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General Probabilistic Computational Framework Applied to Drake–Fermi–Brin Models of Technological Civilizations

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Abstract

Many scientific and engineering domains rely on simple models whose usefulness is limited by uncertain parameters and incompatible formulations. We present a computational framework that converts deterministic, semi-empirical, and heuristic equations into stochastic model families by using bounded parameter representations and Monte Carlo sampling. An explicit semantic layer preserves differences in variable meaning, enabling comparison without forcing structural equivalence. The framework also supports supermodels—weighted mixtures of heterogeneous model families evaluated in a shared diagnostic space. The method is implemented as a reproducible pipeline for five structurally distinct Drake–Fermi–Brin models, with joint and marginal distribution analysis, exploratory clustering, parameter-importance diagnostics, and layered uncertainty decomposition. Results show that model structure and epistemic parameterization materially shape the induced distributions. Comparisons therefore remain conditional on the declared parameter bounds, sampling families, semantic bridges, and model-family weights. Nevertheless, ensemble integration can reveal behavior not visible within individual models. The space of possible supermodel configurations exceeds 10^{27} , illustrating both the scale of the problem and the value of a structured probabilistic workflow. The framework provides an extensible basis for uncertainty propagation and comparison across incompatible models.

Keywords: Monte Carlo simulation; uncertainty quantification; probabilistic modeling; model integration; sensitivity analysis; computational reproducibility; ensemble modeling; scenario analysis; Drake equation; Fermi paradox

1. Introduction

Many scientific and engineering domains are characterized by collections of relatively simple mathematical models whose predictive utility is limited by deep parameter uncertainty, heterogeneous assumptions, and incompatible formulations. In such settings, the primary challenge is not the derivation of new governing equations but the computational integration of existing models into a coherent probabilistic representation that supports uncertainty quantification and systematic comparison.

A representative example is the Drake equation, originally formulated as a heuristic multiplicative decomposition for estimating the number of communicative technological civilizations in the Galaxy:

$$N = R_* f_p n_e f_i f_a L. \quad (1)$$

Here, R_* is the stellar formation rate, f_p is the fraction of stars with planets, n_e is the mean number of habitable planets per planetary system, f_i is the fraction of habitable



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planets on which life emerges, f_i is the fraction on which intelligence emerges, f_a is the fraction that becomes communicative or technologically detectable, and L is the active communicative lifetime. Although this decomposition into astrophysical, biological, technological, and temporal factors remains conceptually useful, substituting highly uncertain inputs with fixed point estimates can create a misleading impression of precision. For this reason, several authors have argued that Drake-like reasoning should be treated probabilistically and computationally rather than deterministically [1–3]. Other formulations address related phenomena, but they often differ from the basic Drake equation in their assumptions, variables, and output semantics.

From a computational perspective, this class of problems belongs to a broader category of uncertainty propagation in multi-model systems, where multiple independently developed formulations describe overlapping aspects of the same phenomenon but cannot be directly combined due to differences in variable definitions, structural assumptions, or scaling interpretations. The central challenge is therefore not merely stochastic sampling but also the construction of a consistent computational layer that preserves model heterogeneity while enabling quantitative comparison.

The aim of this work is to develop a reproducible computational framework for transforming collections of structurally incompatible equations into integrated probabilistic systems under deep uncertainty. The Drake–Fermi–Brin problem is used as a structured test case for this purpose, providing a domain in which multiple competing formulations exist for abundance, lifetime, and expansion processes but lack a unified computational representation. The same methodology applies to general multi-model systems in which structural incompatibility prevents direct aggregation or calibration.

Uncertainty in computational modeling is commonly divided into aleatory and epistemic components. In heterogeneous multi-model systems, the main epistemic sources are parameter, model-form (structural), and semantic uncertainty, with the latter arising when apparently comparable variables have different physical meanings.

Propagation methods include probabilistic techniques, such as Monte Carlo sampling, polynomial chaos, global sensitivity analysis, and Bayesian inference; non-probabilistic representations, including intervals, probability boxes, and convex domains; and hybrid approaches [4–7]. The present framework applies bounded Monte Carlo sampling separately to each model family, preserves distinct model structures, and uses an explicit semantic mapping layer. The resulting distributions remain conditional on the adopted bounds, sampling laws, equations, and semantic assumptions.

To address these challenges, three methodological requirements are imposed. First, all uncertain inputs are represented as bounded distributions and propagated using numerically stable Monte Carlo sampling. Second, models with differing interpretations of key variables, particularly abundance, are not forced into direct equivalence but are instead compared through explicit semantic separation. Third, integration across models is performed only after mapping outputs into a shared diagnostic space that preserves their native meaning.

Within this structure, the paper develops a computational workflow that replaces deterministic evaluation with ensemble-based propagation of uncertainty, enabling the construction of conditional scenario distributions rather than calibrated predictive estimates. The resulting framework supports systematic exploration of how structural assumptions influence emergent distributional behavior across model families.

The main contributions of this work are as follows:

1. A unified computational pipeline for propagating uncertainty across multiple structurally distinct model classes using bounded parameter representations and Monte Carlo simulation.

2. A semantic separation framework that preserves differences in variable meaning across models, preventing invalid aggregation of non-equivalent quantities.
3. A supermodel construction method that integrates heterogeneous model outputs via explicit diagnostic mappings and weighted mixtures in a shared space.
4. A comprehensive diagnostic suite, including joint distribution estimation, marginal analysis, clustering of emergent regimes, and parameter-importance quantification.

The framework is implemented and evaluated using five structurally distinct model classes that represent non-settlement, aggregated, settlement-based, silence-conditioned, and Rare-Earth-filtered formulations. These are combined into weighted supermodels to examine how different structural assumptions influence the resulting probabilistic structure.

The remainder of the paper is organized as follows. Section 2 reviews related work on uncertainty in Drake-like models, stochastic astrobiological modeling, settlement dynamics, SETI non-detection, and Rare-Earth filtering [8–12]. Section 3 introduces the semantic framework for abundance variables. Section 4 presents the computational workflow, bounded triad representation, sampling strategy, and diagnostic estimators. Section 5 defines the model classes, with detailed formulations provided in Supplementary Section S1. Section 6 introduces the supermodel construction. Section 7 presents ensemble results, and Sections 8 and 9 provide interpretation, limitations, and conclusions.

2. Related Work

The computational structure of the problem is related to broader work on uncertainty quantification, stochastic modeling and model comparison. Previous studies have addressed verification, validation, and sensitivity analysis in numerical models [13], parametric reduced-order approximations under uncertainty [14], and Bayesian stochastic up-scaling across model scales [15].

Recent engineering studies further illustrate probabilistic, non-probabilistic and hybrid treatments of bounded and correlated parameter uncertainty [4–7]. These works provide representative examples of mainstream uncertainty-propagation methodologies, but they address single deterministic systems. The present framework differs by preserving several model families with distinct equations, parameter spaces and output semantics, applying bounded Monte Carlo propagation to each family separately, and introducing explicit structural and semantic layers for cross-model comparison.

Drake-like reasoning is best understood as a framework for organizing uncertainty rather than as a calibrated predictive law. Classical Drake formulations separate astrophysical, biological, technological, and temporal factors, but deterministic substitution of point estimates can obscure the scale of the underlying uncertainty. Probabilistic reformulations therefore treat the Drake factors as random variables and examine the induced distribution of possible outcomes rather than a single estimate [2,3,16]. Related Bayesian work on the early emergence of life also emphasizes that evidence from one inhabited planet weakly constrains abiogenesis and intelligence [17]. These studies motivate the present treatment of Drake-like reasoning as a distributional uncertainty-propagation problem.

A second line of work modifies the target quantity of Drake-like models. Some studies estimate the probability that technological species have ever appeared rather than the number currently active [18], while others introduce explicit assumptions about development timescales, stellar populations, and communicative lifetimes [19]. These reformulations show that changing the meaning of the output variable can be as important as changing the numerical value of an input parameter. This issue is central to the present paper, because the abundance variable may denote independent civilizations, source civilizations, or active settled sites depending on the model family.

Settlement and Fermi-paradox models motivate the expansion components of the framework. Brin’s discussion of the Great Silence emphasized that contact and expansion assumptions cannot be reduced to simple island-like extrapolations [8]. Percolation and settlement models further show that incomplete Galactic occupation can occur even when expansion is possible [9], and later simulations demonstrate that settlement dynamics, stellar motion, probe range, and habitability assumptions can strongly affect Fermi-paradox interpretations [10]. Prantzos connected Drake-like abundance parameters with colonization volumes and highlighted the importance of the lifetime factor in determining the spatial reach of technological civilizations [11]. These works motivate treating settlement not merely as a multiplier, but as a change in the semantic meaning of abundance.

Observational non-detection provides an additional modeling constraint, but it is not a direct measurement of civilization prevalence. The cosmic-haystack framework formalizes SETI incompleteness across sky coverage, frequency, sensitivity, time, signal class, and other dimensions [12]. Low-frequency MWA searches and recent large-scale Breakthrough Listen and COSMIC surveys illustrate that null detections remain conditional on exposure, sensitivity, target selection, and signal assumptions [20–22]. For the present paper, the relevant implication is methodological: null detection is represented as diagnostic conditioning rather than as a direct empirical estimate of N or L .

Rare-Earth and Great-Filter arguments represent a different explanatory tradition. Ward and Brownlee argued that microbial life may be common while complex life may require a restrictive conjunction of planetary, geological, and evolutionary conditions [23]. Great-Filter and Galactic-habitability arguments similarly separate abiogenesis, complex life, intelligence, technology, and long-term persistence into distinct filtering stages [24,25]. Recent work has renewed this perspective by emphasizing the possible importance of long-lived continents, oceans, and plate tectonics for complex technological life [26]. In the present framework, Rare-Earth assumptions are therefore treated as scenario-level filters rather than as calibrated empirical frequencies.

Table 1 summarizes how the present study extends the main areas of related work.

Table 1. Main related-work areas and extension of the present study.

Area	Prior Work	Present Study
Computational uncertainty modeling	Develop workflows for uncertainty quantification, model reduction, stochastic up-scaling, and model comparison [13–15].	Applies this logic to Drake–Fermi models using heatmaps, supermodels, clustering, and importance diagnostics.
Probabilistic Drake models	Use distributions instead of fixed Drake parameters [2,3,16].	Propagates bounded triads across several model classes and produces empirical ($\log_{10} L_{\text{active}}, \log_{10} N_{\text{active}}$) distributions.
Modified Drake formulations	Change the target quantity, such as CETI abundance, ever-existing civilizations, or sustainability [18,19].	Treats these changes as semantic differences in what N and L mean.
Settlement and Fermi-paradox models	Model interstellar expansion through settlement, percolation, colonization volumes, or steady states [8–11].	Separates source civilizations from active settled sites and treats expansion as a semantic transformation of N_{active} .

Table 1. Cont.

