

and its associated protein in this paper, especially the trajectory of the production of hax1 and HS_1 with interaction with each other through least action method combining diffusion process[10]. Furthermore, in solving the equation, one stochastic differentiation equation approximates the analytic solution and calculation of MST[11] based on converging with Hamiltonian quantities, finding three convergence points through eigenvalue of position quantities as well as satisfying $H = 0$ and $H_\theta = 0$ where $\theta(P_X, P_Y)$ are momentum quantities.

2.1 switching model with least action

First of all, we consider the dynamics of population of the interaction involved systems as diffusion[12], and thus the Hamiltonian $H(x, \theta)$ is computed with the minimization of action (quasi-potential)[13] instead of some other methods, for instance WKB[14]. With the Lagrangian denoted with respect to Hamiltonian according to LDT: $L(x, y) = \sup_{\theta \in R^n} (\langle y, \theta \rangle - H(x, \theta)) = \langle y, \theta(x, y) \rangle - H(x, \theta(x, y))$. Due to the maximizer $\theta(x, y)$ being implicitly defined by $H_\theta(x, \theta(x, y)) = y$, we calculate the action from quasi-potential: $V(x_1, x_2) = \inf_{T>0} \inf_{\psi \in C_x^2(0, T) S_T(\psi)} = \inf_{T>0} \inf_{\phi \in C_x^2(0, 1)} \inf_{\psi \in C_\phi(0, T) S_T(\psi)} = \inf_{\phi \in C_x^2(0, 1) S(\phi)}$. So that for any $\phi \in C(0, 1)$ the action $S(\phi)$ is given by the equivalent four formula:

$$\begin{aligned} S(\phi) &= \inf_{T>0} \inf_{\phi \in C_\phi(0, T)} S_T(\psi) \\ S(\phi) &= \sup_{\theta: [0, 1] \rightarrow R^n, H(\phi, \theta) = 0} \int_0^1 \langle \phi', \theta \rangle d\alpha \\ S(\phi) &= \int_0^1 \langle \phi', \hat{\theta}(\phi, \phi') \rangle d\alpha \\ S(\phi) &= \int_0^1 \frac{L(\phi, \lambda, \phi')}{\lambda} d\alpha, \lambda = \lambda(\phi, \phi') \end{aligned}$$

Note that $L(x, y)$ is the Lagrangian associated with the Hamiltonian $H(x, \theta)$ with function $\theta(x, y)$ and $\lambda(x, y)$ are implicitly defined for all $x \in D$ and $y \in R^n / 0$ as the unique solution (solution($\theta, \lambda \in R^n X[0, \inf]$) of the system possessing zero value when $\phi' = 0$ or $\lambda(\phi, \phi') = 0$ setting the integrands to zero with: $H(x, \theta) = 0, H_\theta(x, \theta) = \lambda y \leq \text{lambda}$ where the lower bounds for $S(\phi)$ is directly achieved :

$$\begin{aligned} S(\phi) &= \inf_{T>0} \inf_{\phi \in C_\phi(0, T)} S_T(\psi) \\ &\geq \int_0^1 \sup_{H(\phi, \theta)=0} \langle \phi', \theta \rangle d\alpha \\ &\geq \int_0^1 \langle \phi', \theta(\phi, \phi') \rangle d\alpha, \end{aligned}$$

