Chapter 1
Generators, Harmonics and Evolutionary Emergence

James N. Furze and El Hassan Mayad

Abstract Planet Earth was formed around five billion years ago; evolutionary pro-
liferations reach over four billion years. Studies of evolution are made up of differ-
ent fields of study with alternative perspectives. The current work gives a brief
review of these areas, along with modelling techniques applied to date. This chapter
demonstrates the mathematic unification of the different fields of study in order to
further an engineering-based structure for advancement in our understanding of the
pathways which lead to different constructs in life. Computational, biological and
chemical studies lead us to propose that there are two main patterns formed in evo-
lution of life – cellular and molecular.

We used a laboratory simulation to clarify the formation of polymers from mono-
mers under dynamic conditions to set a basis for future simulation. Methods dis-
cussed are of both a Bayesian and Boolean nature. Application of logistic regression
requires partitioning of variance within the systems; after discussing the background
required, we made use of application of higher mathematic technique (multi-
objective genetic algorithm) to generate variance within the different scales of evo-
lution, the result of which was analogous with the Fisher equation model of gene
distribution within populations. The results of the distribution were subjected to
least squares polynomial regression in order to reinforce the rational truth of the
models formed. Each copula distribution was noted in univariate terms and applied
to Sklar's theorem in order to give a concise description of the pathways as alterna-
tive functions. Laboratory simulated data was also subjected to a robust linear

J. N. Furze (✉)
Royal Geographical Society (with the Institute of British Geographers), London, UK

Laboratory of Biotechnology and Valorization of Natural Resources,
Faculty of Sciences-Agadir, Department of Biology, Ibn Zohr University, Agadir, Morocco

Control and Systems Engineering Department, University of Technology-Iraq, Baghdad, Iraq
e-mail: james.n.furze@gmail.com; jamesfurze@hotmail.com

E. H. Mayad
Laboratory of Biotechnology and Valorization of Natural Resources,
Faculty of Sciences-Agadir, Ibn Zohr University, Agadir, Morocco
e-mail: e.mayad@uiz.ac.ma

regression and the resultant variance plotted. Field and laboratory trials validate the existence of triangular relationships within communities; further harmonic constants between interacting species may be found. Variance in the trials showed sine/cosine contraction and expansion, similar to that seen in mathematical and genetic results covered. Extensive use of copular frameworks, Mamdani and refined Takagi-Sugeno-Kang algorithms and additional novel DANCE (differential algorithmic network centred emergence), application of robotic techniques and functional expressions are recommended as primary constructs covering different categories of life in passive and active terms pending their interaction.

Keywords Evolution · Dynamic · Cellular · Molecular · Copula · Simulation · DANCE

1.1 Introduction

Evolution of life's kingdoms spans the last four billion years on Earth. Studies of the creation of life have involved chemistry, physics, biology, biochemistry and astrobiology. Mixtures of inorganic molecules originating in interstellar ices were seen to combine and perform self-replication with respect to their properties (Dworkin et al. 2001); ultimately these molecules formed simple organic structures seen to be capable of performing self-organization due to their chemical and physical properties in dynamic conditions of 'volcanic' Earth. In 'small ponds' assumed to form on early terrestrial landforms, dehydration and rehydration drove molecules far from equilibrium; lipids formed and captured systems of polymers through multiple cycles. This increases the chance that collections of molecules will emerge having one or more functions required for the origin of life, and crucially selection of vesicles encapsulating these polymers led to stepwise increments towards the emergence of functional systems capable of growth, reproduction and evolution (Gordon 1993; Damer and Deamer 2015).

Early life was seen to be 'communal', based purely on chemical/physical properties of molecules in the dynamic conditions of the young Earth (Deamer et al. 2006; Marzban et al. 2014). We can make use of the proposed scenario of volcanic early Earth and draw similarities with processes that occur today in locations such as in the Kamchatka peninsula in Russia or indeed any other volcanic sites.

Starting from a simple, astrophysically relevant, ice mixture (water, methanol, ammonia and carbon monoxide), a complex mixture of compounds, including amphiphiles and fluorescent molecules, is generated in low temperatures by photolysis. Adding additional sources of energy thought to be present on the pre-biotic Earth (such as temperature extremes) similar to geothermal sites enables the build-up of membranous structures from amphiphilic molecules and fats (Lu et al. 2021) and results in formation of simple nucleotide structures and ribose. Hence simple protocells capable of self-replication via RNA-directed processes have been

hypothesized and proved to exist in laboratory conditions which simulate those on early Earth (Schrum et al. 2010; Mungi and Rajamani 2015).