Area	Prior Work	Present Study
Technosignature non-detection	Interpret null results under incomplete search coverage and limited exposure [12,20–22].	Treats silence as model conditioning, not as a direct measurement of civilization prevalence.
Rare-Earth and Great-Filter arguments	Emphasize planetary, geological, evolutionary, Galactic, and anthropic filters [23–26].	Implements Rare-Earth assumptions as scenario-level filters and compares their N – L regimes with Drake and settlement models.

3. Conceptual Framework and Variable Semantics

Drake-like and settlement-based models often use the same abundance symbol to denote different physical quantities. In non-settlement models, abundance typically refers to independently arising active civilizations (N_{civ}), whereas in settlement models it denotes active technological sites (N_{site}) generated by a smaller number of source civilizations (N_{source}). Treating these quantities as equivalent would make the models incomparable.

The plotted abundance variable N_{active} is assigned model-specifically:

$$N_{\text{active}} = \begin{cases} N_{\text{civ}}, & \text{Models I, II, IV,} \\ N_{\text{site}}, & \text{Models IIIA, IIIB–M.} \end{cases} \quad (2)$$

In settlement models, the site multiplicity is defined as

$$Q_{\text{site}} = \frac{N_{\text{site}}}{N_{\text{source}}}, \quad N_{\text{source}} > 0, \quad (3)$$

which quantifies the average number of active sites per source civilization.

Although all models can be visualized in the common $(\log_{10} L_{\text{active}}, \log_{10} N_{\text{active}})$ -plane, the vertical axis carries different semantic meanings depending on the model class. The shared visualization serves only as a diagnostic comparison tool and does not imply physical equivalence between independent civilizations and settled sites.

4. Materials and Methods

4.1. Computational Workflow and Probabilistic Formulation

The study is designed as a controlled computational model-comparison experiment rather than as a single predictive calculation. Let M_k , $k = 1, \dots, K$, denote a model family, Θ_k its uncertain input vector, and $\mathbf{Y}_k = \mathbf{F}_k(\Theta_k)$ its vector of native outputs. The uncertainty-propagation problem is written as

$$\Theta_k \sim P_k, \quad \mathbf{Y}_k = \mathbf{F}_k(\Theta_k). \quad (4)$$

For a Monte Carlo ensemble of size N_{MC} the independent configurations are generated according to

$$\theta_k^{(s)} \stackrel{\text{iid}}{\sim} P_k, \quad \mathbf{y}_k^{(s)} = \mathbf{F}_k(\theta_k^{(s)}), \quad s = 1, \dots, N_{\text{MC}}. \quad (5)$$

Expectations of any integrable diagnostic function g are estimated by the corresponding Monte Carlo average

$$\hat{\mathbb{E}}_{P_k}[g(\mathbf{Y}_k)] = \frac{1}{N_{\text{MC}}} \sum_{s=1}^{N_{\text{MC}}} g(\mathbf{y}_k^{(s)}). \quad (6)$$

The baseline implementation assumes that the components of Θ_k are mutually independent within each realization. Scientifically defensible dependence information is unavailable for most biological, technological, survival and settlement-related parameters.

At the parameter level, each scalar component $\Theta_{k,j}$ of the model-specific input vector is represented by a bounded triad

$$[x_{\min}, x_{\text{peak}}, x_{\max}],$$

where $x_{\min}$ and $x_{\max}$ define the admissible modeling interval and x_{peak} is a central representative value. The associated marginal sampling law is

$$\Theta_{k,j} \sim \mathcal{D}_{k,j}[x_{\min}, x_{\text{peak}}, x_{\max}], \quad (7)$$

where $\mathcal{D}_{k,j}$ denotes one of the bounded distribution families used in the study (bounded lognormal, bounded Gaussian or log-linear).

The selected distribution family forms part of the scenario specification and primarily represents a bounded epistemic state of knowledge rather than an empirically calibrated frequency distribution or posterior. For observationally constrained quantities the triad is anchored to literature estimates; for weakly constrained biological, technological, settlement and survival quantities, it defines an explicitly declared scenario range.

For the Drake-type backbone, the uncertain input vector is

$$\theta = (R_*, f_p, n_e, f_l, f_i, f_a), \quad (8)$$

where the symbols have the same meaning as in Equation (1). As a representative example, the stellar-system formation rate is sampled from its bounded triad as

$$R_* \sim \mathcal{D}_{[R_{*,\min}, R_{*,\text{peak}}, R_{*,\max}]}. \quad (9)$$

The remaining components of θ , namely, f_p , n_e , f_l , f_i , and f_a , are sampled and propagated analogously from their corresponding bounded parameter triads. Parameters in other models are constructed similarly.

The Drake production factor is then a random variable induced by these sampled inputs:

$$C_D(\theta) = R_* f_p n_e f_l f_i f_a. \quad (10)$$

In the inverse formulation used for the principal heatmaps, the abundance axis is also sampled as a bounded distribution,

$$n = N_{\text{active}} \sim \mathcal{D}_{[N_{\text{active},\min}, N_{\text{active},\text{peak}}, N_{\text{active},\max}]}. \quad (11)$$

and the active lifetime is derived from the model equation rather than sampled independently. For the Drake-type inverse relation,

$$L_{\text{active}} = \frac{n}{C_D(\theta)}. \quad (12)$$

Thus, in the inverse N – L construction, L_{active} is the model-implied lifetime associated with a sampled abundance n and a sampled production factor $C_D(\theta)$. It is not an independent input distribution.

The probabilistic output is therefore an induced joint distribution in logarithmic coordinates. Let

$$x = \log_{10} L_{\text{active}}, \quad y = \log_{10} N_{\text{active}}.$$

For the Drake-type inverse model, the corresponding push-forward density is

$$\rho(x, y) = \int \pi(\theta) \pi_N(n) \delta\left(x - \log_{10} \frac{n}{C_D(\theta)}\right) \delta(y - \log_{10} n) d\theta dn. \quad (13)$$

where $\pi(\theta)$ denotes the joint probability density of the uncertain Drake parameters, $\pi_N(n)$ denotes the probability density assigned to the sampled abundance coordinate, and $\delta(\cdot)$ is the Dirac delta distribution.

The heatmap is a discretized estimate of this density. For a bin

$$B_{ij} = [x_i, x_{i+1}) \times [y_j, y_{j+1}),$$

the probability mass assigned to that bin is

$$H_{ij} = \int_{x_i}^{x_{i+1}} \int_{y_j}^{y_{j+1}} \rho(x, y) dy dx. \quad (14)$$

In the Monte Carlo implementation, this integral is approximated by

$$\hat{H}_{ij} = \frac{1}{N_{\text{MC}}} \sum_{s=1}^{N_{\text{MC}}} \mathbf{1}\left[\left(\log_{10} L_{\text{active}}^{(s)}, \log_{10} N_{\text{active}}^{(s)}\right) \in B_{ij}\right], \quad (15)$$

or, for models with diagnostic weights w_s , by

$$\hat{H}_{ij}^{(w)} = \frac{\sum_{s=1}^{N_{\text{MC}}} w_s \mathbf{1}\left[\left(\log_{10} L_{\text{active}}^{(s)}, \log_{10} N_{\text{active}}^{(s)}\right) \in B_{ij}\right]}{\sum_{s=1}^{N_{\text{MC}}} w_s}. \quad (16)$$

A unified workflow is applied to all five single-model classes, but the semantic assignment of N_{active} is model-specific. The complete sampling, semantic-assignment, weighting, probability evaluation and heatmap-construction procedure is summarized in Algorithm A1 in Appendix A.

Table 2 summarizes the main uncertainty sources represented in the Drake–Fermi–Brin framework and indicates how each source is treated in the present Monte Carlo implementation.

Table 2. Classification of the main uncertainty sources addressed in the Drake–Fermi–Brin framework and their treatment in the present study.

Uncertainty Source	Origin in the Model System	Representation or Treatment in the Framework
Parameter uncertainty	Incomplete knowledge of astrophysical, biological, technological, settlement, survival and detection parameters.	Bounded parameter triads, declared sampling distributions, Monte Carlo propagation, distribution-family robustness tests and within-model sensitivity analysis.

Table 2. *Cont.*

Uncertainty Source	Origin in the Model System	Representation or Treatment in the Framework
Model-form/structural uncertainty	Different governing equations, assumptions, mechanisms and causal structures across model families.	Separate preservation of five model families; controlled comparison or mixture only after model-specific simulation.
Semantic uncertainty	Different meanings of apparently comparable output quantities (independent civilizations, source civilizations, and active settled sites).	Native outputs are preserved and connected to shared diagnostic quantities through an explicit semantic mapping layer. A reference site-level bridge and an alternative source-level bridge are compared through a targeted semantic-sensitivity analysis.
Numerical uncertainty	Finite Monte Carlo sample size, numerical integration, density estimation and algorithmic approximation.	Fixed random seeds, Monte Carlo convergence analysis, stored ensembles and reproducible diagnostic computation.

4.2. Bounded Triad Representation

Every uncertain parameter is represented by a bounded triad

$$p \sim [p_{\min}, p_{\text{peak}}, p_{\max}], \quad (17)$$

where $p_{\min}$ and $p_{\max}$ define the admissible modeling range and p_{peak} is the central representative value. The numerical values of the triads are taken from the literature sources listed in Supplementary Section S4. For observationally constrained quantities, they form a conservative literature-based envelope; for weakly constrained biological, technological, settlement, survival and Rare-Earth quantities they define a deliberately broad exploratory range. In all cases the bounds represent epistemic modeling support rather than observational confidence intervals or posterior credible intervals.

This representation was chosen because many Drake-like parameters are too uncertain to support narrow confidence intervals. The same numerical range can encode different epistemic assumptions depending on the chosen sampling distribution (additive, multiplicative, or logarithmic). The triad notation therefore cleanly separates the modeling range from the distribution imposed on that range. All sampled values remain strictly inside the declared bounds.

4.3. Sampling Distributions

Three distribution families are employed. Lognormal sampling captures multiplicative uncertainty, Gaussian sampling captures localized linear uncertainty, and log-linear sampling captures broad logarithmic uncertainty. The choice of distribution family is therefore an explicit part of the model assumption.

For parameters that are intrinsically positive or confined to $[0, 1]$, appropriate positive-support or bounded transformations are applied. The transformation between linear and logarithmic coordinates is non-linear:

$$p_X(x) = p_U(\log_{10} x) \frac{1}{x \ln 10}. \quad (18)$$

Consequently, the same triad produces markedly different density shapes in linear versus logarithmic space. For this reason, all primary results are presented in the $(\log_{10} L, \log_{10} N)$ -plane.

Supplementary Figure S1 in Supplementary Section S2 illustrates how the same bounded triad can lead to different sampled densities depending on whether the uncertainty is represented in linear, lognormal, or log-linear form.

4.4. Targeted Robustness Analysis of Subjective Parameter Triads

To evaluate the sensitivity of the results to the subjective components of the Bounded Triad Representation, we performed a targeted robustness analysis for Model I. The analysis focused on the biological and technological factors f_l , f_i and f_a , because these parameters are weakly constrained and the parameter-importance analysis identifies f_i and f_a as leading contributors to variation in $\log_{10} L_{\text{active}}$.

