**PLANCKIAN INFORMATION (Ip): A NEW MEASURE OF ORDER IN ATOMS, ENZYMES, CELLS, BRAINS, HUMAN SOCIETIES, AND THE COSMOS**

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A new mathematical formula referred to as the Planckian distribution equation (PDE) has been found to fit long-tailed histograms generated in various fields of studies, ranging from atomic physics to single-molecule enzymology, cell biology, brain neurobiology, glottometrics, econophysics, and to cosmology. PDE can be derived from a Gaussian-like equation (GLE) by non-linearly transforming its variable, x, while keeping the y coordinate constant. Assuming that GLE represents a random distribution (due to its symmetry), it is possible to define a binary logarithm of the ratio between the areas under the curves of PDE and GLE as a measure of the non-randomness (or order) underlying the biophysicochemical processes generating long-tailed histograms that fit PDE. This new function has been named the Planckian information, Ip, which (i) may be a new measure of order that can be applied widely to both natural and human sciences and (ii) can serve as the opposite of the Boltzmann-Gibbs entropy, S, which is a measure of disorder. The possible rationales for the universality of PDE may include (i) the universality of the wave-particle duality embedded in PDE, (ii) the selection of subsets of random processes (thereby breaking the symmetry of GLE) as the basic mechanism of generating order, organization, and function, and (iii) the quantity-quality complementarity as the connection between PDE and Peircean semiotics.

1. Introduction

A new mathematical equation known as the Planckian distribution equation (PDE) has been found, during the past 6 years, to apply to various fields ranging from atomic physics to single-molecule enzymology, to whole-cell cell biology, to neuroscience, and beyond [1, 2]. It is shown that PDE can be derived from a Gaussian-like equation (GLE) by transforming the independent variable, x, non-linearly, while keeping the y coordinates unchanged. GLE differs from the Gaussian distribution equation (GDE) by having a pre-exponential factor that is a constant, independent of the standard deviation, σ. There appears to be common mechanisms underlying all Planckian processes (defined as those physical, biophysicochemical or social processes able to generate data that obey the Planckian distribution), including the energy quantization and wave-particle duality [2]. The postulate of the free energy quantization in enzymes is supported by the fitting to PDE of the single-molecule enzyme turnover time histograms [1] (see Fig. 10 below).

When M. Planck (1858-1947) discovered his blackbody radiation equation in 1900, he probably could not have anticipated the fact that his equation, Eq. (1), when generalized in the form of what has variously been called blackbody radiation-like equation (BRE) [1], generalized Planck equation (GPE), or Planckian distribution equation (PDE) [2], Eq. (3) or (4), has been found to fit long-tailed (also called fat-tailed) histograms generated by (i) single-molecule enzyme catalysis (Fig. 10), (ii) protein folding (Fig. 13), (iii) genome-wide mRNA levels in budding yeast (Fig. 14), (iv) genome-wide mRNA levels in human breast tissue, both normal and cancerous (Fig. 15), (v) human T-cell receptor variable region sequence diversity (not shown), (vi) 7-mer frequency distribution in a genome (Fig. 16), (vii) protein length frequency distribution (Figure 17), (viii) decision making in humans (Figure 18), (ix) fMRI (functional magnetic resonance imaging) in human brains before and after a hallucinogen infusion (Fig. 19), (x) electrocorticogram (Fig. 20), (xi) word frequency distribution in a speech (Fig. 21), (xii)
sentence length frequency distribution in written texts (Fig. 22), (xiii) economics (Fig. 23 and 24), and (xiv) polarized cosmic microwave background radiation (Fig. 25). The main objectives of this paper include exploring the possible rationales for the apparent universality of PDE and examining its philosophical and semiotics implications.

2. Methods

2.1. Blackbody radiation

Blackbody radiation refers to the thermally induced emission of photons by material objects that, when left alone, completely absorb photons impinging on them (hence appearing black). An example of blackbody radiation is given in Figure 1, 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 2.

