Heat Dissipation and Self-consistent Nonequilibrium Thermodynamics of Open Driven Systems

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Nonequilibrium thermodynamics of a system in a sustained environment with influx and efflux is usually treated as a subsystem of a large closed "universe". It is still in doubt whether a satisfactory nonequilibrium thermodynamics can be established for an open driven system solely based upon its internal dynamics without involving any further details of the surrounding. In the present work we introduce the notion of *ideal external regenerating systems* which sustains a nonequilibriu steady-state (NESS). Using the master-equation description of motor protein either with or without a regenerating system as an example, we illustrate that the two systems have identical kinetics as well as the traditional Second Law with positive entropy production rate. There is, however, subtle difference in their heat dissipations. In fact, First Law can be established through the minimum work that is required for the external energy regenerating system to keep the NESS. This interpretation makes the heat dissipation well defined in the NESS perspective from the equations of internal dynamics. As a result, the entropy production rate is always equal to the "dissipated" heat in a NESS, leading to a less than 100% efficiency for energy transduction. Moreover, we interpret the housekeeping heat as the ensemble averaged summation of the NESS heat dissipation and NESS entropy change within each transition. The new perspective yields an extended Second Law, which emerges only from driven dynamics with external regenerating systems. It further suggests new ingredients for the thermodynamics of self-organization in driven systems.

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Statistical thermodynamics is the mathematical foundation of our material world in terms of classical physics, on which modern chemistry and biology stand [1]. To address the fundamental issues in complex living organisms such as a cell, there are currently two different perspectives: A classical physicist maintains a world following the Second Law of Thermodynamics and considers a living organism as a *subsystem* in a quasi-stationary state (QSS), due to the the slow changing nature of its environment; engineers and cellular biologists consider the complex systems in a sustained environment which has to be maintained. How to maintain such environment, however, is not a concern to someone who is only interested in the internal, complex dynamics.

This distinction can be best illustrated by two types of laboratory experiments on a motor protein [2], which convert chemical energy from ATP hydrolysis to mechanical work. In the first type, the amount of ATP, ADP and Pi are not controlled. However, due to the excess nature of their amount in solution, their concentrations can be considered approximately constant over the entire duration of a single-molecule experiment. Nevertheless, if an experiment is prolonged for a sufficiently long time, the ATP and ADP+Pi will eventually reach their chemical equilibrium, and the motor protein will cease to execute a directional motion. In the second type of experiments, an ATP-regenerating system is coupled to the motor protein [3]. In this case, the motor protein, as an open chemical system, can reach a nonequilibrium steady state (NESS) while continuously move along its track, even with a constant load [4, 5].

In the kinetic theories of motor proteins [2], both QSS and NESS treatments assume time-independent, constant concentrations of ATP, ADP and Pi, which leads to identical predictions of dynamics as well as similar definitions of free energy. However, the real thermodynamics of the two setups are essentially different [6] : In the QSS, the heat associated with each ATP hydrolysis is its Δh, i.e., enthalpy (or internal energy for system with constant volume) change; while in the NESS, we will show the minimum amount of heat dissipated is the free energy change $\Delta\mu$ of ATP hydrolysis.

The nonequilibrium chemical thermodynamics of QSS is quite traditional, which follows the original idea of Boltzmann and could be very general. Heat, work, entropy, free energy and other thermodynamic quantities are all well defined. However, it could not be built solely on the internal dynamics of the target system and one needs to know nearly every detail of the surroundings e.g. particles in the solution and their interactions [6]. Hence for those engineers or cellular biologists who is only interested in the internal dynamics of the motor protein, another self-consistent thermodynamics is desirable; otherwise even the efficiency of energy transfer could not be well defined and further investigated. Hence in the present work, we shall attempt to develop the second, NESS, perspective, and try to deduce all the important

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nonequilibrium thermodynamic relations solely from internal dynamics in the absence of detailed balance.

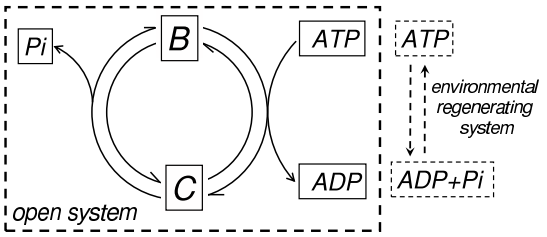

FIG. 1: The thermodynamics of spontaneous ATP hydrolysis and related ATP regenerating process. The entire cycle would have an $\Delta\mu > 0$ amount of work input and the same amount of heat dissipated, where $\Delta\mu$ is just the free energy change of the ATP hydrolysis. See the main text for details.

