



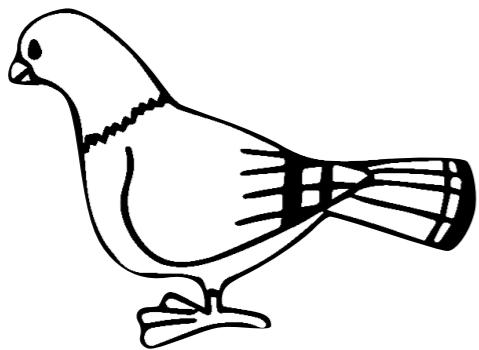
# PLUMED Masterclass

## 21.3: Umbrella sampling

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 @BussiGio





open-source  
freely-available  
C++ library

- enhanced-sampling methods
- free-energy methods
- analysis MD data



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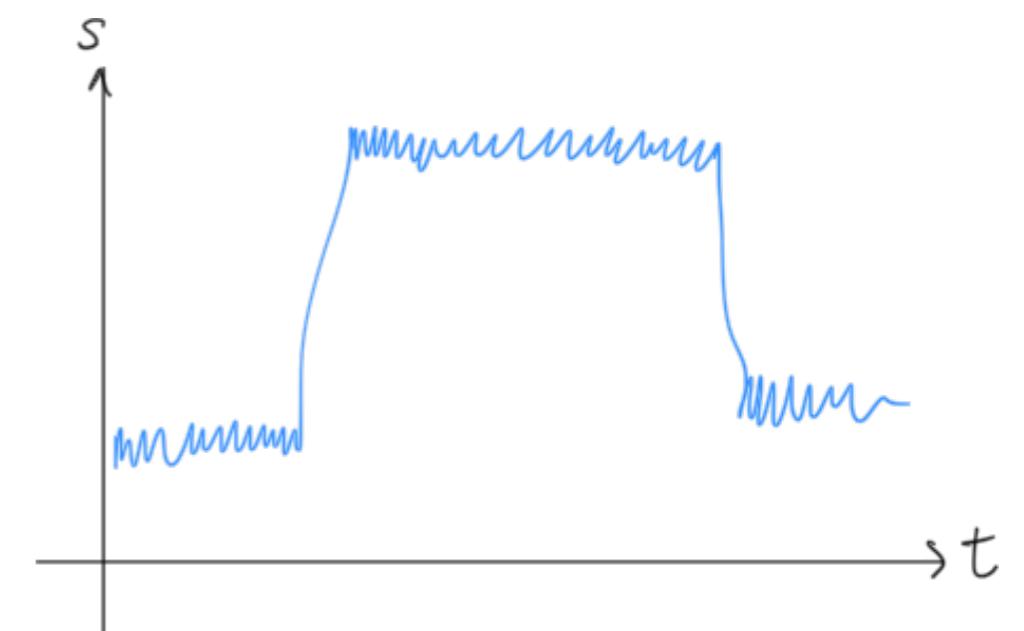
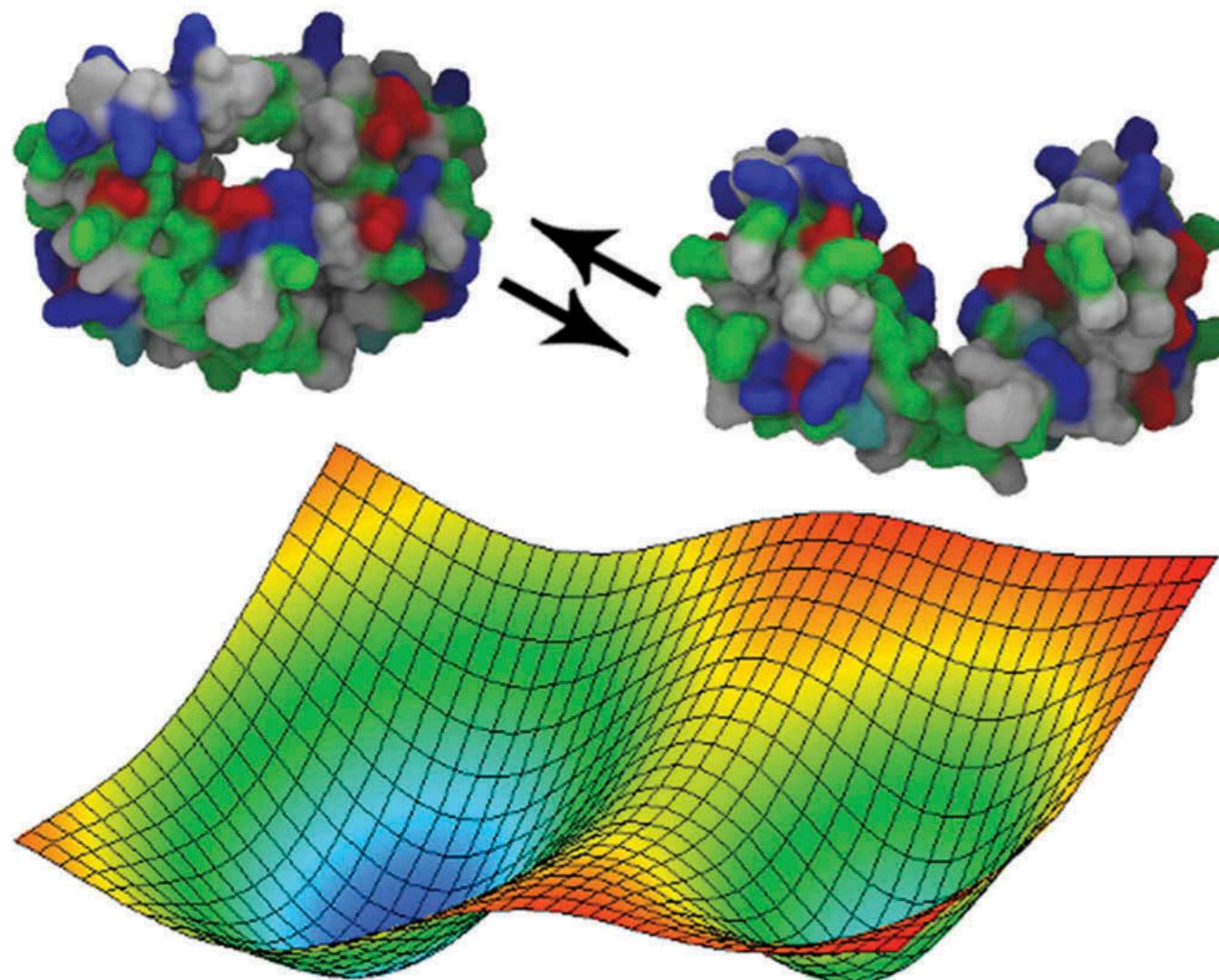


