq)]$ is the sum of the first $n-2$ terms of a geometric progression, having ${}_{(n)}S$ as first term and ${}_nq < 1$ as common ratio.

Remark 2.4: Let (y, z) be any pair of $2n$. Note that the event A: “a given pair (y, z) of $2n$ is prime” cannot be considered random but is only certain or impossible, whether we use the 2.3 definition or the 2.4 definition of prime number. In fact, because of remark 2.1, the pair (y, z) – like any other pair of $2n$ – is prime or not, necessarily, since, for definition 2.5, y and z are both positive integers greater than 1. The probability of A thus admits only two possible values: 0 and 1.

3. Probabilistic puzzle: the heart of Goldbach's conjecture argument

In this section, we present a reasoning that can validate the following:

Goldbach's proposition: Let $M = \{1, 2, \dots, m, \dots\}$ be a set of positive integers, where $m \geq 4 \cdot 10^7$. The definition 2.4 of prime number is also satisfied.

Then, the even number $2m$ can be expressed as the sum of two not necessarily distinct primes.

In this regard, suppose we set up a random mechanism, let's call it Goldbach's proof, – such as the toss of an unrigged die or the extraction with reinserting from an urn – by which a distinctive label, «non-prime» or «prime», is equiprobably and definitively attributed to each element of the infinite set $M - \{1\} = \{2, 3, \dots, m, \dots\}$ and to each member $1_n = 1$ of the sequence $\{1_n\}_{n \in M}$ in such a way that ⁷:

i. Let $\eta, x \in M$, with $\eta \geq x$. Let $F(x_\eta)$ be the relative frequency of the outcome “being a «prime» labeled number” in the first x of η trials, i.e., fixed η , the ratio between the number of positive integers $x_\eta = x$ – related to the index η – of the tuple $(1_\eta, \dots, \eta_\eta)$ that are labeled as «prime» and equal to or less than x and the number x . If $x > 1$, $x_\eta \equiv x_x$ ⁸ and $F(x_x) = F(x) = \Pi(x)/x$.

ii. Let $\eta \in M$ and $\eta \geq 4 \cdot 10^7$. Goldbach's proposition holds if and only if 2η can be written as the sum of two as «prime» labeled positive integers not necessarily distinct.

iii. For every $\eta \in M - \{1\}$, $0 \leq \Pi(\eta + 1) - \Pi(\eta) \leq 1$; ⁹

Within this framework, we make the following five remarks:

Remark 3.1: Let η be any member of the set $\mathbf{N} - \{0, 1\}$. Notation 2.3 and Goldbach's proof, taken together, contain no reason to believe that $F(1_\eta) = \Pi(1_\eta)$. In fact, $F(1_\eta)$ and $\Pi(1_\eta)$ might take different values because they might be the results of random experiments not necessarily identical. It follows that no prime number is necessarily labeled as «prime», nor every labeled «prime» positive integer is necessarily a prime.

⁷ For example, suppose we label as «prime» the positive integer $n+1[1_n]$ with $n \in M$, if the $2n^{\text{th}}$ $[(2n+1)^{\text{th}}]$ roll of an unrigged traditional die leads to an even number; otherwise, $n+1[1_n]$ is a «non-prime» labeled number. This random experiment is possible; its introduction is thus legitimate.

⁸ Then this implies here that, if $x > 1$, both or neither of the terms x_η and x_x are «prime» labeled numbers.

⁹ By hypothesis (See footnote 7) all 2^{2m-1} possible $(2m-1)$ -permutations with repetition of the two distinct labels, «prime» and «non-prime», – assigned to the first $m-1$ members of $M - \{1\}$ and to the first m terms of the sequence $\{1_n\}_{n \in M}$ – are equiprobable, each with probability $p^{2m-1} = (1/2)^{2m-1} \geq 0$, and one of them must occur; so the smallest labeled «non-prime» («prime») positive integer does not necessarily exist. Hence, since $F(x_\eta) = \Pi(x)/x$ may occur for every $\eta, x \in M$ and $\eta \geq x$, we have that i, ii and iii are three compossible and, thus, admissible conditions.

Remark 3.2: Let $\eta \in \mathbb{N}-\{0,1\}$. From remark 3.1 and hypothesis iii, it follows that, unlike necessarily primes, there is no reason to believe that $\eta+1$ is a labeled as «prime» number, if $\Pi(\eta+1) - \Pi(\eta) = 1$; in this case, in fact, according to hypothesis/condition i, both of the following equalities:

$(\eta+1)*F(\eta+1) = \Pi(\eta+1) = {}_1\Pi(\eta+1)$ and $\eta*F(\eta) = \Pi(\eta) = {}_{\text{bis}}\Pi(\eta)$, with $\eta+1$ «non-prime» labeled number, might be satisfied.

Similarly, if $\Pi(\eta+1) - \Pi(\eta) = 0$, we cannot affirm that $\eta+1$ is labeled as a «non-prime» number, in this case, both the relations:

$(\eta+1)*F(\eta+1) = \Pi(\eta+1) = {}_{\text{bis}}\Pi(\eta+1)$ and $\eta*F(\eta) = \Pi(\eta) = {}_1\Pi(\eta)$, with $\eta+1$ «prime» number, might be valid.

Remark 3.3: Let $\eta, x \in M$, with $x \leq \eta \leq 4*10^7$. By i, condition ii is clearly equivalent to saying that any sequence $\{F(x_\eta)\}_{x \in \{1, 2, \dots, \eta\}}$ of relative frequencies of the event “being a «prime» labeled number” in the first x of η trials is such that the declarative sentence: “ 2η can be written as the sum of two as «prime» labeled positive integers not necessarily distinct” has the same truth value of either TRUE or FALSE as Goldbach’s proposition, which, by remark 2.4, is a necessarily true or certainly false statement.

Looking closely, condition ii adds no relevant information either about the truth value of Goldbach’s proposition or, therefore, about the set of all possible sequences (of relative frequencies) of the above type; hence, it does not impact in any way the probability that positive integer η is identified as «prime».

Remark 3.4: Let $\eta \in M-\{1\}$. Let $P(\eta_{\text{«prime»}})$ be the probability that positive integer η is identified as «prime» in the Goldbach proof.

It should also be stressed that the labels assigned to the numbers $1_n = 1 -$ corresponding to the index n – and to n , when n varies over the set $M-\{1\}$, are equiprobably (See footnote 9) and independently chosen, in the sense that the outcome of each of them – to be a «prime» or «non-prime» labeled number – has the same probability $p = 1/2$ to occur and the probability $(1-p) = 1/2$ of not occurring, and it does not influence and is not influenced in any way by that of another or the others. Based on the remarks 3.2 and 3.3, by using the binomial distribution formula (See [8] pp. 600-601) and the famous Bayes’s rule [2], we thus have:

$$P(\eta_{\text{«prime»}}) = \frac{\frac{p * (\eta - 1)! * [p^{\Pi(\eta)-1} * (1-p)^{[\eta-\Pi(\eta)]}]}{[\Pi(\eta) - 1]! * [\eta - \Pi(\eta)]!}}{\frac{\eta! * [p^{\Pi(\eta)} * (1-p)^{[\eta-\Pi(\eta)]}]}{[\Pi(\eta)]! * [\eta - \Pi(\eta)]!}},$$

from which by simplifying we obtain: $P(\eta_{\text{«prime»}}) = F(\eta) = \Pi(\eta)/\eta$.

Remark 3.5: Let $\eta \in M$, $\eta \geq 4 \cdot 10^7$ and $k \in \{0, \dots, \eta-2\}$. Let $(\eta-k, \eta+k)$ be a pair of 2η . Also, if and only if $k > 0$, we assume that the event $E_{(\eta, j)}$ has happened, i.e., that every pair $(\eta-j, \eta+j)$ of 2η , with $j \in \mathbb{N}$ varying in the range 0 to $k-1$, is formed by at least one labeled as «non-prime» positive integer.

According to remark 3.4, the probability ${}_{(\eta)}P_k$ that the pair $(\eta-k, \eta+k)$ of 2η consists of two positive integers both labeled as «prime» may be equal to or greater than

$${}_{(\eta)}S_k = [\Pi(\eta-k)/(\eta-k)] * [\Pi(\eta+k) - 1/(\eta-1)], \text{ if } k \in \{1, \dots, \eta-2\};$$

$${}_{(\eta)}S_k = {}_{(\eta)}P_k = {}_{(\eta)}P_0 = {}_{(\eta)}S_0 = \Pi(\eta)/\eta, \text{ if } k = 0.$$

In fact, if $k \in \{1, \dots, \eta-2\}$, we have

$$\begin{aligned} {}_{(\eta)}P_k &= [\Pi(\eta-k)/(\eta-k)] * \{[\Pi(\eta+k) - 1 - H_{(\eta, j)}]/(\eta+k-2(k-1) - 1 - 1)\} = [\Pi(\eta-k)/(\eta-k)] * \\ &* \{[\Pi(\eta+k) - 1 - H_{(\eta, j)}]/(\eta - k)\}, \text{ where } H_{(\eta, j)} \text{ is the number of pairs of } 2\eta, \\ &\text{excluding the pair } (\eta, \eta), \text{ that belong to the event } E_{(\eta, j)} \text{ and each having only} \\ &\text{one positive integer labeled as «prime» (See Appendix A).} \end{aligned}$$

Now we are equipped to demonstrate the following:

Theorem 3.1: Goldbach's proposition holds.

Proof. Let $m \in M$ and $m \geq 4 \cdot 10^7$. Let ${}_GP(2m)$ be the probability that at least one of the $m-1$ pairs of $2m$ is formed by two positive integers both labeled as «prime» and not necessarily distinct.

Using probability calculus, we can suppose by lemma 2.4 and remark 3.5 that

$${}_GP(2m) \geq P(2m) = {}_{(m)}S_0 + (1 - {}_{(m)}S_0) * {}_{(m)}S_1 + (1 - {}_{(m)}S_0) * (1 - {}_{(m)}S_1) * {}_{(m)}S_2 + \dots + (1 - {}_{(m)}S_0) * (1 - {}_{(m)}S_1) * (1 - {}_{(m)}S_2) * \dots * (1 - {}_{(m)}S_{m-3}) * {}_{(m)}S_{m-2}, \text{ where}$$

$${}_GP(2m) = {}_{(m)}P_0 + (1 - {}_{(m)}P_0) * {}_{(m)}P_1 + (1 - {}_{(m)}P_0) * (1 - {}_{(m)}P_1) * {}_{(m)}P_2 + \dots + (1 - {}_{(m)}P_0) * (1 - {}_{(m)}P_1) * (1 - {}_{(m)}P_2) * \dots * (1 - {}_{(m)}P_{m-3}) * {}_{(m)}P_{m-2}.$$

It follows directly from remark 2.3 and the Rosser-Schoenfeld theorem that

$${}_GP(2m) \geq P(2m) = {}_{(m)}S_0 + (1 - {}_{(m)}S_0) * (1 - m^{-2}), \text{ where } 0 < {}_{(m)}S_0 < 1 \text{ and } q = (1 - {}_{(m)}S) < 1 - [1/\log^2(m+92)]. \quad (3.1)$$

By virtue of condition ii and remark 2.4, Goldbach's proposition necessarily holds iff ${}_GP(2m) \neq 0$, i.e., iff ${}_GP(2m) = 1$, and so, by (3.1), if and only if

$${}_GP(2m) = 1 \geq {}_{(m)}S_0 + (1 - {}_{(m)}S_0) * (1 - m^{-2}).$$

If it were ${}_GP(2m) = 0$, then, by (3.1), we would have

$$({}_m)S_0 + (1 - ({}_m)S_0) \cdot (1 - {}_mq^{m-2}) \leq 0,$$

$$1 - {}_mq^{m-2} \leq -({}_m)S_0 / (1 - ({}_m)S_0),$$

$${}_mq^{m-2} \geq [({}_m)S_0 / (1 - ({}_m)S_0)] + 1 \geq 1.$$

On the other hand, since, if $m \in M$ and $m \geq 67$, $a_m = [1 - 1/\log^2(m)]^{\log(m) \cdot \log(m)}$ and $b_m = (m-2)/[\log(m+92) \cdot \log(m+92)]$ are respectively the general terms of the two strictly increasing sequences $\{a_m\}$ and $\{b_m\}$ of positive real numbers, one can easily check that:

$${}_mq^{m-2} \leq [1 - 1/\log^2(m+92)]^{m-2} \leq e^{-(m-2)/[\log(m+92) \cdot \log(m+92)]} < 0,1 < 1.$$

This would lead to a clear contradiction. Hence, ${}_GP(2m) = 1$. Goldbach's proposition is thus proved.

4 Conclusions

The goal was achieved by combining number theory and probability calculus. Goldbach's strong conjecture – i.e., the assertion: "*Every even natural number greater than 2 can be written as the sum of two prime numbers that are not necessarily distinct*" – has already been verified by computer methods for all even natural numbers up to $4 \cdot 10^{14}$ Bonavoglia [3], Richstein [6] pp.1745-1749. In view of Goldbach's proposition, this statement is thus true for any even integer greater than 2.

However, it is almost impossible to carry out the random experiment "Goldbach's proof" in practice, so much so that if it did occur it would be believed that this process occurred under conditions other than the assumptions under which it is considered theoretically. In fact, with a normal coin that has a fifty percent probability of giving HEAD, the ratio between the number of times you get HEAD in n tosses, with n "large", and the number n is equal to $1/2$ with probability close to 1. But with the coin of numbers labeled as «prime» the relative frequency decreases with each toss and is generally much less than $1/2$. In short, Goldbach's proof is a sort of thought experiment whose only purpose is to explore by means of probability the sequence of primes, highlighting surprising or paradoxical consequences.

Finally, it is still opened a numerical problem: if an even number is the sum of two prime numbers, what are these two numbers? The greater the starting even number, the more difficult it is to identify the two primes that make up its sum.

This essay offers us a different perspective on a long-standing question, anyway, providing a good complement to existing literature.

Appendix A

In the assumptions of remark 3.5, we first show that it is possible to have

$$H_{(\eta, j)} \lesssim (k-1)/\log(\eta-1), \text{ where } \eta \in \mathbb{N}, \eta \geq 4 \cdot 10^7, k \in \{1, \dots, \eta-2\} \text{ and } j \in \{0, \dots, k-1\}.$$

In this regard, suppose that the event $E_{(\eta, j)}$ has occurred and that we know which of the numbers forming the $\eta-1$ pairs of 2η of $E_{(\eta, j)}$ are those labeled as «prime» – e.g., all those of the type $\eta-j$ (or $\eta+j$) and anyway at most one for each pair of 2η of $E_{(\eta, j)}$ –.

Therefore, since $[\Pi(\eta+k-1) - \Pi(\eta) + \Pi(\eta) - \Pi(\eta-k+1) \pm 1]$ is the number of positive integers labeled as «prime» and included in the interval $[n-k+1, n+k-1]$, we can reasonably expect that $H_{(\eta, j)} \approx [\Pi(\eta+k-1) - \Pi(\eta-k+1)]/2$ and, by remark 2.2 and the Rosser-Schoenfeld theorem, that

$$2H_{(\eta, j)} \approx [\Pi(\eta+k-1) - \Pi(\eta-k+1)] \lesssim [(\eta+k-1)/\log(\eta+k-1)] - [(\eta-k+1)/\log(\eta+k-1)] \leq (2k-2)/\log(\eta+k-1) < (2k-2)/\log(\eta-1), \text{ because, as said earlier, we have}$$

$\Pi(68-t)/(68-t) > \Pi(94)/(94)$, for any $t \in \{0, 1, \dots, 66\}$. Hence, we can assume that

$$H_{(\eta, j)} \lesssim (k-1)/\log(\eta-1), \text{ with } \eta \in \mathbb{N}, \eta \geq 4 \cdot 10^7, k \in \{1, \dots, \eta-2\} \text{ and } j \in \{0, \dots, k-1\}. \quad (\text{A.1})$$

Then, since by definition $H_{(\eta, j)} = 0$, if $k = 1$, establish the truth of

$_{(\eta)}P_k = [\Pi(\eta-k)/(\eta-k)]^* \{[\Pi(\eta+k) - 1 - H_{(\eta, j)}]/(\eta-k)\} \geq _{(\eta)}S_k$ means to prove (for $k > 1$) that $[\Pi(\eta-k)/(\eta-k)]^* \{[\Pi(\eta+k) - 1 - H_{(\eta, j)}]/(\eta-k)\} \geq [\Pi(\eta-k)/(\eta-k)]^* \{[\Pi(\eta+k) - 1]/(\eta-1)\}$, which takes the form

$[\Pi(\eta+k) - 1 - H_{(\eta, j)}]/(\eta-k) \geq [\Pi(\eta+k) - 1]/(\eta-1)$. By doing the calculations, we obtain

$$1 - \{H_{(\eta, j)} / [\Pi(\eta+k) - 1]\} \geq (\eta-k)/(\eta-1),$$

$(k-1)/(\eta-1) \geq H_{(\eta, j)} / [\Pi(\eta+k) - 1]$. Thus, applying (A.1), it is sufficient to show that

$(k-1)/(\eta-1) \gg (k-1) / \{[\Pi(\eta+k) - 1] \cdot \log(\eta-1)\}$, and so that

$$1 \gg (\eta-1) / \{[\Pi(\eta+k) - 1] \cdot \log(\eta-1)\}, \text{ where } k \in \{2, \dots, \eta-2\}. \quad (\text{A.2})$$

But (A.2) holds if $\{(\eta-1) / [\log(\eta-1) - (1/2)]\} - 1 \gg (\eta-1)/\log(\eta-1)$.

In fact, by remark 2.2 and using the above-mentioned Rosser-Schoenfeld theorem, we have $(\Pi(\eta+k) - 1) < (\Pi(\eta+k) \geq_{\text{bis}} \Pi(\eta+k) \geq (\eta+k) / [\log(\eta+k) - (1/2)])$, and therefore $(\Pi(\eta+k) - 1) < (\Pi(\eta+k) \geq_{\text{bis}} \Pi(\eta+k) \geq (\eta+k) / [\log(\eta+k) - (1/2)]) > (\eta-1) / [\log(\eta-1) - (1/2)]$,

since, if $\eta \in \mathbb{N}$ and $\eta \geq 67$, $g(\eta) = (\eta - 1)/[\log(\eta - 1) - (1/2)]$ is an increasing function of η greater than 1.

The inequality $\{(\eta - 1) / [\log(\eta - 1) - (1/2)]\} - 1 \gg (\eta - 1) / \log(\eta - 1)$ is satisfied if

$$-\log(\eta - 1) * [\log(\eta - 1) - (1/2)] \gg - (1/2) * (\eta - 1),$$

$$\log^2(\eta - 1) - (1/2) * [\log(\eta - 1)] \ll (1/2) * (\eta - 1), \text{ and even more so, if}$$

$$\log^2(\eta - 1) \ll (1/2) * (\eta - 1).$$

But this last relation is true, because, if $\eta \in \mathbb{N}$ and $\eta \geq 4 * 10^7$, $q(\eta) = (\eta - 1)/\log^2(\eta - 1)$ is an increasing function of η much greater than 2. (See [4] pp. 62-64). Therefore, (A.2) is demonstrated.

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Lie-admissible irreversible biological entanglements and their apparent initiation of hadronic medicine

Federico Inglese* Emanuele Velardo[†]
Ruggero Maria Santilli[‡] and Thomas Vougiouklis[§]

Abstract

In a preceding paper, two of us (R. M. S. and Th. V.) initiated the mathematical representation of life intended as the difference between organic and inorganic molecules, via the Lie-admissible hyperstructural branch of hadronic mechanics representing the size of biological entities, their contact interactions and their irreversibility over time. In this paper, we review the time reversal Lie-isotopic branch of hadronic mechanics, as well as its Lie-admissible covering, by showing that 20th century reversible Lie theories can be extended to an irreversible form by adding symmetric Jordan algebra brackets to antisymmetric Lie brackets. We then introduce, apparently for the first time: a Lie and Jordan admissible axiomatic formulation of the two directions of time; the Lie and Jordan admissible irreversible formulation of biological entanglements; their lack of visible use of energy; and a smooth connection between hadronic uncertainties at small distances and full determinism at classical distances. We then show that biological entanglements can provide a quantitative representation of the behavior by biological entities beyond our sensory perception, with expected diagnostic and curative values suggesting the apparent initiation of the novel hadronic medicine.

Keywords: quantum mechanics, hadronic biology, entanglements.

2020 AMS subject classifications: 16, 18, 81¹

*The Institute for Basic research; federicoinglese@live.it.

[†]The Institute for Basic research; emanuelevelardo@outlook.it

[‡]Corresponding author. The Institute for Basic Research, Palm Harbor, Florida, U.S.A.; research@i-b-r.org.

[§]Democritus University of Thrace, Xanthi, Greece, tvougiou@eled.duth.gr

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1 Introduction

Inspired by the historical 1935 argument by A. Einstein, B. Podolsky and N. Rosen (EPR) that "*quantum mechanics is not a complete theory*" [1] (Fig. 1), in the preceding paper [2] two of us (R. M. Santilli and Th. Vougiouklis) initiated the *mathematical representation of life*, intended as the difference between organic and inorganic molecules, via the *Lie-admissible hyperstructural branch of hadronic mechanics* for:

1.1. A representation of the *actual size* of biological systems and their constituents, such as a collection of cells in condition of mutual contract, or equivalently, of deep entanglement (Fig. 2) with ensuing interactions that generally are *non-linear* (in the wave functions) first studied by W. Heisenberg [3], *non-local* (because extended over surfaces or volumes) first studied by L. de Broglie and D. Bohm [4] and *non-potential* (because of contact, thus zero range character) first studied by R. M. Santilli [5] via the conditions of variational self-adjointness and technically called *variationally non-self-adjoint* (NSA);

1.2. A representation of the irreversibility over time of biological structures via *Santilli Lie-admissible branch of hadronic mechanics* initiated in the 1967 paper [6] (see the 1968 paper [7] for a review of Lie-admissible algebras, and subsequent works [8]-[12]) formulated via *Vougiouklis H_v hyperstructures* [13]-[15];

1.3. The apparent multi-valued character of biological structures which appears to be necessary for attempting a representation of the extreme complexities of life (Fig. 3).

By using a language accessible to the general educated audience, in this paper: we review Einstein's criticisms of quantum entanglements [1] by showing that particles entangled at large mutual distances can only be represented by quantum mechanics as being free; we then review the time reversible Lie-isotopic particle entanglements of hadronic mechanics [16] and show their actual entanglement at large mutual distance due to non-linear, non-local and non-potential/NSA interactions in the overlapping of wave packets of the constituents; we review the implications of Lie-isotopic entanglements for the explicit and concrete representation of Bohm's *hidden variables* [17] with ensuing by-passing of Bell's inequalities [18] and progressive recovering of *Einstein's determinism* [19]-[24].

We then introduce, apparently for the first time: 1) An axiomatic formulation of the two directions of time via an isobimodular structure; 3) A smooth connection between hadronic uncertainties at very small distances and full determinism at classical distances. 3) The *Lie-admissible irreversible biological entanglements* verifying conditions 1.1, 1.2, 1.3, also called hadronic entanglements, and show



Figure 1: *In support of the EPR argument [1] according to which "quantum mechanics cannot be a complete theory," we present nuclear fusions, chemical combustion and the beginning of life that cannot be consistently represented via quantum mechanics due to its strict reversibility over time compared to the known irreversibility of biological systems.*

their lack of visible energy.

