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Uncertainty of the second order

Quasispecies model with inverse Bayesian inference

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Abstract We study the stochastic dynamics of the quasispecies model with inverse Bayesian inference under environmental uncertainty. Inverse Bayesian inference is introduced through the correspondence between Bayesian inference and the replicator equation. We consider environmental uncertainty that is not modeled as the stochastic fitness called uncertainty of the second order. This is in contrast to uncertainty of the first order that can be subsumed by the stochastic fitness. The difference between these two kinds of uncertainty is discussed in the framework of categorical Bayesian probability theory. We analytically show that if the time-scale of inverse Bayesian inference is sufficiently larger than that of Bayesian inference, then the quasispecies model exhibits a noise-induced transition. The theoretical result is verified by numerical simulation.

Keywords Bayesian inference · replicator equation · quasispecies model · category theory · Fokker-Planck equation · noise-induced transition

1 Introduction

According to Bayesian coding hypothesis of cognitive processes, brains encode perceptual information about uncertain environment by probability distributions and use them to perform an approximately Bayes-optimal cognitive computation [10,4]. Inverse Bayesian inference proposed by Arecchi [1] is a process that compensates Bayesian inference by updating the stochastic model in Bayesian inference which usually remains unchanged. It is based on Pöppel's complementary model of temporal perception [13,14]: There exists a content-independent temporal window of a few seconds constituting "subjective present" within which the identity of a perception is produced and maintained. Beyond that temporal window, perceptual changes are allowed. In Arecchi's theory, perception formation based on synchronization of neuronal activity called apprehension corresponds to Bayesian inference, while judgment formation based on comparison among multiple apprehension processes encoded on a language corresponds to inverse Bayesian inference. It is argued that the latter is responsible for creative processes [1]. However, the original presentation of inverse Bayesian inference theory by Arecchi himself is rather informal and has room for interpretation. Gunji et al. [7,6] proposed several mathematical models of inverse Bayesian inference and investigated their behavior by mainly numerical simulation. However, its mathematical nature is still obscure.

In this paper, we reformulate inverse Bayesian inference in its simplest form and study its dynamics theoretically. In particular, we introduce inverse Bayesian inference to the quasispecies model [3] through the correspondence between Bayesian inference and the replicator equation [8] where stochastic models correspond to fitness. The dynamical behavior of the quasispecies model equipped with inverse Bayesian inference under environmental uncertainty is investigated. Environmental uncertainty can be conceived at two different levels. If it is modeled as the stochastic fitness, namely, if it is subsumed by the stochastic model of Bayesian inference, we call it uncertainty of the first order. Otherwise, it is called uncertainty of the second order. It will be shown that if environmental uncertainty is of the second order and if the time-scale of inverse Bayesian inference

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is sufficiently larger than that of Bayesian inference, the quasispecies model exhibits a noise-induced transition. We reveal the mechanism of the transition by deriving and solving the Fokker-Planck equation governing the time evolution of the density of individuals when the number of replicating units is two. Our theory is verified by numerical simulation.

2 Model

In Bayesian inference, knowledge about the world is updated by repeatedly replacing the prior probability $P(h)$ of the hypothesis h by the posterior probability $P(h|d)$ given the data d. The posterior probability is computed by the following Bayes' theorem:

$$P(h|d) = \frac{P(d|h)P(h)}{P(d)}, \tag{1}$$

where $P(d|h)$ is the stochastic model, namely, the conditional probability that the data d is observed given the hypothesis h and $P(d) = \sum_h P(d|h)P(h)$ is the marginal likelihood.