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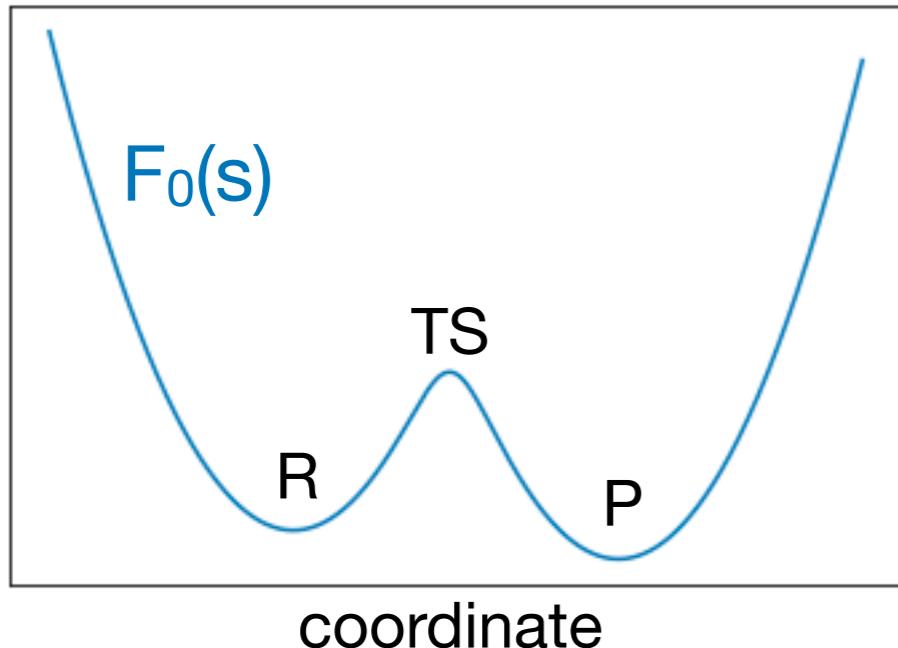


Class	Topic	Lecture I	Lecture II	Instructor
21.1	PLUMED syntax and analysis	January 18, 2021	January 25, 2021	M. Bonomi
21.2	Statistical errors in MD	February 1, 2021	February 8, 2021	G. Tribello
21.3	Umbrella sampling	February 15, 2021	February 22, 2021	G. Bussi
21.4	Metadynamics	March 1, 2021	March 8, 2021	M. Bonomi
21.5	Replica exchange methods	March 15, 2021	March 22, 2021	G. Bussi
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21.7	Performance optimization	April 26, 2021	May 3, 2021	M. Bonomi
21.8	Poster session	May 10, 2021		

