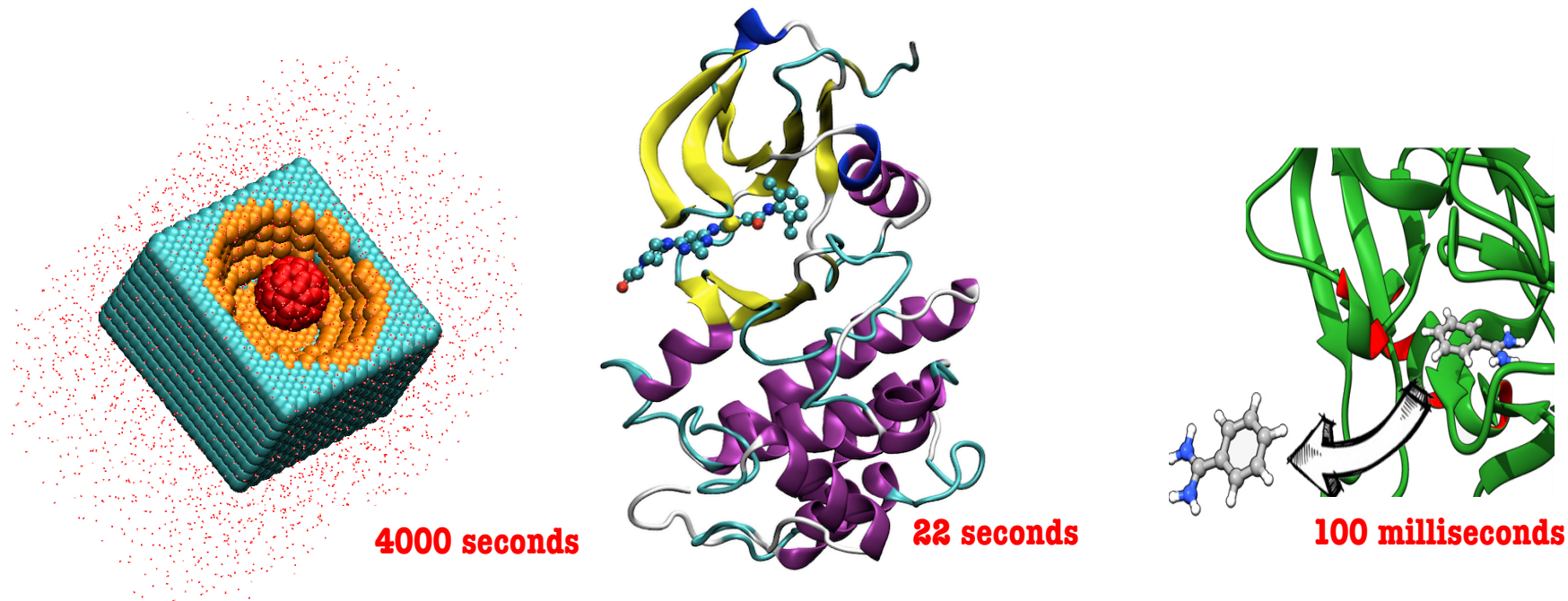


# Identifying and enhancing important fluctuations for sampling molecular systems with rare events



**Pratyush Tiwary**

**Department of Chemistry, Columbia University, New York**

Valsson, Tiwary & Parrinello *Ann. Rev. Phys. Chem.* 2016  
Tiwary & Berne *Proc. Natl. Acad. Sci.* 2016; *J. Chem. Phys.* 2016

# Outline

- Drug unbinding kinetics – a grand challenge for atomistic simulations and enhanced sampling
- Key issues in enhanced sampling:
  - Which collective variables to bias ?
  - How to get unbiased kinetics ?
- Spectral gap optimization of order parameters (SGOOP)
- Applications to fully atomistic simulations of unbinding in explicit water:
  - hydrophobic buckyball and cavity
  - FDA-approved anti-cancer drug and Src kinase
  - BIRB analog and p38 kinase\*
- Summary and outlook

# Acknowledgments

Bruce Berne (Columbia)  
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Axel van de Walle (Caltech/Brown)

SCHRÖDINGER®

**XSEDE**

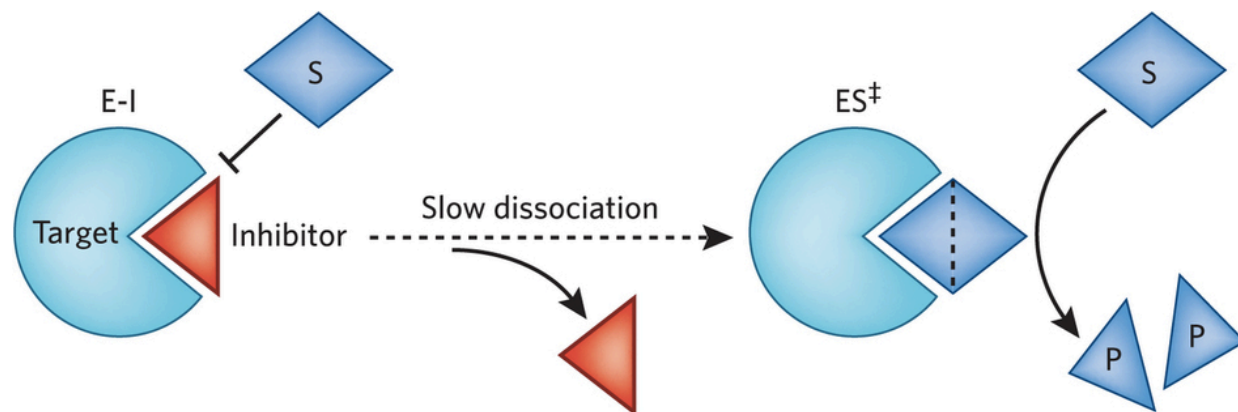
Extreme Science and Engineering  
Discovery Environment

**PLUMED**

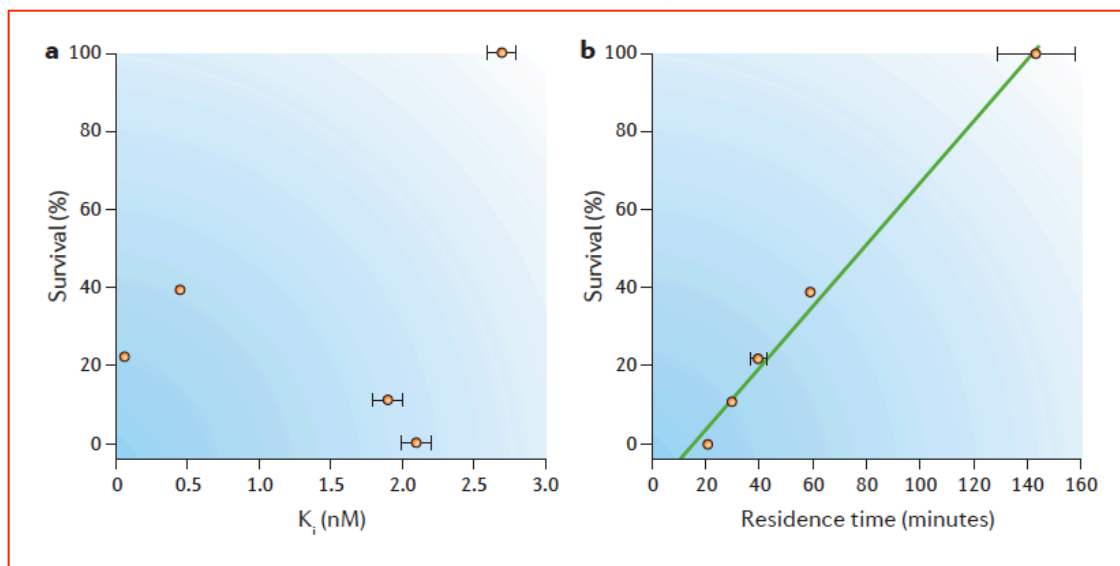


BILL & MELINDA  
GATES foundation

# Why care for drug unbinding kinetics



$$k_{\text{off}} = 1/\text{residence time}$$
$$K_i = k_{\text{off}} / k_{\text{on}}$$



*Copeland,  
Nature Chem Bio 2015*

**Atomistic simulations could rationalize molecular determinants of unbinding kinetics and assist tailor improved drugs**

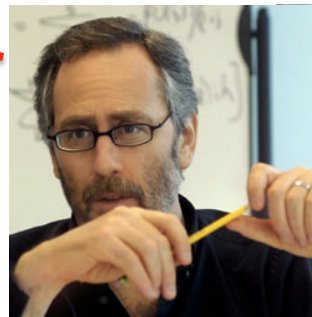
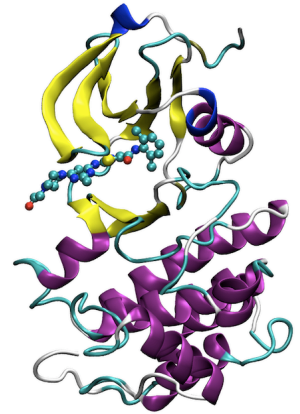
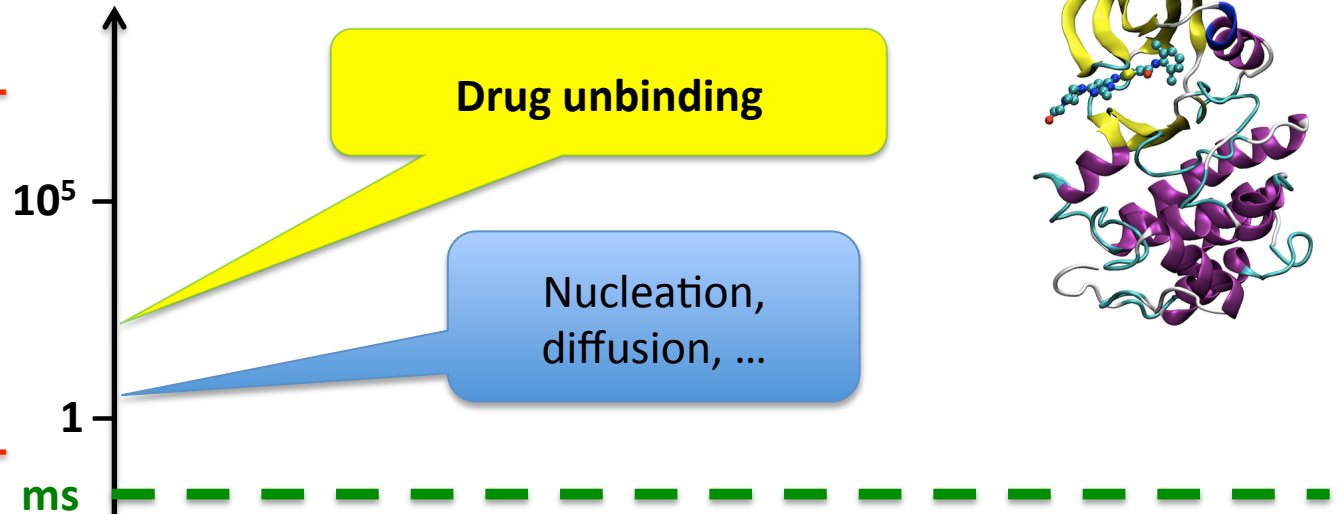
*Pathways, roles of protein flexibility and water*