Inverse Bayesian inference described in [1] can be summarized as follows: First, a hypothesis h^* with the maximum posterior probability is selected after Bayesian inference. The value of the maximum posterior probability is denoted by $P(h^*)$. Next, the left-hand side of Eq. (1) is replaced by $P(h^*)$. If it is solved for $P(d|h)$, then we obtain an update equation for the stochastic model

$$P(d|h) = \frac{P(h^*)P(d)}{P(h)}. \tag{2}$$

However, it is difficult to study inverse Bayesian inference mathematically in the form originally proposed by Arecchi [1]. First, since $P(d|h)$ is not necessarily normalized, namely, $\sum_d P(d|h) \neq 1$ for $h \neq h^*$ in general, a normalization procedure should be introduced. Second, it is obscure whether Eq. (2) is applied to all h or those satisfying certain conditions. Finally, although inverse Bayesian inference is supposed to work in a larger time-scale than that of Bayesian inference, Eq. (2) does not involve such time-scale separation. The first and second problems are caused by the assumption that h^* is selected between Bayesian inference and inverse Bayesian inference. In this paper, we abandon the selection of h^* to avoid these problems and consider a simple form of inverse Bayesian inference: Eq. (1) is just solved for $P(d|h)$. Of course, other formulations are possible. For example, Gunji et al. [6] proposed a different formulation avoiding these three problems: Inverse Bayesian inference was implemented by replacing the least optimal hypothesis with an empirical probability of data. The first and second problems are avoided by the definition of this scheme. The third problem is resolved because replacement of the least optimal hypothesis has little influence on the choice of the most optimal hypothesis when a given data time series is stationary. It works at a longer time scale than Bayesian inference. It was numerically shown that when there is an abrupt change in statistics of the data, this form of inverse Bayesian inference can adapt to the change efficiently [6]. However, its mathematical analysis seems to be difficult since its concrete implementation needs some *ad hoc* assumptions. Here, we focus on a simplified setting where a systematic mathematical analysis is feasible.

Let us rewrite Eq. (1) as

$$P_{t+1}(h) = \frac{P_t(d|h)P_t(h)}{P_t(d)} \tag{3}$$

where subscript t denotes time step. The update equation representing inverse Bayesian inference in the sense of this paper is

$$P_{t+1}(d|h) = \frac{P_{t+1}(h)P_t(d)}{P_t(h)} = P_t(d|h). \tag{4}$$

This just manifests the time-invariance of the stochastic model. However, if the environmental uncertainty is conceived as that of second order, a non-trivial change of inference dynamics occurs as we show below. To fix the third problem, we will introduce a parameter controlling the time-scale of inverse Bayesian inference relative to that of Bayesian inference.

The replicator equation is a basic equation for evolutionary dynamics of organisms [12]. Let us consider a population consisting of N replicating units such as genotypes or phenotypes. We denote the density of individuals of type i by x_i ($x_i \geq 0$, $\sum_{i=1}^N x_i = 1$) and put $\boldsymbol{x} = (x_1, x_2, \ldots, x_N)$. The discrete from of the replicator equation is defined by

$$x_i' = \frac{f_i x_i}{\overline{f}(\boldsymbol{x})}, \tag{5}$$

where f_i is the fitness of type i. In general, f_i is a function of $\boldsymbol{x}$. However, we only consider the case when f_i does not depend on $\boldsymbol{x}$ for simplicity. $\overline{f}(\boldsymbol{x}) = \sum_{i=1}^N f_i x_i$ is the mean fitness. x_i' is the density of type i at the next generation. If mutation between types is introduced, then Eq. (5) becomes the quasispecies model [3]. Let q_{ij} be the mutation probability from type j to type i, then the discrete form of the quasispecies model is defined by

$$x_i(t+1) = \frac{\sum_{j=1}^N q_{ij} f_j x_j(t)}{\overline{f}(\boldsymbol{x}(t))}, \tag{6}$$