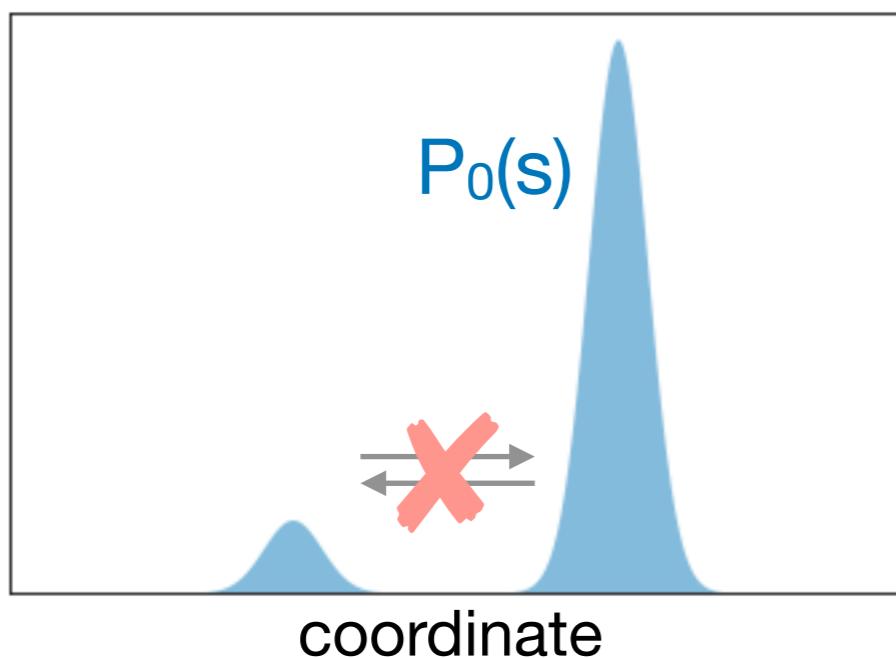
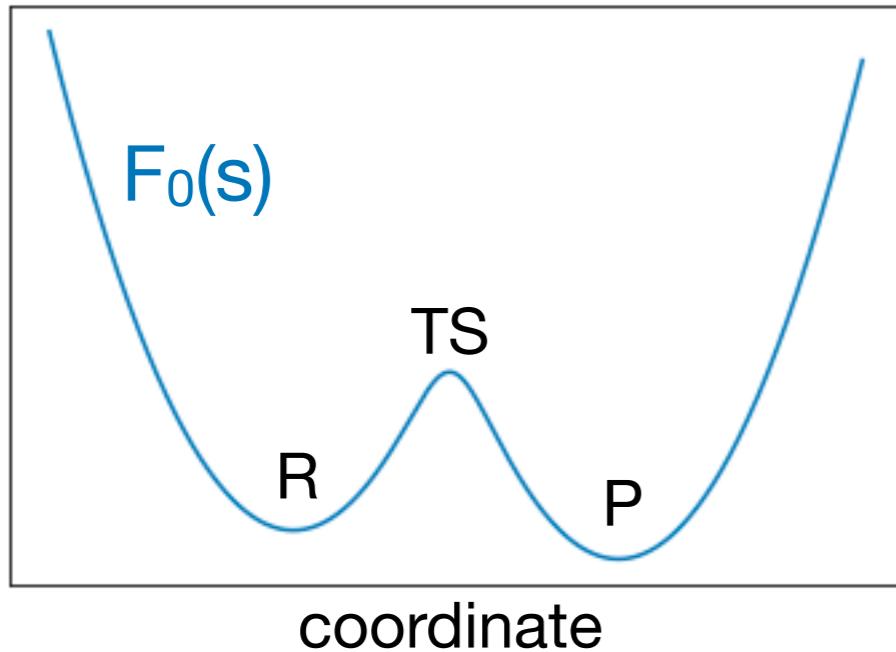
# Rare events



