Planckian distributions in molecular machines, living cells, and brains: The wave-particle duality in biomedical sciences

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Abstract --- A new mathematical formula referred to as the Planckian distribution equation (PDE) has been found to fit long-tailed histograms generated in various fields, including protein folding, single-molecule enzymology, whole-cell transcriptomics, T-cell receptor variable region diversity, brain sciences, and econometrics. PDE can be derived from the Gaussian distribution law by applying the simple rule of transforming the random variable, x, non-linearly, while keeping the Gaussian y coordinate constant. There appears to be a common mechanism underlying all Planckian processes (defined as those physicochemical processes generating numerical data that obey PDE), which has been suggested to be the SID-TEM-TOF mechanism, the acronym for Signal-Induced Deactivation of Thermally Excited Metastable state leading TO Functions. The universal applicability of PDE to many long-tailed histograms is attributed to (i) its role in generating functions and organizations through goal-directed selection of subsets of Gaussian processes, and (ii) the wave-particle duality operating in living systems.

Keywords --- blackbody radiation, fMRI, Planckian distribution equation, single-molecule enzymology, wave-particle duality, whole-cell metabolism, decision-making process

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I. INTRODUCTION

Blackbody radiation refers to the emission of photons by material objects that completely absorb photons impinging on them (hence appearing black). An example of blackbody radiation is given in Figure 1 a) which shows the emission of different wavelength light as a function of temperature. When the light intensity of a blackbody is measured at fixed temperatures, the so-called “blackbody radiation spectra” are obtained as shown in Figure 1 b).

M. Planck (1858-1947) succeeded in deriving the mathematical equation given in Equation (1) that quantitatively accounted for the blackbody radiation spectra. The key to his successful derivation of the so-called Planck radiation equation was his assumption that light is emitted or absorbed by matter in discrete quantities called “quanta of action,” which led to the birth of quantum mechanics revolutionizing physics in the early 20th century [1].

In 2008 [2, Chapter 11], the author noticed that the single-molecule enzyme-turnover-time histogram (see the bar graph in Figure 3 a)) published by Lu et al. [3] resembled the blackbody radiation spectrum at 4000 °K (Figures 1 b) and 2 b)). This observation led me to generalize the Planck radiation equation, Eq. (1), by replacing its universal constants and temperature by free parameters as shown in Equations (2) and (3), the former having 4 parameters, a, b, A and B, and the latter 3 parameters, A, B and C. Depending on the data set to be analyzed, either the 4- or 3-parameter equation can be employed. The
“generalized equation” was originally referred to as the “blackbody radiation-like equation” (BRE) [4], but as the equation was found to apply to more and more data sets, it was thought appropriate to refer to it as either the “generalized Planck equation” (GPE), or more simply as the “Planckian distribution equation” (PDE), in analogy to the Gaussian distribution equation (GDE). The 4-parameter equation can be transformed to the 3-parameter equation utilizing the transforming Equations (4), (5) and

\[ E(\lambda, T) = \frac{2\pi hc^2}{\lambda^5(e^{\frac{hc}{\lambda kT}} - 1)} \]  

where

\[ E = \text{Energy} \]
\[ \lambda = \text{Wavelength} \]
\[ c = \text{Speed of light} \]
\[ k = \text{Boltzmann constant} \]
\[ h = \text{Planck’s constant} \]
\[ e = 2.71828182 \]

The main objective of this paper is (i) to demonstrate the ability of PDE to fit long-tailed histograms reported in many fields, ranging from atomic physics (see Fig. 2) to econophysics (see Figs. 7g and 7h), and (ii) to discuss possible mechanisms underlying individual data sets fitting PDE as well as the common mechanisms underlying the universality of PDE.

\[ [T] = \text{Kelvin (temperature)} \]
\[ [\lambda] = \text{Meters} \]
\[ h = 6.626 \times 10^{-34} \text{J.s} \]
\[ c = 2.998 \times 10^8 \text{m/s} \]
\[ k = 1.381 \times 10^{-23} \text{J/K}. \]

**II. METHODS**

A. Digitization of long-tailed histograms

Due to the difficulties encountered in obtaining the original numerical data of most of the published histograms analyzed in this paper, it was necessary to digitize the graphs of interest in order to test whether they fit the Planckian distribution equation (PDE). Our digitization involved two steps: (i) using either the original graph or after amplifying it by 2-3 fold by xeroxing at an expanded scale, and (ii) digitizing a given histogram either by “hand” using a ruler or by using the digitization program *Paint*.

To test the accuracy of our “hand-digitization” technique, we compared the hand-digitized data set of a published histogram (Figure 2 in [5]) and the original data set of the graph kindly provided by Dr. K. Dill, one of the authors of [5]. When the former was plotted against the latter, a linear correlation was obtained with the equation, \( y = 1.0059x - 0.245 \), with the \( R^2 \) value of 0.9999, indicating that our hand-digitization technique is reliable. Further evidence for this conclusion is provided by Figures 2a, b and c, in which PDE reproduced the blackbody radiation spectra at three different temperatures almost exactly. The numerical values of the parameters of PDE fitting the hand-digitized curves are given in Table 1. The root means square deviations (RMSD) calculated by the *Solver program* in Excel and the visual inspection of Figures 2a, b and c indicate that the agreement between PDE-predicted and the actual blackbody
radiation spectral data hand-digitized by us is excellent.