We then indicate that biological entanglements can provide a physical representation of the behavior of biological entities beyond our sensory perception, with expected diagnostic and curative values and apparent initiation of a new branch of medicine here submitted for the first time under the name of *hadronic medicine*.

We have made an effort to render this paper minimally self-sufficient, with the understanding that a deeper knowledge of the proposed hadronic medicine can be solely reached via the study of the literature in the field (see the originating works [5]-[16]; adjoining studies on the mathematics underlying this study [25] [26]; paper [27] on the classification of hadronic mechanics; [28] for a recent collection of papers; and independent monographs [29]-[36]).

2 Lie-admissible and Jordan-admissible biological entanglements

2.1. Particle entanglements.

According to experimental evidence dating back to the early part of the past century, particles that were initially bounded together and then separated, can continuously and instantaneously influence each other at a distance, (see, e.g., [37] [38] and papers quoted therein), and at the classical level, e.g., for pairs of classical oscillators [39].

As an example, consider a pair of electrons that were initially bonded together into the valence bond and then separated. The entanglement here considered represents the experimental evidence, that when one electron is subjected to a 180°

spin flip, the second electron experiences the same spin flip instantaneously at arbitrary distances without any human intervention or any visible interaction, and the same entanglement appears to occur at the classical level under certain conditions.

2.2. Quantum entanglements.

The experimental evidence on particle entanglements is generally *assumed* to be represented by quantum mechanics for which reason particle entanglements are widely called *quantum entanglement* (Fig. 3). However, Albert Einstein strongly criticized such an assumption because it would imply superluminal communications that violate special relativity.

In support of Einstein's view, Santilli [16] pointed out that, at sufficiently big mutual distances, quantum mechanics can only represent entangled particles as being free.

Recall that quantum mechanics can only represent interactions derivable from a potential V which is *additive* to the kinetic energy K in the Hamiltonian $H = K + V$, while *no* quantum mechanical potential is conceivably possibly to represent continuous and instantaneous interactions at arbitrary distance.

Consequently, the Schrödinger equation for two entangled particles with coordinates r_k , $k = 1, 2$ at a sufficiently big relative distance r on a Hilbert space $\mathcal{H}$ over the field $\mathcal{C}$ of complex numbers is given by (for $\hbar = 1$)

$$\begin{aligned} \Sigma_{k=1,2} \frac{1}{2m_k} p_k \times p_k \times |\psi(r_1) \times \psi(r_2)\rangle &= \\ = [\Sigma_{k=1,2} \frac{1}{2m_k} (-i \frac{\partial}{\partial r_k}) \times (-i \frac{\partial}{\partial r_k})] |\psi(r_1) \times \psi(r_2)\rangle &= \\ = E |\psi(r_1) \times \psi(r_2)\rangle \end{aligned} \quad (1)$$

by, therefore, representing two free particles without any possible or otherwise visible interaction.

Note that, in the event quantum mechanical interactions are detectable at small and/or big distances, they cannot explain the instantaneous action at a distance, such as the indicated electron spin flip.

2.3. Lie-isotopic entanglements.

Recall that the wave packet of a particle fills up the entire universe because it is identically null only at infinity, even though it is measurable with current technologies only in the range of a few $fm = 10^{-13} cm$. Consequently, Santilli [16] proposed that the entanglement of particles is due to the overlapping of their wave packets which is continuous, and instantaneous at arbitrary distance (Fig. 5), by therefore avoiding superluminal interactions.

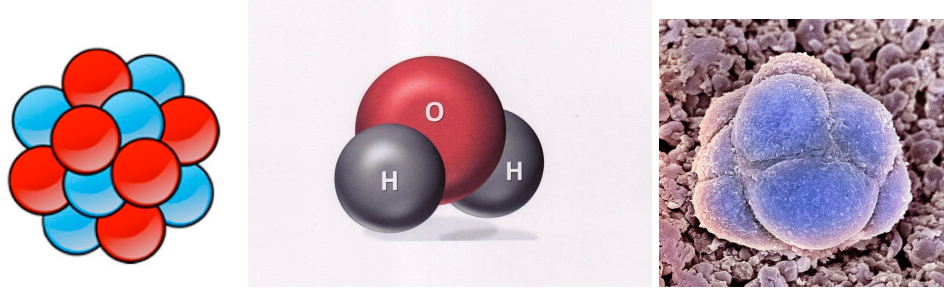


Figure 2: We present examples of physical, chemical or biological systems illustrating their extended constituents in condition of partial mutual penetration, by therefore resulting in the most general known linear and non-linear, local and non-local and potential as well as non-potential interactions.

Additionally, the initial bond of the wave packets of particles causes their synchronicity whose conservation can explain the occurrence of actual physical events, such as a spin flip of a far away particle without any human intervention, without any visible interaction and without any visible use of energy (see Sect 2.5).

Furthermore, Santilli [16] recalled that the interaction caused by the overlapping of wave packets is non-linear, non-local and non-potential/NSA [5], and as such, can be quantitatively represented via the Lie-isotopic branch of hadronic mechanics according to the following main steps.

Recall that quantum mechanics is based on the universal enveloping associative algebra

$$U : \{X_i; X_j \times X_k; 1; i, j, k = 1, 2, \dots, N; \} \quad (2)$$

of Hermitean operators X_i on a Hilbert space $\mathcal{H}$ over a numeric field $F(n, \times, 1)$ with millenary associative product and related unit

$$X_i X_j = X_i \times X_j, \quad (3)$$

$$1 \times X_i = X_i \times 1 \equiv X_i \forall X_i \in U;$$

attached N-dimensional Lie algebra $L \equiv U^-$ with commutation rules

$$[X_i, X_j] = X_i \times X_j - X_j \times X_i = C_{ij}^k X_k; \quad (4)$$

Lie group of transformations with parameters $w \in F$ of an observable $A(w)$

$$A(w) = [\Pi_k e^{X_k w}] A(0) [\Pi_k e^{-i w X_k}]; \quad (5)$$

and related *Lie symmetries and conservation laws*, e.g., for the invariance of a Hamiltonian $X_1 = H(r, p)$ under time evolution with $w = t$ that, for infinitesimal

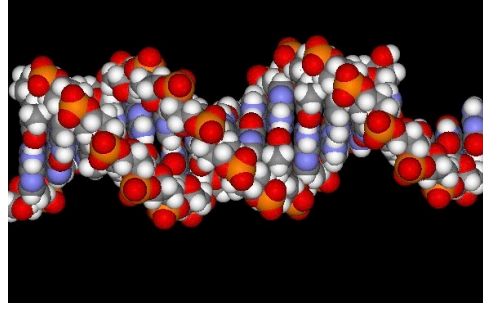


Figure 3: We illustrate the complexity of biological structures by noting that the correlation of two atoms in a DNS, which is mathematically represented by the multiplication can produce an entire organ with billions of atoms, thus suggesting the use of multi-valued hyperstructures [13]-[15] to initiate their quantitative representation.

values of time, implies Heisenberg's equation for an operator $A(t)$

$$i \frac{dA}{dt} = [A, H] = A \times H - H \times A, \quad (6)$$

with ensuing conservation law of the energy

$$i \frac{dH}{dt} = [H, H] = H \times H - H \times H \equiv 0. \quad (7)$$

Lie-isotopic branch of hadronic mechanics, or *isomechanics* for short, is based on the *universal enveloping isoassociative algebra* of the same Hermitean generators X_i (because they are observable) first introduced in the 1983 monograph [8]

$$\hat{U} : \{X_i; X_j \hat{\times} X_k; \hat{1}; i, j, k = 1, 2, \dots, N; \} \quad (8)$$

characterized by the new product

$$X_i \hat{\times} X_j = X_i S X_j, \quad S > 0, \quad (9)$$

called *isoproduct* because verifying the axiom of associativity

$$X_i \hat{\times} (X_j \hat{\times} X_k) = (X_i \hat{\times} X_j) \hat{\times} X_k, \quad (10)$$

and related isounit

$$\begin{aligned} \hat{1} &= 1/S, \\ \hat{1} \hat{\times} X_i &= X_i \hat{\times} \hat{1} \equiv X_i \quad \forall X_i \in \hat{U}, \end{aligned} \quad (11)$$

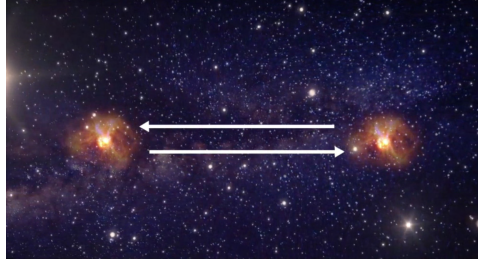


Figure 4: We illustrate the experimental evidence clearly extendable to chemical structures and biological entities according to which two particles or wave packets that were initially bonded together and then separated, can continuously and instantaneously influence each other at arbitrary distances without any human intervention, without any visible energy source.

where $X_i S$ and $S X_j$ are conventional associative products and the quantity S , nowadays called the Santillians [24] [40] [23], is solely restricted by the conditions of being dimensionless and positive-definite while admitting an arbitrary dependence on time t , relative coordinates r , momenta p , density d , wave functions ψ , and any other needed local quantities $S = S(t, r, p, d, \psi, \dots) > 0$, with realization for the non-relativistic entanglement of two particles in Euclidean space [16]

$$S = 1/\hat{1} = \Pi_{\alpha=1,2} \text{Diag.} (a_{1,\alpha}^2, b_{2,\alpha}^2, c_{3,\alpha}^2) \times d_\alpha^2 \times e^{-\Gamma}, \quad (12)$$

$$a, b, c, d > 0, \quad \Gamma > 0, \quad k = 1, 2, 3, \quad \alpha = 1, 2,$$

where: the time-independent parameters $a_{k,\alpha}^2, b_{k,\alpha}^2, c_{k,\alpha}^2$ represent the two volumes of wave overlapping with a radius generally equal to the relative distance r ; the time independent parameters d_α^2 represents the density of the individual wave packets; and Γ represents their non-linear, non- local and non-potential/NSA interactions.

Despite their simplicity, generalized basic assumptions (8)-(11) of isomechanics imply a corresponding generalization of the totality of 20th century applied mathematics into the new *isomathematics* [9] [30] [33] [34] [36] that cannot possibly be reviewed here. We merely limit ourself to recall that isoenvolope (8) is formulated on a Hilbert-Myung-Santilli isospace $\hat{\mathcal{H}}$ [41] with isostate $|\hat{\psi}(\hat{r})\rangle$ over the isofield of isocomplex numbers $\hat{\mathcal{C}}$, $\hat{c} = c\hat{1}$, $c \in C$ [42] with isocoordinates $\hat{r} = r\hat{1}$ and isonormalization

$$\langle \hat{\psi}(\hat{r}) | \hat{\times} | \hat{\psi} \rangle = \langle \hat{\psi}(\hat{r}) | \hat{\times} | \hat{\psi} \rangle = S. \quad (13)$$

Under the correct treatment via isomathematics, isoenvolope (8) uniquely and

unambiguously characterize: 1) The Lie-Santilli isoalgebra [8]

$$[X_i, X_j] = X_i \hat{\times} X_j - X_j \hat{\times} X_i = \hat{C}_{ij}^k \hat{\times} X_k; \quad (14)$$

2) The Lie-Santilli group of isotransformations with isoparameters $\hat{w} \in \hat{\mathcal{C}}$ of an observable $A(w)$

$$\begin{aligned} A(w) &= [\Pi_k \hat{e}^{X_k w i}] \hat{\times} A(0) \hat{\times} [\Pi_k \hat{e}^{-i w X_k}] = \\ &= [\Pi_k e^{X_k S w i}] A(0) [\Pi_k e^{-i w S X_k}], \end{aligned} \quad (15)$$

where we have used the isoexponent $\hat{e}^X = [e^{XS} | \hat{1} = \hat{1}[e^{SX}]$ [9]; 3) Lie-Santilli isosymmetries and conserved quantities generally given by the N generators X_k [8] [30]; 4) The Heisenberg-Santilli isoevolution of an observable $A(t)$

$$i \frac{dA}{dt} = [A, H] = A \hat{\times} H - H \hat{\times} A, \quad (16)$$

with related conservation of the energy for $X_1 = H$, $i \frac{dH}{dt} = [H, H] \equiv 0$; The Schrödinger- Santilli isoeigenvalue equations

$$H \hat{|\psi\rangle} = HS|\hat{\psi}\rangle = \hat{E} \hat{\times} |\hat{\psi}\rangle = E|\hat{\psi}\rangle; \quad (17)$$

and the remaining features of the Lie-isotopic branch of hadronic mechanics [10].

By recalling the expression of the *iso-linear iso-momentum* characterized by the completion of the local Newton-Leibnitz differential calculus into the non-local *iso-differential calculus* [43] (see also [36] for independent mathematical studies)

$$\hat{p} \hat{\times} \hat{\psi}(\hat{r}) = \hat{p} \hat{S}(\hat{r}, \dots) \psi(\hat{r}) = -i \frac{\hat{\partial}}{\hat{\partial} \hat{r}} \hat{\psi}(\hat{r}) = -i \hat{1}(\hat{r}, \dots) \frac{\partial}{\partial \hat{r}} \hat{\psi}(\hat{r}), \quad (18)$$

the non-relativistic version of particle entanglements is characterized by the Schrödinger-Santilli isoequation

$$\begin{aligned} H \hat{|\psi(\hat{r})\rangle} &= HS|\hat{\psi}(\hat{r})\rangle = (\sum_{k=1,2} \frac{1}{2m_k} \hat{p}_k \hat{\times} \hat{p}_k \hat{\times} |\hat{\psi}(\hat{r})\rangle = \\ &= [\sum_{k=1,2} \frac{1}{2m_k} (-i \hat{1} \frac{\partial}{\partial \hat{r}_k}) (-i \hat{1} \frac{\partial}{\partial \hat{r}_k})] |\hat{\psi}(\hat{r})\rangle = \\ &= \{ \sum_{k=1,2} [(-\frac{\hat{1}^2}{2m_k} (\frac{\partial}{\partial \hat{r}_k}) (\frac{\partial}{\partial \hat{r}_k}) - \frac{\hat{1}}{2m_k} (\frac{\partial \hat{1}}{\partial \hat{r}_k}) (\frac{\partial}{\partial \hat{r}_k})] \} |\hat{\psi}(\hat{r})\rangle = \\ &= \{ \sum_{k=1,2} [(-\frac{\hat{1}^2}{2m_k} (\frac{\partial}{\partial \hat{r}_k}) (\frac{\partial}{\partial \hat{r}_k}) - \frac{\Gamma}{2m_k} (\frac{\partial \Gamma}{\partial \hat{r}_k}) (\frac{\partial}{\partial \hat{r}_k})] \} |\hat{\psi}(\hat{r})\rangle = \\ &= \hat{E} \hat{\times} |\hat{\psi}(\hat{r})\rangle = E |\hat{\psi}(\hat{r})\rangle = E |\hat{\psi}(\hat{r}_1)\rangle \hat{\times} |\hat{\psi}(\hat{r}_2)\rangle, \end{aligned} \quad (19)$$

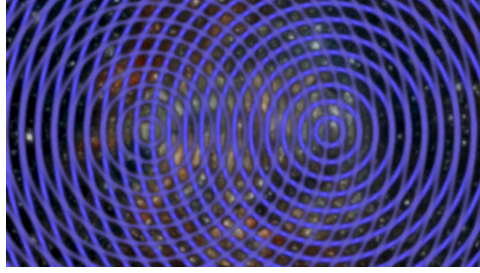


Figure 5: We illustrate the central notion of this paper called "hadronic entanglement" [16] according to which the entanglement of particles of Fig. 4 is due to the overlapping of their wave packets, thus being a continuous and instantaneous physical event at arbitrary distances equally holding for physical, chemical and biological structures.

which identifies the interaction term $-\frac{\Gamma}{2m_k}(\frac{\partial \Gamma}{\partial \hat{r}_k})(\frac{\partial}{\partial \hat{r}_k})$ additive to the kinetic term for two isoentangled particles, which term is completely absent for quantum entanglement (1).

Recall that the primary aim of this paper is to indicate the apparent existence of the entanglement in biological structures which evidently requires a smooth transition from operator settings at particle distances to full determinism at classical distances. This transition has been studied via the following steps:

2.3-I: Bohm's "hidden variables". In 1952, D. Bohm [17] introduced the hypothesis that a number of variables λ may be hidden in the formalism of quantum mechanics in such a way to recover Einstein's determinism [1]. Hadronic mechanics has been constructed for, and has indeed achieved an explicit and concrete realization of Bohm's hidden variables via their identification with the Santillian as being hidden in associativity axiom (10) with new realization

$$\begin{aligned} X_i \hat{\times} X_j &= X_i S X_j = X_i \lambda X_j, \\ X_i \lambda (X_j \lambda X_k) &= (X_i \lambda X_j) \lambda X_k, \end{aligned} \tag{20}$$

by therefore offering a realistic possibility of weakening Heisenberg's uncertainty principle in the transition from its original conception for isolated point-like atomic electrons in vacuum to complex physical, chemical and biological systems with extended constituents under action-at-a-distance potential as well as contact non-potential interactions.

Note that Bohm's hidden variables are represented under the full validity of the abstract axioms of quantum mechanics, only subjected to a broader realization. In fact, at the abstract, realization-free level, quantum and hadronic mechanics coincide to such an extent that they can be expressed via the same equations only subjected to a broader realization of the associative product.

2.3-II. Bell's inequalities. In 1964, J. S. Bell [18] introduced a rigorously proved mathematical theorem according to which a system of quantum mechanical particles with spin $1/2$ does not admit a classical counterpart, by therefore prohibiting the admission of Bohm's hidden variables and any possible reconciliation with Einstein's determinism. The theorem was proved by showing that a certain quantity D^{Bell} representing all possible conditions of the system of spin $1/2$ particles is always *smaller* than the corresponding classical value D^{Clas} ,

$$D^{Bell} < D^{Clas}. \quad (21)$$

In 1998, R. M. Santilli [44] proved a theorem according to which the derivation of Bell's inequality (21) via hadronic mechanics (hm) for *extended* particles with spin $1/2$ in deep mutual entanglement, hence under both Hamiltonian and Santillian interactions, implies the re-definition of Bell's quantity (Eq. (5.8), p. 189 of [44])

$$D^{HM} = \frac{1}{2}(\lambda_1\lambda_2^{-1} + \lambda_1^{-1}\lambda_2)D^{Bell}, \quad (22)$$

which can be equal to the corresponding classical quantity D^{Cl} , by therefore confirming Einstein's view on the possible recovering of classical determinism at small distances.

2.3-III. Einstein's isodeterminism. In 1981, R. M. Santilli [19] submitted the hypothesis that protons and neutrons under the extremely attractive strong nuclear forces should have standard deviations Δr and Δp *smaller* than those of atomic electrons in vacuum (Fig. 6). In 1994, R. M. Santilli [20] proved that said standard deviations are identically null, with ensuing classical determinism, for particles in the interior of black holes.

Following the achievement of maturity of the novel isomathematics, R. M. Santilli [21] (see the review in [22]) finally introduced in 2019 the *Lie-isotopic completion of Heisenberg's uncertainty principle for strong interactions*, nowadays fully applicable to entangled wave packets (Eq. (35), p. 14 of [21])

$$\Delta r \Delta p \approx \frac{1}{2} | \langle \hat{\psi}(\hat{r}) | \hat{\times} [\hat{r}, \hat{p}] \hat{\times} | \hat{\psi}(\hat{r}) \rangle | \ll \frac{1}{2} S = \frac{\lambda}{2} \ll 1. \quad (23)$$

By recalling that the energy, and therefore the density d_α of wave packets decreases in a way inversely proportional to the square of the distance, the above principle establishes that the standard deviations Δr and Δp progressively recover Einstein's classical determinism [1] with the increase of the distance, i.e., with the decrease of the densities d_α of the wave packets, and said deviations are null, $\Delta r = m\Delta p = 0$ for null densities $d_\alpha = 0$ in Eqs. (12) and (23). We reach in this way the needed smooth reconciliation of microscopic hadronic entanglements at very small mutual distances with macroscopic deterministic biological

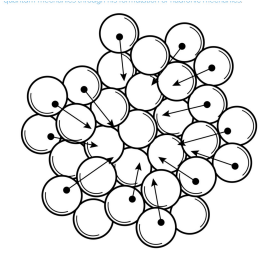


Figure 6: We here illustrate the main argument of the 1981 paper [19] under DOE support according to which protons and neutrons under extremely attractive strong nuclear forces cannot possibly have the same Heisenberg's uncertainties of atomic electrons in vacuum under long range electromagnetic interactions.

entanglements at classical distances (see Ref. [39] and papers quoted therein for experimental evidence of classical, deterministic, mechanical entanglements).

2.4. Lie and Jordan-admissible entanglements.

The main axiomatic assumption of Lie-isotopic entanglements is the systematic use, for all possible products, of the isoproduct $X_i \hat{\times} X_j = X_i S X_j$ which is *invertible* in the sense that the isoproduct to the right of X_i to X_j , here denoted $X_i > X_j = X_i S X_j$ is identical to the isoproduct to the left of X_j to X_i , here denoted $X_i < X_j = X_i S X_j$ resulting in the axiom of product invertibility $X_i < X_j \equiv X_i > X_j$.

Upon due development of the resulting new isomathematics and related methods, the Lie-isotopic entanglement allowed: the first known numerically exact and time invariant representation of; the experimental data for stable nuclei [45]-[47]; the first known attraction between identical electrons in a valence bond despite their extremely big Coulomb repulsion [11]; the first known exact representation of the experimental data of the Hydrogen [48] and water [49] molecule; and other exact representations that had been impossible to achieve via quantum mechanics in one century of research.

Despite the indicated advances, Lie-isotopic entanglements and related methods are *inapplicable* to biological structures because of the invariance of Lie-isotopic formulations under time reversal (as shown, e.g., by the invariance of Heisenberg-Santilli isoequation (16) under anti-Hermiticity), compared to the strict time irreversibility of biological entities.

The first axiomatic formulation of irreversibility over time was reached in 1981 by R. M. Santilli [50], then at the Department of Mathematics of Harvard University, via:

1) The ordering of all isoproducts to the right $X_i > X_j$ in representation of motion forward in time;

2) The ordering of all isoproducts to the left $X_i < X_j = X_i R X_j$ in representation of motion backward in time;

3) The assumption that the isoproducts are characterized by two different, time dependent, forward and backward Santillians to assure irreversibility $R \neq S$.