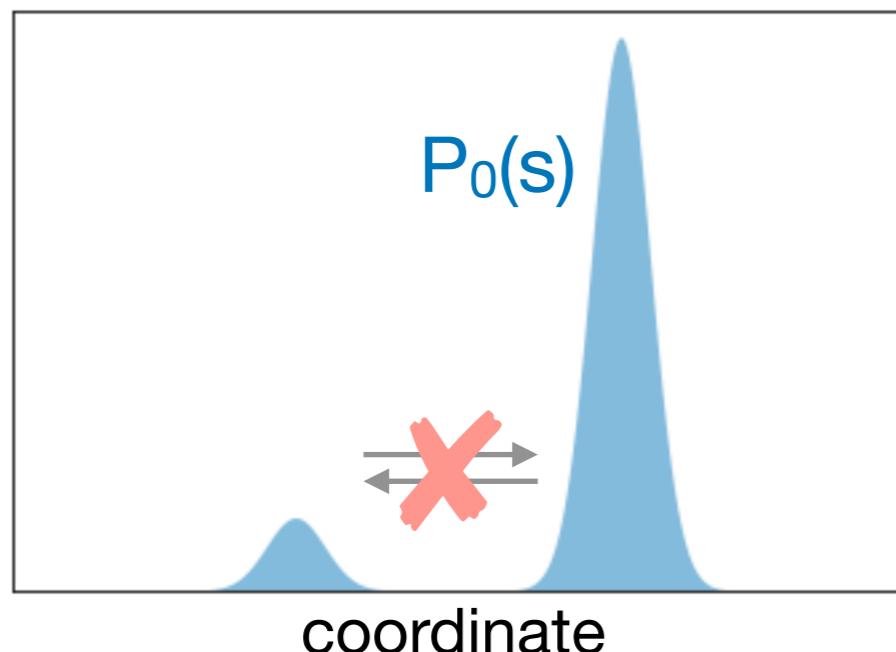
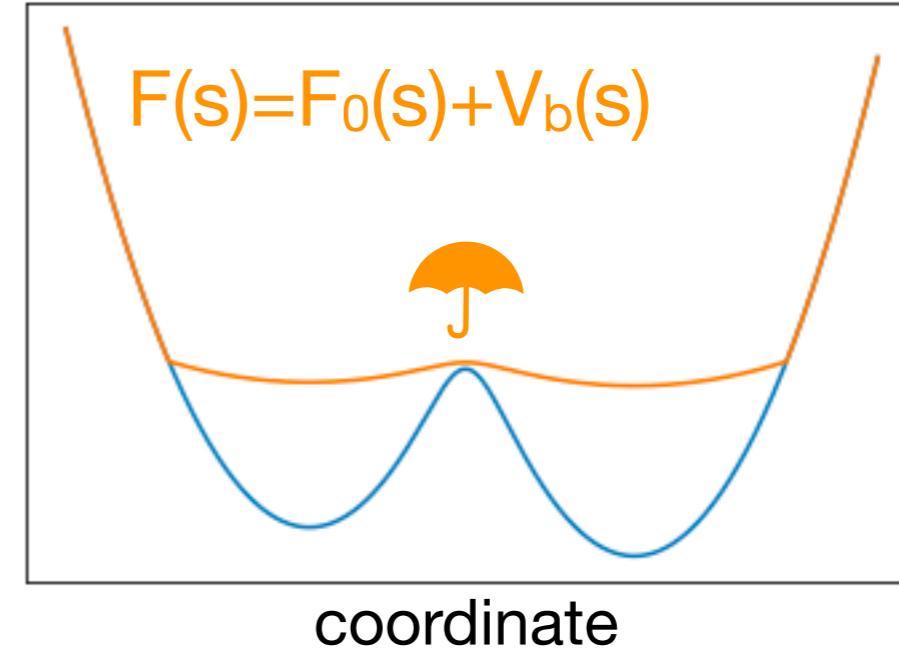
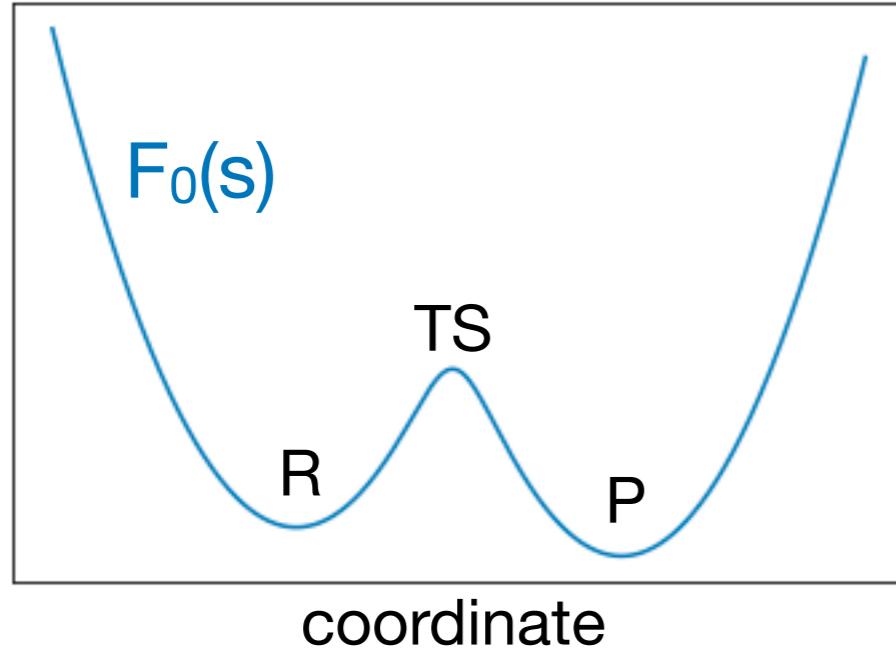
# How biased sampling could help: umbrella sampling