Reactive dynamics of the early Earth were (and still are) present in different dimensions (such as rock formation geodynamic combinations; 3:1 concentrations of formaldehyde-hydrogen cyanide; hydrated/dehydrated cycling). In the orchestra of chaotic molecular collisions, biological evolution formed as a result of a process similar to the formation of geometric fractals. Model formation in three different forms gave rise to different forms of self-replicating 'cells' in different phylogenies (Alicea 2014). However there are several points which are uncertain in the hypothesis of molecular/cellular radiations, and application of a systems approach is the leading current thinking to resolve the difference between cellular and observable/molecular scales of postulated biogenic processes (Grover et al. 2015). Initial evolutionary processes included chemical construction, implying monomer formation, polymerization reactions and formation of complex assemblies. Each of the stages is subjected to selection and differential evolution in variable scenarios. Further modelling is required to resolve evolutionary processes which occurred under alternate environmental scenarios. The future of this work is to expand the complex range of polymerization and molecules formed through experimentation in external dynamic conditions. Logically, variable dynamic conditions lead to different proportional combinations of emergent 'organic' systems (Monnard 2016).

Many models have been used to simplify and operationalize the subtle but complex mechanisms of biological evolution. The so-called toy models are gross simplifications that nevertheless attempt to retain major essential features of evolution, bridging the gap between empirical reality and formal theoretical understanding. Thirteen models which describe evolution qualify as toy models, including the tree of life, branching processes, adaptive ratchets, fitness landscapes and the role of nonlinear avalanches in evolutionary dynamics. Such toy models are intended to capture features such as evolutionary trends, coupled evolutionary dynamics of phenotype and genotype, adaptive change, branching and evolutionary transience (Alicea 2014).

The engineered design of biological processes leads our systematic understanding of evolution, though is at an early stage. Such perspective will develop as a greater volume of previous research is factored, together with increasingly advanced combinatorial Bayesian analysis. A functional-copular approach is proposed using mathematic method, resolving formation of evolutionary pathway functions (Furze et al. 2013a; Schölzel and Friedrichs 2008). Such an approach links together phylogenetic diversification through functional evolutionary adaptation both temporally and spatially over the course of evolution (Manceau et al. 2017). The first of these approaches links phylogenies through common trait structures between lineages, though does not consider the expansive functional range of the traits due to the interactions between the traits themselves. Indeed further research indicates that conserving phylogenetic diversity may often be seen as a poor strategy for conserving functional diversity with evolutionary value (Mazel et al. 2017). However, the link between functional and strategical variation may be resolved by monitoring systems at alternate time scales and in micro-, cellular and macro-ranges. Recent studies have shown that we may enable common structures which link modelling of

life forms and processes in select environments at the macro-scale (Cabral et al. 2016). Considering relations of strategical and functional diversity in Earth systems of high vulnerability accentuates sustainability within ecosystems which continue to evolve (Furze et al. 2017; Basener and Sanford 2018; Lal et al. 2021); such approaches should resolve the variance between genetic trait evolutions at different levels and may be used to feed back and give prediction of functional scenarios in the future. Retaining resilient functional and phylogenetic diversity is a major challenge in conservation today, as pressures on Earth systems result in huge losses to biodiversity amidst heavily polluted backgrounds. It is essential that we align our activities in cooperation with the needs of natural systems, or risk perversion and irretrievable changes to evolutionary pathways through cascades of feedback mechanisms operating ecologically, chemically and as a result of species interactions (Swing 2017). In order to give the appropriate weight of each subject area to the process, combinatorial mathematic method (Furze et al. 2013b), computational theory (Prusinkiewicz and Lindenmayer 1990) and simulations of evolution itself (Damer et al. 2012) have recently been formed to allow for differential scenarios across time periods.

The main motivation of this chapter is to expand/generate the variance which we may use to consider the relationships of how genetic material is formed and evolution takes place in different scales of life and within ecosystems. The use of this mathematics has been criticised due to our lack of knowledge about how the patterns vary and their causes in the first place; a motivation of this study is to clarify the origins of the generative process of evolution and project proliferation pertinent to organisms of all kingdoms.

Life's evolution is proposed to follow two main pathways: cellular and molecular systems operated simultaneously over the same time period of around four billion years. The objectives of this study are to show functions for cellular and molecular evolution, to show a discrete molecular evolutionary function and to show differences between proliferations of the split pathways of evolution (with separate chemical and biological laboratory data). We also show emergence of life within extreme environments from data collected in the field. Finally we form functional mathematics, giving a basis for expansion of evolutionary elements and their pathways, thus forming different constructs. As well as in 'exobiological' systems and explorations (Fortney et al. 2016), this will be relevant in some of the vulnerable ecosystems we are currently failing to protect, including those subject to extreme dynamics present on Earth.