**Table I.** Simulating the blackbody radiation spectral data hand-digitized by the author and inputted into the Planckian distribution equation (PDE), Eq. (2). The b/A ratio is proportional to the width (or spread) of the Planckian distribution.

<table>
<thead>
<tr>
<th>Temperature (°K)</th>
<th>a</th>
<th>b</th>
<th>A</th>
<th>B</th>
<th>RMSD</th>
<th>b/A</th>
</tr>
</thead>
<tbody>
<tr>
<td>3000</td>
<td>1.53x10^5</td>
<td>20.208</td>
<td>4.215</td>
<td>0</td>
<td>0.0121</td>
<td>4.79</td>
</tr>
<tr>
<td>4000</td>
<td>1.34x10^5</td>
<td>14.705</td>
<td>4.061</td>
<td>0</td>
<td>0.0237</td>
<td>3.62</td>
</tr>
<tr>
<td>5000</td>
<td>4.40x10^8</td>
<td>34.952</td>
<td>12.020</td>
<td>0</td>
<td>71.35</td>
<td>2.91</td>
</tr>
</tbody>
</table>

**Figure 2.** The hand-digitized data from the blackbody radiation spectra at a) 3000 °K, b) 4000°K, and c) 5000 °K shown in Figure 1 b) were reproduced almost exactly by the Planckian distribution equation, Eq. (2).

**B. The invariance of the parameter ratios of the Planckian distribution equation (PDE)**

More than one sets of the numerical values of PDE parameters were found to fit a given set of data with comparable accuracies as measured with the root mean square deviation (RMSD) values. For example, when the mRNA level data from human breast cancer tissues [6] that are associated with CGI (kinase binding protein), MAPK (mitogen-activated protein kinase), and ZFP (zinc finger protein) were fit into PDE (see Figure 7 c)), at least four sets of the numerical values each could fit the data more or less equally well (e.g., see Table II). What is interesting is that, although the numerical values of the parameters, a, b, A and B, vary widely, the ratios, b/A, B/b and B/A remain relatively constant. Because the size of the b/A ratio is 10^2-10^3 fold larger than the other two ratios, this ratio was chosen as a representative of a given data set.

**Table II.** The invariance of the parameter ratios of the Planckian distribution function.
### Table

<table>
<thead>
<tr>
<th></th>
<th>a</th>
<th>b</th>
<th>A</th>
<th>B</th>
<th>b/A</th>
<th>B/b</th>
<th>B/A</th>
</tr>
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<tr>
<td>CGI</td>
<td>7.579x10⁶</td>
<td>17.695</td>
<td>4.99</td>
<td>-0.492</td>
<td>3.546</td>
<td>-0.0278</td>
<td>-0.0986</td>
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<tr>
<td></td>
<td>7.398x10⁸</td>
<td>44.233</td>
<td>12.495</td>
<td>-1.230</td>
<td>3.540</td>
<td>-0.0278</td>
<td>-0.0984</td>
</tr>
<tr>
<td></td>
<td>8.000x10⁸</td>
<td>45.072</td>
<td>12.732</td>
<td>-1.253</td>
<td>3.540</td>
<td>-0.0278</td>
<td>-0.0984</td>
</tr>
<tr>
<td></td>
<td>8.090x10⁸</td>
<td>45.031</td>
<td>12.732</td>
<td>-1.249</td>
<td>3.536</td>
<td>-0.0277</td>
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<tr>
<td>MAPK</td>
<td>5.755x10⁶</td>
<td>19.519</td>
<td>7.261</td>
<td>-2.363</td>
<td>2.688</td>
<td>-0.121</td>
<td>-0.325</td>
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<tr>
<td></td>
<td>7.396x10⁸</td>
<td>51.589</td>
<td>19.048</td>
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<tr>
<td></td>
<td>8.000x10⁸</td>
<td>52.519</td>
<td>19.391</td>
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</tr>
<tr>
<td></td>
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<td>52.603</td>
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<td>2.754</td>
<td>-0.114</td>
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<tr>
<td>ZFP</td>
<td>2.219x10⁷</td>
<td>24.175</td>
<td>7.387</td>
<td>-1.098</td>
<td>3.273</td>
<td>-0.045</td>
<td>-0.149</td>
</tr>
<tr>
<td></td>
<td>7.383x10⁸</td>
<td>48.731</td>
<td>14.891</td>
<td>-2.214</td>
<td>3.273</td>
<td>-0.045</td>
<td>-0.149</td>
</tr>
<tr>
<td></td>
<td>8.000x10⁸</td>
<td>49.644</td>
<td>15.170</td>
<td>-2.255</td>
<td>3.273</td>
<td>-0.045</td>
<td>-0.149</td>
</tr>
<tr>
<td></td>
<td>8.080x10⁸</td>
<td>49.610</td>
<td>15.163</td>
<td>-2.250</td>
<td>3.272</td>
<td>-0.045</td>
<td>-0.148</td>
</tr>
</tbody>
</table>

### III. COMPUTATIONAL RESULTS AND DISCUSSIONS

#### A. Simulation of the blackbody radiation spectra with PDE

Figure 2 and Table I demonstrate that PDE (Planckian distribution equation), Eq. (2), can simulate the blackbody radiation spectra at 3000, 4000 and 5000 °K almost perfectly. Comparing Eqs. (1) and (3) and taking into account the fact that B = 0, it follows that parameters A and C of the Planck distribution are related to hc² and hc/k, respectively, the significance of which remaining to be investigated.