Planck succeeded in deriving the mathematical equation, Eq. (1), that quantitatively accounted for the blackbody radiation spectra. The key to his successful derivation of the so-called Planck radiation equation (PRE) was his assumption that light is emitted or absorbed by matter in discrete quantities called “quanta of action,” which revolutionized physics in the early 20th century.

\[
E(\lambda, T) = \frac{2\pi h c^2}{\lambda^4 (e^{h\lambda/kT} - 1)}
\]

where

- \(E\) = Energy
- \(\lambda\) = Wavelength
- \(c\) = Speed of light
- \(k\) = Boltzmann constant
- \(h\) = Planck’s constant
- \(e\) = 2.71828182
- \([T]\) = Kelvin (temperature)
- \([\lambda]\) = Meters
- \(h\) = 6.626.10^{-34} \text{ J.s}
- \(c\) = 2.998.10^8 \text{ m/s}
- \(k\) = 1.381.10^{-23} \text{ J/K}.

2.2. Digitization of Long-tailed Histograms

Due to the difficulties 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 ourselves in the course of testing whether they fit 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 Paint program.

To test the accuracy of our “hand-digitization”
technique, we compared our digitized data set of a published histogram (Figure 2 in [3]) and the original data set of the graph kindly provided by Dr. K. Dill, one of the authors of [3]. When the former was plotted against the latter, a near perfect linear correlation was found (Fig. 3).

Further evidence for this conclusion is provided by Figures 4, 5 and 6, in which the blackbody radiation spectra at three different temperatures are reproduced by PDE (also called BRE, blackbody radiation-like equation) almost exactly.

**Figure 3.** The agreement between the hand-digitized data set of the protein folding free energy histogram in [3] and the original data set of the histogram provided by the authors of [3].

**Figure 4.** The hand-digitized data from the blackbody radiation spectra at 3000 °K were reproduced almost exactly by the Planckian distribution equation, Eq. (2). BRE = blackbody radiation-like equation, synonymous with PDE, Planckian distribution equation.

**Figure 5.** The hand-digitized data from the blackbody radiation spectra at 4000 °K were reproduced almost exactly by the Planckian distribution equation, Eq. (2). BRE = blackbody radiation-like equation, synonymous with PDE, Planckian distribution equation.

**Figure 6.** The hand-digitized data from the blackbody radiation spectra at 5000 °K were reproduced almost exactly by the Planckian distribution equation, Eq. (2). BRE = blackbody radiation-like equation, synonymous with PDE, Planckian distribution equation.

### 2.3. Single-Molecule Enzymology

The technique of measuring the single-molecule enzyme kinetics is outlined in the legends to Figures 7, 8 and 9. The enzyme turnover time histogram shown as a bar graph in Figure 9 was successfully simulated using PDE, Eq. (3), as evident in Figure 10. The double exponential function, Eq. (2), can also simulate the same histogram (not shown) but the double exponential equation used in [4] lacks the parameter, A.

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

(2)

where A, B and C are free parameters.
**Figure 7.** 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. Reproduced from http://www.nigms.nih.gov/News/Reports/single_molecules.htm in 2010.

**Figure 8.** The kinetics of the blinking phenomenon of an isolated single molecule of cholesterol oxidase. One cycle of blinking of the coenzyme is represented by a pair of on- and off states of FAD fluorescence in this figure and the time taken per cycle constitutes one turnover-time of the enzyme. Reproduced from http://www.nigms.nih.gov/News/Reports/single_molecules.htm in 2010.

**Figure 9.** The turnover-time histogram of single-molecule cholesterol oxidase. The turnover times of the enzyme were not constant but varied widely, generating a histogram as shown here. Reproduced from http://www.nigms.nih.gov/News/Reports/single_molecules.htm in 2010. Lu et al. [4] fitted the histogram in Figure 9 with a double exponential function (see the curve). The same data were simulated in Figure 10, using the Planckian distribution equation, Eq. (3).

**Figure 10.** The turnover time histogram of a single-molecule cholesterol enzyme kinetics measured by Lu et al [3] was simulated using the Planckian distribution equation, Eq. (3).

