

Boltzmann statistics as founding principle of microbial growth

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1	Boltzmann statistics as founding principle of
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17 SUMMARY: Microbes are the most abundant living forms on earth and major contributors to the biogeochemical cycles. However, our ability to model their dynamics only relies on empirical laws, 18 19 fundamentally restricting our understanding and predictive capacity in many environmental systems. 20 Preeminent physicists such as Schrödinger and Prigogine have introduced a thermodynamic 21 interpretation of life, paving the way for a quantitative theory. From these seminal contributions 22 have emerged microbial thermodynamics, which allows the prediction of microbial energy allocation. 23 Nevertheless, the link between energy balances and growth dynamics is still not understood. Here 24 we demonstrate a microbial growth equation relying on an explicit theoretical ground sustained by 25 Boltzmann statistics. Historical data from Monod are used to illustrate the experimental accuracy of our law. In addition, two classes of microbial isotopic fractionation behavior are predicted and we 26 27 show how their existence is supported by recent experimental reports. Our work opens the door to 28 the modeling of microbial population dynamics through a thermodynamic state analysis of 29 environmental systems. We anticipate that the predictive power of our law could be used to design 30 and control biotechnological processes and applications. The contribution of microbial reactions to 31 earth biogeochemical cycles could also be more accurately modeled. Importantly, our theory offers a 32 new framework to mathematically assess ecological and evolutionary concepts.

35 "What is life?" was the question asked by Erwin Schrödinger in his famous book (Schrödinger 1944). 36 He opened the debate on how life could be envisioned from the thermodynamic standpoint. Ilyia 37 Prigogine (Prigogine 1955) then made an important contribution by pioneering the application of 38 non-equilibrium thermodynamics to biology, underlying all modern developments of biological 39 flux-force models. Today, thermodynamic state functions are widely applied to living systems at 40 different organization levels (Jørgensen and Svirezhev 2004). The study of microbes, the simplest 41 form of life, however led to a deeper physical conceptualization of the problem (McCarty 1965, Roels 42 1980, Heijnen and Vandijken 1992, Rittmann and McCarty 2001, Kleerebezem and Van Loosdrecht 43 2010). In these contributions, microbial anabolism was linked to catabolism through energy 44 dissipation, sometimes expressed as a universal efficiency factor. A relation between dissipated 45 energy and growth stoichiometry was established, enabling the prediction and calculation of energy 46 and matter balances of microbial growth. However, the key question of the link between microbial 47 thermodynamics and growth kinetics remained unanswered.

At the beginning of the XXth century, chemistry was facing a similar problem which finally resulted in 48 a thermochemical kinetic theory eighty years ago (Eyring 1935). The existence of a high energy 49 50 transition state, resulting from the collision of reactants, was postulated. Statistical physics was 51 invoked to estimate the probability for the colliding molecules to have enough energy to overcome 52 the transition state energy. A link between reaction kinetics and thermodynamic state of the system 53 was thus established. Along a similar path, let us be inspired by the visionary statement made by 54 (Lotka 1922): "The similarity of the [biological] units invites statistical treatment [...], the units in the 55 new statistical mechanics will be energy transformers subject to irreversible collisions of peculiar 56 type-collisions in which trigger action is a dominant feature..."

57 Let us consider the system constituted by a 3D physical space in which a clonal population of N58 microbes is consuming substrates and dividing. Each individual microbe has access to a volume (V_{harv}) in which it can harvest substrates. These elementary volumes define the statistical units of 59 our model. Let us assume that the total volume accessible to the microbes $(N \cdot V_{harv})$ is small 60 61 compared to the rest of the system, the latter being considered as a reservoir. Then, let us also 62 consider a microstate consisting of a specific distribution of substrates molecules in the different 63 statistical units occupied by microbes. Each microstate can then be viewed as a part of a canonical 64 ensemble as defined in the framework of statistical physics. Therefore, the probability for a statistical 65 unit to contain a given number of molecules follows Boltzmann statistics (see supplementary 66 material for the detailed demonstration). Let us assume that the activation of a microbe for a division 67 event is triggered by threshold numbers (v_i) of substrates molecules in its harvesting volume. Then, 68 the proportion of activated microbes is:

$$\frac{N^{\ddagger}}{N} = \prod_{i} \exp\left(-\frac{\nu_{i}}{V_{harv} \cdot [S_{i}]}\right)$$
 (Equation 1)

69 N^{\ddagger} being the number of activated microbes, S_i representing the different substrates.

Threshold numbers of substrate molecules necessary for a division event are related to the stoichiometry of growth:

$$M + \sum_{i} \nu_i S_i \rightarrow 2M + \sum_{j} \nu'_j P_j$$
 (Equation 2)

72 where *M* represents a microbe, P_i metabolic products and v'_i are stoichiometric coefficients.