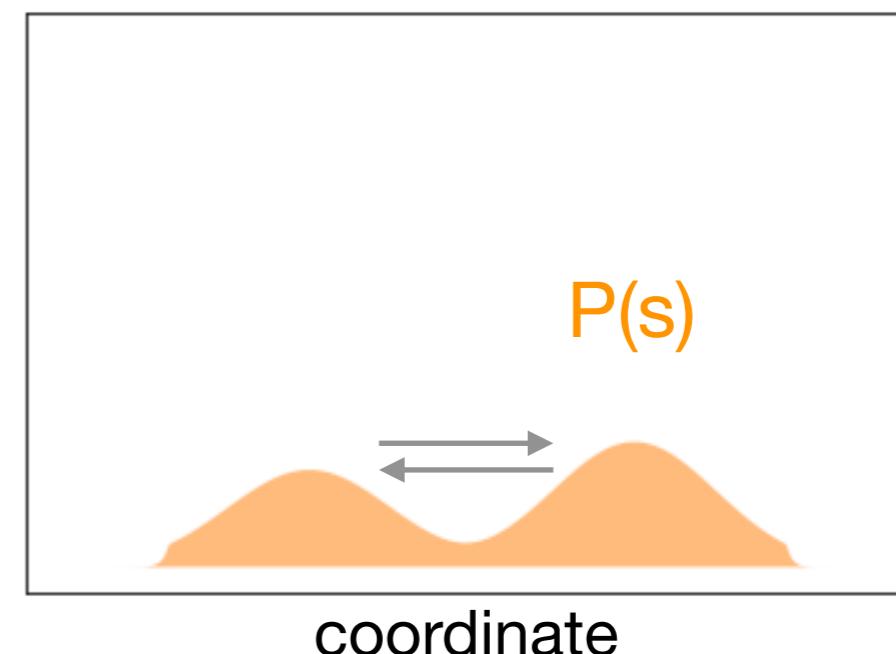
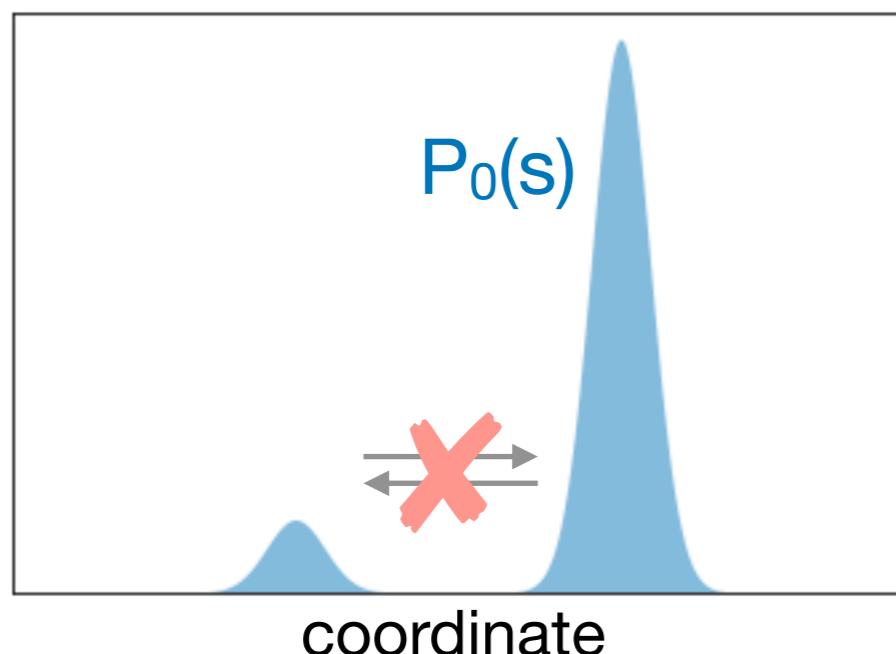
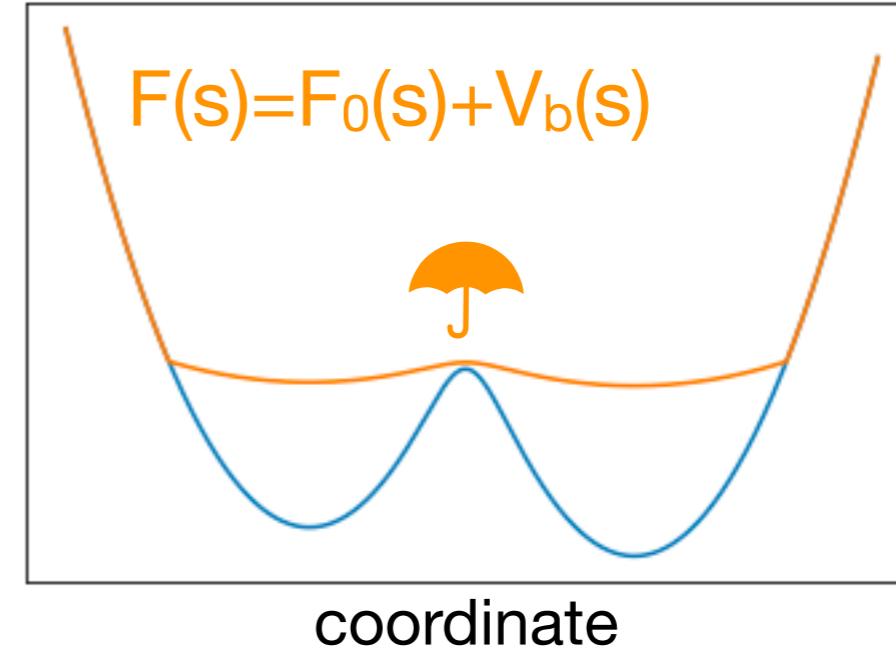
