

The Universal Plausibility Metric (UPM) and Principle (UPP)

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The Universal Plausibility Metric¹⁻³ is an objective quantification of the *plausibility* of extremely low-probability chance hypotheses, models, theories and scenarios. The fact that a possibility has an extremely low probability of occurrence does not necessarily establish its implausibility. Mere possibility, on the other hand, is not an adequate basis for asserting scientific plausibility. Thus a method of objectively measuring the plausibility of any improbable hypothesis is needed. This is provided by The Universal Plausibility Metric (UPM: ξ [xi, pronounced “zai” in American English, “sai” in UK English]).

In addition, a numerical inequality establishes that a highly improbable hypothesis is definitively falsified when its UPM metric of ξ is < 1 . This inequality and *plausibility* bound constitute The Universal Plausibility Principle (UPP).¹ The Principle objectively and quantitatively eliminates from differential lists of possible causes any chance hypothesis with a $UPM < 1$.

Both the UPM and UPP concepts pre-exist and are independent of any particular experimental design and data set. This is an important aspect of the Universal Plausibility Principle’s universality to all areas of science. The UPM and UPP are integral to the scientific method itself.

A UPM should always be calculated for any suggested chance hypothesis, model, theory or scenario independent of, and preferably prior to, experimentation. The probability assessment of that chance scenario that is incorporated into its UPM computation must be objectively assessed and properly calculated. Chance hypotheses cannot be instigated, promoted and

sustained by prejudicial investigator involvement in experimental design (e.g., *directed* evolution; evolutionary *algorithms*; *artificial* selections; *programmed* computer models that steer and/or integrate supposedly random or drunken walk scenarios into hoped-for confirmations of spontaneous emergence).

To arrive at the UPM, we begin with the maximum available probabilistic resources (Ω , upper case Omega)⁴ for any given environment. But Ω could be considered from a quantum OR a classical molecular/chemical perspective. Thus the Ω quantification is broken down first according to the Level (L) or perspective of physicydynamic analysis (${}^L\Omega$), where the perspective at the quantum level is represented by the superscript “q” (${}^q\Omega$) and the perspective at the classical level is represented by “c” (${}^c\Omega$). Each represents the maximum probabilistic resources available at each level of physical activity being evaluated, with the total number of quantum transitions being much larger than the total number of “ordinary” chemical reactions since the Big Bang.

Second, the maximum probabilistic resources ${}^L\Omega$ (${}^q\Omega$ for the quantum Level and ${}^c\Omega$ for classical molecular/chemical Level) can be broken down even further according to the astronomical subset being addressed using the general subscript “A” for Astronomical: ${}^L\Omega_A$ (representing both ${}^q\Omega_A$ and ${}^c\Omega_A$). The maximum probabilistic resources can then be measured for each of the four different specific environments (of each ${}^L\Omega$), where the general subscript A is specifically enumerated with “u” for universe, “g” for our galaxy, “s” for our solar system, and “e” for earth:

Universe ${}^L\Omega_u$

Galaxy ${}^L\Omega_g$

Solar System ${}^L\Omega_s$

Earth ${}^L\Omega_e$ (${}^L\Omega_e$ excludes meteorite and panspermia inoculations)

To include meteorite and panspermia inoculations in the earth metrics, we use the Solar System metrics ${}^L\Omega_s$ (${}^q\Omega_s$ and ${}^c\Omega_s$).

The UPM is the product of the number of functional objects/events/scenarios (f) that are known to occur out of all possible combinations (lower case omega, ω) times the available probabilistic resources (Ω , upper case Omega)⁴ of that particular environment. An example would be the number (f) of functional protein family members all

having the same number of monomers, but varying sequence, known to occur out of sequence space (ω) times the probabilistic resources of whatever environment we are considering (earth [e], our solar system [s], our galaxy [g], or the entire known universe [u]).

The UPM = ξ and is computed according to the following equation:

$$\xi = \frac{f \left({}^L \Omega_A \right)}{\omega} \quad \text{Equation 1}$$

where f represents the number of functional objects/events/scenarios that are known to occur out of all possible combinations (lower case omega, ω), and ${}^L \Omega_A$ (upper case Omega, Ω) represents the total probabilistic resources for any particular probabilistic context. The “L” superscript context of Ω describes which perspective of analysis, whether quantum (q) or a classical (c), and the “A” subscript context of Ω enumerates which subset of astronomical phase space is being evaluated: “u” for universe, “g” for our galaxy, “s” for our solar system, and “e” for earth. Note that the basic generic UPM (ξ) equation’s form remains constant despite changes in the variables of levels of perspective (L: whether q or c) and astronomic subsets (A: whether u, g, s, or e).