Let us consider the common situation where only one substrate (S_{lim}) is limiting the division phenomenon. The nature of this limitation can either be due to the insufficient energy supply brought by S_{lim} or to an elemental stoichiometric restriction.

76 In the case of stoichiometric restriction, the threshold v_{lim} can be deduced from the elemental 77 composition of the microbe M (see supplementary material) consequently determining the 78 proportion of activated microbes.

In the case of energy limitation, v_{lim} depends on the energy allocation during growth, which has been extensively studied (for a review, see Kleerebezem et Van Loosdrecht; (Kleerebezem and Van Loosdrecht 2010)). The energy allocation can be expressed in terms of exergy balance for an elementary microbial division (see supplementary material and Figure 1), leading to the expression of v_{lim} :

$$v_{lim} = \frac{E_M + E_{dis}}{E_{cat}}$$

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 E_{cat} being the catabolic exergy of one molecule of energy limiting substrate, E_M the exergy stored in one microbe, E_{dis} the exergy dissipated during an elementary microbial division which can be calculated as explained in Kleerebezem et Van Loosdrecht; 2010.

This expression can thus be used together with (Equation 1) to infer the proportion of activated microbes as a function of catabolic exergy available. Let us now finally assume that each activated microbe has a probability μ_{max} to divide by time unit. Then comes the expression of microbial growth rate as a function of microbial exergy balance:

$$\mu = \mu_{max} \cdot \exp\left(-\frac{E_M + E_{dis}}{V_{harv} \cdot [S_{lim}] \cdot E_{cat}}\right)$$
 Equation 3

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93 The experimental validity of Equation 3 is illustrated using Monod's historical growth experiments. As 94 shown on Figure 2-A, our law correctly transcribes microbial growth rate dependence on substrate 95 concentration. It exhibits a typical sigmoid shape enabling the modeling of any microbial experimental growth data. Indeed, as stated by Monod: "En fait toute courbe d'allure sigmoïde 96 97 pourrait être ajustée aux données expérimentales. Le choix ne sera donc guidé que par des 98 considérations de commodité et de vraisemblance." (Monod 1942). Interestingly however, our law 99 naturally accounts for the existence of an apparent threshold substrate concentration for growth 100 (Figure 2-A-2), correcting a major flaw of previous empirical equations (Kovarova-Kovar and Egli 101 1998). Although highly encouraging, the ability of our law to correctly represent data from microbial 102 growth experiments is not per se sufficient to support the validity of our theory. We believe that the 103 microbial isotope fractionation phenomenon is providing a more adequate opportunity to challenge 104 the fundamental assumptions sustaining our theory.

According to our law, the microbial isotope fractionation phenomenon can be explained by the variation in catabolic exergy (E_{cat}) due to the differences in thermodynamic properties of light or heavy isotopes, which results in slight differences in substrate consumption rates between isotopomers (see supplementary material). Thus, the kinetic fractionation factor $\alpha_{s/p}$ of substrates towards products (Mariotti, Germon et al. 1981) can be expressed as:

$$\alpha_{S/P} = \alpha_0 \cdot \exp\left(-\frac{E_M + E_{dis}}{V_{harv} \cdot [S_{lim}] \cdot E_{cat}^2} \cdot \Delta E_{cat}^{h-l}\right)$$
Equation 4

110 α_0 being the residual biochemical fractionation factor of the catabolic reaction, ΔE_{cat}^{h-l} represents the 111 difference between exergy of the catabolic reaction involving one molecule of the heavy isotopomer 112 minus the exergy of its light counterpart.

113 It has long been considered that microbial isotopic fractionation was only dependent on the type of 114 metabolism (Mariotti, Germon et al. 1981, Hayes 1993). Recent evidences however increasingly 115 testify that it varies with environmental conditions (Conrad 1999, Conrad 2005). Our theory directly 116 implies the dependence of $\alpha_{S/P}$ to [S]. E_{cat}^2 (see Equation 4). This relationship is depicted on Figure 2-B-1, where increasing catabolic exergy density leads to the convergence of microbial fractionation 117 118 towards an asymptotical value (α_0) whereas the behavior is divergent at low exergy density. 119 Strikingly, the dependency of microbial fractionation on substrate concentration (Valentine, 120 Chidthaisong et al. 2004, Kampara, Thullner et al. 2008, Goevert and Conrad 2009) and on Gibbs 121 energy (Penning, Plugge et al. 2005) was recently evidenced. Moreover, our theory predicts two 122 classes of fractionation behaviours (Figure 2-B-1, upper and lower curves) depending on the 123 thermodynamic properties of light and heavy molecules considered (see supplementary material). 124 Figure 2-B illustrates how experimental data obtained from previous reports (Valentine, 125 Chidthaisong et al. 2004, Penning, Plugge et al. 2005, Kampara, Thullner et al. 2008, Goevert and 126 Conrad 2009) are actually consistent with both predictions. These inferences, based on the 127 mathematical expression deduced from our assumptions, strongly support our theory of microbial 128 growth sustained by Boltzmann statistics of exergy distribution.

