Stochastic Models of Complex Systems

Problem sheet 3

Sheet counts $30/100$ homework marks, **question 3.3 carries double weight**, the others equal.

3.1 Scaling limits

Consider a continuous-time random walk $(X_\tau : \tau \geq 0)$ on $\mathbb{Z}$ with next nearest neighbour jumps and master equation

$$\frac{d}{d\tau}\,\pi_k(\tau) = \alpha\pi_{k-2}(\tau) + (\tfrac{1}{2}-\alpha)\pi_{k-1}(\tau) - \pi_k(\tau) + (\tfrac{1}{2}-\alpha)\pi_{k+1}(\tau) + \alpha\pi_{k+2}(\tau)\,, \quad k \in \mathbb{Z}\,,$$

where $\alpha \in [0, 1/2]$.

(a) Derive the heat equation

$$\frac{\partial}{\partial t}\, f(t,x) = D\,\frac{\partial^2}{\partial x^2}\, f(t,x)$$

in a scaling limit $x = \Delta x\, k$, $t = \Delta t\, \tau$ analogous to the lectures. What is the required relation between Δx and Δt, and what is the value of D (depending on α)?

(b) Take $\alpha = 0$, i.e. consider only nearest neighbour jumps. Add a *weak drift* to the random walk depending on Δx, such that in the same scaling limit as in (a) you get the Fokker-Planck equation

$$\frac{\partial}{\partial t}\, f(t,x) = -c\,\frac{\partial}{\partial x}\, f(t,x) + \frac{1}{2}\,\frac{\partial^2}{\partial x^2}\, f(t,x)$$

for some fixed $c > 0$. Give the master equation of the modified process, and derive the scaling limit analogously to (a).

3.2 Moran model

We consider the Moran model in continuous time, which is a simple model for evolution:
In a population of size N each individuum can be of type A or B. Each individuum independently reproduces at rate 1 passing on its type to the offspring. When this happens, one of the now $N + 1$ individuals is chosen uniformly at random and dies instantaneously, to keep the population size constant to N.
Let X_τ be the number of type A individuals at time τ. Then $X = (X_\tau : \tau \geq 0)$ is a continuous-time Markov chain with state space $S = \{0, \ldots, N\}$.

(a) Find the generator of X and write down the master equation.
Is X irreducible? Does it have absorbing states? What are the stationary distributions?

(b) Rescale space $x = i/N \in [0, 1]$ and set $\pi_i(\tau) = f(\tau, x)\,\frac{1}{N}$. Write the master equation in terms of f and x.
Do a Taylor expansion of the right-hand side up to second order in x. It is (very!) useful to actually do the expansion not for f but for the function $g(\tau, x) := f(\tau, x)x(1 - x)$.

(c) Rescale time appropriately ($t = \Delta t\, \tau$) and derive the Fokker-Planck equation

$$\frac{\partial}{\partial t} f(t,x) = \frac{\partial^2}{\partial x^2}\Big(x(1-x) f(t,x)\Big) \quad \Big(= (\mathcal{L}^* f)(t,x)\Big)$$

in the limit $N \to \infty$. How are Δt and N related?

(d) The limiting process $(Y_t : t \geq 0)$ on $[0,1]$ from (c) is called **Wright-Fisher diffusion**. Give the generator $\mathcal{L}$ of that process, such that $\frac{d}{dt}\mathbb{E}\big(g(Y_t)\big) = \mathbb{E}\big((\mathcal{L}g)(Y_t)\big)$ for observables $g : [0,1] \to \mathbb{R}$.
Show that $\mathbb{E}(Y_t) = \mathbb{E}(Y_0)$ for all $t > 0$ and discuss the limit of Y_t as $t \to \infty$.

(e)* For $Y_0 = 1/2$, derive an equation for $\mathrm{Var}(Y_t)$, solve it, and interpret its solution.

(f)* Repeat the analysis in (a) to (c) with an additional *mutation* rate μ/N, $\mu > 0$ at which an individuum spontaneously changes type.

3.3 Simulation of the contact process. (Sample code on the course webpage)
Consider the contact process $(\eta_t : t \geq 0)$ as defined in Q2.2, but now on the one-dimensional lattice $\Lambda_L = \{1, \ldots, L\}$ with connections only between nearest neighbours and periodic boundary conditions.
The critical value λ_c is defined such that the infection on the infinite lattice $\Lambda = \mathbb{Z}$ started from the fully infected lattice dies out for $\lambda < \lambda_c$, and survives for $\lambda > \lambda_c$. It is known numerically up to several digits, depends on the dimension, and lies in the interval $[1,2]$ in our case.

(a) Simulate the process with initial condition $\eta(x) = 1$ for all $x \in \Lambda$ and several values of $\lambda \in [1,2]$. Plot the number of infected individuals $N_t = \sum_{x\in\Lambda_L} \eta_t(x)$ as a function of time averaging over 100 realizations in a double-logarithmic plot.
What is the expected behaviour of N_t depending on λ for times up to order L?
For a given system size L, find the window of interest choosing $\lambda = 1, 1.2, \ldots, 1.8, 2$ and then use increments 0.01 for λ to find an estimate of the critical value $\lambda_c(L) \in [1,2]$.
Repeat this for different lattice sizes, e.g. $L = 64, 128, 256, 512$, and plot your estimates of $\lambda_c(L)$ against $1/L$. Extrapolate to $1/L \to 0$ to get an estimate of $\lambda_c = \lambda_c(\infty)$.
This approach is called **finite size scaling**, in order to correct for **finite size effects** which influence the critical value.

(b) Simulate the process for $L = 128$ with initial condition $\eta(x) = 1$ for all $x \in \Lambda$ and several (at least 3) values of λ around $\lambda_c(L)$. After an equilibration time $\tau_{equ} = L$, sample from the distribution of the number of infections $N_t = \sum_{x\in\Lambda_L} \eta_t(x)$, i.e. over a time interval of length $\tau_{meas} = L$ count the fraction of time N_t spent in n for each $n \in \{0, \ldots, L\}$. Average this measurement over 100 realizations and plot your estimate of the distribution for all values of λ in a single plot (it might be a good idea to use a log-scale on the y axis). Explain the form of the observed curves.

(c)* Repeat the analysis of (a) on the fully connected graph Λ_L, and compare your estimate of λ_c with the mean-field prediction from Q2.2.