#### B. Gibbs free energy of protein folding

Under normal biological conditions of constant temperature (T) and pressure (P), all spontaneous changes, including protein folding from unfolded to folded states, are driven by a decrease in Gibbs free energy [7, 8], i.e., by a negative Gibbs free energy change, \( \Delta G < 0 \). Conversely, when a protein unfolds, the accompanying free energy change is positive, i.e., \( \Delta G = G_{\text{unfolded}} - G_{\text{folded}} > 0 \), which is referred to as the free energy of protein folding or protein stability [5]. Gibbs free energy G is defined as \( G = H + PV - TS \), where H is enthalpy or heat content, V is the volume of the thermodynamic system under consideration, and S is the entropy of the system. Under the conditions of constant T and P, this equation leads to \( \Delta G = \Delta H + P\Delta V - T\Delta S \) [8]. Based on experimentally determined enthalpy,
entropy, heat capacity, and the length distributions of 4, 3000 proteins from *E. coli*, Dill and his coworkers derived a theoretical equation for protein stability which generated the experimental curve shown in Figure 7a) [5]. As evident in the figure, this theoretical curve can be simulated by the Planckian distribution equation, Eq. (3), with a great precision.

C.1. Single-molecule enzyme catalysis

The technique of measuring the single-molecule enzyme kinetics is outlined in [3]. The enzyme turnover-time histogram shown in Figure 3a) was successfully simulated using the Planckian distribution, Eq. (3), as evident in Figure 3b). The double exponential function, Eq. (7), used in [3], can simulate the same histogram if and only if it is modified by adding A, as shown below:

\[ y = A(e^{-Bx} - e^{-Cx}) \]  

(7)

where A, B and C are free parameters.

**Figure 3.** a) Single molecules of cholesterol oxidase isolated and embedded in gel can be observed to undergo “blinking” of fluorescent light due to its coenzyme FAD which fluoresces when in its oxidized state and is non-fluorescent when it is reduced by its substrate, cholesterol. One cycle of blinking of the coenzyme constitutes one turnover time of the enzyme. The turnover times of the enzyme were not constant but varied widely, generating a histogram as shown here. Lu et al. [3] fitted the histogram with a double exponential function (see the curve). b) The same data as in a) were simulated using the Planckian distribution equation, Eq. (3).

C.2. Quantization of energy levels in enzymes

Just as the fitting of the blackbody
radiation spectra to Planck’s radiation equation, Eq. (1), is synonymous with the *quantization of the energy levels* of electrons in an atom, so it is postulated here that the fitting of the single-molecule enzyme-turnover times of Lu et al. [3] to the Planckian distribution equation, Eq. (2) or (3), as demonstrated in Figure 3b), implies that the conformational states (and hence conformational energy) of an enzyme molecule are quantized. This postulate is consistent with the concept of “conformational substates” of Frauenfelder et al. [9] and the quantization of the Gibbs free energy levels of an enzyme [2, Section 12.14]. Gibbs free energy, G, rather than energy, E, must be considered here because, under the conditions of constant temperature and pressure, it is G, not E, that drives all spontaneous processes in living systems [7, 8]. The quantization of *Gibbs free energy* (hereafter called *energy* for brevity) in enzymes is schematically represented in Figure 4b) in analogy to the energy quantization in atoms shown in Figure 4a).

**Figure 4.** The postulated isomorphism between *energy quantization* in atoms and the discretization/quantization of the conformational states (and hence of Gibbs free energy levels) in enzymes. **(a)** The quantization of the energy levels of electrons in an atom suggested by the fitting of the blackbody radiation spectra with the Planck radiation equation discovered in 1900 [1]. **(b)** In analogy to the quantization of the energy levels of electron in an atom entailed by the Planck’s radiation law, i.e., Equations (1), it is postulated that the fitting of the single-molecule turnover time histogram of cholesterol oxidase by the Planckian distribution law, Eq. (2) or (3), implied a similar quantization of energy levels of enzymes, most likely due to the existence of discrete conformational states of enzymes, denoted as Cᵢ, where the index i running from 1 to n, the number of conformational states of an enzymes [9]. Reproduced from [2, Section 11.3.3.].

Blackbody radiation involves promoting the energy levels (vibrational, electronic, or vibronic) of oscillators from their ground state E₀ to higher energy levels, E₁ through E₆. The wavelength of the radiation (or quantum of action) absorbed or emitted is...
given by $\Delta E = E_i - E_0 = h\nu$, where $E_i$ is the $i^{th}$ excited-state energy level, $h$ is the Planck constant, $\nu$ is the frequency, and $\Delta E$ is the energy absorbed when an oscillator is excited from its ground state to the $i^{th}$ energy level. Blackbody radiation results when electrons transition from a given energy level to a lower energy level within matter, e.g., from $E_1$ to $E_0$, or from $E_2$ to $E_0$, etc. [2, Section 11.3.3].

A single molecule of cholesterol oxidase is postulated to exist in $n$ different conformational states (i.e., conformational substates of Frauenfelder et al. [9]). Each conformational state (also called a conformer, or conformational isomer) is thought to exist in a unique Gibbs free energy level and carries a set of sequence-specific conformational strains (called conformons) [2, Chapters 8 and 11] and can be excited to a common transition state (denoted as $C^\ddagger$) by thermal fluctuations (or Brownian motions), leading to catalysis [2, Section 11.3.3].