**BUT...**



# The grand challenge in MD: timescales beyond milliseconds

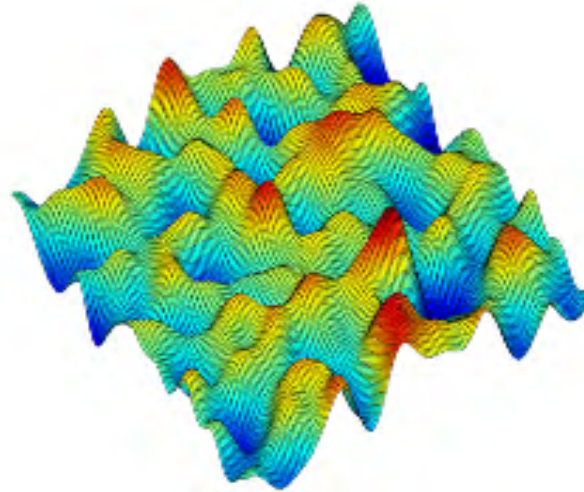
*For accurate statistics*



# Fluctuations that matter: Collective Variables (CV)

Potential Energy Surface  $U(\mathbf{R})$

- ➡ High-dimensional,
- ➡ Rugged



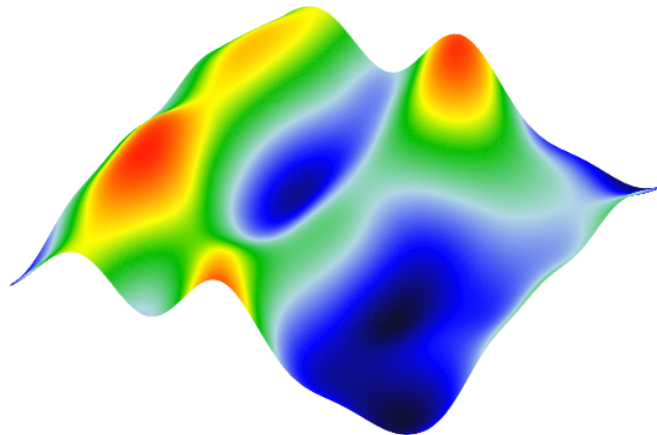
Introduce CVs that  
demarcate relevant stable  
states

- Need not be perfect RC

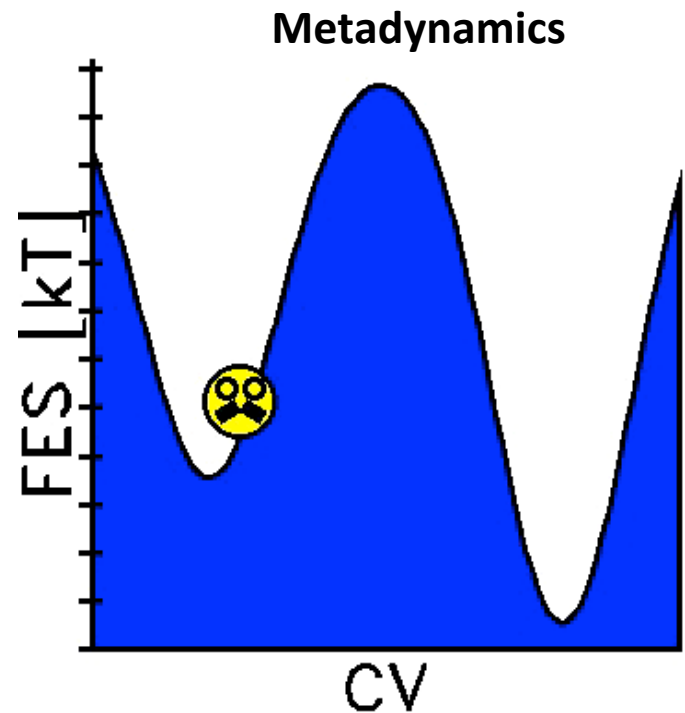
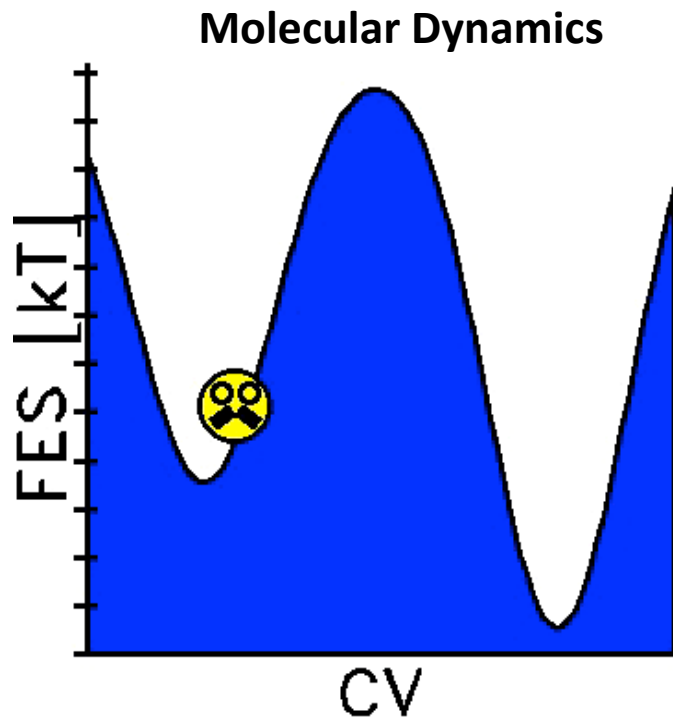
$$\mathbf{s}(\mathbf{R}) = (s_1(\mathbf{R}), s_2(\mathbf{R}), \dots, s_d(\mathbf{R}))$$
$$F(\mathbf{s}) = -\frac{1}{\beta} \log \int d\mathbf{R} \delta(\mathbf{s} - \mathbf{s}(\mathbf{R})) e^{-\beta U(\mathbf{R})}$$

Free Energy Surface  $F(\mathbf{s})$

- ➡ Low-dimensional,
- ➡ Smooth



# Time-dependent enhancement of important fluctuations: Metadynamics



Add repulsive gaussian where you go, as function of chosen collective variable (CV)

Recover all sorts of thermodynamic averages as function of **any** CVs

# Two big problems with enhanced sampling

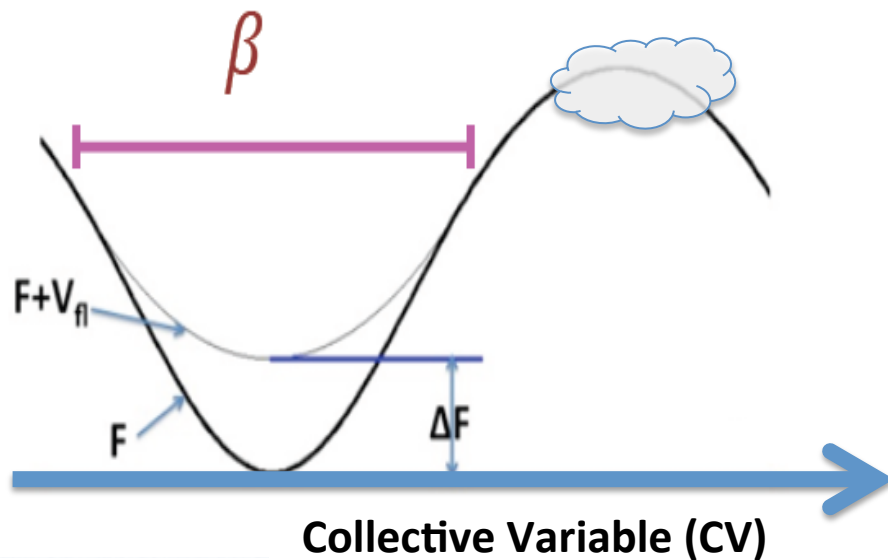
1. Need to presciently identify relevant low-dimensional collective variables

Solution : “Spectral gap optimization of order parameters (SGOOP)”  
Tiwary and Berne, Proc. Natl. Acad. Sci. 2016

2. True dynamical information lost during the course of biasing

Solution : “Infrequent metadynamics”  
Tiwary and Parrinello, Phys. Rev. Lett. 2013

# From metadynamics to dynamics



Acceleration  
factor of rates

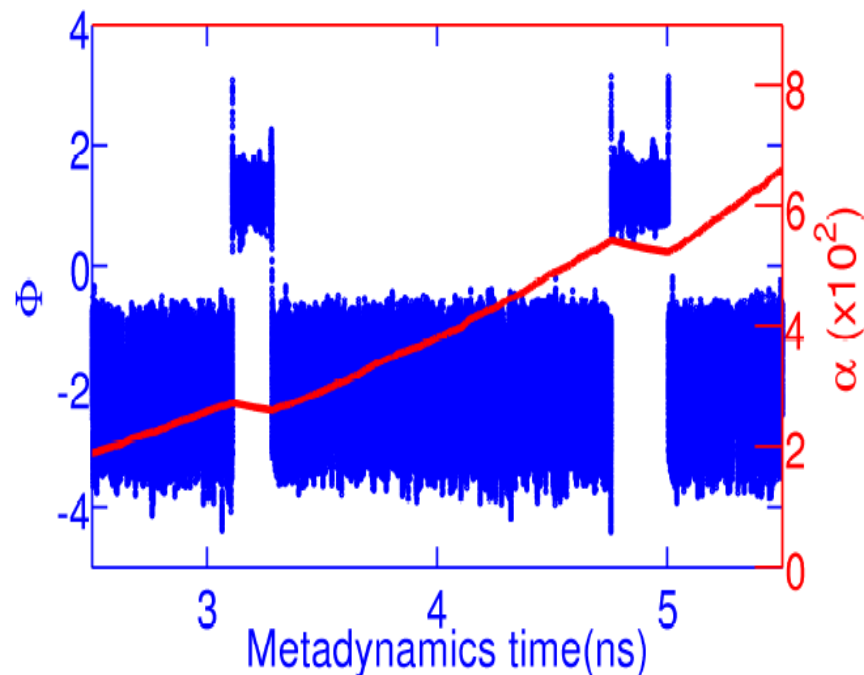
$$k_{\beta \rightarrow \alpha} \propto \kappa \frac{Z_{TS}}{Z_{\beta}} \quad \text{without bias}$$

$$k_{\beta \rightarrow \alpha}^* \propto \kappa \frac{Z_{TS}}{Z_{\beta}^*} \quad \text{with bias}$$

$$\frac{k_{\beta \rightarrow \alpha}^*}{k_{\beta \rightarrow \alpha}} = \frac{Z_{\beta}}{Z_{\beta}^*} = \langle e^{\beta V_{fl}} \rangle^*$$