By noting that the ordered isoproducts $X_i > X_j$ and $X_i < X_j$ are individually associative, the above axioms imply the decomposition of the universal enveloping isoassociative algebra (8) of Lie-isotopic formulations into the Kronecker product of the forward and backward isoenvelopes over the corresponding numeric genofields ${}^<\mathcal{C} \times \mathcal{C}^>$ [42]

$$\begin{aligned}\hat{U} &= {}^<U \times U^>, \\ U^> &: \{X_i; X_i > X_j = X_i S X_j; 1^>; i, j, k = 1, 2, \dots, N\} \\ {}^<U &: \{X_i; X_i < X_j = X_i R X_j; 1^<; i, j, k = 1, 2, \dots, N\} \\ 1^> &= 1/S \neq 1 = 1/R,\end{aligned}\tag{24}$$

resulting in the *Lie-admissible and Jordan-admissible mathematics*, also called *genomathematics* [9] [7] [51] [52].

The jointly Lie and Jordan admissible group of transformations of an observable $A(w)$ is given by

$$\begin{aligned}A(w) &= [\Pi_k \hat{e}^{X_k w i, >}] > A(0) < [\Pi_k e^{-i w X_k, <}] = \\ &= [\Pi_k e^{X_k R w i}] A(0) [\Pi_k e^{-i w S X_k}],\end{aligned}\tag{25}$$

where we have used the genoexponentiations $e^{X, >} = [e^{X R}] 1^>$, $e^{X, <} = {}^<1 [e^{S X}]$ [9], resulting, for small values of the parameter, in the *Heisenberg-Santilli Lie-admissible and Jordan-admissible time evolution* for an observable $A(t)$ (first introduced in the 1967 paper [6], see the 1968 paper [7] for the definition of a jointly Lie-admissible and Jordan-admissible algebra and monographs [8] [10] [12] for subsequent works)

$$\begin{aligned}i \frac{dA}{dt} &= (A, H) = A < H - H > A = A R H - H S A = \\ &= (A T H - H T A) + (A J H + H J A) = [A, H] + \{A, H\},\end{aligned}\tag{26}$$

$$R = T + J, \quad S = T - H,$$

where the totally antisymmetric brackets $[A, H]$ verify the Lie algebra axioms while the totally symmetric brackets $\{A, H\}$ verify the axioms of Jordan algebras, by therefore illustrating the joint Lie and Jordan-admissible character of the main time evolution of hadronic mechanics [6] [7] [8] [10].

In fact, time evolution (26) shows on algebraic grounds that reversible 20th century Lie theories can be extended to represent irreversibility by adding Jordan brackets to Lie brackets in a way reminiscent of supersymmetric theories [61] [62].

On analytic grounds, Santilli's Lie-admissible time evolution (26) shows that irreversibility originates from the forgotten external terms F of Lagrange's and Hamilton's analytic equations, as illustrated by the realization generally used in applications

$$R = 1, \quad S = 1 - F/H, \quad (27)$$

$$i \frac{dA}{dt} = (A, H) = ARH - HSA = [A, H] + AF,$$

which is the operator counterpart, first proposed in paper [55], of the classical, Lie-admissible time evolution of an observable for Hamilton's equations with external terms, whose study was initiated in the 1978 Harvard's memoir [51] and studied in details via Birkhoff-admissible equations in monograph [8] and subsequent works on irreversible processes.

Alternatively, we can say that Jordan algebras provide an operator representation of Lagrange's and Hamilton's *non-conservative* external terms, as illustrated by the *time rate of variation of the energy* of Eqs. (26) for $R = 1$, $S = 1 - F/H$

$$i \frac{dH}{dt} = (H, H) = H(R - S)H = HF, \quad (28)$$

by therefore fulfilling Jordan's dream that his symmetric algebras may, one day, find applications in physics.

We finally mention the Schrödinger- Santilli genoequations

$$\begin{aligned} \langle \psi | < H = \langle \psi | RH = \langle \psi | < E, \\ H > |\psi^> \rangle = HS|\psi^> \rangle = E^> |\psi^> \rangle, \end{aligned} \quad (29)$$

in which irreversibility is assured for $< E \neq E^>$.

All remaining aspects of Lie-isotopic formulations, including the representation of the non-potential origin of entanglements (19), are valid for Lie- and Jordan-admissible entanglements when all their isoproducts are restricted to the right. We shall therefore define our central notion of *organic entanglements*, also called *hadronic entanglements*, as being the extension of Lie-isotopic entanglements (19) with all products being ordered to the right and the forward Santillian being explicitly dependent on time.

Let us note that, since the abstract algebra B with elements $a, b, \dots$ and product $a \star b = aRb - bSa$ is Lie-admissible, i.e., its attached antisymmetric algebra B^-

with product $[a, b] = a \star b - b \star a$ is Lie, it seems natural to assume the algebra B as the universal enveloping *non-associative* algebra of irreversible entanglements.

It is important to note that the 1981 paper [50] selected instead for the axiomatization of time irreversibility the universal enveloping algebra $\langle U \times U \rangle$ in which each branch is isoassociative. This is due to the fact that non-associative enveloping algebras have serious mathematical and physical shortcomings, such as the impossibility to formulate the Poincaré-Birkoff-Witt theorem for a non-associative envelope with consequential impossibility of defining a unique and unambiguous transition from algebras to groups, consequential loss of symmetries and relativities and other shortcomings [63] [64].

2.5. No visible energy in entanglements.

The most mysterious, and therefore, most intriguing aspect of physical, chemical or biological entanglements is that their action occurs without any visible use of energy. We are referring to the case of two electrons of Sect. 2.1 that were initially bonded together and then separated. When the first electron is subjected to a 180 degree spin flit (following the supply of the needed energy), the second far away electron experiences an instantaneous 180 degree spin flip without any visible use of energy.

This intriguing feature was first identified in Sect. 5, p. 819 on of the 1978 memoir [65], studied in detail specifically for valence electrons in Chap. 4, p. 168 on of monograph [11], upgraded in the 2020 paper [66] and can be outlined as follows.

The electron pair valence bond with relative coordinate r can be represented in quantum mechanics by the Schrödinger equation (for $\hbar = 1$)

$$\left[\frac{1}{m_e} p \times p + \frac{e^2}{r} \right] |\psi(r)\rangle = E |\psi(r)\rangle, \quad (30)$$

where the positive sign $+$ of the Coulomb potential $V = +\frac{e^2}{r}$ represents *repulsion*, thus being in gross disagreement with the visual, let alone experimental evidence on the *attraction* in valence pair bonds.

Hadronic mechanics has achieved the numerically exact and time invariant representation of *all* characteristics of valence electron bonds, resulting in a hadronic state called *isoelectronium* [11], via the following simple Santillian

$$S = e^{-V_h/V_c}, \quad (31)$$

exhibiting the Hulten potential (because strongly attractive at short distances)

$$V_h = W \frac{e^{-br}}{(1 - e^{-br})}, \quad (32)$$

where $b^{-1} = 10^{-11}$ cm represents the charge radius of the isoelectronium.

Under value (31), the Schrödinger-Santilli isoequation of the isoelectronium is given by

$$\begin{aligned} & [\frac{1}{m_e} \hat{p} \hat{\times} \hat{p} + V_c] (1 - \frac{V_h}{V_c}) |\hat{\psi}(\hat{r})\rangle = \\ & = [\frac{1}{m_e} \hat{p} \hat{\times} \hat{p} + V_c - V_h] |\hat{\psi}(\hat{r})\rangle = E |\hat{\psi}(\hat{r})\rangle. \end{aligned} \quad (33)$$

Recall that the Hulten potential behaves like the Coulomb potential at small distances, by therefore absorbing the latter irrespective of whether it is attractive or repulsive due to its strength. Therefore, Eq. (33) is well approximated by the reduced form

$$[\frac{1}{m_e} \hat{p} \hat{\times} \hat{p} - V_h] |\hat{\psi}(\hat{r})\rangle = E |\hat{\psi}(\hat{r})\rangle. \quad (34)$$

whose energy spectrum was derived in details in Refs. [?] [11] [66], resulting in the sole value for $n = 1$ (see, e.g., Eqs. (4.15) and (4.17), p. 171 of [11])

$$E = K(\frac{1}{n} - n)^2, = 0, \quad n = 1, \quad (35)$$

(where K is a positive isorenormalization factor) confirming that, *contact non-potential/NSA interactions caused by the overlapping of wave packets provide no contribution to binding energies of entangled particles*, as expected from their very definition [5], and all binding energies are entirely characterized by conventional potential interactions.

This important property has been confirmed by all applications of hadronic mechanics to bound states of extended particles with potential and non-potential interactions, such as electron valence bonds [11], stable nuclei [45]-[47], structure models of elementary particles with detectable constituents [66] and other models. In all cases, the deep entanglement of the wave packet of particles in singled (triplet) coupling resulted to be strongly attractive (repulsive).

In Sect. 2.3 we indicated that a possible mechanism of particle entanglements may be the tendency by synchronized frequencies of wave packets overlapping to remain synchronized, with the understanding that said mechanism and the origin of the related energy are basically unknown at this writing.

Despite that, the lack of visible energy by entanglements may have significant, yet unexplored applications, such as the preference of the *EPR computers* based on entanglements [16] over quantum computers that do not represent entanglements (Sect.2.2), a possible explanation of extremely long bird flights without supplementary food, and other possibilities here left to the interested colleague.

We should indicate that a deeper understanding of the transition from a conventional Coulomb repulsive behavior of electron pairs at large relative distances to their strongly attractive behavior under condition of essentially total entanglement of their wave packets, may imply a generalization of the 20th century notion

of particle (as a unitary irreducible representation of the spinorial covering of the Poincaré symmetry) to the *isoparticles* of hadronic mechanics to characterize an expected mutation of the very structure of the elementary charge [67].

3 Apparent examples of hadronic entanglements

3.1. Foreword.

In this section we review applications in biology of quantum entanglements and reexamine them in terms of hadronic entanglements in view of the insufficiencies of the former reviewed in Sect. 2.2. We then present apparent new application in biology of hadronic entanglements.

3.2. Entanglement in quantum biology.

The ability to sense magnetic fields is common to many animals. This ability can be very useful in nature, especially in migratory species. During research on the perception of magnetic field by robin (*Erithacus rubecola*), the Wiltscho couple discovered that these birds do not perceive the direction of the magnetic field but are aware of its inclination [68]. This opened up several questions about the mechanisms of their sense for magnetic fields, since it behaved in a clearly different way from a normal compass.

Entanglement is currently considered to play a crucial role in the functioning of the robin's sense. According to the hypothesis put forward by Thorsten Ritz and Klaus Schulten, the detection of the magnetic field is carried out thanks to the cryptochromes, proteins present in the eye.

The cryptochrome contains a molecule of FAD with a pair of electrons in entangled state. The hypothesis predicts that when the cryptochrome is hit by photons, loses an entangled electron, and generates a pair of radicals in the state of triplet or singlet. The probability of generating the triplet or singlet has a value dependent on the inclination of the magnetic field. The quantities of radicals in the two different states would then influence the successive reactions, allowing according to mechanisms still unknown, the detection of the inclination of the magnetic field by the robin [69].

3.3. Mother-child information transfer.

Quantum correlation unites all the molecules of a living organism besides them being distant components of a living being since all organisms come from a single cell in the first stage of their formation.

Extending the reasoning, entanglement should relate not only all parts of a living organism but also its descendants.

Since there are cases of transmission of information from mother to child

through unknown pathways, we can consider the possibility that entanglement may play a role in the exchange of information between biological organisms.

The case of a mother who has had a blind child is highlighted. Even if the child cannot see, an experiment has shown that he can acquire visual information from the mother.

The experiment consisted simply in showing letters of the English alphabet or numbers to the two subjects, in two laboratories about 10 km away to isolate the two individuals from any form of communication. The son obviously could not see them and if he tried to guess he could rarely give the right answer, in line with what you would expect from statistical calculations (about 1 out of 26). However, the boy could guess the symbols that were shown to his mother with a greater precision than one would expect from pure chance.

The boy hit 20 numbers out of 58 on the first try and 19 out of 58 on the second. Statistically very significant values, having the boy guessed 34.3% and 32.7% of the times against a theoretical probability of 10%.

During the latter test, the result was even more astonishing: on two attempts with 45 letters, the boy guessed 17 and 12 times (37.8% and 26.2% respectively). A similar result obtained randomly occurs only 1 time out of 10^6 [70].

This case suggests that in a situation of acute need, together with the presence of emotional bond and desire for mutual help, there may be transmission of information, albeit not 100% accurate, from mother to child by apparently telepathic means. Rather than invoking supernatural causes, we suggest entanglement as a possible explanation.

3.4. Correlation between mothers and children during the lactation period.

Another phenomenon that suggests a correlation between mothers and children is lactation. Kary Barber's research suggests that breastfeeding stimulation is influenced by information transfer between mother and child, although again communication is not 100% accurate.

The study involved 19 women who were responsible for keeping a diary of the times when milk was lost, especially during periods when they were away from their baby.

At the same time, those who took care of the child wrote in a second diary the periods when the infant showed signs of discomfort, hunger, or crying.

The results of 10 women were excluded from the experiment because they did not report the data correctly or they never left the baby long enough.

In the remaining nine participants, a correlation was found between child discomfort symptoms and milk loss, which manifested at very close intervals despite the distance that prevented mothers from becoming aware of their child's status through known sensory channels. Of a total of 88 milk losses, 35 occurred during the distress of children. Statistically, in the absence of correlation, there should

have been only 9.

The phenomenon is therefore statistically significant, although imprecise. However, it should be noted that some of the missing correlations could find alternative justifications. 17 of these were associated with a single subject who had the effect during lunch time as a physiological habit. There is also a suspicion that there was an oversight in recording the crying of children in 11 cases [71].

3.5. Entanglement and oncological implications.

If entanglement links the different parts of a common derivation organism, this must be equally true for tumors which usually stem from a single cell. Thus, cancer cells could also be entangled together.

The phenomenon known as the "abscopal effect" is a possible example of a nonlocal effect occurring in different cancer cells. The effect is caused by radiation therapy and consists in weakening of the tumor not only at the site undergoing radiation therapy, but also in cancerous tissues located in organs far from the irradiated area.

It is suggested here, apparently for the first time, that the abscopal effect may be caused by entanglement. Unlike in the cases described above, the effect does not occur in 100% of the cancers undergoing radiation therapy, but in a small percentage of them. In one study, the abscopal effect was observed in 52% of patients [?].

Of course this is not the only possible explanation for the abscopal effect, but a possibility that might be worth investigating.

4 Apparent initiation of hadronic medicine

4.1. Foreword.

The introduction of hadronic mechanics and hadronic entanglements provides a novel approach to understanding complex biological structures at the subatomic level. This framework enables the modeling of biological systems characterized by irreversible, time-dependent interactions, moving beyond the constraints of traditional quantum mechanics, which relies on reversible interactions between point particles. By using the Lie-admissible structure of hadronic mechanics, it is possible to represent extended components such as cells and tissues, offering a theoretical foundation for applications in tissue regeneration and epigenetic reprogramming [2].

4.2. Hadronic Mechanics in Biological Systems.

Hadronic mechanics, with its Lie-admissible structure, overcomes the limitations of traditional quantum mechanics in representing complex biological systems.

Rather than describing cellular components as point particles, hadronic entanglements treat these elements as extended wave packets, allowing for a continuous, dynamic representation. This approach is essential for accurately describing the complex biophysical interactions that characterize cellular tissues and processes of growth and regeneration [2] [73].

Lie-admissible Hv-hyperstructures, which are based on this Lie-admissible framework, map multidimensional cellular interactions and are particularly relevant for depicting intercellular communication.

Thanks to this advanced modeling, Hv-hyperstructures can represent processes that extend beyond simple electrostatic or mechanical interactions, integrating components of dynamic entanglement specific to complex biological systems. This proves advantageous for understanding homeostasis and adaptation processes in variable cellular environments, aspects that classical quantum mechanics cannot fully capture [2] [73].

Another significant aspect of hadronic mechanics is its application in biological systems with irreversible interactions, such as those observed in cellular responses to injuries or degenerative processes. Where classical models fail to represent the progression of irreversible events, hadronic mechanics offers a framework in which cellular states can evolve continuously within a bidirectional entanglement context, allowing researchers to track cellular transitions from healthy to damaged states and vice versa during healing and regeneration processes [2] [74].

4.3. Applications in Computational Biology and Complex Systems.

The integration of hadronic entanglements with quantum computing paradigms, such as quantum annealing, has transformative potential in computational biology. Quantum annealing is particularly relevant for solving complex optimization problems in bioinformatics, such as genome assembly and protein folding, which require substantial computational power due to their high dimensionality and data volume.

4.3.1. Genome Assembly Optimization. Quantum annealing has shown promise in enhancing de novo genome assembly, a process critical for reconstructing genomes without reference sequences, essential in studying novel species and detecting large structural genomic variants. Traditional genome assembly relies on the Overlap-Layout-Consensus (OLC) algorithm, where all-against-all read comparisons must identify overlaps, a computationally intensive task. Quantum annealers, such as those from D-Wave, have demonstrated an ability to address this complexity by leveraging the Quadratic Unconstrained Binary Optimization (QUBO) model, optimizing Hamiltonian paths within the OLC framework to reconstruct the original genome structure with significantly reduced computational time [74] [76].

4.3.2. Protein Folding and Molecular Dynamics. Quantum computing offers a unique advantage in simulating protein folding, a process that determines a protein's function and is critical in many diseases. Classical approaches to protein folding struggle to manage the vast configuration space that proteins can adopt. Quantum algorithms, particularly those based on quantum annealing, enable faster exploration of stable protein configurations by examining entangled quantum states, offering insights into folding pathways and potential misfolding mechanisms that can lead to diseases [77].

4.3.3. Modeling Biological Networks. The extended reach of hadronic mechanics aids in the modeling of complex biological networks, where interactions are often irreversible and multidimensional. Hv-hyperstructures within hadronic mechanics allow for intricate mapping of cellular interactions, capturing the non-linear and time-irreversible dynamics that characterize biological processes. These interactions, described through Lie-admissible structures, support a more holistic representation of biological networks, crucial for understanding metabolic pathways, cellular signaling, and gene regulatory mechanisms [2].

4.3.4. Simulating Quantum Effects in Biomolecular Systems. Quantum coherence and entanglement within hadronic frameworks contribute to simulating quantum behaviors observed in biomolecular systems, such as enzyme catalysis and photosynthesis. These simulations allow for more accurate models of biomolecular interactions, capturing subatomic dynamics otherwise challenging for classical computational methods. As quantum technology matures, the computational models grounded in hadronic mechanics may bridge existing gaps in understanding quantum effects in biological systems [75] [77].

Solving the de novo genome assembly problem using quantum annealers and quantum-inspired (digital) annealing algorithms: (a) raw reads; (b) raw reads are transformed to the overlap-layout-consensus (OLC) graph; (c) finding the Hamiltonian path for the OLC graph is reduced to the QUBO problem; (d) the QUBO problem should be embedded to the architecture of the quantum annealer (D-Wave): for this purpose each logical variable of the the QUBO problem is assigned with several qubits of the quantum annealer; (e) and (f) the Ising problem in QUBO form can be solved using quantum annealers (D-Wave) and quantum-inspired algorithms (SimCIM), correspondingly; (g) the output is the Hamiltonian path; (h) the genome sequence is obtained as the solution [74].

In summary, the fusion of hadronic entanglements and advanced quantum computing techniques stands poised to revolutionize computational biology. By enabling rapid simulations, precise optimizations, and enhanced molecular modeling, these methodologies offer a deeper understanding of complex biological systems, paving the way for novel diagnostic tools and therapeutic applications in

regenerative medicine, cellular reprogramming, and beyond.

4.4. Implications for Tissue Regeneration and Cellular Reprogramming.

Hadronic entanglements offer unique opportunities in regenerative medicine and cellular reprogramming, providing theoretical tools to precisely control rejuvenation and tissue regeneration processes. The transient use of OSKM (Oct4, Sox2, Klf4, c-Myc) reprogramming factors enables "epigenetic rejuvenation," reducing cellular aging markers without inducing full dedifferentiation. Experiments conducted on animal models have shown that this technique can significantly improve muscle and pancreatic regeneration without increasing the oncogenic risk associated with traditional reprogramming methods [73] [76].

4.4.1. Cellular Rejuvenation and Anti-Aging. Hadronic entanglements make it possible to activate controlled cellular rejuvenation processes, preserving cellular identity and reducing oncogenic risks. This approach enables targeted rejuvenation without reverting cells to a pluripotent state, thereby preserving their original function. Epigenetic rejuvenation can be used to counteract aging processes and maintain tissue vitality, opening new possibilities for preventing degenerative diseases and improving quality of life [73].

4.4.2. Tissue Repair and Regeneration. Hadronic mechanics allows for precise manipulation of cellular interactions, promoting the regeneration of damaged tissues. Studies indicate that cells treated with hadronic entanglement methodologies exhibit superior tissue regeneration capabilities, as evidenced in muscle and pancreatic tissue regeneration in experimental models. This approach can be integrated into tissue regeneration strategies to enhance wound healing and reduce scar formation, proving particularly useful for degenerative diseases and the repair of complex tissue injuries [74] [?].

4.4.3. Creation of a Hadronic Algorithm for Biological Time Reversal. Another innovative application of hadronic entanglements is the development of an algorithm for biological time reversal at the cellular level. This algorithm, based on entangled states and principles of hadronic mechanics, manipulates cells' epigenetic properties, allowing them to revert to a biologically younger state. Through the Lie-admissible structure and entangled states, it is possible to modulate the cellular rejuvenation process selectively, minimizing oncogenic risks and providing greater control over cellular processes. The algorithm would find applications in regenerative and anti-aging medicine, offering potential solutions for treating degenerative diseases and extending tissue vitality [2] [73].

4.4.4. Future Prospects and Clinical Applications. The application of hadronic entanglement theory extends to targeted clinical treatments for chronic and degen-

erative conditions, leveraging control over entangled states to modulate specific cellular networks with precision. This advanced control helps reduce side effects while increasing treatment efficacy through optimal customization of therapeutic protocols.

4.4.5. Targeted Medical Treatments. Hadronic entanglements could enhance personalized treatments for complex diseases such as cancer by enabling precise modulation of affected cellular networks. The integration with advanced technologies, such as quantum annealing, could enable highly precise targeting of tumor cells, with reduced side effects and improved therapeutic effectiveness [2].

4.4.6. Advanced Algorithms in Computational Biology. Supported by hadronic entanglements, quantum annealing enables advanced simulations of complex biological phenomena such as protein folding and RNA- DNA interaction, accelerating progress in precision medicine and the design of personalized therapies based on specific genetic structures. This leads to a better understanding of genetic variants and structural mutations, paving the way for targeted treatments for complex genetic disorders [75] [77].

4.4.7. Advanced Diagnostics. Hadronic entanglements have the potential to revolutionize early diagnostics, detecting variations in cellular entangled states to identify diseases at an initial stage. The ability to monitor subatomic changes over time opens the possibility of innovative diagnostic devices capable of identifying diseases at the molecular level with unprecedented accuracy. This approach would improve the precision of early treatments, enhancing therapeutic effectiveness when the disease is most manageable [3]. In conclusion, hadronic mechanics and entanglement theory represent a paradigm shift in biology and computational medicine. Clinical applications range from tissue regeneration to anti-aging medicine, advanced medical treatments, early diagnostics, and algorithms designed to simulate and understand complex biological phenomena. Looking to the future, the opportunity to develop therapeutic protocols based on hadronic algorithms and entanglement techniques could usher in a new era in regenerative medicine and personalized therapy. With further research, these technologies may revolutionize the approach to biology and disease, enabling targeted interventions at the molecular scale and significant improvements in life quality and longevity.