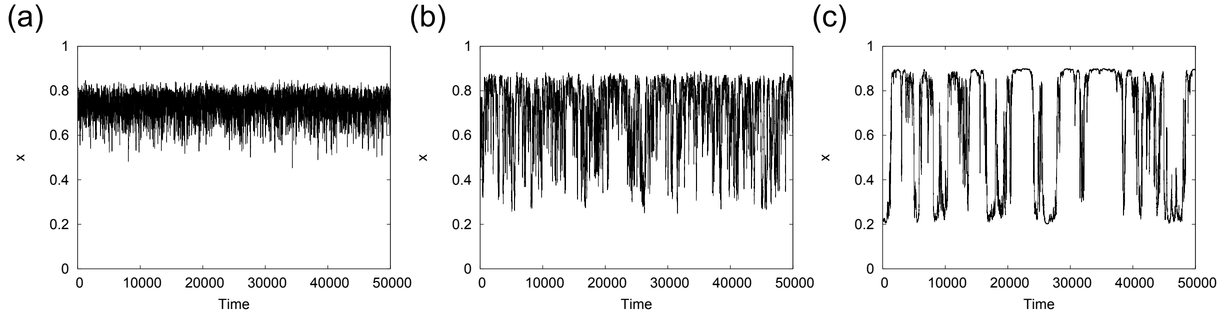

Fig. 1 Time evolution of x. (a) $\alpha = 0.900$, (b) $\alpha = 0.990$ and (c) $\alpha = 0.999$. The values of other parameters are $a = 0.9$, $b = 0.2$, $\overline{r} = \ln 1.2$ and $\sigma^2 = 0.005$.

Table 1 Correspondence between Bayesian inference (1) and the replicator equation (5).

Bayesian Inference	Replicator Equation
Prior Probability $P(h)$	State x_i
Stochastic Model $P(d\|h)$	Fitness f_i
Marginal Likelihood $P(d)$	Mean Fitness $\overline{f}(\boldsymbol{x})$
Posterior Probability $P(h\|d)$	State x_i'

where generation is denoted by t and $x_i(t)$ is the density of type i at generation t.

Harper [8] pointed out the correspondence between Bayesian inference and the replicator equation shown in **Table** 1. Indeed, the former can be seen as a special case of the latter when the fitness is allowed to change stochastically [15]. Uncertainty of environment yielding the stochastic change is modeled by the stochastic model (= the fitness). This kind of uncertainty is called *uncertainty of the first order.* However, it is not necessarily that environmental uncertainty can be always captured by stochastic models. Such unmodeled uncertainty is called *uncertainty of the second order.* If we only consider Bayesian inference, then which perspective we take does not affect the dynamics of $\boldsymbol{x}$. However, in the following, it will be shown that if we introduce inverse Bayesian inference into the quasispecies model through the correspondence in **Table** 1, then a qualitative change can occur in the stochastic dynamics of $\boldsymbol{x}$.

First, we consider the case when environmental uncertainty is conceived as that of the first order. In this case, f_i in the replicator equation is a stochastic variable. By inverse Bayesian inference expressed as Eq. (4), f_i is time-invariant. As one of the simplest cases, let us consider

$$f_i(t) = e^{\overline{r}_i + \xi_i(t)}. \qquad (7)$$

Here, $\overline{r}_i$ is the average of the logarithm of the fitness $f_i(t)$. We assume that $\xi_i(t) \sim N(0, \sigma_i^2)$ and $\xi_i(t)$ and $\xi_j(t')$ are independent for all $t \neq t'$ and all i, j.

Next, let us regard environmental uncertainty as that of the second order. In this case, it is external to the fitness(= the stochastic model). The replicator equation now becomes

$$x_i(t+1) = \frac{e^{\xi_i(t)} f_i(t) x_i(t)}{\tilde{f}(\boldsymbol{x}(t))}, \qquad (8)$$

where $\tilde{f}(\boldsymbol{x}(t)) = \sum_{j=1}^{N} e^{\xi_j(t)} f_j(t) x_j(t)$.

By putting $P_{t+1}(d|h) = f_i(t+1)$, $P_{t+1}(h) = x_i(t+1)$, $P_t(h) = x_i(t)$ and $P_t(d) = \tilde{f}(\boldsymbol{x}(t))$ in Eq. (4), we obtain

$$f_i(t+1) = \frac{x_i(t+1)\tilde{f}(\boldsymbol{x}(t))}{x_i(t)} = f_i(t) e^{\xi_i(t)}. \qquad (9)$$

This is the inverse Bayesian inference counterpart of the replicator equation under environmental uncertainty of the second order.

