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Research Article

Exploring Biogenic Dispersion Inside Star Clusters with System Dynamics Modeling

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ABSTRACT

The discovery of a growing number of exoplanets and even extrasolar systems supports the scientific consensus that it is possible to find other signs of life in the universe. The present work proposes for the first time, an explicit mechanism inspired by the dynamics of biological dispersion, widely used in ecology and epidemiology, to study the dispersion of biogenic units, interpreted as complex organic molecules, between rocky or water exoplanets (habitats) located inside star clusters. The results of the dynamic simulation suggest that for clusters with populations lower than 4 M/ly3 it is not possible to obtain biogenic worlds after 5 Gyr. Above this population size, biogenic dispersion seems to follow a power law, the larger the density of worlds lesser will be the impact rate () value to obtain at least one viable biogenic Carrier habitat after 5 Gyr. Finally, when we investigate scenarios by varying β, a well-defined set of density intervals can be defined in accordance to its characteristic β value, suggesting that biogenic dispersion has a behavior of "minimal biogenic effective" events by interval i.e. once this dose has been achieved, doesn't matter if additional biogenic impact events occur on the habitat.

Keywords: System dynamic; biogenic dispersion; epidemic model; astrobiology; stellar clusters.

INTRODUCTION

Currently, the search for life or signs of life in the universe is a research area with growing interest, not only within the scientific community but within the general public, given the generalized conviction that we are not alone in the universe driven by the discovery of an increasing number of extrasolar systems associated with relatively close stars within our galaxy (Gillon, 2017). It should be noted that these investigations are characterized by their strong interdisciplinary nature because they combine elements of physics, chemistry, biology, geology and mathematics among many other fields, leading to new research questions, new databases and new methods of analysis. (Buettel et. al. 2018). In the particular case of ecology, its interrelations with astronomy are well known since the beginning of the nineties v.gr. the applications of the Hertzsprung-Russell method to population ecology by Keddy (1994) and the vivid description of a space-time ecology by Smolin (1997), Mautner and Park (2017) and Burke et.al. (2018), which point out to the fact that complex ecosystem analysis methods can give novel answers related to the origin and dispersion of life in the universe.

The present work is framed within this line of research when applying principles of population ecology and epidemic theory (Goffman & Newill, 1964) to the study of biogenic dispersion between extrasolar systems inside star clusters. Considering the formidable challenges faced by microbes during the transfer of life from one world to another (Nicholson, 2009) we chose to model, not the dispersion of living entities, but that of complex biomolecules; thus following Bottcher (2018) and Lehn (2002, 2012), we define biogenic units as complex supramolecular entities, which, through non-covalent interactions, can perform processes of individuation, replication, variation and transport of energy and information (Hazen et. al. 2007; Malaterre, 2010; Rimmer et.al 2018), which allows it to carry out emergent phenomena of self-organization of adaptive and evolutionary nature, enabling a multi-step transition from non-living to living matter (de Duve 1991; Rasmussen et. al. 2003; Rasmussen at.al 2014; Popa 2004). An epidemic model is proposed to study the spreading of biogenic units delivered by interstellar objects v.gr.

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comets, meteorites, among extrasolar systems inside a star cluster, leading to the dispersion of biogenicity between exoplanets.

A basic model of biogenic outbreaks inside star clusters

The model for dispersion of biogenic units inside star clusters using an analogy based on the dynamics of epidemic processes (Table 1). This model is based on various assumptions:

- First, it should be noted that the synthesis of organic molecules occurs in the huge clouds of interstellar and circumstellar material, but the development of complex biogenic networks, that can lead to the appearance of life, occurs on aqueous and / or appropriate solid substrates present in Rocky and/or Water worlds. It is important to note that, from the analysis of organic matter in meteorites and other solar system objects, we now know that abiotic synthesis can create a wide range of organic compounds far beyond those found on Earth. This hints that the degrees of complexity and diversity of prebiotic organics are much larger than previously thought.
- Second, taking into account Lin & Loeb (2015), who indicate that life could arise via a spreading mechanism than in a spontaneous pattern; we assume that biogenic units were delivered, via the chaotic exchange of solid materials, to a multiplicity of habitats (H), in this case, the population (N) of Rocky and Water Worlds located within the habitable zones (HZ) of stars associated with extrasolar systems inside a star cluster. But, given that these stellar structures arise primarily in regions of efficient star formation then, the prime targets for biogenic expansion can be regions where newly forming stars and planetary systems are concentrated inside the cluster, where the chances of biogenic units spreading from one solar system to another are greatly enhanced due to the proximity of the systems and lower relative velocities.
- Third, given that the HZ is a dynamic area, recent research indicates that it can cover larger neighborhoods around the stars than previously thought, it is assumed, for simplicity and following Lineweaver & Chopra (2012), that on average, one star has one exoplanet in its habitable zone, so the number of stars equals the number of exoplanets. We assume that the average mass of Rocky and Water Worlds is the Earth Mass (M).
- Fourth, the epidemic analogy: The Biogenic Outbreak follows a typical Kermack and McKendrick's (1927) basic Susceptible, Infected and Recovered (SIR) model, as follows:

$$\frac{dR_H}{dt} = N_H - \beta R_H C_H - \delta R_H \quad (1)$$

$$\frac{dC_H}{dt} = \beta R_H C_H - (\gamma C_H + \delta C_H) \quad (2)$$

$$\frac{dS_H}{dt} = \gamma C_H - \delta S_H \quad (3)$$

Elements of the epidemic process	Elements interpreted in term of		variable
	Infectious disease epidemic	Biogenic dispersion	
host	Individual, population, community by area unit	Rocky or Water worlds by volume units	NH
agent	Infectious material, v.gr. virus	Biogenic units	
Vector agent	Air, water, mosquitoes	Solid material	
infective	Case of disease/ area	Biogenic-Carrier habitats/vol	CH
susceptible	The person who will be infected given infective contact	Biogenic-Receptive habitats/vol	RH
recovered	Immune or death person/ area	Biogenic-free or sterilized habitats/vol	SH
Recovery rate	Death or immunity/time	The rate of elimination of biogenic units/Gyr	▯
Transmission rate	Transmission rate/time	Impact exchange ejecta/Gyr	β
Removal	Death of host/ time	Stellar disruption/Gyr	▯

Table 1. The epidemiological analogy to study biogenic spread inside star clusters

Where, , corresponds Rocky Worlds ~1M⊕ (Hanslmeier, 2018) within the star cluster per volume unit, in the present study, the cubic light year (ly3). It is important to note that in the classic SIR model, the condition S+I+R = constant must be valid, in the present case, this condition is met when S+I+R = N/▯. On the other hand, in accordance with the epidemiological analogy employed, and using the Plausibility of Life (POL) classification proposed by Irwin and Schulze-Makuch (2001), we define three basic populations of Worlds or Habitats (Table 1).

- The Biogenic-Receptive habitats (RH) defined as equivalent to POL of III or moderate habitats characterized by extreme conditions compared with those of Earth but where the minimal criteria of energy, liquid, and complex chemistry in some form are satisfied.
- Similarly, some habitats will lose their biogenic units, the Biogenic-free or Sterilized habitats (SH), due to the action of factors such as Gamma Ray Bursts; these correspond to POL

of IV-low which applies to worlds on which past conditions suitable for the origin of life can reasonably be inferred, prior to the development of conditions so harsh as to make the perseverance of life at present unlikely but conceivable in isolated habitats.

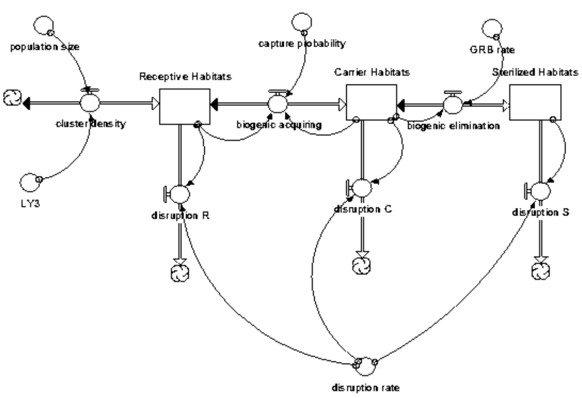
- Finally, some Worlds will support the development of the biogenic units, conforming the set of Biogenic-Carrier habitats (CH) which corresponds to POL of II or favorable habitats, characterized by evidence of the past or present existence of liquid water, availability of energy sources, and where the existence of organic compounds can be inferred. Since organic molecules appear to be pervasive throughout the universe, the last criterion is equivalent to identifying conditions under which they can be reasonably expected to be stable. At least two sites—Mars and Europa— qualify for this category, thus both of them can be classified as Biogenic-Carrier habitats (CH).