C.3. The Energy Quantization as a Prelude to Organization

A possible meaning of the energy quantization invoked in Figure 5 b) to account for the fitting of the single-molecule enzyme kinetic data into the Planckian distribution function, Eq. (2), was proposed in the following quote reproduced from [2, p. 111]:

"Quantization (or discretization) may be essential for any organization, since organization entails selection and selection in turn requires the existence of discrete entities to choose from. In Sections 11.3.3 and 12.12, experimental evidence is presented that indicates that biological processes such as single-molecule enzymic activities . . . , whole-cell RNA metabolism . . . and protein folding . . . are quantized because they all obey mathematical equations similar in form to the blackbody radiation equation . . . that was discovered by M. Planck in physics in 1900 which led to the emergence of quantum mechanics two and a half decades later. . . .

To make the blackbody radiation data fit a mathematical equation, Planck had to assume that the product of energy and time called "action" is quantized in the unit later called the Planck constant, $h$, which has the numerical value of $6.625 \times 10^{-27}$ erg·sec. This quantity seems too small to have any measurable effects on biological processes which occur in the background of thermal fluctuations involving energies in the order of $kT$, where $k$ is the Boltzmann constant, $1.381 \times 10^{-16}$ erg/degree and $T$ is the absolute temperature. The numerical value of $kT$ is $4.127 \times 10^{-14}$ ergs at room temperature, $T = 298$ °K, which is thirteen orders of ten greater than $h$. Thus it appears reasonable to assume that biological processes are quantized in the unit of $k$ rather than in the unit of $h$ as in physics, which leads me to suggest that

"The Boltzmann constant $k$ is to biology what the Planck constant $h$ is to physics."

(4-36)

Thus by combining the evidence for the quantization of biological processes provided by Table 4-6 and Statement (4-36), it appears logical to conclude that

"Biological processes at the molecular and cellular levels are quantized in the unit of the Boltzmann constant $k$."

(4-37)
Elsewhere in [2, p. 110], I also suggested that both information and energy are essential for organization:

“For the purpose of discussing living processes, it appears sufficient to define ‘organization’ as the nonrandom arrangement of material objects in space and time. I have long felt that both energy and information are required for any organization, from the Belousov-Zhabotinsky reaction-diffusion system . . . to the living cell . . . and higher structures. This vague feeling may now be given a more concrete expression by asserting that ‘organization’ is the complementary union of information and energy or that information and energy are the complementary aspects of organization . . . . In other words, the information-energy complementarity may well turn out to be the elusive physical principle underlying all organizations not only in living systems but also nonliving systems including the Universe Itself . . . .”

If these conjectures turn out to be true in the future, the fitting of experimental data into the Planckian distribution equation displayed in Figure 7 may provide the empirical basis for integrating energy quantization, organization, and the information-energy complementarity into a coherent theoretical framework previously referred to as “gnergetics”, defined as the integrated science (-etics) of information (gn-) and energy (-erg) [2, pp. 15-18].

C.4. ‘Raser’ Model of Enzyme Catalysis and the SID-TEM-TOF Mechanism

It seems possible that, just as the blackbody radiation equation of Planck was found to apply to the single-molecule enzyme turnover times of cholesterol oxidase as shown in Figure 3 b) and [2, Chapter 11], so the subatomic mechanisms underlying the phenomenon of laser may apply (analogically) to the molecular mechanism of enzyme action, as indicated in Figure 5 b):
In the mechanism of laser, the input of “pumping” photons, $h\nu_1$, causes the electrons of the atoms constituting the laser medium (e.g., ruby crystal) to undergo a transition from the ground-state energy level to the excited-state energy level (see the 1 to 2 arrow in Fig. 5 a)). The excited state is short-lived, lasting for only about $10^{-12}$ seconds, and lose some of its energy as heat and undergo a transition to a lower energy level called “metastable” state (see the 2 to 3 arrow, Figure 5 a)). Sate 3 is more stable than State 2 but still much more unstable than the ground state (see 1). When there are enough number of electrons in the metastable/excited state (thereby creating the so-called “population inversion”), the arrival of triggering photons, $h\nu_2$, induces the de-excitation of electrons from the metastable excited state back to the ground state (see the 3 to 1 arrow), accompanied by the emission of photons identical to the triggering photons, $h\nu_2$, but larger in number than the original triggering photons, leading to amplification. The emitted photons are “coherent” in that they are identical with respect to (i) amplitude, (ii) frequency, and (ii) phase.

Unlike electrons in atoms that are all in the lowest-energy ground state before absorbing photons, enzymes appear to exist in different ground states to begin with, before thermal excitation (i.e., before absorbing thermal energy), as indicated by the four solid bars in Figure 5 b), which is enabled by the quantization of the Gibbs free energy.