Let

$$z_{\min} = \log_{10} p_{\min}, \quad z_{\text{peak}} = \log_{10} p_{\text{peak}}, \quad z_{\max} = \log_{10} p_{\max}. \quad (19)$$

Two alternative bound scenarios were generated by scaling the logarithmic distances from the peak:

$$z_{\min}^{(s)} = z_{\text{peak}} + s(z_{\min} - z_{\text{peak}}), \quad (20)$$

$$z_{\max}^{(s)} = z_{\text{peak}} + s(z_{\max} - z_{\text{peak}}), \quad (21)$$

where $s = 0.75$ defines the narrowed-bound scenario and $s = 1.25$ defines the widened-bound scenario. Upper bounds for fractional parameters were restricted to unity.

Peak sensitivity was evaluated by moving each peak by 25% of its logarithmic distance toward either the lower or upper bound:

$$z_{\text{peak}}^{(-)} = z_{\text{peak}} + 0.25(z_{\min} - z_{\text{peak}}), \quad (22)$$

$$z_{\text{peak}}^{(+)} = z_{\text{peak}} + 0.25(z_{\max} - z_{\text{peak}}). \quad (23)$$

All parameters other than f_l , f_i and f_a were retained at their baseline specifications.

The baseline bound-and-peak test used a bounded lognormal representation, implemented as a truncated Gaussian distribution in $\log_{10} p$, centered on z_{peak} and restricted to $[z_{\min}, z_{\max}]$. Additional output-level distribution-family checks replaced the bounded-lognormal representations of f_l , f_i and f_a with either log-linear or bounded Gaussian sampling while retaining the original triads.

For each scenario we recorded the median of $\log_{10} L_{\text{active}}$, the 90% interval width

$$W_{90} = q_{0.95}(\log_{10} L_{\text{active}}) - q_{0.05}(\log_{10} L_{\text{active}}),$$

and the changes in the fixed diagnostic-region masses.

Each scenario was evaluated in five independent Monte Carlo runs of $N_{\text{MC}} = 10^5$ samples each. Common random numbers were used across the baseline and alternative scenarios within each run, and the reported values are averages over the five runs. The exact distribution parameterizations, random seeds, seed-specific summaries, and reproduction script are provided in accompanying repository.

4.5. Multiplicative Uncertainty, Silence Conditioning, and Implementation

A central numerical and statistical difficulty in Drake-like modeling is that the main production term is multiplicative. Several factors, especially f_l , f_i , and f_a , are bounded fractions that may span many orders of magnitude. If these factors are sampled directly and multiplied in arithmetic space, small draws can dominate the product, causing the resulting abundance distribution to become highly right-skewed and to assign substantial probability mass to very small values. Equivalently, for a product

$$X = \prod_{j=1}^m X_j, \quad (24)$$

the transformed variable satisfies

$$\log X = \sum_{j=1}^m \log X_j. \quad (25)$$

Thus, uncertainty accumulates additively in log space, while the product itself can vary over orders of magnitude. For independent factors, the variance of the product contains cross-terms:

$$\text{Var}\left(\prod_{j=1}^m X_j\right) = \prod_{j=1}^m (\text{Var}(X_j) + \mathbb{E}[X_j]^2) - \prod_{j=1}^m \mathbb{E}[X_j]^2, \quad (26)$$

so even moderate uncertainty in individual inputs can produce broad output distributions [27]. This motivates the use of bounded input distributions, positivity safeguards, and log-space propagation when estimating Drake-like quantities, and explains why multiplicative uncertainty often produces approximately lognormal or log-skewed output distributions [28].

To mitigate these numerical difficulties, several safeguards are employed. First, all multiplicative models are evaluated with explicit positivity checks and lower-bound safeguards before log-space transformation. These safeguards prevent numerical domination by extreme near-zero production factors while preserving the declared parameter triads. Second, the comparison between Model I and Model II tests whether the fully factorized Drake product $R_* f_p n_e f_l f_i f_a$ produces tail behavior that is not present when the same structure is represented through the aggregate factors F_{astro} and $F_{\text{bioactive}}$. Third, the parameter-importance analysis identifies which inputs dominate the variation in $\log_{10} L_{\text{active}}$, following the broader role of sensitivity analysis in uncertainty propagation [29].

These steps do not remove the structural uncertainty of Drake-like modeling. Rather, they make the tail behavior visible, reproducible, and less dependent on numerical artifacts introduced by multiplying several broad uncertain factors.

Model IIIB-M additionally incorporates observational silence as a conditioning term in the effective survival hazard. Rather than using the Poisson zero-event probability as the default plotting weight, the model modifies the hazard scale through the silence-survivorship factor specified in Supplementary Section S1.2. The ordinary zero-event probability is retained as a diagnostic consistency quantity. With

$$E_{\text{obs}} = \lambda_{\text{det}} T_{\text{det}} + \lambda_{\text{vis}} T_{\text{vis}},$$

the expected number of observable events is

$$\mu_{\text{obs}} = N_{\text{site}} E_{\text{obs}},$$

and the corresponding zero-event diagnostic probability is

$$P_0 = \exp(-\mu_{\text{obs}}).$$

Thus, observational silence affects the lifetime calculation through the effective survival hazard, while P_0 is stored as a diagnostic quantity rather than used as the default Monte Carlo weight. The model equations were implemented in a modular Python framework following Algorithm A1 (see Appendix A). The complete code, configuration files, and random seeds are available in the accompanying repository to ensure reproducibility.

The silence-survivorship factor and the diagnostic zero-event probability should therefore be understood as heuristic, scenario-level conditioning devices. They do not constitute a survey-calibrated multidimensional likelihood [12,30] and must not be interpreted as uniquely constraining civilization lifetime.

4.6. Semantic Empirical Measure and Regime Probabilities

The model outputs are first represented in their native semantics. Let $m \in \{1, \dots, 5\}$ denote the model class and let $s = 1, \dots, N_{\text{MC}}$ index Monte Carlo samples. For every valid sample, the native log-space output is defined as

$$z_{m,s} = \left(\log_{10} L_{\text{active}}^{(m,s)}, \log_{10} N_{\text{active}}^{(m,s)} \right). \quad (27)$$

In Models I, II, and IV, N_{active} denotes independent active civilizations, while in Models IIIA and IIIB-M it denotes active technological sites. Let $w_{m,s}$ denote an optional diagnostic weight for sample s in model m . In the default heatmaps and regime summaries used here, $w_{m,s} = 1$ for all model families. For Model IIIB-M, observational silence is incorporated into the lifetime calculation through the silence-survivorship factor defined in Supplementary Section S1.2. The ordinary zero-event probability P_0 is retained as a diagnostic consistency quantity but is not used as the default plotting weight.

For any region $A \subset \mathbb{R}^2$ in the native $(\log_{10} L_{\text{active}}, \log_{10} N_{\text{active}})$ -plane, the model-specific empirical measure is

$$\hat{\mu}_m(A) = \frac{\sum_{s=1}^{N_{\text{MC}}} w_{m,s} \mathbf{1}[z_{m,s} \in A]}{\sum_{s=1}^{N_{\text{MC}}} w_{m,s}}. \quad (28)$$

This measure is used for individual model heatmaps, marginal diagnostics, and regime summaries.

Supermodel heatmaps require an additional semantic step. Because raw abundance values from different model families do not share the same physical meaning, a common diagnostic abundance variable N^* is introduced. For settlement models (IIIA and IIIB-M), the native site abundance is used directly:

$$N^* = N_{\text{site}}. \quad (29)$$

For Model IV, the non-settlement abundance coordinate is used:

$$N^* = N_{\text{active}} = N_{\text{civ}}.$$

Supermodel integration requires an explicit semantic interface because the native abundance variables of the model families do not denote the same physical entity. The reference bridge used in the original supermodel heatmaps is the site-level bridge

$$N_{\text{site}}^*(m, s) = \begin{cases} N_{\text{civ}}^{(m, s)}, & m \in \{\text{I, II, IV}\}, \\ N_{\text{site}}^{(m, s)}, & m \in \{\text{IIIA, IIIB-M}\}. \end{cases} \quad (30)$$

For a targeted semantic-sensitivity analysis, we additionally evaluate the source-level bridge

$$N_{\text{source}}^*(m, s) = \begin{cases} N_{\text{civ}}^{(m, s)}, & m \in \{\text{I, II, IV}\}, \\ N_{\text{source}}^{(m, s)}, & m \in \{\text{IIIA, IIIB-M}\}. \end{cases} \quad (31)$$

The reference bridge preserves the native active-site abundance of the settlement models, whereas the alternative bridge compares all model families at the level of independently originating civilizations. Neither bridge asserts physical equivalence between civilizations and settled sites. They are alternative diagnostic mappings applied to the same stored native outputs. The baseline figures retain the reference site-level bridge, while the source-level bridge is used only to quantify semantic-mapping sensitivity.

The resulting semantic-sensitivity metrics and the bridge-conditional Bayesian model-averaging results are reported in Section 7 and Supplementary Table S9.

The sensitivity to the semantic bridge is evaluated by post-processing the stored native outputs; no model equations are modified, and no additional baseline Monte Carlo simulations are required. For $b \in \{\text{site, source}\}$, let

$$m_b = \text{med}(\log_{10} N_b^*), \quad W_{90, b} = q_{0.95}(\log_{10} N_b^*) - q_{0.05}(\log_{10} N_b^*).$$

The bridge sensitivity is summarized by

$$\Delta_{\text{med}} = m_{\text{site}} - m_{\text{source}}, \quad R_{W_{90}} = \frac{W_{90, \text{source}}}{W_{90, \text{site}}}, \quad \Delta P_{\text{max}} = \max_r |P_{\text{source}}(\mathcal{R}_r) - P_{\text{site}}(\mathcal{R}_r)|. \quad (32)$$

Here, $P_b(\mathcal{R}_r)$ denotes the conditional Monte Carlo mass assigned to diagnostic region $\mathcal{R}_r$ under bridge b . A positive Δ_{med} indicates that the site-level bridge produces a larger median diagnostic abundance, while $R_{W_{90}} < 1$ indicates that the source-level representation is narrower. These quantities measure sensitivity to the selected semantic mapping; they are not estimates of systematic error relative to a known physical ground truth.

For the reference site-level bridge, the corresponding bridged output is

$$z_{m, s}^* = (\log_{10} L_{\text{active}}^{(m, s)}, \log_{10} N_{\text{active}}^{*(m, s)}). \quad (33)$$

For a supermodel indexed by k , let $\pi_{k, m}$ denote the normalized model-family weight. The bridged supermodel measure is

$$\hat{\mu}_{\text{SM}, k}^*(A) = \sum_{m=1}^5 \pi_{k, m} \frac{\sum_{s=1}^{N_{\text{MC}}} w_{m, s} \mathbf{1}[z_{m, s}^* \in A]}{\sum_{s=1}^{N_{\text{MC}}} w_{m, s}}, \quad \sum_{m=1}^5 \pi_{k, m} = 1. \quad (34)$$

This measure is used for supermodel heatmaps and regime probabilities. Broad regime probabilities for individual models are obtained analogously by integrating the native measure $\hat{\mu}_m$ over chosen regime regions $\mathcal{R}_r$.

