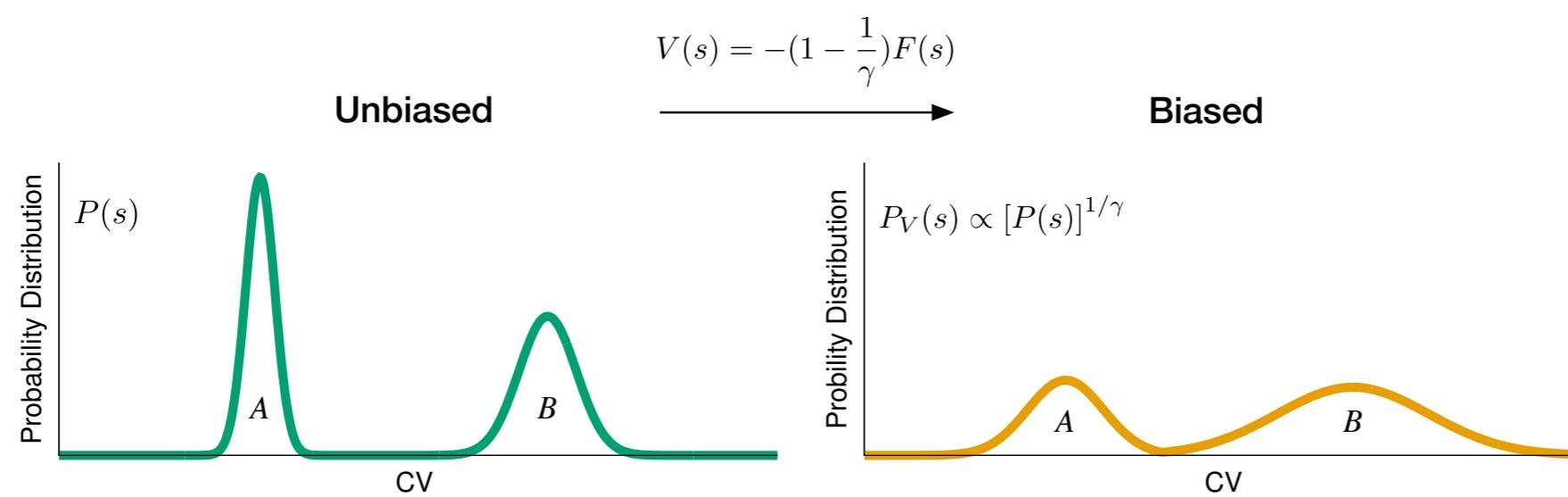


# Enhanced Sampling Methods for Soft Matter Simulations: Metadynamics

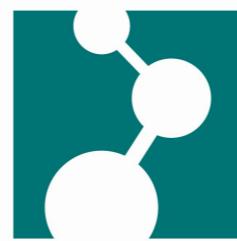


Omar Valsson



MAX-PLANCK-GESELLSCHAFT

Max-Planck-Institut  
für Polymerforschung  
Max Planck Institute  
for Polymer Research



THEORY  
GROUP

## Suggested Readings

Annual Review of Physical  
Chemistry 2016, 67:159-84

Enhancing Important  
Fluctuations: Rare Events  
and Metadynamics from a  
Conceptual Viewpoint

Omar Valsson,<sup>1,2</sup> Pratyush Tiwary,<sup>3</sup>  
and Michele Parrinello<sup>1,2</sup>

<http://doi.org/10.1146/annurev-physchem-040215-112229>

Other useful reviews:

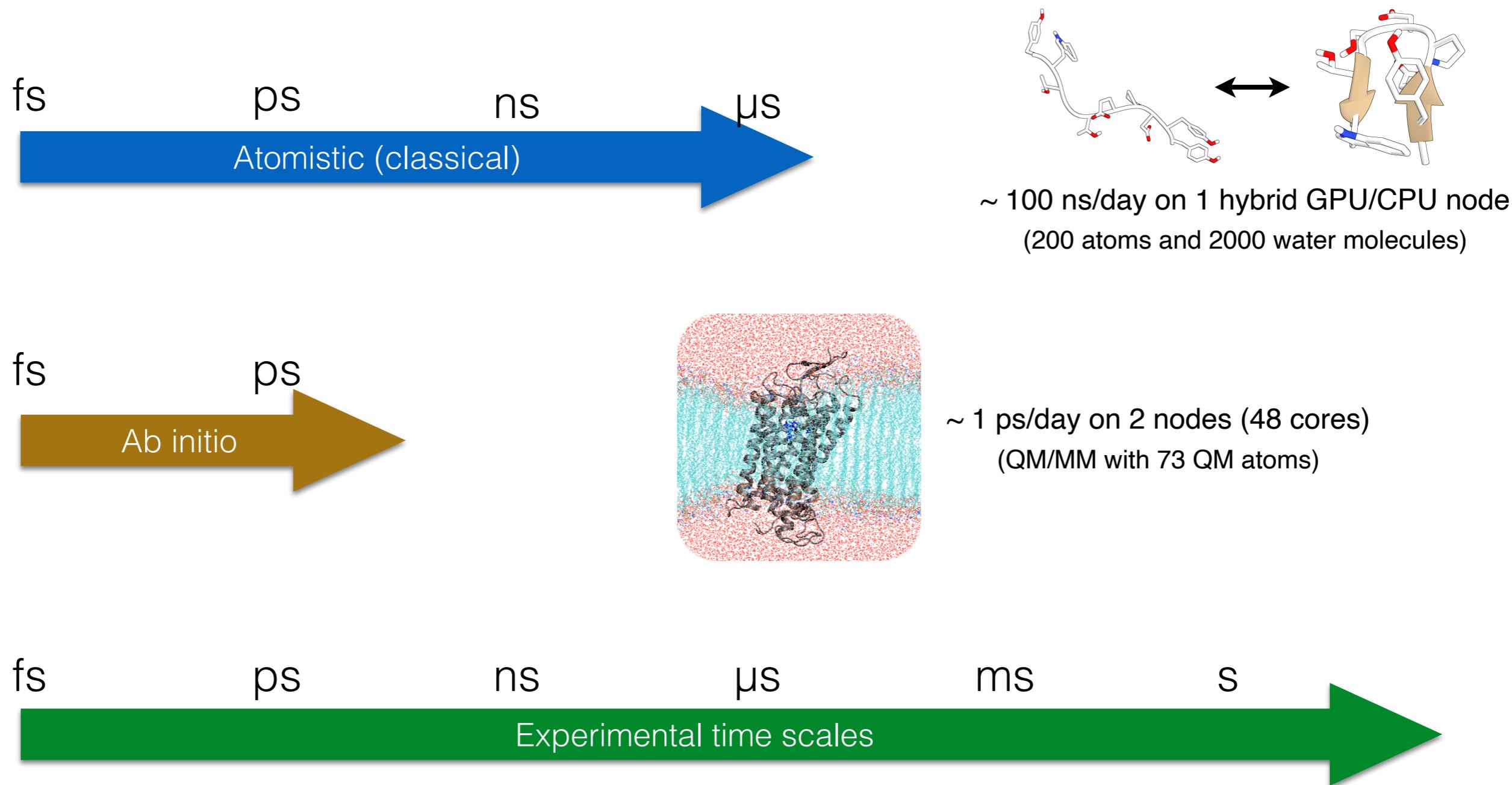
<https://doi.org/10.1038/s42254-020-0153-0>

[https://doi.org/10.1007/978-3-319-44677-6\\_49](https://doi.org/10.1007/978-3-319-44677-6_49)

[https://doi.org/10.1007/978-1-4939-9608-7\\_21](https://doi.org/10.1007/978-1-4939-9608-7_21) (also <https://arxiv.org/abs/1812.08213>)

# Time Scale Problem in Molecular Simulations

# Time Scale Problem in Molecular Simulations

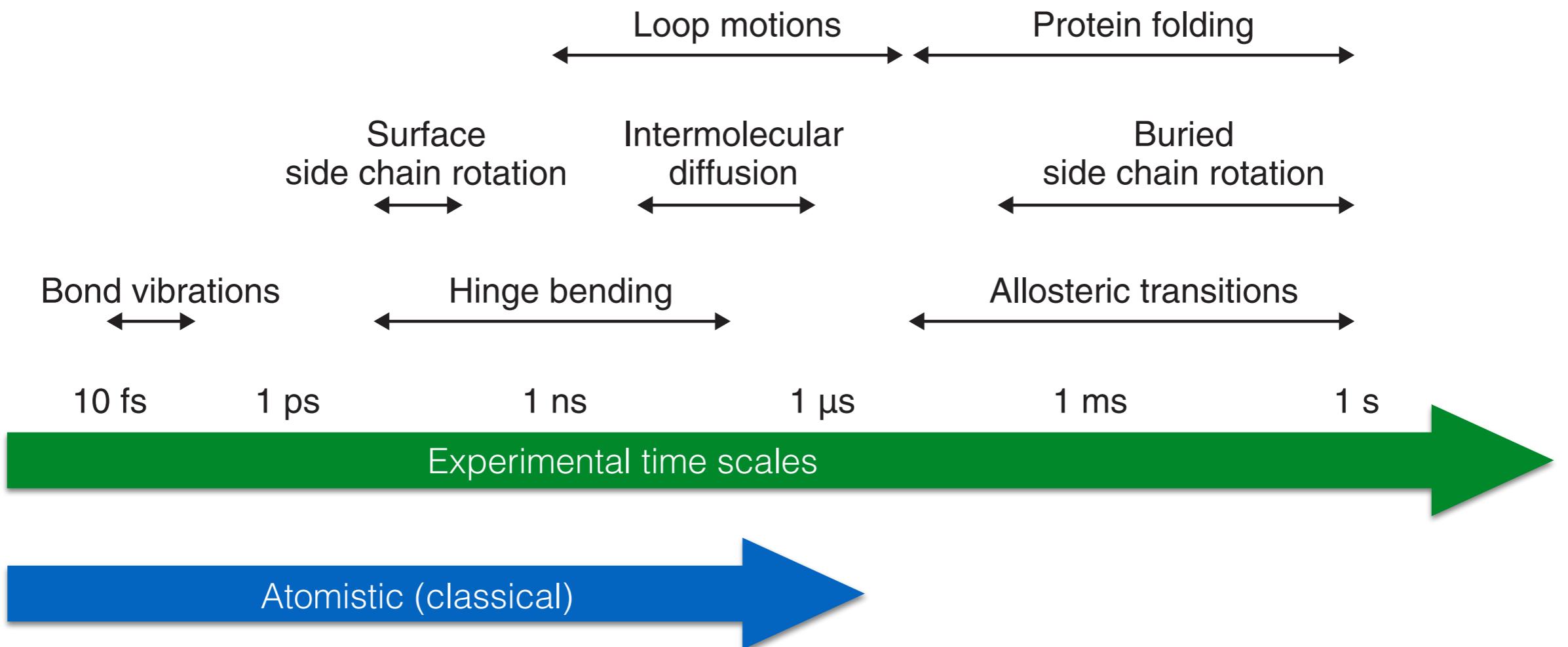


Conventional molecular simulations suffer from a **severe time scale problem**

# Time Scale Problem in Molecular Simulations

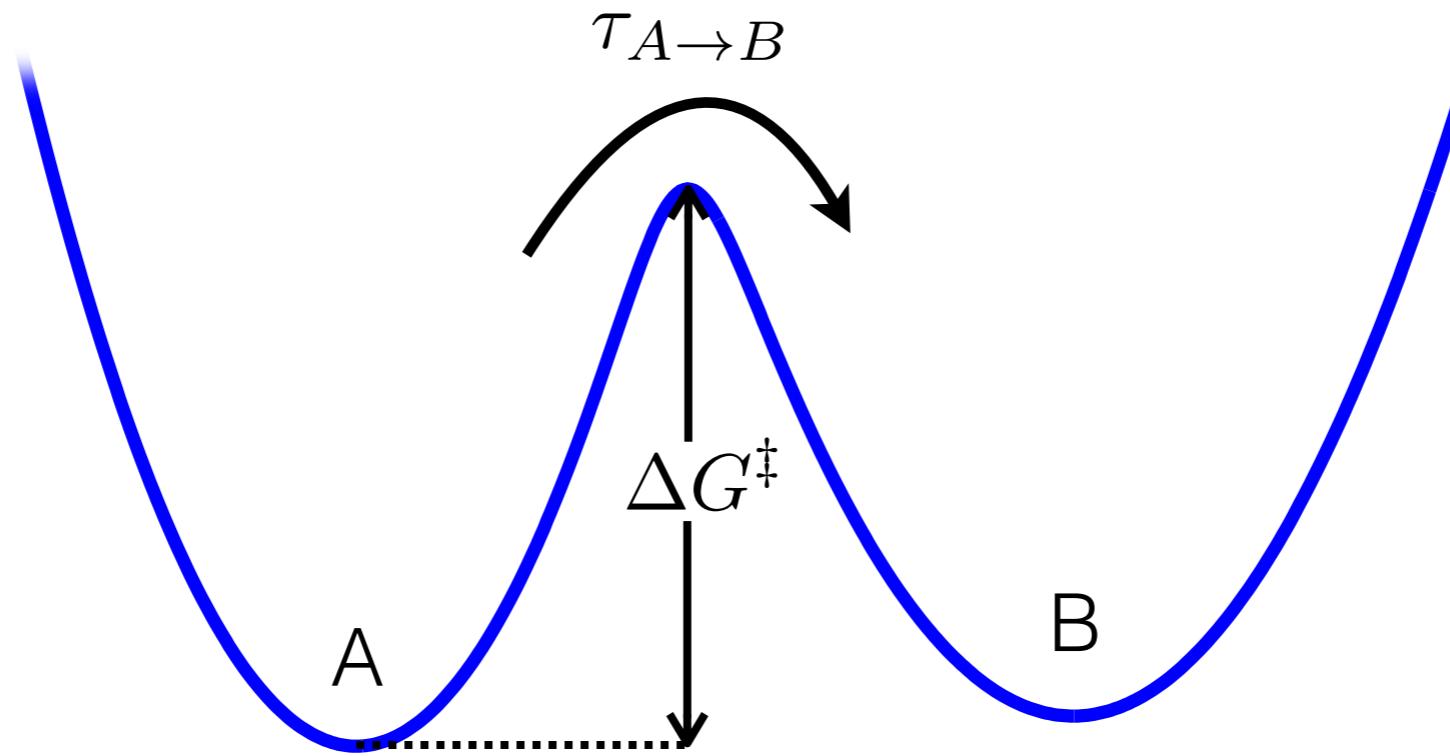
e.g. typical protein motions

Curr. Opin. Pharma. 10 745 (2010)



# Time Scale Problem in Molecular Simulations

Physical system characterized by many metastable states  
separated by high free energy barriers

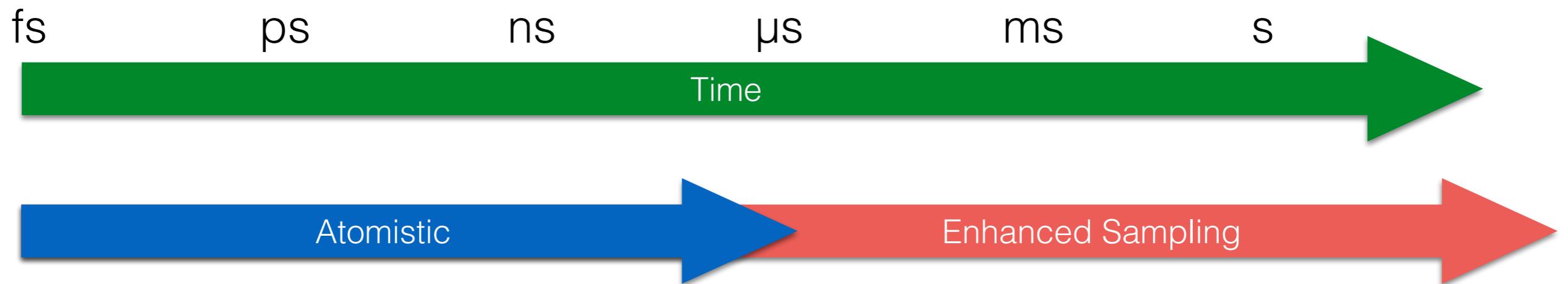


$$\tau_{A \rightarrow B} = \frac{1}{\nu_0 e^{-\Delta G^\ddagger/k_B T}} \propto e^{+\Delta G^\ddagger/k_B T}$$

$\Delta G^\ddagger \gg k_B T \rightarrow$  trapped in a metastable state

barrier crossings are **rare events** on the timescales we can afford

Advanced sampling method needed to bridge time scales

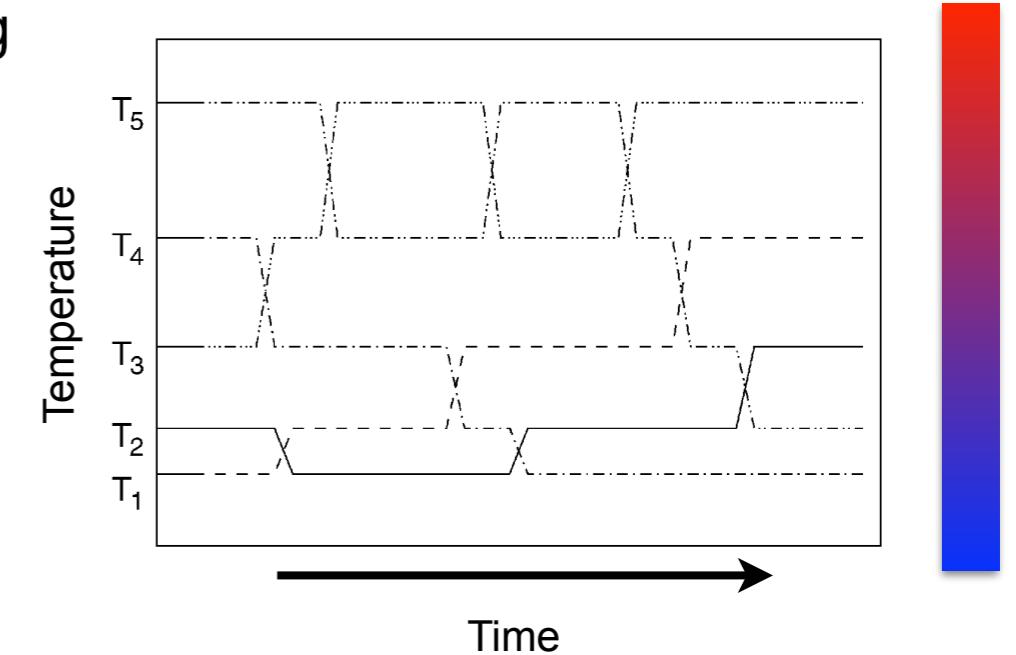


# Solving the Time Scale Problem

Parallel tempering: cross barriers by heating and cooling  
(or more generally replica exchange)

requires generally little information about the system

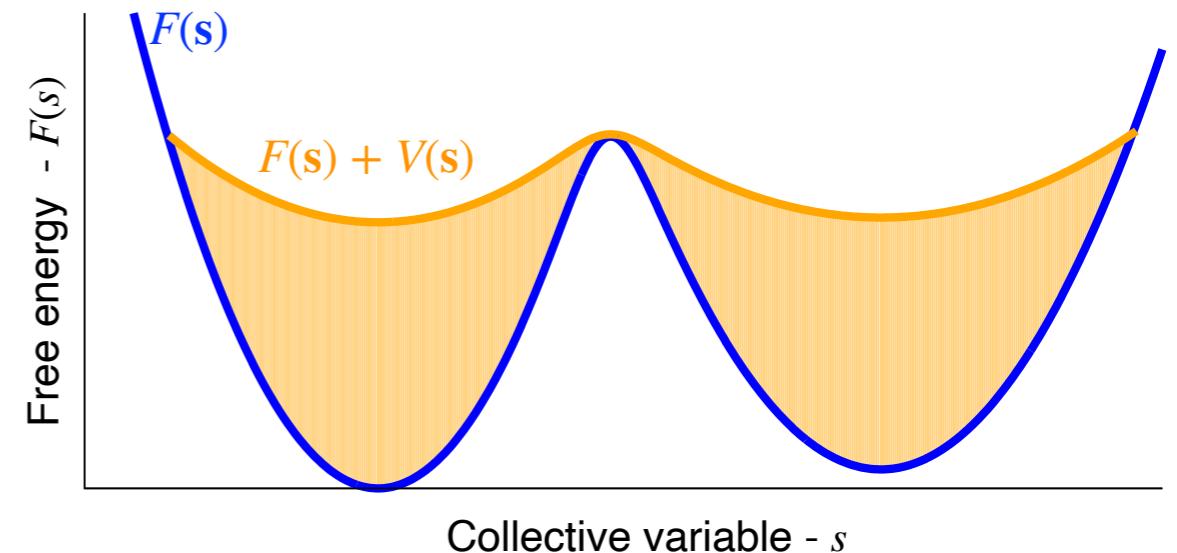
but expensive as we often need many replicas,  
especially for solvated systems