1.2   Methods/Results

1.2.1   The Use of Logistic Regression as a Basis for Simulations of Evolution

Typically, the generalized logistic (Richard's) curve is used to summarize growth models; this takes the following form:

$$Yt = A + \frac{K - A}{\left(C + Qe^{-Bt}\right)^{1/v}}$$

$$(1.1)$$

In (1.1), Y is the dependent variable and t is time. A = the lower asymptote; K = the upper asymptote (carrying capacity when $A = 1$). Effectively these are 'plateau' stages within evolution which may be determined in extreme parameters, including those of volcanic thermal (oceanic) vents (Mullineaux et al. 2018; Deamer and Georgiou 2015). Cycling towards K is mathematically, chemically and biologically related as discussed in the final section of this work; B = growth rate; $v > 0$ affects near which asymptote maximum growth occurs; Q = component related values of $Y(0)$; and C = the maximum distribution of Y (usually 1). The logistic curve may be used as a simplified model for evolution as when displayed graphically it shows a sigmoid growth curve with a Poisson/Gumbel copula route. However, due to the unknown number of multiple elements (non-differentiated) which are in effect in evolutionary terms, its use is highly controversial as the logistic approach does not allow for a clear statement of error due to its non-differentiated form. It is important therefore to make a statement of the precise number of chemical elements dispersing, in order to clarify the error parameters which occur across the period of evolution; secondly it is important to clarify the length of the (approximately 4 billion years) period of evolution without which the logistic curve may not be used (Furze and Zhu 2014). Without the former two sets of variables being clarified, the use of logistic regression is a theoretical model due to Q above and time being undefined.

1.2.2 Translating Evolutionary Data Generation into Biological Terms

1.2.2.1 Evolutionary Data

Evolution operates along two pathways, evolutionary factors or genes are subject to opposing mechanisms of dispersal: conservation and mutation. In the current chapter, these pathways are referred to as cellular and molecular. The conservative cellular process gives a slower evolutionary rate over unit time, though molecular evolution gives a steeper rate over unit time. Gaining from conservation achieves a gain of frequency, though conversely mutating into a new variety results in a loss of frequency. Theoretically evolution consists of both molecular and cellular pathways simultaneously.

In the current study, we simulated the cyclical basis of hydrated/rehydrated, two-phase cycles and following Moore's law of exponential growth in the communities of molecules obtained two curves for cellular and molecular evolutionary pathways as shown in Fig. 1.1.

Figure 1.1 shows a three-dimensional structure which was obtained following Poisson simulation of vectors representing those in cellular [x] and molecular [y]
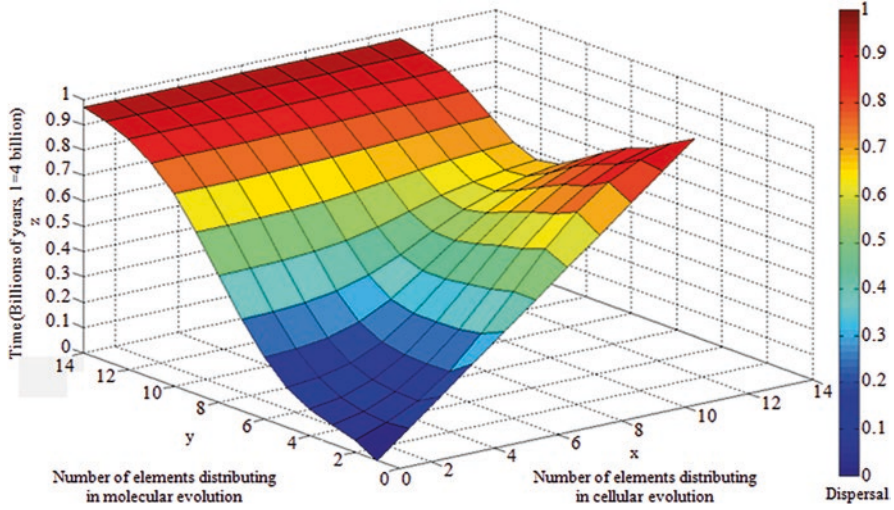
Fig. 1.1 Three-dimensional surface plot of binomial/Poisson distribution of cellular and molecular evolutionary pathways. (Furze and Mayad 2021)

evolution over time [z]. The data for these curves was simulated using a multiple objective genetic algorithm (MOGA) approach (Read et al. 2016; Furze et al. 2017) using a population size of 14 elements. The spread of each curve emulates that which is found following the Fisher equations (Edwards 1994) of natural selection and was also shown in a recent publication (Furze and Mayad 2021).

