

**A coarse graining method
for the identification of transition rates
between molecular conformations**

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"Matheon"

Overview

molecular geometry, $q \in \mathbb{R}^{3n}$

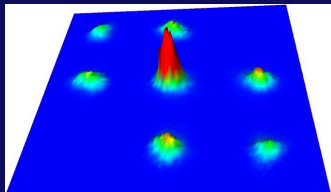
⇓ choose essential degrees of freedom

dihedral space $[-\pi, \pi]^d$

⇓ discretization

ansatz functions $\xRightarrow{\text{HMC/MD}}$

transition matrix



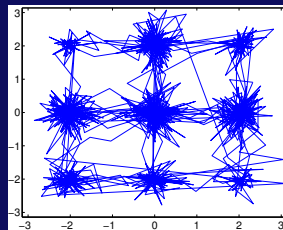
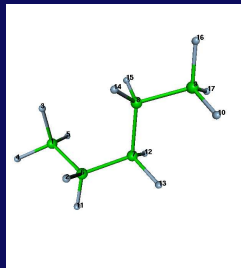
⇓ PCCA+

conformations

aggregation



conformational propagator



Overview

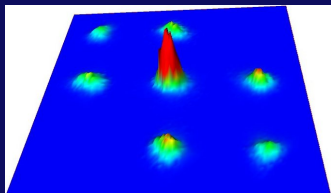
molecular geometry, $q \in \mathbb{R}^{3n}$

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↓ discretization

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transition matrix

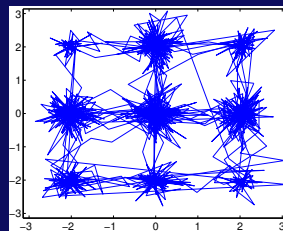
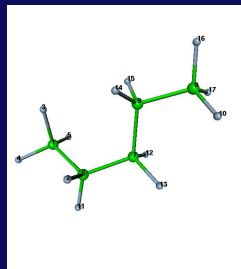
↓ PCCA+

conformations

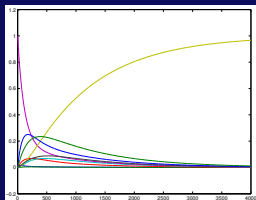
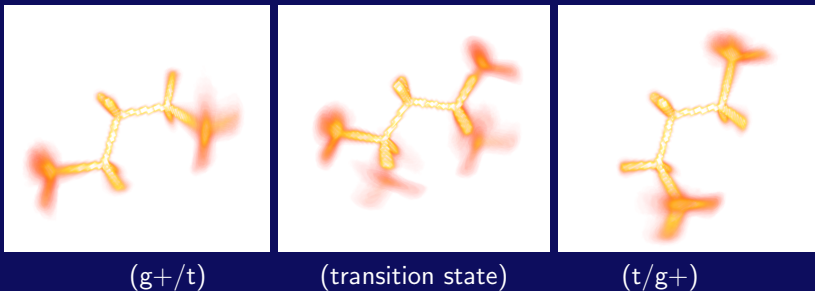
aggregation



conformational propagator



Conformational Propagator



life times, transition probabilities/rates?

Transition Probabilities

Markov chains:

- discrete time sample path $\{X_n\}_{n \in \mathbb{N}}$ (uniform time steps)
- finite state space $E = \{1, \dots, N\}$
- stochastic transition probability matrix

$$P(i, j) = \frac{\#(i \rightarrow j)}{\sum_{k \in E} \#(i \rightarrow k)} \quad i, j \in E$$

Properties:

- **irreducibility** and **positive recurrence** \leftrightarrow

$$\exists! \pi : \quad \pi^\top P = \pi^\top, \quad \sum_{i \in E} \pi(i) = 1$$

- **reversibility**

$$\pi_i P(i, j) = \pi_j P(j, i), \quad \forall i, j \in E$$

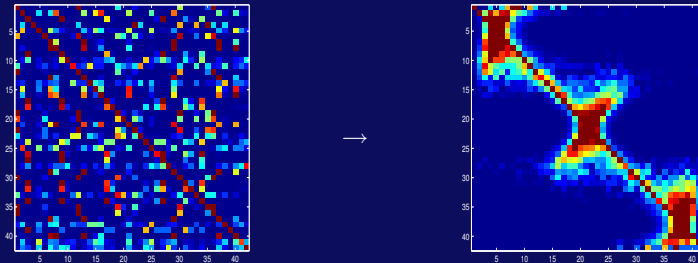
Relative transition frequencies

$$\bar{P} = DP \quad (\text{symmetric}), \quad D = \text{diag}(\pi)$$

- $\bar{P}(i, j) = \frac{\#(i \rightarrow j)}{L-1}$, $i, j \in E$, $L = \text{chain length}$
- $\sum_{i,j=1}^N \bar{P}(i, j) = 1$, $0 \leq P(i, j) \leq 1 \quad \forall i, j \in E$
- $\bar{P}e = \pi$

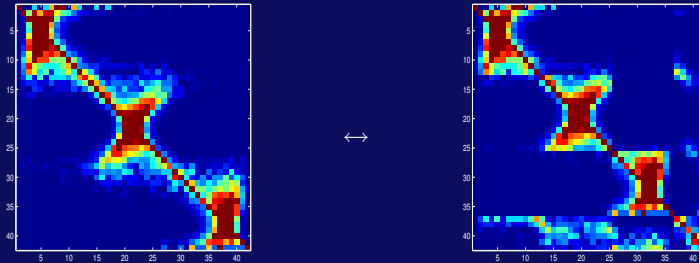
The transition frequencies can be computed directly from the simulation without knowing the stationary distribution!