Algorithm A2 in Appendix A summarizes the construction of native and bridged measures as well as regime-probability summaries.

4.7. Diagnostic Analyses

The simulated ensembles are examined using several complementary diagnostics:

- Heatmaps show the joint density in the native $(\log_{10} L_{\text{active}}, \log_{10} N_{\text{active}})$ -plane.

- Tripanel diagnostics decompose each ensemble into a joint-density map, a marginal lifetime distribution, and a survival (or exceedance) function.
- Supermodel mixtures combine the five base-model ensembles using explicit model-family weights, allowing robustness to be assessed across model classes.
- PCA and k -means clustering identify distinct numerical regimes in the shapes of the lifetime distributions. These clusters are used only as an interpretability diagnostic.
- Parameter-importance grids quantify the relative influence of each sampled input on $\log_{10} L_{\text{active}}$, and secondarily on $\log_{10} N_{\text{active}}$, within each model class. Importance is measured using Random-Forest regression or classification, followed by permutation importance on a held-out test set. The resulting scores are normalized within each model and diagnostic target. To separate the principal uncertainty layers, the accompanying repository reports a balanced hierarchical decomposition of the integrated output variance into within-configuration parameter, model-structural, semantic-bridge, and model-bridge interaction components. The reported shares are conditional on equal representation of the five model families and the two semantic bridges and should not be interpreted as empirical probabilities of the competing physical models.

To quantify uncertainty above the within-model parameter level, we additionally applied a balanced hierarchical variance decomposition to the stored ensembles. For $Y \in \{\log_{10} L_{\text{active}}, \log_{10} N^*\}$,

$$\text{Var}(Y) = V_{\theta} + V_M + V_B + V_{M \times B}, \quad V_{\theta} = \mathbb{E}_{M,B}[\text{Var}(Y \mid M, B)],$$

where the remaining terms are the balanced two-way variance components of the model M , semantic bridge B , and their interaction. Equal model and bridge weights were used. Because the model families have different parameter spaces, this hierarchical decomposition was used instead of forcing a single common-input Sobol design; permutation importance was retained for parameter ranking within each model.

All diagnostics are derived from the same stored Monte Carlo ensemble, ensuring that heatmaps, marginal distributions, supermodel mixtures, clustering analyses, and parameter-importance summaries remain internally consistent.

4.8. Reproducibility and Numerical Safeguards

The baseline pipeline and the revision-specific analyses are reproducible from the code, configuration files, random seeds, and numerical summaries archived in the accompanying repository. The repository supplement contains the robustness-analysis materials (available in the accompanying repository), the balanced layered-uncertainty decomposition and figure (available in the accompanying repository), the clustering-sensitivity diagnostics (available in the accompanying repository), and the observation-informed, semantic-bridge, and bridge-conditional BMA analysis materials.

Numerical safeguards include strict enforcement of parameter bounds, positivity checks before logarithmic transformations, rejection of invalid samples, and consistent semantic labeling of the abundance variable. These safeguards ensure computational consistency across model families, but they do not change the conditional status of the results. Each output distribution is valid only under the corresponding model equations, parameter triads, sampling assumptions, and diagnostic weights.

The results should therefore be interpreted as transparent uncertainty propagation within explicitly defined modeling scenarios.

A multidimensional SETI observation layer based on the cosmic-haystack framework [12] and Bayesian null-detection treatments [30] is derived in Supplementary Section S5 and can reweight stored Monte Carlo samples without modifying the native model equations or the

unchanged baseline figures. A reduced observation-informed application propagates four completeness-corrected external posterior marginals for $\eta_{\text{HZ}} = f_p n_e$ from Bryson et al. [31] through the semantically compatible model families and conditionally reweights the resulting samples using the selected MWA Vela zero-detection survey [20]; the implementation and numerical summaries are reported in Supplementary Section 5.14 and Supplementary Table S10.

5. Model Definitions and Parameter Triads

5.1. Rationale for Model Selection

The five base models were selected for distinct methodological roles. Model I provides the adapted Drake baseline corresponding to the classical equation introduced in Equation (1). Model II recasts the same non-settlement logic in aggregate form as a robustness check. Models IIIA and IIIB-M represent settlement and expansion, either through an explicit spatial kernel or through a coarse-grained active-site multiplier with silence conditioning. Model IV represents the Rare-Earth filtering scenario.

Together, these models provide a compact comparison among classical Drake abundance estimation, aggregate Drake-like reduction, expansionist settlement, silence-conditioned settlement, and Rare-Earth filtering. The aim is not to exhaust all possible models, but to compare a small set of the most popular, interpretable and reproducible modeling assumptions within a unified computational framework.

Because the main-text figures emphasize the contrast between the Drake baseline and the explicit spatial settlement model, Models I and IIIA are defined in full below. Models II, IIIB-M, and IV are summarized briefly here and specified in Supplementary Section S1.

5.2. Model I: Drake Baseline

Model I implements the classical non-settlement Drake baseline. The adapted production factor is

$$C_D = R_* f_p n_e f_l f_i f_a. \quad (35)$$

The model uses the inverse abundance–lifetime relation

$$L_{\text{active}} = \frac{N_{\text{active}}}{C_D} = \frac{N_{\text{active}}}{R_* f_p n_e f_l f_i f_a}, \quad (36)$$

where $N_{\text{active}} = N_{\text{civ}}$ (independent active civilizations). Equivalently, in logarithmic form:

$$\log_{10} L_{\text{active}} = \log_{10} N_{\text{active}} - \log_{10} R_* - \log_{10} f_p - \log_{10} n_e - \log_{10} f_l - \log_{10} f_i - \log_{10} f_a. \quad (37)$$

All uncertain inputs are sampled from the bounded triads listed in Supplementary Table S4 [32–36]. Monte Carlo propagation, semantic assignment, and heatmap construction follow the unified workflow of Section 4.1 and Algorithm A1. Model I serves as the reference against which the reduced (Model II), settlement (Models IIIA, IIIB-M), and Rare-Earth (Model IV) formulations are compared.

5.3. Model II: Reduced Drake Model

Model II is a reduced non-settlement version of Model I. It is included as a robustness test rather than as a new physical mechanism. Whereas Model I keeps the Drake factors fully explicit, Model II groups them into aggregate astrophysical and biological–technological terms. This tests whether the resulting distribution depends on the fully factorized multiplicative structure or remains stable under aggregation.

As in Model I, the abundance variable denotes independently arising active technological civilizations, i.e., $N_{\text{active}} = N_{\text{civ}}$. The two aggregate factors are defined as $F_{\text{astro}} = R_* f_p n_e$ and $F_{\text{bioactive}} = f_l f_i f_a$. The reduced production factor is therefore $C_{\text{red}} = F_{\text{astro}} F_{\text{bioactive}}$.

The inverse abundance–lifetime relation is

$$L_{\text{active}} = \frac{N_{\text{active}}}{C_{\text{red}}} = \frac{N_{\text{active}}}{F_{\text{astro}} F_{\text{bioactive}}}. \quad (38)$$

Because F_{astro} , $F_{\text{bioactive}}$, and N_{active} are sampled probabilistically, Model II induces the following joint density in the $(\log_{10} L_{\text{active}}, \log_{10} N_{\text{active}})$ -plane:

$$\begin{aligned} \rho_{\text{II}}(x, y) = & \int \pi(F_{\text{astro}}, F_{\text{bioactive}}) \pi_N(n) \\ & \times \delta\left(x - \log_{10} \frac{n}{F_{\text{astro}} F_{\text{bioactive}}}\right) \delta(y - \log_{10} n) dF_{\text{astro}} dF_{\text{bioactive}} dn. \end{aligned} \quad (39)$$

Model II therefore differs from Model I not in the semantic meaning of abundance, but in the level at which multiplicative uncertainty is represented. The remaining sampling rules, heatmap construction, and empirical-measure interpretation follow the general computational framework defined in Section 4. The full dimensional check and parameter triads are provided in Supplementary Section S1.1 and Supplementary Table S5.

5.4. Model IIIA: Spatial Settlement-Survival Model

Model IIIA is the explicit spatial settlement model. The plotted abundance is the number of active technological sites ($N_{\text{active}} = N_{\text{site}}$), while N_{source} denotes independent source civilizations. The source production factor is the standard Drake factor $C_D = R_* f_p n_e f_l f_i f_a$.

The spatial component of the model is motivated by Brin’s original settlement formulation [8]. In that formulation, the number n_j of active sites settled or explored by technological species j is

$$n_j = 4\pi B f_g n_e \int_0^{R(j)} r^2 \exp\left[-\frac{R(j) - r}{vL'}\right] dr, \quad (40)$$

where B is the stellar number density, $R(j)$ is the radius of the approximately spherical region reached by species j , v is the effective expansion velocity, and L' is the characteristic survival time of an individual settled site. The exponential term accounts for the decreasing probability that sites settled earlier remain active at the time of observation.

Settlement is governed by the effective target density $\rho_{\text{set}} = B f_g n_{e, \text{br}} p_{\text{set}}$. For a source civilization of age t , the expansion time and scale are $\tau(t) = \max(t - t_{\text{delay}}, 0)$ and $\beta(t) = v_{\text{eff}} \tau(t)$.

The local settlement integral is

$$I_{\text{loc}}(R, \beta) = \int_0^R r^2 \exp\left(-\frac{r}{\beta}\right) dr, \quad \beta > 0, \quad (41)$$

with closed form

$$I_{\text{loc}}(R, \beta) = \beta^3 \left[2 - \exp\left(-\frac{R}{\beta}\right) \left(\left(\frac{R}{\beta}\right)^2 + 2\frac{R}{\beta} + 2 \right) \right]. \quad (42)$$

One source civilization generates

$$N_{\text{site}}^{(1)}(t) = 1 + 4\pi \rho_{\text{set}} I_{\text{loc}}(R, \beta(t)) \quad (43)$$

active sites. These sites suppress the local hazard component:

$$\lambda(t) = \lambda_{\text{corr}} + \frac{\lambda_{\text{loc}}}{1 + \left(\frac{N_{\text{site}}^{(1)}(t) - 1}{N_{50}} \right)^{\gamma}}. \quad (44)$$

With cumulative hazard $H(t) = \int_0^t \lambda(u) du$ and survival function $S(t) = \exp[-H(t)]$, the active lifetime is

$$L_{\text{active}} = \int_0^{T_{\text{max}}} S(t) dt. \quad (45)$$

The active source count is $N_{\text{source}} = C_D L_{\text{active}}$. The active-site abundance used for heatmaps is

$$N_{\text{site}} = C_D \int_0^{T_{\text{max}}} S(t) N_{\text{site}}^{(1)}(t) dt. \quad (46)$$

Equivalently,

$$Q_{\text{site}} = \frac{\int_0^{T_{\text{max}}} S(t) N_{\text{site}}^{(1)}(t) dt}{\int_0^{T_{\text{max}}} S(t) dt}, \quad N_{\text{site}} = N_{\text{source}} Q_{\text{site}}. \quad (47)$$

For $N_{\text{source}} > 0$, the site multiplicity is $Q_{\text{site}} = N_{\text{site}}/N_{\text{source}}$. The stored output is $(\log_{10} L_{\text{active}}, \log_{10} N_{\text{site}})$. Parameter triads are listed in Supplementary Table S6 [37].