Focus on few relevant slow degrees of freedom  
i.e. collective variable based methods

generally less expensive

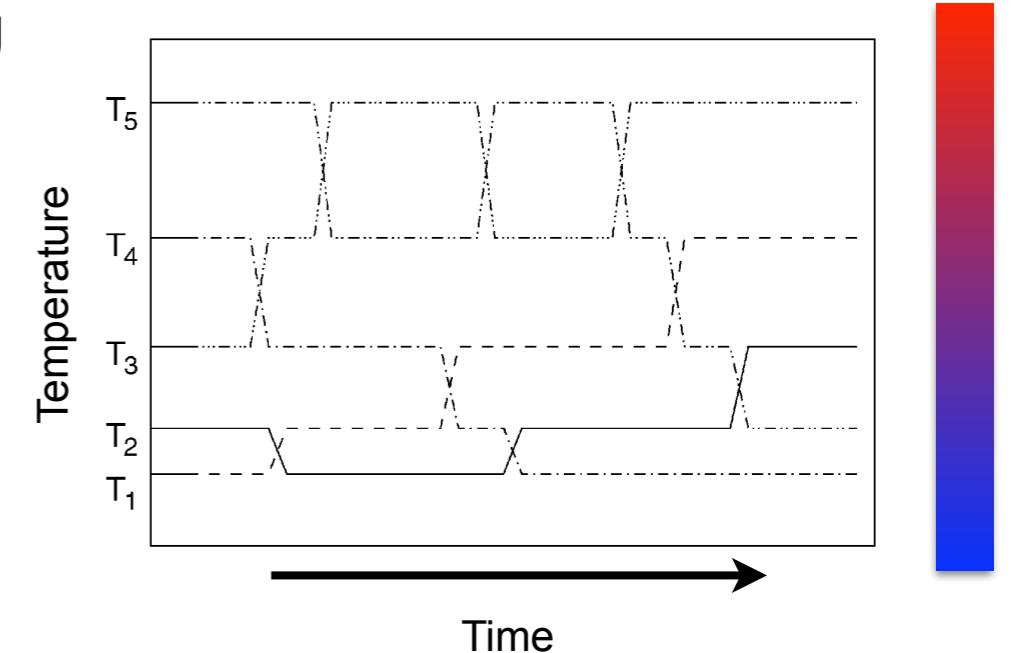
but requires knowledge about the system



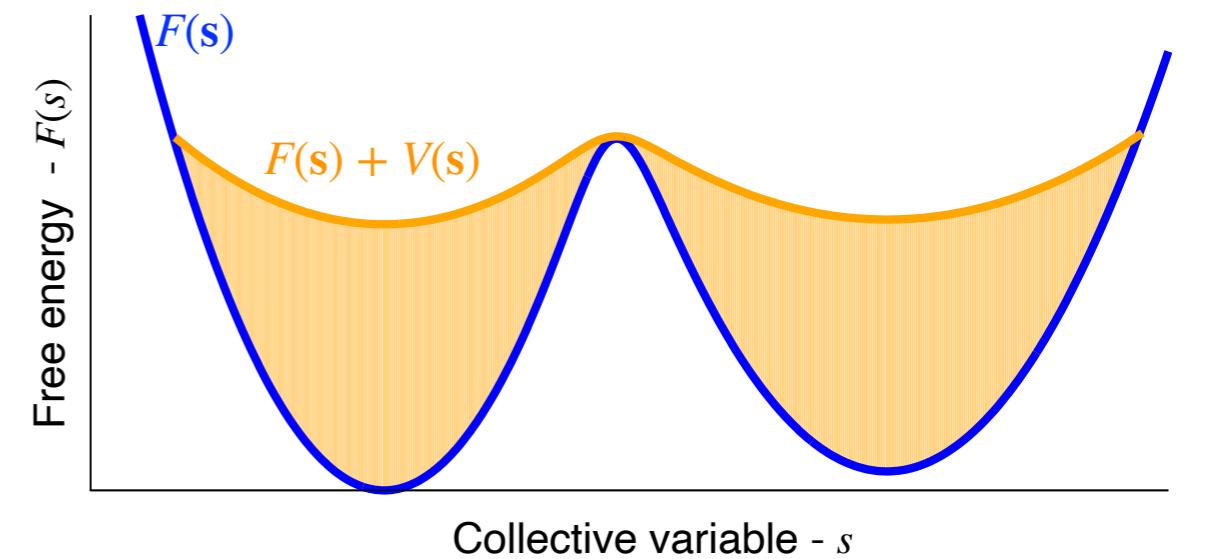
# Solving the Time Scale Problem

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but expensive as we often need many replicas,  
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Focus on few relevant slow degrees of freedom  
i.e. collective variable based methods  
generally less expensive  
but requires knowledge about the system



# Collective Variables (CVs) and CV-based Enhanced Sampling Methods

# Mapping to a Lower Dimension

Start by reducing the description of the problem to a reduced number of variables

$$\mathbf{R} = (\mathbf{r}_1, \mathbf{r}_2, \mathbf{r}_3, \dots, \mathbf{r}_N) \in \mathbb{R}^{3N}$$

high-dimensional space ( $\sim 10^4\text{-}10^6$ )  
hard to understand



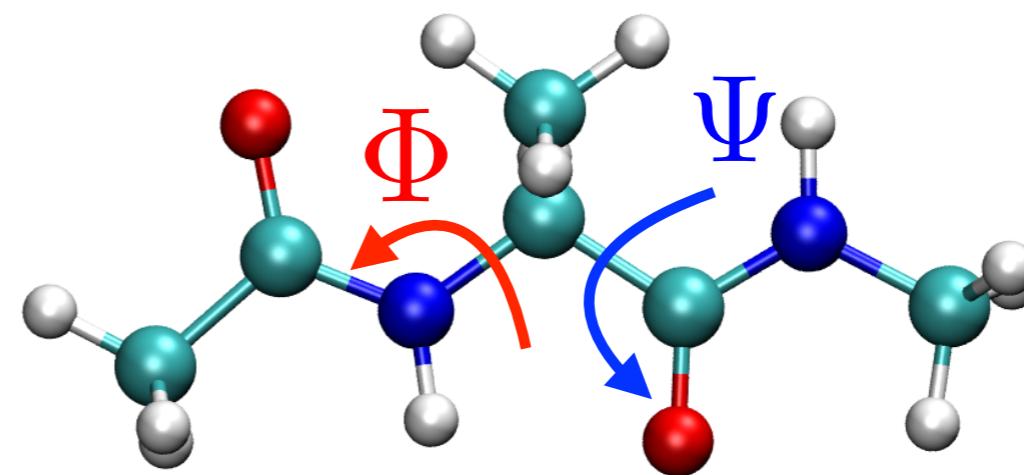
$$\mathbf{s}(\mathbf{R}) = (s_1(\mathbf{R}), s_2(\mathbf{R}), \dots, s_d(\mathbf{R})) \in \mathbb{R}^d \quad d \ll 3N \quad (\text{generally } \sim 1\text{-}3)$$

Coarse-grained descriptors or order parameters, generally called  
**collective variables (CVs)**

Often highly non-linear functions of  $\mathbf{R}$

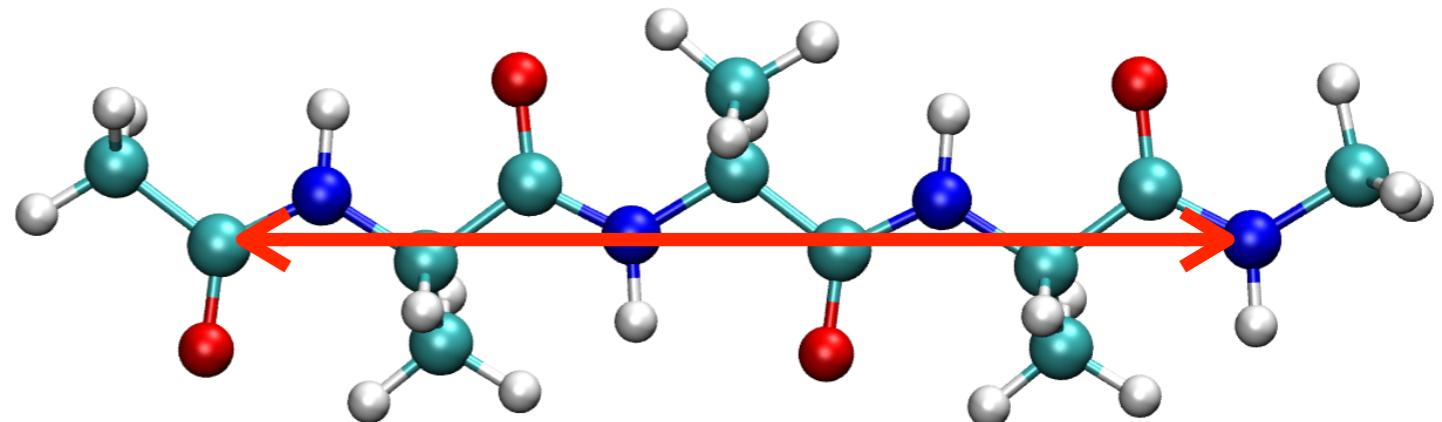
# Examples of Collective Variables

Dihedral angles



Distances

$$d_{i,j} = \|\mathbf{r}_i - \mathbf{r}_j\|$$



# Examples of Collective Variables

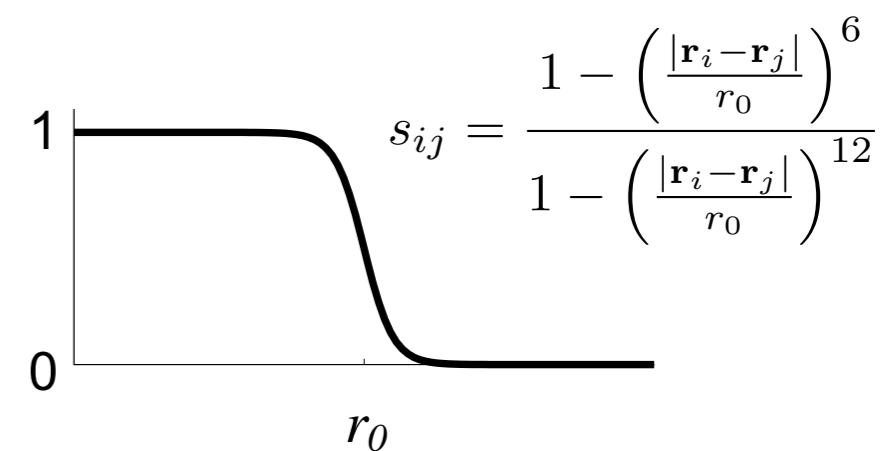
Root mean square deviation (RMSD) from a reference structure

$$RMSD = \sqrt{\frac{1}{n} \sum_i^n ||\mathbf{r}_i - \mathbf{r}_i^{ref}||^2}$$

Coordination numbers (e.g. number of hydrogen bond)

$$CN = \sum_{i \in A} \sum_{j \in B} \frac{1 - \left( \frac{|\mathbf{r}_i - \mathbf{r}_j|}{r_0} \right)^6}{1 - \left( \frac{|\mathbf{r}_i - \mathbf{r}_j|}{r_0} \right)^{12}}$$

continuous switching function



Radius of gyration

$$R_g = \left( \frac{\sum_i m_i |\mathbf{r}_i - \mathbf{r}_{COM}|^2}{\sum_i m_i} \right)^{1/2}$$

$$\mathbf{r}_{COM} = \frac{\sum_i m_i \mathbf{r}_i}{\sum_i m_i}$$

And many more ....

## Mapping to a Lower Dimension

Boltzmann distribution

$$P(\mathbf{R}) = \frac{e^{-\beta U(\mathbf{R})}}{\int d\mathbf{R} e^{-\beta U(\mathbf{R})}} \quad \beta = \frac{1}{k_{\text{B}} T}$$

## Mapping to a Lower Dimension

Boltzmann distribution

$$P(\mathbf{R}) = \frac{e^{-\beta U(\mathbf{R})}}{\int d\mathbf{R} e^{-\beta U(\mathbf{R})}} \quad \beta = \frac{1}{k_B T}$$

Distribution (marginal) of **CVs** obtained by integrating over all other degrees of freedom

$$P(\mathbf{s}) = \int d\mathbf{R} \delta [\mathbf{s} - \mathbf{s}(\mathbf{R})] P(\mathbf{R}) = \langle \delta [\mathbf{s} - \mathbf{s}(\mathbf{R})] \rangle$$

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Boltzmann distribution

$$P(\mathbf{R}) = \frac{e^{-\beta U(\mathbf{R})}}{\int d\mathbf{R} e^{-\beta U(\mathbf{R})}} \quad \beta = \frac{1}{k_B T}$$

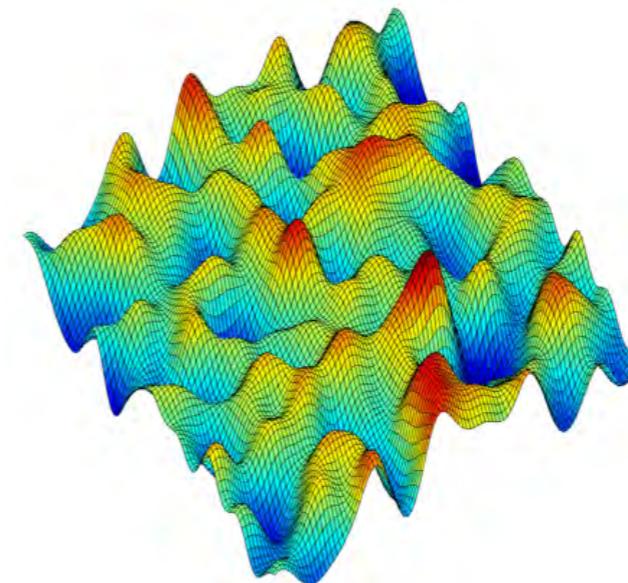
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so-called **Free Energy Surface (FES)** given by the negative logarithm

$$F(\mathbf{s}) = -\frac{1}{\beta} \log P(\mathbf{s}) = -\frac{1}{\beta} \log \int d\mathbf{R} \delta [\mathbf{s} - \mathbf{s}(\mathbf{R})] e^{-\beta U(\mathbf{R})} + C$$

# Mapping to a Lower Dimension



C. Dellago

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

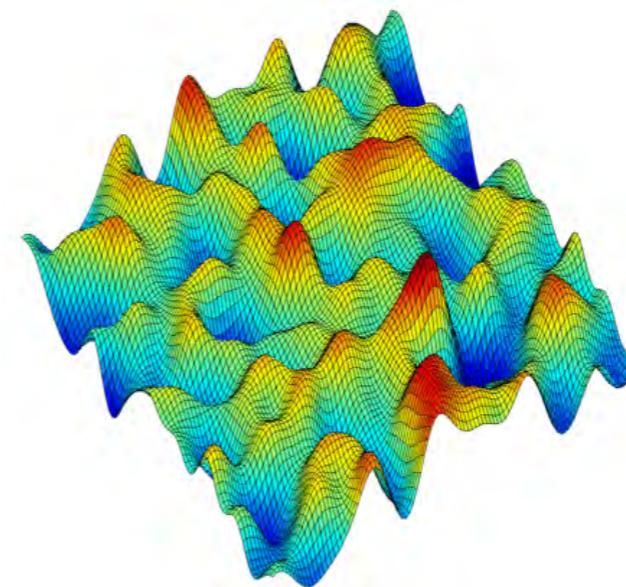
- High-dimensional,  $\mathbf{R} \in \mathbb{R}^{3N}$
- Rugged

# Mapping to a Lower Dimension

C. Dellago

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

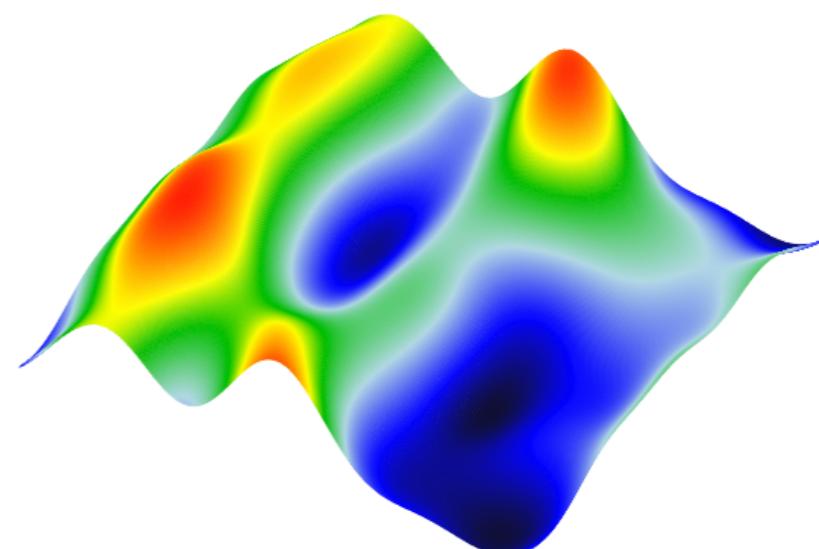
- High-dimensional,  $\mathbf{R} \in \mathbb{R}^{3N}$
- Rugged



CVs  $\mathbf{s}(\mathbf{R}) = (s_1(\mathbf{R}), s_2(\mathbf{R}), \dots, s_d(\mathbf{R}))$

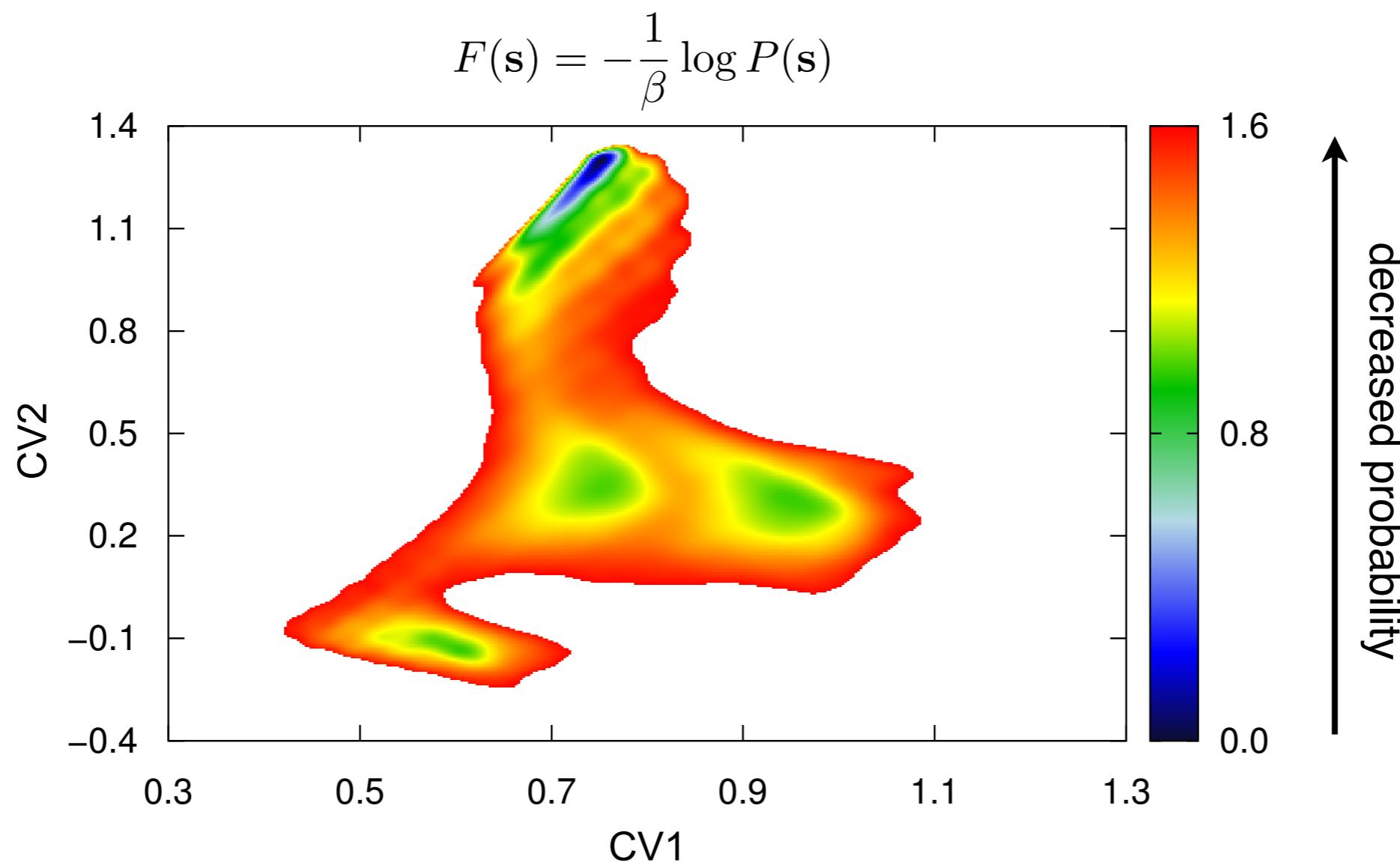
Free Energy Surface  $F(\mathbf{s})$

- Low-dimensional,  $\mathbf{s} \in \mathbb{R}^d$
- Smooth



# Free Energy Surface

The FES normally what we are interested in obtaining gives information about metastable states, their relative stability, and the free energy barriers



# Estimating the Free Energy Surface

The FES is also defined as

$$F(\mathbf{s}) = -\frac{1}{\beta} \lim_{t \rightarrow \infty} \log N(\mathbf{s}, t)$$

where  $N(\mathbf{s}, t)$  is a normalized histogram

$$N(\mathbf{s}, t) = \frac{1}{t} \sum_{t'}^t \delta [\mathbf{s} - \mathbf{s}(\mathbf{R}(t'))]$$

Therefore, should be possible to estimate the FES from histogram accumulated in a unbiased simulation of finite length

