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 $4 \ M_{\odot}/\text{ly}^3$ 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 ($\beta^{-0.46}$) value to obtain at least one viable biogenic Carrier habitat after 5 Gyr. Finally, when we investigate scenarios by varying $\beta$, a well-defined set of density intervals can be defined in accordance to its characteristic $\beta$ value, suggesting that biogenic dispersion has a behavior of “minimal infective dose” 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

Biogenic dispersion; epidemic model; System dynamics; 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. 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 (Tielens, 2013), but the development of complex biogenic networks (Cronin & Walker, 2019), that can lead to the appearance of life, occurs on aqueous and / or appropriate solid substrates present in Rocky and/or Water worlds (Hanslmeier, 2018). 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 (Meringer and Cleaves 2017).

- 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 (Mautner, 1997). 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 (Adams & Spergel (2005).

- Third, given that the HZ is a dynamic area, recent research indicates that it can cover larger neighborhoods around the stars than previously thought (Kasting et.al., 2014), 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\(_{\oplus}\)).
Fourth, the epidemic analogy: The Biogenic Outbreak follows a typical Kermack and McKendrick’s (1927) basic Susceptible, Infected and Recovered (SIR) model, as follows:

\[
\frac{dR_H}{dt} = N_H - \beta R_H C_H - \delta R_H \tag{1}
\]

\[
\frac{dC_H}{dt} = \beta R_H C_H - (\gamma C_H + \delta C_H) \tag{2}
\]

\[
\frac{dS_H}{dt} = \gamma C_H - \delta S_H \tag{3}
\]

Where, \(N_H = C_H + R_H + S_H\), corresponds Rocky Worlds \(\sim 1\text{M}_\oplus\) (Hanslmeier, 2018) within the star cluster per volume unit, in the present study, the cubic light year \((\text{ly}^3)\). It is important to note that in the classic SIR model, the condition \(S+I+R = \text{constant}\) must be valid, in the present case, this condition is met when \(S+I+R = N/\delta\). 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 \((R_H)\) 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 \((S_H)\), 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 \((C_H)\) 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 \((C_H)\).

In relation to the model parameters, \(\beta\) corresponds to the transmission rate i.e. the average number of contacts of between Biogenic-Receptive and Biogenic-Carrier habitats \((\beta R_H C_H)\) 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, \(\gamma\) is the rate at which Biogenic-Carrier Worlds become Biogenic-free ones. Finally, \(\delta\) 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 $\beta$, $\gamma$ and $\delta$ based on dimensional analysis of the model equations (1), (2) and (3), are expressed as events by Gyr$^{-1}$.

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

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

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.

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 0.0003 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 ($pc^3$) 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 pc$^3$ to 34.6959 cubic light years (ly$^3$). iii) our assumption of one world by star, we adopt a working population ranging from 0.004 $M_{\odot}$ / ly$^3$ to 288 $M_{\odot}$ /ly$^3$.

Dynamic rates

The contact rate ($\beta$) was interpreted as impact exchange ejecta events, occurring in planetary systems, of comets, meteoroids, asteroids and other small bodies carrying biogenic units. For $\beta$ 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 ($\beta$) could have plausible...
values ranging from $10^{-3}$ to $10^3$ 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 ($\gamma$), this has the meaning of the elimination probability of all biogenic units from their Carrier habitats ($C_H$) 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 $\gamma$, we consider the case where $\delta=\beta=0$, and we see from (2) that $C_H = C_0 \exp(-\gamma^*t)$. Setting $t=5$ Gyr and $C_H/C_0 = 0.1$ (implying that 90% of them were wiped out), we find $\gamma = 0.5$ sterilization events by Gyr$^{-1}$.

Respecting to disruption rate ($\delta$), 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 $\delta$, we consider the case where only disruption occurs ($\gamma=\beta=0$); then, we use (3) to obtain $S_H = S_0 \exp(-\delta^*t)$. Based on the references provided in this work, we choose $t = 10$ Myr and $S_H/S_0 = 0.2$ (because 80% are lost) in this equation, thus yielding $\delta = 160.9$ 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 $4 M_{\odot}/\text{ly}^3$, like those estimated near the Sun (0.004 stars/ly$^3$), there are no possibility to obtain one viable Carrier habitat, neither employing $\beta = 10^3$. 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 Stimulated 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.
On the other hand, when we investigate scenarios by varying $\beta$, 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 ($\beta$) 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 $\approx \beta^{-0.46}$ (figure 2a). Furthermore, a well-defined set of density intervals can be defined in accordance to its characteristic $\beta$ value v.gr., the interval between 4 and 4.3 $M_\oplus$/ly$^3$ with $\beta= 10^3$; the interval between 4.4 to 7 $M_\oplus$/ly$^3$ with $\beta= 10^2$; From 7.1 to 24 $M_\oplus$/ly$^3$ with $\beta= 10^1$; ; From 25 to 115 $M_\oplus$/ly$^3$ with $\beta= 10^0$; ; From 116 to 288 $M_\oplus$/ly$^3$ with $\beta= 10^{-1}$, 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.

Data accessibility. https://datadryad.org/stash/share/ooWbLs5hyixq5tvX3XnRM1LQtbFHS5x7fwI1k1WTjYc

Competing interests. The authors declare no competing interests.

Authors contribution. JB proposed the central ideas of the present work, in addition, he modeled the biogenic dispersion. DCS contributed with the concepts of applied ecology for the model.

Acknowledgements. To CIINAS CORP for the given support represented by the use of its facilities to carry out this work.
APPENDIX 1

A. Stock Flow diagram of the Biogenic Outbreak inside star Clusters

![Diagram of stock flow model](image_url)

B. Stock Flow Model parameter summary

| Parameter                  | Value       | Unit               | Meaning                                                                 |
|----------------------------|-------------|--------------------|-------------------------------------------------------------------------|
| GRB rate ($\gamma$)        | 0.5         | Events/Gyr         | The rate of elimination of biogenic units by Gamma Ray Burst             |
| Capture probability ($\beta$) | $10^{-3}$-$10^{3}$ | Events/Gyr | Impact exchange events                                                  |
| Disruption rate ($\delta$)  | 160.9       | Events/Gyr         | Stellar disruption                                                      |
| Population size ($N_H$)    | 0.004 to 288| $M_\oplus/Ly^3$    | Rocky worlds ($M_\oplus$)                                              |

Initial Stock Conditions

| Biogenic-Carrier Habitats ($C_H$) | $N_H/3$ | $M_\oplus/Ly^3$ | Biogenic-Carrier Worlds/habitats                                      |
| Biogenic-Receptive habitats ($R_H$) | $N_H/3$ | $M_\oplus/Ly^3$ | Biogenic-Receptive Worlds                                             |
| Biogenic-Sterilized habitats ($S_H$) | $N_H/3$ | $M_\oplus/Ly^3$ | Biogenic-free or sterilized Worlds/habitats                          |

Flows

| Flow                        | Function                          | Meaning                                      |
|-----------------------------|-----------------------------------|----------------------------------------------|
| 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 |
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