2.4. The Generalization of the Planck Radiation Equation (PRE) to Fit Single-Molecule Enzyme Kinetic Data

In 2008 [1, Chapter 11], I noticed that the single-molecule enzyme-turnover-time histogram (Fig. 9) published by Lu et al. [4] resembled the blackbody radiation spectrum at 4000 °K (Figures 2). This
observation led me to generalize the Planck radiation equation, Eq. (1), by replacing its universal constants and temperature with free parameters as shown in Equations (3) and (4), the former having 4 parameters, a, b, A and B, and the latter 3 parameters, A, B and C. Depending on the data set under analysis, either the 4- or the 3-parameter equation has been found convenient. The 4- and 3-parameter equations can be interconverted using the transforming Equations (5), (6) and (7).

The “generalized equation” is referred to either as the as “blackbody radiation-like equation” (BRE) [1], the “generalized Planck equation” (GPE), or the “Planckian distribution equation” (PDE) [2] in analogy to the Gaussian distribution equation (GDE).

\[
y = \frac{a}{(Ax + B)^5} \cdot \frac{1}{e^{b(Ax + B)} - 1} \quad (3)
\]

\[
y = \frac{A}{(x + B)^5} \cdot \frac{1}{e^{C(x + B)} - 1} \quad (4)
\]

\[A = a/A^5\]  
\[B = B/A\]  
\[C = b/A\]  

2.5. A Suggested Common Mechanism underlying Blackbody Radiation and Enzyme Catalysis

Blackbody radiation (Figures 1 and 2) involves thermally induced promotion of the energy levels (vibrational, electronic, or vibronic) of oscillators from their ground state \(E_0\) to higher energy levels, \(E_i\) through \(E_6\), as schematically depicted in Figure 11. The wavelength of the radiation (or quantum) 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. Blackbody radiation results when excited electrons transition from a given energy level to a lower energy level within matter, e.g., from \(E_1\) to \(E_0\), from \(E_2\) to \(E_0\), etc.

Just as the fitting of the blackbody radiation spectra to Planck radiation equation is synonymous with the quantization of the energy levels of electrons within an atom, so it was thought reasonable to postulate that the fitting of the single-molecule enzyme turnover time histogram to the Planckian distribution equation (as demonstrated in Figure 10) implies the discretization of the conformational states of an enzyme molecule in agreement with the concept of “conformational substates” of Frauenfelder et al. [5], which, in turn, is synonymous with the quantization of the Gibbs free energy levels of an enzyme [1]. This idea is schematically represented in Figure 12.

![Figure 11. The quantization of the energy levels of electrons in atoms.](image1)

![Figure 12. The postulated quantization of the free energy of an enzyme molecule thereby generating discrete energy levels within an enzyme similar to the atomic orbitals in atoms.](image2)
exist in different Gibbs free energy levels and carries a set of sequence-specific conformational strains (or conformons) [1, Chapters 8 and 11] and can be excited to a common transition state (denoted as C‡) by thermal fluctuations (i.e., Brownian motions), whose de-excitation being postulated to lead to catalysis [1, Section 11.3.3; 2].

3. Results, Discussions, and Conclusions

As already alluded to above, PDE has been found to fit long-tailed histograms generated from various fields of inquiries in both natural and human sciences, as summarized below.

3.1. Protein Folding

The Gibbs free energy changes accompanying protein folding have been measured by various investigators and summarized in [3]. These data have been found to fit PDE as shown in Figure 13. The theoretical curve fits the empirical data almost exactly except toward the tail end where the theoretical curve rises above the empirical one. The area between these two curves is estimated to be about 5% of the total area which would correspond to approximately 200 proteins. These proteins may have thermodynamic properties that cannot be estimated by their chain length, N, alone and implicate other factors including conformational strains (referred to as conformons in [1, 6] or as frustrations by P. W. Anderson [7, 8]) that raise the ground-state free energy levels and hence reduce the associated activation free energies for the denaturation of these proteins.

Figure 13. Fitting to PDE of the folding free energies of 4,300 proteins isolated from E. coli [3].