Grubmueller PRE 1995  
Voter, JCP 1997 + PRL 1997  
Tiwarý & Parrinello, PRL 2013

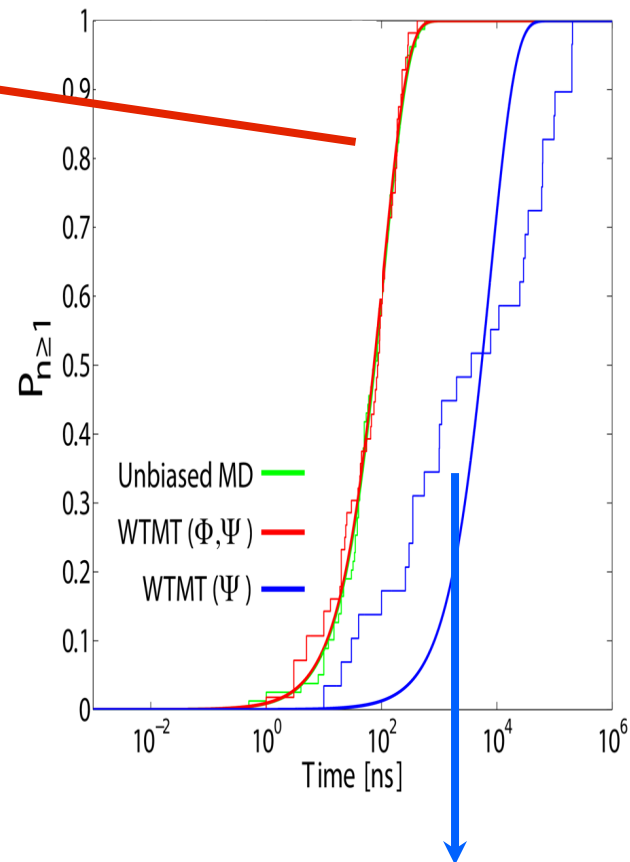
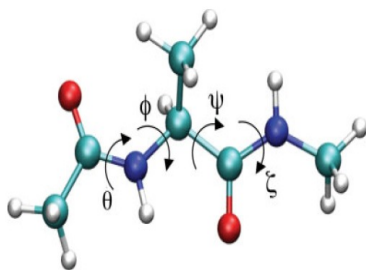
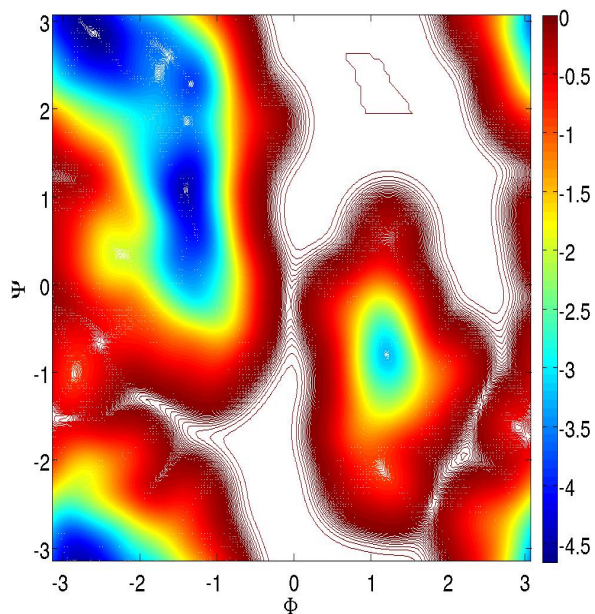
# Doing away with TS knowledge : Infrequent Metadynamics



- Transitions are rare-but-fast: make bias deposition slower than time in bottleneck
- Can identify *a posteriori* if requirements met – **TS corruption will introduce memory into dynamics**
- Other approaches can complement this: Mccarty, Valsson, Tiwary, Parrinello PRL 2015

# Check memoryless-ness through Poisson behavior *a posteriori*

small KS statistic  
large  $p$ -value ( $\sim 0.9$ )  
uncorrupted dynamics



large KS statistic  
small  $p$ -value ( $\sim 1\text{E-}4$ )  
corrupted barriers and dynamics

# Problems with enhanced sampling: #1

Need to presciently identify  
relevant low-dimensional collective variables  
(possibly from a larger dictionary of choices)

Solution :

“Spectral gap optimization of order parameters (SGOOP)”

Tiwary and Berne, Proc. Natl. Acad. Sci. 2016



## Is it even possible to solve this problem?

Statistical mechanics does not tell us what the relevant variables are. This is our choice. If we choose well, the results may be useful; if we choose badly, the results (while still formally correct) will probably be useless.

- Robert Zwanzig

*Nonequilibrium Statistical Mechanics*

(Ch. 8, “Projection Operators”)

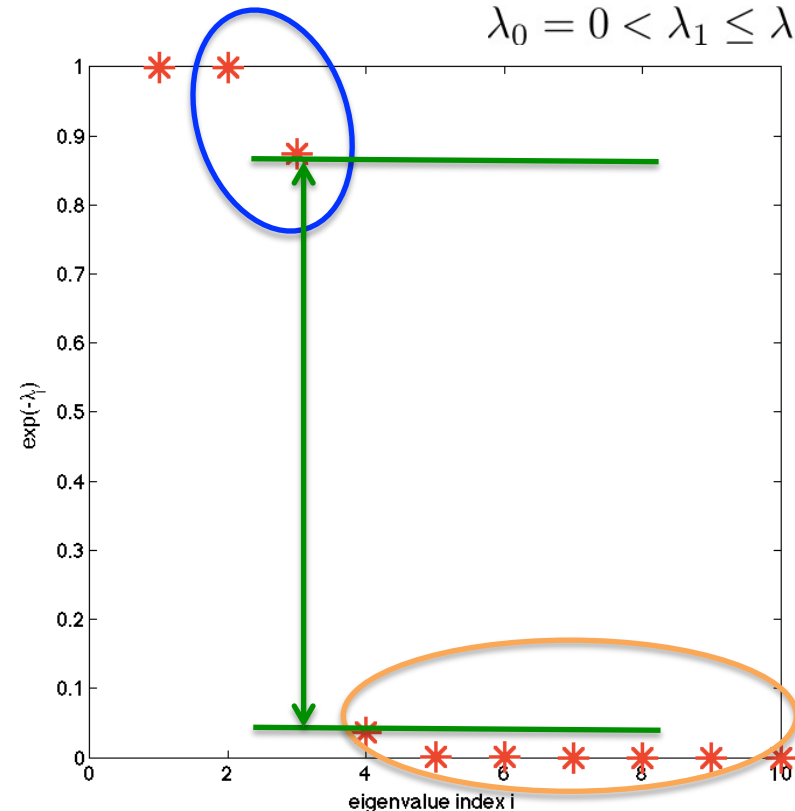
# Quantifying the importance of low-dimensional CV through spectral gap of unbiased dynamics

$$\partial_t p(\vec{r}, t) = \mathcal{L}(\vec{r}) p(\vec{r}, t)$$

$$p(r, t) = \phi_0(r) + \sum_{n \neq 0} c_n \phi_n(r) e^{-\lambda_n t}$$
$$\lambda_0 = 0 < \lambda_1 \leq \lambda_2$$

← How (unbiased) probability of being in CV region  $(r, r+dr)$  evolves in space and time

← Solution



## Motivation :

When projected on low dimensional CVs, the best CV will show best **timescale separation** into visible visible slow and orthogonal fast processes – highest **spectral gap**

## Challenge :

Given **limited stationary and dynamical knowledge** in rare event molecular systems, how to quantify spectral gap for various CVs?

# Maximum entropy over paths and Caliber

ET Jaynes, ARPC 1980

Presse, Ghosh, Lee, Dill RMP 2013

$$\text{Entropy over states} = -\sum_a p_a \log p_a$$

$$\text{Entropy over paths} = -\sum_{\tau} p_{\tau} \log p_{\tau} = -\sum_{a,b} p_a k_{a,b} \log k_{a,b}$$

$$\text{Caliber} = \underbrace{-\sum_{a,b} p_a k_{a,b} \log k_{a,b}}_{\text{Path entropy}} + \underbrace{\sum \rho_i * [\langle A^i \rangle - A_{obs}^i]}_{\text{Constraints}}$$

Maximum caliber relation between transfer matrix and stationary probabilities

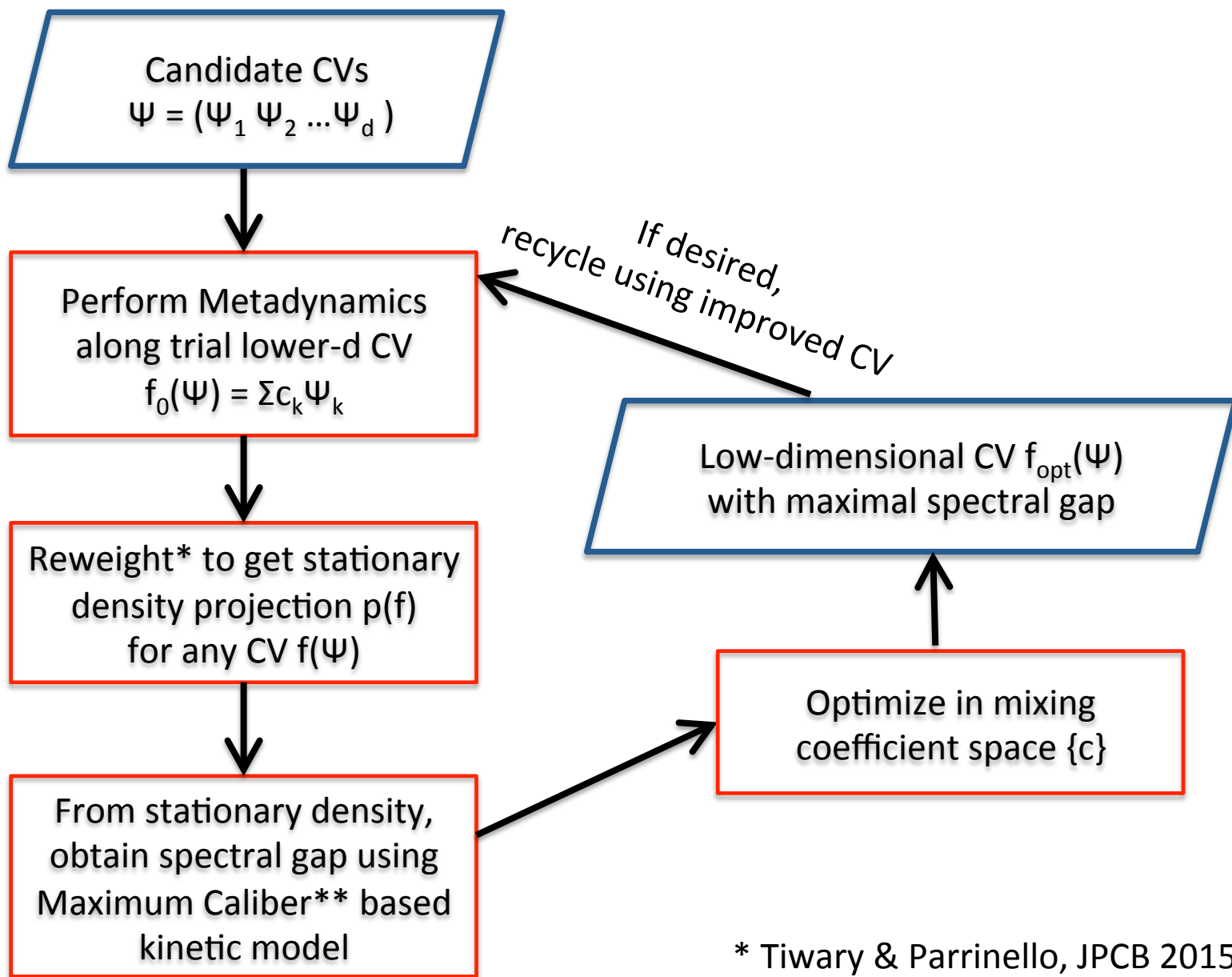
$$k_{a,b} = \sqrt{\frac{p_b}{p_a}} e^{-\sum \rho_i A_{a,b}^i}$$