129 Equation 3 introduces a flux-force relationship between microbial growth rate and exergy. Our law 130 applied to mixed cultures thus opens the door to the modeling of microbial population dynamics 131 through a thermodynamic state analysis of environmental systems. Implemented into engineering 132 models for environmental bioprocesses such as ADM1 for anaerobic digestion (Batstone, Keller et al. 133 2002), it could naturally transcribe the well-known dependence of microbial activity to 134 thermodynamic conditions, correcting a major flaw of current kinetic models (Kleerebezem and van 135 Loosdrecht 2006, Rodriguez, Lema et al. 2006). At a larger scale, our law offers the possibility to 136 integrate the various fluxes resulting from multiple biochemical reactions through the concept of 137 exergy and to infer from it the growth and dynamics of microbial engines that drive earth's biogeochemical cycles (Falkowski, Fenchel et al. 2008). More fundamentally, our law offers a 138 139 mathematical framework to consistently assess thermodynamic ecological principles such as the 140 maximum power (Lotka 1922, Lotka 1922, DeLong 2008), maximum exergy (Jørgensen and Svirezhev 2004) or minimum entropy production (Prigogine 1955) principles to go one step further in the 141 142 fundamental scientific quest aiming to unveil "what is life".







Figure 1: General principle of an elementary microbial division as sustained by Boltzmann statistics. (A) Representation of substrate molecules (dots) distribution depicting those falling within microbial harvesting volumes (circles) and highlighting activated microbes (red) for which enough substrate molecules are available to trigger an elementary division act. (B) Graphical representation of microbial exergy levels along division coordinates. Microbial exergy (E_M) is augmented by the catabolic exergy within the harversting volume ($E_{cat} \cdot [S_{lim}] \cdot V_{harv}$). Reaching the threshold catabolic exergy ($E_M + E^{\ddagger}$), the microbe is activated (a state denoted X^{\ddagger}), and an irreversible division process is triggered, associated with exergy dissipation ($E_{dis} = E^{\ddagger} - E_M$), resulting in two microbes.





156 Figure 2 : Experimental evidences supporting Boltzmann sustained microbial growth. (A-1) Growth rate of E. coli as a 157 function of glucose concentrations under aerobic conditions (Monod 1942). The plain curve shows the fit of Equation 3 158 on the data. The dashed curve shows the fit of a Monod equation. (A-2) Detail of the growth rate/concentration 159 dependency at low substrate concentration showing that the mathematical expression of our law naturally accounts for 160 the existence of an apparent substrate threshold concentration for growth. (B-1) Isotopic microbial fractionation factor (α) as a function of substrate concentration times the square of the catabolic exergy (X-axis) as predicted from our 161 162 microbial growth theory. Two classes of behaviour are predicted depending on thermodynamic properties of the isotopomers considered. The upper curve corresponds to the case $\Delta E_{cat}^{h-l} < 0$ for which α decreases when $([S] \cdot E_{cat}^2)$ 163 164 increases and could be named "microbial overfractionation". The lower curve (i.e. "microbial underfractionation") corresponds to the case $\Delta E_{cat}^{h-l} > 0$ for which α increases with $([S] \cdot E_{cat}^2)$. Surprisingly, in this case, our law predicts that 165 166 microbial isotopic fractionation can either enrich (α <1) or deplete (α >1) reaction products in heavy isotope depending 167 on ($[S] \cdot E_{cat}^2$). (B-2) Experimental data from (Penning, Plugge et al. 2005) (triangles); and (Valentine, Chidthaisong et al. 2004) (circles); on ¹³C isotopic fractionation associated with hydrogenotrophic methanogenesis confirming the existence 168 169 of microbial overfractionation. (B-3) Experimental data from (Goevert and Conrad 2009); on ¹³C isotopic fractionation 170 associated with aceticlastic methanogenesis confirming the existence of microbial underfractionation. The inversion of 171 isotopic enrichment factor as predicted from our theory appears to be supported by this set of experimental data. (B-4) 172 Experimental data from (Kampara, Thullner et al. 2008) including fractionation factor obtained after 50% (triangles) or 173 70% (circles) of toluene degradation under aerobic conditions. This graph illustrates the consistency of the microbial 174 underfractionation prediction with another type of element (hydrogen/deuterium fractionation) further supporting the 175 strong dependency of biological fractionation on the thermodynamic properties of isotopomers. See suplementary 176 material 2 for detailed calculations.

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