A simple cyclic reaction system coupled with a regenerating system — Fig. 1 shows a simple biochemical reaction cycle $B \to C \to B$ coupled to ATP hydrolysis. The ATP, ADP and Pi concentrations are maintained by an "external" regenerating system:

$$B + ATP \underset{k_{-1}}{\overset{k_1}{\rightleftharpoons}} C + ADP, \quad C \underset{k_{-2}}{\overset{k_2}{\rightleftharpoons}} B + P_i. \tag{1}$$

After completing a reaction cycle (1), the net effect is one ATP being hydrolyzed to ADP+Pi. At the meantime, the regenerating system would convert ADP+Pi back to ATP externally. This is the essential difference between NESS and QSS which results in one ATP hydrolysis after one cycle. Standard thermodynamics tells us the chemical potentials of each species are defined as

$$\begin{aligned}
&\mu_B = \mu_B^o + k_BT\ln[B], \quad \mu_C = \mu_C^o + k_BT\ln[C],\\
&\mu_{ATP} = \mu_{ATP}^o + k_BT\ln[ATP],\\
&\mu_{ADP} = \mu_{ADP}^o + k_BT\ln[ADP],\\
&\mu_{P_i} = \mu_{P_i}^o + k_BT\ln[P_i].
\end{aligned} \tag{2}$$

At chemical equilibrium, $\mu_B + \mu_{ATP} = \mu_C + \mu_{ADP}$ and $\mu_B + \mu_{P_i} = \mu_C$, i.e. $k_1[B]^{eq}[ATP]^{eq} = k_{-1}[C]^{eq}[ADP]^{eq}$ and $k_2[C]^{eq} = k_{-2}[B]^{eq}[P_i]^{eq}$, which also leads to the thermodynamic constrains

$$\begin{aligned}
\mu_B^0 + \mu_{ATP}^0 - \mu_C^0 - \mu_{ADP}^0 &= k_BT\ln\left(k_1/k_{-1}\right),\\
\mu_C^0 - \mu_B^0 - \mu_{P_i}^0 &= k_BT\ln\left(k_2/k_{-2}\right).
\end{aligned} \tag{3}$$

Each intrinsic chemical potential can be decomposed into $\mu^0 = h^0 - Ts^0$, where h^0 and s^0 are the intrinsic enthalpy and entropy respectively. Then for a single occurrence of the hydrolysis cycle in Fig. 1, the heat dissipation is

$$\begin{aligned}
h_d &= (h_B^0 + h_{ATP}^0 - h_C^0 - h_{ADP}^0) + (h_C^0 - h_{P_i}^0 - h_B^0)\\
&= h_{ATP}^0 - h_{ADP}^0 - h_{P_i}^0.
\end{aligned} \tag{4}$$

There is an "external step" for the regenerating system converting ADP+Pi back to ATP after each completion of a cycle. The minimum work (non-PV work) it has to do is the free energy difference between ADP+Pi and ATP, i.e.

$$W_{min} = \mu_{ATP} - \mu_{ADP} - \mu_{P_i}, \tag{5}$$

with corresponding enthalpy changes back from $h_{ADP}^0 + h_{P_i}^0$ to h_{ATP}^0. The external regenerating system that accomplishes the minimum work is called "ideal".

Therefore, the energy dissipation of this external step in the environment, in the form of heat, is

$$h_d^{ext} = W_{min} - (h_{ATP}^0 - h_{ADP}^0 - h_{P_i}^0). \tag{6}$$

We note that h_d^{ext} is just the entropy change for the ATP hydrolysis.

Hence the total heat dissipation of a single forward biochemical cycle in a drive system with regeneration is

$$\begin{aligned}
Q_{tot} &= h_d + h_d^{ext}\\
&= W_{min} = \Delta\mu = \mu_{ATP} - \mu_{ADP} - \mu_{P_i} = k_BT\ln\gamma,
\end{aligned}$$

where $\gamma = \frac{k_1k_2[ATP]}{k_{-1}k_{-2}[ADP][P_i]} > 1$ is the affinity for the reaction cycle. The affinities now has a clear thermodynamic meaning in such a driven cycle, and all the external work is dissipated while the system remains steady.