3.2. Single-Molecule Enzyme Kinetics

(See Section 2.3 and Figure 10)

3.3. RNA Metabolism in Budding Yeast

When glucose is replaced with galactose as nutrient, budding yeast cells exhibit massive changes in the copy numbers (from 0 to several hundreds) of its mRNA molecules encoded by 6,300 genes. Garcia-Martinez et al. [9] measured the levels of over 5,000 mRNA molecules at 6 time points (0, 5, 120, 360, 450, and 85 minutes after the 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 classes or bins to generate a histogram shown in Figure 14. As can be seen, the fitting of the histogram to PDE is excellent.

Figure 14. The histogram of the genome-wide mRNA levels measured in budding yeast at 6 timer points over a period of 850 minutes after replacing glucose with galactose. The experimental data are almost exactly reproduced by PDE, Eq. (4).

3.4. RNA Metabolism in Human Breast Tissues

Perou et al. [10] measured the mRNA levels of 8,102 genes in the normal cells, and 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. A total of 4,740 x 20 = 94,800 mRNA levels were divided into 60 bins to generate a histogram shown in Figure 15. Again the experimental curve fitted the
Planckian distribution equation, Eq. (3), with great precision.

3.5. 7-Mer Frequency Distribution

Zhou and Mishra [11] studied the statistics of short DNA segments in different genomes by performing a large-scale non-overlapping mer-frequency distribution analysis. The 7-mer frequency distribution in *Pyrococcus abyssi* shown in Figure 16 can be simulated by PDE almost exactly. The deviation of the PDE curve from the Gaussian-like distribution is thought to reflect the participation of some non-random processes in generating the numbers embodied in the histogram.

**Figure 16.** 7-Mer frequency distribution in the *Pyrococcus abyssi* genome [11].

3.6. Protein Length Frequency Distribution in *Haemophilus influenzae*

The protein length frequency distribution in a bacterium [12] is shown in Figure 17. This long-tailed histogram could be fit into three different distribution equations – PDE, log-normal, and gamma, indicating that the fitting of long-tailed histograms to PDE is not necessarily unique and there exist other equations that can fit the same histogram with more or less equal facility.

**Figure 17.** Protein length frequency distribution in *Haemophilus influenzae* is simulated by three different mathematical equations – PDE, the log-normal distribution and the gamma distribution.

3.7. Human Decision Making

The drift-diffusion model (DDM) of decision-making is a widely utilized in behavioral neurobiology [13, 14, 15, 16]. DDM accurately reproduces the decision-time histograms (see Experimental in Figure 18), reflecting the well-known phenomena [13] that it takes the brain longer to process more difficult tasks than easier ones.
3.8. Hallucinogen-Induced fMRI Signals from Human Brains

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. Carhart-Harris et al. [21] measured the fMRI signals from the brains of 15 healthy volunteers before and after the intravenous infusion of the hallucinogen psilocybin. 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 studied (2° visual, 1° visual, motor, DAN, auditory, DMN, R-FP, L-FP, salience), four regions exhibited pronounced changes in their fMRI signals measured as increases in the deviations of the local signals from the 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 individual voxel signals from the group-mean fMRI signal are calculated and grouped into bins and their frequencies are counted, histograms are obtained such as shown in Figure 19, which could be reproduced by PDE, Eq. (3), reasonably well. The numerical values of the parameters of the PDE fitting these two histograms differed, especially the b/A ratios, which increased from 0.93 to 1.62 by the psilocybin infusion.

The fitting of the fMRI signals to PDE indicates potential application of PDE to quantitative studies of the consciousness in humans and to developing CNS-active drugs affecting the state of consciousness and pain.

3.9. Human Electroencephalogram

The histogram of the electrocorticograms measured from the human brain [22, Fig. 6/1] can be simulated by
PDE. The deviation of the PDE curve from the Gaussian-like distribution indicates that the neurobiological processes underlying the ECoG signals in the rabbit olfactory system are not random but organized and the degree of this organization can be quantified using PDE and its conjugate Gaussian-like equation (GLE) as shown in Eq. (8).

Figure 20. The histogram of the electrocorticograms can be simulated with PDE.

3.10. Word/Phrase Length Distribution in a Speech

The histogram of the word/phrase frequency distribution in a speech delivered by J. Kerry in 2004 can be fit into either PDE or the Menzerath-Altmann equation discovered by glottometricians [23, 24].