It is possible that, when an enzyme molecule absorbs enough thermal energies through Brownian motions, it is excited to the transition state lasting only for a short period of time, probably for $10^{-14}$ to $10^{-12}$ seconds, the periods of chemical bond vibrations. The thermally excited enzyme is thought to undergo a transition to a more stable state called the “metastable” or “activated” state lasting probably up to $10^{-9}$ seconds. It appears that the metastable/activated state can be deactivated in two ways – (i) spontaneously (as in “spontaneous emission” in laser), and (ii) induced by substrate binding (as in “induced emission”). During spontaneous deactivation of the active/metastable state of an enzyme, the excess energy may be released as uncoordinated random infrared photons, whereas, during the substrate-induced deactivation, the excess energy of the enzyme-substrate complex may be released in a coordinated manner, resulting in catalysis, just as the triggering photon-induced de-activation of population-inverted electrons in atoms results in the amplification of emitted photons in laser.

The enzyme catalytic mechanism depicted in Figure 5 b) may be referred to as the SID-TEM-TOF mechanism because it embodies the following three key processes:

(i) **Substrate- or Stimuli-Induced Deactivation** in Step 4,
(ii) **Thermally Excited Metastable** state in the 1 to 2 and 2 to 3 steps
(iii) **leading TO** Function i.e., catalysis, in the 3 to 1 Step.

It is here postulated that the SID-TEM-TOF mechanism underlies many processes (and/or their records/results) that obey the Planckian distribution, Eqs. (2) or (3).
**D. RNA levels in budding yeast**

When glucose is switched to galactose within a few minutes, budding yeast cells undergo massive changes in the copy numbers (from 0 to several hundreds) of its mRNA molecules encoded by 6,300 genes over the observational period of hours [10,11]. Garcia-Martinez et al. [10] measured the levels of over 5,000 mRNA molecules at 6 time points (0, 5, 120, 360, 450, and 85 minutes) after glucose-galactose shift using microarrays, generating over 30,000 mRNA level data points. Of these data, 2159 mRNA levels were chosen arbitrarily and grouped into 250 bins to generate a histogram shown in Figure 7b) (see Experimental). As can be seen in this figure, the histogram fits the Planckian distribution almost exactly, with RMSD value of 10.64. The numerical values of the Planckian distribution parameters are given in Table IV, Row b).

**E. RNA levels in human breast tissues**

Perou et al. [6] measured the mRNA levels of 8,102 genes in the normal cells, the breast cancer tissues before and after treating with the anticancer drug, doxorubicin, in 20 breast cancer patients using microarrays. Of 8,102 genes, we analyzed 4,740 genes and their transcripts from 20 patients. A total of 4,740 x 20 = 94,800 mRNA levels were divided into 60 bins to generate a histogram shown in Figure 7c) (see Experimental). Again the experimental curve fitted the Planckian distribution equation with great fidelity, the RMSD value being 368.8. (It should be pointed out that the magnitude of the RMSD values depend on the total number of the points in the data set; the greater the number of data points, the greater is the RMSD even if the fit between the experimental and theoretical curves are comparable by visual inspection.)

**F. Human T-cell receptor variable region gene sequence diversity**

The T-cell receptor consists of two chains, α and β, and each chain in turn consists of the transmembrane, constant and variable regions. The variable regions of T-cell receptors, called CDR3 (Complement Determining Region 3), recognize pathogens and initiate an immune response. The CDR3 length between conserved residues ranges from 20 to 80 nucleotides. Murugan et al. [12] analyzed the nucleotide sequence data of T-cell beta chain CDR3 regions obtained from nine human subjects, each subject generating on average 232,000 unique CDR3 sequences. The germline DNA encoding the beta chain of human T-cell receptors has 48 V-genes, 2 D-genes and 13 J-genes. These gene segments are recombined via a series of stochastic recombination mechanisms catalyzed by appropriate enzymes to generate a large repertoire of CDR3 sequences. Each CDR3 sequence can be viewed as the result of a generative event describable by several random variables, including V-, D- and J-gene choices.

From the set of observed CDR3 sequences, Murugan et al. [12] was able to construct a mathematical equation called the *generative probability function* that predicts the probability of generating CDR3 sequence \( \sigma \), \( \text{P}_\text{gen}(\sigma) \). \( \text{P}_\text{gen}(\sigma) \) is the sum of the probabilities of all recombination events involved in producing CDR3 sequence \( \sigma \). A typical example of the CDR3 sequence histogram predicted by \( \text{P}_\text{gen}(\sigma) \) for one subject is given in Figure 7d) (see Experimental). This histogram was obtained by transforming the original left long-tailed histogram to the right long-tailed histogram by replacing \(- \log \text{P}_\text{gen}(\sigma)\) with (30 -
\(|P_{\text{gen}}(\sigma)|\), where \(|P_{\text{gen}}(\sigma)|\) is the absolute value of \(P_{\text{gen}}(\sigma)\). (It was subsequently found that the original left long-tailed histogram could be fitted into PDE just as well, without any transformation.) As evident in Figure 7 d), the agreement between the \(P_{\text{gen}}(\sigma)\) distribution and the Planckian distribution is excellent.

G. Decision-time histogram

The drift-diffusion model (DDM) of decision-making is a widely employed theoretical model in behavioral neurobiology [13, 14, 16, 17, 18]. DDM accurately reproduces the decision-time histograms (see Experimental in Figure 7 e)), reflecting the well-known phenomena [13] that it takes the brain longer to process more difficult tasks than easier ones. Figure 6 a) depicts the two essential features of DDM, i.e., (i) the Gaussian-distributed drift rates (i.e., the rates of evidence accumulation in the brain), which can be represented as \(\tan \alpha\), where \(\alpha\) is the arctangent of the drift rate, \(D/t\), with \(D\) as the decision threshold (i.e., the level at which, when reached by accumulating evidence, a decision is made) and \(t\) is the time when a decision is made, and (ii) the non-linear relation between the independent variable of the Gaussian distribution function and the decision times.