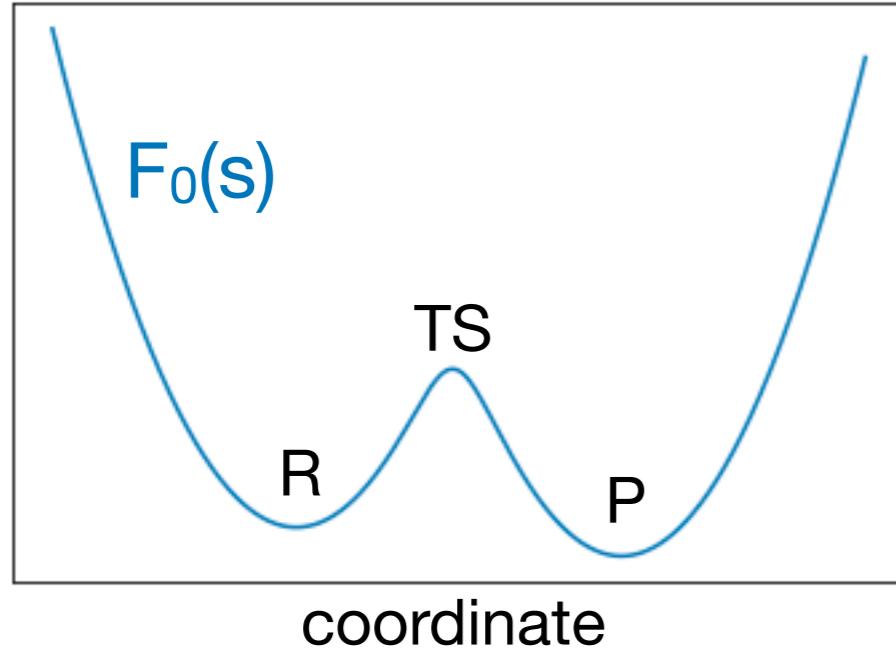
# How biased sampling could help: umbrella sampling