5 Concluding remarks

In this paper we have reviewed:

5.1) Einstein's criticisms of quantum entanglements by showing that particles entangled at large mutual distances can only be represented by quantum mechan-

ics as being free.

5.2) The time reversible Lie-isotopic particle entanglements of hadronic mechanics at large mutual distance due to non-linear, non-local and non-potential interactions in the overlapping of the wave packets of the constituents.

5.3) The implications of Lie-isotopic entanglements for the explicit and concrete representation of Bohm's hidden variables with ensuing by-passing of Bell's inequalities and progressive recovering of Einstein's determinism for biological entities.

In this paper we have then introduced, apparently for the first time:

5.4) An axiomatic formulation of the two directions of time via an isobimodular structure.

5.5) A smooth connection between hadronic uncertainties at very small distances and full determinism at classical distances.

5.6) The Lie and Jordan-admissible irreversible biological entanglements verifying conditions 1.1, 1.2, 1.3.

5.7) The lack of visible energy by the mechanism of entanglement with intriguing open applications.

5.8) A possible quantitative representation via the Lie and Jordan-admissible irreversible entanglements of the behavior by biological entities beyond our sensory perception.

5.9) Possible diagnostic and curative values of biological entanglements.

In conclusion, the representation by hadronic mechanics of non-linear, non-local and non-potential interactions between the wave packets of the constituents of biological entities appears to initiate a new quantitative branch of medicine submitted in this paper under the name of *hadronic medicine*.

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Comparison of aggregation methods used in online reviews: a critical analysis

Maria Grazia Olivieri*
Elisa Fiorenza†

Abstract

With digitalization, online reviews have become a crucial component of consumer decisions and are an important source of feedback on products and services. Users can make informed choices using online review systems such as e-commerce platforms, social media, and others. However, the collection and analysis of these reviews raises a number of questions regarding reliability, representativeness and accuracy. Since they directly influence users' choices, the methods used to aggregate review scores are extremely important. In this article, we explore the most common aggregation methods for rating online reviews on the Amazon platform, with a particular focus on the arithmetic mean. Although these methods are easy to implement, they do not always accurately reflect the overall quality of a product. We then critically analyze how more sophisticated approaches can minimize some of the limitations of the mean, such as the so-called recency bias; propose more robust solutions and alternative approaches that can provide a more accurate representation of the overall rating, improving the quality of aggregated ratings.

Keywords: aggregation methods; arithmetic mean; online reviews; alternative methods; recency bias; weighting.

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* Ecampus University, Novedrate, Italy; mariagrazia.olivieri@uniecampus.it.

† Universitas Mercatorum, Rome, Italy; elisa.fiorenza@unimercatorum.it

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1. Introduction

In the e-commerce and service industries, online reviews have become an important factor influencing customers' purchasing behavior and business strategies, and thus their purchasing decisions [9]. With millions of reviews shared every day, review sites offer a seemingly comprehensive overview of the products and services they offer. Users rely on these reviews to make purchasing decisions, while recommendation systems use review aggregations to recommend products. The aggregation methods that are used to calculate the overall rating of a service or product online do not always guarantee the reliability and usefulness of the aggregated reviews. Platforms, such as Amazon and the like, use simple statistical methods as a review aggregation system, which they then integrate with more specific algorithms. Fundamental to user trust is the ability to correctly combine reviews into a single score. In order to aggregate individual ratings into a complete one, which reflects the quality of the service or product, online platforms collect thousands of ratings; this requires more effective and fair tools and methods [10]. Among them, the arithmetic mean is most often used because it is considered easy to implement and because it is believed to provide a fair representation of users' opinions; however, it has several critical problems. Among the main problems are its sensitivity to extreme values, the arithmetic mean can be significantly affected by extremely positive or negative reviews, which do not necessarily reflect the average consumer experience [30]; bias in skewed distributions, in cases of highly skewed review distributions (e.g., if most reviews are positive, but there are some very negative reviews), the arithmetic mean may not accurately represent the quality perceived by the average consumer; furthermore, it ignores variability, that is, the arithmetic mean ignores the dispersion of ratings, which can be an important indicator of product or service quality [19]. This paper provides a critical analysis of the arithmetic mean, and proposes alternative methods that can provide more robust and representative approaches to address these limitations. It is very important that review platforms adopt more sophisticated aggregation techniques to improve the quality of information provided to consumers and ensure more informed purchasing decisions. User credibility, quality of review content, sentiment expressed, and consistency between reviews are some of the qualitative factors that could influence the final rating that these conventional methods tend to ignore. Recency bias is also a major problem with these systems [16]. When more recent reviews, which often represent temporary changes, updates, or trends, have an excessive impact on the overall review aggregation, recency bias occurs. This phenomenon can lead to a distortion of a product's rating, giving an inaccurate image of its real value in the long run. Review aggregation is a complex process that uses different statistical and machine learning techniques to summarize the opinions expressed by users. In this paper, we will examine how recency bias affects these methodologies, discuss its implications and propose solutions to reduce its effect [11]. The aim is to provide a comprehensive and informed picture of how online review platforms could evolve to better respond to users' needs, contributing to improve the quality of information available in the decision-making process.

The paper is structured in 4 Sections: in Section 1 the Introduction, in Section 2 we present a brief literature review on the different aggregation methods that online platforms use for review evaluation; in Section 3 we analyze the basic arithmetic mean method in

Amazon online reviews, its critical issues and proposing alternative aggregation methods. Furthermore, recency bias and its manifestation in online reviews are described, then its influence on the different aggregation methods proposed; in Section 4 we present the conclusions.

2. Literature review

In the literature, several articles have discussed the use of different online review aggregation techniques, from the traditional arithmetic mean to the use of the median, probabilistic models and more sophisticated advanced approaches such as Bayesian models; in order to improve the accuracy of aggregated reviews, reduce bias and provide a more representative summary of users' experiences. Several researchers then provide an in-depth analysis of various review aggregation methods, discussing both the limitations of traditional approaches and the advantages of alternative methods to improve the reliability and representativeness of ratings in online review sites. According to [26], the authors present a comprehensive overview of opinion analysis and sentiment analysis, considering different online review aggregation methods and analyzing the challenges in combining feedback from different sources. The paper describes the use of arithmetic mean as a traditional aggregation technique, and then analyzes more advanced techniques such as review weighting. [12] address the problem of rating score prediction in online review sites by examining the importance of the textual content of reviews. The authors propose an approach that integrates textual information with numerical ratings of reviews to improve rating prediction, suggesting that prediction errors can be reduced compared to using the arithmetic mean, or purely numerical tools, by using well-integrated textual information. [28] considers different online review aggregation techniques, among which he offers a comprehensive overview of sentiment analysis and opinion mining. He analyzes the tone and emotion behind user reviews, combining these techniques with numerical aggregation methods in order to obtain more accurate and representative ratings of products or services. [5] study the impact that online reviews have on product prices and competition among major online retailers. The authors, in order to reduce bias, analyze the use of aggregation systems, proposing more reliable methods, capable of influencing customers' opinions and actions. [22] in their study address the problem of incorrect reviews, demonstrating, through a method that automatically detects "opinion spam", how aggregation techniques can be used to find and delete biased reviews; influencing the reliability of review aggregation systems. [27] present a method based on sentiment analysis technique and intuitionistic fuzzy set theory to rank alternative products through online reviews. In the method, the online reviews of alternative products regarding the features are crawled using crawler software. Again, [14] propose two mechanisms for classifying online product reviews: one classifies reviews based on their expected usefulness, consumer orientation, and the other, which involves a producer orientation, classifies reviews based on their expected effect on sales. These tools have the ability to combine econometric analysis with text mining techniques in general, with subjectivity analysis in particular. [8] study different aggregation techniques in e-commerce contexts and the economic role of online reviews. The authors highlight how

the distribution of scores and the reputation of users can influence the aggregation system. The paper highlights in particular the fact that trust in reviews depends both on the average quality of scores and on the historical behavior of users who contribute to reviews. The overall reliability of ratings can be improved by using more advanced aggregation techniques, such as weighting reviews by user reputation. In fact, traditional methods, such as simple arithmetic mean, are not sufficient to address the complexities caused by recency bias, low-quality reviews, and differences in opinion. In [23], the author focuses on the representativeness of online review distributions to study how extreme bias and conformity affect it; and to determine whether the representativeness is altered by online review requests. The success of the Internet economy depends on representative consumer reviews online. [29] in his study he considers different scenarios, describing their properties. Specifically, the author considers a type of bias that occurs in online product reviews in the sequence in which these reviews are written. [13] in their study demonstrate that dimensional review bias, which arises from consumers' heterogeneity and their multidimensional product preferences and experiences, weakens information transfer among consumers. The authors use a novel text mining approach to identify and quantify two types of dimensional distortion from text reviews: dimensional rating bias and dimensional preference bias. Furthermore, they add a quantitative approach to reduce dimensional rating bias. They examined the effectiveness and application of bias and de-bias techniques in unidimensional and multidimensional rating systems.

3. Critical analysis of the aggregation methods

Online review aggregation is a critical activity for online platforms such as Amazon, TripAdvisor, Yelp, and other e-commerce and travel sites, which collect millions of user opinions. The ability to correctly aggregate reviews into a single score (e.g., the average rating of a product or service) is essential to user trust in the platforms themselves [17]; Amazon is one of the largest and most influential online review platforms in the world. Users create a large database of reviews by writing reviews of the products they purchase; these reviews help other customers in their purchasing decisions, making them more informed, because they influence the ranking of the products themselves and their visibility on the platform. However, to be reliable and transparent, reviews depend largely on how individual scores are combined into an overall rating. Amazon currently uses the arithmetic mean as a basic method to aggregate review scores; it is a simple tool to determine the average score of star ratings left by users. It has several limitations that risk compromising the accuracy and representativeness of the final rating. The aim of this article is to analyze the use of the arithmetic mean as an aggregation method for evaluating online reviews, examine its limitations; and then compare it with other alternative aggregation methods that could improve the accuracy and reliability of ratings. Median, weighted mean, sentiment analysis, machine learning offer promising solutions to overcome the limitations of traditional arithmetic method, improve the representativeness of ratings, and reduce the bias effects of extreme ratings [4]. The

implementation of more sophisticated and transparent approaches could not only improve consumer trust, but also promote a fairer and more reliable review platform.

The traditional methods of aggregation

One of the most common methods of aggregating reviews on platforms like Amazon is the arithmetic mean. This method uses a star rating system (for example, 1 to 5 stars) to determine the average score of each review a product has received. A numerical summary of the overall quality of a product can be obtained using the arithmetic mean, which helps users make better choices. A vacuum cleaner, sold on Amazon, has received numerous reviews that include the following star ratings (Table 1):

	Stars				
	Stars (st_i)				
	5*	4*	3*	2*	1*
Reviews (r_i)	50	30	10	5	5

Table 1. 100 reviews of an Amazon product

The arithmetic mean of the review score, which we indicate with $\bar{x}$, can be calculated with the following formula where st_i indicates the stars and r_i the reviews obtained:

$$\bar{x} = \frac{\sum_{i=1}^n (st_i \cdot r_i)}{\sum_{i=1}^n (r_i)} \quad (1)$$

$$\bar{x} = \frac{(5 \cdot 50) + (4 \cdot 30) + (3 \cdot 10) + (2 \cdot 5) + (1 \cdot 5)}{50 + 30 + 10 + 5 + 5} = \frac{415}{100} = 4.15$$

In this case, the average product rating $\bar{x}$ is 4.15 stars.

The arithmetic mean has obvious advantages: it is a simple method to calculate and implement, which provides an immediate summary of reviews; the average rating is easily understandable for users and gives them a quick indication of the overall quality of a product [25]. If the reviews are far apart and appear to be conflicting, using the average as an aggregation method may not be appropriate to express the reality of user opinion. If a product has many extremely positive reviews and only a few 1-star reviews, the average may not accurately represent the quality of the product, creating a misleading impression. If a product has 92 5-stars reviews and 6 1-star reviews, the average will be 4.75 (approximate), which may seem very positive, but may not reflect the fact that some people have very negative reviews. Again, the mean does not take into account the content of the reviews, only the numerical results. For example, a 3-stars review may be very thorough and point out small flaws in the product, while a 5-stars review may be very superficial. The mean cannot distinguish between a rating that describes a product as "good but with room for improvement" and a rating that describes a product as "excellent." Finally, it does not capture sentiment, which means that the arithmetic mean

cannot distinguish between positive and negative reviews that talk about different aspects of the product, such as quality or customer service. It does not indicate which aspects are praised or criticized. When using the average as an aggregation tool for online reviews, all reviews, regardless of when they were recorded, contribute equally to the final score. Recency bias can distort the perception of product quality, especially for customers who only look at the most recent reviews. A product on Amazon has the following reviews: 100 past reviews, many of which were very positive, with an average rating of 4.8 stars; ten additional reviews were written for the product in the last few weeks, with an average rating of 2-stars, indicating emerging quality issues. If someone looks only at the most recent reviews, they might think the product has a very low rating, even though most of the reviews have been positive. However, if the arithmetic mean does not take these recent changes into account, the average score may still be high, representing an overall rating that does not accurately reflect recent issues.

$$\text{before recent reviews} = \frac{(4.8 \cdot 100)}{100} = 4.8$$

$$\text{after recent reviews} = \frac{(4.8 \cdot 100) + (2 \cdot 10)}{110} = 4.55$$

Users typically rely more on recent reviews in their purchasing decisions because they believe they are more reliable than older reviews. It goes without saying that if a product has been reviewed negatively in the recent period, the user may have a negative impression, even if the rating derived from the arithmetic mean is high, due to older positive reviews. Therefore, recency bias significantly influences perceptions of online reviews when scores are aggregated using the arithmetic mean. To address this issue, platforms such as Amazon are working to implement systems that balance older and more recent reviews, giving customers a more accurate impression of the quality of the product. Despite its limitations, the arithmetic mean remains a simple and useful tool for having a general overview of product reviews; combining it with other aggregation methods would lead to a more accurate and complete analysis.

The weighted mean μ is a method certainly more complex than the arithmetic mean and is used when you want to give greater weight to certain reviews or categories of reviews. Unlike the arithmetic mean, where each value has equal weight, the weighted average multiplies each value (such as a review score) by a "weight" that changes its importance. In online reviews on Amazon or other e-commerce platforms, the weighted average is used to assign different weights to reviews based on factors such as:

- date of publication (recency bias);
- user reliability (for example, whether a review comes from a verified user or a user who actually purchased the product);
- quality of the review (detailed reviews, reviews with photos, reviews that receive approval from other users as "helpful");
- rating by feature categories (e.g. quality, durability, ease of use).

To calculate it, given n ratings x_i , which represent the stars received, they are multiplied by a specific weight w_i (which can be assigned based on different factors) and then the results are added. The total is then divided by the sum of the weights w_i :

$$\mu = \frac{\sum_{i=1}^n (x_i \cdot w_i)}{\sum_{i=1}^n (w_i)} \quad (2)$$

It is specified that Amazon, in assigning weights to the reviews useful for calculating the weighted average, uses several combined factors to decide how much a review "counts". The main criteria with which Amazon assigns weights: verified purchase; review date; helpfulness voted by other users; reviewer reliability; review content.

Let us now consider a weighted approach in which more importance is given to the most recent reviews; assigning them an increasing weight and using a weighting system based on the publication date. Specifically, the most recent review (review 10) is given the greatest weight, and decreasing weights for reviews that are more distant in time (Table 2).

<i>Reviews</i>	<i>Time</i>	<i>Stars</i>	<i>Weights</i>
Review 1	1 december	2 stars	0.5
Review 2	3 december	3 stars	0.9
Review 3	3 december	1 star	1.1
Review 4	6 december	2 stars	1.4
Review 5	8 december	3 stars	1.8
Review 6	9 december	2 stars	2
Review 7	10 december	3 stars	2.4
Review 8	11 december	5 stars	2.7
Review 9	13 december	5 stars	3
Review 10	14 december	5 stars	3.4

Table 2. Amazon reviews in two weeks considering relative weights

Let's calculate the weighted average μ :

$$\begin{aligned} \mu &= \frac{(2 \cdot 0.5) + (3 \cdot 0.9) + (1 \cdot 1.1) + (2 \cdot 1.4) + (3 \cdot 1.8) + (2 \cdot 2) + (3 \cdot 2.4) + (5 \cdot 2.7) + (5 \cdot 3) + (5 \cdot 3.4)}{0.5 + 0.9 + 1.1 + 1.4 + 1.8 + 2 + 2.4 + 2.7 + 3 + 3.4} \\ &= 3.63 \end{aligned}$$

The weighted average turns out to be about 3.63, while the arithmetic mean is 3.1. As for the benefits of weighted average, this aggregation method allows you to give more weight to higher quality reviews, increasing the accuracy of the product rating; it can help give more weight to the latest reviews, which may indicate improvements or changes to the product; it allows for the application of custom weights for a variety of factors, such as user verification, review quality, date, etc., improving the accuracy of the aggregation.

But it also has some critical issues: determining the right weights can be difficult and requires subjective evaluation; there may be a risk of manipulating the results, for example, by giving too much weight to positive reviews and reducing the importance of negative reviews if the weights are not determined correctly. Finally, the quality of the final result strongly depends on the quality of the assigned weights; if these are not chosen carefully, the weighted average may not accurately reflect the overall experiences of users [33].

If the weight assigned to recent reviews is greater than that assigned to older ones, the final score will suffer from recency bias, that is, the product may seem better or worse than it actually is based on past reviews.

A product received 10 initial very positive reviews (average of 5-stars) and then, in the last few days, received 5 very negative reviews (average of 1-star). If you give more weight to recent reviews in the weighted average, the final rating of the product will be influenced mainly by the more negative reviews, even though most of the past reviews were positive.

- Initial reviews (average 5-stars rating): 10 reviews, weight 1
- Recent reviews (average 1-star rating): 5 reviews, weight 2 (given the greater weight for recent reviews)

We will have:

$$\mu = \frac{(5 \cdot 10 \cdot 1) + (1 \cdot 5 \cdot 2)}{(10 \cdot 1) + (5 \cdot 2)} = 3$$

Although most of the reviews are positive, the final score of the product is heavily influenced by the most recent reviews, which are all negative. Recency bias, when more recent reviews are given very high weights, can have a significant impact on the weighted average of reviews; in this case, it leads to a lowering of the final score, giving a negative impression of the product. Platforms like Amazon, in order to provide a more accurate representation of the quality of the product, try to balance the weight of reviews based on a number of factors, but there is always the possibility that more recent reviews influence the final rating too much.

Let's always consider the same Amazon product, let's see what happens if we use the median as an aggregation method. The median is another method of aggregating reviews that can be used as an alternative to the arithmetic mean or weighted mean. Unlike the mean, which treats all review scores equally, the median focuses on the central score of a data set, that is, the value that separates the lower half from the upper half of the sample. In the context of online reviews, the median is calculated by sorting all reviews in ascending or descending order and taking the value that is in the center of the distribution [1]. If there is an even number of data points, the median is the average of the two middle values:

1. Sort review scores in ascending order
[1, 2, 2, 2, 3, 3, 3, 5, 5, 5]
2. The median is the average of the two central values being the number of even reviews (10 reviews),

$$Med = 3$$

In this case, recency bias does not significantly impact the median; because the median depends on the relative position of the scores and not on the magnitude of the most recent scores. The most recent reviews are all positive (5 points), but the median remains the same. If there were many more high reviews, the median could still remain stable unless the total number of reviews changes the center position. In other words, the median is less sensitive to changes in review value than the arithmetic mean, which is directly affected by extreme scores (such as very high recent reviews). When you want to avoid biases due to particularly positive or negative recent reviews, the median can be a useful aggregation method. It has several advantages over the arithmetic mean. It is less sensitive to extreme values, or outliers, in fact very high or very low ratings do not influence the median. Additionally, the median provides a more realistic view of what "most" users think of the product. If a product has many negative reviews but also many extremely positive reviews, the mean may not accurately reflect the average user experience. In such cases, the median may be a more representative measure of the "typical" user experience. However, it also has some issues; it doesn't reflect the overall distribution, meaning it doesn't provide information about the number of reviews in each rating range (e.g., 1-star or 5-stars). The median is unable to show that there are a sizable number of unhappy consumers when a product has a large number of 1-star ratings but few 5-stars evaluations. It also disregards the "strength" of the reviews; for example, two 5-stars reviews and one 1-star review may provide a 5-stars median, but it won't make the disparity in the scores obvious. The median is less prone to recency bias than the mean since it concentrates on the reviews' core value. To avoid bias, it is important to ensure that all reviews are adequately considered and that any weights are carefully calibrated.

Sophisticated approaches

Sentiment analysis

Sentiment analysis is a Natural Language Processing (NLP) technique that aims to determine whether a text expresses a positive, negative, or neutral sentiment. When applied to online reviews, sentiment analysis can provide a general indication of how users perceive a product or service [20]. However, recency bias (the tendency to give more weight to recent reviews than older ones) can affect the results of sentiment analysis.

Let's consider the same Amazon product, this time we take into account the sentiment expressed by consumers (Table 3). Recent reviews are much more positive than early reviews, and so recency bias could impact the overall sentiment analysis of the product.

<i>Review</i>	<i>Time</i>	<i>Content</i>	<i>Sentiment</i>
Review 1	1 december	"I wouldn't buy it again!"	Negative
Review 2	3 december	"The design is nice, but the display quality isn't the best."	Neutral
Review 3	3 december	"I've been having problems with the	Negative

		<i>camera, I can't take decent pictures."</i>	
Review 4	6 december	<i>"The phone is very slow, the battery drains quickly."</i>	Negative
Review 5	8 december	<i>"Audio is great, but battery life could be better."</i>	Neutral
Review 6	9 december	<i>"I don't like the operating system, too complicated."</i>	Negative
Review 7	10 december	<i>"Overall satisfactory product, but there are better!"</i>	Neutral
Review 8	11 december	<i>"This phone is awesome! All day battery life, beautiful screen!"</i>	Positive
Review 9	13 december	<i>"Very satisfied, great display and long lasting battery."</i>	Positive
Review 10	14 december	<i>"Awesome phone, amazing speed, highly recommended!"</i>	Positive

Table 3. Amazon reviews considering the sentiment

The most recent reviews (last 3) are all very positive, while the oldest reviews (first 7) are mostly negative or neutral. Now let's see how the sentiment analysis might change depending on whether we consider only the most recent reviews or all reviews.

Without considering recency bias

Suppose we apply a simple sentiment analysis to all reviews (without weighting them by date) using a sentiment analysis model that classifies reviews as positive, negative, or neutral.

	Sentiment		
	Negative	Neutral	Positive
Review	4	3	3

Since there are more negative reviews (4) than positive reviews (3), the overall sentiment will be negative, even though there are many recent positive reviews. However, the influence of older reviews may diminish the impact of recent positive reviews. Recency bias has not been taken into account, and so the final result is still affected by many initial reviews that are negative. The overall rating may not accurately reflect current reality, especially if the product or service has recently received a series of very positive reviews; the simple sentiment average is also influenced by older negative reviews.