The difference between uncertainty of the first order and that of the second order can be made clearer when they are interpreted in categorical Bayesian probability theory [2]. In categorical Bayesian probability theory, one works with a category $\mathcal{P}$ whose objects are certain measurable spaces and whose morphisms are conditional probabilities between them. Modeling environmental uncertainty as that of the first order corresponds to extending a measurable space to a larger one. On the other hand, uncertainty of the second order can be regarded as introducing a stochastic transformation on the set of conditional probabilities. Let H be the set of hypotheses and D the set of data. For simplicity, let us consider the case when both H and D are finite sets. The set of morphisms from H to D is denoted by $\mathcal{P}(H, D)$. Then, a morphism in $\mathcal{P}$ is just a $|D| \times |H|$ stochastic matrix. In regard to the replicator equation, $H = \{1, 2, \ldots, N\}$ and D is a singleton set $\{\bullet\}$. The latter expresses a static environment. $\mathcal{P}(H, D)$ should

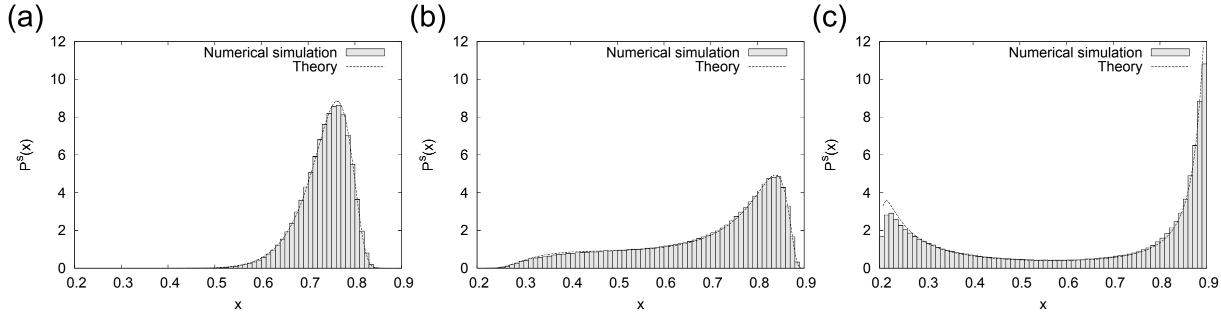

Fig. 2 Stationary probability distribution of x. The theoretical line (18) and the result of numerical simulation are compared. (a) $\alpha = 0.900$, (b) $\alpha = 0.990$ and (c) $\alpha = 0.999$. The values of other parameters are the same as those in **Fig.** 1. The numerical probability distributions were obtained from the frequency of x over 2^{20} time steps after discarding initial 10000 time steps in a single trial from a random initial condition.

be extended to the set of non-negative matrices which is denoted by $\widetilde{\mathcal{P}}(H, D)$ since the fitness is not normalized. The N-tuple of fitness $\boldsymbol{f} = (f_1, f_2, \ldots, f_N)$ constitutes a morphism from H to D. The fitness f_i is the "conditional probability" given i. Let us extend D to a larger set E, where E is the set of different environments. A morphism from H to E is a non-negative matrix $F := (f_{ei})_{e\in E,\ i\in H}$ where f_{ei} is the fitness of i in environment e. F is the stochastic fitness resulting from uncertainty of the first order. On the other hand, uncertainty of the second order can be expressed as a stochastic transformation $U : \widetilde{\mathcal{P}}(H, D) \to \widetilde{\mathcal{P}}(H, D)$. In the above case considered for the replicator equation, $U[\boldsymbol{f}(t)] = \left(f_i(t)e^{\xi_i(t)}\right)_{1\le i\le N}$. If U is combined with inverse Bayesian inference (4), it yields Eq. (9): $\boldsymbol{f}(t+1) = U[\boldsymbol{f}(t)]$. Note that D remains a singleton set. In summary, uncertainty of the first order operates at the object level, but that of the second order does at the morphism level.