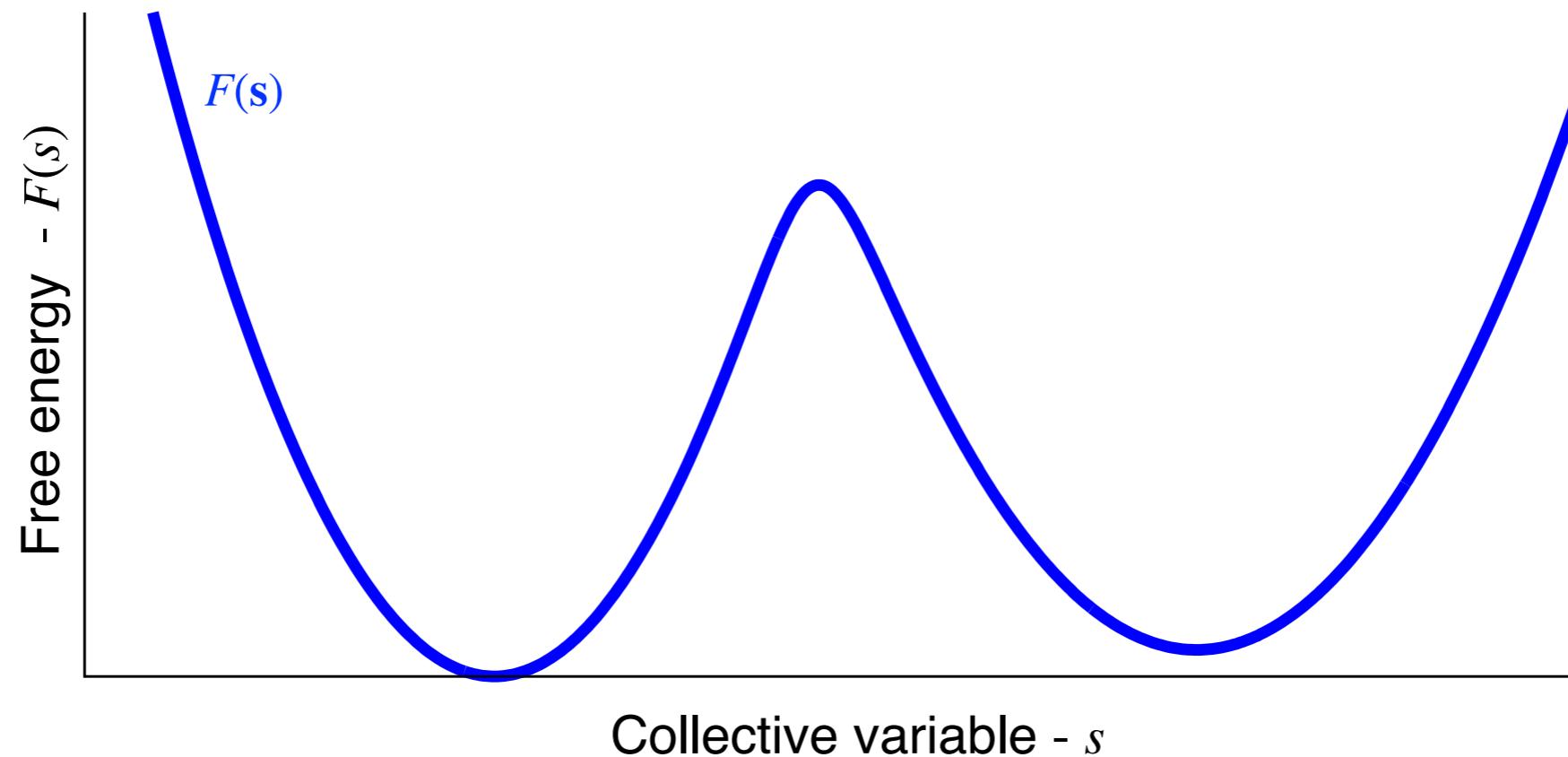
$$F(\mathbf{s}) = -\frac{1}{\beta} \log N(\mathbf{s}, t)$$

However, this rarely works due to sampling problems

# Umbrella Sampling

Torrie and Valleau, J. Comp. Phys. 1977

The basic idea behind many enhanced sampling methods



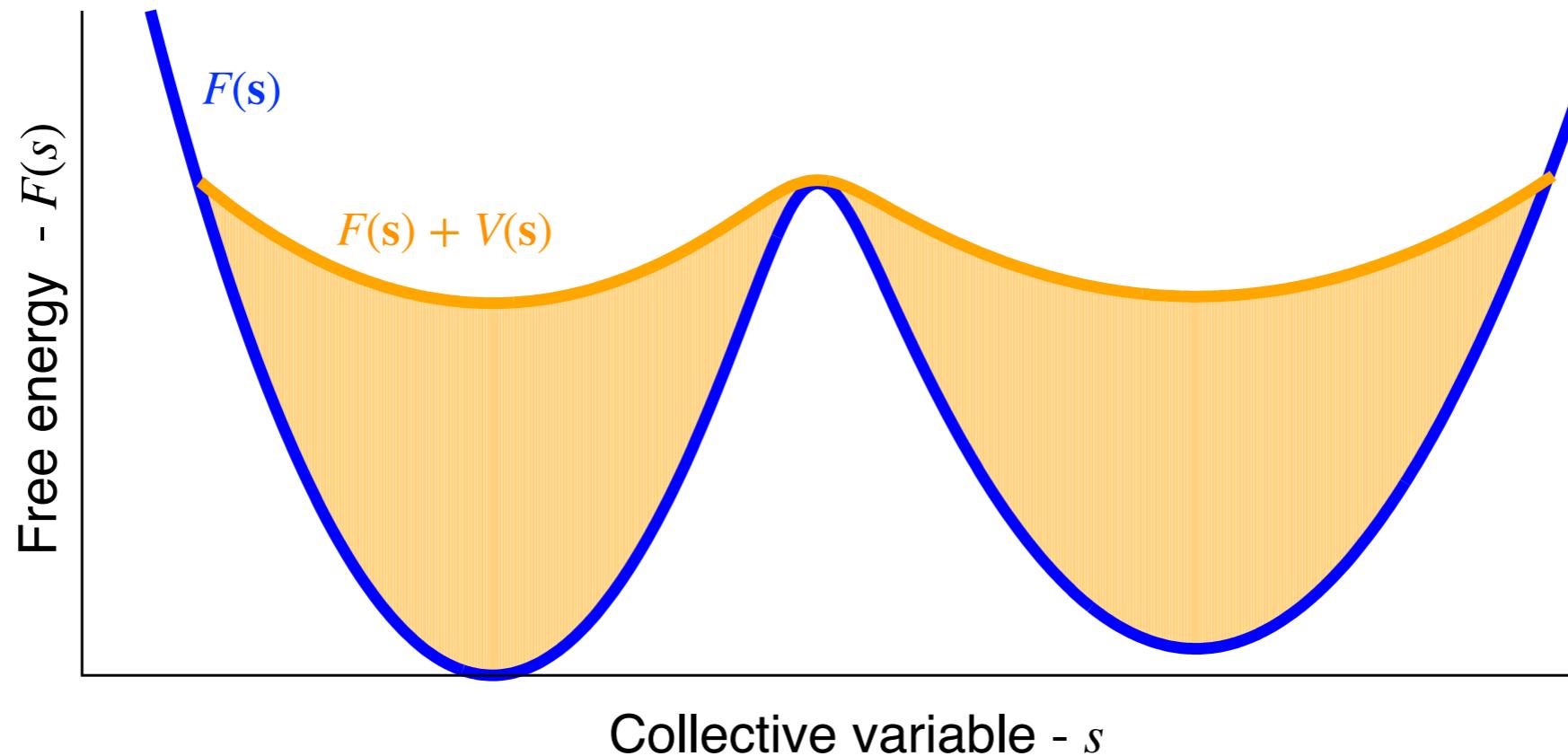
# Umbrella Sampling

Torrie and Valleau, J. Comp. Phys. 1977

The basic idea behind many enhanced sampling methods

Introduce a bias potential  $V(s)$  that acts in the space spanned by the slow CVs

$$U(\mathbf{R}) \rightarrow U(\mathbf{R}) + V(s(\mathbf{R}))$$



# Umbrella Sampling

Torrie and Valleau, J. Comp. Phys. 1977

The basic idea behind many enhanced sampling methods

Introduce a bias potential  $V(\mathbf{s})$  that acts in the space spanned by the slow CVs

$$U(\mathbf{R}) \longrightarrow U(\mathbf{R}) + V(\mathbf{s}(\mathbf{R}))$$

Sample a “easier” biased distribution

$$P_V(\mathbf{R}) = \frac{e^{-\beta[U(\mathbf{R})+V(\mathbf{s}(\mathbf{R}))]}}{\int d\mathbf{R} e^{-\beta[U(\mathbf{R})+V(\mathbf{s}(\mathbf{R}))]}} \propto P(\mathbf{R}) e^{-\beta V(\mathbf{s}(\mathbf{R}))}$$

The biased CV distribution is then

$$P_V(\mathbf{s}) = \int d\mathbf{R} \delta[\mathbf{s} - \mathbf{s}(\mathbf{R})] P_V(\mathbf{R}) \propto e^{-\beta[F(\mathbf{s})+V(\mathbf{s})]}$$

## Umbrella Sampling - Reweighting

Can obtain unbiased ensemble averages by weighting each configuration by the bias acting on it

$$P(\mathbf{R}) \propto P_V(\mathbf{R}) e^{\beta V(\mathbf{s}(\mathbf{R}))}$$

$$\langle O(\mathbf{R}) \rangle = \frac{\langle O(\mathbf{R}) e^{\beta V(\mathbf{s}(\mathbf{R}))} \rangle_V}{\langle e^{\beta V(\mathbf{s}(\mathbf{R}))} \rangle_V}$$

e.g. the FES for any CVs

$$F(\tilde{\mathbf{s}}) = -\frac{1}{\beta} \log \left\langle \delta [\tilde{\mathbf{s}} - \tilde{\mathbf{s}}(\mathbf{R})] e^{+\beta V(\mathbf{s}(\mathbf{R}))} \right\rangle_V$$

Note that these relations are only valid if the bias is stationary  
(i.e. does not change with time)

## How to Select a Good Bias Potential

Assume that we can take the bias potential as

$$V(\mathbf{s}) = - \left(1 - \frac{1}{\gamma}\right) F(\mathbf{s})$$

where  $\gamma \geq 1$  is a parameter

Inserting this  $V(\mathbf{s})$  into

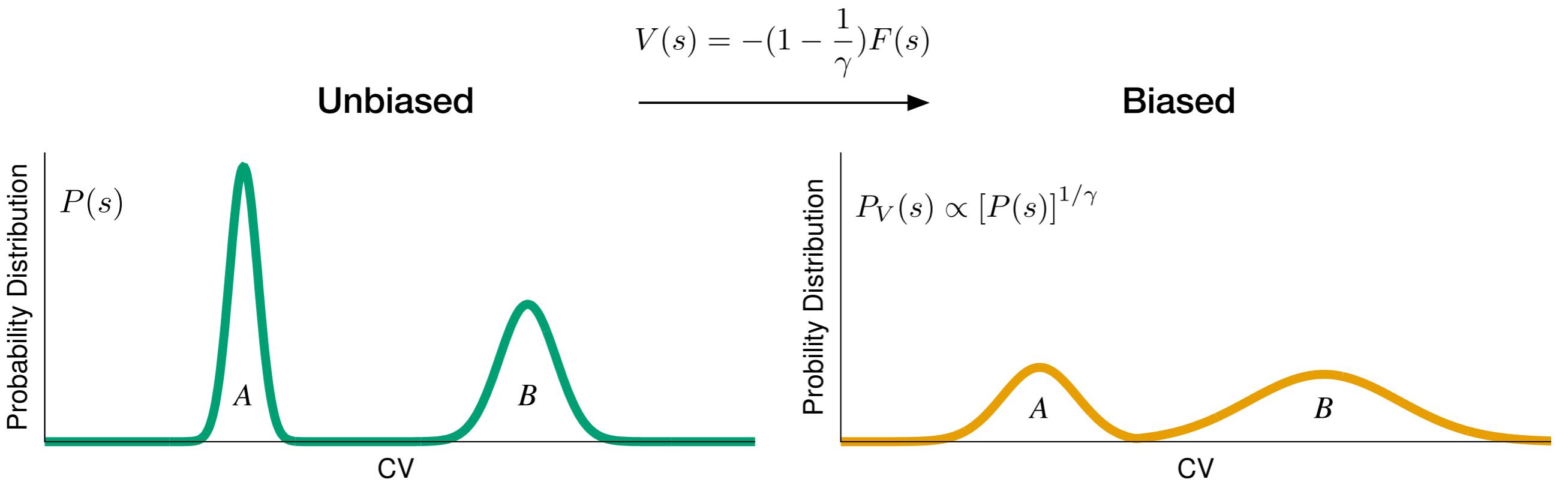
$$P_V(\mathbf{s}) \propto e^{-\beta[F(\mathbf{s})+V(\mathbf{s})]}$$

gives

$$P_V(\mathbf{s}) \propto [P(\mathbf{s})]^{1/\gamma}$$

so called well-tempered distribution

# Well-Tempered Distribution



Enhanced fluctuations of the CVs  $\Rightarrow$  easier to cross barriers

Flatten the sampling as compared to unbiased distribution  $P(s)$

## Well-Tempered Distribution

By using

$$P_V(\mathbf{s}) \propto [P(\mathbf{s})]^{1/\gamma} \quad \text{and} \quad F_V(\mathbf{s}) = -\frac{1}{\beta} \log P_V(\mathbf{s})$$

we obtain

$$F_V(\mathbf{s}) = \frac{1}{\gamma} F(\mathbf{s}) \quad (\text{ignoring unimportant additive constants})$$

sampling on an effective FES where barriers have been reduced by a factor of  $\gamma$

optimal  $\gamma$  such that effective barriers are around few  $k_B T$  and easily crossed

## Uniform Distribution

Taking the limit  $\gamma \rightarrow \infty$  gives

$$V(\mathbf{s}) = -F(\mathbf{s})$$

$$P_V(\mathbf{s}) \propto 1$$

Uniform sampling of CVs

Complete disappearance of free energy barriers

Many enhanced sampling (“flat histogram”) methods aim to achieve such a bias potential

but, generally not optimal

- spend a lot of time sampling irrelevant regions high in free energy
- better to just enhance CV fluctuations with a finite value of  $\gamma$

## Constructing the Bias Potential

However cannot use directly

$$V(\mathbf{s}) = - \left( 1 - \frac{1}{\gamma} \right) F(\mathbf{s})$$

as it depends on the FES  $F(\mathbf{s})$  which is the very quantity we want to obtain

Can instead iteratively on the fly build a bias potential that in the long-time limit gives this solution

Metadynamics

Laio and Parrinello, Proc. Natl. Acad. Sci. U.S.A. 2002,  
Barducci, Bussi, and Parrinello, Phys. Rev. Lett. 2008

Variationally Enhanced Sampling

Valsson and Parrinello, Phys. Rev. Lett. 2014

# General Requirements on CVs

The CVs that are biased must generally:

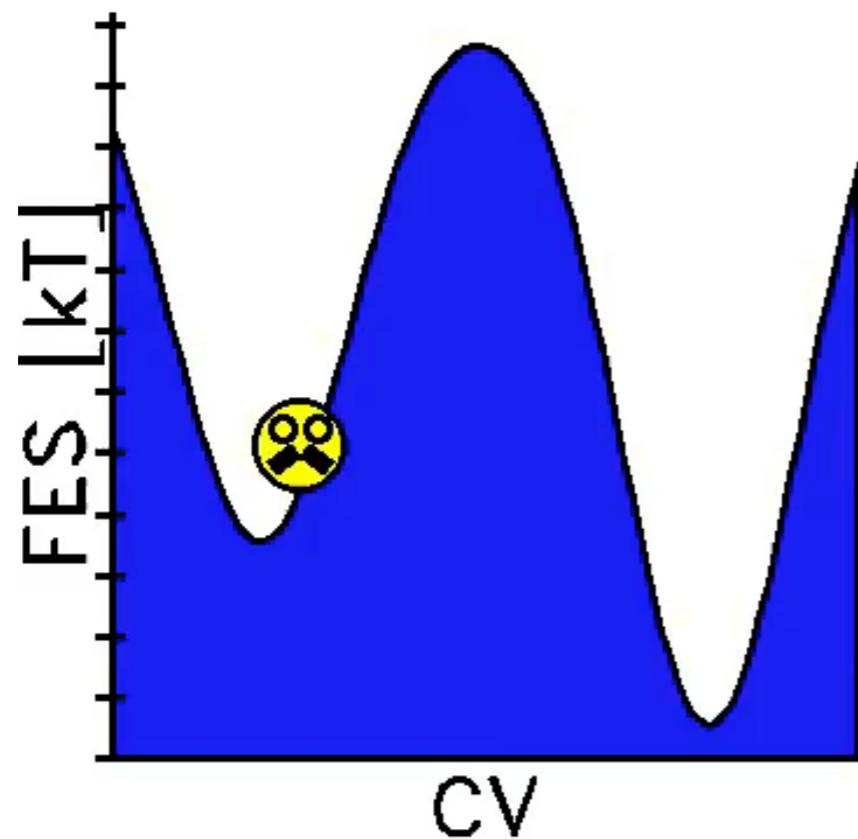
- be few in number (~1-3)  
although there some extensions that allow for overcoming this
- have continuous derivatives  
technical requirement for MD to have continuous forces
- distinguish all the relevant metastable states
- include all slow modes of the system  
not always possible, but there are ways to tackle this

# Metadynamics

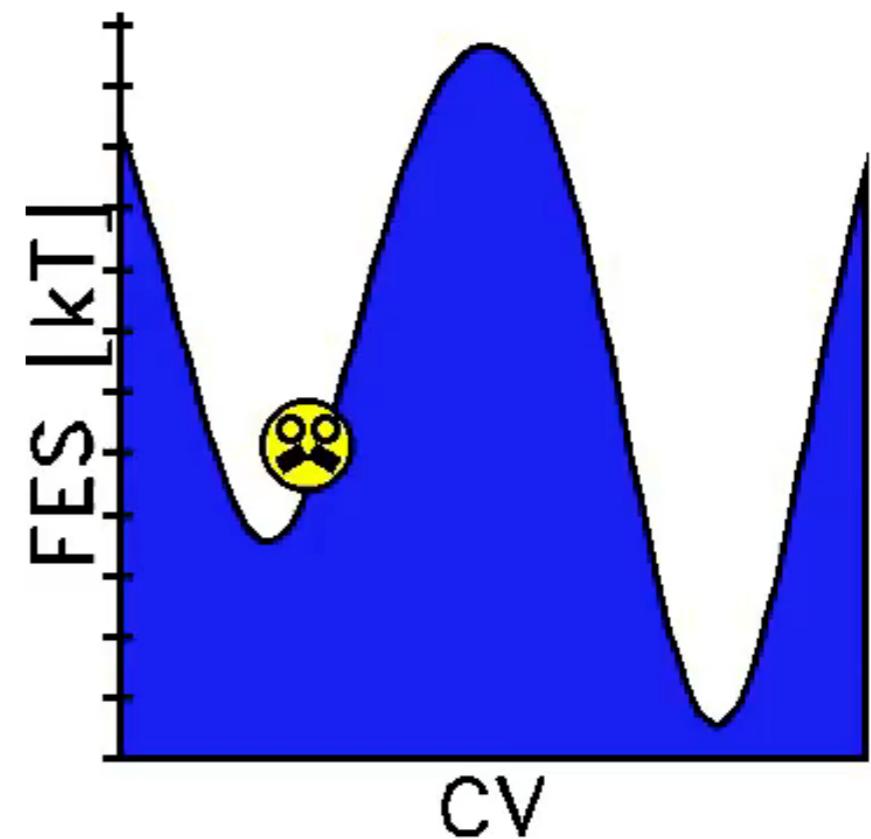
# Metadynamics

Deposit repulsive Gaussian biasing kernels everywhere you go in CV space  
→ pushes you over the barriers

Unbiased Molecular Dynamics



Metadynamics



## Well-Tempered Metadynamics

Iteratively builds a bias by periodically updating it according to

$$V_n(\mathbf{s}) = V_{n-1}(\mathbf{s}) + G(\mathbf{s}, \mathbf{s}_n) \exp \left[ -\frac{1}{\gamma - 1} \beta V_{n-1}(\mathbf{s}_n) \right]$$

where

$$G(\mathbf{s}, \mathbf{s}_n) = W_0 \exp \left( -\sum_i^d \frac{(s_i - s_{n,i})^2}{2\sigma_i^2} \right)$$

is a Gaussian biasing kernel of height  $W_0$  that is centered at the current CV location  $\mathbf{s}_n = (s_{n,1}, s_{n,2}, \dots, s_{n,d})$  and scaled by

$$\exp \left[ -\frac{1}{\gamma - 1} \beta V_{n-1}(\mathbf{s}_n) \right]$$

## Well-Tempered Metadynamics

The update is performed every  $N_G$  steps

between updating steps  $n$  and  $n+1$  the bias reads

$$V_n(\mathbf{s}) = \sum_{k=1}^n W_k \exp \left( - \sum_i \frac{(s_i - s_{k,i})^2}{2\sigma_i^2} \right)$$

where  $W_k$  is the Gaussian height for the Gaussian deposited at step  $k$

$$W_k = W_0 \exp \left[ -\frac{1}{\gamma - 1} \beta V_{k-1}(\mathbf{s}_k) \right].$$

# Well-Tempered Metadynamics

The scaling factor in the update

$$V_n(\mathbf{s}) = V_{n-1}(\mathbf{s}) + G(\mathbf{s}, \mathbf{s}_n) \exp \left[ -\frac{1}{\gamma - 1} \beta V_{n-1}(\mathbf{s}_n) \right]$$

decreases to zero as  $1/n$

$$\exp \left[ -\frac{1}{\gamma - 1} \beta V_{n-1}(\mathbf{s}_n) \right] \sim \frac{1}{n}$$

The bias thus reaches a quasi-stationary state (i.e. does not change with time), this is important for reweighting

