Conditional entropic approach to nonequilibrium systems with weak fluctuation correlation

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\textbf{Abstract:} A conditional entropic approach is discussed for nonequilibrium complex systems with a weak correlation between spatiotemporally fluctuating quantities on a large time scale. The weak correlation is found to constitute the fluctuation distribution that maximizes the entropy associated with the conditional fluctuations. The approach is illustrated in diffusion phenomenon of proteins inside bacteria.

\textbf{Keywords:} weak correlation; conditional entropy; protein diffusion in bacteria
1. Introduction

Consider a nonequilibrium complex system divided into a lot of small spatial regions or “blocks”, each of which is in a local equilibrium state characterized by dynamics of two different fluctuating quantities (e.g., the local temperature). The time scale of these dynamics is much larger than that of a typical local dynamics (e.g., the one of a random walker). Denoting random variables by \( x \) and \( y \), which express two such quantities, the joint probability distribution is given here by \( g(x, y) = g(x \mid y)f(y) \), where \( g(x \mid y) \) is the conditional distribution describing the probability of \( x \), given a value of \( y \), and \( f(y) \) is the marginal distribution describing the probability of \( y \). The conditional entropy associated with \( g(x \mid y) \) at a given value of \( y \), say \( y_0 \), is then as follows:

\[
S[g] = -\int dxg(x \mid y_0)\ln g(x \mid y_0),
\]

which is of the form of the Shannon entropy [1].

In recent years, various discussions have been developed about using the maximum entropy principle [2] for describing nonequilibrium complex systems organized hierarchically by different dynamics on largely-separated time scales, e.g., as in Refs. [3-10]. There, the joint entropy concerning both the fast variable and the slow variable or the marginal entropy relevant to the slow one has been treated as the quantity to be maximized, for example. Such a direction seems to be pertinent due to the existence of the time-scale separation.

Motivated by a recent work in Ref. [11] (see also Ref. [12]), suppose that \( x \) and \( y \) are not fully statistically independent, the notion of which is referred to as weak correlation between \( x \) and \( y \). To realize this, write the conditional distribution as \( g(x \mid y) = e^{h(x \mid y)} \), where \( h(x \mid y) \) is a suitable function and is approximately constant in terms of \( y \) in the sense that it can be expanded around at \( y = y_0 \), with \( y_0 \) being the
average value of $y$, up to the first order of $y - y_0$: $h(x \mid y) \equiv h_0(x) + h_1(x)(y - y_0)$ with $h_0(x) = h(x \mid y_0)$ and $h_1(x) = h'(x \mid y_0)$, where the prime denotes differentiation with respect to $y$. $h_1(x)$ should be small but still finite so that this expansion is valid in the whole range of $y$. Thus, the conditional distribution is found to be

$$g(x \mid y) \sim g(x \mid y_0)\exp[(y - y_0)h_1(x)],$$

(2)

which offers the marginal distribution $g(x) = \int dy g(x, y)$ given by

$$g(x) \sim g(x \mid y_0) \exp[-y_0h_1(x)]\int dy f(y)\exp[h_1(x)y].$$

(3)

As shown in Refs. [11,12], the existence of the weak correlation is essential for describing the marginal distribution (see Section 3).

In this article, we discuss a conditional entropic approach to nonequilibrium complex systems with the weak correlation between different fluctuations on a large time scale. Such a weak correlation is shown to constitute the conditional distribution $g(x \mid y_0)$, maximizing the entropy associated with the conditional fluctuations. We also illustrate the approach in diffusion phenomenon of histonelike nucleoid-structuring proteins (known as DNA-binding proteins) inside living *Escherichia coli* bacteria.

2. Maximization of conditional entropy and weak correlation

Clearly, the behavior of the conditional distribution on the left-hand side of Eq. (2) is dominantly determined by $g(x \mid y_0)$. In what follows, we show that $g(x \mid y_0)$ is
realized in terms of the weak correlation \( h_1(x) \), which is meant in the sense that the \( x \)
dependence of \( h_0(x) \) comes only from \( h_1(x) \) itself except possible additional quantities
irrelevant to the weak correlation, if the maximization of the conditional entropy in Eq.
(1) is considered. It is noticed that such a realization is not necessarily the case at the stage
of Eq. (2), in general.

Under the assumption that \( h_1(x) \) is given, the normalizability of \( g(x \mid y) \) requires
the conditional distribution to satisfy the following condition:

\[
\int dx \, g(x \mid y_0) h_1(x) = 0, \tag{4}
\]

where the expansion of the exponential factor in Eq. (2) up to the first order of \( h_1(x) \) as
well as the normalization condition on \( g(x \mid y_0) \) has been taken into account. Therefore,
together with a possible constraint on the average of a certain quantity, \( Q(x) \), i.e.,
\[
\int dx \, g(x \mid y_0) Q(x) = \bar{Q}, \tag{5}
\]
and further constraints if any), the maximization of the
conditional entropy in Eq. (1) reads