In order to discuss the time-scale of inverse Bayesian inference relative to that of Bayesian inference, we extend Eq. (9) as follows:

$$f_i(t+1) = \left(f_i(t)e^{\xi_i(t)}\right)^{\alpha} f_i(0)^{1-\alpha}, \tag{10}$$

where $0 \le \alpha \le 1$. $\alpha = 1$ recovers Eq. (9) and $f_i(t) = f_i(0)$ when $\alpha = 0$. If we put $\overline{r}_i := \ln f_i(0)$ when $\alpha = 0$, Eq. (8) becomes the replicator equation under environmental uncertainty of the first order.

Let $r_i(t) := \ln f_i(t)$. Then, Eq. (10) is

$$r_i(t+1) = \alpha r_i(t) + (1-\alpha)\overline{r}_i + \alpha\xi_i(t). \tag{11}$$

Thus, $r_i(t)$ is an AR(1) process with mean $\overline{r}_i$ and variance $\alpha^2\sigma_i^2/(1-\alpha^2)$ for $\alpha < 1$. Its characteristic time-scale is $\tau = -1/\ln\alpha$.

We can introduce inverse Bayesian inference into the quasispecies model in the same way. $x_i(t+1)$ is replaced by the i-th element of vector $Q^{-1}\boldsymbol{x}(t+1)$ in Eq. (9). Here, $Q = (q_{ij})$ is the mutation matrix and we assume that its inverse Q^{-1} exists. Q^{-1} always exists when the non-diagonal elements of Q are sufficiently small. The resulting equation governing time evolution of r_i is the same as that for the replicator equation. In summary, equation of the quasispecies model with inverse Bayesian inference is

$$x_i(t+1) = \frac{\sum_{j=1}^{N} q_{ij}e^{\overline{r}_j+\xi_j(t)}x_j(t)}{\sum_{j=1}^{N} e^{\overline{r}_j+\xi_j(t)}x_j(t)} \tag{12}$$

under environmental uncertainty of the first order and

$$x_i(t+1) = \frac{\sum_{j=1}^{N} q_{ij}e^{r_j(t)+\xi_j(t)}x_j(t)}{\sum_{j=1}^{N} e^{r_j(t)+\xi_j(t)}x_j(t)}, \tag{13}$$

$$r_i(t+1) = \alpha r_i(t) + (1-\alpha)\overline{r}_i + \alpha\xi_i(t) \tag{14}$$

under environmental uncertainty of the second order.

3 Results

In this section we study dynamical behavior of Eqs. (13) and (14) when $N = 2$. Since $\sum_{i=1}^{N} x_i(t) = 1$ holds for the quasispecies model Eq. (6) due to $\sum_{i=1}^{N} q_{ij} = 1$, Eqs. (13) and (14) can be simplified as follows. If we put $x := x_1$, then $x_2 = 1 - x$. Let $q_{11} = a$ and $q_{12} = b$ $(0 < b < a < 1)$. Note that the other components of the mutation matrix Q are given by $q_{21} = 1 - q_{11} = 1 - a$ and $q_{22} = 1 - q_{12} = 1 - b$. Let $r(t) := r_1(t) - r_2(t)$ and $\overline{r} := \overline{r}_1 - \overline{r}_2$. We can assume $\overline{r} \ge 0$ without loss of generality. For $\xi(t) := \xi_1(t) - \xi_2(t)$ and $\sigma^2 := \sigma_1^2 + \sigma_2^2$, $\xi(t) \sim N(0, \sigma^2)$ holds. From these notations, Eqs. (13) and (14) when $N = 2$ reduce to

$$x(t+1) = \frac{ae^{r(t)+\xi(t)}x(t) + b(1-x(t))}{e^{r(t)+\xi(t)}x(t) + (1-x(t))}, \tag{15}$$