# Well-Tempered Metadynamics

Can be rigorously proven that in the long-time limit the bias fulfills

$$V(\mathbf{s}, t) = - \left(1 - \frac{1}{\gamma}\right) F(\mathbf{s}) + c(t)$$

↑  
constant independent of  $\mathbf{s}$



$$P_V(\mathbf{s}) \propto [P(\mathbf{s})]^{1/\gamma}$$

thus, in the long time limit we obtain the well-tempered distribution

furthermore, can directly obtain the FES from the constructed bias

## Well-Tempered Metadynamics - Reweighting

Need to account for time-dependence of bias when reweighting

$$P(\mathbf{R}, t) = P_V(\mathbf{R}) e^{\beta[V(\mathbf{s}(\mathbf{R}), t) - c(t)]}$$

$$\langle O(\mathbf{R}) \rangle = \left\langle O(\mathbf{R}) e^{\beta[V(\mathbf{s}(\mathbf{R})) - c(t)]} \right\rangle_V$$

where the time-dependent constant  $c(t)$  is calculated as<sup>a</sup>

$$c(t) = \frac{1}{\beta} \log \frac{\int d\mathbf{s} \exp \left[ \frac{\gamma}{\gamma-1} \beta V(\mathbf{s}, t) \right]}{\int d\mathbf{s} \exp \left[ \frac{1}{\gamma-1} \beta V(\mathbf{s}, t) \right]}$$

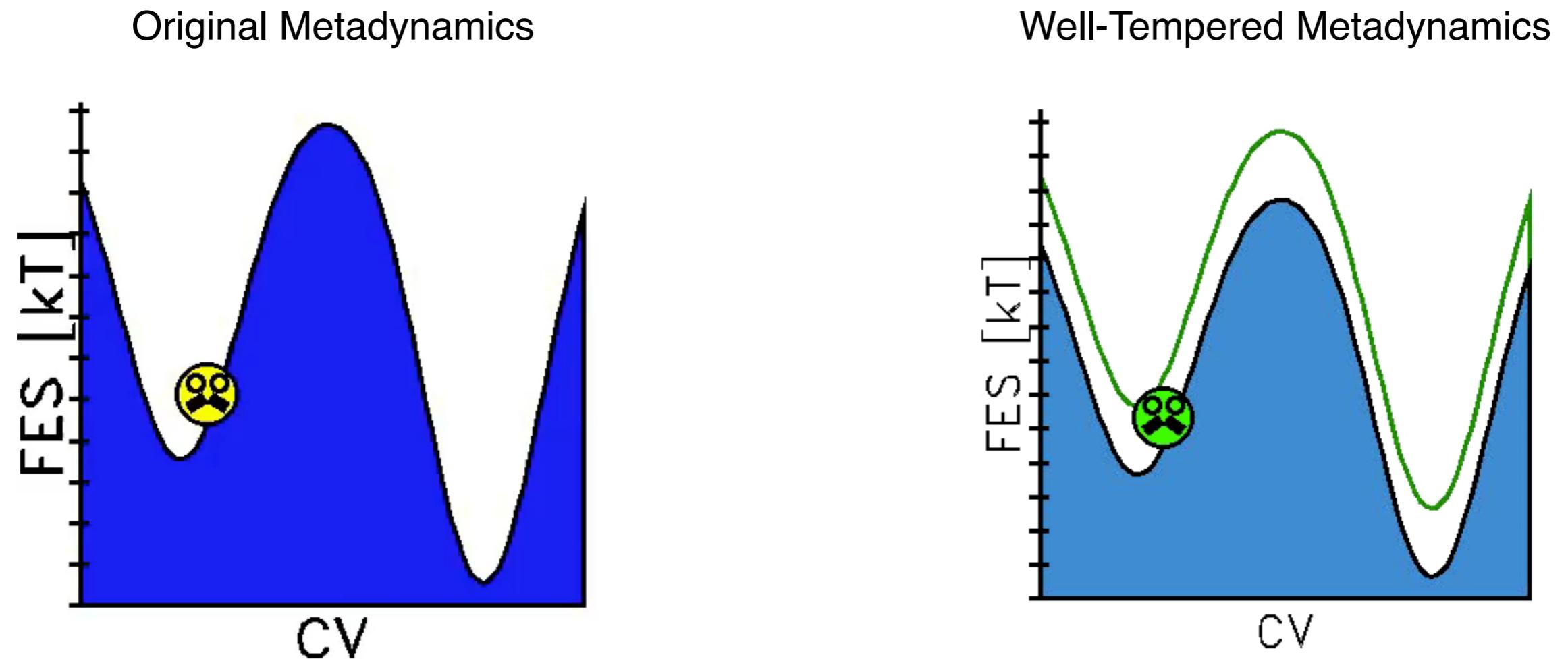
valid when the bias has reached a quasi-stationary state

<sup>a</sup>Tiwary and Parrinello, JPCB, 2014

# Metadynamics

In the original version of Metadynamics the biasing kernel was not scaled  
this corresponding to the  $\gamma \rightarrow \infty$  limit and  $V(s) = -F(s)$  (flat histogram)

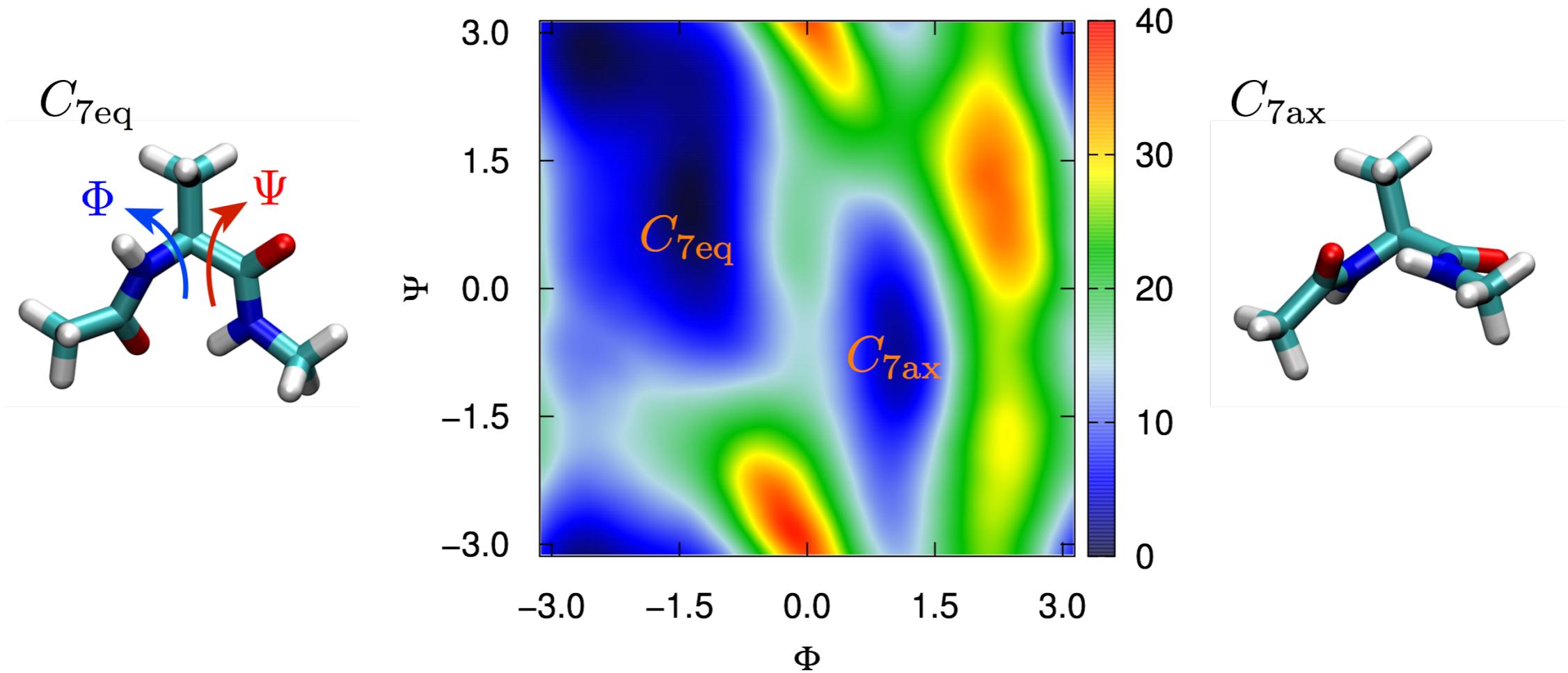
However, hard to converge



Convergence greatly improved by the well-tempered version described here

# Exemplifying System - Alanine Dipeptide

Alanine dipeptide in vacuum - Backbone dihedral angles  $\Phi, \Psi$  as CVs

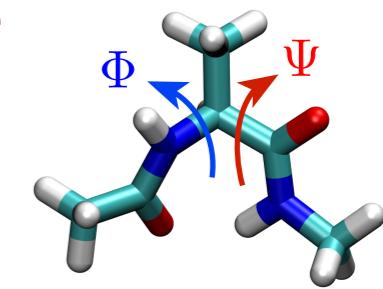


Two metastable basins,  $C_{7\text{eq}}$  and  $C_{7\text{ax}}$

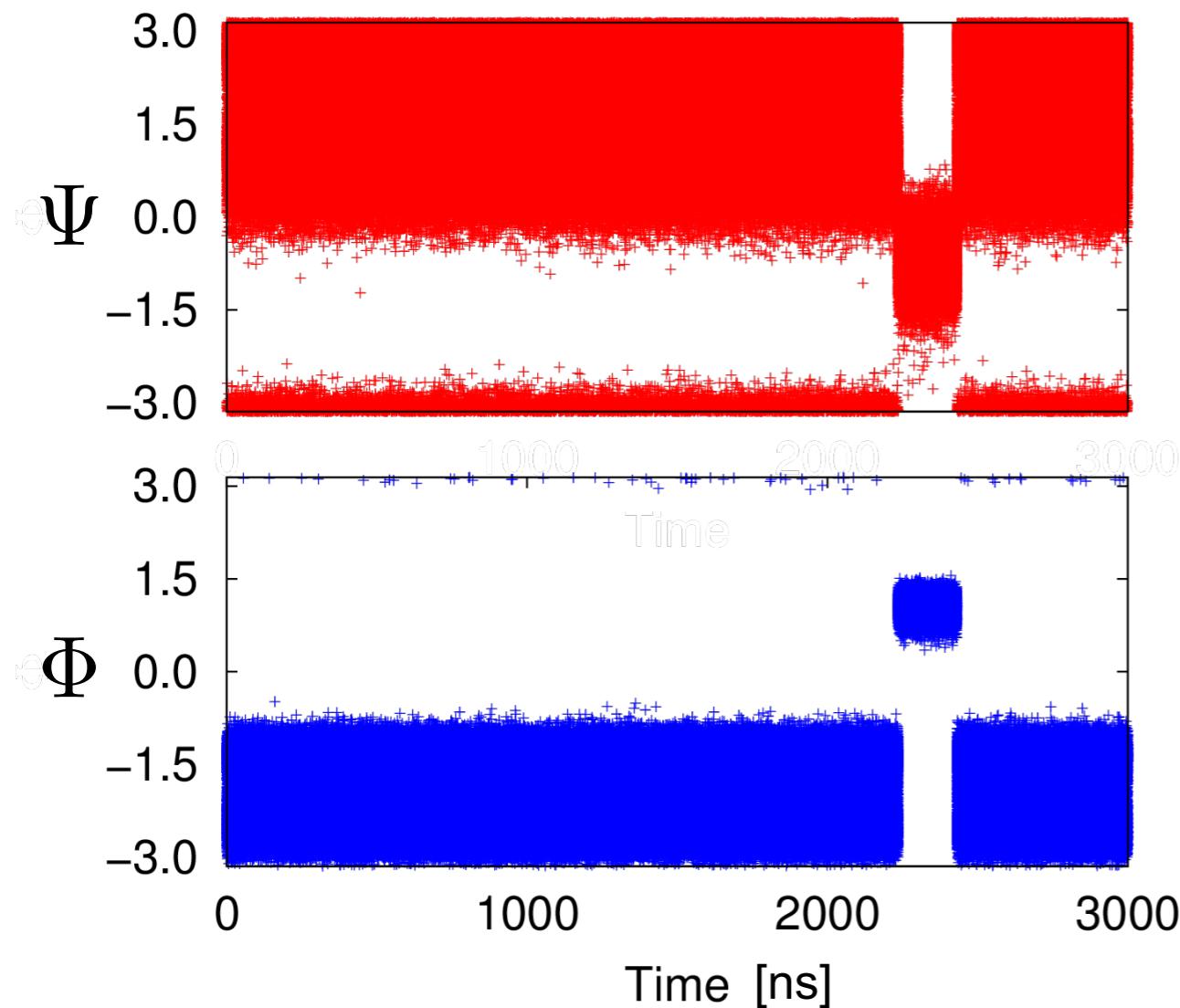
barrier around 34 kJ/mol (16  $k_B T$ )

mean transition time around 28  $\mu\text{s}$

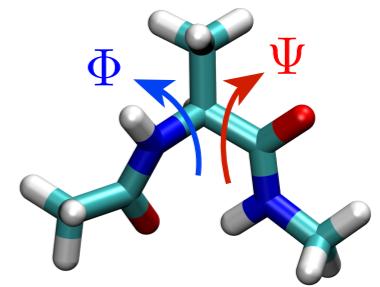
# Exemplifying System - Alanine Dipeptide



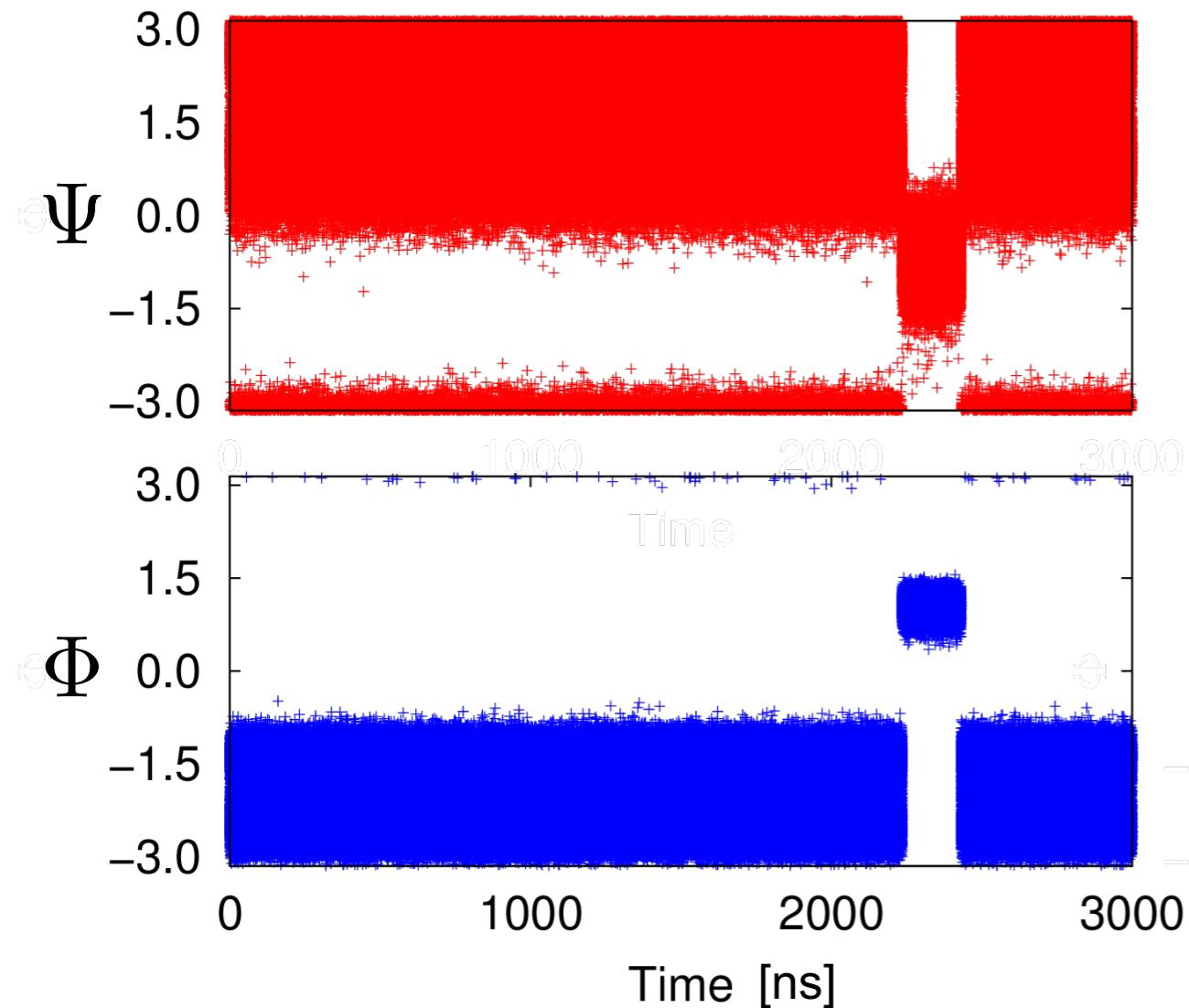
Unbiased molecular dynamics



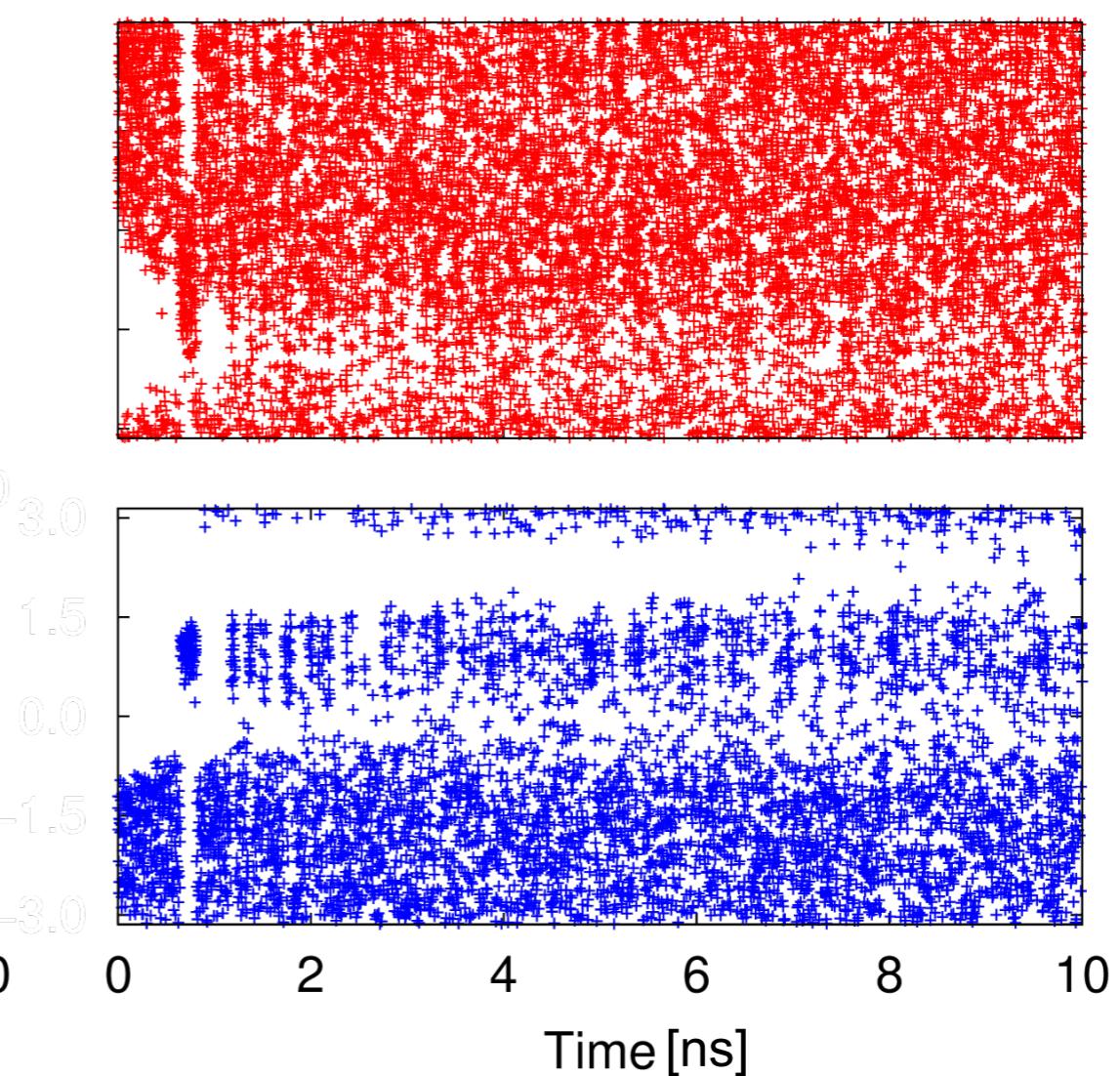
# Exemplifying System - Alanine Dipeptide



Unbiased molecular dynamics



Metadynamics



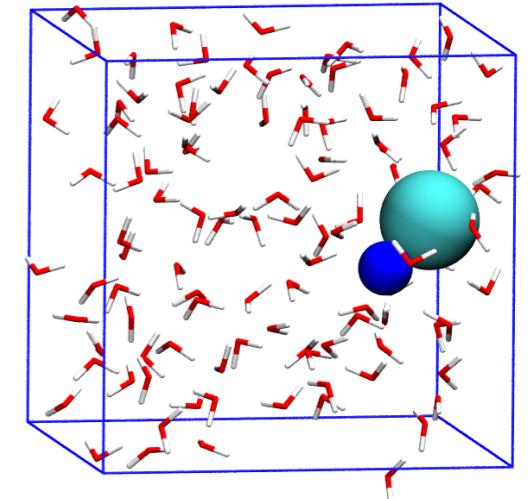
Note the difference of 300 in the time scale!