We see the central importance of cycle kinetics from this simple example. Before a completion of a cycle, the regenerating system needs not to do anything to maintain the environment, and all the work done to "the system" is potentially reversible. This has been emphasized by T.L. Hill; a similar argument was put forward by Landauer for the thermodynamics of computation [7].

Master equation model and thermodynamic constrains — The above analysis for a single biochemical cycle can be generalized to any dynamical model with a master equation: Let us consider a motor protein with N different conformations $R_1, R_2, \cdots, R_N$. Suppose that the system is kept in a close contact with a large heat reservoir with constant temperature T and pressure. For simplicity, the concentration of every substance is assumed to be independent of its position, and there is no external input or output of mechanical energy.

Let k_{ij} be the first-order, or pseudo-first-order rate constants for reaction $R_i \to R_j$. Assume only one of them is coupled with the energy source, i.e., ATP and ADP:

$$ATP + R_1 \underset{\tilde{k}_{21}}{\overset{\tilde{k}_{12}}{\rightleftharpoons}} ADP + R_2,$$

where $\tilde{k}_{12}$ and $\tilde{k}_{21}$ are both second-order reaction constants, and denote $k_{12} = \tilde{k}_{12}[ATP]$, $k_{21} = \tilde{k}_{21}[ADP]$ as the pseudo-first-order rate constants. For simplicity, here we omit the Pi release step, since what we want to emphasize here is only the reaction $R_1 \to R_2$ can have a driving force.

Let c_i be the concentration of R_i. Once the concentrations of ATP and ADP are sustained, the stochastic dynamics of all the motor proteins are independent, in

which case we could substitute the concentration with probability. By the law of mass action, such a linear system could be described in terms of a mathematical model

$$\frac{dc_i(t)}{dt} = \sum_j \left(c_j k_{ji} - c_i k_{ij}\right). \tag{7}$$

If there is no external mechanism to keep the concentrations of ATP and ADP, then the time evolution of $[ATP]$ and $[ADP]$ is

$$\frac{dc_T}{dt} = -\frac{dc_D}{dt} = -\tilde{k}_{12} c_T c_1 + \tilde{k}_{21} c_D c_2. \tag{8}$$

Classical equilibrium thermodynamics for closed chemical system tells us that there is a unique dynamic and chemical equilibrium $\{c_1^{eq}, c_2^{eq}, \cdots, c_N^{eq}, c_T^{eq}, c_D^{eq}\}$ which satisfies the detailed balance condition $c_i^{eq} k_{ij} = c_j^{eq} k_{ji}$, where $k_{12} = \tilde{k}_{12} c_T^{eq}$ and $k_{21} = \tilde{k}_{21} c_D^{eq}$.

Similar to (2), each species has a chemical potential $\mu_i(c_i) = \mu_i^0 + k_B T \ln c_i$, where the internal chemical potential μ_i^0 obeys the Boltzmann's law $\mu_i^0 = -k_B T \ln c_i^{eq}$+const. When the system reaches chemical equilibrium, the chemical potentials of different components are the same, i.e. $\mu_i(c_i^{eq}) = \mu_j(c_j^{eq})$, and $\mu_1(c_1^{eq}) + \mu_T(c_T^{eq}) = \mu_2(c_2^{eq}) + \mu_D(c_D^{eq})$, where $\mu_T(c_T) = \mu_T^0 + k_B T \ln c_T$ and $\mu_D(c_D) = \mu_D^0 + k_B T \ln c_D$ are the chemical potentials of ATP and ADP respectively.

Then it gives the relation between μ^0's and k_{ij}'s of the system, i.e.

$$\mu_i^0 - \mu_j^0 = k_B T \ln \frac{k_{ij}}{k_{ji}}, \quad \mu_T^0 - \mu_D^0 = k_B T \ln \frac{c_D^{eq}}{c_T^{eq}},$$
$$\mu_1^0 + \mu_T^0 - \mu_2^0 - \mu_D^0 = k_B T \ln \frac{\tilde{k}_{12}}{\tilde{k}_{21}}.$$

QSS in a larger closed system with detailed balance — In this case, the whole system is closed including ATP and ADP; its final dynamical equilibrium is a chemical equilibrium. The total free energy of the system is

$$\begin{aligned} F^{close} &= \sum_i c_i \mu_i + c_T \mu_T + c_D \mu_D \\ &= k_B T \sum_i c_i \ln \frac{c_i}{c_i^{eq}} + c_T \ln \frac{c_T}{c_T^{eq}} + c_D \ln \frac{c_D}{c_D^{eq}}, \end{aligned}$$

and which always decreases until it reaches to its minimum at equilibrium:

$$\frac{dF^{close}(t)}{dt} = -k_B T \sum_{i>j} (c_i k_{ij} - c_j k_{ji}) \ln \frac{c_i k_{ij}}{c_j k_{ji}} \le 0. \tag{9}$$

The term $f_d^{close} = -dF^{close}(t)/dt$ is called *free energy dissipation rate* [8].