5.5. Model IIIB-M: Scalar Settlement Model with Null-Silence Conditioning

Model IIIB-M is a coarse-grained settlement-survival analog of Model IIIA. Instead of resolving an explicit spatial settlement kernel, it represents settlement through a scalar active-site multiplier M_{site} . The model retains the settlement-model semantic assignment $N_{\text{active}} \equiv N_{\text{site}}$, while N_{source} denotes the corresponding independent source-civilization count. In this formulation, L_{active} is not inferred from a prescribed active-site abundance. Instead, the model first computes a settlement-reduced effective hazard, in which the local hazard component is reduced by site redundancy while the correlated hazard floor remains unchanged. Observational silence then enters through a silence-survivorship conditioning factor that modifies the effective survival hazard. The resulting L_{active} determines the source population via $N_{\text{source}} = C_D L_{\text{active}}$, and the scalar settlement multiplier then gives the active-site abundance as $N_{\text{site}} = M_{\text{site}} N_{\text{source}}$, up to the finite Galactic capacity used in the simulations.

Model IIIB-M computes the active lifetime from a silence- and settlement-adjusted hazard via the closed-form expression

$$L_{\text{active}} = \frac{1 - \exp\left(-\frac{\lambda_{\text{base}}}{A_{\text{sil}}} T_{\text{max}}\right)}{\frac{\lambda_{\text{base}}}{A_{\text{sil}}}}, \quad (48)$$

where λ_{base} incorporates local hazard reduction through the scalar site multiplier M_{site} , and the silence-survivorship factor is given by

$$A_{\text{sil}} = \left(1 + \frac{T_{\text{sil}}}{T_{50,\text{sil}}}\right)^{\eta_{\text{sil}}}.$$

The model is used to test whether settlement-like abundance amplification persists under a simpler site-multiplier formulation with diagnostic silence conditioning. The full equations, silence-conditioning formulation, dimensional check, and parameter triads are provided in Supplementary Section S1.2 and Supplementary Section S4, Supplementary Table S7.

5.6. Model IV: Rare-Earth Filtering Model

Model IV represents a Rare-Earth filtering scenario. It is a non-settlement model with $N_{\text{active}} = N_{\text{civ}}$, but unlike Models I and II, it does not compute the active lifetime from an inverse Drake production relation. Instead, planetary and Galactic filtering factors define a filtered Rare-Earth potential scale,

$$N_{\text{pot,RE}} = N_* n_e f_g f_{pm} f_m f_j f_{me}.$$

Here, $N_* n_e$ denotes the potential habitable-site scale, f_g is the Galactic habitable fraction, and f_{pm} , f_m , f_j , and f_{me} denote Rare-Earth planetary, architectural, and evolutionary filters.

The characteristic active lifetime is computed as

$$L_{\text{active}} = \frac{N_{\text{pot,RE}}}{R_* n_{e,\text{den}}}.$$

The denominator $R_* n_{e,\text{den}}$ acts as a Drake-like normalization rate. Thus $N_{\text{pot,RE}}$ is an intermediate filtered potential scale, not the plotted abundance variable.

For heatmaps and regime summaries, $N_{\text{active}} = N_{\text{civ}}$ is sampled as a separate comparative active-abundance coordinate using the triad reported in Supplementary Table S8. Model IV therefore tests how Rare-Earth filtering shifts the lifetime distribution while retaining the non-settlement abundance semantics of independently active civilizations.

6. Integrated Supermodel Construction

The five base models induce probability distributions with different native meanings of abundance. Direct comparison of raw outputs is therefore not meaningful. Instead, each model output is first mapped into a common diagnostic variable N^* , after which the model-specific measures are combined into a single supermodel measure.

Let $m \in \{\text{I, II, IIIA, IIIB-M, IV}\}$ index the model class, θ_m its parameter vector, $\pi_m(\theta_m)$ its sampling density, and $w_m(\theta_m)$ its diagnostic weight (when applicable). The bridged log-space output of model m is

$$z_m^*(\theta_m) = (\log_{10} L_{\text{active}}^{(m)}(\theta_m), \log_{10} N^{*(m)}(\theta_m)).$$

For the baseline SM1–SM5 stress tests, Models I, II, and IV contribute their non-settlement abundance coordinate $N_{\text{civ}} = N_{\text{active}}$, while Models IIIA and IIIB-M contribute their native active-site abundance N_{site} under the reference site-level bridge defined in Equation (30). The alternative source-level bridge defined in Equation (31) is evaluated separately in the semantic-sensitivity and bridge-conditional BMA analyses.

For a controlled supermodel scenario indexed by k , the diagnostic mixture coefficients are constructed from positive scenario factors $a_{k,m} > 0$ according to

$$\pi_{k,m} = \frac{a_{k,m}^{-1}}{\sum_{j=1}^5 a_{k,j}^{-1}}, \quad \sum_{m=1}^5 \pi_{k,m} = 1. \quad (49)$$

The coefficients $\pi_{k,m}$ are scenario-mixture coefficients rather than posterior model probabilities. The values $a_{k,m} \in \{0.1, 1, 10\}$ define symmetric order-of-magnitude perturbations around the neutral reference value $a_{k,m} = 1$. They are used to examine how the integrated diagnostic distribution responds when a selected model family is deliberately emphasized or suppressed. They are not inferred from observational evidence and are not intended to rank the physical plausibility of the model families.

The integrated supermodel density on the diagnostic space is given by the mixture of the five bridged push-forward measures:

$$\rho_{\text{SM},k}^*(x, y) = \frac{\sum_{m=1}^5 \pi_{k,m} \times \int_{\Theta_m} w_m(\theta_m) \pi_m(\theta_m) \delta(x - \log_{10} L_{\text{active}}^{(m)}(\theta_m)) \delta(y - \log_{10} N^{*(m)}(\theta_m)) d\theta_m}{\int_{\Theta_m} w_m(\theta_m) \pi_m(\theta_m) d\theta_m}. \quad (50)$$

Equation (50) defines the continuous population-level supermodel measure. In the implementation, it is not evaluated analytically. The reported heatmaps, marginal distributions, and regime probabilities are obtained from its Monte Carlo approximation through the empirical measures defined in Section 4.6.

Individual model heatmaps estimate the component measures, whereas supermodel heatmaps estimate the integrated distribution $\rho_{\text{SM},k}^*(x, y)$.

Five controlled scenario-weighted stress tests are examined: SM1 (neutral), SM2 (Rare-Earth suppressed), SM3 (Rare-Earth favored), SM4 (settlement suppressed), and SM5 (settlement favored). These mixtures are not additional physical models, and their coefficients are not estimates of $p(M_m | D)$. Their sole purpose is to test the sensitivity of the integrated diagnostic distribution to deliberate changes in the relative representation of Rare-Earth and settlement-based model families. The role of each scenario is summarized in Supplementary Section S1.4, Supplementary Table S1.

Estimating the Number of All Models and Supermodels

To illustrate the counting procedure, consider Model II, which contains three bounded uncertain quantities. Since each quantity can be assigned one of three probability distributions, the model admits $3 \times 3 \times 3 = 27$ distinct distributional configurations. Applying the same counting principle to all five model families yields

$$3^7 + 3^3 + 3^{19} + 3^{20} + 3^9 = 4,649,067,765$$

native distributional specifications in total.

A supermodel does not evaluate these configurations only in isolation. Instead, it is formed by selecting one distributional configuration from each model family included in the mixture and combining the selected models in a shared diagnostic space. Consequently, the full Cartesian product $\prod_m K_m$ enumerates the model-specification combinations; for the declared K_m this product already exceeds 10^{27} . This follows because the five model families contain 7, 3, 19, 20, and 9 sampled inputs, so assigning one of three distributions independently to each input gives

$$3^{7+3+19+20+9} = 3^{58} \approx 4.71 \times 10^{27}$$

possible combinations. These combinations correspond to alternative assignments of input-distribution families across the component models. As a simple illustration, a toy two-slot supermodel with two independent Model II choices would already admit $27^2 = 729$ possible combinations.

This construction lies at the heart of the computational approach. Rather than deriving conclusions from any single model or from one particular set of assumptions, the framework examines which futures become more or less probable when different combinations of semantically related but structurally incompatible models are integrated. By systematically varying modeling choices across the entire ensemble, the supermodel reveals collective

patterns and robustness properties that cannot be observed within any individual model in isolation.

7. Results

The Monte Carlo simulations are reported as empirical distributions in the model-specific ($\log_{10} L_{\text{active}}, \log_{10} N_{\text{active}}$)-plane. This section presents the main heatmaps, super-model comparisons, clustering diagnostics, and parameter-importance summaries. Additional heatmaps and supporting diagnostics are provided in Supplementary Section S2.

All reported quantities are derived from the semantic empirical measure (Equation (28)) and the supermodel construction (Equation (50)). The figures should therefore be interpreted as conditional Monte Carlo distributions under the specified model equations, parameter triads, sampling rules, and diagnostic weights.

In particular, the reported distributions are baseline scenario distributions rather than posterior estimates calibrated against the complete historical record of SETI non-detections. The theoretical procedure for transforming them into survey-conditioned posterior distributions is provided in Supplementary Section S5.

A separate observation-informed analysis was therefore performed without replacing the baseline figures: published exoplanet occurrence constraints were propagated through the compatible model families, and a selected SETI null result was applied through conditional Bayesian importance reweighting. The broad density structure remained similar to that of the baseline ensembles, while the model-dependent shifts in medians, 90% intervals, and effective sample sizes are summarized in Supplementary Table S10.

7.1. Robustness to Subjective Triad Specifications

Table 3 summarizes the targeted robustness analysis for Model I. Narrowing the logarithmic distances between the bounds and peaks by 25% shifted the median $\log_{10} L_{\text{active}}$ by -0.149 dex and reduced the 90% interval width by approximately 18%. Widening the corresponding distances by 25% produced a median shift of $+0.268$ dex and increased the interval width by approximately 11%.

Table 3. Targeted robustness analysis for the subjective biological and technological triads in Model I. Median shifts and interval-width ratios are relative to the bounded-lognormal baseline. The last two columns give conditional Monte Carlo masses in the short-lived and long-lived-localized diagnostic regions.