In relation to the model parameters, β corresponds to the transmission rate i.e. the average number of contacts of between Biogenic-Receptive and Biogenic-Carrier habitats () mediated by the chaotic exchange events of solid materials between these types of Worlds (Mautner, 1997; Napier, 2004; Belbruno et. al 2012; Petigura et.al 2013; Ginsburg et.al, 2018; Lingam & Loeb, 2018). On the other hand, ▯ is the rate at which Biogenic-Carrier Worlds become Biogenic-free ones. Finally, ▯ corresponds to the disruption rate of the different kind of habitats i.e. The fraction of the total disruption contributed by tidal shocks (Baumgardt & Makino, 2002; Kalirai & Richer, 2010). The units for β, ▯ and ▯ based on dimensional analysis of the model equations (1), (2) and (3), are expressed as events by Gyr-1.

The system dynamics modeling approach

Having defined the basic model for the biogenic outbreak inside star clusters, we proceed, following the epidemiological approach, to develop a versatile strategy to study dynamically complex issues of the model through the identification, description, and simulation of feedbacks and processes that drive system behavior. The stock-flow (SF) diagram and their parameters, corresponding to the differential equations of the Biogenic Outbreak model, are presented in Appendix 1.

Appendix 1



Stock Flow diagram of the Biogenic Outbreak inside star Clusters

STOCK FLOW MODEL PARAMETER SUMMARY			
Parameter	Value	Unit	Meaning
GRB rate (▯)	0.5	Events/Gyr	The rate of elimination of biogenic units by Gamma Ray Burst
Capture probability (β)	10-3-103	Events/Gyr	Impact exchange events
Disruption rate (▯)	160.9	Events/Gyr	Stellar disruption
Population size (NH)	0.004 to 288	M▯/Ly3	Rocky worlds (M▯)
Initial Stock Conditions			
Biogenic-Carrier Habitats (CH)	NH/3	M▯/Ly3	Biogenic-Carrier Worlds/ habitats
Biogenic-Receptive habitats (RH)	NH/3	M▯/Ly3	Biogenic-Receptive Worlds
Biogenic-Sterilized habitats (SH)	NH/3	M▯/Ly3	Biogenic-free or sterilized Worlds/ habitats
Flows			
Disruption C	Function		Carrier Habitats*disruption rate
Disruption R	Function		Receptive Habitats*disruption rate
Disruption S	Function		Sterilized Habitats*disruption rate
Biogenic elimination	Function		Carrier Habitats*GRB rate
Biogenic acquiring	Function		Capture probability*Receptive Habitats*Carrier Habitats

Stock Flow Model parameter summary

Population size

Following the epidemic analogy, and given that the range of star population densities existing in nature is immense, v.gr., the population density of stars at the center of the nearby Andromeda spiral galaxy has been determined to equal 100,000 solar masses per cubic light-year, while the density at the center of the Ursa Minor dwarf elliptical galaxy is only 0.00003 solar masses per cubic light-year (Gregersen, 2010; Marx & Pfau, 1997), we choose, as reference, the globular clusters, where stars may reach a density between 100 and 1,000 stars per cubic parsec (pc3) and also, the density of stars near our sun, estimated at about 0.14 star per cubic parsec. Thus, taking in i) an interval between 0.14 to 10,000 stars per cubic parsec ii) the equivalence of 1 pc3 to 34.6959 cubic light years (ly3). iii) our assumption of one world by star, we adopt a working population ranging from 0.004 M□ / ly3 to 288 M□ /ly3.

