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ORIGINAL ARTICLE

Mathematical model for adaptive evolution of populations based on a complex domain

Rabha W. Ibrahim [a], **M.Z. Ahmad** [b], **Hiba F. Al-Janaby** [b,*]

[a] *Faculty of Computer Science and Information Technology, University Malaya, 50603, Malaysia*
[b] *Institute of Engineering Mathematics, Universiti Malaysia Perlis, 02600 Arau, Perlis, Malaysia*

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Abstract A mutation is ultimately essential for adaptive evolution in all populations. It arises all the time, but is mostly fixed by enzymes. Further, most do consider that the evolution mechanism is by a natural assortment of variations in organisms in line for random variations in their DNA, and the suggestions for this are overwhelming. The altering of the construction of a gene, causing a different form that may be communicated to succeeding generations, produced by the modification of single base units in DNA, or the deletion, insertion, or rearrangement of larger units of chromosomes or genes. This altering is called a mutation. In this paper, a mathematical model is introduced to this reality. The model describes the time and space for the evolution. The tool is based on a complex domain for the space. We show that the evolution is distributed with the hypergeometric function. The Boundedness of the evolution is imposed by utilizing the Koebe function.

1. Introduction

Consider a population evolves agreeing with the method containing mutations and natural assortment, and some of its quantitative traits are modified progressively. The question is: what is the rate of this modification? The speed of evolution is critical in constant competition of classes and is of significant practical prominence in relation to present day phenomena such as, adaptation of endangered species to changing environmental conditions or adaptation of pathogens to existing methods of treatment. Measurable method of evolution dates back at least to Fisher's (1930) book, which enclosed his well-known "Fundamental Theorem of Natural Selection", affirming that *the rate of increase of the mean fitness of a population at any moment of time, attributed to natural selection, equals the genetic variance of fitness of that population at that moment of time*. The following question is, of course, what concludes this variance in the population fitness, and how to predict it?

Though diverse epigenetic and genetic methods stand elaborated in the development plus preservation of altered tissues, the evolution of population can be determined by the relative significance of an asymmetric and the symmetric cell differentiation, cell divisions and death. A central issue in evolutionary

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* Corresponding author.
E-mail addresses: rabhaibrahim@yahoo.com (R.W. Ibrahim), mzaini@unimap.edu.my (M.Z. Ahmad), fawzihiba@yahoo.com (H.F. Al-Janaby).

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genetics is to calculate whether a population accrues damaging or beneficial mutations.

The equivalent proteins and genes stay perceived to be important for instruction of various tissues. This unity and conservation of straightforward procedures entail that their mathematical models can employ crossways the spectrum of pathological and normal growth. An androgynous population accumulates damaging mutations and, consequently, its fitness will grow. On the other hand, it newly rotated out that useful mutations are additional ample than formerly supposed.

One recognizes that the technique of demonstrating such schemes remains to utilize a discrete family of ordinary differential equations labeling dynamics of cells at various maturation phases and evolution between the phases. These consequently entitled multi-compartmental models stay founded by the condition that in every lineage of cell originators there occurs a discrete sequence of maturation phases, which are consecutively crossed. Nevertheless, it is besides flattering increasingly strong that the differentiated originator's system such sequence only beneath homeostatic assumptions. A devoted cell usually arranges a continuous sequence, which may include incremental phases, the measure of which could be changeable (Biktashev, 2014; Alfaro and Carles, 2014; Britton et al., 2015; Abasi et al., 2015; Gerleea and Altrock, 2015; Chao et al., 2015; Landguth et al., 2015). As an application, cell differentiation devoid of cell divisions is detected throughout neurogenesis. Furthermore, in certain tissues such as the mammary gland, different phases of differentiation stand not well recognized.

This clarification appeals not simply to the essential biological question of whether the cell differentiation is a continuous or a discrete development and what is the amount of cell difference, nevertheless correspondingly to how to select a suitable forming method. Is the pace of maturation (commitment) verbalized by continuous divisions, or is maturation a continuous development decoupled from proliferation? The conventional interpretation in ordinary hematopoiesis appears to be opposite. To discuss these questions and to consider the impact of potential continuous transformations of the differentiation procedure, one can impose a classical method based on partial differential equations of transport category and compare this method to its discrete complement. The argument of disappearance is a multi-compartmental method of a discrete gathering of cell subpopulations, which stood newly suggested in Marciniak-Czochra et al. (2009) and Doumic et al. (2011) to study the dynamics of the hematopoietic scheme with cell proliferation and differentiation structured by a nonlinear feedback loop.

Hitherto an additional category of evolution is selection. This income that various alleles could have various susceptibilities for resampling, for instance, various amounts at which they resemble. An auxiliary element might be migration, i.e., genetic substantial is communicated among various populations for the reason that the individuals booming this substantial travel from one population to the following.

Analysis of populations has approximately continuously depended on processes founded on estimated gene identities or heterozygosities, because of these connections to variance and the binary nature of sexual reproduction and diploid inheritance. The corresponding processes and their numerous simplifications for divided populations have likewise played a central role in evolutionary biology and population genetics. This method highlights the frequent alleles by introducing in them much more weight than their population fraction, and multi-level hierarchical additive partitioning is not typically likely with heterozygosity-based measures (Landguth et al., 2015).

Investigators in numerous castigations have progressively documented that variety inside populations and compositional differentiation between populations cannot be completely categorized by a single measure. For example, ecologists have touched a consensus (Chao et al., 2014) that instead of one or a few diversity measures, it is best to practice a multifaceted diversity measure parameterized to totally describe the class abundance distributions in ecological assemblages. By analogy, moreover to measures based on heterozygosity, complementary abundance-sensitive measures that are sensitive to less frequent alleles are needed to portray a more complete picture of allele frequency distribution or differentiation among populations.

Mathematics is frolicking an ever more significant character in the physical and biological sciences. The technique followed in most texts on these topics (e.g., electrodynamics, quantum mechanics, classical mechanics, modern physics, mathematical biology, chemical biology, etc.) is forum-getting at the problem as a differential equation that is associated with one of several special differential equations (Bessel's, Hermite's, Legendre's, Laguerre's, etc.). All the above equations have solutions in term of special functions. The most important special function is the hypergeometric function (Seaborn, 1991)

$$pF_q(a_1,\ldots,a_p;b_1,\ldots,b_q;z)=\sum_{n=0}^{\infty}\frac{(a_1)_n\ldots(a_p)_n}{(b_1)_n\ldots(b_q)_n}\frac{z^n}{n!},$$

where $(x)_n$ is the Pochhammer symbol. The hypergeometric function is utilized to test, classify and analyze various types of biological process (Gurarie and King, 2014).

In this paper, a mathematical model is presented for this certainty. The method designates the time and space for the evolution. The tool is based on a complex domain for space. Therefore, we utilize some of the concepts in geometric function theory, such as univalent function. We show that the evolution is distributed with the hypergeometric function. The Boundedness of the evolution is imposed by utilizing the Koebe function. This new method allowed us to understand the fitness of the population geometrically. The changing with respect to time and space is formulated by employing the concept of fractional calculus in real as well as in a complex domain.

2. Material and methods

In this section, we select some recent mathematical models.

2.1. Adaptive dynamics

Adaptive dynamics is essentially apprehensive with qualitative questions such as stability of evolution, the direction of evolution, steady states and speciation due to branching. On the quantitative stage, the fundamental for adaptive dynamics is the following canonical equation:

$$\frac{dM}{dt}=\kappa(M)\frac{dr(M,x)}{dx}\bigg|_{x=M},$$