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Evo-SETI SCALE to measure Life on Exoplanets

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ABSTRACT

Darwinian Evolution over the last 3.5 billion years was an increase in the number of living species from 1 (RNA?) to the current 50 million. This increasing trend in time looks like being exponential, but one may not assume an exactly exponential curve since many species went extinct in the past, even in mass extinctions. Thus, the simple exponential curve must be replaced by a stochastic process having an exponential mean value. Borrowing from financial mathematics ("Black–Scholes models"), this "exponential" stochastic process is called Geometric Brownian Motion (GBM), and its probability density function (pdf) is a lognormal (not a Gaussian) (Proof: see ref. Maccone [3], Chapter 30, and ref. Maccone [4]). Lognormal also is the pdf of the statistical number of communicating ExtraTerrestrial (ET) civilizations in the Galaxy at a certain fixed time, like a snapshot: this result was found in 2008 by this author as his solution to the Statistical Drake Equation of SETI (Proof: see ref. Maccone [1]). Thus, the GBM of Darwinian Evolution may also be regarded as the extension in time of the Statistical Drake equation (Proof: see ref. Maccone [4]). But the key step ahead made by this author in his Evo-SETI (Evolution and SETI) mathematical model was to realize that LIFE also is just a *b*-lognormal in time: every living organism (a cell, a human, a civilization, even an ET civilization) is born at a certain time *b* ("birth"), grows up to a peak *p* (with an ascending inflexion point in between, *a* for adolescence), then declines from *p* to *s* (senility, i.e. descending inflexion point) and finally declines linearly and dies at a final instant *d* (death). In other words, the infinite tail of the *b*-lognormal was cut away and replaced by just a straight line between *s* and *d*, leading to simple mathematical formulae ("History Formulae") allowing one to find this "finite *b*-lognormal" when the three instants *b*, *s*, and *d* are assigned.

Next the crucial Peak-Locus Theorem comes. It means that the GBM exponential may be regarded as the geometric locus of all the peaks of a one-parameter (i.e. the peak time *p*) family of *b*-lognormals. Since *b*-lognormals are pdf-s, the area under each of them always equals 1 (normalization condition) and so, going from left to right on the time axis, the *b*-lognormals become more and more "peaky", and so they last less and less in time. This is precisely what happened in human history: civilizations that lasted millennia (like Ancient Greece and Rome) lasted just centuries (like the Italian Renaissance and Portuguese, Spanish, French, British and USA Empires) but they were more and more advanced in the "level of civilization". This "level of civilization" is what physicists call ENTROPY.

Also, in refs. Maccone [3] and [4], this author proved that, for all GBMs, the (Shannon) Entropy of the *b*-lognormals in his Peak-Locus Theorem grows LINEARLY in time. The Molecular Clock, well known to geneticists since 50 years, shows that the DNA base-substitutions occur LINEARLY in time since they are neutral with respect to Darwinian selection. In simple words: DNA evolved by obeying the laws of quantum physics only

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(microscopic laws) and not by obeying assumed "Darwinian selection laws" (macroscopic laws). This is Kimura's neutral theory of molecular evolution. The conclusion is that the Molecular Clock and the *b*-lognormal Entropy are the same thing.

At last, we reach the new, original result justifying the publication of this paper. On exoplanets, molecular evolution is proceeding at about the same rate as it did proceed on Earth: rather independently of the physical conditions of the exoplanet, if the DNA had the possibility to evolve in water initially. Thus, Evo-Entropy, i.e. the (Shannon) Entropy of the generic *b*-lognormal of the Peak-Locus Theorem, provides the Evo-SETI SCALE to measure the evolution of life on exoplanets.

1. Purpose of this paper

This paper describes recent developments in a new statistical theory describing Evolution and SETI by mathematical equations. This we call the Evo-SETI mathematical model of Evolution and SETI.

Now the question is: whenever a new exoplanet is discovered, where does that exoplanet stand in its evolution towards life as we have it on Earth nowadays, or beyond? This is the central question of Evo-SETI.

In this paper we show that the (Shannon) Entropy of *b*-lognormals answers such a question, thus allowing the creation of an EVO-SETI SCALE.

2. During the last 3.5 billion years life forms increased like a (lognormal) stochastic process

Let us look at Fig. 1: on the horizontal axis is the time t, with the convention that negative values of t are past times, zero is now, and positive times are future times. The starting point on the time axis is $ts = -3.5\ 10^9$ years i.e. 3.5 billion years ago, the time of the origin of life on Earth that we assume to be correct. If the origin of life started earlier than that, say 3.8 billion years ago, the coming equations would still be the same and their numerical values will only be slightly changed. On the vertical axis is the number of species living on Earth at time t, denoted $L(t)$. This "function of the time" we do not know in detail, and so it must be regarded as a random function, or stochastic process, with the notation $L(t)$ standing for "life at time t". In this paper we adopt the convention that capital letters represent random variables, i.e. stochastic processes if they depend on the time, while lower-case letters mean ordinary variables or functions.

3. Mean value of the lognormal process $L(t)$

The most important ordinary, continuous function of the time associated with a stochastic process like $L(t)$ is its mean value, denoted by

$$m_L(t) \equiv \langle L(t) \rangle. \tag{1}$$

The probability density function (pdf) of a stochastic process like $L(t)$ is assumed in Evo-SETI Theory to be a lognormal, that is, its equation reads

$$L(t)\_\mathrm{pdf}(n; M_L(t), \sigma, t) = \frac{e^{-\frac{[\ln(n) - M_L(t)]^2}{2\sigma_L^2 (t-ts)}}}{\sqrt{2\pi}\sigma_L \sqrt{t-ts}\, n} \tag{2}$$

$$\text{with } \begin{cases} n \ge 0, \\ t \ge ts, \end{cases} \text{ and } \begin{cases} \sigma_L \ge 0, \\ M_L(t) = \text{arbitrary function of } t. \end{cases}$$

This assumption is in line with the extension in time of the statistical Drake equation, namely the foundational and statistical equation of SETI, as shown in ref. [1].

The mean value (1) is of course related to the pdf (2) by the relevant integral in the number n of living species on Earth at time t, that is

$$m_L(t) \equiv \int_0^\infty n \cdot \frac{e^{-\frac{[\ln(n) - M_L(t)]^2}{2\sigma_L^2 (t-ts)}}}{\sqrt{2\pi}\sigma_L \sqrt{t-ts}\, n}\, dn. \tag{3}$$

The "surprise" is that this integral (3) may be computed exactly with the key result that the mean value $m_L(t)$ is given by

$$m_L(t) = e^{M_L(t)} e^{\frac{\sigma_L^2}{2}(t-ts)}. \tag{4}$$

In turn, the last equation has the "surprising" property that it may be inverted exactly, i.e. solved for $M(t)$:

$$M_L(t) = \ln(m_L(t)) - \frac{\sigma_L^2}{2}(t-ts). \tag{5}$$

4. $L(t)$ initial conditions at ts

Now about the initial conditions of the stochastic process $L(t)$, namely about the value $L(ts)$. We shall assume that the positive number

$$L(ts) = Ns \tag{6}$$

is always exactly known, i.e. with probability one:

$$\Pr\{L(ts) = Ns\} = 1. \tag{7}$$

In the practice, Ns will be equal to 1 in the theories of evolution of life on Earth or on an exoplanet (i.e., there must have been a time ts in the past when the number of living species was just one, let it be RNA or something else). On the contrary, Ns will be equal to the number of living species just before the asteroid/comet impact in the theories of mass extinction of life on a planet.