\[
\delta_s \left\{ S[g] - \lambda \left( \int dx \, g(x \mid y_0) - 1 \right) + \sigma \left( \int dx \, g(x \mid y_0) h_1(x) - 0 \right) + \kappa \left( \int dx \, g(x \mid y_0) Q(x) - \bar{Q} \right) \right\} = 0,
\]

where \( \lambda, \sigma, \) and \( \kappa \) are the set of the Lagrange multipliers concerning the constraints
relevant to the normalization condition, the weak correlation, and the average value,
respectively, and \( \delta_s \) stands for the variation with respect to \( g(x \mid y_0) \). The stationary
solution of Eq. (5) is given by
\[ 
\hat{g}(x \mid y_0) \propto \exp[\sigma h_1(x) + \kappa Q(x)], 
\]

which in fact shows that the conditional distribution at \( y = y_0 \) is realized by the weak correlation, highlighting its novel aspect. Later, the crucial importance of fluctuation distributions will be mentioned, [see the discussion after Eq. (15) below].

A point to be emphasized here is that in contrast to the works [3-10] mentioned earlier, the quantity to be maximized is the conditional entropy associated with the slowly fluctuating variable, recalling the dominant role of \( g(x \mid y_0) \) in Eq. (2).

3. **Protein diffusion in bacteria**

We here illustrate our approach of maximum conditional-entropy principle in the diffusion of histonelike nucleoid-structuring proteins inside living *Escherichia coli* bacteria observed in a recent experiment in Ref. [13] (see also Ref. [14]). Below, we will see that \( x \) and \( y \) correspond to describe the diffusion-exponent fluctuations and the temperature fluctuations, respectively.

The proteins distributed over the bacteria exhibit a highly heterogeneous diffusion in the sense that at the level of individual trajectories, the mean square displacement of a given protein scales for elapsed time, \( t \), as

\[ 
\Delta x^2 \sim D_\alpha t^\alpha. 
\]

where \( D_\alpha \) is the diffusion coefficient and the distribution of its dimensionless numerical values obeys asymptotically the following power law
\[ \varphi(D_\alpha) \sim D_\alpha^{-\gamma-1} \]  

with \( \gamma \approx 0.97 \), whereas the diffusion exponent, \( \alpha \), follows a non-trivial broad distribution in the range \( 0 \leq \alpha \leq 2 \). Regarding the latter, the case with \( \alpha \neq 1 \) \( (\alpha > 0) \) is called anomalous diffusion [15], which is under vital investigation in the literature (see, e.g., Refs. [16-18] for recent reviews). It is noted that for small elapsed time, only normal diffusion, i.e., \( \alpha = 1 \), has been observed, for which the distribution of the diffusion coefficient, \( D \), decays as a power law, \( \varphi(D) \sim D^{-\mu} \) with \( \mu \approx 1.9 \).

In the experiment, the analysis of the mean square displacement in an ensemble average (i.e., an average of square displacement over all of the individual trajectories) has yielded both an average diffusion coefficient and an average diffusion exponent. What is remarkable there is the fact [13] that the former increases significantly, whereas the latter increases only slightly, with respect to the cell age (or, equivalently cell length).

In Ref. [11], based on these experimental facts and the assumption of the Einstein relation [19], i.e., \( D \propto 1/\beta \) with the inverse temperature, \( \beta \equiv 1/(k_B T) \), where \( k_B \) is the Boltzmann constant, the concept of the weak correlation between the diffusion-exponent fluctuations and the temperature fluctuations has been introduced.

Therefore, in the present case, \( x \) and \( y \) correspond to \( \alpha \) and \( \beta \), respectively.

We shall see this point in detail. According to Ref. [11], in consistent with the power-law nature of the diffusion coefficient, the following \( \chi^2 \) distribution has been proposed for the temperature fluctuations [20]:

\[
f(\beta) = \frac{1}{\Gamma(\mu)} \left( \frac{\mu}{\beta_0} \right)^\mu \beta^{\mu-1} \exp \left( -\frac{\mu \beta}{\beta_0} \right),
\]  

(9)
where \( \beta_0 \) is the average value of \( \beta \in (0, \infty) \) and \( \Gamma(\mu) \) is the Euler gamma function. Also, with the following relation assumed like the Einstein relation, which seems to be experimentally supported [11], (see also Ref. [21])

\[
D_\alpha = D_{\alpha, \beta} \sim \frac{c}{s^\alpha \beta}.
\]  

(10)

where \( s \) is a typical time characterizing displacement of the protein and \( c \) is a positive constant, the form of an inverse gamma distribution has been suggested for the dimensionless numerical values of \( D_\alpha \), given a value of \( \beta \), as an explicit form of \( \varphi(D_\alpha) \), in consistent again with the power-law nature. This distribution gives the conditional distribution obtained by \( g(\alpha | \beta) = |\partial D_{\alpha, \beta} / \partial \alpha | \varphi(D_\alpha) \) in the range \( 0 \leq \alpha \leq 2 \), which behaves as

\[
g(\alpha | \beta) \propto s^{\gamma \alpha} \exp\left[ -\frac{\gamma a(\beta)}{c} s^\alpha \right]
\]  