1.2.2.2 Fisher Expansion of Evolution

Let the distribution frequency of any gene in a population be x_i, where $0 \leq x_i \leq 1$. Then take the fitness that the gene confers upon the organism as w_i, where $0 \leq w_i \leq 1$. Regarding the locus where x_i acts, all genes competing for that spot have an average fitness of $\bar{w}$ such that $0 \leq \bar{w} \leq 1$. In the case that the new gene is fitter than average, then $w_i > \bar{w}$. We can now denote the change in frequency x_i, x_i', x_i'' in each generation approximately as follows:

$$\text{First generation } x_i = x_i \tag{1.2}$$

$$\text{Second generation } x_i' = x_i w_i / \bar{w} \tag{1.3}$$

$$\text{Third generation } x_i'' = x_i' w_i / \bar{w} \tag{1.4}$$

This is converted to a Fisher equation, by the frequency, Δx_i, as:

$$\Delta x_i = x_i^{'} - x_i \tag{1.5}$$

$$= x_i w_i / \overline{w} - x_i \tag{1.6}$$

$$= x_i \left(w_i / \overline{w} - 1 \right) \tag{1.7}$$

This shows that the fitter w_i makes an individual above $\overline{w}$, the greater is $w_i - \overline{w}$, so the faster x_i spreads until $\overline{w}$ rises to w_i.

Suppose a population of any given species has 1000 individuals. One individual has an allele, 'x_2', resistant to high acidity ($w_2 = 1$), and the other 999 'x_1' individuals have only 50% resistance ($w_1 = 0.5$). With low acidity, each generation ($w_i - w$) = 0, so x_2 does not increase ($\Delta x_2 = 0$). Yet once increased acidity is present, x_1 halves each generation, while x_2 increases its frequency from $x_2 = 0.001$ to $x_2 = 1.0$ by about the 18th generation.

The equation for the front curve of Fig. 1.1 is established. This shows a conserved sequence. Both curves are logistic, although the Fisher equation is iterative.

$$\Delta x_i = x_i \left(w_i / \overline{w} - 1 \right) \tag{1.8}$$

Illustrating a standard logistic convention, as in the following equation:

$$X_i = \varepsilon_i / \left(1 + \varepsilon_i \right) \tag{1.9}$$

1.2.2.3   Cellular and Molecular Evolution

Each component spread of Fig. 1.1 is shown in Figs 1.2 and 1.3 along with their least squares regression coordinates (through the 7th degree polynomial), as processed through Matlab (Version 2018a).

In Figs. 1.2 and 1.3, 'e' is notation for times 10 to the power. Shown in Figs. 1.2 and 1.3, the elements were dispersed over unit time. The difference between the curves is due to the coefficient factor ($\partial 1$) being lower in cellular evolution (larger scale, fewer elements, lower fitness), achieving a lower independent 'generator' of the curve; these are defined further in Table 1.1 which gives the rules for linear, quadratic and cubic distributions.

In Table 1.1, C represents cellular; M represents molecular; and rules 1, 2 and 3 represent the distributions shown in the case of cellular and molecular distributions, as such they may be shown in concise terms (Furze and Mayad 2021) by the expression:

$$F_i \le \sum_{j=1}^{n} M_j B_{ji}, \left(i = 1, \ldots n \right) \tag{1.10}$$
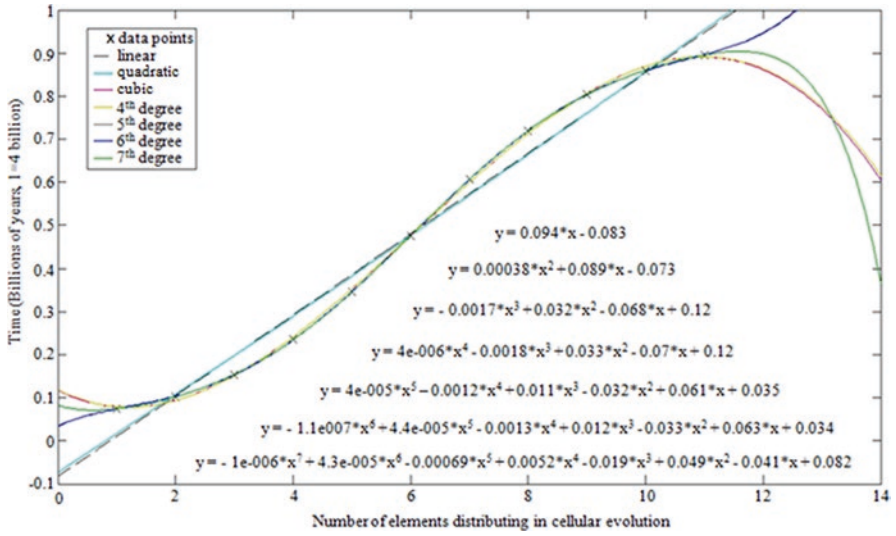
Fig. 1.2 Two-dimensional cellular evolution binomial distribution. (Furze and Mayad 2021)
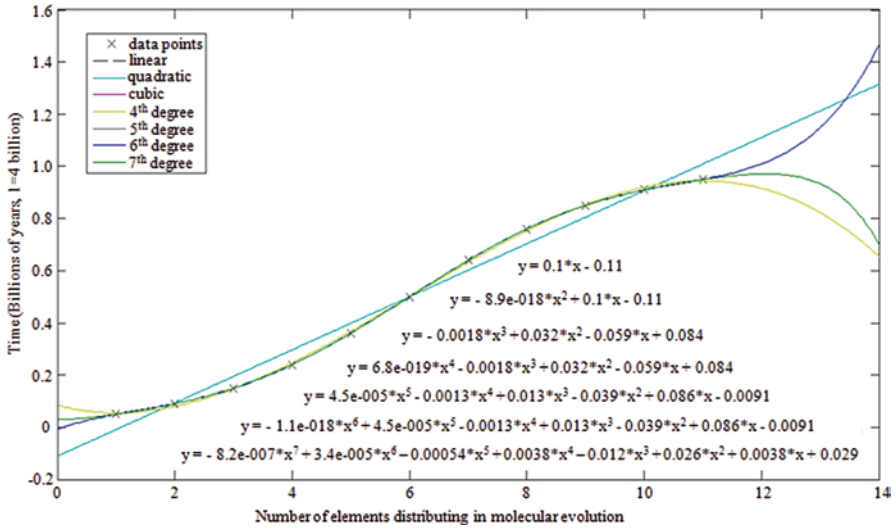