Because of these two features, the Gaussian-distributed drift rates can produce a right-long-tailed decision-time histogram as shown in Figure 6 b), where the right-long tailed distribution was derived from the Gaussian distribution based on two operations: (i) transform the x coordinates of the Gaussian distribution (obtained by hand-digitizing the Gaussian curve found at http://en.wikipedia.org/wiki/Normal_distribution) to \(D/\tan \alpha\), and (ii) retain the y coordinates of the Gaussian distribution unchanged. As Figure 6 b) demonstrates, the Gaussian distribution transformed according to Operations (i) and (ii) above coincides with the Planckian distribution based on \(x\), demonstrating that the Planckian distribution can, in principle, be derived from the Gaussian distribution based on DDM; i.e., DDM can act as the bridge between the Gaussian and Planckian distributions.

As shown in Figure 7 e), the experimentally observed decision-time histogram was almost exactly simulated by the Planckian distribution equation. Just as random mechanisms can be claimed to underlie the Gaussian distribution, so it is here claimed that the SID-TEM-TOF (Signal-Induced Deactivation of Thermally Excited Metastable state leading TO Function) mechanism underlies the Planckian distributions. The SID-TEM-TOF mechanisms, in turn, can be viewed as the generalized Raser model of enzyme catalysis (Figure 5 b)).

It would be convenient to define as the “Planckian processes” all those processes in nature that obey the Planckian distribution equation or law, just as the Gaussian processes can be defined as those processes that obey the Gaussian distribution law. Since random processes are implicated in all Gaussian processes, so it would be reasonable to assume that, underlying all Planckian processes, there exists one or more non-random mechanisms common to many, if not all, Planckian processes. One of such common mechanisms is suggested to be the SID-TEM-TOF mechanism, i.e., Figure 5 b), or its equivalent.

The mathematical relation between the Gaussian and Planckian distributions can be established based on the drift-diffusion model (DDM) of decision making [18]. It should be noted that \(t\) and \(x\) are synonymous (Figure 6 a)). The Planckian distribution can be derived from the Gaussian distribution based on the simple algorithm...
consisting of two steps – (i) change $x$ to $D/\tan \alpha$, where $\alpha$ is the arctan of $D/x$, where $D$ is the decision threshold, and (ii) keep the $y$ coordinates unchanged.

**Figure 6. a)** A schematic representation of the drift-diffusion model (DDM) of decision making adopted from [18].  
**b)** The derivation of the Planckian distribution from the Gaussian distribution based on the DDM of decision making.

*H. fMRI signals from the human brain before and after psilocybin*
The functional magnetic resonance imaging (fMRI) technique, when applied to the human brain, allows neuroscientists to monitor neuronal firing activities in different regions of the brain noninvasively within seconds of infusing a psychedelic drug such as psilocybin. Carhart-Harris et al. [15] measured the fMRI signals from the brains of 15 healthy volunteers before and after the intravenous infusion of psilocybin lasting for 60 seconds. The subject’s consciousness, cerebral blood flow (CBF), and fMRI signals responded within seconds. CBF values decreased in all regions of the brain and the subject reported that their “thoughts wandered freely”. Out of the 9 brains regions examined (2° visual, 1° visual, motor, DAN, auditory, DMN, R-FP, L-FP, salience), four regions exhibited significant changes in their fMRI signals characterized by increases in the deviations of the local signals from their mean, i.e., an increase in variance. By “local” is meant to indicate brain tissue volume elements (voxels) measuring a few mm in linear dimensions. When the distances of the signals from individual voxels from the group-mean fMRI signal are calculated and grouped into bins and their frequencies are counted, histograms are obtained such as shown in Figures 7f), which could be fitted reasonably well to the Planckian distribution equation (see Planckian). The numerical values of the Planckian distribution equation fitting these two histograms differed, especially the b/A ratios which increased from 0.93 to 1.62 by the psilocybin infusion (see Row f in Table IV).

I. The ultraviolet catastrophe in econophysics

The Rayleigh-Jeans law [19] predicts that the power of radiation emitted by a heated body increases with the frequency raised to a fourth power. This exponential law works fine at long wavelengths but fails dramatically at short wavelengths, leading to the so-called the “ultraviolet catastrophe” [20].

Some physicists [21] have suggested that the distribution of incomes in a society can be modeled using the Boltzmann-Gibbs equation, a power law, making the analogy that money can be treated as energy (see Table III). Again this statistical mechanical approach works fine for high income levels but fails badly at low income levels (see Figures 7g) and h)). However, the Planckian distribution law, Eq. (2), fits the 1996 and 2013 US annual income distributions almost exactly.

If we assume that the exponential distributions shown in Figures 7g) and h) are analogous to the Rayleigh-Jeans law and the Planckian distributions to the Planck radiation law, Equation (1), we can reasonably conclude that the deviation of the exponential distributions from the observed income distributions are analogous to the ‘ultraviolet catastrophe’ in the physics of over one hundred years ago.