Dynamic rates

The contact rate (β) was interpreted as impact exchange ejecta events, occurring in planetary systems, of comets, meteoroids, asteroids and other small bodies carrying biogenic units. For β determination, we considered the work of Scharf and Cronin (2016) who, using a heuristic formula based on a Poisson distribution, proposed that impact ejecta exchange (β) could have plausible values ranging from 10-3 to 103 events by Gyr-1, taking into account that this exchange occurs between exoplanets with parallel chemistries and chemical evolution which could, in principle, amplify the development of molecular complexity and abiogenesis probabilities. Also, it is important to note that in young clusters the exoplanets seem to be subject to events like the Late Heavy Bombardment (Lisse et.al. 2013; Bottke et. al. 2017) which could exert a substantial increment over the impact exchange ejecta events.

Regarding the sterilization rate (□), this has the meaning of the elimination probability of all biogenic units from their Carrier habitats by the action of the cosmic the Gamma-Ray Burst (GRB), phenomenon equivalent of the well-known procedure of surface sterilization using high energy radiation, but also events that threads life like supernovae (Melott et. al., 2015) and AGNs could be considered (Lingam et.al., 2019). Following Piran and Jimenez (2014), We use, as a benchmark value 0.9, given that probability of at least one long GRB of 100kJ/m2 having occurred in the past 5 Gyr with enough flux to produce significant life extinction is 90%. In order to estimate the appropriate value for □, we consider the case where □=β=0, and we see from (2) that CH = C0 exp(-□*t). Setting t=5 Gyr and CH/C0 = 0.1 (implying that 90% of them were wiped out), we find □ = 0.5 sterilization events by Gyr-1.

Respecting to disruption rate (□), and following Adams (2010) who quotes that of the total number of clusters with more than 1000 stars, 80% of them dissolve quickly after 10 million years, and following also Kalirai & Richer (2010), who obtain similar results, we adopt 0.8 as a key value. To estimate □, we consider the case where only disruption occurs (□=β=0); then, we use (3) to obtain SH = S0 exp(-□*t). Based on the references provided in this work, we choose t = 10 Myr and SH/S0 = 0.2 (because 80% are lost) in this equation, thus yielding □ = 160.9 disruption events by Gyr-1.

RESULTS AND DISCUSSION

The exploration using the dynamic simulation of the biogenic dispersion within stellar clusters following an epidemic outbreak yields a series of interesting results. Taking into account simulation results where it is possible to obtain at least one Biogenic Carrier habitat after 5 Gyr as a critical cut-off, we found that for worlds populations with densities below 4 M□/ly3, like those estimated near the Sun (0.004 stars/ly3), there are no possibility to obtain one viable Carrier habitat, neither employing β = 103. This behavior can be interpreted as the well-known "social distancing" effect. Also, it is remarkable that after the first 0.3 Gyr (Figure 1) density decreases 25% in the case of Biogenic carrier worlds, but close to 94% for Sterilized worlds. These results suggest that biogenic dispersion would be associated with migration patterns in relation to their host star, and the dynamics of the star linked to its main sequence evolution.

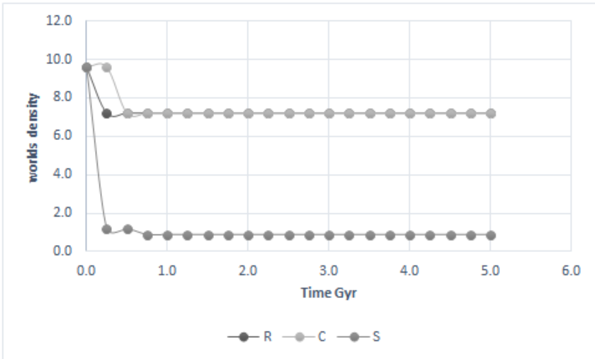


Figure 1. Biogenicity survival curves of worlds

Figure 1. Biogenicity survival curve for a population of 28.8 rocky planets by cubic light year, split between the three types of exoplanets considered, under a β=1 interaction rate. At the end of a period of 5 Gyr 25% of the exoplanets are of a biogenic nature.