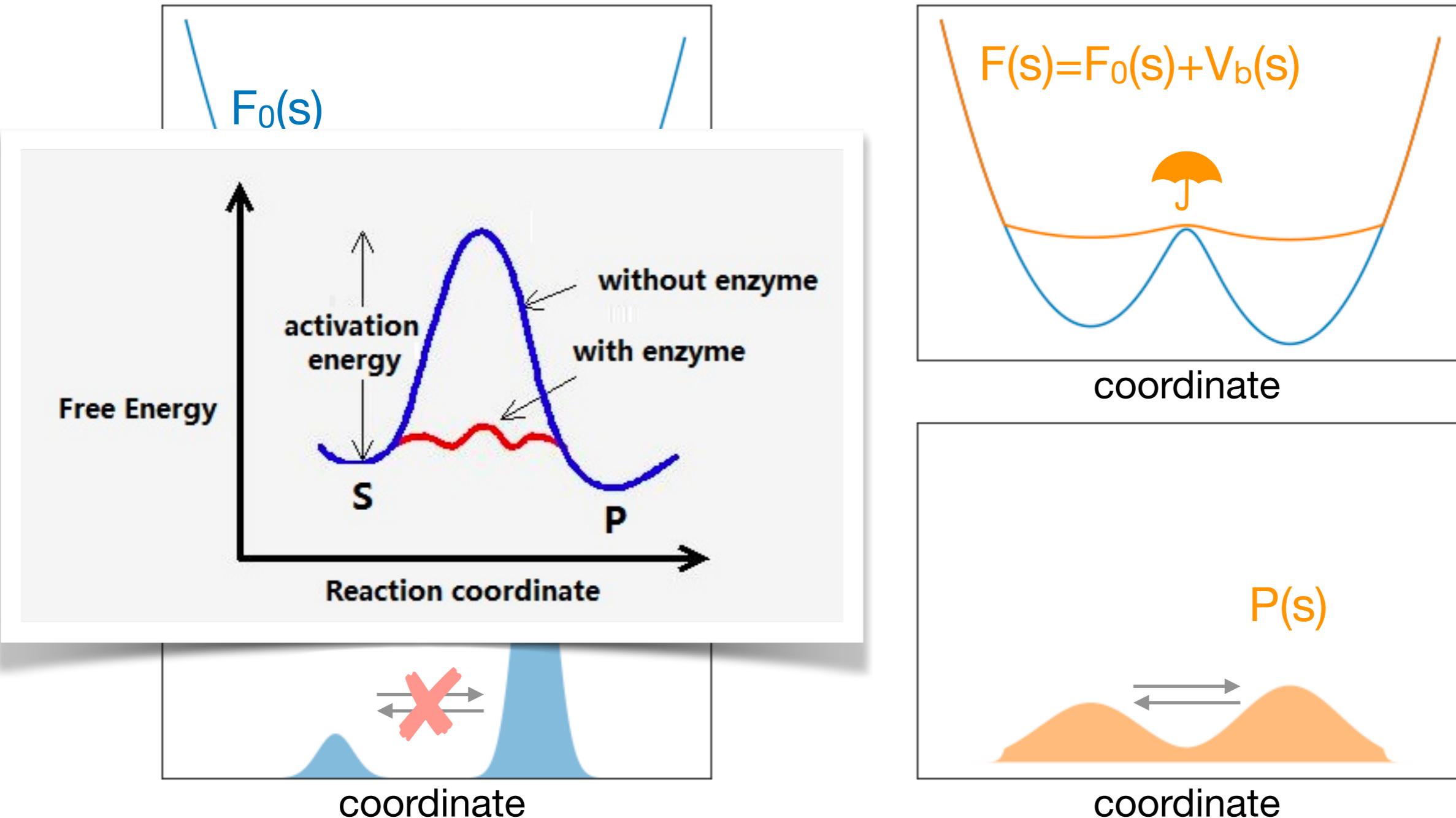
# How biased sampling could help: umbrella sampling