Also Bicout & Szabo JCP 1998

Hummer NJP 2005

# Spectral gap optimization of order parameters: SGOOP

Tiwary and Berne, PNAS 2016

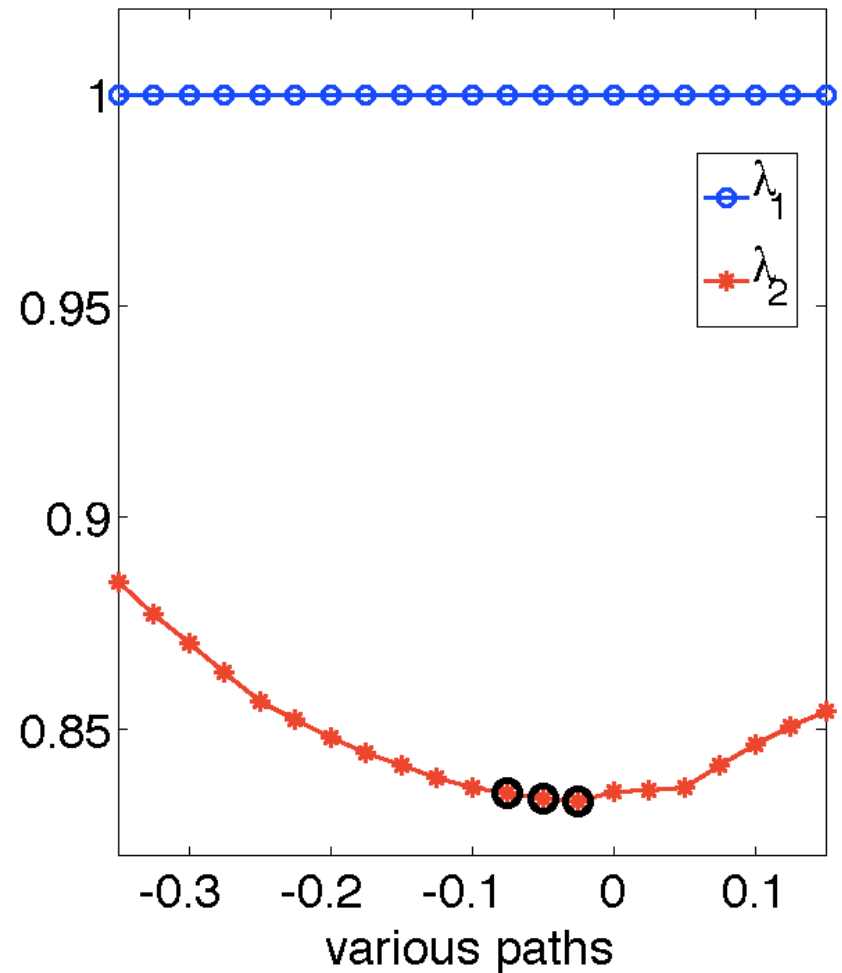
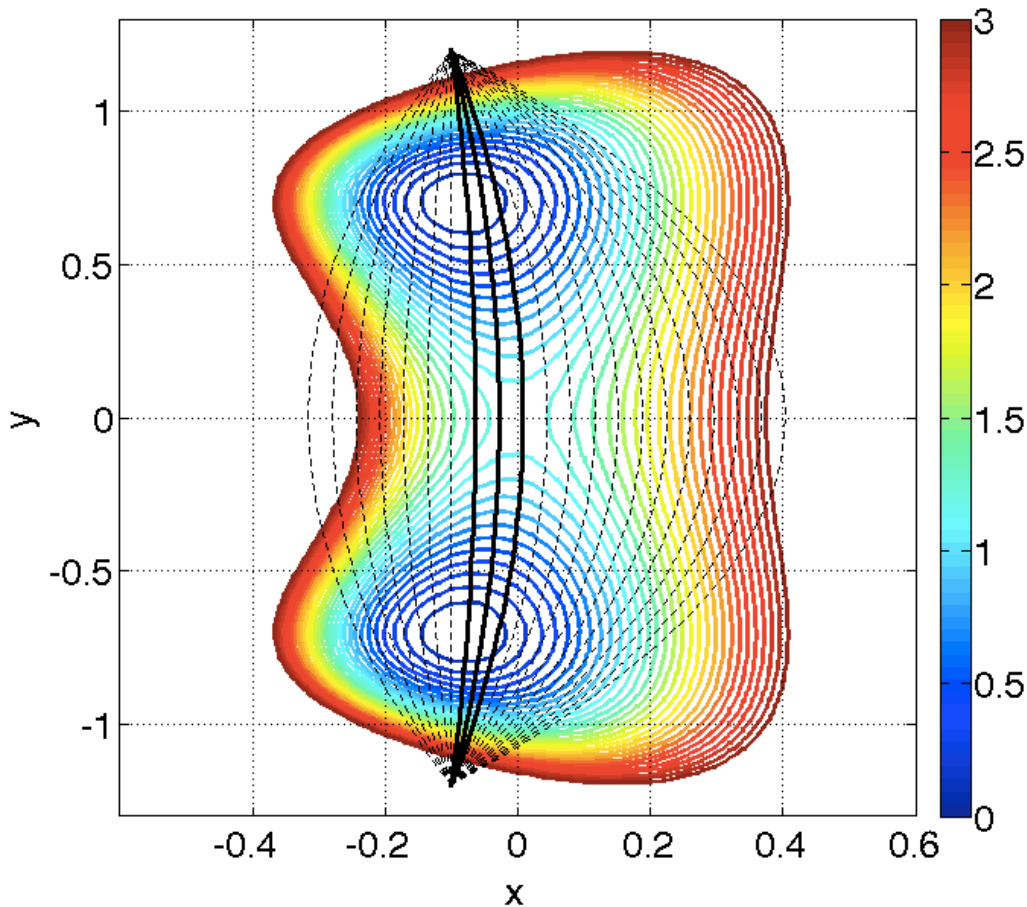


$$k_{a,b} = \sqrt{\frac{p_b}{p_a}} e^{-\rho}$$

\* Tiwary & Parrinello, JPCB 2015

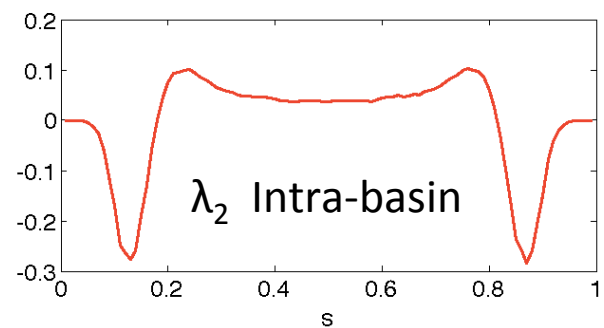
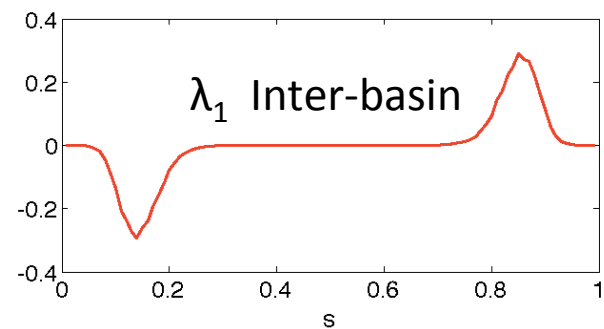
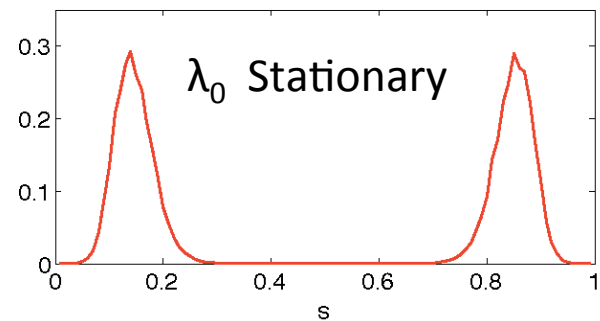
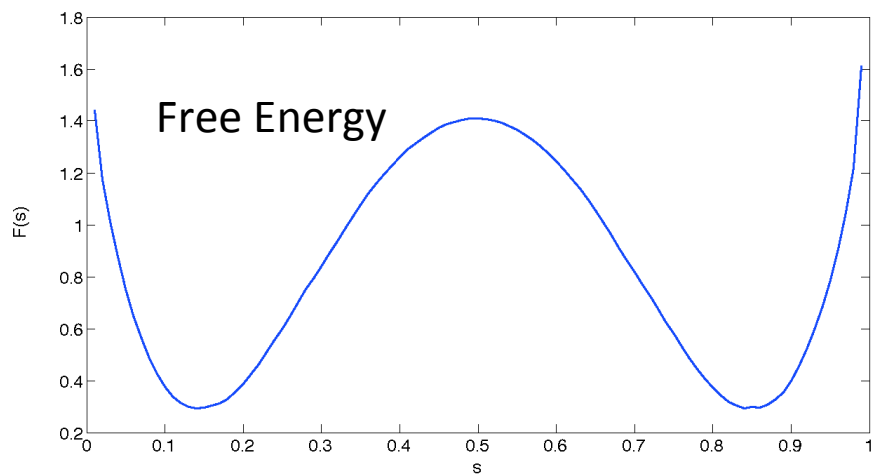
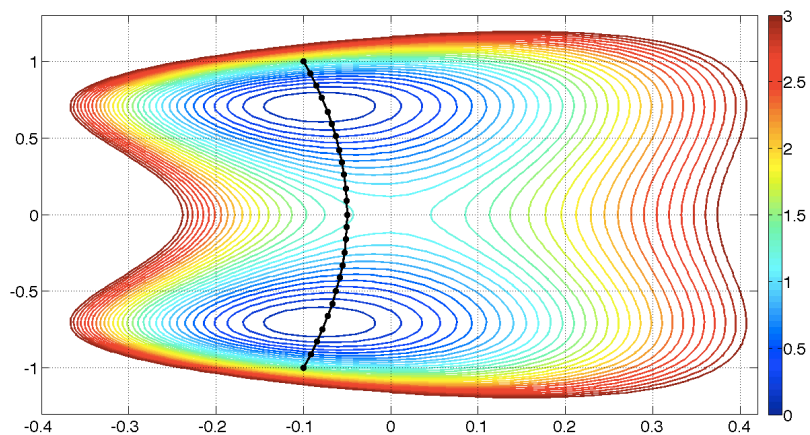
# 2-d model potential with path CVs