$$r(t+1) = \alpha r(t) + (1-\alpha)\overline{r} + \alpha\xi(t). \tag{16}$$

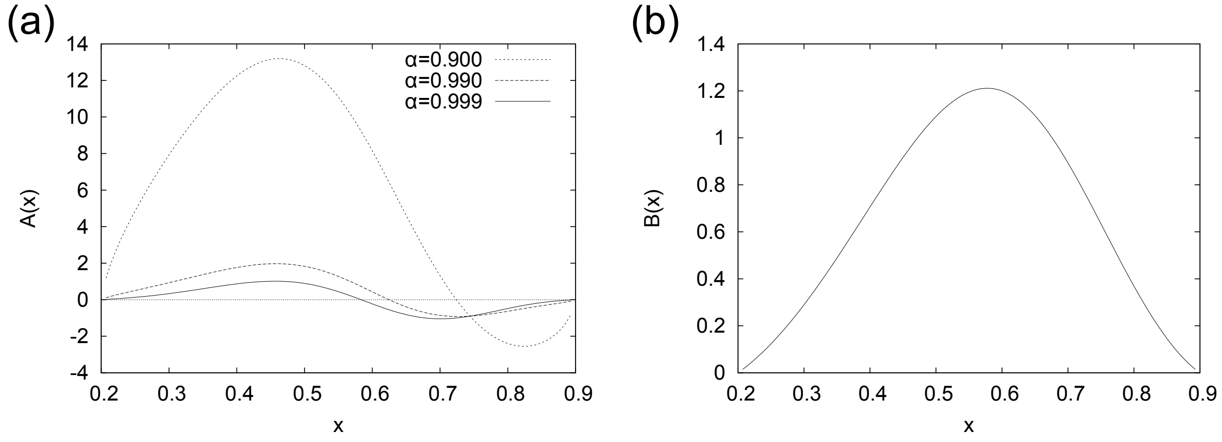

Fig. 3 The two terms in the right-hand side of the Fokker-Planck equation (21). (a) The drift term $A(x)$ (22). (b) The diffusion term $B(x)$ (23). The values of parameters are the same as those in **Fig.** 1.

When $\xi(t)$ can be ignored in Eq. (15) and consequently we can assume that $r(t) = \overline{r}$, it has a unique globally stable fixed point x^* satisfying

$$\overline{r} = \ln \frac{(1-x)(x-b)}{x(a-x)}. \tag{17}$$

x^* can be obtained explicitly by solving the quadratic equation Eq. (17):

$$x^* = \frac{ae^{\overline{r}} - b - 1 + \sqrt{(ae^{\overline{r}} - b - 1)^2 + 4b(e^{\overline{r}} - 1)}}{2(e^{\overline{r}} - 1)}.$$

The other solution is discarded since it is negative. Hence, we can expect that $x(t)$ fluctuates around x^* at stationarity when both σ^2 and the variance of $r(t)$ are small ($\gamma := \alpha^2\sigma^2/(1-\alpha^2) \ll 1$). In **Fig.** 1 (a), we can observe such behavior by numerical simulation ($x^* = 0.744\ldots$ in **Fig.** 1). However, if α is increased while fixing σ^2, a qualitative change in the dynamics of $x(t)$ seems to occur. As shown in **Figs.** 1(b) and (c), $x(t)$ switches stochastically between a neighborhood of $x = b$ and that of $x = a$ if α is sufficiently large. Such change of dynamical behavior can also be seen by plotting the frequency distribution of $x(t)$. The distribution changes from a unimodal type peaked at $x = x^*$ to a bimodal type peaked around $x = b$ and $x = a$ (**Fig.** 2).