# Metadynamics Reweighting

Can use reweighting to obtain FESs for CVs not biased

Example: association/dissociation of NaCl in aqueous solution  
(from a tutorial in the VES code, see later)

Biased CV: Na-Cl distance

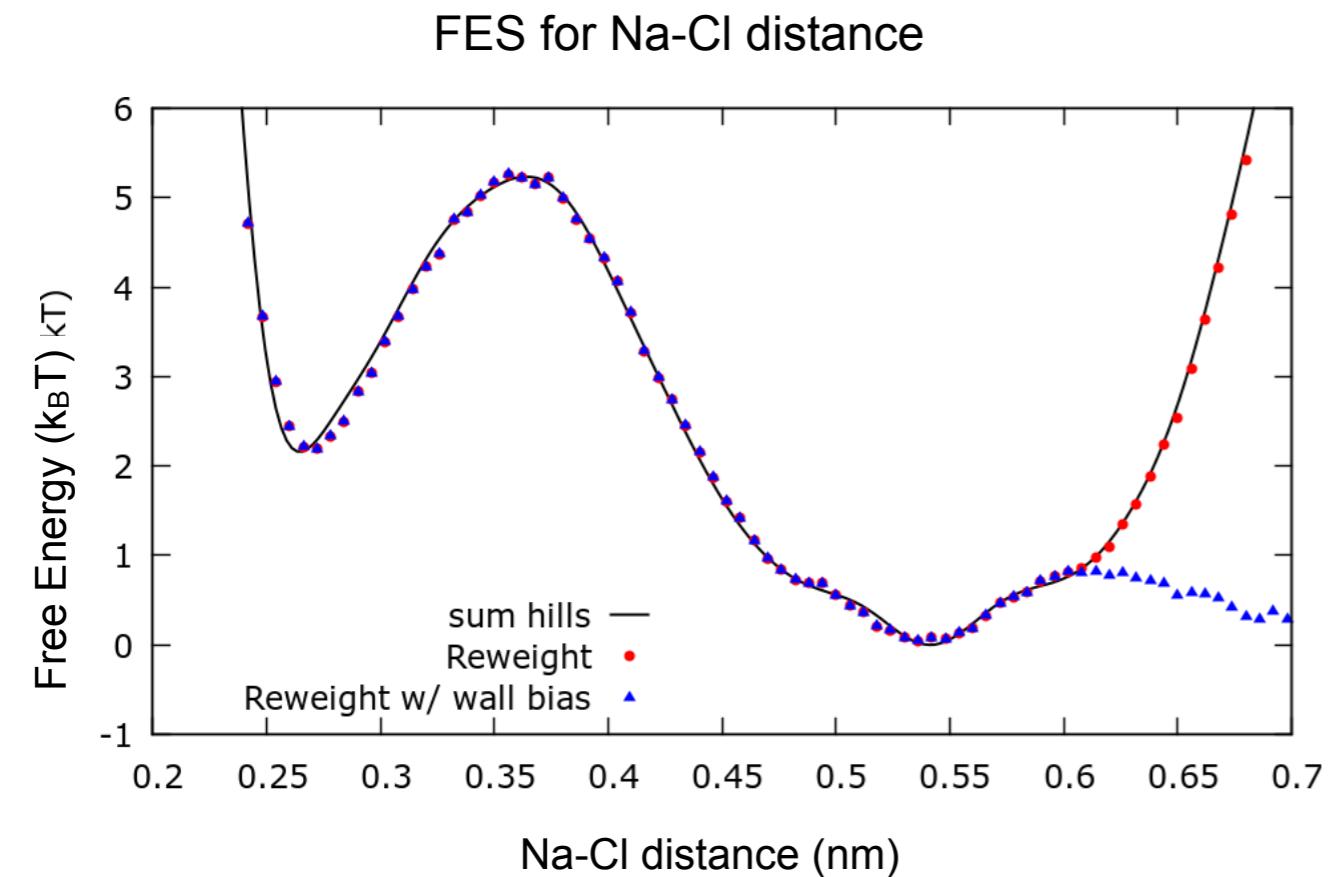
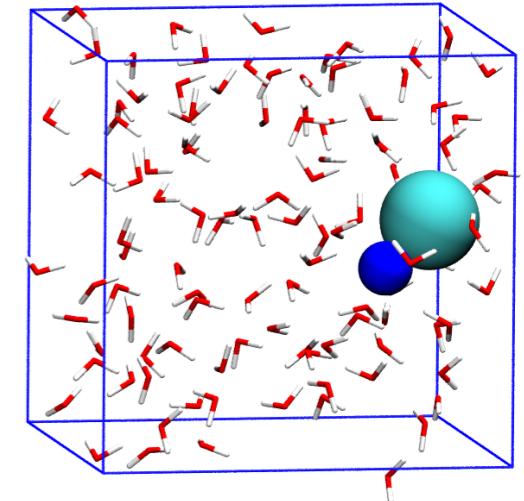


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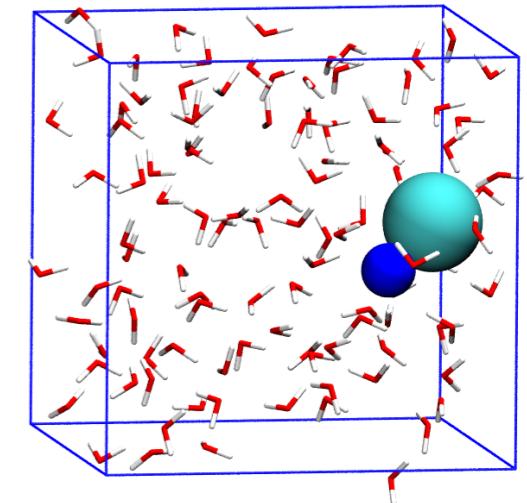
Reweighting can also be used to check the results,  
or to correct for the usage of constraints

# Metadynamics Reweighting

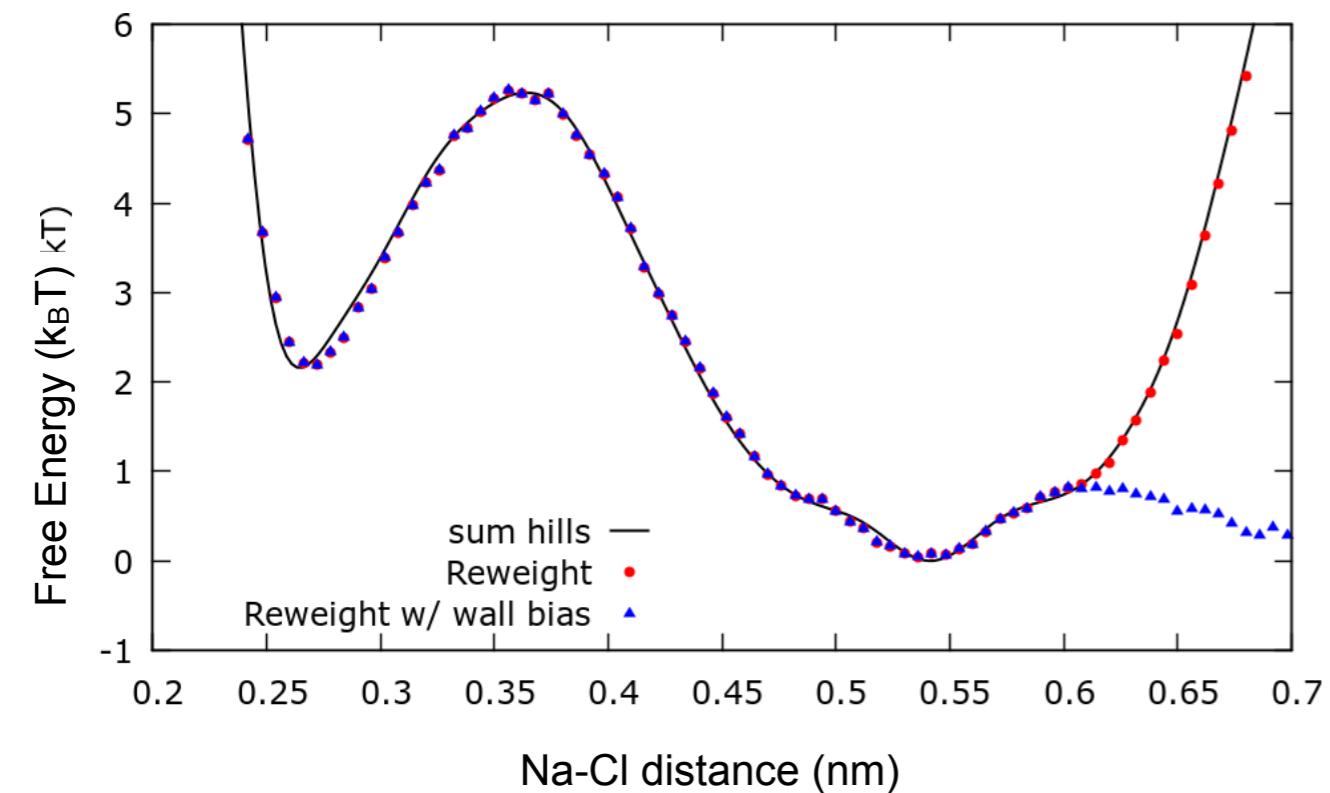
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Example: association/dissociation of NaCl in aqueous solution  
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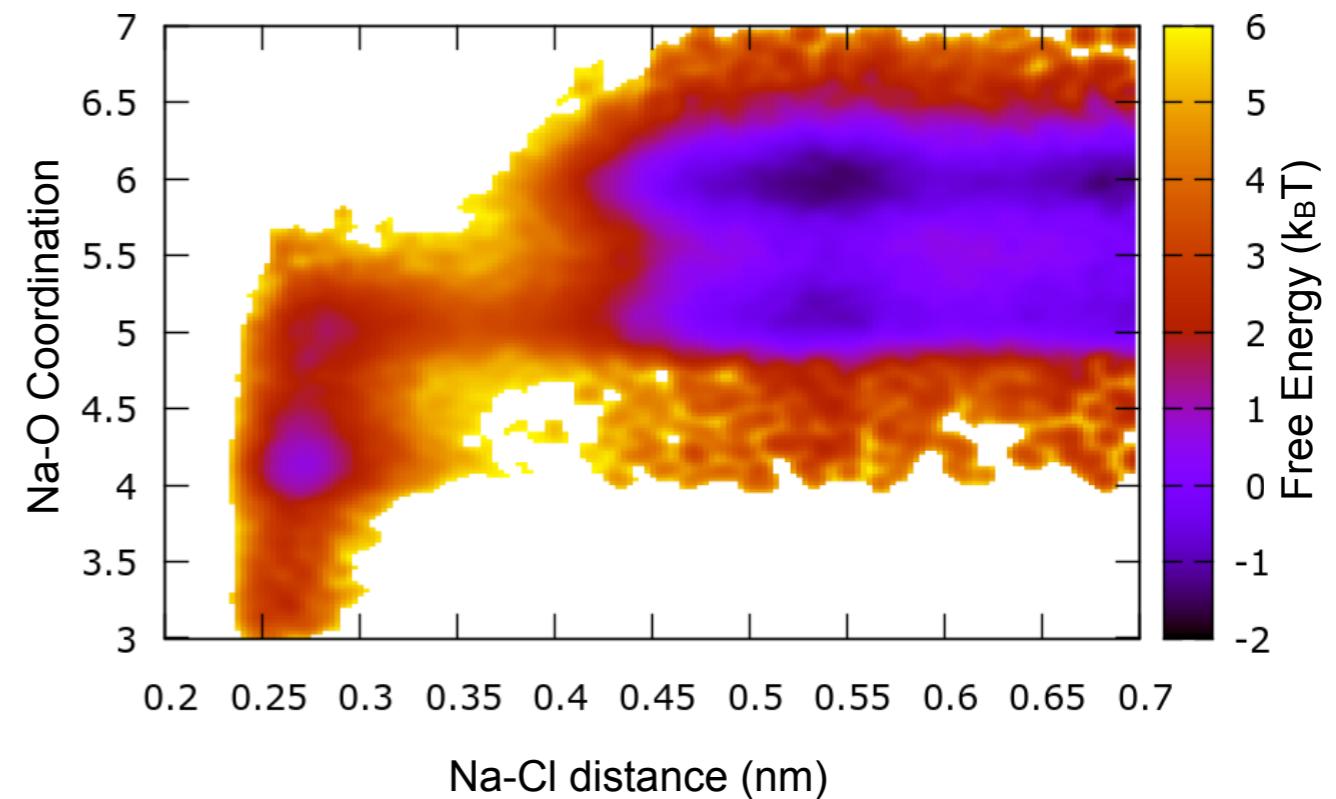
Biased CV: Na-Cl distance



FES for Na-Cl distance



FES for Na-Cl distance + Na-O Coordination



Reweighting can also be used to check the results,  
or to correct for the usage of constraints

# Extensions of Metadynamics

- Parallel-Tempering MetaD  
Helps sampling missing slow CVs
- Well-Tempered Ensemble  
Can be used to reduce the number of replicas needed for parallel-tempering
- Bias Exchange MetaD  
Employ many CVs via replica exchange strategy
- Parallel-Bias MetaD  
Employ many CVs within one replica via 1D potentials
- Multiple Walkers MetaD  
Shared bias between multiple copies, reduces human time needed for convergence
- Adaptive Gaussians MetaD  
Gaussian whose shape adapt to the FES
- Infrequent MetaD for obtaining kinetics  
Obtain kinetics of rare event from biased simulations

See Ann. Rev. Phys. Chem. 2016, 67:159-84 for further information and original references

# PLUMED

MD Code

e.g. Gromacs, LAMMPS, CP2K, OpenMM, ...



PLUMED 2

[www.plumed.org](http://www.plumed.org)

**PLUgin for MolEcular Dynamics (open source)**

wide range of collective variables available

**metadynamics**, umbrella sampling, steered MD, ...

easy to use, extensive tutorials, ...

# Well-Tempered Metadynamics

the input parameters for a metadynamics simulations are

$N_G$  how often we deposit Gaussians

$W_0$  the initial Gaussian height

$\gamma$  bias factor

$\sigma_i$  width (standard deviations) of deposited Gaussians

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# Well-Tempered Metadynamics

typical values

$N_G$  ~ 500-1000 steps for molecular dynamics simulation

~ 1-10 steps for Monte Carlo simulation if each MC move is not too “small”

$W_0$  fraction or around  $k_B T$ , e.g.  $0.1*k_B T$  to  $1.0*k_B T$

$\gamma$  ideally a value that makes the effective free energy barriers to be on the order of few  $k_B T$

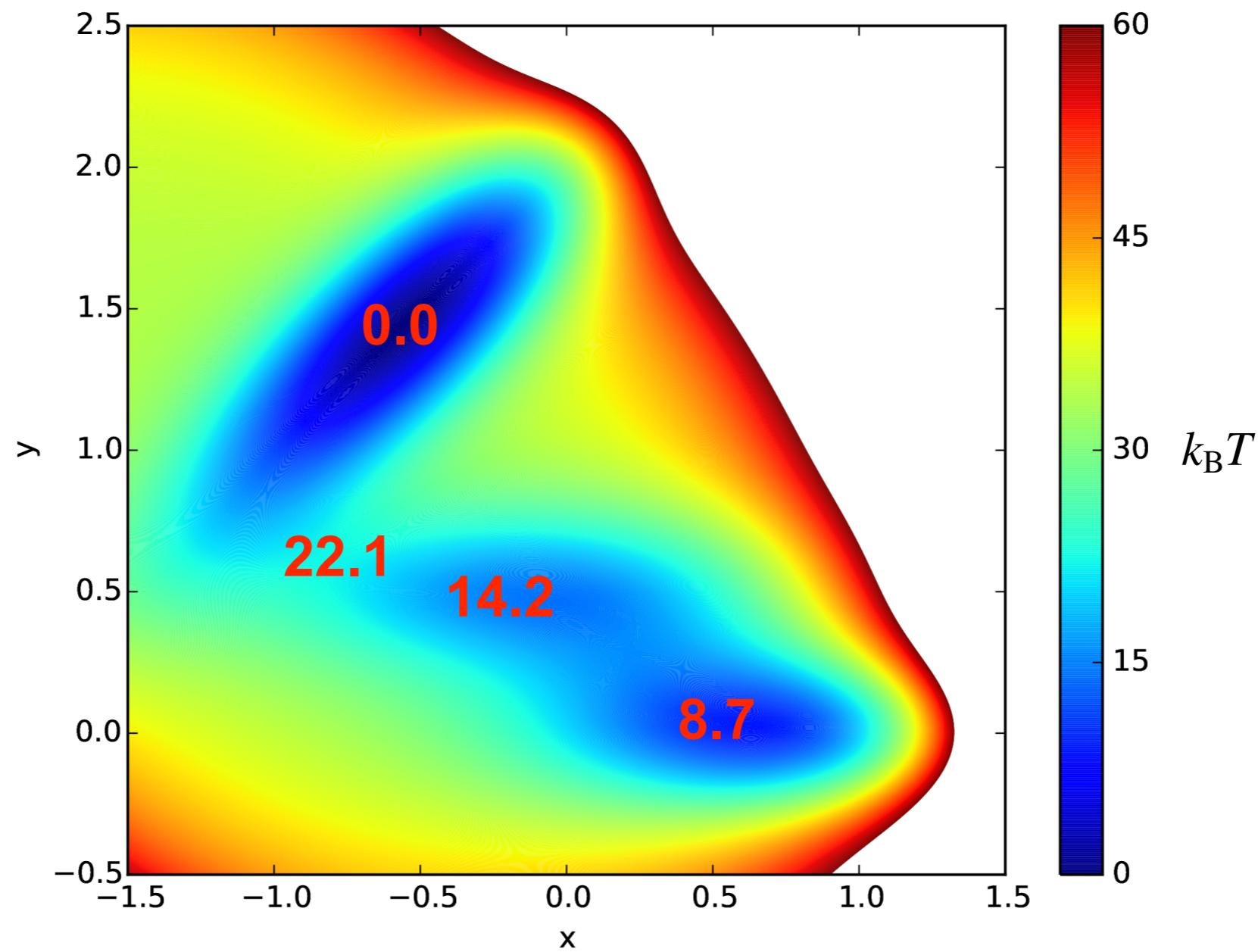
too low value will not enhance the sampling enough while too large value will lead to slow convergence

$\sigma_i$  on the order of the fluctuation (i.e. standard deviations) of the CVs observed in unbiased simulations, e.g. 0.5-1.0 of the unbiased fluctuations

# Exemplifying System - Mueller Brown Potential

One particle on a two-dimensional potential energy surface

$$U(x, y) = \sum_{i=1}^4 A_i \exp [a_i(x - x_0)^2 + b_i(x - x_0)(y - y_0) + c_i(y - y_0)^2] + C_0$$

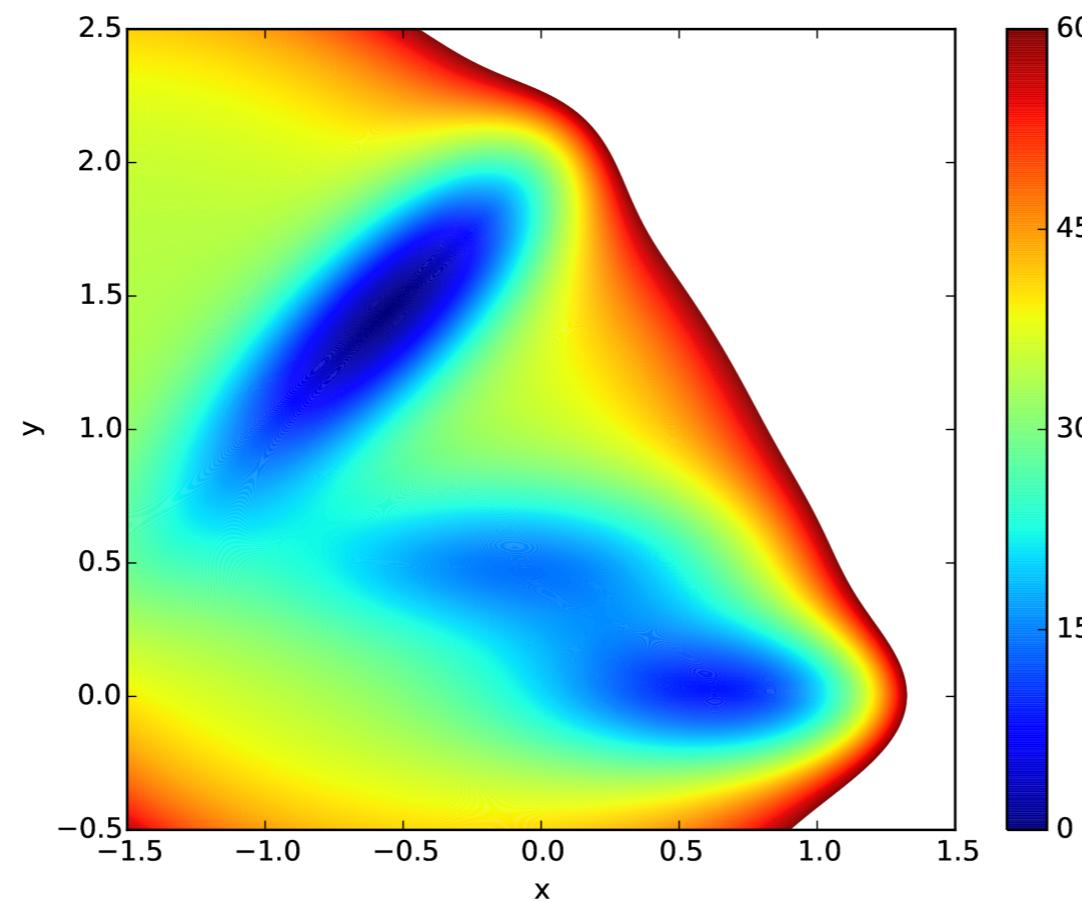


## Exemplifying System - Mueller Brown Potential

$$F(\mathbf{s}) = -\frac{1}{\beta} \log \int d\mathbf{R} \delta [\mathbf{s} - \mathbf{s}(\mathbf{R})] e^{-\beta U(\mathbf{R})}$$