With recency bias

Now consider the impact of recency bias. Suppose we decide to weight the most recent reviews so that they have a higher weight than the older reviews (Table 4). A simple technique would be to assign increasing weight to the most recent reviews (e.g., the highest weight goes to the latest review, the second highest weight goes to the second-to-last review, and so on).

<i>Review</i>	<i>Weights (w_i)</i>
Review 1	0.5
Review 2	0.9
Review 3	1.1
Review 4	1.4
Review 5	1.8
Review 6	2
Review 7	2.4
Review 8	2.7
Review 9	3
Review 10	3.4

Table 4. Amazon reviews by assigning a weight

Each positive, negative or neutral review is then weighted according to the associated weight. The weighted average of sentiment s is calculated, denoted by μ_s :

$$\mu_s = \frac{\sum_{i=1}^n (s \cdot w_i)}{\sum_{i=1}^n (w_i)} \quad (3)$$

s	<i>Negative</i>	<i>Neutral</i>	<i>Positive</i>
	-1	0	1

μ_s

$$= \frac{(-1 \cdot 0.5) + (0 \cdot 0.9) + (-1 \cdot 1.1) + (-1 \cdot 1.4) + (0 \cdot 1.8) + (-1 \cdot 2) + (0 \cdot 2.4) + (1 \cdot 2.7) + (1 \cdot 3) + (1 \cdot 3.4)}{0.5 + 0.9 + 1.1 + 1.4 + 1.8 + 2 + 2.4 + 2.7 + 3 + 3.4}$$

$$= 0.21$$

The weighted sentiment μ_s is around 0.21, which is a positive value, indicating that overall, considering the recency bias, the overall sentiment of the reviews is positive. This is a significant change from the unweighted average (which would have given a negative or neutral value), thanks to the influence of very positive recent reviews. By applying recency bias (weighting the most recent reviews), sentiment analysis can provide a more accurate assessment of current user perceptions, as more recent reviews are emphasized [2]. This approach takes into account changes in sentiment over time.

Cluster Evaluation System

Clustering is a sophisticated aggregation method that allows you to group reviews into homogeneous classes based on similar properties, such as score, review content, sentiment, or themes [15]. Clusters are formed, and an aggregate score is calculated for each group [31]; the impact of recency bias can strongly influence clustering results, especially if recent reviews are significantly more positive than older ones.

A product, such as a smartwatch, receives 10 reviews over the course of a month. The reviews are distributed such that the first 7 reviews are negative or neutral, while the last 3 reviews are very positive. The impact of recency bias can lead to a bias in clusters, causing newer (positively oriented) reviews to be treated as more relevant, while older (often negative) reviews are excluded or undervalued in the clustering process.

<i>Reviews</i>	<i>Time</i>	<i>Stars</i>	<i>Content</i>
Review 1	1 december	2 stars	"Battery life is too short."
Review 2	3 december	3 stars	"Interface is complicated to use."
Review 3	3 december	1 star	"Not satisfied, connection with phone is unstable."
Review 4	6 december	2 stars	"I don't like the operating system, too complicated."
Review 5	8 december	3 stars	"Watch is ok, but not what I expected."
Review 6	9 december	2 stars	"Display quality is poor."
Review 7	10 december	3 stars	"Design is nice, but I don't find many useful features."
Review 8	11 december	5 stars	"Great smartwatch, easy to use and very accurate."
Review 9	13 december	5 stars	"I love this smartwatch! Excellent features and beautiful design."

Review 10	14 december	5 stars	"I love it, perfect for sports and daily life!"
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Table 5. Amazon reviews for clustering

Older reviews (December 1st to December 10th) are generally negative or neutral, while newer reviews are all very positive.

Review clustering without considering recency bias

Reviews can be classified into two clusters with a clustering method such as K-means: one for positive ratings and one for negative ratings. The clustering is based only on the ratings and content of the reviews, without considering the period in which they were written. Clustering process:

1. Rating features: Each review is visualized as a point in the feature space, where the rating and sentiments (positive, negative, or neutral) are the main features.
2. Application of K-means: it is an unsupervised clustering algorithm, which means that it does not require a labeled dataset to train it. The goal of K-means is to divide a dataset into K number of clusters, where each cluster contains data points that are similar to each other [18]. The method works iteratively and tries to minimize the variability within each cluster while maximizing the distance between the clusters. K-means follows these steps [24]:
 - Selection of two initial clusters (one positive and one negative).
 - Assignment of reviews to clusters based on their proximity to centroids (mean values of clusters).
 - Recomputation of centroids based on reviews assigned to each cluster.
 - Iteration until the final clusters are established.

	<i>Clusters</i>	
	<i>1 (Negative)</i>	<i>2 (Positive)</i>
<i>Number of Reviews</i>	7	3

Cluster 1 (Negative): Reviews with a score of 2 and 3, or Reviews: 1, 2, 3, 4, 5, 6, 7.

Cluster 2 (Positive): Reviews with a score of 5, or Reviews: 8, 9, 10.

In this case, recency bias has not been taken into account. The older reviews, which are predominantly negative, are all grouped into the negative cluster, while the more recent reviews are all in the positive cluster. While the clustering appears to accurately reflect overall sentiment, it does not take into account the effect that more recent reviews may have in balancing the overall sentiment. If a product has significantly improved over time, the clusters will not adequately reflect this without considering the importance of the date.

Clustering weighted for recency bias

Now let's introduce a recency bias into the clustering process. Consider the Table 2. Performing clustering with weights:

- Review Weighting: Each review is given a higher weight if it is more recent.
- Weighted Clustering: We use a clustering algorithm that takes into account the weights assigned to each review. The review with the highest weight will have a greater influence on the final cluster result.

With recency bias applied, the clustering algorithm will be more influenced by recent reviews with high scores. Therefore, even though the number of negative reviews may be higher, recency bias will cause recent reviews with high ratings to influence the clustering result more. Clustering result with recency bias:

- Cluster 1 (Negative): Clustering may likely assign some of the older reviews (those with low scores) to the negative cluster, but the influence of recent reviews with high scores will cause negative reviews to be less prominent.
- Cluster 2 (Positive): The cluster of positive reviews will likely be much larger, due to the influence of the higher weights of recent reviews.

In this case, the recency bias will have a significant impact on the clustering result. Recent reviews (very positive) will shift the center of the positive cluster, while older reviews (often negative) will be less influential in determining the location of the center of the negative cluster. Clustering is more influenced by recent reviews, which are much more positive [21]. However, this approach could lead to a distorted representation of the overall sentiment of the product, as the clusters focus on the most recent reviews, ignoring older reviews that may be negative.

4. Conclusions

Online reviews are a critical tool for consumers, but traditional aggregation methodologies, such as arithmetic mean, fail to provide reliable results when reviews have skewed distributions, recency bias, or heterogeneous content; arithmetic mean struggles to capture the nuanced and dynamic nature of user feedback. Quantitatively, the analysis highlighted, for example, in a case where 90% of the reviews were positive but only 10% were recent and negative, the arithmetic mean remained high (4.75), masking potential product issues. More sophisticated and accurate solutions are offered by the implementation of alternative methods such as clustering, sentiment analysis, machine learning and MCDM [32]. For example, applying weights to the review dates shifted the sentiment score from slightly negative to positive, clearly showing the influence of recent

improvements in product quality. As for multi-criteria methods, as expected from future research, the integration of these techniques appears promising, allowing aggregation based on a broader range of variables, and they also improve the reliability of overall ratings. These sophisticated methods can help Amazon shoppers receive more accurate and representative product ratings. Continued innovation in aggregation techniques is essential to improve the online shopping experience and ensure that reviews accurately represent the quality of products sold. In the future, we plan to try to use multi-criteria decision-making methods, which consider multiple aspects of reviews (quality, usefulness, truthfulness, user involvement) and which are gaining attention for their ability to address the problems of traditional methods.

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An introduction to iso-, geno- and hyper-mathematics and their applications in physics, chemistry and biology

Emanuele Velardo*

Abstract

In this work, the author reviews recent advances on isomathematics, genomathematics and hypermathematics that were initiated by the Italian-American scientist Ruggero Maria Santilli for the invariant representation of reversible and irreversible systems of extended constituents in conditions of deep mutual entanglement with conventional linear, local and potential interactions represented by the conventional Hamiltonian H plus non-linear, non-local and non-potential interactions represented by the Santillian S in the axiom-preserving iso-, geno- and hyper-completion $A \hat{\times} B = ASB$ of the millenary old associative product of operators $A \times B = AB$. We then review and present, apparently for the first time, new advances in physics, chemistry and biology which are permitted by iso-, geno- and hyper-mathematics, but impossible for 20th century applied mathematics.

Keywords: Lie-isotopic, Lie-admissible, hyperstructural mathematic, biological structures, hadron mechanics

2020 AMS subject classifications: Find your subject classification at <https://mathscinet.ams.org/msnhtml/msc2020.pdf>.¹

*The Institute for Basic Research, Palm Harbor, Florida, USA; emanuelevelardo1999@gmail.com

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1 Foreword

Many important advances in science and technology have been generated by advances in mathematics. Consider, for example, the fundamental importance of the development of differential calculus for our modern knowledge or the discovery of complex numbers, without which there would be no contemporary electronics, or quantum mechanics.

By using a language accessible to the general scientific audience, in this paper we present an introduction to isomathematics, genomathematics and hypermathematics that were initiated by the Italian-American scientist Ruggero Maria Santilli (Biographical Notes <http://www.i-b-r.org/Sir-Santilli-bionotes-05-15-21.pdf>) during his Ph. D, studies in the 1960's at the University of Torino, Italy [1]-[3], continued in the late 1970's at Harvard University under DOE support [4]-[7], completed at the Institute for Basic Research, Palm Harbor, Florida [8]-[15], studied by numerous scholars [16]-[28] at a number of international workshops and conferences [29]-[37] and recently applied for significant advances [81]-[73] in mathematics, physics, chemistry and biology that would not have been possible with 20th century mathematics.

The primary aim of the studies is the representation of microscopic systems, such as particles, molecules or cells, composed by *extended* constituents in condition of partial mutual penetration/entanglement with ensuing conventional/potential as well as contact/non-potential interactions, said systems having the following classification for conditions of increasing complexity:

1.1. Closed/isolated, thus time reversal invariant systems, such as stable nuclei, molecules or cells, that can be represented via the single-valued *Santilli's Lie-isotooic mathematics* [17] [26] also known as *isomathematics*, where the prefix "iso" indicates in its Greek meaning the preservation of the abstract axioms of 20th century applied mathematics.

1.2. Open/non-conservative, thus time irreversible systems, such as nuclear fusions, chemical combustions or embryos, which can be represented via the single-valued *Santilli's Lie-admissible mathematics* [23] [26], also known as *genomathematics*, where the prefix "geno" indicates in its Greek meaning the generalization of the abstract axioms of 20th century applied mathematics.

1.3. Biological systems, such as a cell or a DNA, which can be represented via the multi-valued *Santill-Vougiouklis Lie-admissible hyperstructural mathematics* [1]- [10] [45]-[47], also known as *hypermathematics* for short, where the prefix "hyper" indicates in its Greek meaning the use of generalized multi-valued operations.

Following a rudimentary review of the above new mathematics, we present

intriguing new applications in physics, chemistry and biology.

2 Isomathematics

2.1 Elements of isotopic methods

Isomathematics was initiated in 1978 by R. M. Santilli [4] [5] at Harvard University for the representation of time reversal invariant systems with Hamiltonian plus contact, zero-range non-Hamiltonian interactions between extended constituents (particles, molecules or cells). The representation of the additional contact non-Hamiltonian interactions was achieved via a generalization of the conventional associative product of a set of elements $\xi : \{A, B, \dots; AB = A \times B; 1\}$ into the associativity preserving, thus isototoic form called isoproduct [5]

$$A \hat{\times} B = A \times \hat{S} \times B, \quad (1)$$

$$A \hat{\times} (B \hat{\times} C) = (A \hat{\times} B) \hat{\times} C,$$

with compatible generalization of the right and left multiplicative unit 1 of 20th century mathematics into the form $\hat{1} = 1/\hat{S}$ called the isounit

$$\hat{1} \hat{\times} A = A \hat{\times} \hat{1} \equiv A \quad \forall A \in \xi, \quad (2)$$

where the positive- definite quantity $\hat{S}$, called the *Santillian* [81] [82] [72] [73] represents the extended size of particles, molecules or cells and their non-Hamiltonian interactions with realizations for a two-body system of the type

$$\begin{aligned} \hat{S} &= 1/\hat{1} = \\ &= \sum_{k=1,2} \text{Diag.}(1/n_k, 1/n_k, 1/n_k, 1/n_k) \times e^{-\Gamma(t,r,p,\psi,\dots)} \ll 1, \quad (3) \\ k &= 1, 2, \Gamma > 0, \end{aligned}$$

where n_k^2, n_k^2, n_k^2 represent the semi-axes, n_k^2 the density and Γ the non-potential interactions of the extended constituents.

Santilli isomathematics [25] is characterized by the isotopies of the totality of 20th for century applied mathematics with no known exceptions because any treatment mixing the use of the isoproduct $A \hat{\times} B$ with the conventional product $A \times B$ is afflicted by catastrophic mathematical and physical inconsistencies [52].

As an example, the isoproduct can be obtained via a simple non-unitary transformation of the conventional product

$$\begin{aligned} U1U^\dagger &= \hat{1} \neq 1, \\ U(AB)U^\dagger &= (UAU^\dagger)(UU^\dagger)^{-1}(UBU^\dagger) = A' \hat{\times} B', \\ \hat{S} &= (UU^\dagger)^{-1}, \end{aligned} \tag{4}$$

and the same holds for the map of a conventional theory into its isotopic image.

However, the resulting *non-unitary theory* is structurally inconsistent when formulated on conventional spaces over conventional fields [52] and has to be reformulated with the full use of isomathematics, beginning with the reformulation of the non-unitary into an *iso-unitary transformation*

$$\begin{aligned} U &= \hat{U} \times \hat{S}^{1/2}, \\ UU^\dagger &= \hat{U} \hat{\times} U^\dagger = \hat{U}^\dagger \hat{\times} U = \hat{1}, \end{aligned} \tag{5}$$

and then passing to the entire formulation in terms of the isoproduct, isonumbers, isospaces, isodifferential calculus, etc.

In the following subsections, we present an introduction to the various branches of isomathematics that are needed for correct formulations. At this moment, we mention the important *Lie-Santilli isothory* [5] [17], which includes the isotopies of an N -dimensional Lie algebra with Hermitean generators $\xi : \{X_i, X_j \times X_j; 1\}$

$$[X_i, X_j] = X_i \hat{\times} X_j - X_j \hat{\times} X_i = C_{ij}^k \hat{\times} X_k, \tag{6}$$

and the isotopies of the corresponding Lie transformation group

$$A(t) = \Pi_k^{iX_k \times \hat{S} \times w} \times A(0) \times e^{-iw \times \hat{S} \times X_k}. \tag{7}$$

As an illustration of the significance of Santilli's isotopies, we mention that, for the case in which the parameter w represents an infinitesimal period of time t and the generator X_k is the Hamiltonian H , isotransformation isogroup (4) implies the *Heisenberg-Santilli time evolution* [5]

$$\hat{I} \frac{dA}{dt} = [A, \hat{H}] = A \hat{\times} H - H \hat{\times} A = A \hat{S} H - H \hat{S} A, \tag{8}$$

where conventional potential interactions are represented by the Hamiltonian H , while the extended size of the constituents and their non-potential interactions are represented by the Santillian $\hat{S}$. Note that Eq. (6) is invariant under anti-

Hermiticity, and therefore, can solely represent variationally nonselfadjoint (VNS) [4] time reversal invariant systems such as stable nuclei or stable molecules.

We should also note that isomathematics has permitted the progressive recovering of Einstein's determinism under strong interactions [81] [82], the first known numerically exact and time invariant representation of nuclear data [95] and nuclear stability [96], the first known attractive force between the identical electrons of a valence bond despite their extreme Coulomb repulsion [13] with ensuing first known exact representation of molecular data [65] [66], the first known mathematical representation of life [72] and other applications.

Additional applications of isomathematics in physics, chemistry and biology are outlined in Sections 8, 10 and 11, respectively.

2.2 Classification of isotopies

The characteristics of all possible topologically different isounits, first done by J. V. Kadeisvili [19] identifies all possible new mathematics:

Class I: the isounity is a positive defined Hermitian matrix.

Class II: the isounity is a negative defined Hermitian matrix.

Class III: includes preceding classes and isounits of undefined sign.

Class IV: includes previous classes and the case $\hat{1} = 0$

Class V: includes the previous classes and isounities with arbitrary characteristics thus being distribution, functions, et al.

Evidently, all the above isounits have one single value and the same holds for the isoproduct. Later on, for applications to biology, the above classification has to be extended to include multi-valued isounits and isoproducts.

2.3 Isofields

As it is well known, experimental verifications of a given theory produce numbers that, for consistency, have to be elements of the numeric field on which the theory is defined. The generalization of the basic unit 1 into the isounit $\hat{1}$ implies the loss of conventional fields with ensuing lack of consistent experimental verifications of isotopic theories.

In 1993, while visiting the Joint Institute for Nuclear Research in Dubna, Russia, Santilli [42] proved that the abstract axiom of a numeric field do not necessarily require the multiplicative unit to be the number 1 because it can be an arbitrary quantity $\hat{1}$ provided it is invertible. In this way Santilli introduced the new *isonumbers* and *isofields* that verify all axioms of a numeric field, thus being suitable for experimental verifications.

Let $F = F(a, +, \times, 0, 1)$ be a field with additive unit 0 and multiplicative unit 1. An "isofield" $\hat{F} = \hat{F}(\hat{a}, +, \hat{\times}, 0, \hat{1})$ [42] (see also monograph [20]) is a ring characterized by the operations $(+, \times)$ where $+$ is the conventional sum with unit 0 and $\hat{\times}$ is the new multiplication with isounit $\hat{1}$ whose elements $\hat{n} = n \times \hat{1}$, called isonumbers, obey the isoproduct

$$\hat{n} \hat{\times} \hat{m} = \hat{n} \times \hat{S} \times \hat{m} = (n \times m) \times 1 = c \in \hat{F}, \quad (9)$$

where $\hat{S} = \hat{1}^{-1}$ is the same Santillian of Eq. (9). Consequently, all conventional operations on numbers are similarly generalized [42] [8] [?].

It should be noted that, being an axiom-preserving generalization of the standard number theory, Santilli's isonumber theory is straightforward, although conceptually it requires a conceptual effort in understanding that, when projected in our three-dimensional space over the Reals, *Santilli's isonumbers* $\hat{n} = n \times \hat{1}$ *represent volumes*, as evident from the realization of the isounit from Santillian (5)

$$\hat{n} = n \times \hat{1} = n \Sigma_{k=1,2} \text{Diag.}(n_k^2, n_k^2, n_k^2). \quad (10)$$

Rather than being a mathematical curiosity, the indicated conception of isonumbers is necessary for the invariant representation of the dimensions, shape and density of the constituents to such an extent that said feature has to be carried over at all levels of treatments.

The isofields considered above are of Class I with $\hat{1} > 0$ and are at the foundation of isomathematics. Class II isofields have a negative-definite isounit $\hat{1} < 0$, characterize the *isodual isomathematics* for the description of antimatter [15] which is interconnected with isomathematics by an anti-Hermitean map called *isoduality* and indicated with an upper index d , e.g.,

$$\hat{1} > 0 \rightarrow \hat{1}^d = -\hat{1} < 0. \quad (11)$$

The isodual isofields $\hat{F}^d = \hat{F}^d(\hat{n}^d, +, \hat{\times}^d)$ are characterized by isodual numbers $\hat{n}^d = -\hat{n}^\dagger$ and isodual isoproduct with isodual Santillian $\hat{S}^d = -\hat{S}$.

2.4 Isospaces

An Euclidean space $E(x, \delta, R)$ with metric $\delta = \text{Diag.}(1, 1, 1) \in R$ is characterized by the Euclidean distance as an invariant quantity between two points x and y over the field of real numbers R

$$(x - y)^2 = (x^i - y^i) \delta_{ij} (x^j - y^j) \in R(n, +, \times). \quad (12)$$

An *iso-Euclidean isospace*, also called an *Euclid-Santilli isospace*, [43] $\hat{E}(\hat{x}, \hat{\Delta}, \hat{R})$ [43] (see also monographs [8] [25]) is an N-dimensional metric space defined on

a Class III isoreal isofield $\hat{R}(\hat{n}, +, \hat{x})$ with an $N \times N$ -dimensional isounit $\hat{1}$, isocoordinates $\hat{x} = x \times \hat{1}$ and isometric $\Delta = \delta \hat{1} \in \hat{R}$ with *isodistance* between two isopoints

$$(\hat{x} - \hat{y})^2 = \left[(\hat{x}^i - \hat{y}^i) \hat{\times} \hat{\Delta}_{ij} \hat{\times} (\hat{x}^j - \hat{y}^j) \right] \times \hat{1} \in \hat{R}, \quad (13)$$

characterized by the isometric

$$\hat{\delta} = \hat{S} \times \delta. \quad (14)$$

An *iso-Minkowskian isospace*, also called a *Minkowski-Santilli isospace* first introduced in the 1983 Ref. [43], is characterized by the *isometric* $\hat{\Omega} = \hat{\eta} \times \hat{1} = (\hat{S} \times \eta) \hat{1} \in \hat{R}$ where η is the familiar Minkowskian metric $\eta = (1, 1, 1, -1)$ and it is at the foundation of relativistic treatments of systems of extended particles with potential and non-potential interactions.

Recall that, to characterize metric spaces over the reals, the elements of metrics δ and η must be real numbers $n \in R$. Similarly, to characterize isospaces over the isoreals, the elements of isometrics Δ and Ω must be isoreal isonumbers $\hat{n} \in \hat{R}$.

2.5 Isodifferential calculus

Let us recall that, by the mid 1990's, the virtual entirety of 20th century applied mathematics had been isotopically generalized. Nevertheless, the resulting physical theories were afflicted by serious inconsistencies with particular reference to the inability to achieve a representation invariant over time of the dimensions, shape and density of particles, molecules and cells as requested by experimental verifications.

Following years of trials and errors, Santilli finally identified in 1995 the origin of the inconsistencies as being due to the use of the conventional Newton-Leibnitz differential calculus within the context of isotopic theories because the former can only be defined at isolated points while isotopic theories are conceived to represent volumes.

This observation led Santilli to the discovery of the *isodifferential calculus*, first presented in the 1995 monograph [8], applied in the subsequent monograph [9] to the generalization of quantum into *hadronic mechanics* and extensively presented in the 1996 memoir [44] which, in essence, is a calculus defined on volumes with evident applications in all quantitative sciences, including engineering.