For each conformational state i of the motor protein, the internal entropy $Ts_i^0 = h_i^0 - \mu_i^0$. Thus the entropy of the entire system could be defined as $\tilde{S}^{close} = S^0 + S^{close}$, where $S^0 = \sum_i s_i^0 c_i + s_T^0 c_T + s_D^0 c_D$ and $S^{close} = k_B \left[\sum_i (-c_i \ln c_i) - c_T \ln c_T - c_D \ln c_D\right]$. Then the evolution of entropy becomes

$$\frac{d\tilde{S}^{close}}{dt} = e_p^{close} - \frac{\tilde{h}_d^{close}}{T}, \tag{10}$$

where

$$\begin{aligned} \tilde{h}_d^{close} &= \frac{1}{2} k_B T \sum_{i>j} (c_i k_{ij} - c_j k_{ji})(h_i^0 - h_j^0) \\ &\quad + k_B (c_1 k_{12} - c_2 k_{21})(h_T^0 - h_D^0) \end{aligned}$$

is the heat dissipation, and the *entropy production rate* $T e_p^{close} = f_d^{close}$ [1, 4, 10]. The entropy of the system increases due to entropy generated in spontaneous processes and decreases when heat is expelled into the surrounding.

If one only regards the motor protein as the unique target system, and define $\tilde{S}^{motor} = \sum_i s_i^0 c_i - k_B \sum_i c_i \ln c_i = \tilde{S}^{close} - \tilde{S}^{ATP,ADP}$, then we have

$$\frac{d\tilde{S}^{motor}}{dt} = e_p^{motor} - \frac{\tilde{h}_d^{motor}}{T}, \tag{11}$$

where $e_p^{motor} = e_p^{close}$, and $\tilde{h}_d^{motor} = \tilde{h}_d^{close} + T \cdot \frac{d\tilde{S}^{ATP,ADP}}{dt}$. Here we notice that the definition of entropy as well as entropy production rate is not dependent upon the mechanical details of the environment, but the traditional definition of heat, i.e. $\tilde{h}_d^{close}$, is, which involves the entropy change in the solution resulting from the reaction [6]. One needs to overcome such a non-self-consistence in order to set up a thermodynamic framework solely from the internal dynamics of the target system.

Thermodynamics of nonequilibrium driven system— With the presence of an external regenerating mechanism, the concentrations of ATP and ADP would be kept invariant. The system is not at equilibrium in general [9]. Recall that each μ^0 could be decomposed into $h^0 - Ts^0$, hence for each individual occurrence of the transition $R_i \to R_j$, the heat dissipation is $h_i^0 - h_j^0$ which is not coupled with the regenerating system. However, for the real driven reaction step $ATP + R_1 \rightleftharpoons ADP + R_2$, the total heat dissipation should be $(h_1^0 + \mu_T) - (h_2^0 + \mu_D)$ following the above analysis of the simple example in Fig. 1.

Therefore the heat dissipation rate in such a driven open system is

$$\begin{aligned} \tilde{h}_d^{open}(t) &= k_B T \sum_{i>j} \left(c_i(t) k_{ij} - c_j(t) k_{ji}\right)(h_i^0 - h_j^0) \\ &\quad + k_B T \left(c_1(t) k_{12} - c_2(t) k_{21}\right)(\mu_T - \mu_D) \end{aligned}$$

Furthermore, in the stationary NESS:

$$\begin{aligned} \tilde{h}_d^{ness} &= k_B T \sum_{i>j} \left(c_i^{ss} k_{ij} - c_j^{ss} k_{ji}\right)(\mu_i^0 - \mu_j^0) \\ &\quad + k_B T \left(c_1^{ss} k_{12} - c_2^{ss} k_{21}\right)(\mu_T - \mu_D) \\ &= k_B T \sum_{i>j} \left(c_i^{ss} k_{ij} - c_j^{ss} k_{ji}\right) \ln \frac{k_{ij}}{k_{ji}}. \end{aligned} \tag{12}$$

The rigorous derivation of (12) is based on the fact that in an NESS, its kinetics and thermodynamics can be decomposed into different cycles [1, 4, 10].

