

# Practical Course on Molecular Dynamics and Trajectory Analysis

## Episode 5: Trajectory analysis

Jordi Villà i Freixa

Universitat de Vic - Universitat Central de Catalunya  
Facultat de Ciències, Tecnologia i Enginyeries (FCTE)

*jordi.villa@uvic.cat*

MD Course and Trajectory Analysis  
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  - Preprocessing and cleanup
  - Velocities and inertia
  - Reduction and clustering
  - Free energies and surfaces
  - Statistics and confidence
  - Summary

# Pre-analysis pipeline

- 1 Convert and clean trajectories with `simulatePdb.py` or `simulateGromacs.py`.
- 2 Align structures and strip irrelevant solvent.
- 3 Define atom subsets and write DCD/NetCDF for downstream analysis.

Scripts from the OpenMM Application Layer. [2]

# Velocities and distributions

- 'StateDataReporter' and 'DCDReporter' build histograms of  $v_i$  and energies.
- By the equipartition theorem:  $\langle K \rangle = \frac{3N}{2} k_B T$  for classical systems.
- Monitoring  $C(t) = \langle A(0)A(t) \rangle$  reveals the relevant timescales.

# RMSD and alignments

$$\text{RMSD}(t) = \sqrt{\frac{1}{N} \sum_{i=1}^N \|\mathbf{r}_i(t) - \mathbf{r}_i^{\text{ref}}\|^2}.$$

- Use the Kabsch algorithm for optimal rotations.
- Document with `simulateAmber.py` and per-replica CSV output.

# Radius of gyration and inertia tensor

$$I_{ab} = \sum_i m_i (r_i^2 \delta_{ab} - r_{ia} r_{ib}) .$$

- Eigenvalues of  $I$  describe global anisotropy.
- Monitor  $R_g^2 = \frac{1}{N} \sum_i m_i \|\mathbf{r}_i - \mathbf{r}_{\text{CM}}\|^2$  per replica.

# Extremes and contacts

- Binary maps with a 0.45 nm cutoff generate contact matrices.
- Columns represent domain changes detected by `simulateCharmm.py`.

$$C = \langle (\mathbf{x} - \langle \mathbf{x} \rangle)(\mathbf{x} - \langle \mathbf{x} \rangle)^T \rangle.$$

- Project onto the leading eigenvectors and define event axes.
- Relate to `coarse_grained_polymer.py` to compare slow modes of polymers and proteins.



# Hierarchical clustering

- Use average linkage and silhouette index to decide  $k$ .
- Poor choices yield empty microstates; prefer progressive trials.

# Transitions and graphs

- State graphs (see 'graph.png') represent kinetic channels.
- Annotated edges reflect fluxes measured by OpenMMTools scripts.

# Eigenvalues and modes

$$C\mathbf{w} = \lambda\mathbf{w}, \quad \lambda \in \mathbb{R}_+.$$

- Dominant modes identify collective motions.
- Save projections to feed Markov models.

# Density functions

$$g(r) = \frac{1}{4\pi r^2 \rho} \left\langle \sum_{i \neq j} \delta(r - r_{ij}) \right\rangle.$$

- Compare with `argon-chemical-potential.py` for validation.
- Use reweighted histograms to estimate  $F(r) = -k_B T \ln g(r)$ .

# Free energy surfaces and barriers

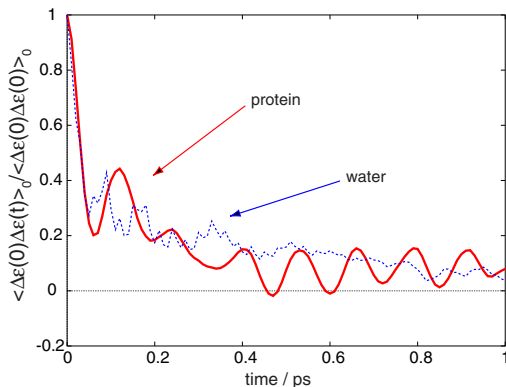
- Projection  $F(s) = -k_B T \ln P(s)$  requires robust CVs.
- Integrate with 'umbrella sampling' windows and combine with MBAR.
- Compare 1D profiles with `simulateAmber.py`.
- Validate using manually overlapping histograms.

# Bootstrap and blocking

- Resample blocks to estimate variances.
- Autocorrelations (see `bs_autocorrelation.pdf`) determine the block size.

# Block autocorrelations

Autocorrelation of the energy gap  
in water and protein for the LADH system



$$\sigma_{\bar{A}} = \frac{\sigma_A}{\sqrt{N_{\text{eff}}}}, \quad N_{\text{eff}} = \frac{N}{g}, \quad g = 1 + 2 \sum_t \rho(t).$$



- Generate RMSD/RMSF/radius of gyration tables with `simulateCharmm.py`.
- Export CSV/HDF for easy handoff to PyEMMA/Deeptime.

## Summary and next step

- Preprocess without artifactual PBC.
- Stable CVs and converged histograms.
- Reports with errors and documented trajectories.
- Use the prepared features as input for PyEMMA/Deeptime.

# References I

- [1] OpenMM Cookbook. *Autocorrelation example from Selecting Values for Simulation Parameters*. CC BY-SA 4.0. URL: [https://openmm.github.io/openmm-cookbook/latest/notebooks/tutorials/simulation\\_parameters.html](https://openmm.github.io/openmm-cookbook/latest/notebooks/tutorials/simulation_parameters.html) (visited on 01/12/2026).
- [2] OpenMM developers. *OpenMM application guide*. Reference for scripting and workflow examples. 2024. URL: <https://docs.openmm.org/latest/userguide/application.html>.