Let dx be the conventional differential of an Euclidean coordinate x . Santilli isodifferential calculus is characterized by all possible generalized differentials $\hat{d}\hat{x}$ of an iso-Euclidean isocoordinate $\hat{x} = x \times \hat{1}(x, \dots)$, whose isounit $\hat{1}$ has an explicit dependence on the local coordinate x , such to verify the limit condition

$$\text{Lim } \hat{d}_{\hat{1} \rightarrow 1} \hat{x} = dx. \quad (15)$$

Let us define as *isofunction* the quantity $\hat{f}(\hat{x}) = f(\hat{x}) \times \hat{1}$ with value in $\hat{F}$. Then, an infinite succession $\hat{f}_1, \hat{f}_2, \hat{f}_3, \dots$ is strongly isoconvergent to a value $\hat{f}$ when:

$$\lim_{k \rightarrow \infty} |\hat{f}_k - \hat{f}| = 0. \quad (16)$$

A strongly convergent series is also strongly isoconverging. However, a strongly isoconverging series is not necessarily strongly converging.

The isofield $\hat{E}(\hat{x}, \hat{\delta}, \hat{R})$ with coordinates $\hat{x} = \{\hat{x}^k\}$, $k = 1, \dots, N$ and isometric $\hat{\delta} = \hat{S} \times \delta$ on the isoreals, admits per isounit a matrix $N \times N$ of class III, $\hat{1} = \left(\hat{I}_i^j\right) = \hat{S}^{-1} = \left(\hat{S}_i^j\right)^{-1}$ with line element

$$\hat{x}^i \hat{\delta}_{ij} \hat{x}^j = \hat{x}^i \hat{S}_i^j \delta_{jm} \hat{x}^m = \hat{x}_i \hat{\delta}^{ij} \hat{x}_j = \hat{x}^k \hat{x}_k = \hat{x}_k \hat{x}^k. \quad (17)$$

The isodifferentials of first order of covariant and contravariant coordinates are given respectively by [8] [44] [24])

$$\hat{d}\hat{x}^k = \hat{1}_k^i(x, \dots) dx^i, \quad (18)$$

$$\hat{d}\hat{x}_k = S_k^j(x, \dots) dx_j.$$

The isodifferentials expressed in this way allow the calculation of the corresponding isoderivatives:

$$\hat{f}'(\hat{a}^k) = \frac{\hat{d}\hat{f}(\hat{x})}{\hat{d}\hat{x}^k} \Big|_{\hat{x}^k=\hat{a}^k} = \hat{S}_k^i \frac{df(x)}{dx^i} \Big|_{x^k=\hat{a}^k}, \quad (19)$$

$$\hat{f}'(\hat{a}_k) = \frac{\hat{d}\hat{f}(\hat{x})}{\hat{d}\hat{x}_k} \Big|_{\hat{x}_k=\hat{a}_k} = \hat{I}_k^i \frac{df(x)}{dx_i} \Big|_{x_k=\hat{a}_k},$$

which are at the foundation of all applications of isomathematics.

Recall that integration is defined as the inverse of the differentiation, e.g., $\int dx = x$. Consequently, isointegration can be defined as being the isoinverse of isodifferentiation

$$\int \hat{d}\hat{x} = \left(\int \hat{1}\right)(Sd\hat{x}) = \hat{x}. \quad (20)$$

Nineteen years later, the mathematician Svetlin Georgiev discovered Santilli's isodifferential calculus [44] and published a monumental volume of works in the field, including eight monographs [24] [25] [26].

2.6 Iso-Euclidean geometry

An *isoline* [8] [26] is defined as the image of the ordinary line on the reals under the lifting $R(n, +, \times) \rightarrow \hat{R}(\hat{n}, +, \hat{x})$ and the position of its isopoints (images in

the isospace of the points of the line) is described by the isocoordinates $\hat{x} = \hat{I}x$ whose isoorigin is $\hat{0} = \hat{I}0$

The isodistance from two isopoints is then given by

$$\hat{1} \left(\hat{x} - \hat{x}' \right) \hat{1} = \hat{1} \left(\hat{x} - \hat{x}' \right) \times \hat{S} \times \left(\hat{x} - \hat{x}' \right) \hat{1}^{\frac{1}{2}} \times \hat{1}. \quad (21)$$

The value of the distance between two points is different for the line and isospace. This result leads to a number of intriguing implications in mathematics and physics such as a newly developed propulsion method called geometric propulsion [15], which is based on the movement of an isopoint from one isocoordinate to another by altering the underlying geometry rather than the conventional motion or the point in space.

Let us consider now the three-dimensional Euclidean vector space $V[r, +, \odot, -, R(n, +, \times)]$. The Class I isotopies of the three-dimensional Euclidean vector space, called iso-Euclidean isovector isospaces, are given by the same set of contravariant vectors $r = (x, y, z)$ reformulated as "isovectors"

$$r = (x, y, z) \rightarrow \hat{r} = r \times \hat{1} = (\hat{x}, \hat{y}, \hat{z}) = (x \times \hat{I}, y \times \hat{I}, z \times \hat{I}). \quad (22)$$

In the conversion from Euclidean vector space to iso-Euclidean isovector isospace, the following quantity is invariant [9]:

$$Length \times Unity = Isolength \times Isounity. \quad (23)$$

In the 3-dimensional space, the isounit is a matrix 3×3

$$\hat{1} = \hat{S}^{-1} = Diag(b_1^{-2}, b_2^{-2}, b_3^{-2}). \quad (24)$$

Furthermore, isoseparation coincides with conventional separation:

$$\hat{r}^2 = (r_k \times r^k) \times \hat{I} = \left(r^i \times \hat{S} \times \delta_{ij} \times r^j \right) \times \hat{1} = r^2 \times \hat{S} \times \hat{S}^{-1} = r^2. \quad (25)$$

If length and unit were invariant, instead of their product, it would be a different geometry from the isogeometry, because $\delta \rightarrow \delta \times \hat{1}$ rather than $\delta \rightarrow \delta \times \hat{S}$.

The isodistance [8] [26] from two points $P_1(x_1, y_1, z_1)$ and $P_2(x_2, y_2, z_2)$ is the isoscalar

$$\hat{D}_{12} = \hat{1} (\hat{r}_1 - \hat{r}_2) \hat{1} = [(\hat{x}_1 - \hat{x}_2)^2 b_1^2 + (\hat{y}_1 - \hat{y}_2)^2 b_2^2 + (\hat{z}_1 - \hat{z}_2)^2 b_3^2]^{\frac{1}{2}} \times \hat{I} \in \hat{R} \quad (26)$$

where $\hat{r}_1$ and $\hat{r}_2$ represent the isovectors from the origin to P_1 and P_2 .

By indicating with d the Euclidean distance between two points and with $\hat{D} = D \times \hat{1}$ the corresponding isoeuclidean distance between two isounits, the following rule is valid:

$$\begin{aligned} D > d &\longleftrightarrow \det \hat{1} < 1, \\ D < d &\longleftrightarrow \det \hat{1} > 1. \end{aligned} \quad (27)$$

Consequently, an object has different dimensions and shape in Euclidean and Isoeuclidean geometries. An internal observer to the isoeuclidean isospace may appear to the external observer arbitrarily smaller or larger. Also, the isodimensions can vary in time and can be arbitrarily moved in the future or past of the external observer, as well as be in motion without the application of any force.

For example [15], the enormous distance of stars in Euclidean space can be made as small as desired in an isoeuclidean isospace.

The equation of an isoret isoline is given by one of the following forms:

$$\hat{a} \times \hat{x} + \hat{b} \times \hat{y} + \hat{c} \times \hat{z} + \hat{d} = (a \times x + b \times y + c \times z + d) \times \hat{I} = 0,$$

$$\left\{ \begin{array}{l} \hat{x} - \hat{x}_1 - \hat{p} \times \hat{a}_1 = (x - x_1 - pa_1) \times \hat{I} = 0 \\ \hat{y} - \hat{y}_1 - \hat{p} \times \hat{a}_2 = (y - y_1 - pa_2) \times \hat{I} = 0, \\ \hat{z} - \hat{z}_1 - \hat{p} \times \hat{a}_3 = (z - z_1 - pa_3) \times \hat{I} = 0, \end{array} \right\} \quad (28)$$

with $a, b, c, d \in R$ and $\hat{a}, \hat{b}, \hat{c}, \hat{d} \in \hat{R}$.

The representation of an isoline in isovectoral notation is given by

$$\hat{r}_k - \hat{r}_{1k} - \hat{n} \times \hat{a} = (r_k - r_{1k} - na_k) \times \hat{I}. \quad (29)$$

The isogeometric propulsion [15] moves a point $P_1(x_1, y_1, z_1)$ into a point $P_2(x_2, y_2, z_2)$ which lies on the same line connecting $P_1(x_1, y_1, z_1)$ to the origin by means of the following steps:

1) The geometry underlying point P_1 is isotopically raised with the resulting isodistance to another point P_2 .

2) The isotopy is chosen according to the law:

$$D_{01} = (x_1^2 b_1^2 + y_1^2 b_2^2) \times \hat{I} = d_{02} \times \hat{I}, \quad (30)$$

with the simplest possible solution

$$b_1^2 = \frac{x_2^2}{x_1^2}; b_2^2 = \frac{y_2^2}{y_1^2}; b_3^2 = \frac{z_2^2}{z_1^2}; Det.\hat{I} > 1. \quad (31)$$

3) The geometry is then returned to the original Euclidean form.

The isogeometric propulsion shown here is a purely mathematical notion, although its possible actual realization has been studied by R. M. Santilli [15] via means which can alter the fundamental units of space and time.

In the iso-Euclidean geometry we can introduce the isoangle $\hat{a}$ as a generalization of the ordinary angle with isotrigonometric isocoordinates [8]

$$isocos\hat{a} = \frac{x_1 b_1^2 x_2 + y_1 b_2^2 y_2}{(x_1 b_1^2 x_1 + y_1 b_2^2 y_1 + x_2 b_1^2 x_2 + y_2 b_2^2 y_2)^{\frac{1}{2}}}. \quad (32)$$

By introducing the angular Santillian $\hat{S}_a = b_1 b_2$ and the angular isounit $\hat{1}_a = b_1^{-1} b_2^{-1}$ the formula of the isoangle is given by

$$\hat{a} = b_1 b_2 a = \hat{S}_a a = \hat{1}_a^{-1} a. \quad (33)$$

2.7 Isoaxioms of the iso-Euclidean geometry

The above isogeometric properties allow the identification of the isoaxioms of the isoeuclidean isogeometry (see also [8] [26]):

Isoaxiom I: There exists one and only one isostraight isoline from one isopoint to another isopoint.

Isoaxiom II: An isosegment can be prolonged continuously into an isostraight line from each end.

Isoaxioms III: For any given center and isoradius there is one and only one isosphere.

Isoaxioms IV: All isoright isoangles are equivalent.

Isoaxioms V: For each given isosegment between two isopoints there exist only two isoparallel lines, one per each isopoint, which are isoperpendicular to that isosegment.

2.8 Isodual iso-Euclidean geometries

Class I iso-Euclidean isogeometry is used in physics for characterizing matter [8].

Class II isodual isoeuclidean isogeometry is used in physics for the characterization of antimatter [15].

Class III isogeometry seems particularly suitable for applications in theoretical biology [14].

The reversal of the sign of time on conventional spaces over conventional fields leads to the violation of causality. The only known alternative to avoid this problem in the study of antimatter is Santilli's map [15] of the entire geometry into an anti-automorphic image called isoduality:

$$1 \longrightarrow 1^d = -1. \quad (34)$$

The isodual iso-Euclidean isospaces are obtained via the the isodual map of the original isovectors.

The fundamental invariants of Euclidean or iso-Euclidean geometries are iso-selfdual, that is invariant under isoduality

$$\begin{aligned} r^2 &= r^{d2d}, \\ \hat{x}^2 &= \hat{x}^{d2d}. \end{aligned} \tag{35}$$

This property has important physical implications for the representation of antimatter because it implies that its isodual space is hidden but co-existing within our space.

The equations for isoret and isodual angle are respectively given by:

$$\begin{aligned} \hat{a}^d \hat{\times}^d \hat{x}^d + \hat{b}^d \hat{\times}^d \hat{y}^d + \hat{c}^d \hat{\times}^d \hat{z}^d + \hat{d}^d &= (a \times x + b \times y + c \times z + d) \times \hat{I}^d = 0, \\ \hat{a}^d &= b_1^d b_2^d a^d = -\hat{a}. \end{aligned} \tag{36}$$

Isoduality can represent the movement back in time in a causal way allowing for the causal representation of antimatter with Dirac's negative energies. This representation is also useful for the study of biological structures.

2.9 Representation of biological structures in isospaces

Biological structures can be represented by isospheres in isoeuclidean spaces [14]. The isosphere in a three-dimensional Euclidean space $\hat{E}(\hat{r}, \hat{\delta}, \hat{R})$ with diagonal isounity is the isotopic image of an ordinary sphere with equation

$$\hat{r}^2 = \hat{x}^2 + \hat{y}^2 + \hat{z}^2 = \hat{R}^2. \tag{37}$$

Similarly the isodual isosphere in space $\hat{E}^{d2d}(\hat{r}^{d2d}, \hat{\delta}^{d2d}, \hat{R}^{d2d})$ has the equation

$$\hat{r}^{d2d} = \hat{x}^{d2d} + \hat{y}^{d2d} + \hat{z}^{d2d} = \hat{R}^{d2d}, \tag{38}$$

of which a particular case is the isodual sphere, namely, the image of the sphere of Euclidean space

$$\hat{r}^{d2d} = (-\hat{x}^2 - \hat{y}^2 - \hat{z}^2) \times I^d = R^2 \times I^d. \tag{39}$$

The perfect sphericity in Euclidean space is given by

$$I_x = I_y = I_z = +1, \tag{40}$$

but in general an iso-Euclidean space admits the property

$$I_x = b_1^{-2} \neq I_y = b_2^{-2} \neq I_z = b_3^{-2} \neq +1. \tag{41}$$

Spinning hadrons are represented as isospherical in the isospace although their projection on ordinary spaces have an arbitrary shape with a compact topology, thus including all possible deformations which maintain the basic rotational symmetry [9].

Anti-hadrons are instead represented as isodual isospherical because all the characteristics have changed sign, while conventionally anti-hadrons are represented with the same geometry used for hadrons, thus being insufficient for their distinction.

For the simple case of an isocircle of radius 1 in the isoplane, the coordinates are given by [8]:

$$x = isocos\hat{\theta} = b_1^{-1}cos\hat{\theta}, \quad (42)$$

$$y = isosin\hat{\theta} = b_2^{-1}sin\hat{\theta}, \quad (43)$$

$$\hat{\theta} = b_1b_2\theta, \quad (44)$$

$$r^2 = xb_1^2x + yb_2^2y = b_1^2isocos^2\hat{\theta} + b_2^2isosin^2\hat{\theta} = cos^2\hat{\theta} + sin^2\hat{\theta} = 1. \quad (45)$$

The Class I isosphere unifies the sphere and all its ellipsoidal deformations and the same holds for the Class II isodual isosphere. The Class III isosphere unifies the sphere and all quadrants. Currently known physical applications are restricted to class I and II isospheres since there is no known physical phenomenon which can alter, for example, ellipsoids in paraboloids.

3 Connections with non-Euclidean geometries

The first non-Euclidean property of iso-Euclidean isospace is that it is curved unless the isometric is independent from local coordinates, but dependent on remaining variables $\hat{\delta} = \hat{\delta}(t, \dot{r}, \ddot{r})$.

In fact a given n-dimensional iso-Euclidean space admits the non-null Christoffel symbols [53]

$$\Gamma_{hk}^l = \frac{1}{2}\hat{\delta}^{ij} \left(\frac{\partial \hat{\delta}_{kj}}{\partial r^h} + \frac{\partial \hat{\delta}_{jh}}{\partial r^k} - \frac{\partial \hat{\delta}_{hk}}{\partial r^j} \right), \quad (46)$$

that characterize quantities such as the curvature tensor

$$R_{lh}^j = \frac{\partial \Gamma_{rh}^l}{\partial r^k} - \frac{\partial \Gamma_{rk}^l}{\partial r^h} - \Gamma_{qk}^j \Gamma_{lh}^q - \Gamma_{qh}^l \Gamma_{lk}^q, \quad (47)$$

which is identically null when the isometric is independent of local coordinates.

It should be noted that the above notion of curvature emerges when iso-Euclidean spaces are projected on our spaces over conventional fields because, isospaces over isofields are *isoflat* due to their topologically equivalence to conventional spaces.

The emergence of curvature on an isopath was unexpected, so this feature was identified 12 years after the identification of the iso-Euclidean geometry. This property allows a geometric unification of special and general relativities into the unit of relativistic quantum theories [54].

Lobacevski geometries are projections of iso-Euclidean geometries in the Euclidean space. The following transformations

$$x' = \frac{x + a}{1 + ax}, \quad (48)$$

$$y' = \frac{y(1 - a^2)^{\frac{1}{2}}}{1 + ax}, \quad (49)$$

map lines into lines and circles into circles. Hence, the Lobacevski geometry is a special case of the broad class of isotopies.

A similar situation exists for the Minkowskian, Riemannian, symplectic and other geometries which can all be described as special cases of iso-Euclidean geometries.

In summary, the geometries studied in this section are the following [8] [9]:

- 1) Iso-Euclidean geometry of Class I, used for the characterization of biological structures evolving forward in time;
- 2) Isodual Isoeuclidean geometry of Class II, used for the characterization of biological structures evolving backward in time.
- 3) Isogeometry of Class III, used for the characterization of biological structures requiring time-inversions.
- 4) Iso-Euclidean geometries of Class IV, used for biological structures with singularities.
- 5) Iso-Euclidean geometry of Class V, used for the most general possible isotopic representation of biological structures.

4 Isotopies of classical methods

The fundamental equations of contemporary mechanics are Newton's equations for a system of N particles with non-null masses in the second-order form [4]

$$m_a \frac{dv_{ka}}{dt} = F^{SA}(t, r, v) + F_{ka}^{NSA}(t, r, v), \quad (50)$$

$$a = 1, 2, 3 \dots N; k = 1, 2, 3 (= x, y, z); v_{ka} = \frac{dr_{ka}}{dt}; m_a \neq 0. \quad (51)$$

But classical and quantum methods are structurally insufficient for the representation of biological systems.

To begin, all contemporary classical and quantum formulations are solely applicable to local-differential systems, as demanded by the underlying topology and geometry, while we are primarily interested in non-local integral systems. Also, the above methods are solely applicable to particles represented as perennial and immutable massive points, while we are interested in representing particles as extended, non-spherical and deformable. Finally, the contemporary formulations of Lagrange's and Hamilton's equations can only represent a rather small class of Newton's equations.

Fundamental analytic problem: Identify generalized analytic methods which achieve a direct universality for the representation of all possible well behaved nonlinear, nonlocal and non-Hamiltonian systems [5].

The first solution to the above problem was achieved by the creators of analytical mechanics, Lagrange and Hamilton themselves, because they formulated their famous equations, not in the form currently used in mathematics, physics and biology, but the one with external terms that represent precisely the forces F^{NSA} , i.e. the contact forces that cannot be represented by potentials.

It should be recalled that in Newtonian mechanics the potential $U(t, r, v)$ must be linear in the velocities to avoid a redefinition of the mass,

$$U(t, x, v) = U_k(t, x) v^k + U_0(t, x), \quad (52)$$

and the Newton equation becomes

$$\begin{aligned} & \left\{ m \frac{dv_k}{dt} - \frac{d}{dt} \frac{\partial U(t, x, v)}{\partial v^k} + \frac{\partial U(t, x, v)}{\partial x^k} - F_k^{NSA}(t, x, v) \right\}^{NSA} \\ &= \left\{ m \frac{dv_k}{dt} - \frac{\partial U(t, x, v)}{\partial x^s} \frac{dv^s}{dt} + \frac{\partial U_0(t, x)}{\partial x^k} - F_k^{NSA}(t, x, v) \right\}^{NSA} = 0, \end{aligned} \quad (53)$$

namely, they are not in general derivable from Lagrange's or Hamilton's equations.

The first step in the application of all isotopies is the identification of the independent variables and related basic generalized units. The independent variables in Newton's equations are time t , coordinates r and velocities v .

So, we have time isounit, space isounit and velocity isounit

$$\hat{I}_t = \hat{T}_t^{-1}, \quad (54)$$

$$\hat{I}_r = \hat{T}_r^{-1}, \quad (55)$$

with total isounit

$$\hat{I}_{tot} = \hat{I}_t \times \hat{I}_v \times \hat{I}_r. \quad (56)$$

The isotopic lifting of Newton's equations in isospace $\hat{S}(t, r, v)$ of Class III known under the name of *Newton-Santilli isoequations* [44] are given by

$$\begin{aligned}\hat{\Gamma}_k(\hat{t}, \hat{r}, \hat{v}) &= \hat{m} \frac{d\hat{v}_k}{d\hat{t}} - \frac{\hat{d}}{d\hat{t}} \frac{\partial \hat{U}(\hat{t}, \hat{r}, \hat{v})}{\partial \hat{v}^k} + \frac{\partial \hat{U}(\hat{t}, \hat{r}, \hat{v})}{\partial \hat{r}^k} = \\ &= \hat{m} \frac{d\hat{v}_k}{d\hat{t}} - \frac{\partial \hat{U}_k(\hat{t}, \hat{r})}{\partial \hat{r}^l} \frac{d\hat{x}^l}{d\hat{t}} + \frac{\partial \hat{U}_0(\hat{t}, \hat{r})}{\partial \hat{r}^k} = 0,\end{aligned}\quad (57)$$

where $\hat{m}$ is the "isotopic mass", the image of the Newtonian mass in the isospace and $\hat{d}$ is the isodifferential.

The important properties of Eqs. (57) are their direct universality for the representation of all possible Newton's equations (53) directly in the frame of the experimenter, and Eqs. (57) are indeed derivable from an isotopic variational principle [44].

The studies here presented introduce a representation of the actual extended, non-spherical and deformable forms of particles at the primitive Newtonian level, which then persists in classical analytical representations as well as in maps up to the operator form. Newton-Santilli isoequations actually achieve these goals by laying down the foundations for possible new advances in various fields. The goal is achieved through the new degrees of freedom of the generalized unity of theory that are evidently absent in conventional Newtonian, classical and quantum formulations.

As a simple example, suppose that the body considered is a rigid spheroidal ellipsoid with semiaxes $n_1^2, n_2^2, n_3^2 = \text{constants}$. This form is directly represented by the Santillian of the theory in the simple diagonal form $\hat{T} = \text{diag}(n_1^2, n_2^2, n_3^2)$

$$m \hat{T}_k^l \frac{dv_i}{dt} - \hat{T}_k^l \frac{d}{dt} \frac{\partial U_l(t, r)}{\partial v^l} v^s + \hat{T}_k^l \frac{\partial U_0(t, r)}{\partial v^l} = 0. \quad (58)$$

Moreover, the nonspherical character of the shape emerges only in the projection in ordinary spaces, because at the isotopic level all particles are represented via the isosphere, i.e., the perfect sphere in isospace

$$\hat{r}^2 = (x^1 n_1^{-2} x^1 + x^2 n_2^{-2} x^2 + x^3 n_3^{-2} x^3) \times \hat{I} \in \hat{R}(\hat{n}, +, \hat{\times}). \quad (59)$$

The representation of shapes more complex than the spheroidal ellipsoids is possible with non-diagonal isounits. The representation of the deformations of the original shape due to motion within resistive media or other reasons, can be achieved via a suitable functional dependence of the Santillian $\hat{T}_k^i$ in velocities, pressure, etc.