utilizing the first equation of the four. Furthermore, $S(\phi)$'s upper bound can also be obtained through defining a minimizing sequences $(T_k, \psi_k)_{k \in N}$ with the following rescaling process: For every $k \in N$ let: $\lambda_k(\alpha) = \max(\lambda(\phi(\alpha), \phi'(\alpha)), \frac{1}{k}), \alpha \in [0, 1], B_k(\alpha) = \int_0^{\text{alpha}} \frac{1}{\lambda_k} da, \alpha \in [0, 1], T_k(\alpha) = B_k(1), \psi_k(t) = \phi(B_k^{-1}(t)), t \in [0, T_k]$. Specifically, the inverse of B_k is approximated with the Brownian standard σ_x satisfying the $\alpha'(t) = \lambda_k(\alpha(t))$ and thus $\frac{1}{k} \leq \alpha'(t) \leq |\lambda_k|_{\inf} \leq \inf$ holds for all $t \in [0, T_k]$ with the absolute continuity of $\alpha(t)$. And thus, the ψ_k is continuous in the whole time sequence $(0, T_k)$, enabling the inverse process: $t = \alpha(t) = G_k(\alpha)$ with $dt = da/\lambda_k$ and $\phi'(\text{alpha}) = \psi'_k(t)G'_k(\alpha) = \frac{\psi_k(t')}{\lambda_k(\alpha)}$. Thus,

$$S_{T_k}(\phi_k) = \int_0^{T_k} \frac{L(\phi, \phi' \lambda_k)}{\lambda_k} d\alpha$$

leading to the upper bound switching the integrate and limitation with $k \rightarrow \inf$, and with the proof in appendix B(in another work with landscape model) fulfilling the first order and second order conditions: $\phi' = \frac{H_\theta(\phi, \theta)}{\lambda}$ is negative definite during the θ maximizing process: $\frac{L(\phi, \lambda, \phi')}{\lambda} = \sup_{\theta \in R^n} (\langle \phi', \theta \rangle - \frac{H(\phi, \theta)}{\lambda})$ and guaranteeing them both fulfilled by $\theta = \theta(\phi, \phi')$ with the second equation, so that upper-bound here is the same as the integrands of the lower bound as well as holds the $\theta = 0$ when the $\lambda = 0$ is satisfied, and therefore: $\frac{L(\phi, \lambda, \phi')}{\lambda} = \langle \phi', \theta \rangle - \frac{H(\phi, \theta)}{\lambda} = \langle \phi', \theta \rangle, \theta = \theta(\phi, \phi')$

The calculation can be found completely in Appendix B.

2.2 diffusion Approximation with numerical methods on the convert ratio referencing bacteria sensing and MTS on difference mapping

As we want to study the switching model interpreting the process

explicitly, we thus combine the deterministic[15] background of the switching between on and off and give out one stochastic model based on the explicit (ordinary differential equation) ODE of the numbers of mRNA and proteins. Although the final model referencing the quorum sensing model of bacteria in changing environment[16]) removes the dimers but it is used in the first place while cancelled out in the quasi steady state according to its far more faster production and degradation rate comparing to transcription and translation.(Simplified mechanism sees Appendix A). Start from the bistability of the metastability[17] of the two state model, with the absorbing boundary conditions, $\rho_0(x*, t) = 0$ and the identification of mean transition rate with principal eigen value λ_ϵ^0 , the quasi-stationary approximation of $\rho_n(x, t) = C_0 * \exp(-\lambda_\epsilon^0 t) * \phi_\epsilon^0(x, n)$. Furthermore, with the quasi-potential satisfying

$\sum_{n=0, 1} S_n(x)(A_{n,m}(x) + \phi'_m(x)\delta_{n,m})F_m(x) = 0, H = 0.5 * (g_x^2 p_x^2 + g_y^2 p_y^2) + p_1 * \phi_1 + p_2 * \phi_2$ where p_i is the momentum conjugate to the generalized coordinate x_i , where $g_i = \sqrt{(S_i^2 f_i + X_i/\tau_i)}$ (For more specific study of the ϕ_1 and ϕ_2 as the interacted diffusive speed, most studies applies WKB equations.) Since we focus on the transform between two status of the two populations, mRNA (of HS-1) X_n and proteins Hax1 Y_n as the system.(with dimer Z of production rate k_{XY} and degradation rate k_P)[18] and the degradation rate of HS_1 and hax1, as K_X and K_Y , separately. From the original ODES:

$$\begin{aligned} \frac{dZ}{dt} &= k_{XY}XY - k_Z Z \\ \frac{dX}{dt} &= -k_{XY}XY + k_Z Z - k_X X + V_X * \frac{Z}{(K_X + Z) + X_0} \\ \frac{dY}{dt} &= -k_{XY}XY + k_Z Z + V_Y * \frac{Z}{(K_Y + Z)} + V_Y - k_X X \end{aligned}$$

where X_0 and Y_0 are the initial volumes or baseline volumes of these two populations and with instant volume as V_X and V_Y and due to the zero value of $\frac{dP}{dt}$, the term of P can be replaced through:

$$\begin{aligned} P &= \frac{k_{XY}}{K_P} XY \\ \frac{dX}{dt} &= -k_X X + V_X * \frac{k_{XY}}{K_P} XY + X_0 = -k_X X + V_X * \frac{1}{(1 + \frac{K_X k_P}{k_{XY}})} + X_0 \\ \frac{dY}{dt} &= -k_Y Y + V_Y * \frac{k_{XY}}{K_P} XY + Y_0 = -k_Y Y + V_Y * \frac{1}{(1 + \frac{K_Y k_P}{k_{XY}})} + Y_0 \end{aligned}$$

Considering the transform of X(Upstream only), in the first step as degradation as the first term of right of the upper formula, the degradation part of X with k_X which can be interpreted as the Poisson process and rewrite into $-\frac{\mu_1}{\exp^{P_X}}$, and in the second term, the coefficient of degradation part of X, $C1$ is denoted as $\frac{V_X * k_X}{\mu_1}$. Mean while with the assumption of continuous Markov chain, where the convert ratio of Y is n, the $\frac{k_{XY}}{K_P} * X * Y$ is equivalent to $(\frac{Y}{X+Y})^n$ so that the whole degradation part becomes $\frac{C1 * \mu_1}{1 + (\frac{Y}{X+Y})^n} \exp^{P_X}, \frac{C2 * \mu_2}{1 + (\frac{Y}{X+Y})^n} \exp^{P_Y}$ (*1) and the final transform rate of mRNA number X and proteins Y are:

$$\frac{C1}{1 + (\frac{Y}{X+Y})^n} (\exp^{P_X} - 1) - \mu_1 * X(\exp^{-P_X} - 1) \text{ and } \frac{C2}{1 + (\frac{Y}{X+Y})^n} (\exp^{P_Y} - 1) - \mu_2 * Y * (\exp^{-P_Y} - 1) \text{ where, the coefficient of degradation part of Y } C2 \text{ denoted as } \frac{V_Y * k_Y}{\mu_2}, \text{ as the reciprocal of the other population ratio. And as Y stands for the number of the proteins, X for the number of the mRNA separately with m and n as their translation and transcription rate. With the total sum of the system molecule numbers assumed as X+Y, we have the Hamiltonian:}$$

$$\frac{C1}{1 + (\frac{Y}{X+Y})^n} (\exp^{P_X} - 1) - \frac{\mu_1 * X}{(\exp^{-P_X} - 1)} + \frac{C2}{1 + (\frac{Y}{X+Y})^n} (\exp^{P_Y} - 1) - \frac{\mu_2 * Y}{(\exp^{-P_Y} - 1)}$$

,where P_X, P_Y are calculated setting $H = 0$ and $H_\theta = 0$, and conversion rate which can be calculated as $\frac{dy}{dx}$ specifically here, letting the first term equals the second and third equals the fourth term. (Complete see Appendix B) Note that: each single DNA population(hax1 and HS_1) has its own degradation rate when considering about its mRNA computation, and the other population's protein is taken as the intake, promoting its population when as normals binding onto the according site of persisters, activating it. Vice versa, thus, the two populations have similar structured formula describing each degradation and population under the dual interacted population. The mean switching time is calculated based on the solution of the SDE: $z' = z + \sqrt{(\frac{N_c}{N}) * \sqrt{1 + 2 * e^{-z^2}} * \eta}$,