Reordering of states such that there are n_C blocks $\mathcal{C} = \{C_1, \dots, C_{n_C}\}$.



Grade of membership $\chi(i, j) \in [0, 1]$:

$$\chi(i, j) = \begin{cases} 1 & \text{if state } i \text{ belongs to cluster } j \\ 0 & \text{else} \end{cases}$$



There are states which cannot be assigned uniquely to one of the clusters.

Grade of membership $\chi(i, j) \in (0, 1)$: state i belongs to cluster j with probability $\chi(i, j)$

- $\sum_{j=1}^{n_C} \chi(i, j) = 1 \quad \forall i \in E$
- $0 \leq \chi(i, j) \leq 1 \quad \forall i \in E, j \in \mathcal{C}$

Robust Perron Cluster Analysis (PCCA+) (Deufhard, Weber, 2004)

$$\chi = XA$$

- X : eigenvectors of P

$$PX = \lambda X, \quad \lambda \approx 1$$

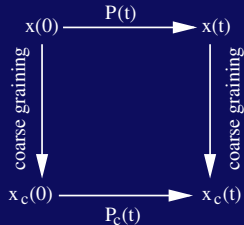
- A : non-singular transformation matrix

Propagation of Densities

- $x_i(t)$: probability to be in state i at time t

$$\sum_{i=1}^N x_i(t) = 1, \quad 0 \leq x_i(t) \leq 1$$

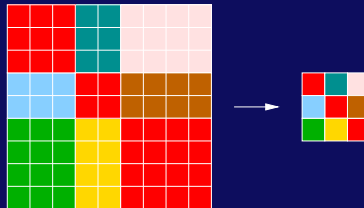
- propagation of densities: $\mathbf{x}(t) = P^\top(t)\mathbf{x}(0)$
- Chapman-Kolmogorov: $P(nt) = P^n(t)$
- goal: **coarse graining** – propagation of densities $\mathbf{x}(t) \in \mathbb{R}^{n_c}$, $n_c \ll N$



Clustering of states:

- frequencies:

$$\bar{P}_c(k, l) = \sum_{i \in C_k, j \in C_l} \bar{P}(i, j) = \chi(:, k)^\top \bar{P} \chi(:, l)$$



- probabilities:

$$P_c = \tilde{D}^{-1} \bar{P}_c = \tilde{D}^{-1} \chi^\top D P \chi$$

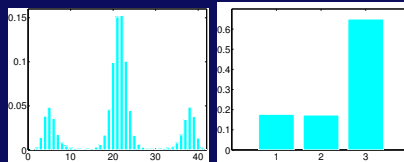
Coarse Graining Operators

$$P_c = \tilde{D}^{-1} \chi^\top D P \chi := I^\top P R^\top$$

Definition:

- **restriction** $R : \mathbb{R}^N \mapsto \mathbb{R}^{n_C} : R = \chi^\top$
- **interpolation** $I : \mathbb{R}^{n_C} \mapsto \mathbb{R}^N : I = D \chi \tilde{D}^{-1}$

Transformation of densities: $x^c = R x^f, \quad x^f = I x^c$



Main goal – commutative diagram: $R P^\top(t) x(0) = P_c^\top(t) R x(0)$
 :(Not satisfied for a hard clustering!

Define

$$\hat{P}_c := (RI)^{-\top} I^\top PR^\top$$

Properties:

- \hat{P}_c is diagonalizable:

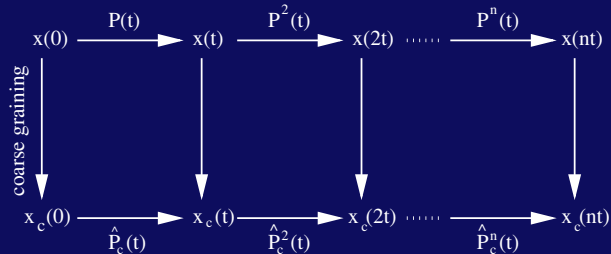
$$\hat{P}_c = A^{-1}\Theta A$$

- invariant density: $\hat{P}_c^\top \tilde{\pi} = \tilde{\pi}$, $\tilde{\pi} = R\pi$, $\pi = I\tilde{\pi}$
- correct row sum: $\sum_{j=1}^{n_C} \hat{P}_c(i, j) = 1 \quad \forall i \in \mathcal{C}$
- positivity: $\sim \{0 \leq \hat{P}_c(i, j) \leq 1 \quad \forall i, j \in \mathcal{C}\}$
- $RP^\top(t)x(0) = \hat{P}_c^\top Rx(0)$