## Largest spectral gaps = minimum energy paths

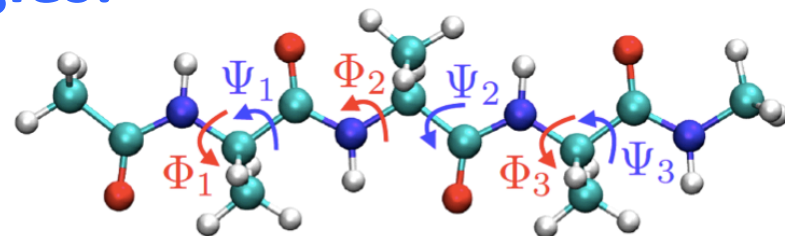


Model potential: De Leon, Berne JCP 1981  
Path CVs: Branduardi, Gervasio, Parrinello JCP 2007

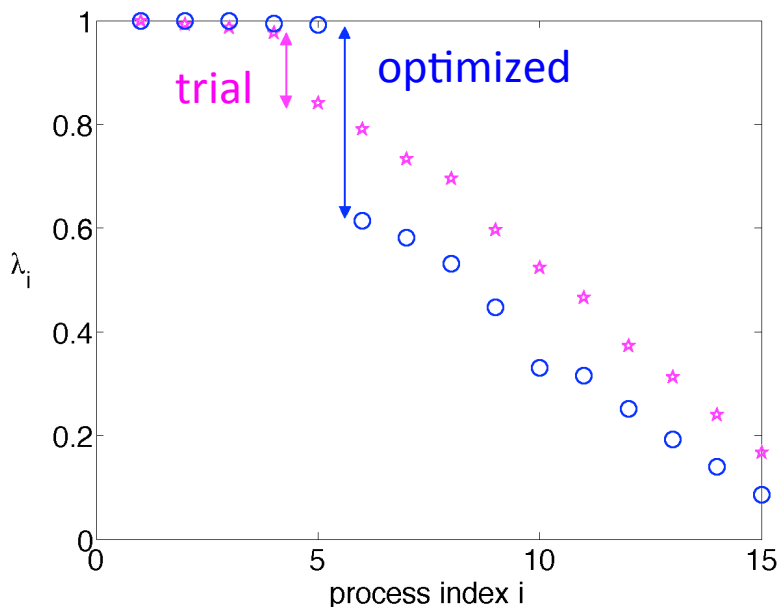
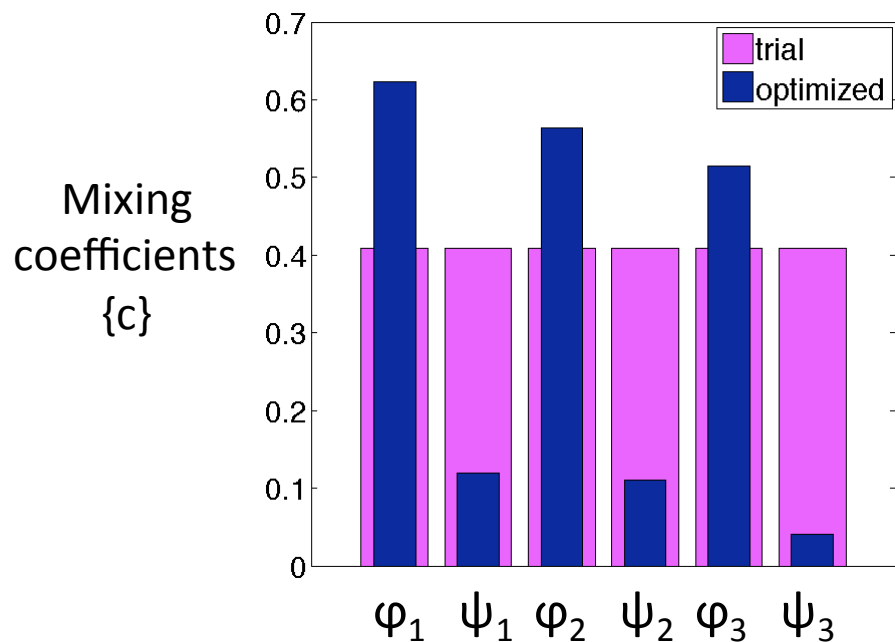
# Inter-basin and intra-basin eigenvectors



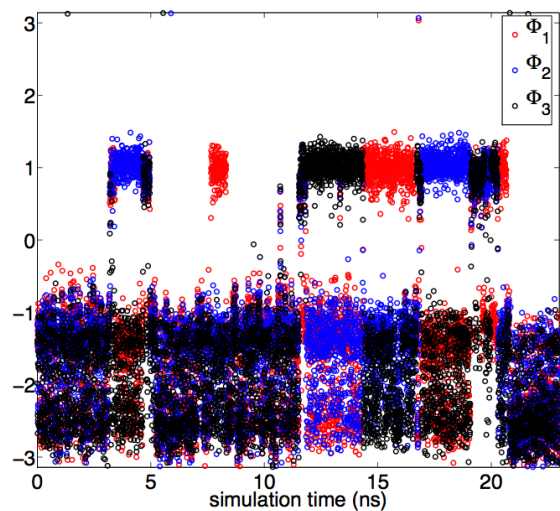
# SGOOP in action for free energies: Ace-Ala<sub>3</sub>-Nme



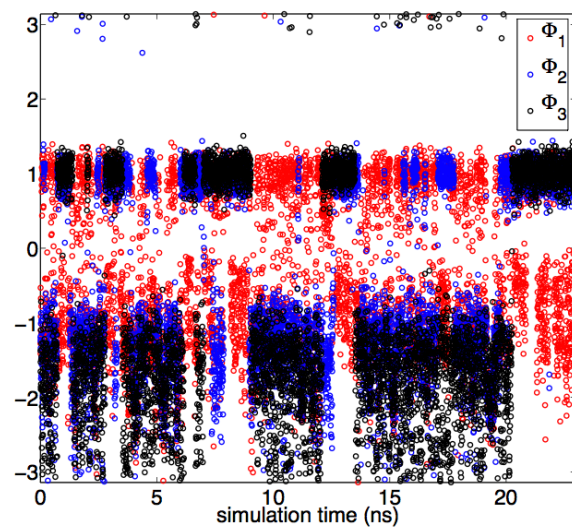
- **Objective:** find 1-d CV biasing which will maximize 6-d exploration



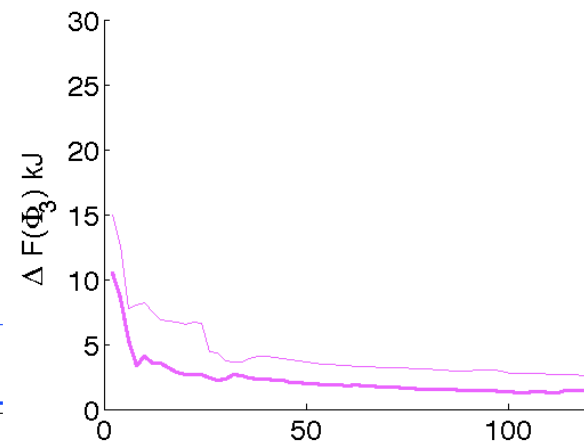
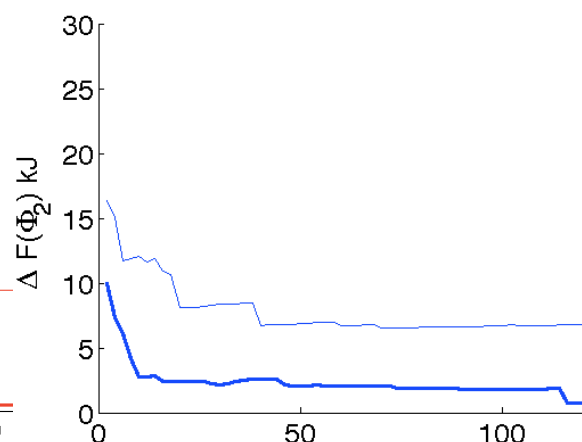
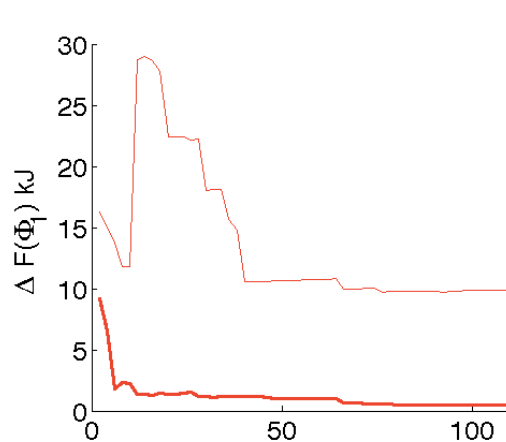
# Several orders of magnitude improvement in FES convergence speed



Trajectories biasing trial CV



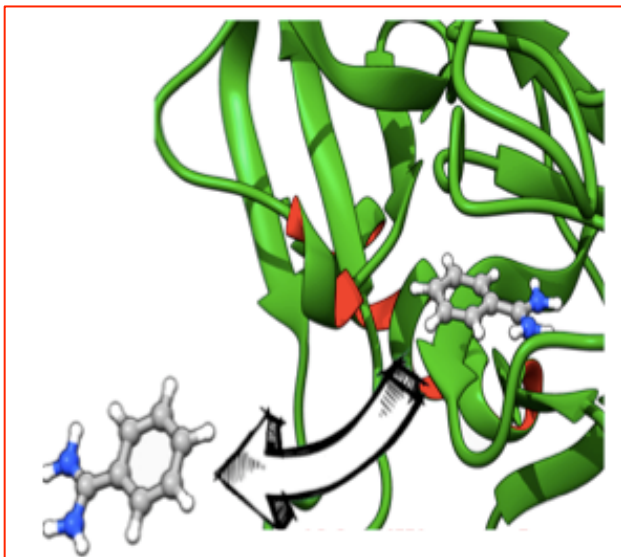
Trajectories biasing optimized CV



Error relative to reference FES for trial CV (thin line) and optimized CV (thick line)