The resolution of the ultraviolet catastrophe in physics in the early decades of the 20th century with the discovery of Planck’s radiation law introduced a new concept into physics, i.e., quantum of action, as the unit of organizing matter and energy in abiotic systems. Similarly, the resolution of the “econophysics” version of the ultraviolet catastrophe with the Planckian distribution equation demonstrated in Figures 7g) an h) may introduce another novel concept into natural and human sciences – the quantization of organization in terms of the Planckian information, $I_P$, defined as follows:

$$I_P = \log_2 \frac{[\text{AUC(P)}]}{[\text{AUC(G)}]} \text{ bits} \quad (8)$$
where AUC(P) stands for the area under the curve of the Planckian distribution and AUC(G) the area under the curve of the Gaussian distribution whose rising phase coincides with the rising phase of the Planckian distribution [22]. These and related ideas are collected in Table III.

Table III. A comparison between the ‘ultraviolet catastrophes’ in quantum physics and econophysics.

<table>
<thead>
<tr>
<th>Ultraviolet Catastrophe in Quantum Physics</th>
<th>Econophysics</th>
</tr>
</thead>
<tbody>
<tr>
<td>1  energy</td>
<td>money</td>
</tr>
<tr>
<td>2  frequency</td>
<td>annual income</td>
</tr>
<tr>
<td>3  blackbody radiation spectra</td>
<td>annual income distribution</td>
</tr>
<tr>
<td>4  laws of thermodynamics (energy, entropy, work)</td>
<td>laws of organization &amp; selection (energy, entropy, information; i.e., gnergy [2])</td>
</tr>
<tr>
<td>5  Boltzmann-Gibbs law</td>
<td>Planckian distribution law</td>
</tr>
<tr>
<td>6  $y = ae^{-bx}$</td>
<td>$y = a/(Ax + B)^2/(e^{b(Ax + H)} - 1)$</td>
</tr>
<tr>
<td>7  organization of energy in atoms</td>
<td>organization of income in society (?)</td>
</tr>
</tbody>
</table>

![a) Protein folding](image1.png) ![b) RNA levels in budding yeast](image2.png)
Figure 7. The universality of the Planckian distribution. a) protein folding [5]; b) RNA metabolism in unicellular organism [2, Chapter 12]; c) RNA metabolism in human breast tissues [6]; d) human T-cell variable region gene diversity [12]; e) the decision-time histogram of the human brain [13, 16, 17, 18]; f) fMRI (functional magnetic resonance imaging) data from human brains before and after the arterial infusion of psilocybin [15]; g) the annual income distribution in the US in 2013 [21]; and h) the annual income distribution in the US in 1996 [21].

The numerical values of the parameters of the Planckian distribution equation fitting the diverse sets of data shown in Figure 8 are summarized in Table 3.

Table IV. The numerical values of the parameters of the Planckian distribution, Equations (2) or (3), that fits the histograms shown in Figure 8. The italicized lower values in the last row are the post-psilocybin values.

<table>
<thead>
<tr>
<th>Histogram</th>
<th>a</th>
<th>b</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>b/A</th>
</tr>
</thead>
<tbody>
<tr>
<td>a) Protein folding</td>
<td>1.24x10^{14}</td>
<td>368.3</td>
<td>9.45</td>
<td>6.82</td>
<td>-</td>
<td>38.97</td>
</tr>
<tr>
<td>b) RNA levels (yeast)</td>
<td>-</td>
<td>-</td>
<td>1.11x10^{12}</td>
<td>13.962</td>
<td>159.30</td>
<td></td>
</tr>
<tr>
<td>c) RNA levels (breast tissues)</td>
<td>8x10^{10}</td>
<td>40</td>
<td>8</td>
<td>1.7</td>
<td>-</td>
<td>5.00</td>
</tr>
<tr>
<td>d) DNA sequence</td>
<td>-</td>
<td>-</td>
<td>7.019x10^{0}</td>
<td>0.063</td>
<td>25.00</td>
<td></td>
</tr>
<tr>
<td>e) Decision times</td>
<td>8.5x10^{11}</td>
<td>101.49</td>
<td>0.1077</td>
<td>6.345</td>
<td>-</td>
<td>942.34</td>
</tr>
<tr>
<td>f) fMRI signals</td>
<td>7.6x10^{10}</td>
<td>107.67</td>
<td>115.9</td>
<td>0</td>
<td>-</td>
<td>0.928</td>
</tr>
<tr>
<td></td>
<td>4.4x10^{10}</td>
<td>43.17</td>
<td>26.7</td>
<td>0</td>
<td>-</td>
<td>1.617</td>
</tr>
<tr>
<td>g) US income 2013</td>
<td>1.10x10^{12}</td>
<td>275.4</td>
<td>1.93</td>
<td>36.87</td>
<td>-</td>
<td>142.60</td>
</tr>
<tr>
<td>h) US income 1996</td>
<td>1.60x10^{12}</td>
<td>247.6</td>
<td>1.71</td>
<td>17.33</td>
<td>-</td>
<td>144.91</td>
</tr>
</tbody>
</table>

J. The MPM category: Mechanism, Phenomenon, and Model

The concept of a mathematical category is universal in that it can be applied to all fields of human intellectual activities from physics, to chemistry, to biology, to mathematics, and to philosophy [23]. One example of a category that has a universal applicability consists of the triad of mechanism, phenomenon, and model as diagrammed in Table V. This so-called MPM category can be viewed as a type which has many tokens, including semiotics, the study of signs [25, 26] (see Row 6 in Table V).
Table V. The MPM category. For a definition of a category, see [24].