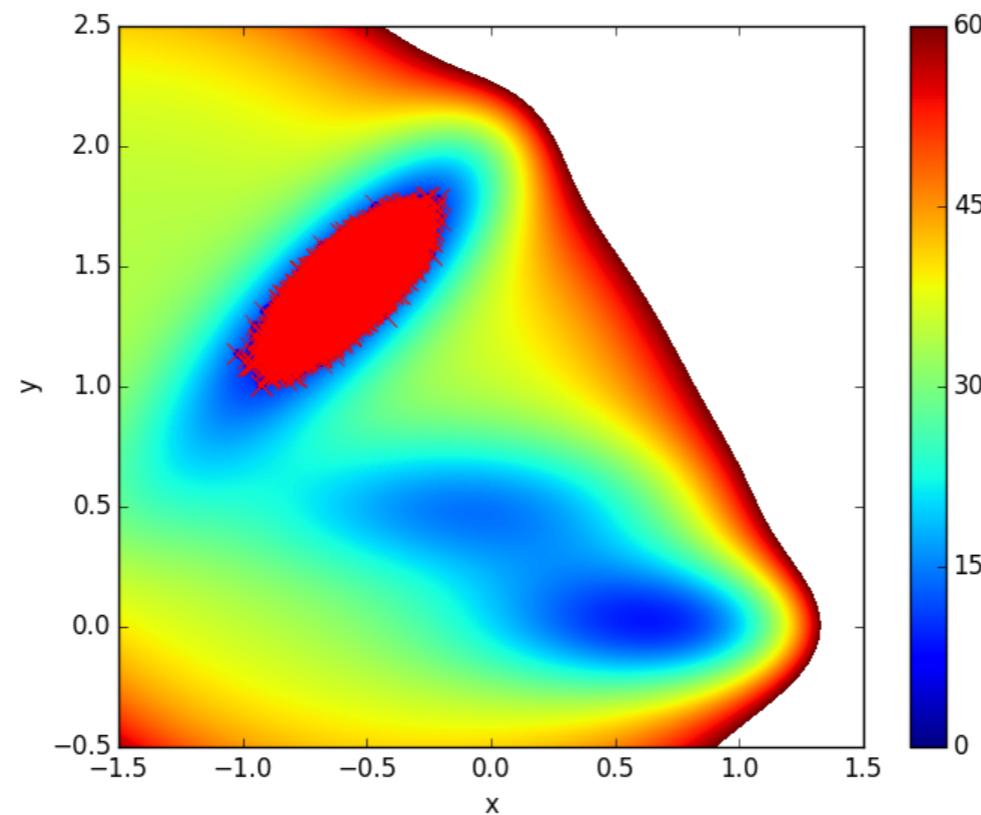
$x$  and  $y$  as CVs  $\Rightarrow$  the FES is just given by  $U(x,y)$

$$F(x, y) = U(x, y)$$

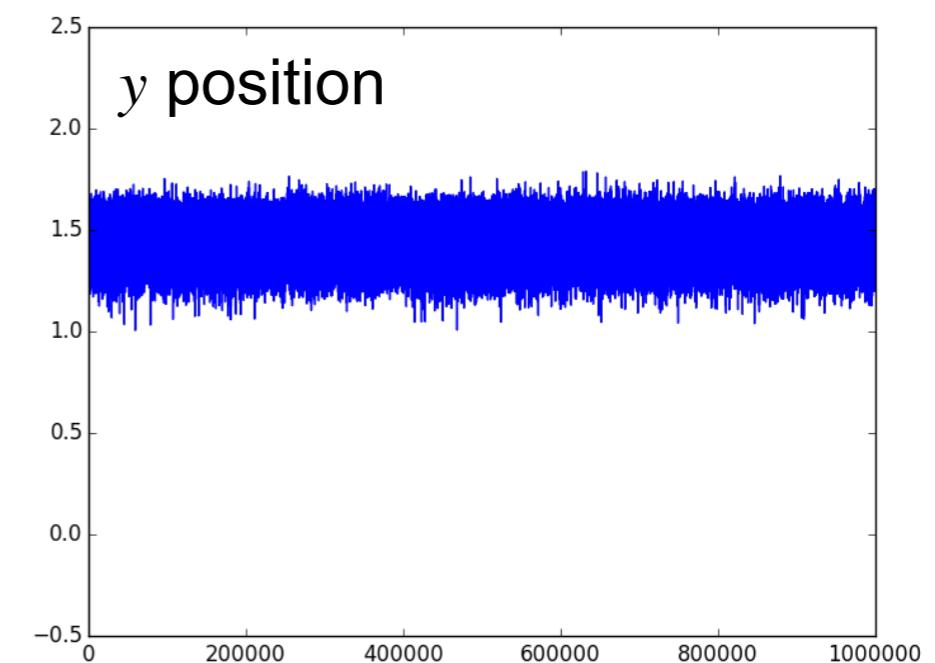
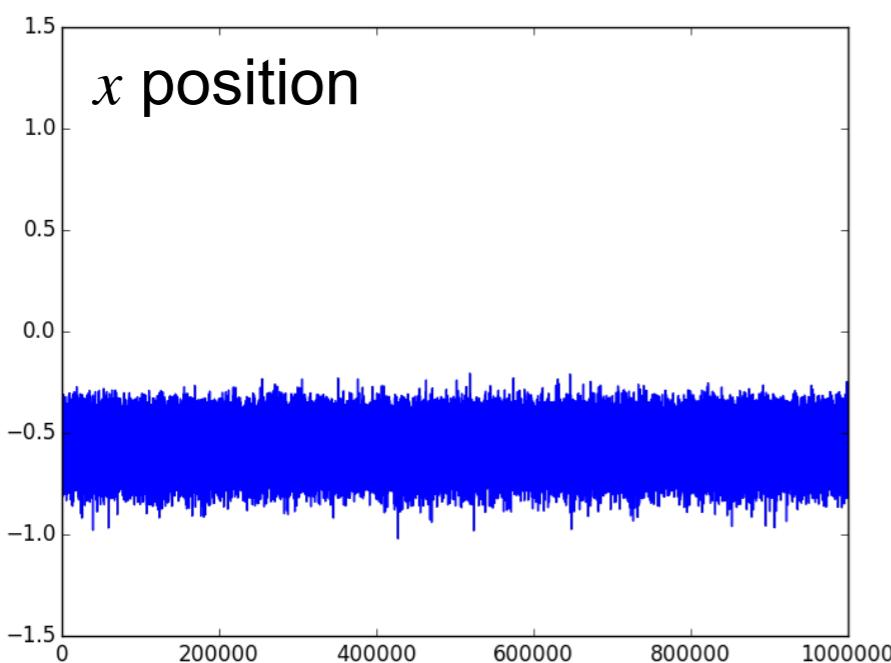


# Unbiased Monte Carlo Simulations

Unable (or rare) to cross barriers in unbiased MC simulations

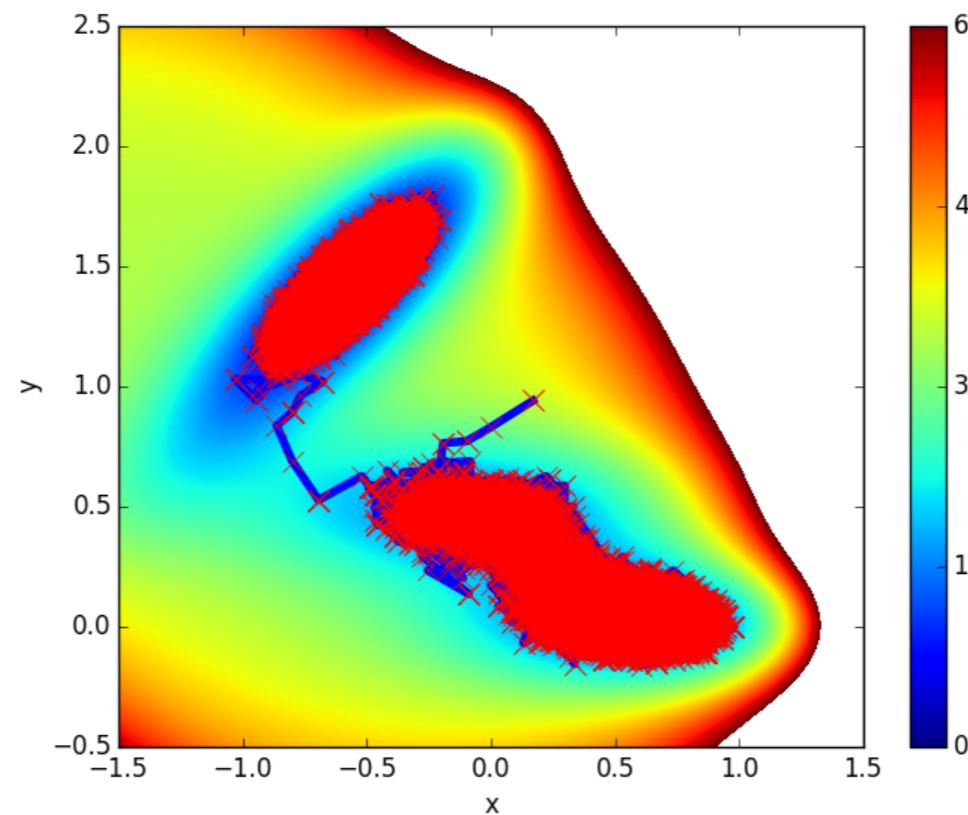


$10^6$  MC step

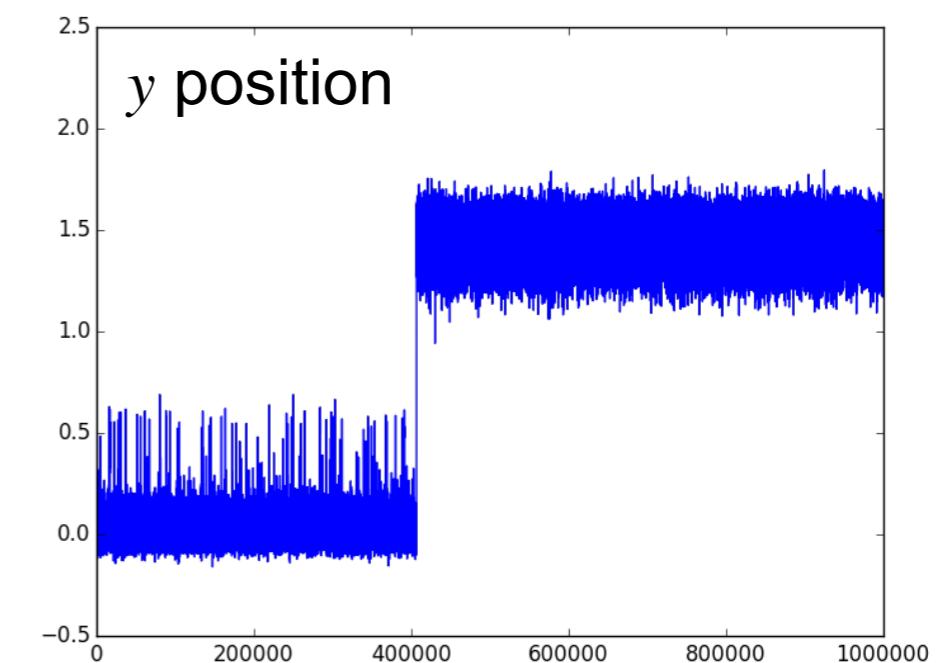
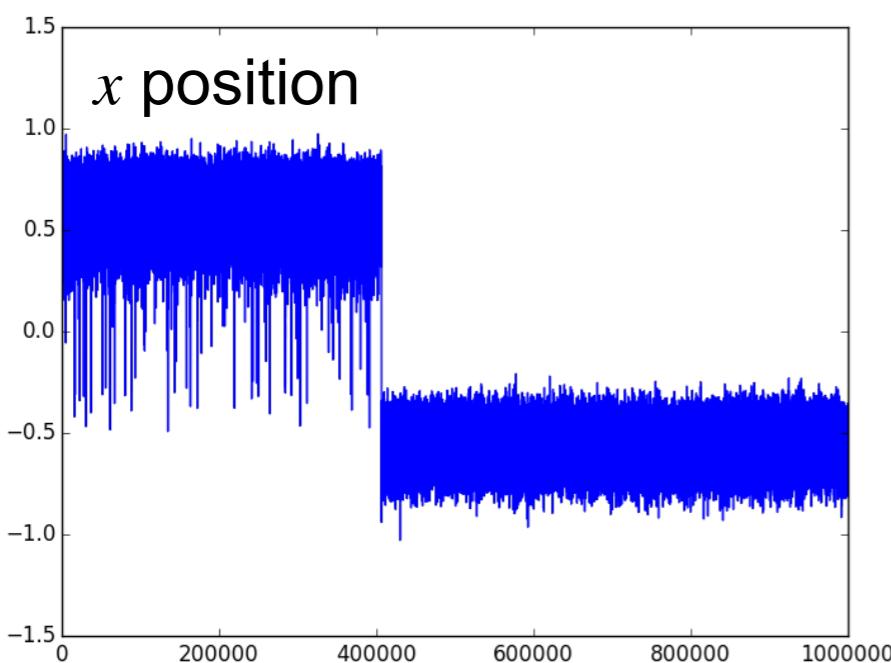


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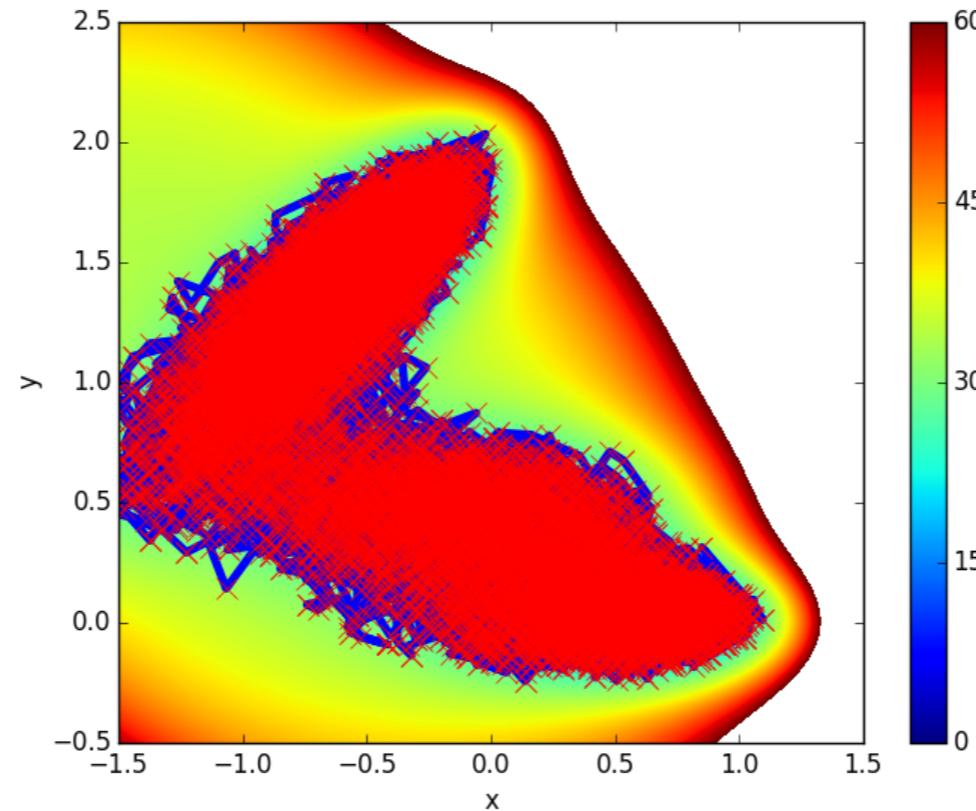


$10^6$  MC step



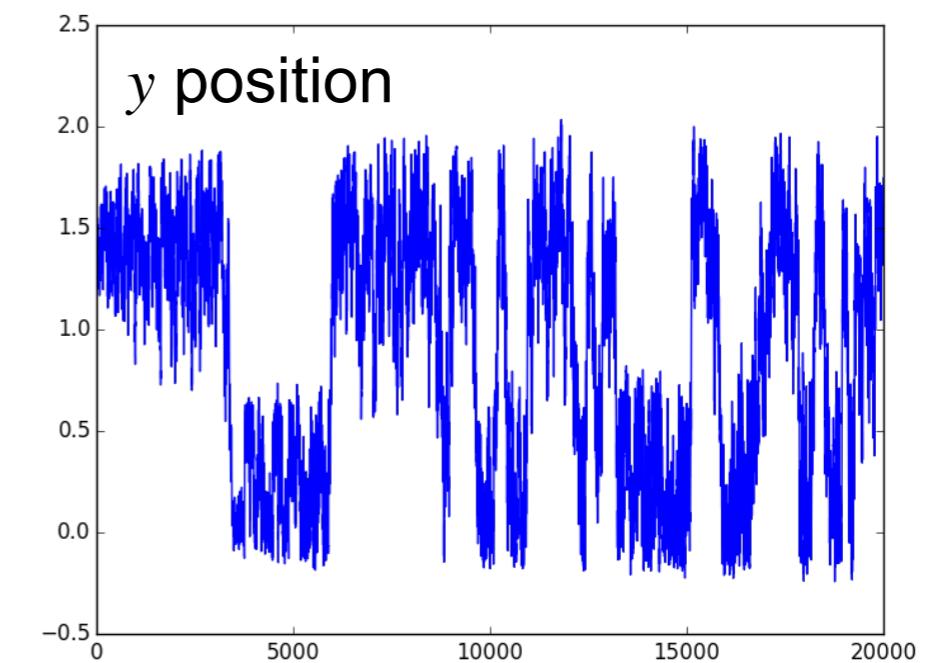
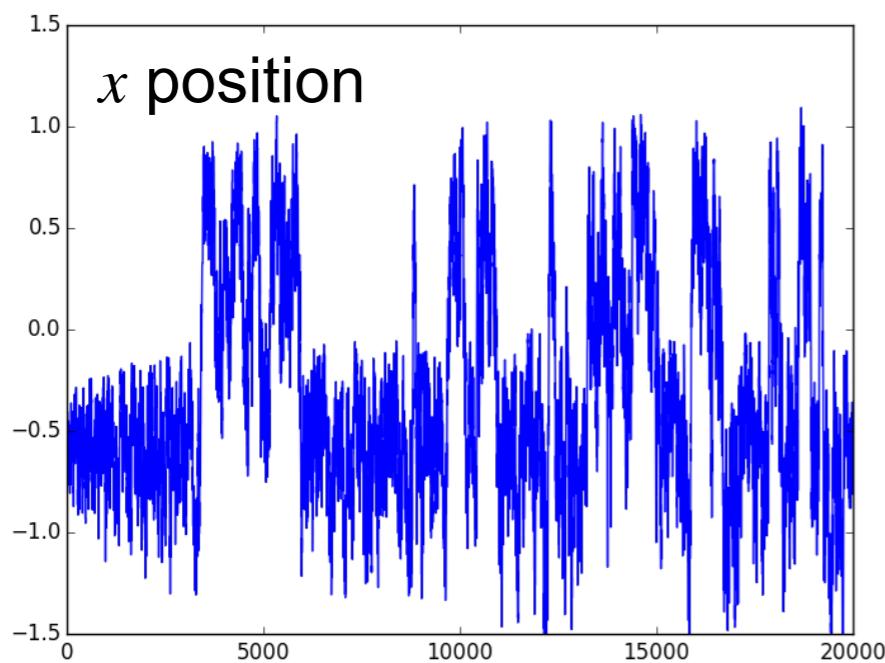
# Metadynamics Simulations

Greatly enhanced barrier crossings with Metadynamics



$2 \times 10^4$  MC step

much less than for the  
unbiased run before!