For each state i, the internal entropy $Ts_i^0 = h_i^0 - \mu_i^0$. Thus the entropy of the open system could be defined as $\tilde{S}^{open} = S^0 + S^{open}$, where $S^0 = \sum_i s_i^0 c_i$ and $S^{open} = -k_B \sum_i c_i \ln c_i$. Then the evolution of entropy becomes

$$\frac{d\tilde{S}^{open}}{dt} = e_p^{open} - \frac{\tilde{h}_d^{open}}{T}, \tag{13}$$

where $e_p^{open} = k_B \sum_{i>j} (c_i k_{ij} - c_j k_{ji}) \ln \frac{c_i k_{ij}}{c_j k_{ji}}$ is the entropy production rate [1, 4, 10]. The "heat term" $\tilde{h}_d^{motor} (= \tilde{h}_d^{open})$ in Eq. (11) now finally becomes real heat and is completely independent of the any details on the regenerating system.

One could easily notice that the entropy $\tilde{S}^{open} = \tilde{S}^{motor}$, and more important $Te_p^{open} = Te_p^{motor} = Te_p^{close} = f_d^{close}$. This reflects the different perspective of Boltzmann/Gibbs and Prigogine for the traditional Second Law: Gibbs states free energy never increase in a closed, isothermal system; while Prigogine states that the entropy production is non-negative in an open system, which can be defined solely from internal dynamics. They are equivalent.

The free energy of the open system

$$\tilde{F}^{open} = H^0 - T\tilde{S}^{open} = \mu^0 - TS^{open},$$

where $H^0 = \sum_i h_i^0 c_i$ is the enthalpy, and $\mu^0 = \sum_i \mu_i^0 c_i$ is the internal (conditional) free energy of the system. But the evolution of such a free energy function would not always decrease any more, which spurred the discovery of relative entropy (See below).

Efficiency for the chemical energy transduction to mechanical energy — A mechanical system coupled fully reversibly to a chemical reaction system, with a constant force F_{mech} resisting the mechanical movement driven by the chemical gradient, will not alter the value of W_{min}. Rather it reduces the amount of entropy production as well as the heat dissipation when the F_{mech} is small. When the F_{mech} is greater than the stalling force, the entropy production increases again and the mechanical energy is being converted into chemical potential, i.e., the chemical flux is against the chemical potential. This scenario has been realized in the reversely run F_0F_1 ATPase becoming a ATP synthetase [2].

Quantitatively, in the case of chemical to mechanical transduction, the energy conservation in steady state is

$$W_{min} \times J_{c\to m} = \tilde{h}_d^{ness} + P_{mech},$$

where P_{mech} is the mechanical power, and the efficiency $\eta = \frac{P_{mech}}{\tilde{h}_d^{ness} + P_{mech}} \leq 1$. In the opposite direction, the above P_{mech} and $J_{c\to m} < 0$. Hence, $\eta = \frac{W_{min} \times |J_{c\to m}|}{W_{min} \times |J_{c\to m}| + \tilde{h}_d^{ness}} \leq 1$. Note that in NESS, $T \cdot e_p^{ness} = \tilde{h}_d^{ness}$, hence we conclude that whether the energy transduction is chemical to mechanical or the opposite, the entropy production is always equal to the total heat "dissipation", which is nonnegative resulting in a less than 100% efficiency. Although such an expression of energy transduction efficiency has been used in many previous works [11], its physical meaning becomes more clear now.

On the other hand, the reversal of chemomechanical energy transduction would not occur if the coupling is not fully reversible. For example, a load from viscous drag force. The direction of the force is always against the stochastic flux that generates movements.

Relative entropy and housekeeping heat in nonequilibrium open driven system — So far, based on existing classical thermodynamics, we have obtained a self-consistent picture for the nonequilibrium driven system. In fact, one can see a distinction between Clausius' and Kelvin's historical statements on the 2nd law: The former is about the spontaneity of a transient process, i.e. the non-negativity of f_d^{close}, while the latter is about a cyclic process with non-negative e_p^{open} in a NESS.