Fig. 1.3 Two-dimensional molecular evolution binomial distribution. (Furze and Mayad 2021)

Table 1.1 Rational polynomials give rules for elements dispersing through evolution (Furze and Mayad 2021)

Rule	Variables									
	$\partial 1$		$\partial 2$		$\partial 3$		$\partial 4$		ε	
	C	M	C	M	C	M	C	M	C	M
1. $Z = \partial 1x + \partial 2 \pm \varepsilon$	0.094	0.1	−0.083	0.11					0.13898	0.14225
2. $Z = \partial 1x^2$ $+\partial 2x + \partial 3 \pm \varepsilon$	0.00038	−8.9e−18	0.089	0.1	0.073	−0.11			0.13854	0.14225
3. $Z = \partial 1x^3 + \partial 2x^2$ $+\partial 3x + \partial 4 \pm \varepsilon$	−0.0017	−0.0018	0.032	0.032	−0.068	0.059	0.12	0.084	0.020352	0.02251

In (1.10) *F* represents the function of data *i* in the space of Fig. 1.2 and Fig. 1.3, *n* represents the number of elements, *j* is the spread of data *i*, *M* represents the mid-point of the linear regression and *B* represents the *Z* matrix space. Increasing the dynamic in the ratio of opposing conditions (such as hydrolysis-condensation reactions; volatile agents; amount of heat/light) on the elements dispersing in the above Poisson distributions would result in translation of the copula distributions. This may be seen as a generator function for the cellular/molecular 'switch'. The difference, subject to error (variance) in both cellular and molecular pathways, represents the fuzzy integral and consequently defines the membership functions which may be used in the following Laplace equation:

$$A = \int_u \mu A \ldots (y)/y$$

(1.11)

In (1.11) $\int_u$ stands for the union of fuzzy singletons (elements dispersing) and μA is the grade of membership in *A* (or *y*). '…' is used to represent the iterative process which may be repeated through additional dispersed elements.

The copula type we apply is referred to as a Gumbel, represented by the following:

$$\phi G_u = \left(-\log G_u\right)^{\theta G_u}$$

(1.12)

ϕG is the set generator of the union equal to the negative logarithm of the generator union, G_u raised to the power of the symmetrical difference, Θ in the generator union itself (Wang et al. 2012; Alhadlaq and Alzaid 2020; Aldhufairi et al. 2020; Ota and Kimura 2021). Further copula exploration should reveal mathematic relations around the error of the dispersed elements of cellular and molecular evolution, which gives consistent exploration of the Bayesian (discrete) nature of the distributions. Carrying out these steps via hybrid genetic algorithm and functional expansion elucidates the variance between distributions fills in the mathematic gaps to make use of logistic relations.

Although we have not clarified enough of the structural error to make use of the logistic regression expression (1.1) shown earlier, we may link the distributions

with use of Sklar's theorem (Sklar 1959; Durante et al. 2013), which states that multivariate distributions may be expressed as copula functions and evaluated as a two-dimensional distribution function. Univariate distribution functions ($F_1, \ldots F_n$) can be linked to a multivariate distribution function, H as shown:

$$H(x_1, \ldots, x_n) = C\big(F_1(x_1), \ldots, F_n(x_n)\big) \tag{1.13}$$

given that H is a unifying term that summarizes Hilbert space harmonics of discrete univariate distribution functions, which may be given in Laplacian rule-based systems (with sinusoidal variations).