In particular, Newton-Santilli isoequations permit a novel representation of nonpotential, variationally nonselfadjoint forces of the type

$$m \frac{dv_k}{dt} - F_k^{NSA}(t, r, v) = \hat{I}_k^l m \frac{d\hat{T}_l^j v_j}{dt}, \quad (60)$$

while leaving unchanged the representation of conventional self-adjoint forces.

5 Isotopies of Hamiltonian mechanics

Newton-Santilli isoequations can be derived from a first-order isovariational principle [4] [9].

$$\hat{A} = \int_{t_1}^{t_2} L(t, x, v, a...) dt = \int_{\hat{t}_1}^{\hat{t}_2} L(\hat{t}, \hat{x}, \hat{v}) d\hat{t}, \quad (61)$$

along an isodifferentiable path

$$\begin{aligned} \delta \hat{A}(P) &= \int_{\hat{t}_1}^{\hat{t}_2} (\delta \hat{r}^k \frac{\partial}{\partial \hat{r}^k} + \delta \hat{v}^k \frac{\partial}{\partial \hat{v}^k}) \hat{L}(\hat{P}) d\hat{t} = \\ &= \int_{\hat{t}_1}^{\hat{t}_2} \left(\frac{\partial \hat{L}}{\partial \hat{r}^k} - \frac{d}{d\hat{t}} \frac{\partial \hat{L}}{\partial \hat{v}^k} \right) \hat{L}(\hat{P})(P) \delta \hat{r}^k d\hat{t}. \end{aligned} \quad (62)$$

By introducing the following isodifferentials into the isospace $\hat{S}(t, \hat{r}, \hat{p}) = \hat{E}(t) \times \hat{E}(r, \delta, \hat{R}) \times \hat{E}(p, \delta, \hat{R})$

$$d\hat{t} = I_t dt; d\hat{r}^k = \hat{I}_k^l dr^l; \frac{\partial r^l}{\partial r_j} = \delta_j^l; d\hat{p}^k = \hat{I}_k^l dp^l, \quad (63)$$

with isounits

$$I_2 = \text{diag}(\hat{I}_t, \hat{I}, \hat{T}); T_2 = \text{diag}(\hat{T}_t, \hat{T}, \hat{I}), \quad (64)$$

and the isocanonical momentum

$$\hat{p} = \frac{\partial \hat{L}(\hat{t}, \hat{r}, \hat{v})}{\partial \hat{v}} = \hat{m} \hat{v}_k - \hat{U}_k(\hat{t}, \hat{r}), \quad (65)$$

the iso-Hamilton equations, also called Hamilton-Santilli isoequations [17]-[24] are given by

$$\frac{\partial \hat{r}^k}{\partial \hat{t}} = \frac{\partial H(\hat{t}, \hat{r}, \hat{p})}{\partial \hat{p}_k}, \quad (66)$$

$$\frac{\partial \hat{p}_k}{\partial \hat{t}} = - \frac{\partial H(\hat{t}, \hat{r}, \hat{p})}{\partial \hat{r}^k}. \quad (67)$$

6 Isotopies of quantum mechanics

The isotopy of the simple quantization via a variational principle led Santilli to the identification of the isotopies of the Schrödinger equations at the foundation of hadronic mechanics first achieved in the 1983 monograph [5] which can be reviewed as follows.

Consider the isounitary operator $\hat{U}$ which describes the evolution over time of a hadronic isostate

$$\hat{\psi}' = \hat{U} \hat{\times} \hat{\psi} = e^{i\hat{H}t} \hat{\times} \hat{\psi} = e^{iHSt} \times \hat{I} \hat{\times} \hat{\psi} = e^{i\hat{H}St} \times \hat{\psi}, \quad (68)$$

$$\hat{U} \hat{\times} \hat{U}^\dagger = \hat{U}^\dagger \hat{\times} \hat{U} = \hat{I}, \quad (69)$$

resulting in the *Schrödinger-Santilli isoequation*

$$\hat{H} \hat{\times} |\hat{\psi}\rangle = \hat{E} \hat{\times} |\hat{\psi}\rangle = E |\hat{\psi}\rangle, \quad \hat{E} = E \hat{1} \in \hat{R}, \quad E \in R, \quad (70)$$

with isoexpectation values of an observable $\hat{H}$

$$\langle \hat{H} \rangle = \frac{\langle \hat{\psi} | \hat{\times} \hat{H} \hat{\times} | \hat{\psi} \rangle}{\langle \hat{\psi} | \hat{\times} | \hat{\psi} \rangle}. \quad (71)$$

Note that the same Hamiltonian H has basically different eigenvalues in quantum mechanics (qm) and hadronic mechanics (hm), as transparent from the presence of the isotopic element in hadronic expressions

$$H |\psi\rangle = E_{qm} |\psi\rangle \hat{S} |\hat{\psi}\rangle = E |\hat{\psi}\rangle, \quad E_{qm} \neq E_{hm}. \quad (72)$$

7 Elements of genotopic methods

While isotopic formulations are naturally set to represent total conservation laws under nonconservative internal effects, genotopic formulations generally admit no conserved quantity, because they have been conceived [56] to characterize time-rate-of-variations of a given quantity of which conservation is an evident particular case. Genotopies are therefore ideally suited to represent the nonconservative events such as nuclear fusions, chemical combustions or the growth of biological structures.

Santilli genotopies are based on a further extension of numbers: the genonumbers. These are characterized by the two alternating multiplications to the right and left, denoted by the symbols $>$ and $<$ respectively [56].

The ordering is compatible with other properties and axioms of number theory, such as commutativity, associativity, etc.

You can then use ordered fields to the left to represent motion backward in time ${}^{<F}(a, +, <)$ and ordered fields to the right to represent motion forward in time ${}^{>F}(a, +, >)$.

The genodifferential calculation is based on the following forward and backward genodifferentials

$$\hat{d}^>r_k = \hat{I}_k^>\hat{l}dr_l \quad (73)$$

$${}^{<}\hat{d}r^k = {}^{<}\hat{I}_l^k dr^l. \quad (74)$$

The related genotopic elements

$$\frac{\partial^>}{\partial r^{k>}} = S_k^l \frac{\partial}{\partial r^l}, \quad (75)$$

$$\frac{{}^{<}\partial}{{}^{<}\partial r^k} = R_k^l \frac{\partial}{\partial r^l}, \quad (76)$$

are called the forward and backward Santillians, from which we obtain the Heisenberg-Santilli genoequations [5] for the representation of the time rate of variation of observables

$$\begin{aligned} i\frac{dA}{dt} &= (A, H) = A < H - H > H = A {}^{<}SH - HS {}^{>}A, \\ i\frac{dH}{dt} &= H({}^{<}R - S {}^{>})H \neq 0. \end{aligned} \quad (77)$$

8 Element of hyperstructural methods

Hyperstructures are some of the most complex mathematical structures conceived by mathematicians until now. Part of their complexity is due to their virtually endless variety of formulations and realizations which evidently multiply the difficulties for their selection and realization into a form suitable for applications. The need for the hyperstructures in theoretical biology is unavoidable because the isotopic and genotopic methods are effective up to a certain complexity of the systems considered.

A central mathematical property of the hyperstructures is that of being multi-valued, that is, products which traditionally have only one value, may assume a series of ordered different values. This central feature of hyperstructure has a clear potential for new frontiers in theoretical biology, because it is particularly suited to represent, say, the birth of a new cell in which the original number of entities was one and the final number of entities is two, which is precisely a realization of the notion of multivaluedness.

While the generalized units of isotopies and genotopies are given by simple single-valued quantities, hyperunits have the form

$$(I^>) = (I_1^> (r, t, \dot{r}, \ddot{r}) I_2^> (r, t, \dot{r}, \ddot{r}) \dots), \quad (78)$$

from which we derive the hyperfield $(\hat{F}^>)((\hat{a}^>), +, (>))$ defined from a conventional numerical field $F(a, +, \times)$ with elements

$$(\hat{a}^>) = a \times (\hat{I}^>), \quad (79)$$

and related hypermultiplication

$$(\hat{a}^>)(>)(\hat{\beta}^>) = (\hat{a}^>) \times (S_1, S_2 \dots) \times (\hat{\beta}^>), \quad (80)$$

where the forward hyper-Santillian is given by $(S) = (S_1(t, r, \dot{r} \dots), S_2(t, r, \dot{r} \dots) \dots)$.

The forward hyperdifferential calculus, apparently introduced here for the first time, can be defined via the forward hyperdifferentials with corresponding forward hyperderivatives with the corresponding ordered multiplications.

$$(\hat{d}^>) r^k = (\hat{I}_i^>{}^k) \times dr^i. \quad (81)$$

The first and perhaps most important implication of the hyperstructures is the generalization of the four directions of time [15] into multivalued forms of the type

- 1) Forward hypertime $(\hat{t}^>) = t \times (\hat{I}_t^>); (\hat{I}_t^>) = (\hat{S}_t^{-1})$
- 2) Conjugated forward hypertime $(^<\hat{t}) = t \times (^<\hat{I}_t); (^<\hat{I}_t) = (\hat{R}_t^{-1}) = (\hat{I}_t^>)^{\dagger}$
- 3) Backward hypertime $(\hat{t}^>)^d = -(\hat{t}^>); (\hat{I}_t^>)^d = -(\hat{I}_t^>)$
- 4) Conjugated backward hypertime $(^<\hat{t})^d = -(^<\hat{t}); (^<\hat{I}_t)^d = -(^<\hat{I}_t)$

In addition to the invariant

$$Length \times Unity = Hyperlength \times Hyperunity, \quad (82)$$

another invariant characterizing time in biological systems is given by

$$(t_2 - t_1) \times \hat{T} \times (t_2 - t_1) \times \hat{I} = (t_2 - t_1)^2 \times 1, \quad (83)$$

$$(t_2 - t_1) \times \hat{T}^d \times (t_2 - t_1) \times \hat{I}^d = (t_2 - t_1)^2 \times 1, \quad (84)$$

$$\begin{aligned}
 (t_2 - t_1) \times \hat{T}^> \times (t_2 - t_1) \times \hat{I}^> &= \\
 (t_2 - t_1) \times \hat{T}^< \times (t_2 - t_1) \times \hat{I}^< &= \\
 (t_2 - t_1) \times \hat{T}^{>d} \times (t_2 - t_1) \times \hat{I}^{>d} &= \\
 (t_2 - t_1) \times \hat{T}^{<d} \times (t_2 - t_1) \times \hat{I}^{<d} &= \\
 (t_2 - t_1)^2 \times 1. &
 \end{aligned} \tag{85}$$

By means of hyperunity one can generalize the action as a hyperaction and define the forward hypernewton equations

$$(\hat{m}^>) \frac{(\hat{d}^>)(\hat{v}_k^>)}{\hat{d}\hat{t}^>} - (F_k)(\hat{t}^>, \hat{r}^>, \hat{v}^>); k = x, y, z. \tag{86}$$

With an analogous logic, we also arrive at the equations hyperlagrange and hyperhamilton equations.

9 Applications in physics

As we have seen, the implications of hadronic mechanics in physics are numerous and can only be examined to a limited extent in this work, including:

9.1. Bohm's hidden variables

Hadronic mechanics was conceived in 1978 [83] (see also the subsequent studies [5] [9]) to provide explicit and concrete realizations of Bohm's hidden variables [57] [58] via the Santillian S of isoproduct (1) and realizations of type (5) [9] [59] [60], as a result of which *Bohm's variables are hidden in the associative product*, by therefore confirming Bohm's view on the possible recovering of classical determinism for operator formulations.

9.2. Entanglements

The main objective of hadronic mechanics is the representation of extended wave packets in conditions of deep mutual entanglements with ensuing non-linear, non-local and non-potential interactions that, evidently, are not representable via the Hamiltonian.

R. M. Santilli [61] has first proved the exact character of Einstein's criticism of "quantum entanglements" (i.e., the representation of entanglements via quantum mechanics) because, when the entangled particles are at large mutual distances r , there is no known interconnecting interaction derivable from a potential $V(r)$.

In this case, the Hamiltonian of quantum mechanics $H = K + V$ reduces to the kinetic energy $H = K + V = K = \sum_{k=1,2} (1/2m_k) p_k^2$ and consequently, *quantum mechanics can only represent entangled particles as being free*.

Santilli has then shown that the non-Hamiltonian interactions of particle entanglements admit a full quantitative representation via the Santillian S of the isoassociative product (1) [61] [73], by therefore achieving a quantitative representation of particle entanglements in reversible, irreversible and multi-valued conditions at the foundation of seminal advances in physics, chemistry and biology [62].

9.3. Isorelativities

Isotopies allow axiom-preserving generalizations of Galileo and Einstein special relativity into broader relativities for the representation of particles in deep mutual entanglement, nowadays known as *iso-Galilean and isospecial relativities* or *isorelativities* for short, that were first proposed by R. M. Santilli in paper [63] of 1983 on the Lorentz-Santilli generalization $\hat{SO}(3.1)$ for extended particles of the Lorentz symmetry $SO(3.1)$ for point-like particles of special relativity. Santilli then studied isospecial isorelativity in numerous works, including Refs. [11] [12] [54] and others.

The basic isoaxioms for the relativistic motion of extended particles in the k -direction of inhomogeneous and anisotropoic physical media with local density n_{4k} , are:

ISOAXIOM-I: The speed of light within (transparent) physical media is given by:

$$C_k = \frac{c}{n_{4k}}. \quad (87)$$

ISOAXIOM-II: The maximal causal speed within physical media is given by:

$$V_{max,k} = c \frac{n_k}{n_{4k}}. \quad (88)$$

ISOAXIOM-III: The addition of speeds within physical media follows the isotopic law:

$$V_{tot,k} = \frac{\frac{V_{1k}}{n_k} + \frac{V_{2k}}{n_k}}{1 + \frac{V_1 V_2}{c^2} \frac{n_{4k}^2}{n_k^2}}. \quad (89)$$

ISOAXIOM-IV: The dilation of time, the contraction of lengths, the variation of mass and the energy equivalence within physical media follow the isotopic laws:

$$t'_k = \hat{\gamma}_k t, \quad (90)$$

$$\ell'_k = \hat{\gamma}_k^{-1} \ell, \quad (91)$$

$$m'_k = \hat{\gamma}_k m, \quad (92)$$

$$\hat{E}_k = m V_{max,k}^2 = m c^2 \frac{n_k^2}{n_{4k}^2}, \quad (93)$$

where:

$$\hat{\beta}_k = \frac{\frac{v_k}{n_k}}{\frac{c}{n_{4k}}}, \quad (94)$$

and

$$\hat{\gamma}_k = \frac{1}{\sqrt{1 - \hat{\beta}_k^2}}. \quad (95)$$

ISOAXIOM-V: The frequency shift within physical media follows the isotopic law (for null aberration)

$$\omega_k = \hat{\gamma} \left(1 - \hat{\beta}_k \cos(\hat{\alpha}) \right) \omega. \quad (96)$$

For experimental verifications of the above isoaxioms in transparent media, including the first known causal representation of the superluminal electrons originating the Cherenkov light, see [54] and [62].

Santilli's isotopic formulation of gravitation, including a geometric representation of interior and exterior gravitation and their apparent resolution of some of century-old open problems of Einstein's general relativity are presented in Sections 8.2 and 8.3 of [54] (see also the problem of the origin of gravitation outlined in point 3 of Sect. 9.4).

9.4. Isocosmology

Isoaxiom V has been verified by a series of accurate experiments in Earth's atmosphere done in the USA and Europe (see [74] and papers quoted therein), where Einstein's relativity is inapplicable because the axioms of special relativity require our space-time to be homogeneous and isotropic, while our atmosphere is inhomogeneous and anisotropic, thus implying the inapplicability of the geometrical foundations of special relativity in favor of the Minkowski-Santilli isogeometry and related isotopic covering of the Poincaré symmetry $\hat{\mathcal{P}}(3.1)$ [53].

The Doppler-Santilli Isoaxiom V admits the expansion for the frequency shift of light propagating in our atmosphere

$$\Delta\omega = \pm \frac{v_k}{c} \pm H_k d, \quad (97)$$

where: H_k is (approximately) a constant; d is the distance covered by light; $\pm \frac{v}{c}$ is the standard Doppler effect, and $\pm H d$ is the new Santilli isoshift describing the decrease (increase) of the frequency for light propagating within a gaseous

medium at low (high) temperature without any relative motion between the source, the medium and the observers.

In particular, the latter effect known as isoredshift (isoblueshift) essentially consists of the release of energy by light to (acquisition of energy by light from) the medium, thus requiring no relative motion, and these new effects have received a rather wide experimental verification, firstly, for individual laser lights, and secondly, for the solar spectrum [62].

Santilli's isoredshift phenomenon is of fundamental importance for our understanding of nature and the cosmos because it provides a consistent alternative explanation of the cosmological redshift to the current interpretation via the expansion of the universe. In fact, said phenomenon suggests that light loses energy on its way to the solar system due to interaction with the intergalactic medium mostly composed by extremely cold Hydrogen gas.

Within the indicated experimental setting, the background microwave radiation results to be due to the continuous release by intergalactic Hydrogen of the energy continuously acquired by intergalactic light during its travel to reach Earth.

Independently from the experimental verification on Earth [74], Santilli's isoredshift representation of the cosmological redshift of galactic light and related cosmological isosymmetry $\hat{P}(\exists.\infty)$, also known as *Santilli's isocosmology* [64], are preferable over the representation via the expansion of the universe because the latter implies the Big Bang theory, namely, a theory with a multitude of problems still unresolved after decades of studies [110].

It should also be recalled that Einstein, Hubble, Hoyle, Zwicky, Fermi, de Broglie and other famous scientists died without accepting the expansion of the universe because the representation of Hubble's law on the cosmological redshift of galactic light with the Doppler axiom of special relativity, $z = Hd = \frac{v}{c}$ (where now H is Hubble's constant and d is the travel of galactic light to reach us) implies a return to the Middle Ages with Earth at the center of the universe due to the dependence of the redshift from all possible *radial directions from Earth* [62] [110].

9.5. Heisenberg's uncertainty principle

R. M. Santilli has additionally shown that Heisenberg's uncertainty principle for electromagnetic interactions is inapplicable for extended nucleons under strong nuclear interactions by therefore creating the grounds for advances in nuclear physics that would be otherwise impossible.

Santilli first submitted the hypothesis of the inapplicability of Heisenberg's uncertainty principle in nuclear physics in the 1981 paper [75] written at Harvard University under DOE support because, in view of the strength of nuclear forces, the standard deviations for nuclear constituents must be *smaller* than the corresponding deviations for atomic electrons orbiting in vacuum around their nuclei,

which hypothesis was confirmed in the 1994 paper [76] on the uncertainties under gravitational collapse. The progressive recovering of Einstein's determinism with the increase of the nuclear density was proved in the 2019 paper [77] and elaborated in details in Refs. [78]-[80] (see independent reviews [81] [82]), resulting in a new principle originally submitted under the name of *Einstein's isodeterminism* [77] and nowadays known as *hadronic isodeterminism*.

In summary, the recovery of determinism is evidenced by the formula

$$\begin{aligned} \Delta r \Delta p &\simeq \frac{1}{2} \langle \hat{\psi}(\hat{r}) | * [\hat{r}, \hat{p}] * | \hat{\psi}(\hat{r}) \rangle = \\ &= \frac{1}{2} \langle \hat{\psi}(\hat{r}) | \hat{S}[\hat{r}, \hat{p}] \hat{S} | \hat{\psi}(\hat{r}) \rangle = \frac{1}{2} \int_{-\infty}^{+\infty} \hat{\psi}(\hat{r})^\dagger \hat{S} \hat{\psi}(\hat{r}) d\hat{r} = \frac{1}{2} S \end{aligned} \quad (98)$$

generalising Heisenberg's uncertainty principle in conditions where quantum mechanics is unapplicable.

9.6. Pauli's exclusion principle

An important contribution by R. M. Santilli in need of experimental verification has been the apparent lack of universal validity of Pauli's exclusion principle in physics.

The studies in the field initiated with the 1978 paper [83] written at Harvard University under DOE support indicating the need for experimental verifications of Pauli's exclusion principle beginning with its title. The studies were then continued in the 1990 paper [84] and completed in the 1998 paper [85] on the generalized structure of the notion of spin for extended particles under contact non-Hamiltonian interactions (see also [79]).

The inapplicability of Pauli's exclusion principle in nuclear physics was readily suggested on axiomatic grounds from the inapplicability of quantum mechanics for nucleons under deep entanglements, with ensuing non-linear, non-local and non-potential interactions [49], under which conditions there is no possibility of a consistent formulation of said principle.

The progressive inapplicability of Pauli's exclusion principle in atomic structures is predicted from the increase of the entanglement of orbital electrons with increase of the atomic number due to the experimentally established decrease of inter-orbital distances.

Said entanglements of orbital electrons cause a structural generalization of the $SU(2)$ -spin Lie symmetry into the Lie-Santilli $\hat{S}\hat{U}(2)$ -spin isosymmetry [85] whose spin for the fundamental representation remains $1/2$, but the isostates are generalized due to an explicit and concrete realization of Bohm's hidden variables by the Santillian S which has to be included in *all* possible products [84], with ensuing lack of general antisymmetric character of the isostates.

For example, to represent the entanglement of orbital electrons, the antisymmetric state $|\psi(x, y)\rangle = \sum_{x,y} N(x, y) |x, y\rangle$, $N(x, y) = -N(y, x)$ representing

Pauli's exclusion principle on a Hilbert space $\mathcal{H}$ over the field of complex numbers $\mathcal{C}$, has to be mapped into the isotopic form $|\hat{\psi}(\hat{x}, \hat{y})\rangle = \Sigma_{\hat{x}, \hat{y}} M(\hat{x}, \hat{y}) S|\hat{x}, \hat{y}\rangle$, $\hat{x} = x\hat{1}$, $\hat{y} = y\hat{1}$ on an iso-Hilbert isospace $\hat{\mathcal{H}}$ over the isofield $\hat{\mathcal{C}}$, where the isocoeficient M may remain antisymmetric on $\hat{\mathcal{H}}$ over $\hat{\mathcal{C}}$, but the projection of the term MS on our space-time is, in general, no longer antisymmetric.

9.7. The structure of unstable particles

It should be indicated that, thanks to the new mathematics, relativities and physical laws, hadronic mechanics has permitted basically new quantitative *structure models* of unstable particles which: 1) Have physical constituents produced free in their decays; 2) Admit mechanisms for the spontaneous character of the decays; and 3) Achieve compatibility with conventional $SU(3)$ -type *classifications* of particles, including:

1) The representation of all characteristics of the π^0 meson, including charge radius, mass, spin, charge, magnetic moment, mean life and spontaneous decays, in which the π^0 is a hadronic bound state of an electron e^- and a positron e^+ ("compressed positronium" down to 1 fm of mutual distances), whose spontaneous decay is due to electron-positron annihilation (see the original proposal in Section 5.1 of the 1978 paper [83], recent update [80] and papers quoted therein). The $\pi^\pm$ mesons are characterized by a hadronic bound state of a π^0 meson and an $e^\pm$ electron totally immersed/entangled in its structure, with ensuing Lie-isotopic angular momentum equal but opposite to the spin for stability and null total angular momentum [83] [80]. The remaining mesons result to be hadronic bound states of $e^\pm$, π^0 and $\pi^\pm$ in conditions of total mutual immersion/entanglement.