Scenario	Δmed	$W_{90}^{\text{alt}}/W_{90}^{\text{base}}$	$P(\mathcal{R}_{\text{short}})$	$P(\mathcal{R}_{\text{long,loc}})$
Baseline (bounded lognormal)	0.000	1.000	29.6%	13.3%
Bounds narrowed 25%	-0.149	0.816	30.7%	6.6%
Bounds widened 25%	$+0.268$	1.111	24.5%	20.7%
Peaks $\rightarrow$ lower bounds	$+1.199$	1.081	7.7%	43.0%
Peaks $\rightarrow$ upper bounds	-0.356	0.958	40.2%	7.7%
Log-linear sampling	$+1.615$	1.368	9.1%	53.5%
Bounded Gaussian sampling	-1.055	0.736	66.9%	1.0%

Each scenario was evaluated in five independent Monte Carlo runs of $N_{\text{MC}} = 10^5$ samples each. Common random numbers were used across the baseline and alternative scenarios within each run, and the values reported in Table 3 are averages over the five runs. The baseline uses the same parameter triads and sampling rules as the Model I baseline reported elsewhere in the manuscript.

Greater sensitivity was observed when the peaks of the weakly constrained biological and technological factors were modified. Moving their peaks toward the lower bounds increased the median inferred lifetime by 1.199 dex and increased the long-lived-localized

diagnostic mass from 13.3% to 43.0%. Moving the peaks toward the upper bounds shifted the median by -0.356 dex and reduced the long-lived-localized mass to 7.7%.

The output-level distribution-family test produced still larger changes. Relative to the bounded-lognormal baseline, log-linear sampling increased the median $\log_{10} L_{\text{active}}$ by 1.615 dex, whereas bounded Gaussian sampling decreased it by 1.055 dex. Between-run variation was small relative to the scenario-induced median shifts. The exact distribution parameterizations, random seeds, and seed-specific numerical summaries are provided in the accompanying repository together with the reproduction script.

The inverse Drake relation and the qualitative dependence of lifetime on the biological and technological production factors are preserved in every scenario. However, the quantitative location and width of the lifetime distribution, as well as the mass assigned to the fixed diagnostic regions, depend materially on the selected peaks and sampling families. Moderate perturbations of the bounds have smaller effects than changes in the peaks or distribution family.

These findings reinforce the intended interpretation of the framework. The reported ensembles are conditional uncertainty-propagation results under explicitly declared epistemic assumptions, rather than observationally calibrated predictions. Robustness should therefore be assessed at both the structural level and the parameter-specification level.

7.2. Basic Model Distributions

The five base models produce empirical distributions in the $(\log_{10} L_{\text{active}}, \log_{10} N_{\text{active}})$ -plane. In Models I, II, and IV, N_{active} denotes independently active civilizations, whereas in Models IIIA and IIIB-M it denotes active technological sites. The common plotting plane therefore enables comparison, but it does not remove the semantic difference between civilizations and settled sites.

Figure 1 presents the two principal reference cases: the non-settlement Drake baseline (Model I) and the explicit spatial settlement model (Model IIIA). Note that the coordinate scales differ between the two panels, so direct visual comparison of the distributions should be made with caution. The red dot in each panel indicates the weighted empirical mean of the corresponding simulated distribution in log-space. The remaining basic-model heatmaps are provided in Supplementary Section S2 (Supplementary Figures S2–S4).

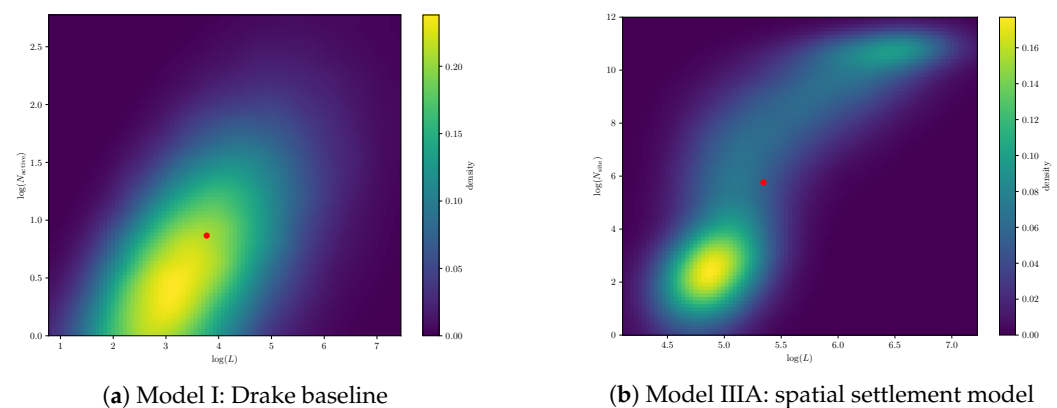


Figure 1. Representative heatmaps for the basic model families. Panel (a) shows the non-settlement Drake baseline. Panel (b) shows the explicit spatial settlement model. The mean coordinates, labeled with a red dot, are (3.8, 0.9) in panel (a) and (5.3, 5.8) in panel (b).

Model I exhibits the baseline inverse Drake structure: for a sampled abundance N_{active} , longer inferred lifetimes occur when the sampled production factor C_D is smaller. In Model IIIA the meaning of abundance changes to the number of active technological sites ($N_{\text{active}} = N_{\text{site}}$). Settlement of additional planets increases longevity, but the growth is sub-linear because the correlated hazard floor λ_{corr} remains unaffected. Nevertheless,

the overall effect of settlement is substantial: across the Monte Carlo ensemble, the mean active lifetime increases by approximately a factor of thirty relative to the non-settlement baseline (see Figure 1). When a civilization settles around one hundred planets, its expected active lifetime is roughly ten times longer than in the corresponding Drake-type scenario.

Model IIIB-M provides a coarse-grained settlement comparison by replacing the spatial kernel with a scalar active-site multiplier and adding silence conditioning through the effective survival hazard. Model IV represents the contrasting Rare-Earth filtering case, which moves probability mass toward lower-abundance regimes.

Taken together, the five basic distributions show that the main differences arise from model structure and abundance semantics, rather than from numerical parameter variation alone.

7.3. Supermodel Heatmaps

The supermodel outputs are controlled scenario-weighted mixtures of the bridged base-model ensembles. SM1 defines the neutral reference mixture, SM2 and SM3 respectively suppress and emphasize the Rare-Earth model, while SM4 and SM5 respectively suppress and emphasize the settlement models. These configurations are used as structural stress tests rather than as posterior rankings of the model families. Figure 2 compares the neutral reference mixture with the settlement-emphasizing scenario. The remaining supermodel heatmaps are provided in Supplementary Section S2 (Supplementary Figures S5–S7).

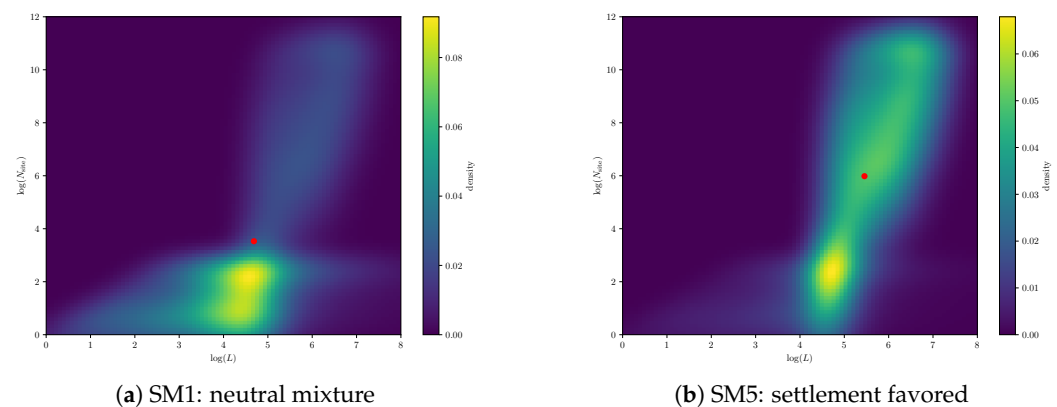


Figure 2. Representative supermodel heatmaps. Panel (a) shows the neutral mixture, while panel (b) shows the settlement-favoring mixture. The comparison illustrates how increasing the weight of settlement models shifts probability mass toward higher-abundance outcomes. The mean coordinates, labeled with a red dot, are (4.7, 3.5) in panel (a) and (5.5, 6.0) in panel (b).

Under the controlled transition from SM1 to SM5, the combined scenario-mixture coefficient assigned to the settlement models increases from 0.40 to $20/23 \simeq 0.87$, because the scenario factors enter as $\pi_i \propto a_i^{-1}$. This deliberate perturbation shifts probability mass mainly toward larger active-site counts N_{site} , while the displacement along the L_{active} -axis remains comparatively modest. The change should therefore be interpreted as a response to an imposed structural emphasis, not as evidence that the settlement models are more probable.

The alternative source-level bridge produced substantial abundance shifts within the settlement model families. Relative to the reference site-level bridge, the median of $\log_{10} N^*$ decreased by 2.953 dex in Model IIIA and by 2.969 dex in Model IIIB-M. The corresponding maximum absolute changes among the fixed diagnostic-region masses were 19.9 and 12.3 percentage points, respectively.

For the neutral equal-family reference mixture, the median bridge shift was smaller, 0.108 dex, although the source-level 90% interval width was only 0.469 times the corresponding site-level width and the maximum diagnostic-region mass change was 6.4 percentage

points. The complete semantic-sensitivity and bridge-conditional BMA results are reported in Supplementary Table S9.

This pattern suggests that the reduction in local extinction risk improves survival, but the presence of the correlated hazard floor λ_{corr} limits the extent to which additional settled sites can further extend active lifetimes. Consequently, the dominant effect of favoring settlement models is an increase in the number of active sites, with more limited gains in lifetime.

A second notable feature is the change in the distribution of lifetimes. In the neutral mixture (SM1), substantial probability mass remains in shorter-lifetime regimes. In the settlement-favoring mixture (SM5), this mass in the short-lifetime region is markedly reduced, while probability mass in the longer-lifetime region becomes more prominent. Within this settlement-emphasizing stress test, the increased contribution of the settlement models raises the number of active sites and reduces the relative contribution of the shortest-lived scenarios in the integrated mixture. As a result, longevity in SM5 is about 100 times longer than in basic Drake models I and II. The remaining supermodel heatmaps are provided in Supplementary Section S2 (Supplementary Figures S5–S7).

7.4. Clustering and Parameter Importance

Clustering and parameter-importance diagnostics provide complementary views of the Monte Carlo output. Clustering provides an exploratory view of numerical substructure in the simulated ensemble, while parameter-importance analysis reveals which inputs most strongly influence the simulated distributions.