Figure 21. The fitting of the word or phrase-length frequency distribution into PDE or the Menzerath-Altmann equation [23, 24]

3.11. Sentence-Length Frequency Distribution in Texts

The sentence length frequency distribution in private letters shown in Figure 22 [24] can be almost exactly reproduced by PDE, indicating that the selection of words in private letters was performed non-randomly, since random selection of words would have resulted in a Gaussian-like distribution.

Figure 22. The sentence length frequency distribution in private letters [2] fitting PDE.

3.12. Econophysics

The Rayleigh-Jeans law [25] 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” [26].

Some physicists [27] have suggested that the distribution of incomes in a society may be modeled using the Boltzmann-Gibbs equation making the analogy that money can be treated as energy (see Table I below). Again this statistical mechanical approach works fine for high income levels but fails badly at low income levels (see Figures 24 and 25). However, PDE, Eq. (3), fits both the 1996 and 2013 US annual income distributions almost exactly.
If we assume that the exponential distribution shown in Figures 24 and 25 are analogous to the Rayleigh-Jeans law and the Planckian distribution to the Planck radiation law, Eq. (1), we can reasonably conclude that the deviation of the exponential distributions from the observed income distributions are analogous to the ‘ultraviolet catastrophe’ in physics of about a century ago [26].

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 24 and 25 may introduce another novel concept into natural and human sciences – the quantization of organization in terms of what may be called the Planckian information, \( I_P \), defined as follows:

\[ I_P = \log_2 \left[ \frac{\text{AUC}(P)}{\text{AUC}(G)} \right] \text{ bits} \]  

(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-like distribution whose rising phase coincides with the rising phase of the Planckian distribution [2]. These and related ideas are collected in Table I.

It should be pointed out that what was referred to as the Gaussian equation (GE) in Fig. 6 and Eq. (8) in [2] is erroneous and should be replaced by “Gaussian-like equation (GLE):

\[ y = A e^{-(x - \mu)^2/2\sigma^2} \]  

(9)

where A is a free parameter. In GE, A is not free but a function of \( \sigma \), which makes it difficult to make the rising phase of GE to coincide with the rising phase of PDE. But this problem does not arise with GLE as exemplified in Figs. 15, 16, 20, 22, 24 and 26.

Figure 23. The US annual income distribution in 1996 fits PDE better than the exponential function used by some physicists [ ].

Figure 24. The US annual income distribution in 2013 fits the exponential function up to the lowest income.

<table>
<thead>
<tr>
<th>Table I. A comparison between the ‘ultraviolet catastrophes’ in quantum physics and econophysics.</th>
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<tr>
<td>Ultraviolet Catastrophe in</td>
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<tr>
<td>Quantum Physics</td>
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</table>

3.13. Cosmology

Although PDE has been found to fit almost exactly most fat-tailed histograms generated in various disciplines that we have examined so far (over 30), the polarized CMB (Cosmic Microwave Background) data as shown in Figure 26 is an exception in that the data could not be made to fit PDE exactly using the Solver program in Excel. The falling phase of the CMB polarization curve is thinner than PDE curve and considerably fatter than the Gaussian-like curve.

As can be seen in Figures13 through 25, if PDE fits the rising phase of the histogram, it fits the falling phase of the histogram as well, except the polarized CMB data in Figure 26. The areas under the curves (AUC) of the Gaussian-like distribution (GLE), the CMB data, and PDE were found to be, respectively, 10.3, 13.97, and 16.98 units. From these numbers, we can calculate the Planckian information, \( I_P \), defined as

\[
I_P = \log_2 \left( \frac{\text{AUC(PDE)}}{\text{AUC(GLE)}} \right). \tag{10}
\]

\[
= \log_2 (16.98/10.3) = 0.721 \text{ bits}
\]

which is equivalent to selecting 70 out of 100, i.e., the information needed to select or generated by selecting 70 out of 100 possibilities.

Our current interpretation of the Planckian information is that it represents the degree of organization of a physical system (in contrast to the Boltzmann-Gibbs entropy which represents the disorder/disorganization of a physical system), whether the system involved is atoms, enzymes, cells, brains, human societies, or the Universe.