(11)

with \( a(\beta) \) being a positive quantity that can be expanded as \( a(\beta) \equiv a_0 + a_1 (\beta - \beta_0) \) with \( a_0 \equiv a(\beta_0) \) and \( a_1 \equiv a'(\beta_0) \): \( a_1 \) is small to realize the weakness of correlation and is required to be negative in conformity with the cell-age dependence mentioned above [11]. Accordingly, \( h_i(\alpha) \) takes the following form:

\[
h_i(\alpha) = \frac{\gamma a_1}{c} \left( \left\langle s^\alpha \right\rangle_\alpha - s^\alpha \right),
\]  

(12)
where \( \langle \cdot \rangle_{\alpha} \) stands for the average with respect to \( g(\alpha \mid \beta_0) \) over \( \alpha \in [0, 2] \). With Eqs. (9), (11), and (12), the marginal distribution \( g(\alpha) \) is found to be given by

\[
g(\alpha) \sim g(\alpha \mid \beta_0) \frac{\exp[-\beta_0 h_1(\alpha)]}{[1-(\beta_0/\mu) h_1(\alpha)]^{\mu}} \tag{13}
\]

with \( 1-(\beta_0/\mu) h_1(\alpha) > 0 \) in a good agreement with the experimental data (see Fig. 2 in Ref. [11]). In Ref. [12], it has quantitatively been examined how largely the conditional distribution is modulated by the weak correlation.

Therefore, taking the diffusion exponent \( \alpha \) as the quantity \( Q \), from Eqs. (6) and (12), we obtain the following conditional distribution:

\[
\hat{g}(\alpha \mid \beta_0) \propto \exp[\sigma h_1(\alpha) + \kappa \alpha]. \tag{14}
\]

This becomes identical to \( g(\alpha \mid \beta_0) \) in Eq. (11) after the following choices are made:

\[
\sigma = \frac{a_0}{a_1}, \quad \kappa = \gamma \ln s, \tag{15}
\]

where it is understood that all quantities are dimensionless. It is obvious that the condition in Eq. (4) is indeed fulfilled by Eq. (14) with Eq. (15).

Thus, we see that the weak correlation governs the conditional distribution in the present case of the protein diffusion in bacteria.
We wish to mention several works, in which the statistical property of fluctuations is of crucial importance for describing the displacement distribution. In Ref. [11], it has been shown, in view of so-called superstatistics [22], which is a “statistics of statistics” with two largely-separated time scales, that the temperature fluctuation distribution in Eq. (9) has successfully led to $q$-Gaussian distribution [23] (also called a Pearson-type VII distribution [24]), which decays as a power law, observed experimentally for displacements of the proteins [13] (see Fig. 4 in Ref. [11]): the fluctuation distribution is superstatistically incorporated into a process of fractional Brownian motion [25,26] that offers a unified description of anomalous diffusion as well as normal diffusion based on a fractional operator [27] (see Ref. [28] for a recent development about modelling anomalous diffusion toward such a direction). Thus, the conditional distribution in Eq. (11) should play a central role for describing the displacement distribution on a sufficiently long time scale, for which it is nonnegligible as discussed in Ref. [11]. The non-Gaussian diffusion has also been found to emerge from superstatistical frameworks with the distribution of the diffusion-coefficient/size fluctuations [29-32] or that of the diffusion-exponent fluctuations [33,34] (see also, e.g., Refs. [35-37]).

Finally, we point out the following. Fluctuations have experimentally been observed in other biological systems, e.g., as in Refs. [38-41]. The influence of protein conformational fluctuation to fluctuating diffusivity has been studied in Ref. [42]. In addition, a recent experimental work in Ref. [43] has reported a mild dependence of the diffusion exponent of telomeres in cells on temperature at the statistical level. This fact may imply the existence of the weak correlation between their fluctuations.

4. Concluding remarks

We have developed a conditional entropic approach to nonequilibrium complex systems with the weak correlation between slowly fluctuating quantities. Maximizing the conditional entropy associated with such fluctuations, we have shown that the conditional fluctuation distribution is realized in terms of the weak correlation. We have also demonstrated the present approach for diffusion of histonelike nucleoid-structuring proteins in living *Escherichia coli* bacteria.
We make some comments on relevant issues. It may be of interest to examine, in the present context, the deviation of the fluctuation distribution from its reference distribution [44] and a formal analogy of diffusivity fluctuations to thermodynamics [45], both of which are based on an entropic approach. A discussion has been made about (non-)Markovianity of the diffusion process that takes into account the diffusion-exponent fluctuations, for which the case of virus capsids in cells is treated [46]. In this respect, a recent experimental result about virus capsids in Ref. [47] is intriguing, where heterogeneous diffusion has been observed.

Acknowledgment

This work has been supported in part by a Grant-in-Aid for Scientific Research from the Japan Society for the Promotion of Science (No. 21K03394).

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