<table>
<thead>
<tr>
<th>Discipline</th>
<th>Phenomenon (P)</th>
<th>Models (M)</th>
<th>Mechanisms (M)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Physics</td>
<td>Blackbody radiation (Fig. 1)</td>
<td>Planck radiation equation (Eq. 1)</td>
<td>Transitions between atomic orbitals (Fig. 5 a)</td>
</tr>
<tr>
<td>2. Chemistry</td>
<td>Chemical reactions</td>
<td>Kinetic equations or laws (zero\textsuperscript{th}, first, second order, etc.)</td>
<td>Molecular mechanisms (e.g., electrophilic or nucleophilic attacks)</td>
</tr>
<tr>
<td>3. Biology</td>
<td>Enzyme catalysis</td>
<td>Planckian distribution law (Fig. 3 b))</td>
<td>SID-TEM-TOF mechanisms (Fig. 5 b))</td>
</tr>
<tr>
<td></td>
<td>Cell biology</td>
<td>Planckian distribution law (Fig. 7 b), the Bhopalator model [28])</td>
<td>Conformon-driven IDS underlying all cell functions [2, Section 12.15]</td>
</tr>
<tr>
<td>Evolution</td>
<td>Zeldovich-Shakhnovich model [29]</td>
<td>Protein stability- and comparative genomic data-based mechanisms [29]</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Planckian distribution (Fig. 7 e)</td>
<td>SID-TEM-TOF mechanisms (Fig. 5 b))</td>
</tr>
<tr>
<td></td>
<td>fMRI signals [15]</td>
<td>Planckian distribution (Figs. 7 f)</td>
<td>SID-TEM-TOF mechanisms (Fig. 5 b))</td>
</tr>
</tbody>
</table>
K. The Universality of the Planckian distribution

As evident above, the Planckian distribution equation, Eqs. (2) or (3), has been found to fit the experimental data measured from a surprisingly wide range of disciplines, from atomic physics (i.e., blackbody radiation) to enzymology, to cell biology, and to brain neurophysiology (Figure 7). These unexpected findings may indicate that, underlying all the varied phenomena obeying the Planckian distribution equation, there exists a common mechanism, just as all the phenomena obeying the Gaussian distribution law implicate a common mechanism, namely, random processes. The connection between the Gaussian and the Planckian distributions may not be as haphazard as it may appear from this casual statement but much more substantial.

Another possible common mechanism underlying the universal applicability of the Planckian distribution equation may be sought in the postulated universality of the wave-particle duality in all organized material systems, from atoms to cells to brains to the Universe itself, and this possibility is partially supported by the fact that the first term of the Planck radiation equation, Eq. (2), is related to the number of standing waves in a physical system. This idea is depicted in Figure 8.
IV. CONCLUSIONS

A. The universality of the Planckian distribution. We have demonstrated that the Planckian distribution, Eqs. (2) or (3), is a new distribution law, comparable to the Gaussian distribution, that applies to a wide range of experimental data measured from atoms, biopolymers, living cells, and brains (Figure 7). One plausible explanation for these unexpected findings is that, underlying all Planckian processes, there are common physical processes mediated by ‘standing waves’ (electromagnetic, gravitational, mechanical, and concentration) as represented by the first term in the Planckian distribution law, Eq. (2). The number of standing waves present within a system is determined by the volume and topology of the system being heated, as schematically represented in Figure 8.

B. Planckian processes as selected Gaussian processes. Many, if not all, Planckian processes may derive from the
subset of Gaussian (or random/chaotic) processes that have been selected because of their functional roles in physical systems under given environmental conditions. The mechanisms enabling such a function-realizing selection processes may be identified with the SID-TEM-TOF mechanism which is in turn dependent on the Raser model of enzyme catalysis (Figure 5 b).

C. The wave-particle duality in biomedical sciences. Since (i) the Planckian distribution, Eqs. (2) or (3), consists of two components – one related to the number of standing waves per volume and the other to the average energy of such oscillatory modes, (ii) the wave aspect of the Planck radiation equation is fundamental in accounting for not only blackbody radiation spectra but also subatomic organization of atoms in terms of atomic orbitals, and (iii) the Planck distribution applies to both atoms (Figure 2 a), b) and c)) and living systems (Figures 7 a), b), c), d), e), f), g) and h)), it appears logical to infer that the wave aspect of the wave-particle duality plays a fundamental role in the behavior of living structures and processes in biology and medicine. In other words, it may be impossible for biomedical scientists to completely account for living processes, both normal and diseased, without taking into account their wave aspect along with their particle aspect.

D. Science as an irreducible triad of data, mathematical models, and mechanisms. The concept of an irreducible triad is basic to the triadic philosophy of C. S. Peirce [25, pp. 1-16]. Applying this concept to the definition of science leads to the conclusion that science cannot be defined in terms of two or less of the triad, i.e., data (also known as measurement), mathematical models, and physical mechanisms. We may refer to this philosophical position as the M x M x M or M³ doctrine of science, where the first M stands for measurement, the second for mathematical models, and the third for physical mechanisms, all of which are simultaneously required to define science. The M³ doctrine of science described here may be viewed as a token or example of the MPM category defined in Table V.

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REFERENCES

http://www.cspeirce.com/rsources/76defs/76defs.htm