Based on Figure 26, the Planckian information associated with the polarized CMB data was found to be 0.44 bits which contrasts with the \( I_P \) associated with the Planckian distributions (and hence the blackbody radiation) of 0.72 bits, the difference being almost 2 fold. One possible interpretation of this difference would be that the polarized CMB radiation 'lost' some of its information about the order or the organization of the Big Bang due to the randomizing effects of the galactic dust. (It is hoped that that this interpretation can be experimentally tested by experts in the field.)
3.14. **Category Theory**

The quantitative fittings PDE of the long-tailed histograms generated from various fields of inquires as demonstrated in this paper can be understood if we utilize the concepts and principles developed in the mathematical theory of categories. Qualitative characterization of the concepts of categories and functor are provided by the following quotations:

(a) “Comparison and analogy are fundamental aspects of knowledge acquisition. We argue that one of the reasons for the usefulness and importance of Category Theory is that it gives an abstract mathematical setting for analogy and comparison, allowing an analysis of the process of abstracting and relating new concepts. This setting is one of the most important routes for the application of Mathematics to scientific problems.” [28]

(b) “We view a category as giving a fairly general abstract context for comparison. The objects of study are the objects of the category. Two objects, A and B, can be compared if the set C(A,B) is non-empty and various arrows A \longrightarrow B are ‘ways of comparing them’. The composition corresponds to: If we can compare A with B and B with C, we should be able to compare A with C.” [28]

(c) “…a functor . . is a way of comparing categories, . . . “ [28].

(d) “Different branches of mathematics (human knowledge; my addition) can be formalized into categories. These categories can then be connected together by functors. And the sense in which these functors provide powerful communication of ideas is that facts and theorems (regularities; my addition) proven in one category (discipline; my addition) can be transferred through a connecting functor to yield proofs of analogous theorems in another category. A functor is like a conductor of mathematical truth (my emphasis)” [29].

3.15. **A comparison between Shannon entropy and the Planckian information, \( I_P \)**

There is no doubt that a close formal similarity exists between the mathematical equations of H and S (see Rows 1 and 3, Column 1 in Table II). But this is a shallow and superficial reason for giving both functions the same name, 'entropy', without first checking that both mathematical functions share some common principles or mechanisms. Since the meaning of 'entropy' in thermodynamics is relatively well established (e.g., a measure of disorder, obeying the Second Law), giving this same name to the H function may lead to unwittingly attributing the same thermodynamic meanings of entropy to H. In fact many prominent scientists and mathematicians unfortunately have taken this road, in my opinion, thereby creating confusions among scholars.

As already stated, a new equation called the Planckian distribution equation (PDE) (see Row 3, Column 2 in Table II) was derived in 2008 from the Planck radiation equation (PRE) (see Row 1, Column 2, Table II) with free parameters, a, b, A and B. For convenience, we define "Planckian processes" as those physicochemical, biomedical, or socioeconomic processes that generate numerical data that fit PDE, and there are many such processes found in natural and human sciences [1, 2]. In a certain sense, H function of
Shannon is related to the S function of Boltzmann as PDE is related to PRE. Therefore, if there are functors connecting PDE and PRE (e.g., energy quantization, wave-particle duality) as I strongly believe, it is likely that there may well be at least one functor connecting H and S, which I do not believe is the Second Law as some physicists and mathematicians have claimed. One possible functor connecting H and S may well turn out to be "variety" or "complexity" as suggested by Wicken [31, p. 186].

In addition to the "mathematical functors" described above, there may be "non-mathematical" or "qualitative" functors connecting H and S on the one hand and PDE and PRE on the other, and I suggest that these what may be called "qualitative functors" may be identified with the Peircean sign triad or semiosis as indicated in the bottom portion of Figure 27.