2) The representation of all characteristics of the $\mu^\pm$ leptons, including charge radius, mass, spin, charge, *anomalous* magnetic moment, mean life and spontaneous decay, in which the $\mu^\pm$ leptons are bound states of an electron-positron pair and an $e^\pm$ at mutual distances bigger than 1 fm , i.e., being such for the ground state of the angular momentum to be null, resulting in a state with spin 1/2 [83] [80]. The first and only known numerically exact and time invariant representation of the *anomalous magnetic moment of the muons* via relativistic hadronic mechanics is presented in the recent paper [86]. The structure of the remaining leptons follows bootstrap guidelines similar to those for mesons.

3) Stars initiate their lives as aggregates of Hydrogen that increase by accretion during their travel in Hydrogen rich intergalactic spaces. When the pressure in their interior reaches sufficient values, stars synthesize the neutron n as a "compressed Hydrogen atom" [87], i.e. as an electron e^- compressed inside the hyperdense proton p^+ . Thereafter, Stars initiate the synthesis of Deuterons D from a proton and a neutron, after which they initiate the production of light.

In view of the above fundamental character, R. M. Santilli dedicated decades of research to the neutron synthesis and did achieve the first and only known, exact and invariant representation of *all* characteristics of the neutron as a hadronic bound state of an electron and a proton at the non-relativistic and relativistic levels (see the review in [62] and original references quoted therein).

Jointly, Santilli dedicated an additional decade of experimentations on the laboratory synthesis of the neutron from a commercially available Hydrogen gas [89], resulting in the production and sale by the U.S. publicly traded company Thunder Energies Corporation of the Directional Neutron Source (DNS), namely, an equipment producing on demand a flux of thermal neutrons synthesized from a Hydrogen gas in the desired direction and with the desired intensity [90].

By recalling that stars initiate their lives as being aggregates of Hydrogen and, thanks to the new hadronic uncertainty principle, Santilli achieved a rigorous reduction of all matter in the universe to protons and electrons in conditions of increasing complexities, thus requiring more advanced mathematics [44].

Additionally, in his 1974 paper [92] while being in the faculty of the Institute for Theoretical Physics at MIT, Santilli proved the Poincaré hypothesis that the exterior gravitational field $G_{\mu\nu} = R_{\mu\nu} = \frac{1}{2}Rg_{\mu\nu}$ of a *neutral* massive body is entirely representable via the electromagnetic *tensor* $T_{\mu\nu}^{int}$ characterized by the rotating interior changes.

Note that the Poincaré-Santilli origin of gravitation cannot be consistently studied via Einstein's general relativity because: the former deals with the interior gravitational problem while the latter solely deals with the exterior gravitational problem; the former requires a "source" of the gravitational field which is prohibited by the latter as a necessary condition to represent gravitation via the curvature of space; the former entirely reduces the mass/energy of a "neutral" body to the interior electromagnetic field $G_{\mu\nu} = KT_{\mu\nu}^{int}$, while the latter do admit the field $G_{\mu\nu} = R_{\mu\nu} = \frac{1}{2}Rg_{\mu\nu} = K'T_{\mu\nu}^{Ext}$ in the right-hand-side of the field equations, but only for the *total charge* of the body whose contribution to gravitational field, e.g., of Earth, is of the order of $T_{\mu\nu}^{ext} \approx 10^{-35}G_{\mu\nu}$, thus being ignorable for the study of the origin of gravitation; and for other insufficiencies of general relativity studied in works [93] [94].

In view of the above momentous implications, the supporters of the conjecture that unidentifiable point-like quarks are the physical constituents of the hyperdense neutron, to achieve credibility, should prove that at the time of the neutron synthesis the permanently stable proton and electron disappear to be replaced by the hypothetical quarks and additionally, at the time of the spontaneous decay of the neutron, the hypothetical quarks should disappear and be replaced by the permanently stable proton and electron [88].

9.8. The structure of stable nuclei

Thanks to all preceding mathematical, theoretical and experimental advances, Santilli additionally achieved the first and only known exact and invariant hadronic representation of *all* characteristics of the Deuteron [95], as well as its stability [96], despite the natural instability of the neutron and the strongly repulsive protonic Coulomb forces, resulting in a model which is extendable to all stable nuclei [97].

9.9. HyperFusions

As it is well known, the repulsive Coulomb force between natural, thus positively charged nuclei, acquires such extreme values at mutual distances of the order of 1 fm to prohibit the achievement of sustainable and controllable nuclear fusions.

To initiate studies toward the resolution of the above Coulomb barrier, Santilli proposed the synthesis via specially designed hadronic reactors of pseudo-nuclei, which are hadronic bound states of electrons and nuclei that, for sufficiently small values of the atomic number, are negatively charged, thus being attracted by natural positively charged nuclei, resulting in inevitable nuclear fusions called HyperFusions [98]- [99].

The existence of Santilli's pseudo-nuclei has been confirmed by experiments [100] which also provide a disproof of Heisenberg's uncertainty principle in nuclear physics. The sustainable production of excess thermal energy over the used energy has been independently certified in Refs. [101]-[104] jointly with the lack of harmful radiations.

10 Applications in chemistry

The application of hadronic mechanics to chemistry has naturally opened the way to new advances, marking the beginning of "hadronic chemistry" [13], with new interpretations and predictions in the field of chemical bonds as well as phenomena such as superconductivity.

10.1. Molecules

Following the achievement of maturity in 1996 of isomathematics [44] and related isomechanical branch of hadronic mechanics [8] [9], Santilli confronted the central open problem of quantum chemistry: the lack of representation in one century of the *attraction* between identical electron pairs in valence bonds as existing in nature, with ensuing lack of a quantitative representation of molecular structures. In fact, the *repulsive* Coulomb force between identical electron pairs at valence mutual distances reaches such astronomical values (of about 230 Newtons) that cannot be overcome by any existing, quantum chemical valence bond.

Santilli first wrote a series of papers reviewed from Chapter 4 on of the 2001 monograph [13] on the generalization of the quantum notion of point like *particles*

under the Poincaré symmetry $P(3.1)$ into extended *isoparticles* in deep mutual entanglement under the spinorial covering of the Poincaré symmetry $\hat{P}(3.1)$ [53], Santilli then achieved the first and only known *attraction* between the identical electrons of a valence pair [13] reviewed in details in Appendix B, resulting in the new notion of valence bonds called *strong isovalence bonds* which are characterized by very small values of the Santillian S , with ensuing rapid convergence of perturbative series.

Thereafter, Santilli and the chemist Donald Shillady achieved the first known exact and invariant representation of binding energies as well as electric and magnetic moments of the Hydrogen [65] and water [66] molecules.

10.2. Magnecules

Following the achievement of a quantitative representation of molecular structures, Santilli confronted a second, century old, open problem in chemistry particularly important for fuel combustions and clean environmental usages: the rather general belief that the valence bond and related chemical species of *molecules* can represent the bond of all possible clusters existing in the universe.

Following due mathematical, theoretical and experimental studies, after two centuries of dominance in chemistry by the chemical species of molecules, Santilli introduced in the 1998 memoir [107] the new chemical species of *molecules* which are stable clusters comprising individual atoms (such as H, O, C), dimers (like $H-O, C-H$), and conventional molecules (e.g., $H_2, C-O, H-O-H$) bonded together by opposing magnetic polarities of toroidal polarizations of atomic orbitals, either existing in nature, e.g., in biological structures, or industrially induced in spherical atomic distributions (see [13] and quoted references). Note that the term "magnecules" was introduced by Santilli to distinguish them from conventional "molecules" as well to emphasize the magnetic origin of their bond.

To substantiate the existence of magnecules, Santilli conducted systematic measurements on gases created by DC arcs submerged in liquids [107] and the use of a gas chromatograph-mass spectrometer (GC-MS) equipped with an infrared detector (IRD). The key findings from these experiments include the detection of peaks with mass up to 1,000 atomic mass units (a.m.u.) that cannot be explained via molecular bonds, all detected peaks having no IRD signature against the existence of distinct IR signatures for molecules.

Additionally, magnecules demonstrated stability at ambient temperatures and pressures and exhibited properties not accountable via molecular bonds, such as: anomalous combustion temperatures; anomalous energy content; anomalous adhesion to substances; and other features.

10.3. Liquids

Following the achievement of a quantitative representation of molecular structures

and the discovery of the new chemical species of magneccules, Santilli confronted a third, century old, open basic problem in chemistry: the attractive force between water molecules in their liquid state.

The transition of the water states from liquid to gas indicates that the attractive force between water molecules ceases to exist at the boiling temperature, by therefore suggesting that liquid water has a magnecular structure [70] and, more specifically, that $100^{\circ}C$ is the Curie temperature of the water magnecular bond.

An inspection of the water molecule $H-O-H$ indicated that the two H -atoms of the water molecule have precisely the toroidal distribution of magnecular structures, thus having magnetic polarities North-South along the two symmetry axes that can bond with opposite polarities resulting in the conception of liquid water as a state in which each water molecule is bonded to four other water molecules.

Needless to say, the confirmation of the magnecular structure of liquid water would imply that all liquids have the same structure [70]. As an example, the elementary constituents of ordinary gasoline are gasoline molecules while the gasoline liquid state would be characterized by magnecular bonds of gasoline molecules.

10.4. Magnecular fuels

The above mathematical, theoretical and experimental studies lead to the industrial development and sale by the U. S. publicly traded company Magnegas Corporation and others of a variety of new gaseous fuels with magnecular structure synthesized from liquid feedstock among which we mention: the new gaseous fuel magnegas with complete combustion (no combustible contaminants in the exhaust, i.e., no C-O, no HC, etc.) [13]; the new chemical species of Magnesium-Hydrogen whose specific weight and energy content are a multiple those of the conventional Hydrogen $H-H$ [67]; the new gaseous and combustible form of water (called by Santilli the HHO gas) which contains all needed oxygen for combustion [68]; and others (for details, see monograph [108]).

10.5. HyperCombustion

The combination of the studies reported in this and in the preceding section lead Santilli to the proposal of the new *hypercombustion* [71] which consists in the clean combustion of fossil fuels via specially designed sparks suitable to activate the HyperFusions of Sect. 9.9 in parts per millions without harmful radiations, by therefore multiplying the power output of fossil fuels, whose sole gaseous exhaust is Carbon Dioxide CO_2 that can be collected and recycled into Carbon and Oxygen via the hadronic reactors of Sect. 9.9.

11 Applications in biology

The biological studies reported in this section were initiated in the 1990's by the Australian concilogist C. Illert [27] with his discovery that the time evolution of sea shells cannot be consistently represented in the Euclidean space of our sensory perception because requiring a generalized space with two values for each coordinate (see Appendix A for details).

Independently from C. Illert, R. M. Santilli introduced in the early 1980's iso-, geno- and hyper- mathematics for novel physical advances and proposed in 1994 their applications to biology [14].

Following initial studies by a number of biologists, the next important event in the field occurred with the first and only known quantitative representation of life intended as the difference between inorganic and organic molecules by R. M. Santilli and the Greek mathematician Thomas Vougiouklis [72].

The next significant event has been the application to biology by E. Velardo and F. Inglese of the lifelong physical studies on entanglements by R. M. Santilli [111] (see also the related studies on correlations of Appendix C), which studies have shown that a number of anomalous actions by biological entities, which are generally considered to be supernatural, can in fact be quantitatively represented as due to the entanglement of the wave packets of biological constituents.

Additionally, Santilli's magnecules (Sect. 10.3) have important applications in biology due to their crucial role for the liquid state of water, and therefore, for the entire body of a living organism.

Additionally, magnecules have an important role for expected new advances in other biological aspects. For instance, it has been shown that a human DNA does not have six billions valence electrons necessary to bond its billion atoms into a collection of molecules. Consequently, in Santilli's view, the DNA cannot be consistently qualified as being a "molecule" because it appears to have an extremely complex chemical composition including, of course, molecules, but also magnecules as outlined in Sect. 10, as well as additional, more complex chemical species currently under study, such as that of the multivalued "hypermagnecules".

Also, A. L. Kalcker has advanced the hypothesis that HHO magnecule plays a fundamental role in physiology in the oxidation and energy production of the organism [69].

Needless to say, Santilli's iso geno- and hyper-mathematics are expected to have intriguing applications to our notion of time. Consider, for instance, our instinctive perception of time. When investigating any physical, chemical or biological structure, we instinctively assume that they have our own time.

Biological structures represented with isotopic, genotopic and hyperstructural methods generally have their own/intrinsic time which is generally different than our own perception of time [14], both in its rate of flow and in its direction, as well

as being of progressively increasing complexity depending on the complexity of the system considered.

Assume the isotopic representation of certain biological structures. The problem which has to be addressed and resolved in due time is whether we are referring to a purely mathematical property or to an actual intrinsic behavior of nature.

For these studies, consider the following isoinvariant [8]

$$D \times I_t = \hat{D} \times \hat{I}_t, \quad (99)$$

where: D is the considered time interval; I_t is our unit of time (e.g., $I_t = 1 \text{ sec}$); $\hat{D}$ and $\hat{I}_t$ are the corresponding isotopic forms.

From this invariant it is possible to derive the time interval of the organism considered because, in the event the unit of time becomes an isounit with values $\hat{I}_t = 10 \times I_t$. Then, the intrinsic time flow of the considered biological structure must decrease tenfold with respect to our time flow as a necessary condition for the entity to be perceived by our senses as evolving with our time.

The new isomathematics suggests that there are infinite dimensions of time and that time appears one-dimensional only when projected into our sensory perception.

Studies have shown that isotopic representations of biological structures may perform a closed loop inside the forward light cone, i.e., the capability of initiating at one point t in space-time, move arbitrarily forward or backward in time and then returning to the original time t . The emergence of multivalued hyperstructures is simply unavoidable if one reflects a moment on the fact that the cells of a complex organism are all generally different, thus requiring different isounits of space and time.

A similar argument is valid with regard to space, since space itself can be different from one organism to another. Thus, the perceived shapes can differ depending on the observer as well as the dimensions (an object can be perceived as very small or very large in different isogeometries) [14] and the evolution over time of the shape goes against our intuition.

For example, an object of 0.03 cm in diameter expressed in a unit of 1 cm appears to be 300 cm in a unit of 0.0001 cm.

Hyperstructures can cause changes in size such as isotopie, and also an increase or decrease of the same dimensionality. We are not sure of the correctness of this description but we believe that our perception of space is insufficient for quantitative scientific studies in biology.

We should also not forget that simple observations of the behavior of plants indicate quite clearly the existence of anomalous space behaviors, that is, space behavior anomalous with respect to our perception of space. We have all observed plants from ordinary seeds grown inside bottles which stop their growth without

reaching the walls, or the rather peculiar growth of plants along directions compatible with their environment. Since plants do not have eyes, the existence of a space behavior in biological structures beyond our perception appears to be evident. The only issue which is open on scientific grounds is its correct quantitative representation.

The implications for locomotion are interesting. Biological structures represented with isotopic, genotopic and hyperstructural methods can perform internal motion according to Santilli "geometric propulsion" [15] that is, the possibility of locomotion from one point to another via the alteration of the geometry itself, without any actual motion or application of a Newtonian force.

Appendix A: Isotopic representation of sea shells

C. Illert [27] has shown that a graphic or computer representation of sea shell growth require multivalued Euclidean spaces subsequently formulated by R. M. Santilli as hyperspaces [14]. In fact, the use of the Euclidean geometry alone does not allow to represent sea shell growth because they are first distorted and then break in computer simulations.

Therefore Illert has shows the possibility of obtaining a correct representation of sea shell *Angaria delphinus* by doubling the number of dimensional axes.

The equations describing the shell are:

$$x = ae^{\alpha\Phi} (1 + e^{\Phi} \cos(2\gamma\Phi)) \cos\Phi, \quad (100)$$

$$y = ae^{\alpha\Phi} (1 + e^{\Phi} \cos(2\gamma\Phi)) \sin\Phi, \quad (101)$$

$$z = be^{\beta\Phi} \sin(\gamma\Phi). \quad (102)$$

The Lagrangian must have a structure of the type:

$$L = K_1 (\psi \times \psi)^n + K_2 (\psi \times \xi)^m + K_2 (\xi \times \xi)^m. \quad (103)$$

The growth of the shell is simulated correctly with the isolagrangian:

$$\hat{L} = \left[K_1 \left(\frac{\hat{d}\xi}{\hat{d}t} \hat{\times} \frac{\hat{d}\xi}{\hat{d}t} \right)^{\hat{n}} + K_2 \left(\frac{\hat{d}\xi}{\hat{d}t} \times \xi \right)^{\hat{m}} + K_2 (\xi \times \xi)^{\hat{p}} \right] \hat{I}. \quad (104)$$

Similar representations are possible for all sea shells.

Appendix B: Isotopic representation the valence bonds

Quantum mechanical isotopies (hadronic mechanics) has been able to represent the attraction between the two identical electrons in valence bonds outlined in Sect. 10. This result can be reviewed as follows.

Thanks to the use of hadronic mechanics, Santilli has first shown in the 1978 memoir [83] the existence of a new electron-positron bound state in relation to positronium (the only bound state predicted by quantum mechanics) which is identifiable with π^0 meson (Sect. 9.7) due to the non-local and non-Hamiltonian interaction of the wave packets. These interactions can be represented via the Hulthen potential, which is predominant over the Coulomb interaction when distances are very short.

The model therefore provides a quantitative representation of the transition of the positronium into the π^0 -meson

$$(e_{\uparrow}^-, e_{\downarrow}^+)_{QM} \longrightarrow \pi_0 = (e_{\uparrow}^-, e_{\downarrow}^+)_{HM}. \quad (105)$$

This phenomenon also provides a quantitative representation of the Cooper pairs in superconducting materials and studies conducted by Animalu and Santilli [109] show full compatibility of this hypothesis with experimental tests of superconductivity.

A Cooper Pair (CP) can then be represented via a structure similar to that of valence bonds

$$CP = (e_{\uparrow}^-, e_{\downarrow}^-)_{HM}, \quad (106)$$

the model has also been able to predict the experimental behavior of the material $YBa_2Cu_3O_6$, giving further scientific credibility to the model.

The modified Schrödinger equation is then given by

$$\left(\frac{1}{2m} \hat{p}_k S \hat{p}^k + \frac{e^2}{r} \hat{I} - z \frac{e^2}{r} \right) S \hat{\psi}_{\uparrow}(t, r) = E \hat{\psi}_{\uparrow}(t, r), \quad (107)$$

where the term $-z \frac{e^2}{r}$ denotes the potential of the electric field of the atomic nucleus, since the valence electrons are not isolated in space.

An explicit expression of the Santillian was first located in [83] and it is given by:

$$\hat{I} = i/\hat{S} = e^{-\langle \hat{\psi}_{\uparrow} | \hat{\psi}_{\downarrow} \rangle} \simeq 1 - \langle \hat{\psi}_{\uparrow} | \hat{\psi}_{\downarrow} \rangle \frac{\psi_{\uparrow}}{\psi_{\downarrow}} + \dots \quad (108)$$

$$\hat{S} = e^{+\langle \hat{\psi}_{\uparrow} | \hat{\psi}_{\downarrow} \rangle} \simeq 1 + \langle \hat{\psi}_{\uparrow} | \hat{\psi}_{\downarrow} \rangle \frac{\psi_{\uparrow}}{\psi_{\downarrow}} + \dots \quad (109)$$

leading to the Hulthen potential, which expresses the contact potential:

$$V_0 \frac{e^{-\frac{r}{R}}}{1 - e^{-\frac{r}{R}}} \simeq V_0 \frac{R}{r}, \quad (110)$$

with $V_0 = e^2 \langle \hat{\psi}_{\uparrow} | \hat{\psi}_{\downarrow} \rangle$.

It is a great achievement that the isotopic model of the pion π^0 correctly predicts all meson characteristics such as resting energy, charge, radius, magnetic moment and even decay time.

The result becomes all the more remarkable when it has been extended to unstable mesons and unstable baryons, including the representation of neutron synthesis from protons and electrons, a process of great importance that occurs in stars. The new isotopic structure of the neutron $n = (p+, e-)_H M$ synthesized in stars should have significant repercussions also in theoretical biology.

In conclusion, we observe that quantum mechanics can be considered a special case of hadronic mechanics in which $\langle \hat{\psi}_\uparrow | \hat{\psi}_\downarrow \rangle = 0$; $\hat{I} = 1$, and occurs when the superposition of the wave packets of two electrons (at the origin of the non-local interaction) becomes negligible.

Appendix C: Isotopic representation of correlations

In particle physics the Bose-Einstein correlation has been experimentally detected in the proton-antiproton annihilation at both high and low energies. It may be recommendable to briefly outline the latter correlation because its reformulation in theoretical biology is straightforward. In the Bose-Einstein correlation, the $p - \bar{p}$ fuse together into a state called the fireball, which then decays rapidly into various particles whose end results are mesons (obeying the Bose-Einstein statistics) which, even though at large distances, are correlated.

In the 1992 memoir [112], R. M. Santilli has shown that quantum mechanics cannot consistently represent the Bose-Einstein correlation (see also paper [113]) in view of the following insufficiencies. Protons and antiprotons are not ideal spheres with points in them, but are instead constituted by some of the densest media measured in laboratory by mankind until now. Being the result of the mutual penetration of the hyperdense protons and antiprotons, the fireball is therefore one of the most general known non-local integral systems. But nonlocal-integral interactions are non-Hamiltonian both conceptually and technically. It then follows again that quantum mechanics is not expected to be exactly valid for the Bose-Einstein correlation in view of its central requirement of representing everything with one single quantity, the Hamiltonian.

But even assuming that the above insufficiency is by-passed via not so infrequent machinations to preserve old knowledge (e.g., the addition in the Hamiltonian of the "nonlocal-integral potential" (which, has no mathematical or physical sense), quantum mechanics still remains structurally unable to represent correlation in an exact way.

This is due to the limitations of its very axioms as compared to the experimental evidence of the correlation. As an example, the two-body quantum mechanical

axiom of expectation value of the n- point correlation function is given by

$$C_n = \sum_k (< k, a|k, a > + < k, b|k, b >,) \quad (111)$$

thus lacking the cross terms $< k, a|k, b >$ representing the correlation. By comparison, the axiom of isoexpectation values of hadronic mechanics is given by

$$\hat{C}_n = \sum_{k,i,j} \left(< k, a|\hat{S}_{kk}|k, a > + < k, b|\hat{S}_{kk}|k, b > + < i, a|\hat{S}_{ij}|j, b >, \right) \quad (112)$$

and exhibits precisely the cross terms needed for a description of correlation from first axiomatic principles.

In current "semiphenomenological models", the cross terms are introduced via a number of artificial methods which, however, violate the quantum axiom of expectation values, thus confirming Santilli's view [112] that quantum mechanics cannot provide an axiomatically and physically consistent description of the Bose-Einstein correlation.

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