Figure 3 presents two complementary visualizations of the settlement-favored supermodel SM5. Panel (a) shows a three-dimensional surface plot of the joint density in the $(\log_{10} L_{\text{active}}, \log_{10} N_{\text{site}})$ -plane, highlighting the overall shape and peaks of the distribution. Panel (b) shows the same SM5 ensemble projected onto the first three principal components, with samples colored according to k -means cluster membership. These two representations offer different viewpoints of the same underlying distribution: the surface plot emphasizes the global density structure, while the PCA projection provides an exploratory view of numerical substructure within the supermodel rather than a physical classification.

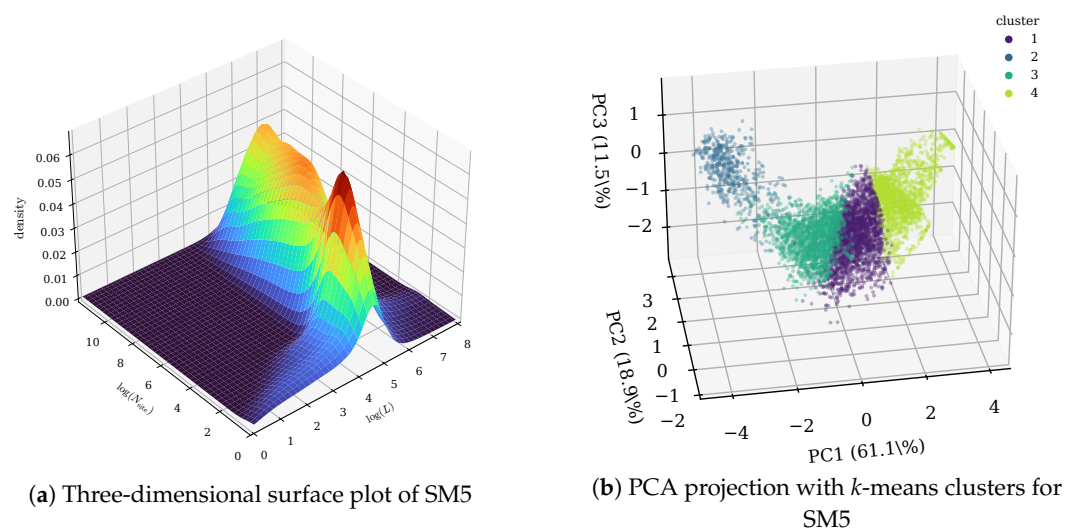


Figure 3. Complementary visualizations of the settlement-favored supermodel SM5. Panel (a) shows the three-dimensional surface of the joint density in logarithmic lifetime–abundance space. Panel (b) displays a sample-level PCA projection of the same Monte Carlo ensemble, colored by k -means cluster membership. Panel (b) displays the $k = 4$ solution selected from the elbow diagnostic as an exploratory visualization. This solution is not claimed to be uniquely optimal, and the resulting

groups are not interpreted as physical classes. The surface plot reveals the global shape of the distribution, while the PCA plot shows numerical substructure within SM5.

Candidate values of k for the k -means visualization were evaluated using the within-cluster sum-of-squares elbow diagnostic and the silhouette score. The silhouette criterion favored a coarser partition, whereas the principal elbow occurred at $k = 4$. A separate Gaussian-mixture analysis evaluated candidate component counts using AIC and BIC and favored a finer partition. Because Gaussian-mixture information criteria evaluate a likelihood-based mixture model rather than k -means, they were not used to select k for the k -means visualization. The diagnostics therefore did not identify a common unique optimum. We display the $k = 4$ solution on the basis of the elbow diagnostic solely as an exploratory representation of numerical substructure, not as an inferred classification of physical regimes. The numerical elbow, silhouette, Gaussian-mixture AIC, and Gaussian-mixture BIC diagnostics are reported in the accompanying repository together with the corresponding analysis script.

AIC, BIC, and maximized log-likelihood are not used to rank the Drake–Fermi–Brin base models or supermodels because these models are not fitted to a common set of observations using comparable likelihoods. The baseline outputs are conditional scenario distributions generated under specified equations, parameter triads, semantic mappings, and mixture weights. The survey likelihood introduced in Supplementary Section S5 is used for Bayesian importance reweighting, but it does not constitute a common fit of all model families and therefore does not support an AIC/BIC ranking of those families. In the present analysis, AIC and BIC are used only for the separate Gaussian-mixture clustering sensitivity check.

The sample-level PCA projection indicates that SM5 is not homogeneous but contains several distinct numerical regions. The most separated region lies on the high-settlement, high-abundance branch and is dominated by configurations with strong spatial settlement and large active-site counts, in some cases approaching the imposed Galactic carrying capacity. Other regions correspond to moderate settlement, longer but less saturated lifetimes, and a mixed cloud of lower-abundance or weak-expansion outcomes. Thus, even within a single supermodel, different combinations of modeling assumptions produce distinct numerical regions rather than statistically optimized physical regimes.

Parameter-importance analysis provides a complementary perspective by quantifying the relative influence of each sampled input on the model outputs. Figure 4 compares the importance grids for the two core models. In Model I, the biological and technological Drake factors (f_i and f_a) together with the sampled abundance axis dominate the variation in $\log_{10} L_{\text{active}}$. In Model IIIA, the sampled abundance axis and settlement-related parameters become the leading contributors, reflecting the additional influence of site generation and survival dynamics. The importance scores are normalized Random-Forest permutation-importance diagnostics computed on held-out Monte Carlo samples and should not be interpreted as calibrated causal effects. The auxiliary-model importance grids are provided in Supplementary Section S2, Supplementary Figure S8.

The layered decomposition (Supplementary Figure S9) assigns 54.4% of the variance in $\log_{10} L_{\text{active}}$ to within-configuration parameter uncertainty and 45.6% to model structure; the bridge terms vanish because the semantic bridge does not modify the native lifetime. For $\log_{10} N^*$, parameter uncertainty contributes 32.0%, model structure 51.9%, the bridge 6.4%, and the model–bridge interaction 9.7%. Thus, structural and semantic choices jointly account for 68.0% of the balanced abundance variance.

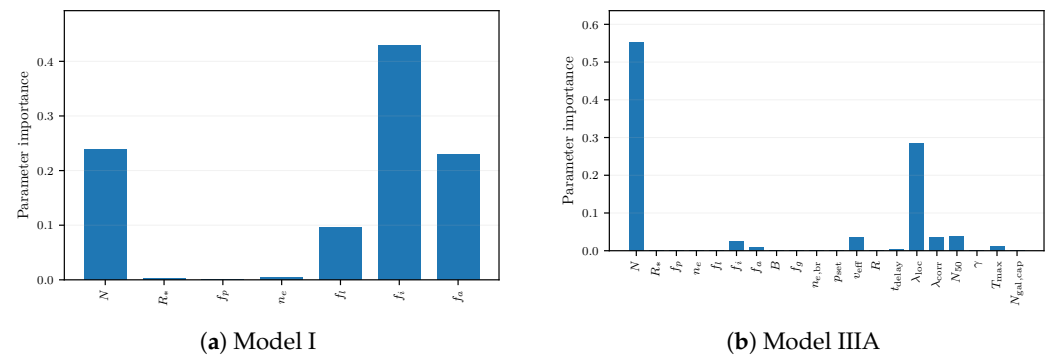


Figure 4. Representative parameter-importance grids for the main-text model comparison. Panel (a) shows the Drake-type baseline, while panel (b) shows the explicit spatial settlement model. Bars indicate normalized Random-Forest permutation-importance scores computed on held-out Monte Carlo samples.

8. Discussion

This work introduced a general computational framework for integrating heterogeneous and structurally incompatible mathematical models into unified probabilistic representations under deep uncertainty. Rather than targeting improved prediction within a specific domain, the objective was to establish a reproducible methodology for uncertainty propagation, cross-model comparison, and controlled integration of model families that cannot be reconciled at the equation level.

The framework replaces deterministic evaluation with ensemble-based Monte Carlo propagation over bounded parameter spaces. Each formulation is transformed into a stochastic model family whose outputs are interpreted as empirical distributions in a shared diagnostic space. Uncertainty is therefore treated as the primary computational object across multiple structurally distinct formulations, rather than a secondary property of individual models.

A key methodological contribution is the separation between native model semantics and diagnostic representation. Instead of enforcing equivalence between variables with different meanings, the framework introduces a controlled semantic mapping layer that preserves structural distinctions while enabling consistent comparison. On this basis, the concept of a supermodel is defined as a weighted mixture of heterogeneous model families operating in a common diagnostic space, enabling systematic study of how structural assumptions affect emergent distributional behavior.

From a computational standpoint, the framework implements a three-level decomposition of uncertainty: parameter uncertainty (bounded triads and stochastic sampling), structural uncertainty (multiple non-equivalent model classes), and semantic uncertainty (mapping between native and diagnostic variables). These components are implemented in a unified Monte Carlo pipeline that supports joint density estimation, marginal analysis, regime clustering, and parameter-importance analysis—all derived from the same ensemble.

The methodology is general and extensible to settings where independently developed models describe overlapping phenomena but differ in assumptions, variable definitions, or structure. In such cases, it provides a reproducible way to construct comparable probabilistic representations without requiring model homogenization.

Within the Drake–Fermi–Brin application, the framework shows how structural assumptions about rarity, expansion, and survival produce qualitatively different distributional regimes. These outcomes should be interpreted as conditional consequences of model structure rather than empirical claims. In particular, settlement-based and Rare-Earth formulations shift probability mass in the lifetime–abundance space by up to two

orders of magnitude, demonstrating strong sensitivity to model class selection and semantic assumptions.

Overall, the contribution is a computational methodology for uncertainty propagation and integration of heterogeneous models under deep uncertainty, implemented in a reproducible Monte Carlo framework with explicit semantic control.

Several limitations follow directly from the computational design. First, results depend on bounded parameter triads, which represent scenario ranges rather than inferred distributions; alternative choices may shift outcomes. The baseline implementation additionally assumes independent parameter sampling. Potential dependencies among astrophysical, biological, technological, and settlement-related quantities may alter the induced output distributions. Such dependencies should be represented through scientifically defensible joint distributions, copula-based sampling, or other dependence-aware uncertainty representations when sufficient information becomes available. Second, Monte Carlo estimates are subject to sampling error and convergence effects, particularly in tail regimes. Third, the semantic bridge between model families is non-unique. The site-level and source-level bridges tested here produce materially different abundance dispersions and diagnostic-region masses. These differences quantify sensitivity to the selected semantic mapping rather than systematic error relative to a known physical ground truth.

Fourth, the SM1–SM5 coefficients are externally specified scenario-mixture coefficients used for controlled structural stress tests; they are not model priors, posterior probabilities, or evidence-based rankings. The separately reported BMA weights remain conditional on the selected candidate-model set, semantic bridge, MWA Vela likelihood, equal model priors, and declared effective-detectability prior. Finally, the baseline ensembles are not fully calibrated observational predictions and remain intended primarily for structural comparison; the separate observation-informed robustness analysis constrains the empirically accessible planetary occurrence factor and conditionally reweights the simulated populations under explicit SETI detectability assumptions.