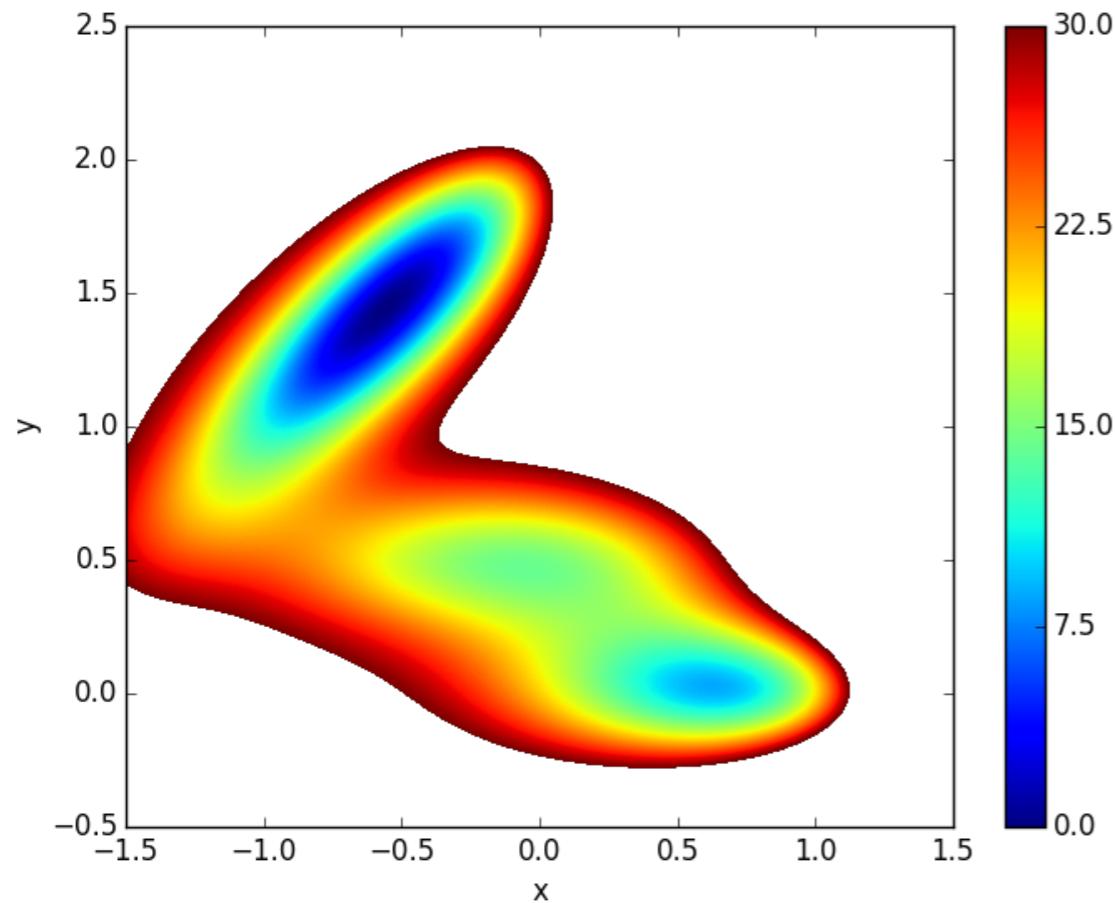


# Metadynamics Simulations

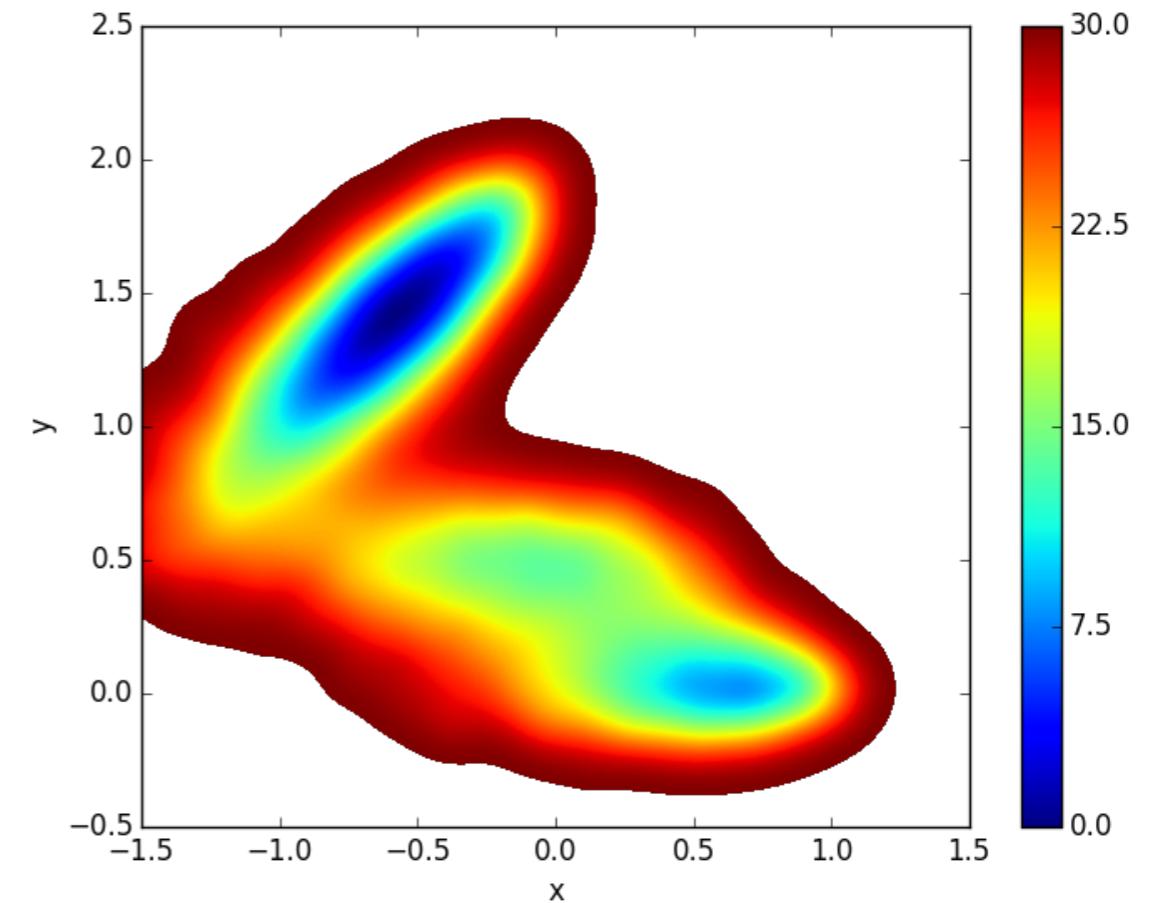
FES/PES from Metadynamics in good agreement with the exact potential

$2 \times 10^4$  MC step

Exact Potential

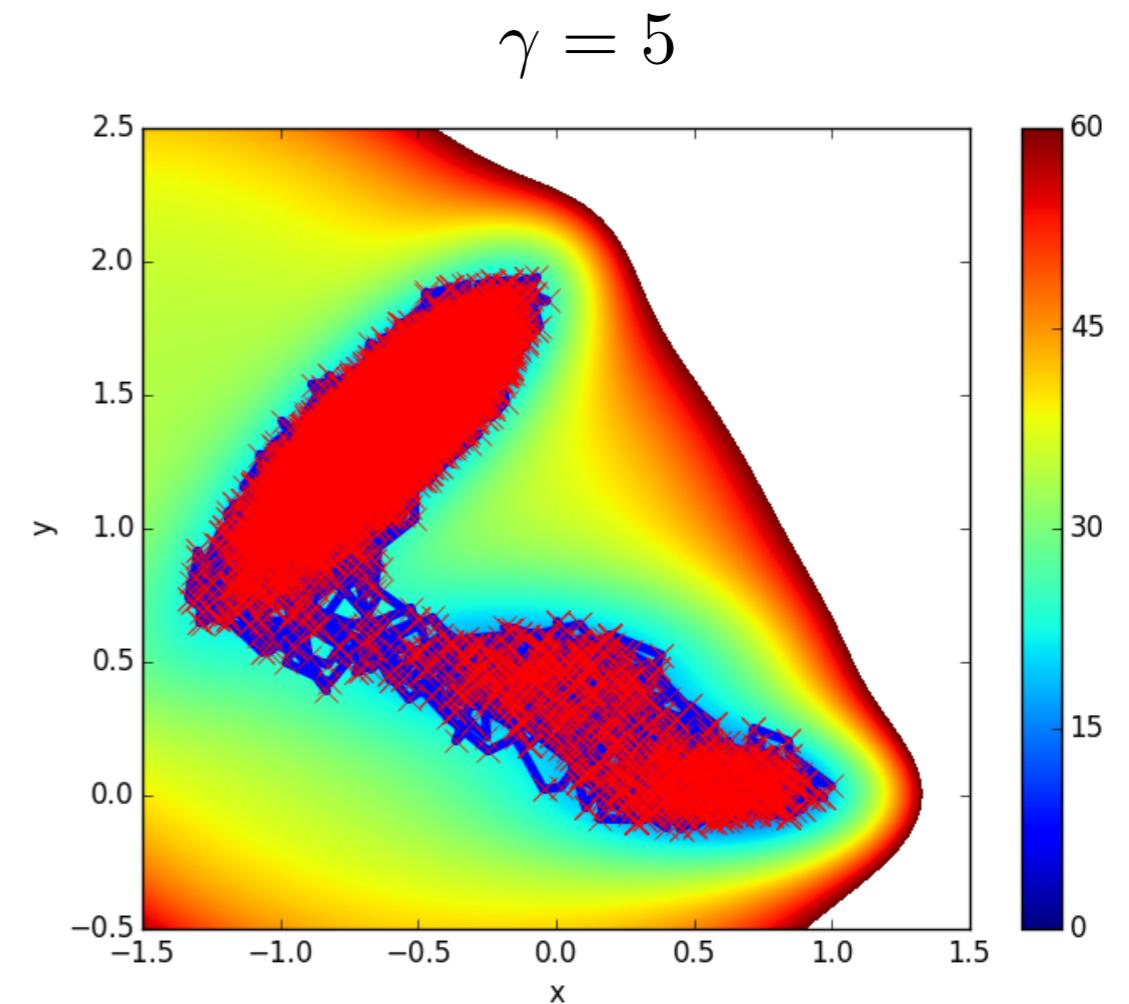
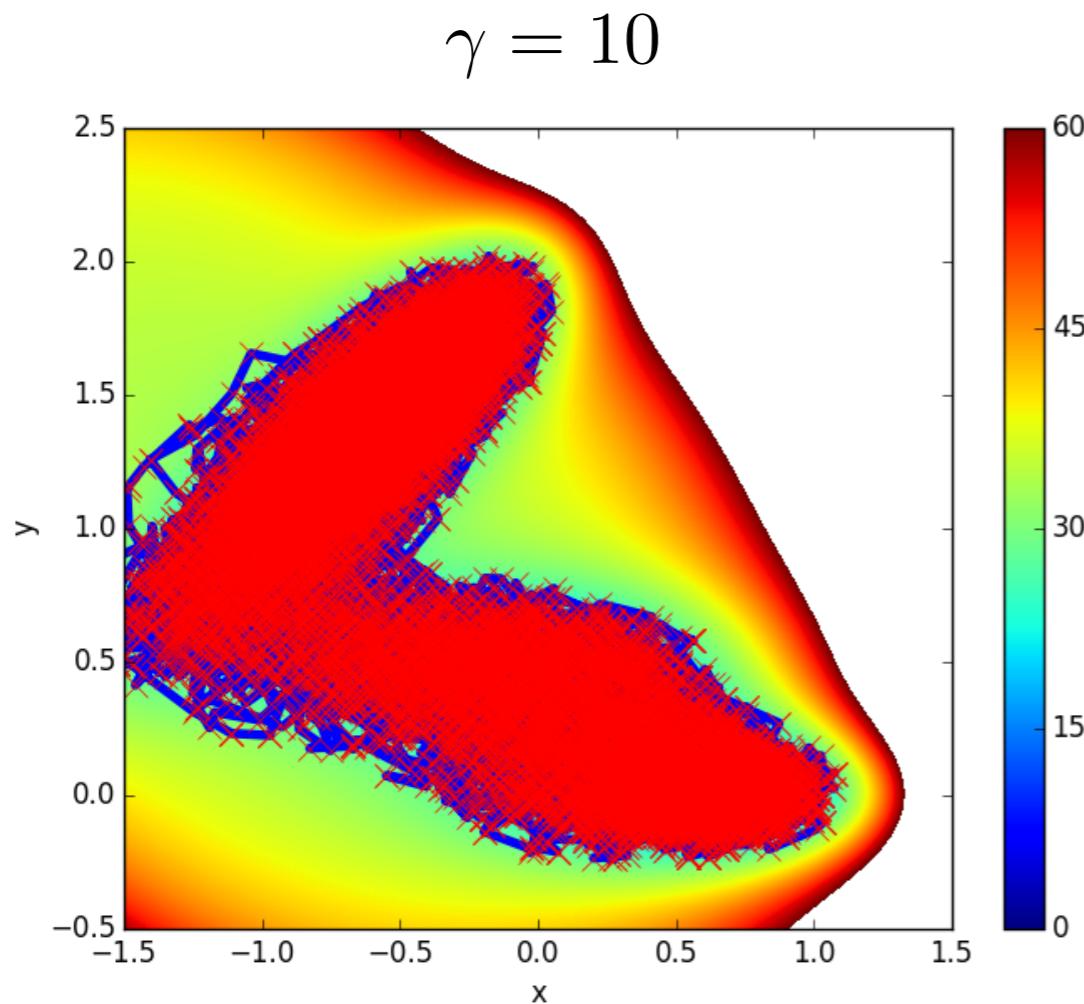


Estimate from Metadynamics



# Metadynamics Simulations

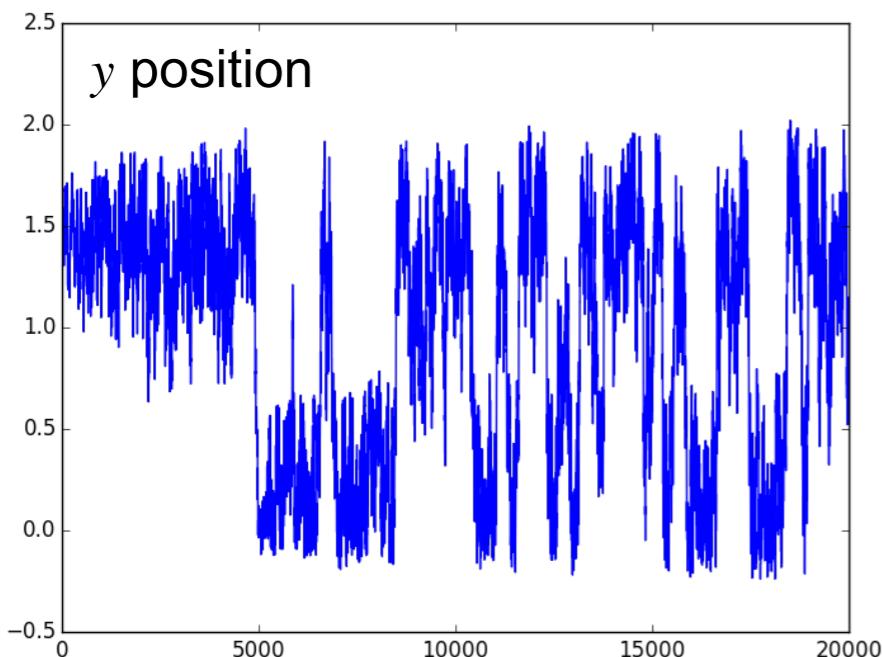
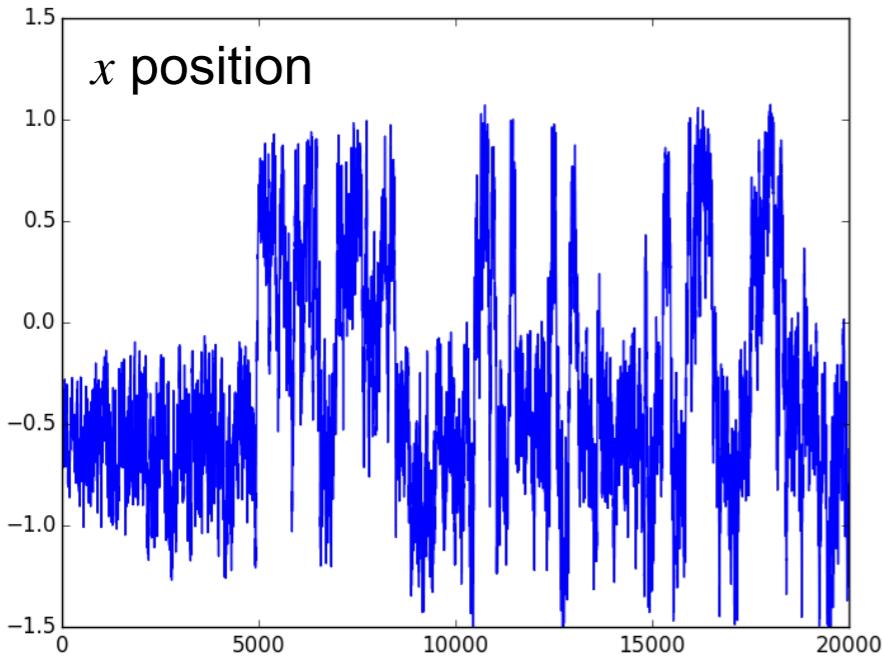
## Effect of the bias factor



# Metadynamics Simulations

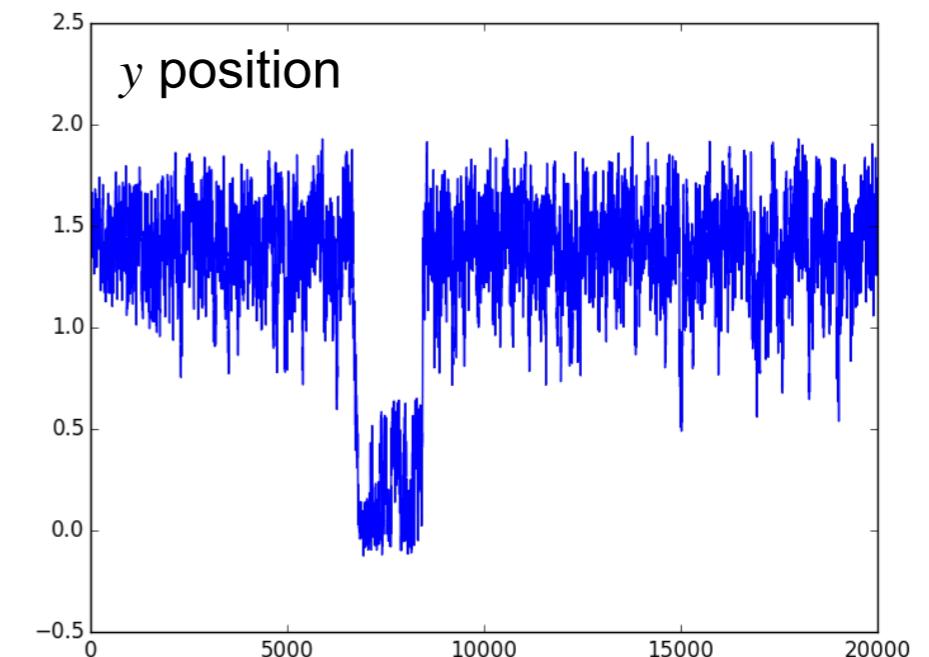
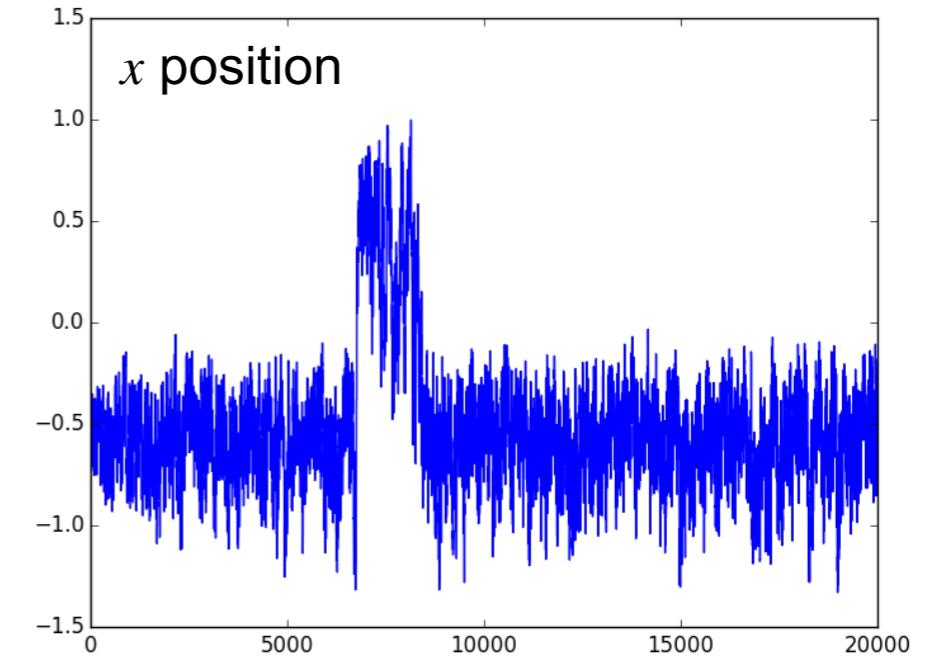
Effect of the bias factor

