Enhanced Sampling Simulations of protein aggregation

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# Misfolding and aggregation

- Misfolding and aggregates are associated with diseases:
  - Alzheimer's
  - Parkinson
  - Cystic Fibrosis
- marker for these disease are amyloid fibril deposits
  - 4.7 Å between β-strands perpendicular to fibril axis
  - 6-10 Å between neighboring β-sheets
- but toxic species: solvable oligomers rather than fibrils?



### FIBER STABILITY AND TOXICITY



#### Jiang et al Elife. 2013. 2:e00857



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# Cylindrin β-barrel amyloid oligomers

- six identical 11-residue peptides that form out-of-register antiparallel β-strands in the shape of a barrel, instead of the in-register β-strands typically observed in amyloid fibrils
- Model for solvable toxic oligomers
- What determines stability of the oligomers?
- On or off pathway to formation of unsolvable fibrils?
- Mechanism of toxicity?



# Cylindrin as Model System (a) fibril (b) barrel







# Folding and Aggregation Landscape?



- Folding takes > ms s; aggregation takes even longer: ≈ h d
- Computational effort increases exponentially with system size (including solvent!)

# **Requirements on Sampling Methods**

- Find local minima
- Escape out of local minima and continue search

# Can be achieved by:

- Improved/adaptive steps
- Improved/adaptive weights



### Replica Exchange Sampling (Parallel Tempering)

- The probability of crossing barriers increases with temperature



- Walk in temperature, replica exchange with  $\min(1, \exp(\Delta\beta\Delta E))$ ,  $\beta = 1 / k_B T$ 



### **Replica Exchange with Tunneling**

F. Yasar, N.A. Bernhardt & U.H.E. Hansmann, J. Chem. Phys., 143 (2015) 224102.

- Common situation: exchange move leads to energetically unfavorable state in Multi-Markov-chain →low acceptance rate
- But if accepted, the system quickly evolves to a state with energies similar to the state before the exchange move.
- Examples: proteins in explicit solvent, resolution exchange
  - Number of replicas increases rapidly with system size, otherwise low acceptance rates
  - Simulation time increases, too, as more time required for round trips
- How to "tunnel" through the unfavorable "transition state"?



### **Replica Exchange with Tunneling**

F. Yasar, N.A. Bernhardt & U.H.E. Hansmann, J. Chem. Phys., 143 (2015) 224102



- Microcanonical molecular dynamics from A to A' (B to B')
- Conditional exchange of configurations, with kinetic energies rescaled such that total energies E(B") = E(A') and E(A") = E(B')

$$v''_{A} = v'_{A} \sqrt{\frac{E_2 - E_{pot}(q'_{A})}{E_{kin}(v'_{A})}} \qquad \qquad v''_{B} = v'_{B} \sqrt{\frac{E_1 - E_{pot}(q'_{B})}{E_{kin}(v'_{B})}}$$

• Microcanonical molecular dynamics from A" to  $\hat{A}$  (B" to  $\hat{B}$ )

- The configurations  $\hat{A}$  and  $\hat{B}$  are accepted with probability  $\exp(-\beta_1(E_{pot}(\hat{q}_A) - E_{pot}(q_B) - \beta_2(E_{pot}(\hat{q}_B) - E_{pot}(q_A)))$
- If rejected, the simulation continues with configurations A and B

### **Systems With Competing Attractors**

N.A. Bernhardt, W. Xi, W. Wang and U.H.E. Hansmann, JCTC 12 (2016) 5656.

- Problem: conversion between structures
- "feeding" of physical model by Go-model(s) $E = E_{phys} + \lambda E_{Go}$



- Replicas walk between Helix and Sheet folds.
- Measurements only at  $\lambda=0$  (no bias)
- Low Acceptance rate → use RET!

#### First Test: helix and sheet forming peptides N.A. Bernhardt, W. Xi, W. Wang and U.H.E. Hansmann, JCTC **12** (2016) 5656.

- **AFP:** 11 residue long polypeptide sequence ELLEKLLEKEK has 51% helicity at physiological temperature
- BFP: 16 residue long C-terminus of the B domain of protein G, known to form β-hairpins with a frequency of 42%



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### Walk in lambda-space

N.A. Bernhardt, W. Xi, W. Wang and U.H.E. Hansmann, JCTC 12 (2016) 5656.



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### Go Model feeding does not lead to Bias

N.A. Bernhardt, W. Xi, W. Wang and U.H.E. Hansmann, JCTC 12 (2016) 5656.

RET simulations were compared to REMD simulations

AFP		
	% Helix	% Hairpin
RET	42	0
REMD	53	0
Experiment	51	0
BFP		
	% Helix	% Hairpin
RET	% Helix 0	% Hairpin 48
RET REMD	% Helix 0 0	% Hairpin 48 38



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# Walk in λ-Space

H. Zhang, W. Xi, U.H.E. Hansmann and Y. Wei, JCTC, 13 (2017) 3936



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# Walk in λ-Space

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### Free Energy Landscape

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# *In vitro* and patient-derived Aβ-fibrils

- *In vitro* generated Aβ-fibrils are polymorphic
- In patient-derived fibrils only one form found J-X Lu et al., Cell 154 (2013) 1257
- This difference is not because of higher stability of patient-derived form!
  E.J. Alred, E.G. Scheele, W.M. Berhanu & U.H., JCP, 141 (2014) 175101.
- Are some Aβ-fibril structures "infectious"?

# Comparison of the two polymorphic forms of A $\beta$ wild-type and A $\beta_{1-40}$ E22 $\Delta$



Aβ<sub>1-40</sub> WT Angew. Chem. Int. Ed. 2015, 54, 331 – 335 J Am Chem Soc 2011,133:16013-16022

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### **Cross-seeding and infectious strains**

- $A\beta_{1-40}$  WT fibrils can be seeded with  $A\beta_{1-40}$  E22 $\Delta$  nuclei
- But not  $A\beta_{1-40} E22\Delta$  fibrils with  $A\beta_{1-40}$  WT nuclei
- Polymorphism of Aβ wild type
- Aβ wild type can form "infectious" strains



Neurodegener Dis 2014;14:151–159 ;Angew. Chem. Int. Ed. 2015, 54, 331–335

### Hybrid model simulation are used to study interconversion of two forms



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