In biological context we may refer to equation (1.11) as an expression of evolutionary harmonics used to summarize differential algorithmic network centred emergence (DANCE). The Gumbel Copula has been used to represent data of climatic and dynamical systems; thus (1.12) may be discretely applied to represent individual expressions of categories of life and their generation (such as that of unicellular life, microbial populations and macro-ecological populations). The elements which represent the dynamic conditions which form the union in the copula give a Poisson/skewed or sinusoidal pattern. This pattern is represented at all scales throughout life, from genetic bottlenecks imposed in vulnerable locations, island landmasses or indeed by the levels of volatile agents and extremes imposed on populations of life-units as a result of modern anthropic 'extractive' approaches. Harsh changes have been present throughout the changing conditions on planet Earth (Judson 2017). Harmonic expressions summarize complex life constructs in order that we can gain greater understanding of the parameters of life (Brack 2004; Furze and Mayad 2021) and their effects on the emergence of novel life systems.

Fundamental evolutionary patterning has been represented through Moore's law of exponential growth, the Fisher equation of natural selection (respecting genetic factors) and by using an expansive mathematical basis.

1.2.3   Laboratory Simulated Polymer Formation

Laboratory studies were carried out in order to concisely define the resolution of molecular evolution; polymers resembling nucleic acids can be synthesized from monomers in simulated hydrothermal conditions undergoing wet-dry cycles. In order to establish a formula that can describe the yield of polymers, variables to be included are as follows:

1. Fraction of monomers becoming polymers in each cycle by simple ester bond synthesis (Fe)
2. Fraction of polymers being hydrolysed back to monomers in each cycle (Fh)
3. Fraction of polymers being synthesized on a template in each cycle (Ft)
4. Fraction of monomers being degraded in each cycle (Fd)
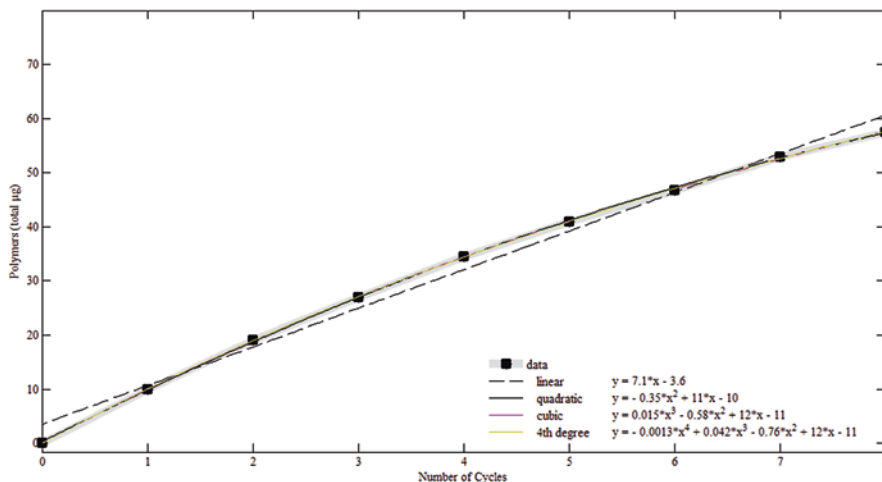5. Number of cycles

Fig. 1.4 An established framework for laboratory simulated data of polymer formation, assuming hydrolysis, degradation and template refeeding are absent

In the above, 1–4 are constants that may be chosen.

For instance, in the simplest case, assume that no polymers are hydrolysed. Now suppose that we start out with 100 μg of monomers and that 10% of them become polymerized in the first cycle. At the end of the first cycle, we will have 10 μg of polymers and 90 μg of monomers remaining.

Given the assumption that there is a 10% yield of polymers and that we use 100 micrograms of monomers at the start, data obtained is shown in Fig 1.4.

