Broken detailed balance at mesoscopic scales in active biological systems

Ramanuj Raman MS21271

Introduction

Systems in thermodynamic equilibrium are not only characterized by time-independent macroscopic properties, but also satisfy the principle of detailed balance in the transitions between microscopic configurations. A thermodynamic equilibrium is characterized by the fact that all microscopic states are equally accessible, and the probability of a transition between two states is equal to the probability of the reverse transition.

In contrast, most of living systems are characterized by out of equilibrium scenario and characterized by directed fluxes through chemical states which breaks principle of detailed balance at molecular scale. For instance, metabolic and enzymatic processes drive closed-loop fluxes through the system's chemical states. Non-equilibrium driving of a system can boost intercellular transport, accuracy of transcription, chemotaxis and accuracy of sensory preception. So to understand the cell function it is important to understand whether the system is in equilibrium or not, which is not a simple task.

In this paper, we'll explore the **probability flux analysis (PFA)** a non invasive method to understand and quantify this broken detailed balance in real, nosiy, mesoscopic system.

Model

To understand this approach we'll consider a model 1D bead string model. We'll consider two scenario where we have two beads are attached to heat bath with two beads attached to bath with temperature T_1 and T_2 such that $T_1 \neq T_2$ generating a temperature gradient and hence driving it out of equilibrium. One can also analyse the same situation in equilibrium where $T_1 = T_2$.

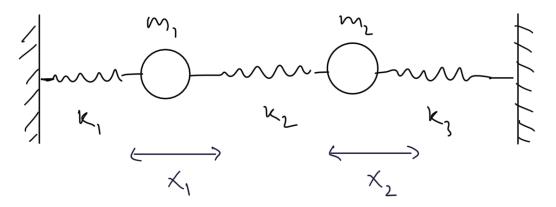


Figure 1: Bead string model

The equation of motion of the above system in lagenvin dynamics system [1]

$$m\frac{\mathrm{d}^2x_1}{\mathrm{d}t^2} = -k_1x_1 - k_2(x_1 - x_2) - \gamma m\frac{\mathrm{d}x_1}{\mathrm{d}t} + \eta_1(t) \tag{1}$$

$$m\frac{\mathrm{d}^2x_2}{\mathrm{d}t^2} = -k_3x_2 - k_2(x_2 - x_1) - \gamma m\frac{\mathrm{d}x_2}{\mathrm{d}t} + \eta_2(t) \tag{2}$$

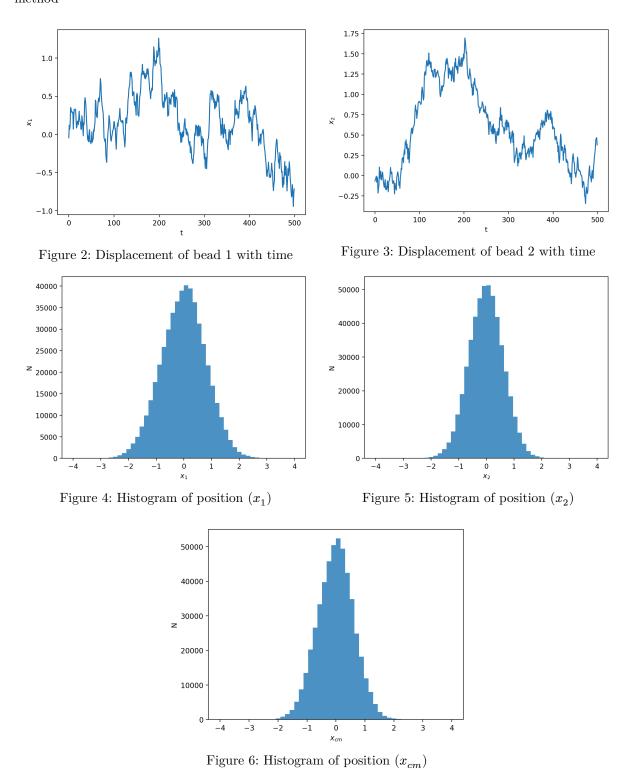
Now in the overdamped limit we have

$$\gamma \frac{\mathrm{d}x_1}{\mathrm{d}t} = -\frac{k_1}{m}x_1 - \frac{k_2}{m}(x_1 - x_2) + \eta_1(t) \tag{3}$$

$$\gamma \frac{\mathrm{d}x_2}{\mathrm{d}t} = -k_3 x_2 - k_2 (x_2 - x_1) + \eta_2(t) \tag{4}$$

Dynamics of beads with time

We can numerically solve Eq. 3 and Eq. 4 to get the dynamics of the system using Euler-Maruyama method



Probability flux analysis

In equilibrium, systems obey detailed balance—transitions between any two microstates are equally likely in both directions, so there's no net "flow" or flux in phase space. Here is the method to calculate the probability flux in a system.[2]

1. Define the system state space

Choose relevant degrees of freedom, in our case we'll consider the position (x_1) and (x_2) of the beads.

2. Discretize the State Space

Divide the continuous phase space into a coarse-grained grid (called CGPS). Each grid box is a "state bin".

3. Collect Transitions Between States

Track how often the system moves from state/bin $a \to b$ and $b \to a$ and denote these counts as N_{ab} and N_{ba} .

4. Compute Net Flux

Define the net probability flux between bins as:

$$\omega_{ab} = \frac{N_{ab} - N_{ba}}{t} \tag{5}$$

Flux arrows are plotted from bin $a \to b$ with a length proportional to the net flux ω_{ab} .

Results

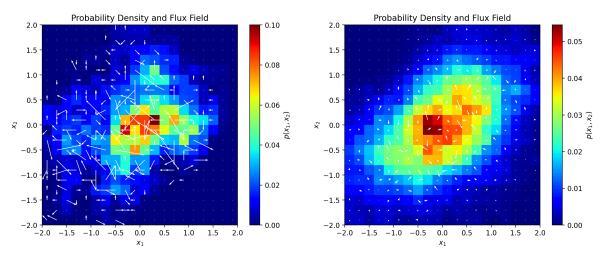


Figure 7: Simulation when $T_1 = T_2$ for N = 1000 time steps

Figure 8: Simulation when $T_1 \neq T_2$ for N = 1000 time steps

Observing the above results from simulations of a 1D bead string system one can observe closed loop fluxes in Figure 8 but the simulations results aren't as good as shown in [2]

Code

Find the code for the simulations here.

Bibliography

- [1] N. Pottier, *Nonequilibrium Statistical Physics: Linear Irreversible Processes*. in Oxford Graduate Texts. OUP Oxford, 2009.
- [2] C. Battle *et al.*, "Broken detailed balance at mesoscopic scales in active biological systems," *Science*, vol. 352, no. 6285, pp. 604–607, 2016, doi: 10.1126/science.aac8157.