The reported variance shares are conditional on equal representation of the five model families and two bridges and should not be interpreted as empirical probabilities of the competing physical models.

The survey-specific SETI update remains conditional on assumptions concerning transmitter prevalence, signal power, frequency coverage, bandwidth, intermittency, directionality, temporal overlap, and recovery efficiency, which cannot be identified uniquely from a null result. The reduced MWA Vela application in Supplementary Section S5.14 therefore evaluates an explicit range of effective detectability assumptions, while full multi-dimensional calibration using multiple surveys remains outside the scope of this study.

The targeted robustness analysis demonstrates that moderate changes in the widths of the biological and technological triads produce comparatively limited shifts in the Model I lifetime distribution. In contrast, changes in the triad peaks and sampling families can alter the median lifetime and diagnostic-region masses substantially. Consequently, the numerical probabilities associated with individual diagnostic regions should not be interpreted independently of the declared parameter bounds, peaks, and sampling laws. The present test is restricted to the dominant weakly constrained factors in Model I and does not constitute an exhaustive robustness analysis of every parameter in Supplementary Section S4 or every model family. A systematic multi-model analysis of alternative bounds, dependence structures, and distribution families remains an important direction for future work.

The baseline analysis assumes mutual independence of the sampled parameters within each Monte Carlo realization. When scientifically defensible correlation information becomes available, the framework can be extended to joint distributions, copula-based

sampling, or other dependence-aware methods without changing the overall computational structure. Extensions also include improved sampling methods such as quasi-Monte Carlo and Latin hypercube designs for better convergence in high dimensions. Sensitivity analysis can be strengthened using variance-based global methods to separate parameter, structural, and semantic effects.

Future work may complement the present cross-model decomposition with model-specific first- and total-order Sobol indices for individual parameter effects and interactions. Future work should extend the bridge-conditional BMA analysis to multiple non-overlapping SETI surveys, alternative model and bridge priors, and more complete survey-selection functions. Automated semantic alignment could reduce reliance on manually defined bridges. Finally, scaling to larger ensembles of model classes would allow broader exploration of structural uncertainty beyond the current five-model system.

9. Conclusions

This work developed a general computational framework for integrating heterogeneous and structurally incompatible mathematical models into a unified probabilistic representation under deep uncertainty. The objective was not prediction in a specific domain, but a reproducible methodology for uncertainty propagation, cross-model comparison, and semantic control across incompatible formulations.

The approach replaces deterministic model evaluation with ensemble-based Monte Carlo propagation over bounded parameter spaces. Each model is transformed into a stochastic family whose outputs are interpreted as empirical distributions in a shared diagnostic space, making uncertainty the central computational object.

A key element is the separation between native model semantics and diagnostic representation. A controlled mapping layer preserves differences in variable meaning while enabling comparison in a common coordinate system. On this basis, supermodels are defined as weighted mixtures of heterogeneous model families, enabling analysis of how structural assumptions shape distributional outcomes.

The framework distinguishes three uncertainty levels: parameter uncertainty (bounded sampling), structural uncertainty (multiple model classes), and semantic uncertainty (cross-model mapping). These are implemented in a unified Monte Carlo pipeline that supports joint density estimation, regime analysis, and parameter importance extraction from a single ensemble.

The method is general and applicable to multi-model systems with incompatible assumptions and variable definitions. It enables the construction of comparable probabilistic representations without forcing structural homogenization.

In the Drake–Fermi–Brin case study, differing structural assumptions produce substantially different regimes, with settlement-based and Rare-Earth formulations shifting probability mass across the lifetime–abundance space by up to two orders of magnitude. This highlights strong sensitivity to model structure and semantic assumptions.

The framework was additionally evaluated through the reduced observation-informed analysis reported in Supplementary Section S5.14. This analysis propagated external exoplanet occurrence constraints and applied conditional Bayesian reweighting using the selected SETI null result while retaining the original baseline ensembles and model equations.

A targeted perturbation analysis further showed that the main structural relationship is preserved under alternative triad specifications, although quantitative lifetime distributions remain sensitive to the assumed peaks and sampling families of weakly constrained biological and technological parameters.

Overall, the contribution is a reproducible Monte Carlo-based computational methodology for uncertainty propagation and integration of heterogeneous models with explicit semantic control.

Supplementary Materials: The following supporting information can be downloaded at <https://www.mdpi.com/article/10.3390/computation14080181/s1>: Supplementary Sections S1–S5, including detailed auxiliary-model specifications (S1), additional figures (S2), diagnostic-region summaries (S3), parameter triads (S4), and the multidimensional SETI observation layer (S5).

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Data Availability Statement: The baseline simulation code, parameter definitions, random seeds, generated numerical summaries, and revision-specific analyses are available in the institutional repository at <https://repo.ijs.si/julijastopar/drake-brin-civilizations> (accessed on 3 August 2026). The standalone Supplementary Materials are archived on Zenodo at <https://doi.org/10.5281/zenodo.21705348> (accessed on 3 August 2026).

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Appendix A. Algorithms

The algorithms below summarize the Monte Carlo workflow and the semantic-bridging procedure used to construct native model measures, supermodel measures, and regime summaries.

Algorithm A1 Monte Carlo workflow used for basic models

Require: model type m , parameter triads, sampling distribution, random seed, sample count N_{MC} , heatmap bins B_{ij}

- 1: Initialize the random-number generator with the specified seed
- 2: Load model equations, parameters, semantic assignments, and output configuration
- 3: **for** each Monte Carlo sample $s = 1, \dots, N_{MC}$ **do**
- 4: Sample all uncertain parameters required by model m from their bounded triads
- 5: Compute derived production factors, settlement quantities, hazards, or filters required by model m
- 6: **if** $m \in \{I, II, IV\}$ **then**
- 7: Sample or compute the independent-civilization abundance $N_{civ}^{(m,s)}$
- 8: Assign the plotted abundance

$$N_{active}^{(m,s)} = N_{civ}^{(m,s)}$$

- 9: Store $N_{source}^{(m,s)} = N_{civ}^{(m,s)}$, $N_{site}^{(m,s)} = N_{civ}^{(m,s)}$, $Q_{site}^{(m,s)} = 1$
as storage aliases only; these are not interpreted as physical settlement quantities
 - 10: **else if** $m \in \{IIIA, IIIB-M\}$ **then**
 - 11: Compute or sample the source-civilization abundance $N_{source}^{(m,s)}$
-

```

12:      Compute the active-site abundance  $N_{\text{site}}^{(m,s)}$ 
13:      Assign the plotted abundance
                                     
$$N_{\text{active}}^{(m,s)} = N_{\text{site}}^{(m,s)}$$


14:      if  $N_{\text{source}}^{(m,s)} > 0$  then
15:          Compute the site multiplicity
                                     
$$Q_{\text{site}}^{(m,s)} = \frac{N_{\text{site}}^{(m,s)}}{N_{\text{source}}^{(m,s)}}$$


16:      end if ▷ end if  $N_{\text{source}} > 0$ 
17:  end if ▷ end if model class  $m$ 
18:  Evaluate the model-specific equation to obtain  $L_{\text{active}}^{(m,s)}$ 
19:  if  $m = \text{IIIB-M}$  then
20:      Compute the silence-conditioning factor and the diagnostic zero-event probability  $P_0$ 
21:  end if
22:  Set the default plotting and regime-summary weight
                                     
$$w_{m,s} = 1$$


23:  if  $L_{\text{active}}^{(m,s)} > 0$  and  $N_{\text{active}}^{(m,s)} > 0$  then
24:      Compute logarithmic coordinates
                                     
$$x_{m,s} = \log_{10} L_{\text{active}}^{(m,s)}, \quad y_{m,s} = \log_{10} N_{\text{active}}^{(m,s)}$$


25:      Store sampled inputs, derived quantities, and semantic outputs
      store  $L_{\text{active}}^{(m,s)}, N_{\text{active}}^{(m,s)}, N_{\text{civ}}^{(m,s)}, N_{\text{source}}^{(m,s)}, N_{\text{site}}^{(m,s)}, Q_{\text{site}}^{(m,s)}, (x_{m,s}, y_{m,s}),$  and  $w_{m,s}$ 
26:      Add the sample to the corresponding heatmap bin  $B_{ij}$ 
27:  end if ▷ end if valid log-space sample
28: end for
29: Normalize heatmaps using Equation (15)
    or Equation (16)
30: Generate supermodels, clustering outputs, and importance grids from the stored ensemble

```

Algorithm A2 Semantic measures, bridge construction, and regime probabilities

Require: Stored ensembles from Algorithm A1; diagnostic weights $w_{m,s}$; supermodel penalties $a_{k,m}$; regime regions $\mathcal{R}_r \subset \mathbb{R}^2$

```

1: for each model  $m = 1, \dots, 5$  do
2:   for each valid sample  $s = 1, \dots, N_{\text{MC}}$  do
3:     Read  $L_{\text{active}}^{(m,s)}, N_{\text{active}}^{(m,s)}, N_{\text{civ}}^{(m,s)}, N_{\text{site}}^{(m,s)}, w_{m,s}$ , and semantic outputs from Algorithm A1
4:     Compute

```

$$z_{m,s} = \left(\log_{10} L_{\text{active}}^{(m,s)}, \log_{10} N_{\text{active}}^{(m,s)} \right)$$

```

5:      if  $m \in \{I, II, IV\}$  then
6:          Set

$$N^{*(m,s)} = N_{\text{civ}}^{(m,s)} = N_{\text{active}}^{(m,s)}$$

7:      else if  $m \in \{IIIA, IIIB-M\}$  then
8:          Set

$$N^{*(m,s)} = N_{\text{site}}^{(m,s)}$$

9:      end if ▷ ends supermodel abundance bridge assignment
10:     Compute

$$z_{m,s}^* = (\log_{10} L_{\text{active}}^{(m,s)}, \log_{10} N^{*(m,s)})$$

11:     end for
12:     Construct the native model measure  $\hat{\mu}_m$  using Equation (28)
13: end for
14: for each supermodel  $k$  do
15:     Compute normalized mixture weights

$$\pi_{k,m} = \frac{a_{k,m}^{-1}}{\sum_{j=1}^5 a_{k,j}^{-1}}, \quad m = 1, \dots, 5$$

16:     Construct  $\hat{\mu}_{\text{SM},k}^*$  using Equation (34)
17:     for each regime region  $\mathcal{R}_r$  do
18:         Compute

$$\hat{p}_{k,r}^* = \hat{\mu}_{\text{SM},k}^*(\mathcal{R}_r)$$

19:     end for
20: end for
21: for each model  $m = 1, \dots, 5$  do
22:     for each regime region  $\mathcal{R}_r$  do
23:         Compute

$$\hat{p}_{m,r} = \hat{\mu}_m(\mathcal{R}_r)$$

24:     end for
25: end for
26: return native model measures, bridged supermodel measures, and regime-probability
    summaries

```

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