

Practical Course on Molecular Dynamics and Trajectory Analysis

Episode 6: Markov models with PyEMMA

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MD Course and Trajectory Analysis
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- 1 Episode 6: Markov models with PyEMMA
 - Motivation and theoretical background
 - Trajectory preparation
 - Feature representation
 - Time-lagged Independent Component Analysis
 - Discretization
 - MSM estimation
 - Spectral analysis and validation
 - Transition Path Theory

Why Markov State Models?

- Molecular dynamics (MD) simulations generate high-dimensional trajectories $\{\mathbf{X}_t\}_{t=0}^T$.
- Relevant molecular processes occur on timescales much longer than MD timesteps.
- MSMs provide a statistical coarse-graining into discrete states with Markovian dynamics.
- Enable computation of long-timescale kinetics, populations, and pathways.

From continuous dynamics to a Markov chain

- Consider a stochastic process \mathbf{X}_t in phase space Ω .
- Partition Ω into disjoint sets $\{S_1, \dots, S_N\}$.
- Define a discrete process $X_t \in \{1, \dots, N\}$:

$$X_t = i \quad \text{if } \mathbf{X}_t \in S_i.$$

- Markov assumption at lag time τ :

$$P(X_{t+\tau} = j \mid X_t = i, \dots) \approx P(X_{t+\tau} = j \mid X_t = i).$$

Preparing molecular trajectories

- Input trajectories from MD engines (OpenMM, Gromacs, AMBER, ...).
- Preprocessing:
 - Remove periodic boundary artifacts.
 - Align structures to a reference.
 - Remove solvent if not used as features.
 - Subsample to a uniform timestep Δt .
- Validate trajectories: energy stability, RMSD convergence.

Feature extraction

- Each frame is mapped to a feature vector $\mathbf{x}_t \in \mathbb{R}^d$.
- Typical features:
 - Interatomic distances or contacts.
 - Dihedral angles.
 - Ligand–protein distances.
- Features should resolve slow collective motions.

Covariance structure

$$\bar{\mathbf{x}} = \langle \mathbf{x}_t \rangle,$$
$$C_0 = \langle (\mathbf{x}_t - \bar{\mathbf{x}})(\mathbf{x}_t - \bar{\mathbf{x}})^T \rangle.$$

- Averages over all frames and trajectories.
- C_0 captures instantaneous correlations.

Time-lagged covariance

$$C_{\tau} = \langle (\mathbf{x}_t - \bar{\mathbf{x}})(\mathbf{x}_{t+\tau} - \bar{\mathbf{x}})^T \rangle.$$

- Measures correlations persisting over lag time τ .
- Slow processes correspond to large time-lagged correlations.

Generalized eigenvalue problem

$$C_\tau \mathbf{w}_i = \lambda_i C_0 \mathbf{w}_i.$$

- Eigenvectors \mathbf{w}_i define tICs.
- Projection:

$$y_{i,t} = \mathbf{w}_i^T \mathbf{x}_t.$$

Implied timescales

$$t_i = -\frac{\tau}{\ln \lambda_i}.$$

- Estimates relaxation timescales of slow modes.
- Plateaus vs. τ indicate robust dynamics.

Clustering into microstates

- Project data onto first m tICs.
- Cluster in reduced space (e.g. k -means).
- Each frame assigned to a discrete state i .

Discrete trajectories

- Continuous trajectories become symbol sequences:

$$X^{(n)} = (x_0^{(n)}, \dots, x_{T_n}^{(n)}).$$

- These sequences define the MSM input.

Transition counts

$$C_{ij}(\tau) = \sum_t \mathbb{I}(X_t = i, X_{t+\tau} = j).$$

- Counts transitions from i to j at lag time τ .

Transition matrix

$$T_{ij}(\tau) = \frac{C_{ij}(\tau)}{\sum_k C_{ik}(\tau)}.$$

- Row-stochastic matrix.
- Interpreted as conditional probabilities.

$$\pi_i T_{ij} = \pi_j T_{ji}.$$

- Expected for equilibrium simulations.
- Enforcing reversibility reduces statistical noise.

Stationary distribution

$$\pi^T T = \pi^T.$$

- π_i gives equilibrium populations.
- Free energies:

$$F_i = -k_B T \ln \pi_i + \text{const.}$$

Eigenvalues and timescales

$$T \mathbf{r}_i = \lambda_i \mathbf{r}_i, \quad t_i = -\frac{\tau}{\ln \lambda_i}.$$

- $\lambda_1 = 1$ corresponds to equilibrium.
- Spectral gap indicates timescale separation.

Chapman–Kolmogorov test

- Markovianity check:

$$T(n\tau) \approx T(\tau)^n.$$

- Agreement validates chosen lag time.

Committor function

- Define reactant set A and product set B .
- Forward committor:

$$q_i = \sum_j T_{ij} q_j, \quad q_i = 0 \ (i \in A), \ q_i = 1 \ (i \in B).$$

$$f_{ij} = \pi_i T_{ij} q_i (1 - q_j).$$

- Identifies dominant reactive pathways.

References I