# SGOOP for ligand unbinding



Many possible  
order parameters :

Ligand conformation/orientation

Ligand - binding pocket  
separation

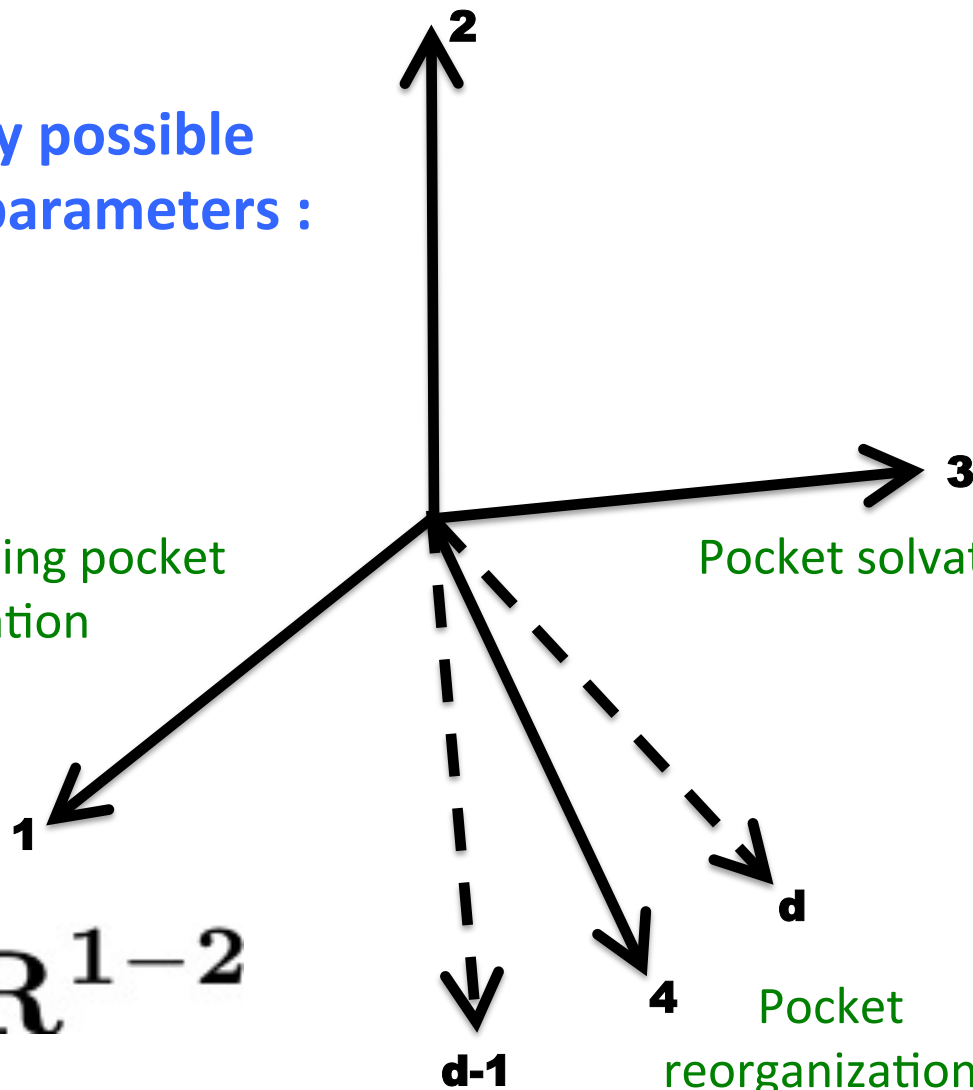
Pocket solvation

Pocket  
reorganization/  
flexibility

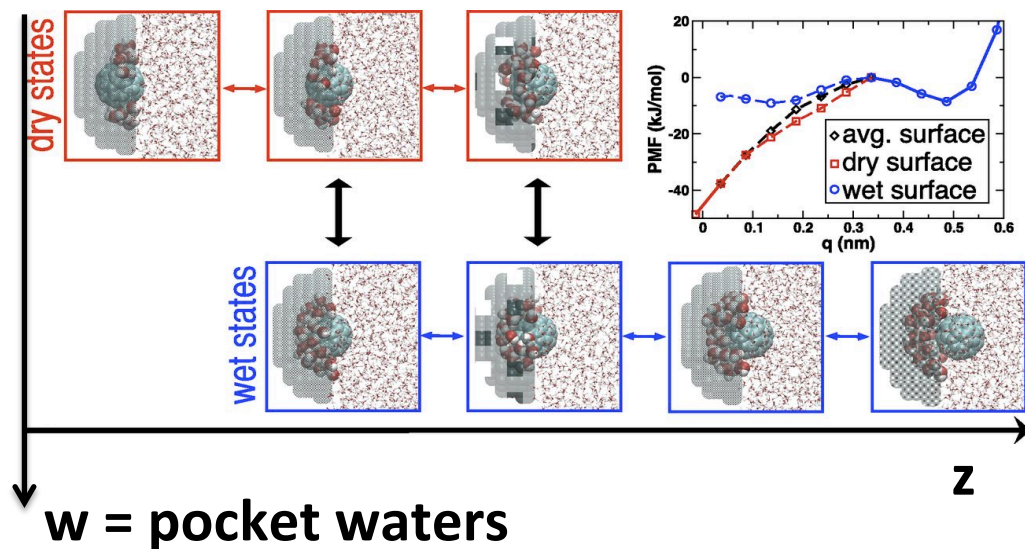
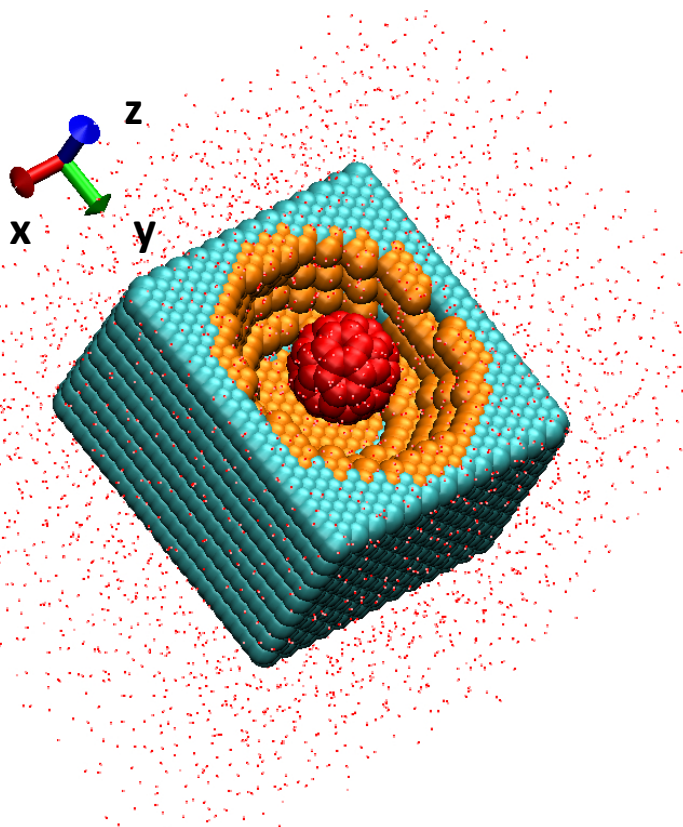
$$\mathbf{R}^{3N} \mapsto \mathbf{R}^d \mapsto \mathbf{R}^{1-2}$$

Intuition /  
non-equilibrium MD

SGOOP



# Buckyball-cavity unbinding in explicit TIP4P water



**Objective:** find optimal 1-d CV of the form

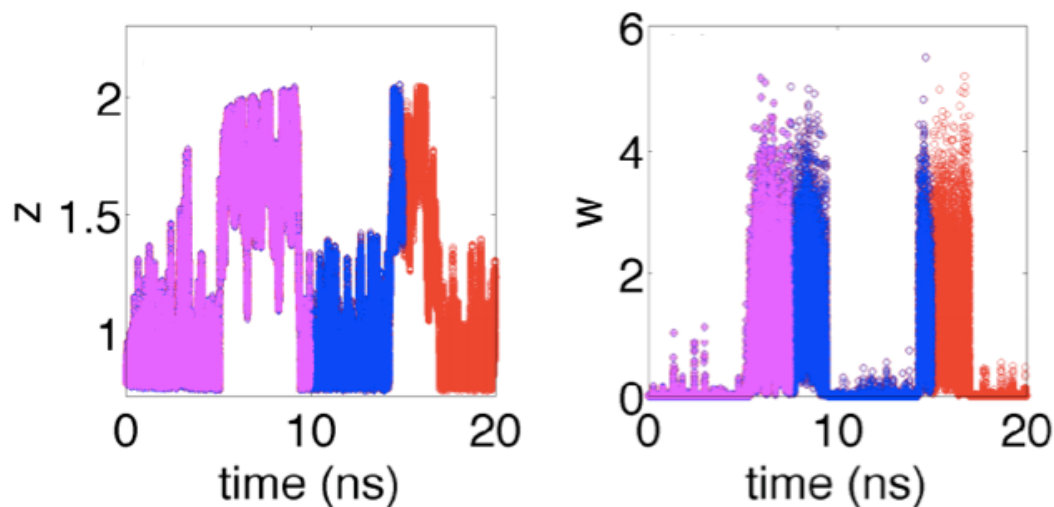
$$\Psi(z, w) = \{z + m_w w; m_w \geq 0\}$$

$m_w$  quantifies the “wetness” of CV

Mondal, Morrone, Berne PNAS 2013  
 Tiwary, Mondal, Morrone, Berne PNAS 2015  
 Tiwary and Berne JCP 2016

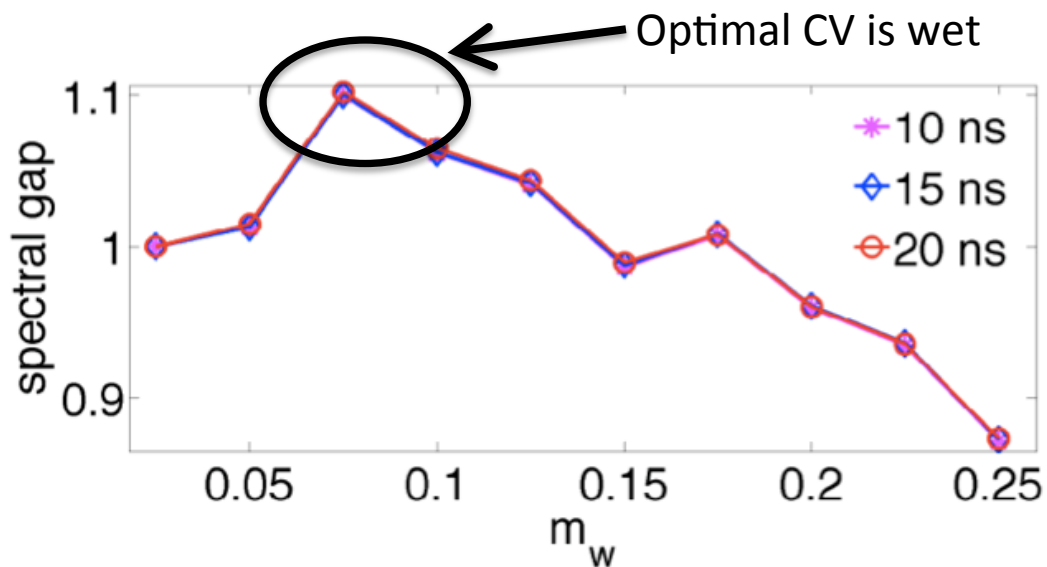
# SGOOP: How much do cavity water fluctuations really matter for driving unbinding?