In the following, we theoretically investigate the reason why such transition phenomenon of the distribution of x occurs. In the limit of $\alpha \to 1$, the time-scale of $r(t)$ becomes extremely larger than that of $x(t)$. Consequently, $r(t)$ can be regarded as a constant in Eq. (15). Moreover, if σ^2 is sufficiently small, then we can expect that $x(t)$ approximately satisfies Eq. (17) with the left-hand side replaced by $r(t)$. On the other hand, the stationary distribution of $r(t)$ is given by a normal distribution with mean $\overline{r}$ and variance γ, which is denoted by $P_R^s(r)$. Hence, the stationary distribution of x is approximately

$$P^s(x) = P_R^s(r(x))\frac{dr}{dx}, \tag{18}$$

where $r(x) = \ln((1-x)(x-b)/(x(a-x)))$ and $dr/dx = -1/(1-x) + 1/(x-b) - 1/x + 1/(a-x)$. In **Fig.** 2, Eq. (18) is compared with numerical simulation. One can see that they agree well. Thus, the transition from the unimodal distribution to the bimodal one can be understood as follows: $r = r(x)$ is an increasing function of x and diverges to the negative infinity as x approaches to $x = b$ and diverges to the positive infinity as x approaches to $x = a$. Since the variance of r diverges as $\alpha \to 1$, the probability of x concentrates around $x = b$ and $x = a$ where the expansion rate of the change of variables from x to r by Eq. (18) is large.

This transition phenomenon can be understood in a different point of view. First, we can approximate the discrete-time AR(1) process (16) by the following continuous-time Ornstein-Uhlenbeck process since our interest is the situation where the time-scale of $r(t)$ is large, namely, $\tau \gg 1$:

$$dz = (\ln\alpha)\, z dt + b dW_t, \tag{19}$$

where W_t is the Wiener process, $z(t) := r(t) - \overline{r}$ and $b := \alpha\sigma\sqrt{2\ln\alpha/(\alpha^2-1)}$. Next, we can derive a stochastic differential equation governing time evolution of x by applying Ito's formula to the change of variables from z to x:

$$dx = \left((\ln\alpha)\, z\frac{dx}{dz} + \frac{1}{2}b^2\frac{d^2x}{dz^2}\right)dt + b\frac{dx}{dz}dW_t. \tag{20}$$

Finally, the corresponding Fokker-Planck equation for the probability distribution of x is derived as [5]

$$\frac{\partial P(x,t)}{\partial t} = -\frac{\partial}{\partial x}\left(A(x)P(x,t)\right) + \frac{1}{2}\frac{\partial^2}{\partial x^2}\left(B(x)P(x,t)\right),$$

(21)

where

$$A(x) = -\frac{z(x)}{\gamma z'(x)} - \frac{z''(x)}{z'(x)^3} \tag{22}$$

and

$$B(x) = \frac{2}{z'(x)}. \tag{23}$$

Here, $'$ denotes differentiation with respect to x and we performed a time-scale transformation ($(\ln \alpha^{-1})\gamma t$ is replaced by t). One can check that the unique stationary solution of Eq. (21) is Eq. (18). The drift term $A(x)$ and the diffusion term $B(x)$ are shown in **Fig.** 3 (a) and (b), respectively. For each value of α, there exists a unique x^{**} such that $A(x^{**}) = 0$ in the interval (b, a). If we ignore the diffusion term, then x is attracted to x^{**}. However, as $\alpha \to 1$, the attractive force to x^{**} becomes small. On the other hand, the diffusion term is bell-shaped on (b, a) and thus takes smaller values around both ends of (b, a). Moreover, it does not depend on α. Consequently, as $\alpha \to 1$, the effect of the diffusion term becomes dominant and the boundaries of (b, a) work as quasi-absorbing states. Such mechanism of the transition from a unimodal distribution to a bimodal distribution due to the effect of a multiplicative noise is known as Noise-Induced Transition (NIT) [9]. It was recently revisited in the field of theoretical biology and is also called Noise-Induced Symmetry Breaking [11]. Note that the stochastic switching behavior yielded by NIT is different from that resulting from a bistable potential. The former can occur even when the deterministic part of the model equation has a unique globally stable stationary solution as in Eq. (15). On the other hand, the latter requires two different locally stable stationary solutions.