(change of propagation and restriction)

- extension to **time steps** nt , $n \in \mathbb{N}$: $x(nt) = P^{n\top}(t)x(0)$

$$RP^{n\top}(t)x(0) = \hat{P}_c^{n\top}(t)Rx(0)$$



Idea:

- generalization of the coarse graining process to **arbitrary times** $t > 0$
- description of the dynamic behavior in terms of the **infinitesimal generator** Q

$$\dot{x}(t) = Q^\top x(t)$$

Coarse Grained Kinetics

$$Q = \lim_{t \rightarrow 0^+} \frac{P(t) - id}{t}$$

Master equation:

$$\dot{x}(t) = Q^\top x(t) \quad \rightarrow \quad x(t) = \exp(tQ^\top)x(0)$$

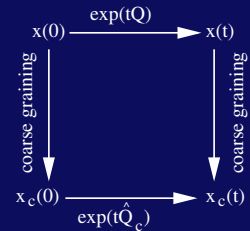
Define

$$\hat{Q}_c := (RI)^{-\top} I^\top QR^\top$$

Properties:

- \hat{Q}_c is diagonalizable:

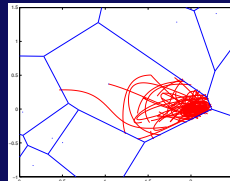
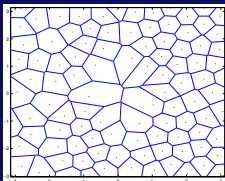
$$\hat{Q}_c = A^{-1} \Lambda A$$
- invariant density: $\hat{Q}_c^\top \tilde{\pi} = 0$, $\tilde{\pi} = R\pi$, $\pi = I\tilde{\pi}$
- conservation of mass: $\sum_{j=1}^{n_C} \hat{Q}_c(i, j) = 0 \quad \forall i \in \mathcal{C}$
- positivity: $\sim \{0 \leq \hat{Q}_c(i, j) \quad \forall i, j \in \mathcal{C}, i \neq j\}$



commutative!

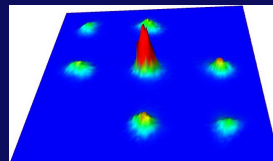
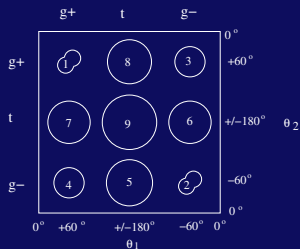
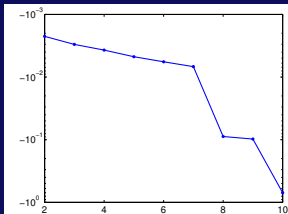
Example

1. Discretization
2. Molecular Simulation
 - Merck Molecular Force Field
 - generation of 3000 points per cell according to the Boltzmann distribution by hybrid Monte-Carlo sampling with umbrella strategies and Gelman-Rubin convergence indicator
 - propagation by MD until the trajectories leave their starting cell



Example

3. Computation of Q
4. Cluster Analysis



weights = {0.0036, 0.0032, 0.0640, 0.0680, 0.1248, 0.1232, 0.1140, 0.1567, 0.3426}

$h^{-1} = \{10.39, 11.38, 361.68, 334.35, 198.91, 227.31, 172.40, 235.74, 283.64\}ps$

P. Deuffhard, Ch. Schütte: *Molecular Conformation Dynamics and Computational Drug Design*. In J. M. Hill and R. Moore, editors, *Applied Mathematics Entering the 21st Century*. ICIAM 2003, Sydney, Australia, 2004.

P. Deuffhard, M. Weber: *Robust Perron Cluster Analysis in Conformation Dynamics*. In M. Dellnitz, S. Kirkland, M. Neumann, and Ch. Schütte, editors, *Lin. Alg. Appl. - Special Issues on Matrices and Mathematical Biology*, Vol. 398C, pp 161-184. Elsevier Journals, 2005.

M. Weber: *Meshless Methods in Conformation Dynamics*. PhD thesis, FU Berlin, Februar 2006. Verlag Dr. Hut, München, 2006.

S. Kube, M. Weber: *Coarse Grained Molecular Kinetics*. ZIB-Report 06-35.

ZIB Scientific Computing:

Dept. Numerical Analysis and Modelling:

Peter Deufhard, Marcus Weber, Susanna Kube

Dept. Scientific Visualization:

Hans-Christian Hege, Daniel Baum, Johannes Schmidt-Ehrenberg

Cooperation:

FU Biocomputing:

Christof Schütte, Wilhelm Huisinga, Evelyn Dittmer

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