Short metadynamics with trial CV =  $z$

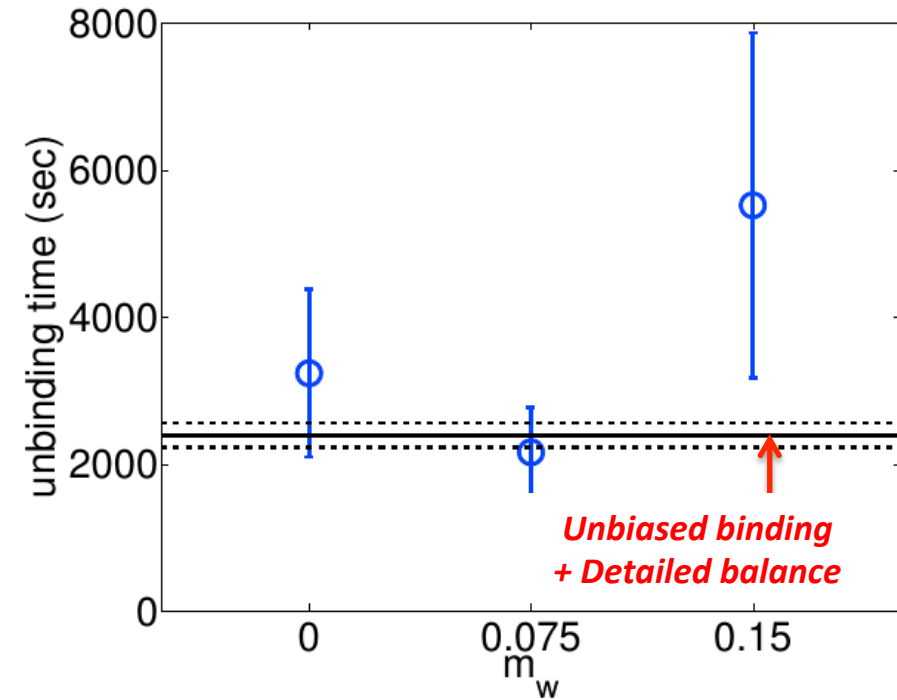


Robust spectral gap estimates for different CVs

$$\Psi(z, w) = \{z + m_w w; m_w \geq 0\}$$

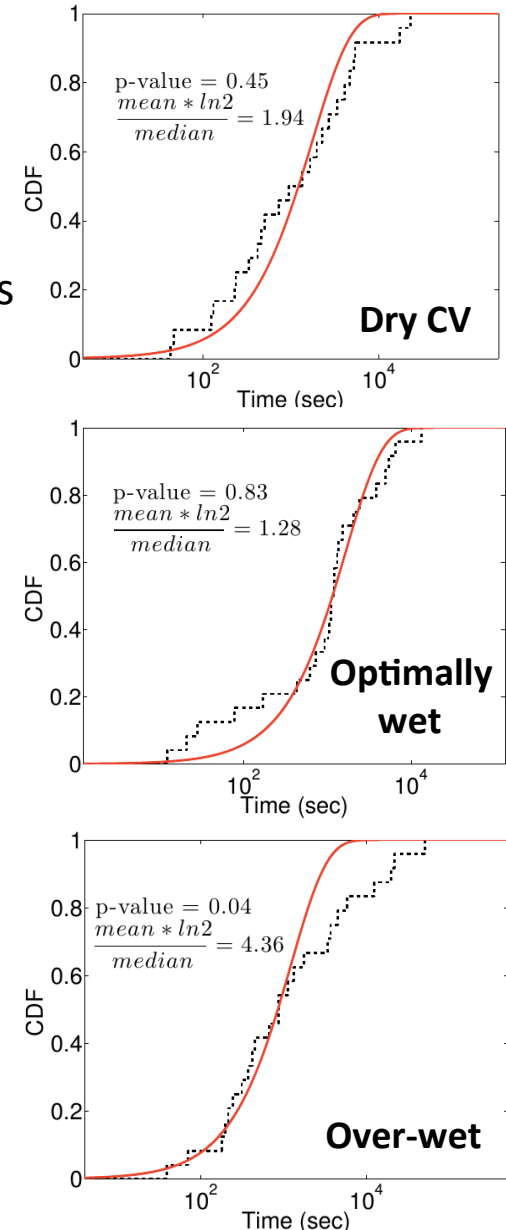


# Optimally wet CV gives the most accurate unbinding time through infrequent metadynamics



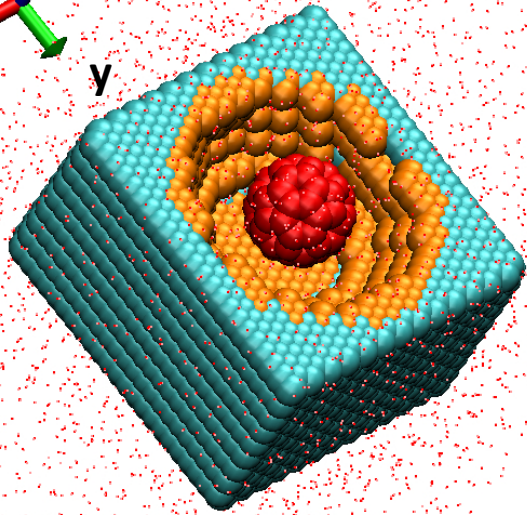
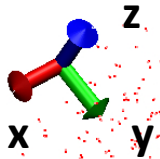
Infrequent metadynamics on optimally wet CV gives best agreement with detailed balance and unbiased binding time estimate

Infrequent metadynamics on optimally wet CV gives best Poisson fits:

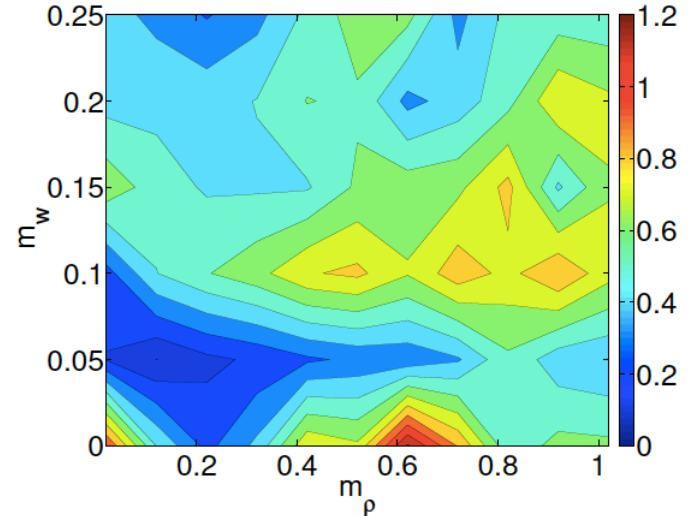


# What if buckyball has no steric constraints?

$$\rho = \sqrt{x^2 + y^2}$$



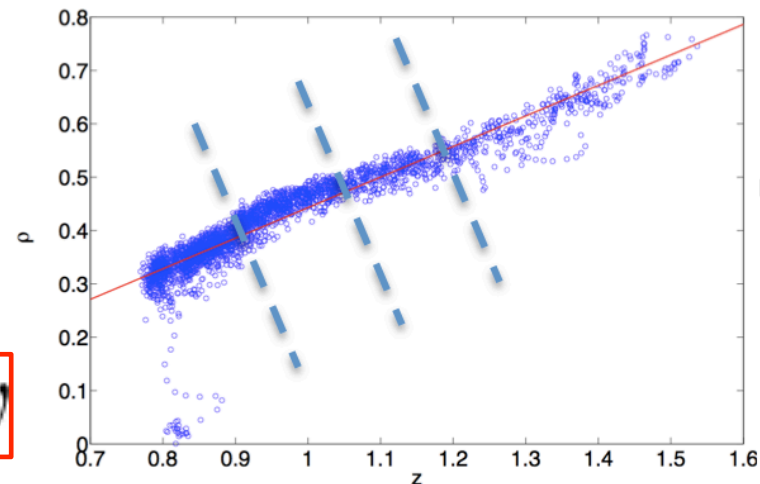
Contour map  
of spectral gaps



Water density fluctuations now become a  
driven rather than driving variable -  
**Buckyball rolls along the sides, water follows**