Recently, a more general nonequilibrium thermodynamic theory has been put forward for Markov processes including master equation systems [8]. For an open, driven system, one has the relative entropy [8, 10]

$$H\left(\{c_i\} \| \{c_i^{ness}\}\right) = k_B T \sum_i c_i \ln \left(c_i / c_i^{ness}\right), \tag{14}$$

where c_i^{ness} is the steady state concentration of state i. Interestingly, several new mathematical inequalities have been obtained [8]: $H\left(\{c_i\} \| \{c_i^{ness}\}\right) \geq 0$; its time derivative

$$f_d^{open} = -\frac{d}{dt} H\left(\{c_i(t)\} \| \{c_i^{ness}\}\right) \geq 0; \tag{15}$$

and a decomposition $f_d^{open} = Te_p^{open} - Q_{hk}$ in which Q_{hk} is called *housekeeping heat* [8, 12]:

$$Q_{hk}(t) = k_B T \sum_{i>j} (c_i k_{ij} - c_j k_{ji}) \ln \left(\frac{c_i^{ness} k_{ij}}{c_j^{ness} k_{ji}} \right) \geq 0. \tag{16}$$

The novel mathematical results (15) and (16) beg for a thermodynamics interpretations in the simple example of motor protein. In the NESS perspective, the heat dissipation for the transition $i \to j$ is $Q_{ij} = k_B T \ln (k_{ij}/k_{ji}) + T(s_i^0 - s_j^0)$ no matter coupled with the driving force or not; and meanwhile, the steady-state entropy also could be defined along a stochastic trajectory [13] as $\Delta S_{ij} = k_B \ln \left(c_i^{ness}/c_j^{ness}\right) + (s_j^0 - s_i^0)$ [14].

Therefore, the Q_{hk} in (16) is just ensemble averaged summation of ΔS_{ij} and Q_{ij}. Housekeeping heat is really the driven characteristic of the system. For master equation with detailed balance, which correspond to closed system, $Q_{hk} = 0$ and $T\Delta S_{ij} + Q_{ij} = 0$, which matches the classic definition of equilibrium entropy difference through a reversible process. In this case, the H in (14) is precisely the free energy deviation from the equilibrium [15], and then Eq. (15) is reduced to (9), with $f_d^{close} = Te_p^{close}$.

Traditional and extended Second Law of thermodynamics — Due to the evolution of entropy (13) and the nonnegativity of entropy production rate, the traditional Second Law reads

$$\frac{d\tilde{S}^{open}}{dt} \geq -\frac{\tilde{h}_d^{open}}{T}.$$

One can further rewrite (13) as

$$\frac{d\tilde{S}^{open}}{dt} = (e_p^{open} - \frac{Q_{hk}}{T}) - \frac{\tilde{h}_d^{open} - Q_{hk}}{T} = \frac{f_d^{open}}{T} - \frac{Q_{ex}}{T},$$

where the excess heat Q_{ex} is the difference between $\tilde{h}_d^{open}$ and Q_{hk} [8]. Therefore, an extended Second Law emerges [8]

$$\frac{d\tilde{S}^{open}}{dt} \geq -\frac{Q_{ex}}{T}.$$

It is different from and stronger than the traditional Second Law, only for really driven system with $Q_{hk} > 0$.

Summary and discussion — Is there anything beyond Clausius/Boltzmann's notion about the Second Law of Thermodynamics? If we regard the entropy production e_p as the total entropy increase of the isolated "universe" and h_d as the entropy change of the medium, then the equation from Prigogine $dS = e_p - \frac{h_d}{T}$ is nothing but a restatement of the entropy increase principle of any isolated system. It is somehow true, but not exact. The most important contribution of Prigogine's NESS perspective is trying to build a self-consistent thermodynamics solely in terms of the internal dynamics of open driven system. It is also the motivation of the present article.

A real driven system is referred to a physical or biological system with a *sustained* source and sink with chemical potential difference. But fundamental physics considers such a setup only approximate: In an absolute sense, the source and sink has to be slowly delay toward its own equilibrium (QSS). Therefore, it is generally believed that if one includes all the relevant part of "environment" into an enlarged system with detailed balance, then the NESS perspective would disappear. However, such a physical argument begs a resolution on the mathematical level for the analysis. If one considers (a) NESS and QSS as two different perspectives of a same system; then it is surprising that they have different heat dissipation; if (b) one considers them as different systems, then it is even more surprising their dynamics and free energy accounting are identical. We believe this is very much a similar problem faced Gibbs when he developed his different ensemble theories for the *equation of state*: Whether one consider canonical and isobaric ensembles same or different, the important issue is that they *both* give same macroscopic thermodynamic relations; but they give different heat capacity: C_v and C_p.

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