The respective values of each ${}^L \Omega_A$ is calculated and provided in the original source peer-reviewed publication of the Universal Plausibility Metric (UPM) and Principle (UPM)¹:

Quantum perspective:

$$\begin{aligned} {}^q \Omega_u &= \text{Universe} = 10^{140} \\ {}^q \Omega_g &= \text{Galaxy} = 10^{127} \\ {}^q \Omega_s &= \text{Solar System} = 10^{117} \\ {}^q \Omega_e &= \text{Earth} = 10^{102} \end{aligned}$$

Classical Perspective

$$\begin{aligned} {}^c \Omega_u &= \text{Universe} = 10^{108} \\ {}^c \Omega_g &= \text{Galaxy} = 10^{96} \\ {}^c \Omega_s &= \text{Solar System} = 10^{85} \end{aligned}$$

$${}^c\Omega_e = \text{Earth} = 10^{70}$$

The Universal Plausibility Principle (UPP) states that *definitive operational falsification* of any chance hypothesis is provided by the inequality of:

$$\xi < 1$$

Inequality #1

This definitive operational falsification holds for hypotheses, theories, models, or scenarios at any level of perspective (q or c) and for any astronomical subset (u, g, s, and e). The UPP inequality's falsification is valid whether the hypothesized event is singular or compound, independent or conditional. Great care must be taken, however, to eliminate errors in the calculation of complex probabilities. Every aspect of the hypothesized scenario must have its probabilistic components factored into the one probability ($p = f/\omega$ when events are independent) that is used in the UPM. Many such combinatorial possibilities are joint or conditional. This requires more complex probabilistic mathematics.

Suppose 10^3 *biofunctional* polymeric sequences of monomers (f) exist out of 10^{17} possible sequences in sequence space (ω), all of the same number (N) of monomers. That would correspond to one chance in 10^{14} of getting a functional sequence by chance ($p = 10^3/10^{17} = 1/10^{14} = 10^{-14}$ of getting a functional sequence). If we were measuring the UPM from the perspective of a classical chemical view on earth over the last 5 billion years (${}^c\Omega_e = 10^{70}$), we would use the following UPM equation (#1 above) with substituted values:

$$\xi = \frac{f({}^L\Omega_A)}{\omega} = \frac{10^3 \times 10^{70}}{10^{17}}$$

$$\xi = \frac{10^{73}}{10^{17}} = 10^{56}$$

Since $\xi > 1$, this particular chance hypothesis is shown unequivocally to be plausible and worthy of further scientific investigation. Upon investigating further, however, we find that we must also factor in the probability of getting *any* biopolymer spontaneously in a prebiotic environment. The sequence space ω must include factors such as heterochirality, unwanted *non*-peptide-bond formation half the time, and the large number of non-

biological amino acids present in any prebiotic environment. This greatly increases ω , and would tend to substantially reduce the probability p of naturalistic abiogenesis.⁵ Axe measured the probability of a random 150-residue primary structure producing *any* functional short protein, despite many allowable monomeric substitutions, to be only one in 10^{74} sequences.⁶ If only one 150-residue polypeptide in 10^{45} have all peptide bonds needed for biological folding, and only one in 10^{43} would have only left-handed amino acids (excluding glycine), the correct calculation of ω would be one string out of 10^{162} ($10^{74} \times 10^{45} \times 10^{43}$). Under those circumstances, the UPM of getting any one functional 150-residue protein in a prebiotic environment using ${}^c\Omega_u$ would be less than 1. The notion would be falsified.

Summary: No extremely low-probability hypothetical plausibility assertion should survive peer-review without subsection to the UPP inequality standard of formal falsification. The UPP specifies that the UPM (xi) of any hypothesis, model, theory, or scenario must be greater than 1 to merit further expenditure of grant resources and labor. Concomitantly, a $\xi < 1$ definitively falsifies any hypothetical proposition in any field of science.

References:

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