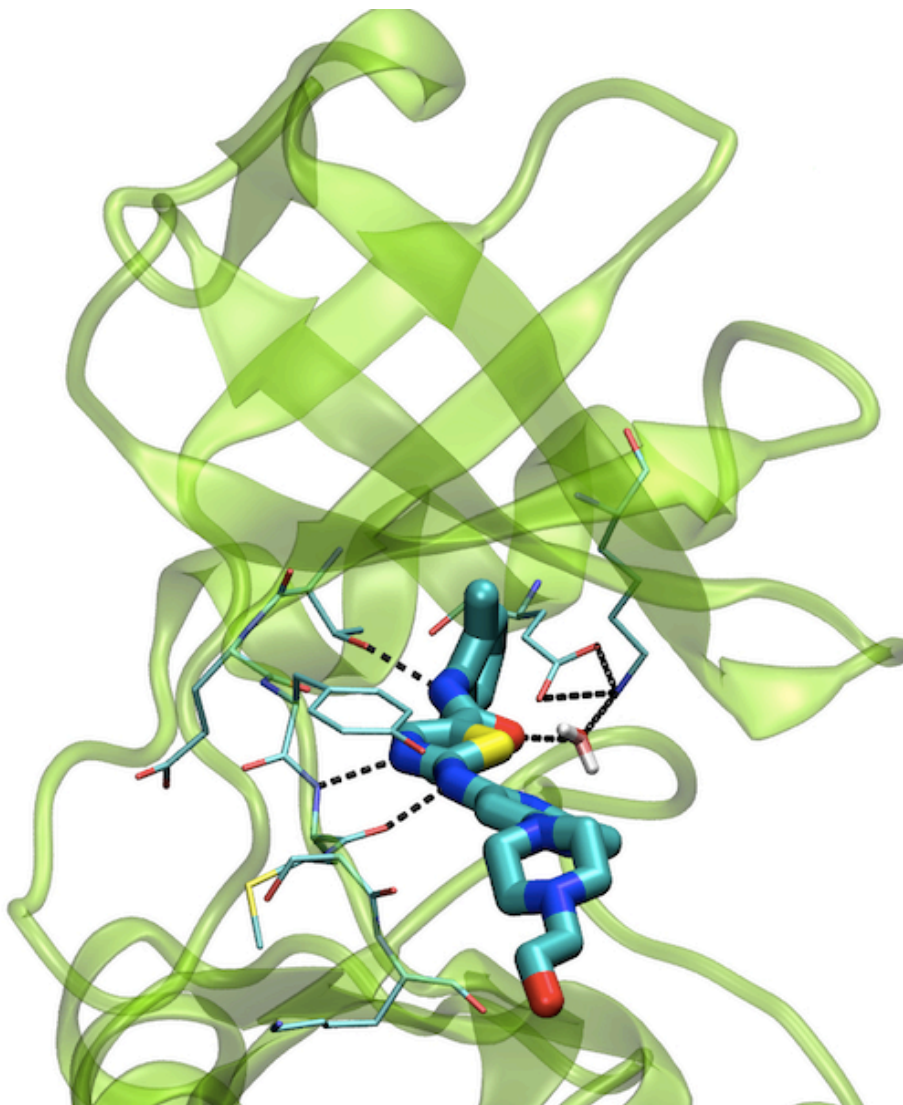
**Objective:** find optimal 1-d CV  
of the form

$$\Psi_{ideal} \approx z + 0.6\rho + 0.0w$$





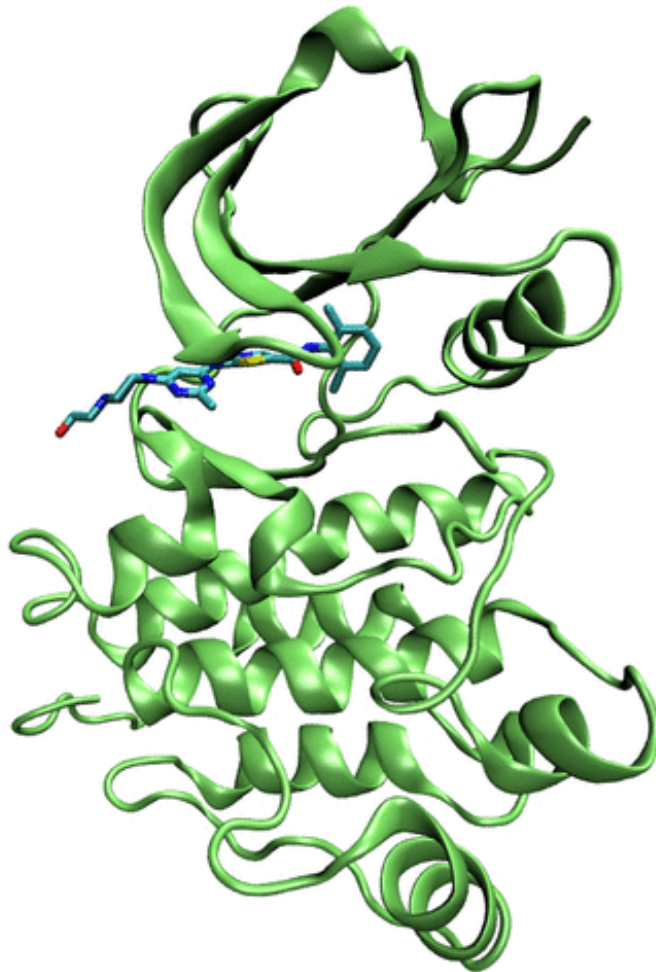
# Anti-cancer drug Dasatinib (Sprycel<sup>®</sup>, Bristol-Myers Squibb) from Src kinase



- ATP = energy currency  
Kinase = ATM card
- Previous works<sup>1,2</sup> studying binding
- 2 CVs:
  - (1) distance between H-bond formers
  - (2) solvation state of binding pocket

1. Shan, Shaw and co-workers, JACS 2011
2. Mondal, Friesner, Berne JCTC 2014
3. Shan, Kuriyan, Shaw et al PNAS 2009

# Anti-cancer drug Dasatinib (Sprycel<sup>®</sup>, Bristol-Myers Squibb) from Src kinase



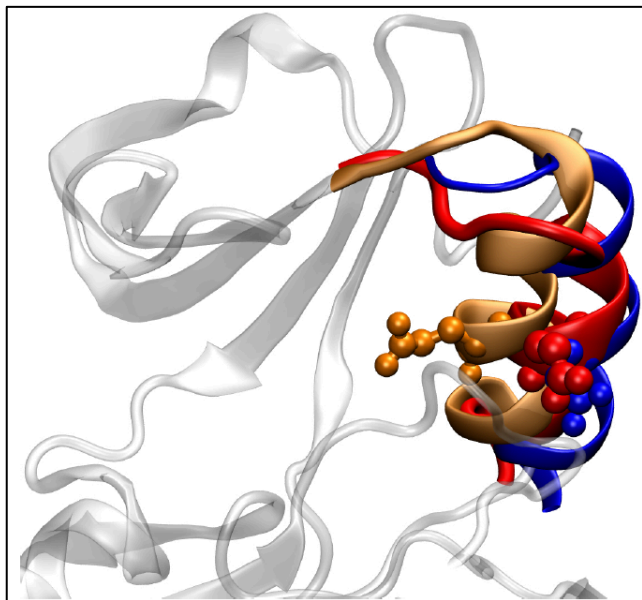
Using acceleration factor,  
our residence time  
estimate<sup>1</sup> = **20 +/-9 sec**

Experiments<sup>2</sup> = **18-900 sec**

**Variety of other detailed,  
intriguing findings – stay  
tuned for our paper<sup>1</sup>**

1. Tiwary, Mondal & Berne, under preparation
2. Shaw, Seeliger et al PNAS 2009;  
Seeliger, Soellner ACS Chem Bio 2016

# Coupled water-protein fluctuations matter



States #2-4

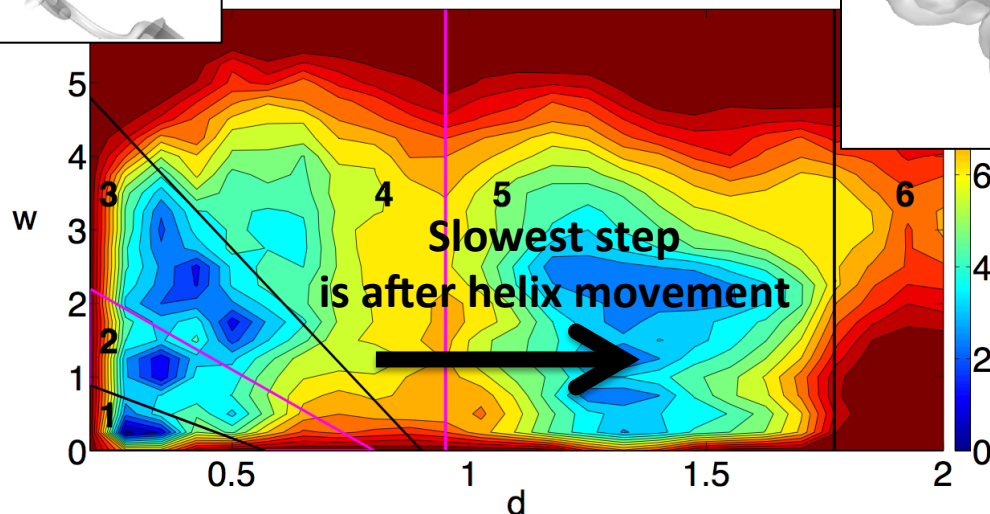
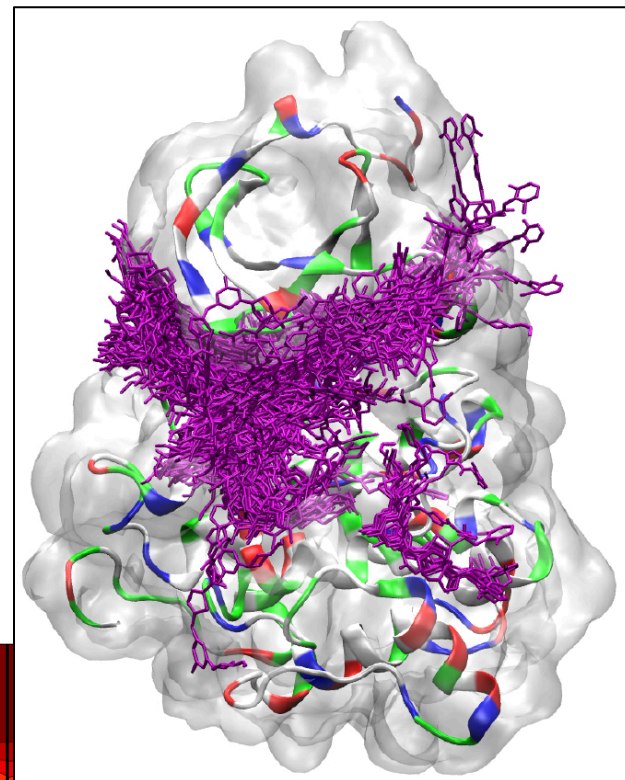
Orange =  $\alpha$ C helix in

Red =  $\alpha$ C helix out (this work)

Blue =  $\alpha$ C helix out (expt.)

State #6

Surface and bulk diffusion



Free energy landscape as function of  
d (Ligand-protein separation) and w (pocket hydration)



# Summary and outlook

- Recent progress in enhanced sampling with CVs allows obtaining dynamics and thermodynamics of rare-event (bio)molecular systems with statistical accuracy
- Successful applications to ligand unbinding kinetics – buckyball, trypsin-benzamidine, Src-Dasatinib, p38-BIRB
- Mixing order parameters into low-dimensional form is critical for methods such as metadynamics and umbrella sampling – SGOOP helps with quick and systematic refinement of CVs in hard to sample rare event systems
- Collective variables as tools to study molecular systems, that can be iteratively refined – **they are both input and output for enhanced sampling**