<table>
<thead>
<tr>
<th>Table II.</th>
<th>A comparison between Shannon entropy and the Planckian distribution equation.</th>
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<tbody>
<tr>
<td></td>
<td>Shannon H</td>
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<tr>
<td>1. Original equation</td>
<td>Boltzmann equation for entropy S (1872-5)</td>
</tr>
<tr>
<td></td>
<td>S = k \ln W</td>
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<tr>
<td></td>
<td>which was generalized by Gibbs as</td>
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<tr>
<td></td>
<td>S = - k \sum P_i \log P_i</td>
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<tr>
<td>2. Insight or mechanisms</td>
<td>Microscopic explanation of macroscopic measurements in thermodynamics</td>
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<tr>
<td>3. New equations as a generalization of the original equation</td>
<td>Shannon equation formulated in 1948</td>
</tr>
<tr>
<td></td>
<td>H = - K \sum P_i \log_2 P_i</td>
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<td></td>
<td></td>
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<tr>
<td>4. Significance</td>
<td>S measures the thermally induced disorder of a physical system, while H measures the variety or complexity of a message source of a communication system</td>
</tr>
<tr>
<td>5 Domain of applications</td>
<td>Any field generating a probability distribution, P_i, regardless of whether or not organized into regular patterns.</td>
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3.16. A Unified Theory of the Amount of Information (UTAI)

Statistical entropy $S$ and Shannon entropy $H$ can be viewed as instantiations or TOKENS of the more abstract definition of information given in Eq. (11) below, which may be viewed as the information TYPE.

$$I = A \log_2 (B/C)$$  \hspace{1cm} (11)

where $A = \text{proportionality constant}$, $B = \text{the number of possible messages available at the message source}$, and $C = \text{the number of messages selected}$.

Although both $H$ and $S$ share the same name "entropy", their meanings are not the same in that, e.g., $S$ in isolated systems increase with time and temperature but $H$ does not \cite{1, pp. 97-101}. In other words, $S$ obeys the Second Law of thermodynamics but $H$ does not. This is demonstrated in the thought experiment called the "Bible test" \cite{1, see Footnote c in Table 4.3}.

Information can be thought of as resulting from a selection process characterized by a ratio, $B/C$, in Eq. (11).

Many investigators have suggested that information has three distinct aspects – (i) quantity, (ii) meaning, and (iii) value. It is important to keep in mind that UTAI can only deal with the AMOUNT of information, not its meaning nor its value.

There are many kinds of information just as there are many kinds of energies (chemical, electrical, gravitational, kinetic, potential, nuclear, solar, electromagnetic, etc.). Hence we can speak of Boltzmann’s $S$ as “molecular information”, Shannon’s $H$ as "probability-dependent information (?)", and $I_p$ as the Planckian information (see Table III). The meanings of these different kinds of information would depend critically on the detailed mechanisms of selection operating at the message source level of the communication system under consideration.

More generally "information" can be defined as the correlation between the source (or the 'object' in the language of Peircean semiotics) and the receiver ('interpretant') of a communication system. The message carried by the messenger ('sign' or 'representamen') in the communication system can be identified with "information". The net result of such a mediated process can be described as the 'information flow' from the source to the receiver.

Just as the Peircean sign is an irreducible triad (i.e., it cannot be defined without all of the 3 nodes, i.e., object, representamen, and interpretant \cite{2, see Row 6 in Table V} , connected by the three edges representing 'natural process', 'mental process', and 'information flow', so I maintain that 'information' is another "irreducible triad" (of source, messenger, and receiver).

The UTAI may be considered as the ‘quantitative functor’ connecting the mathematical aspects of communication, and I predict that there is the ‘qualitative functor’ (in agreement with the assumed principle of quantity-quality complementarity \cite{30}) that connects the qualitative aspects of communication and semiotics. This predicted qualitative functor may be identified with natural and formal languages, both of which belonging to the class of the irreducible triad (see Fig. 27).

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Table III. A unified theory of the amount of information carried by a sign:
*AUC = area under the curve of the Planckian distribution equation, \( y = \frac{(a/(A + x + B)^5)}{(e^{b/(A + x + B)} - 1)} \), or the Gaussian-like equation, \( y = A e^{-\frac{(x - \mu)^2}{2\sigma^2}} \), where A is a free parameter. I_{P} is thought to be a new measure of organization or order.

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References


http://en.wikipedia.org/wiki/Rayleigh%E2%80%93Jean_s_law
[26] Ultraviolet catastrophe.
http://en.wikipedia.org/wiki/Ultraviolet_catastrophe