$$\gamma = 10$$

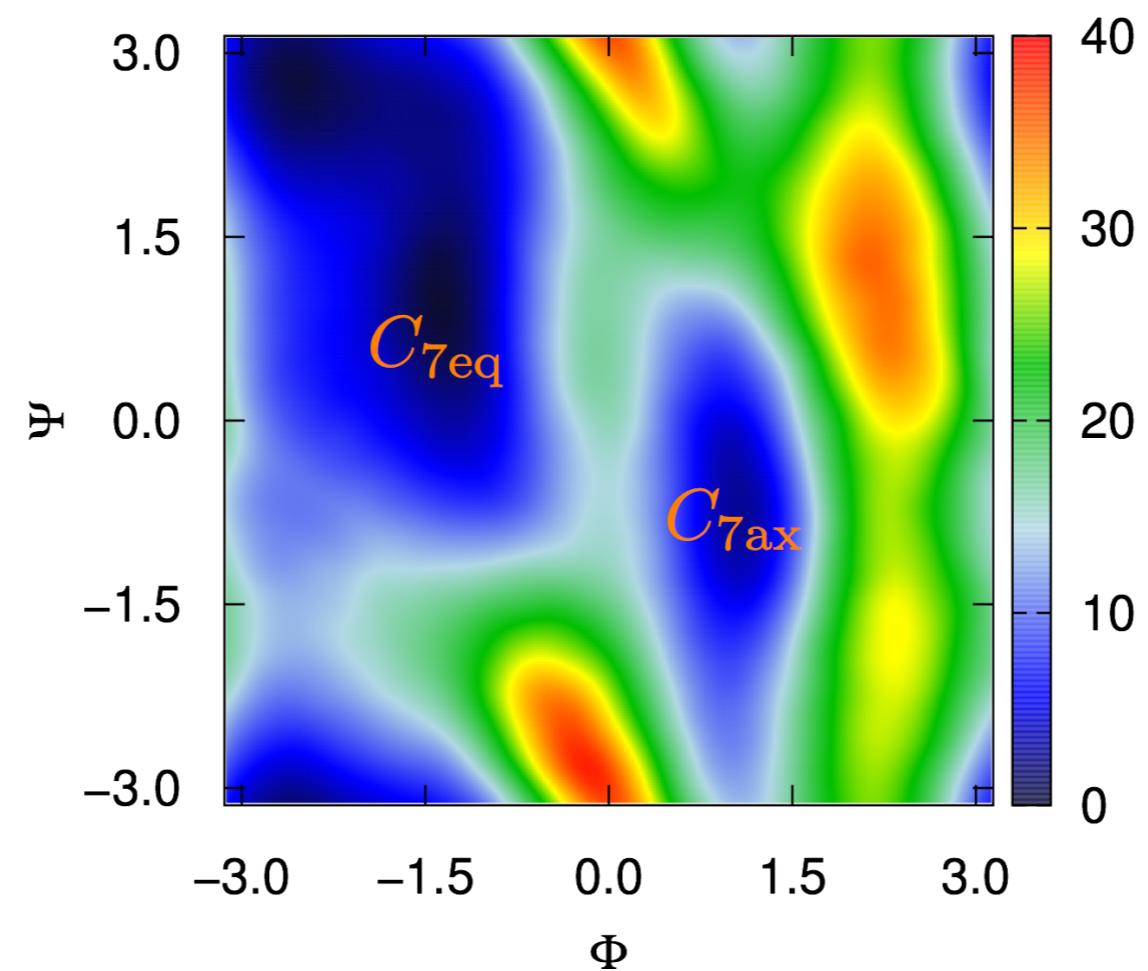
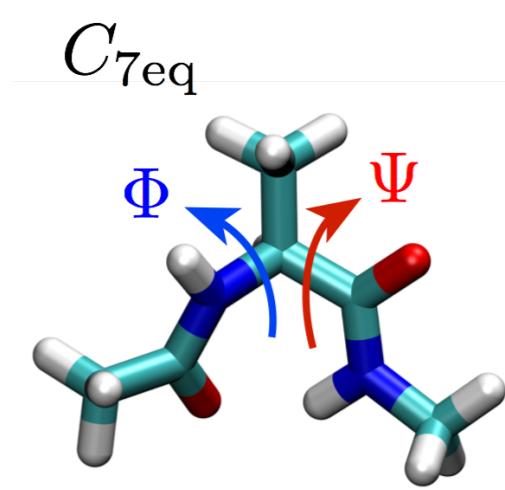


value of 5 not sufficient to overcome barriers

$$\gamma = 5$$

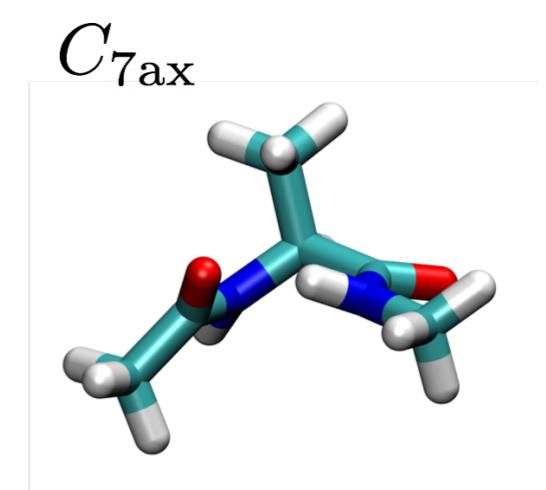


# Missing Slow CVs

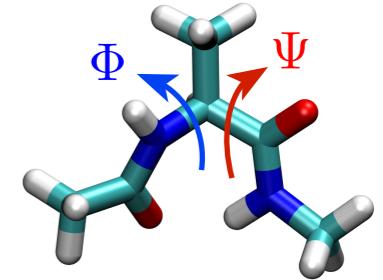


$\Psi$  fast CV

$\Phi$  slow CV

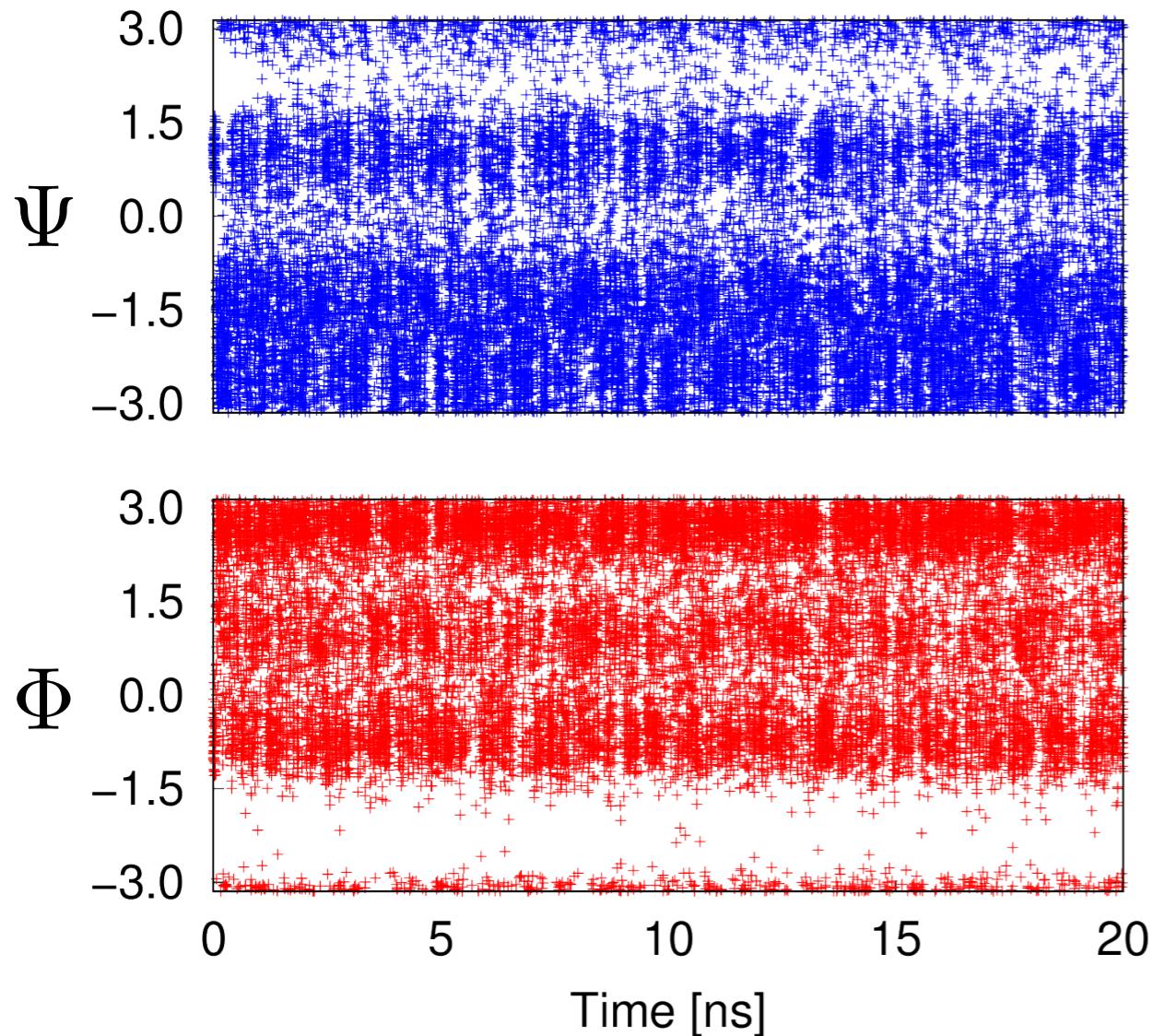


# Missing Slow CVs

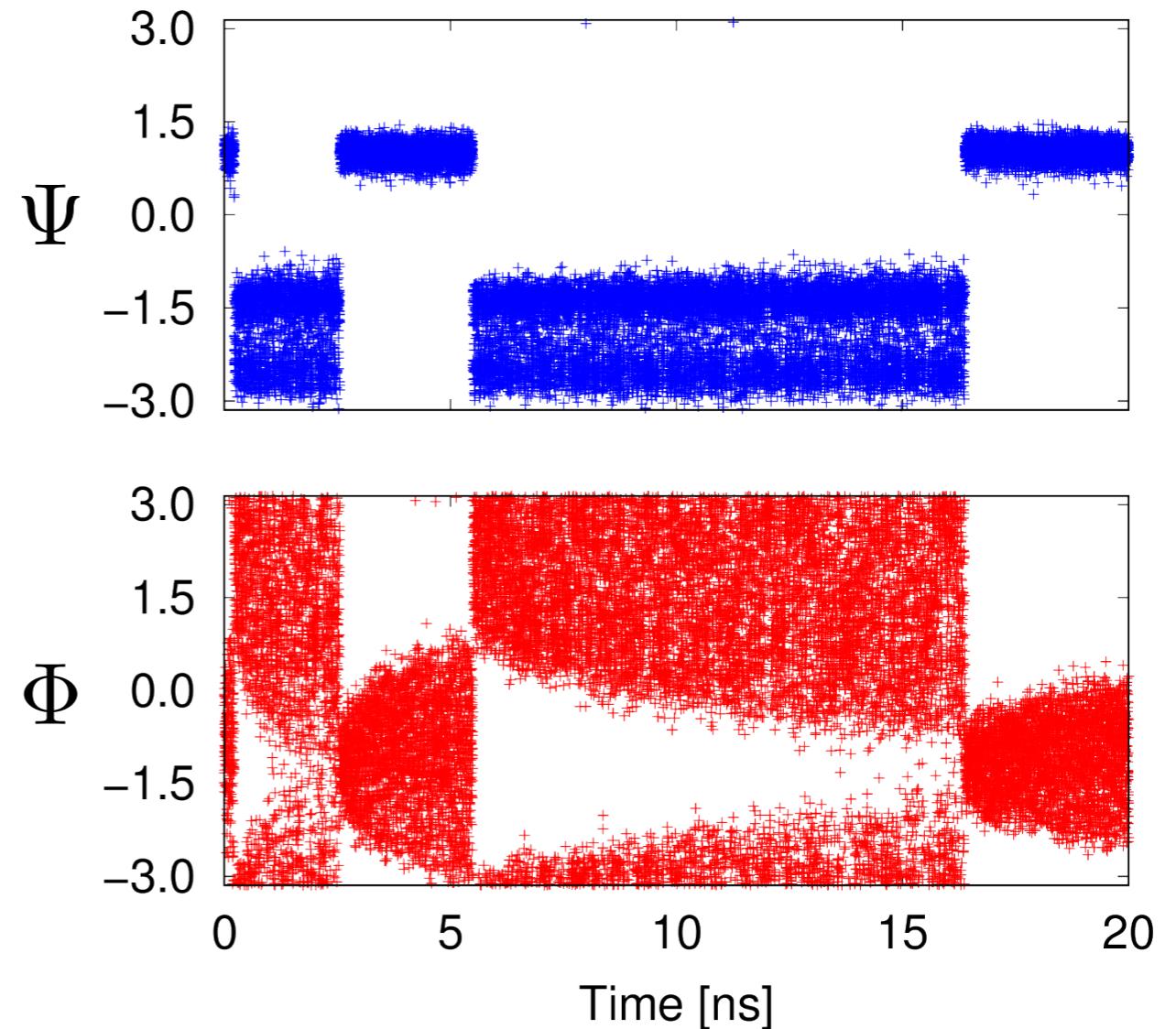


$\Phi$  slow CV /  $\Psi$  fast CV

biasing only slow CV  $\Phi$



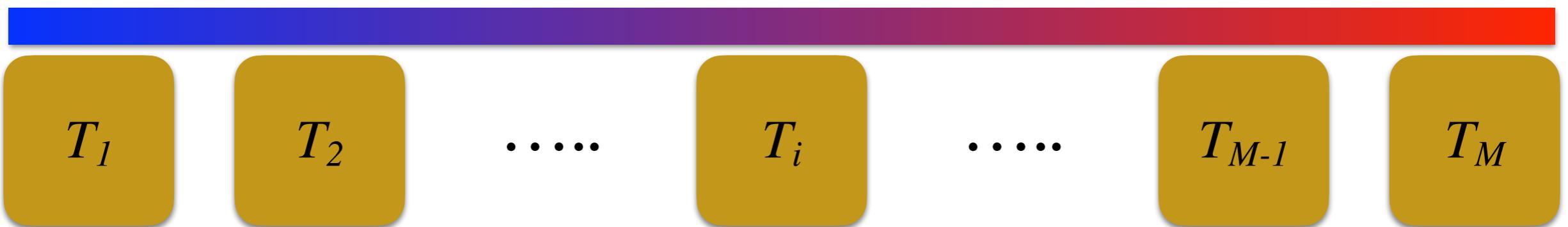
biasing only fast CV  $\Psi$



hysteresis behavior in  $\Psi$  if we are missing slow CV  $\Phi$   
such behavior is quite general

# Parallel-Tempering + Metadynamics

Can combine Metadynamics with parallel-tempering (or other replica exchange method)



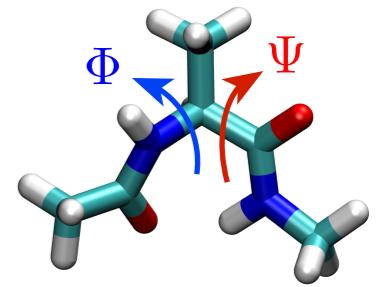
Reduces the requirement on the quality of the metadynamics CVs as parallel-tempering will help sampling the slow degrees of freedom not included in the CV set.

Metadynamics will also assist in sampling transition states and higher lying metastable free energy basins that are generally poorly sampled in parallel-tempering (as it reproduces canonical sampling)

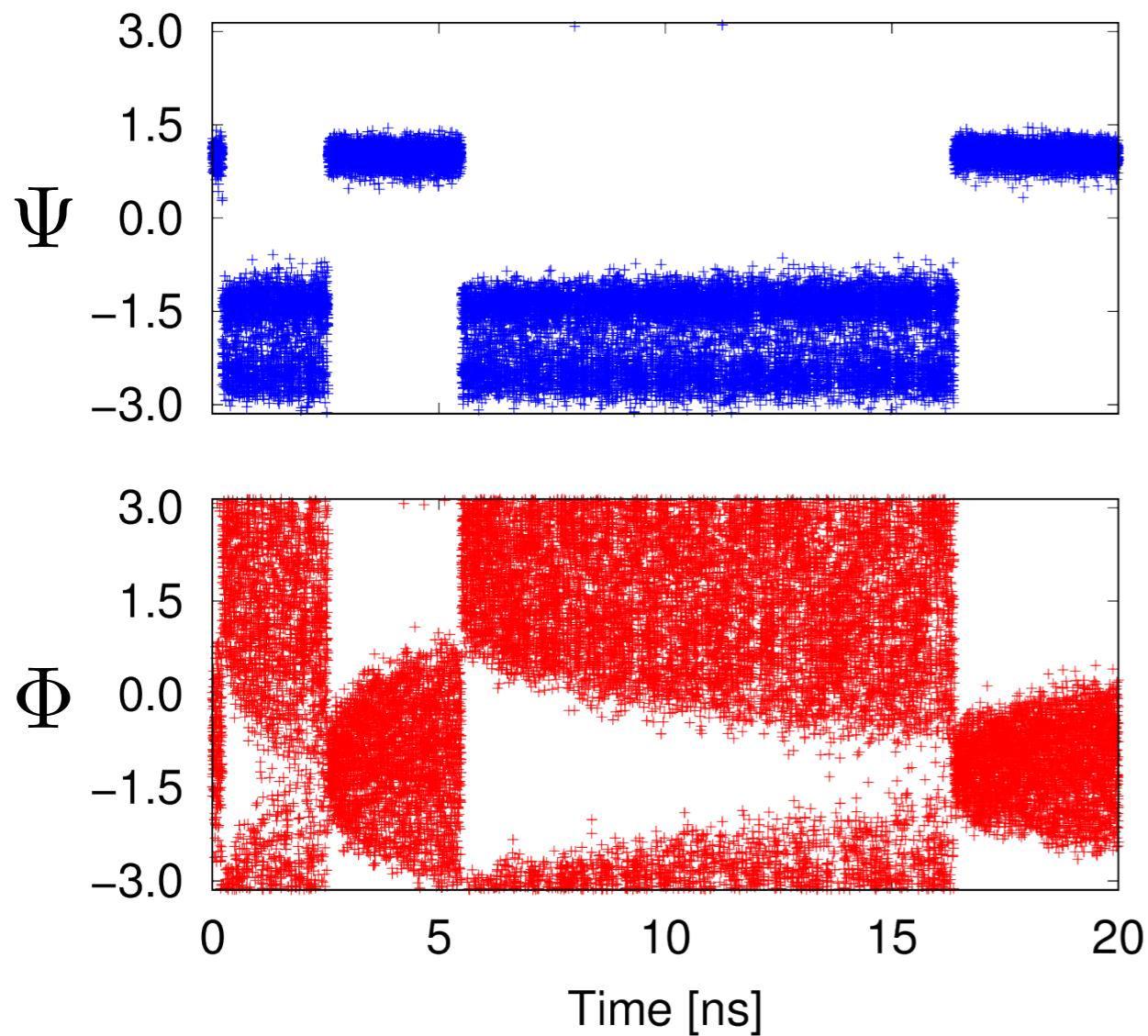
However, parallel-tempering can require a large number of replicas, especially for solvated biomolecules. One way to circumvent this is to employ the so-called well-tempered ensemble (PT-WTE)

# PT+MetaD Helps with Missing Slow CVs

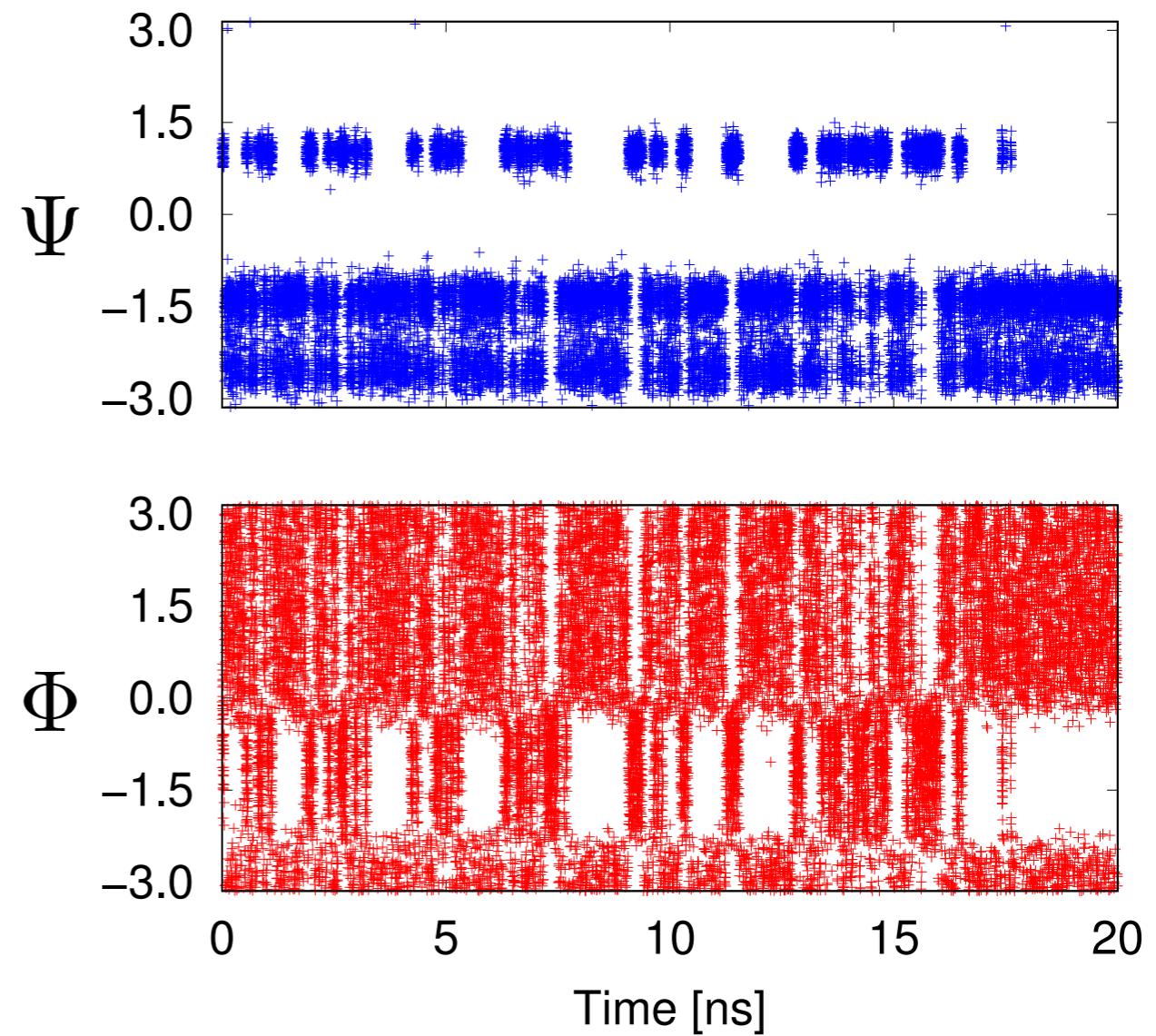
$\Phi$  slow CV /  $\Psi$  fast CV



Metadynamics  
biasing only fast CV  $\Psi$



Metadynamics + PT  
biasing only fast CV  $\Psi$



Combining with parallel-tempering mends hysteresis behavior