Here, only the case of $N = 2$ was theoretically analyzed. We conjecture that the same mechanism is responsible for generating the swiching behavoir in higher dimensional cases $N > 2$. In **Fig.** 4, we show an example of time evolution of $\boldsymbol{x}$ for $N = 3$ when the switching behavior is observed. In general, it is known that the solutions of the quasispecies model converge to a unique stationary solution when the matrix $W := (q_{ij} e^{\overline{r}_j})$ has a unique largest eigenvalue [12]. For the values of parameters in **Fig.** 4, Eq. (13) has a unique globally stable stationary solution $(x_1^*, x_2^*, x_3^*) \approx (0.407, 0.324, 0.269)$ when all fluctuation terms $\xi_i(t)$ can be ignored and $r_i(t) = \overline{r}_i$ (Stationary solutions can be obtained by solving a cubic equation derived from Eq. (13). The other two solutions contain negative components and hence are discarded). Thus, the switching behavior in **Fig.** 4 cannot be explained by stochastic jumps between multiple locally stable stationary solutions.

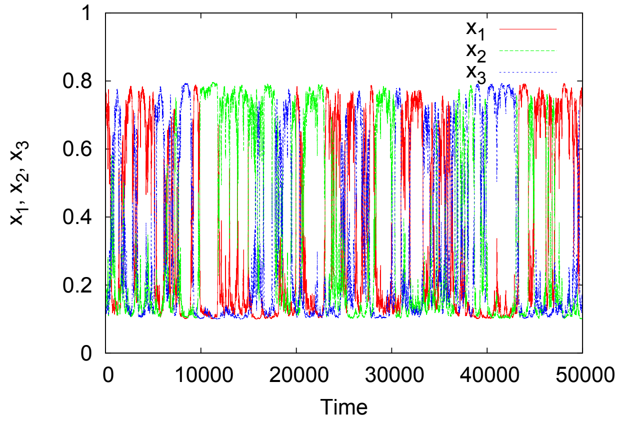

Fig. 4 Time evolution of $\boldsymbol{x}$ for $N = 3$ with the switching behavior. Parameters are: $\alpha = 0.999$, $\sigma^2 = 0.001$, $\overline{r}_1 = \ln 1.2$, $\overline{r}_2 = \ln 1.1$, $\overline{r}_3 = 0$, $q_{ii} = 0.8$ and $q_{ij} = 0.1$ for $1 \leq i \neq j \leq 3$.

4 Discussion

The aim of this paper was to explore mathematical nature of inverse-Bayesian inference. We introduced inverse Bayesian inference to the quasispecies model through the correspondence between Bayesian inference and the replicator equation and investigated its dynamical behavior in uncertain environment. We pointed out that there are two kinds of the way to conceive environmental uncertainty. Uncertainty of the first order is the one that is modeled by the stochastic model of Bayesian inference. Uncertainty of the second order is the one that is not. When they are interpreted in the categorical Bayesian probability theory, the former operates at the object level and the latter does at the morphism level. It was shown that NIT occurs in the quasispecies model with inverse Bayesian inference under uncertainty of the second order when the time-scale of inverse Bayesian inference is sufficiently larger than that of Bayesian inference. On the other hand, such a qualitative change of dynamical behavior never occurs under uncertainty of the first order. In our model, the power of inverse Bayesian inference exhibits only when it is combined with uncertainty of the second order.

In Arecchi's theory, change of hypothesis constituting an aspect of creative cognitive processes is considered as a jump from one peak to another peak on a multimodal fitness landscape [1]. In contrast, our theory predicts that stochastic switching between hypotheses can occur even on a unimodal fitness landscape if uncertainty of the second order is at work. In real-world cognitive processes involving creative jumps, the mechanism of switching could be different case-by-case. The two mechanisms can be distinguished by measuring how average time to reach from one hypothesis to another hypothesis called mean first passage time depends on control parameters [11]. Thus, although our theory presented in this paper is abstract, it proposes a different scenario that can in principle be tested by experiments.

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