The reduction in residual variance (error) resulting from higher polynomial orders accounts for the increase in accuracy closer to the theoretical model formed from a genetic evolutionary basis such as the Fisher equation, the distribution of which is analogous to that of the data shown in Figs. 1.1, 1.2 and 1.3. The residual variance follows a sine wave pattern, the parameters of which are shown in Fig. 1.5 and indicated in the earlier steps of 1–5 which establish the conditions for the cycle. Plotting linear, quadratic, cubic and fourth-degree polynomials through Fig. 1.4 data gives a result which is consistent with the simulated data pattern shown in Figs. 1.2 and 1.3 (contact for further details). Differentiating via the Taylor expansion to a higher polynomial (up to 7th order) will account for prediction of unknown variables of hydrolysis, degradation and template refeeding; however these are not shown in Fig. 1.5 due to the instability of higher-order polynomials. More laboratory and simulated studies are required to establish this point in reality. Research in this area works towards establishing the parameters for rule bases and scenarios for alternative scales of cellular and molecular evolution (Bains 2020) in variable settings of life systems. The latter may well lead to sets of data (Tugrul et al. 2019; Taylor et al. 2020; van den Hoogen et al. 2020; Echeverría-Londoño et al. 2018; Albrecht et al. 2018), which translate the distributions of Fig 1.1 to satisfy a full cone, respecting biological, chemical and geological research.
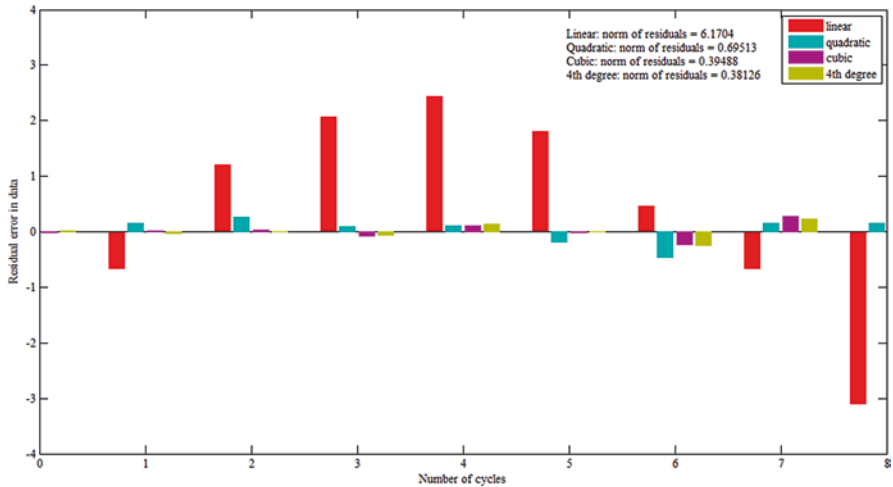
Fig. 1.5 Residual error of laboratory simulated data for molecular evolution

Research of extreme dynamics and gradient effects is essential to determine not only the formation of life but factors which determine its variance. Considering terrestrial systems enables the recognition of emergent populations, essentially triangular relations in life constructs and the sinusoidal waves, which represent the greater copula harmonics (multiple functions or strings of life present) in evolution.

1.3   Discussion: Evolutionary and Numerical Connotations

We have shown the bidirectional nature of molecular and cellular evolution using theoretical and laboratory-based data; the expansion of evolution is also consistent with that which takes place in extreme dynamics in the field (Furze and Mayad 2021) where ancient ternary groupings of life's constructs were seen. The laboratory-based data brings us closer to a concise definition of the resolution on which we must consider chemical and biological reactions and interactions in order to construct a concise algorithmic basis for evolution. A suggested future direction is to first construct algorithms in accordance with differential scenarios using a Mamdani Fuzzy basis (Mamdani 1974) and then with the more refined parameters of a Takagi-Sugeno-Kang Fuzzy basis (Takugi and Sugeno 1985). These higher mathematic techniques enable us to build scenarios, which cater for the evolution of the different categories of life that exist today. Such methods also illustrate the expanding and contracting nature of evolution which occurs as illustrated through the pattern of variance which is followed in dynamic evolution, also documented in the proposed use of Markov chains to describe evolution (Djordjevic 2015). The pattern followed may be reflected through sine/cosine relations such as those which are present in the

Fourier transform. Research in this area is ongoing, although differential algorithmic network centred emergence (DANCE) and harmonic evolutionary algorithmic resilience (HEAR) have recently been identified to give a basis for passive and active interactions between individuals, species and even trophic proportionality (Furze and Mayad 2021). Copula (distribution) expansion identifies similarity in biological/theoretical patterns with laboratory simulated patterns (all of which share the same variance patterns).

We have met our original objectives of linking the functions for molecular and cellular evolution together through the use of Sklar's theorem and combinatorial approaches of MOGA, laboratory and field studies (Furze and Mayad 2021; Filali et al. 2021). Continued use of these methods is proposed to confirm the categories of life present within different kingdoms in existence today. We have shown the mathematical basis on which different categories of copulas may be formed. Excitingly the use of the generator Gumbel equation (1.12) enables us to numerically observe the state of evolution in the conditions of any given time period.

Regarding chemical/genetic formations and the potential laboratory scenarios shown in Fig. 1.5, the special cases of hydrolysis, template refeeding and damaging processes should be considered in future research. A combination of laboratory, computer simulated and mathematic exploration produces rational rule structures which feed back to experimental and field results in order to reflect the dynamics operating. Processes such as template refeeding give an exponential increase in polymer formation and may be detected beyond the third polynomial level. Depurination (loss of adenine from monomers) simulation should result in the presence of shorter peaks and troughs given the correct resolution is observed for molecular systems. The number of times that we differentiate to get the polynomials logically indicates the number of processes which are occurring in order that we see the effects. This can be tested in laboratory/field conditions. Given that we establish the main sets of variables operating within a systematic approach to evolution, there is great potential for expansion of evolutionary copulas to show the formation of different constructs. Hence concise statements can be used to show different nodes of evolution throughout the categories of life. Variance and indeed rational truth of the evolutionary operating systems can be generated mathematically. Advancing through complex polynomials and validating their presence within copulas holds great promise for our understanding of evolution as decreased variance in the evolution of cellular and molecular systems is shown. Extensive use of higher mathematics, dispersal methods, rational polynomials and an algorithmic basis enables use of Markov chains across various categories of life; additionally this will produce Bayesian vectors for use in logistic regression. Integrating fieldwork and different laboratory methods gives practical indication of the variance, which may be shown mathematically.