On the other hand, when we investigate scenarios by varying β, a strategy very common in ecological epidemiology, biogenic dispersion shows the following pattern, the larger the density of worlds lesser will be the impact rate (β) value necessary to obtain, at least, one viable Biogenic Carrier habitat after 5 Gyr, which can be described as a power law where world density (figure 2a). Furthermore, a well-defined set of density intervals can be defined in accordance to its characteristic β value v.gr., the interval between 4 and 4.3 M□/ly3 with β= 103; the interval between 4.4 to 7 M□/ly3 with β= 102 ; From 7.1 to 24 M□/ly3 with β= 101; ; From 25 to 115 M□/ly3 with β= 100; From 116 to 288 M□/ly3 with β= 10-1 , as can be observed in (figure 2b). this result suggest that biogenic dispersion has a behavior of "minimal infective dose" or "minimal biogenic effective" events by interval i.e. once this dose has been achieved, doesn't matter if additional biogenic impact events occur on the habitat.

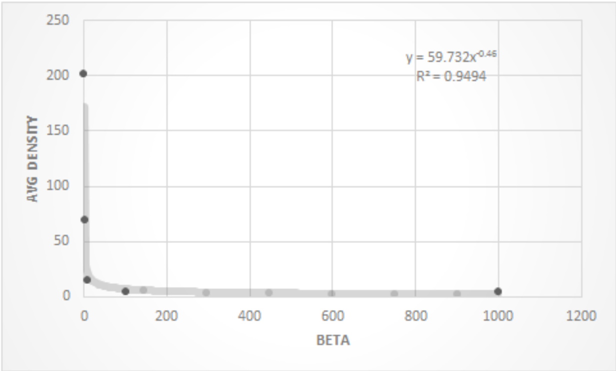


Figure 2a. Behavior of the population (Average density) under the β variation scenario

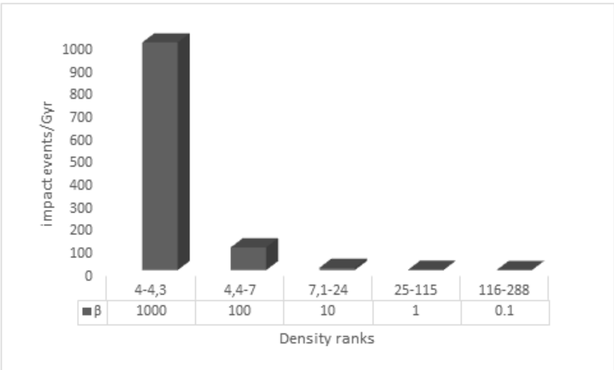


Figure 2b. Minimal Biogenic effective impact events

Figure 2. a) A power law behavior seems to rule the relationship between the population density of rocky planets and the rate of impact exchange ejecta events needed to develop at least one biogenic-carrier exoplanet at the end of the 5 Gyr period. b) The histogram represents the number of impact exchange events found for population density intervals, which seems to indicate that to achieve biogenicity implementation, what could be called minimum effective dose is required.

These results suggest that biogenic dispersion seems to be more feasible in the center of the stellar clusters, when the planets are in juvenile stages and some of their habitability characteristics begin to be defined depending on migration patterns in relation to their host star. In accordance with, the cluster center can be viewed as a huge biogenic reactor, where complex biochemical species are actively formed and transmitted, becoming to implant itself in the exoplanets with the appropriate characteristics through the impact ejecta events.

Following Goffman (1964), epidemic theory can be employed to develop more sophisticated models. For example, a limitation of the present SIR model is that, in all the simulation scenarios used, the complex biogenic units has been assumed to reach the exoplanets by meteorites, comets, cosmic dust or some other source, which are capable to evolve under the habitability conditions of the Rocky and Water worlds. However, scenarios may arise in which, once biocomplexity begins to develop, these worlds are not affected by impact ejecta events that transmit their biogenicity to other worlds. These scenarios can be studied with a SEIR type model, Susceptible, Exposed, Infected and Recovered, which contemplate the fact of having worlds that, although they develop biocomplexity (Exposed), are not infectious, that is, they cannot transmit biogenicity to other habitats. This approach may generate results that complement those found in the present study, because contemplates the possibility that there are immense abiogenic clusters, although perfectly habitable (Cockell, 2014). The concurrence of the dispersion of complex biogenic units using epidemic theory, with suitable habitability conditions, what we call Biogenic Space, the appearance of life in an extrasolar system would be possible.

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