Determining variation in life and its processes certainly requires use of multi-objective genetic algorithms and subsequent functional scenario generation; however with use of the higher mathematics we work towards discretely qualifying life parameters, the overstepping of which of course lead to changes in life processes and hence evolution. Evolution of processes and species proliferations is indirectly

guided by feedback and feed-forward of the same life systems as well as the environments within which they are found. Naturally it is imperative that the process is not destroyed at the 'preliminary' stages (e.g. by chemical imbalances). In order to establish discrete parameters across different scales of evolution, we suggest further exploration in extreme and dynamic environments in both terrestrial and aquatic systems.

Evolutionary emergence of soil community diversity may be 'forced' (induced), in the extremes of pH and drought. This leads us to suggest that within extreme environments there are activators (effectors) and actuators (causal) of diversity across the vast range of macro-ecological species and ecosystems found on Earth (Novikov and Copley 2013; Adams et al. 2016, Khanal et al. 2015; De Marchi et al. 2017; Furze and Mayad 2021). Expansion of the evolutionary generator (Gumbel copula), Eq. (1.12), for cellular/molecular systems enables calculation of differential algorithmic network centred emergence (DANCE), also expressed as a stochastic integral Laplacian expression, Eq. (1.11) – stating evolution at any given set of differential parameters. Harmonic evolutionary algorithmic resilience (HEAR) represents an accelerator of evolution between differing levels of suppression in communities. In the case that the difference is great (overlapping), suppression is effective and the organism (or element) is termed as active [1]. In the case that the difference is minimal (smoother or aligned), there is no suppression and the organism (or element) is classified as passive [0]. HEAR thus enables application of binary terms of evolution.

1.4   Conclusion

The current chapter shows that copula distributions may be used to account for sets of variables, which occur within evolution. Rules on which the curves can be reconstructed may be stated in both cellular and molecular terms. The key linking processes of Earth's diversity are pathogenicity and virulence complexes found within the soil and other growth environments across evolution. Microbial and macro-species contain orthologs with both normal and promiscuous activities, which are triggered by genetic mutation events over time. Further experimentation is required to identify members of edaphic, terrestrial, aquatic and atmospheric environments within ternary groups. It may be interpolated that the microbial community begets the macro-ecological community and thus enables levels of primary ecological production. Investigation of the soil environment and other microbiomes may be of assistance in making the best use of resources (nutrients) in terms of their availability in even the most extreme environments.

The ranges of extremes within which cascades of evolution may be observed require further investigation, in order that threshold values can be identified around which general increases or decreases in diversity are seen. It follows that directional trends should be observed in which clades of species assemblages adapted to different sets of extremes will form. The formation of such monotypic conditions is

detrimental to maximum diversity throughout life as it leads to dramatic species losses as conditions change. The relations, which expand throughout evolution, require urgent investigation, as when concentrations of diversity are present, discrete chemical pathway changes may result in lack of evolutionary potential. The additive effect of species assemblages and chemical pathways being 'misdirected' by harsh changes in their environment has drastic consequences on species numbers across greater time scales.

The use of remote monitoring and robotic techniques is suggested to sample extreme environments, which are analogous with the state of Earth at the beginning of evolution. We envisage that an increased range of samples would help us to define the complete (Fourier) transform series for evolution. From the latter, we may also make use of alternative functions (such as the cone function and its inverse) to show contraction and expansion of evolutionary patterns. The use of radial functions holds great promise for the mathematic categorization of life. This chapter is the first to suggest the use of generators of diversity; further we identify the presence of harmonic relationships in biological and chemical systems. Considering the harmonics of life leads us to observe emergence in all environmental settings, it has been identified that virulence and pathogenicity are key factors warranting further investigation in evolutionary constructs. We propose future work should overlap the formation of model structures in linguistic terms with biochemical (laboratory) and field studies to further emphasize the complexity of life and its constructs.

Given that within life constructs the combined harmonics of life operate in cooperative/synergistic terms, perhaps future work may query the very nature of triangular pirouettes in Hilbert space itself; do extremes exist in Hilbert space or are they just our biological perspectives of frequency, oscillation and density, which parameterize novel mathematic expressions such as extremum seeking algorithms? Combinatorial mathematic, topological and unified field theory explorations are imminent in this exciting field to bring evolutionary emergence and sustainability of life constructs to the fore for the benefit of both human and other life systems. Given that we acknowledge our interdependence, role and position in the array of Earth's beauty, we must understand and categorize biological diversity in order to impose appropriate protection of the highest order.

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