# How biased sampling could help: umbrella sampling



# How biased sampling could help: umbrella sampling



Disfavor reactant and product (i.e. favor transition state), like a biological enzyme

# Unbiasing the result

$$P(t_1, \dots, t_M) \propto \prod_{j=1}^M \left( e^{-\beta V_b(s_j)} p_j \right)^{t_j}$$

how much the bias  $V_b$  affects the probability

number of times state  $j$  was visited

product over all states

unbiased probability of observing state  $j$

# Unbiasing the result

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how much the bias  $V_b$  affects the probability

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product over all states

Find  $p$  that maximises the likelihood

$$w(s) \propto e^{+\beta V_b(s)}$$

Averages can be computed by reweighting

$$\langle A \rangle = \frac{\sum_j A_j w(s_j)}{\sum_j w(s_j)}$$

# Unbiasing the result

$$P(t_1, \dots, t_M) \propto \prod_{j=1}^M \left( e^{-\beta V_b(s_j)} p_j \right)^{t_j}$$

how much the bias  $V_b$  affects the probability

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product over all states

Find  $p$  that maximises the likelihood

Weight more if system went there even if disfavored

$$w(s) \propto e^{+\beta V_b(s)}$$

Averages can be computed by reweighting

$$\langle A \rangle = \frac{\sum_j A_j w(s_j)}{\sum_j w(s_j)}$$

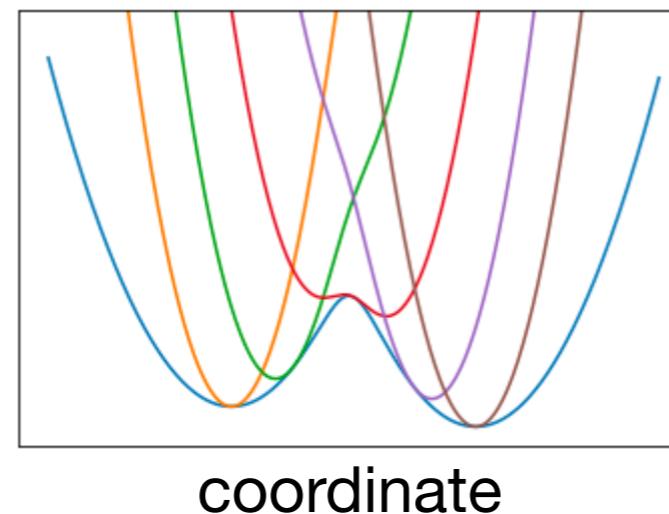
# Multiple-windows umbrella sampling

Each simulation estimates the profile for a narrow range of the biased variable

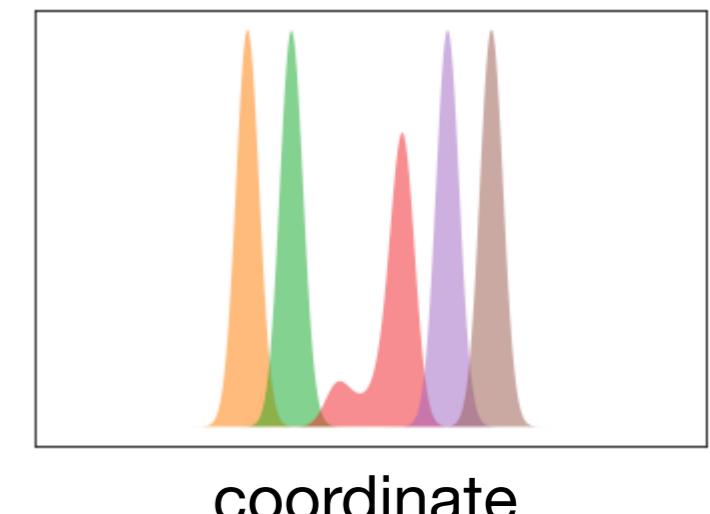
stiffness

$$V_b^j(s) = \frac{k}{2} (s - s_j)^2$$

↑  
interpolate  
between  
reactant and  
product



Overlapping histograms



# Combining multiple simulations: WHAM

$$P(t_1^1, \dots, t_M^N) \propto \prod_{j=1}^M \prod_{k=1}^N \left( c_k e^{-\beta V_b^k(s_j)} p_j \right)^{t_{kj}}$$

product over all states and all trajectories

how much the  $k$ -th bias affects the probability

make sure each probability is normalized

number of times state  $j$  was visited in traj  $k$

unbiased probability of observing state  $j$

Diagram illustrating the components of the WHAM equation:

- Product over all states and all trajectories
- how much the  $k$ -th bias affects the probability
- make sure each probability is normalized
- number of times state  $j$  was visited in traj  $k$
- unbiased probability of observing state  $j$

# Combining multiple simulations: WHAM

$$P(t_1^1, \dots, t_M^N) \propto \prod_{j=1}^M \prod_{k=1}^N \left( c_k e^{-\beta V_b^k(s_j)} p_j \right)^{t_{kj}}$$

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Find  $p$  that maximises the likelihood

$$c_k = \frac{1}{\sum_j e^{-\beta V_b^k(s_j)} w(s_j)}$$

$$w(s) \propto \frac{1}{\sum_k c_k e^{-\beta V_b^k(s)}}$$

Self-consistent equations

# Combining multiple simulations: WHAM

$$P(t_1^1, \dots, t_M^N) \propto \prod_{j=1}^M \prod_{k=1}^N \left( c_k e^{-\beta V_b^k(s_j)} p_j \right)^{t_{kj}}$$

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make sure each probability is normalized

unbiased probability of observing state  $j$

number of times state  $j$  was visited in traj  $k$

Find  $p$  that maximises the likelihood

Averages can be computed by reweighting

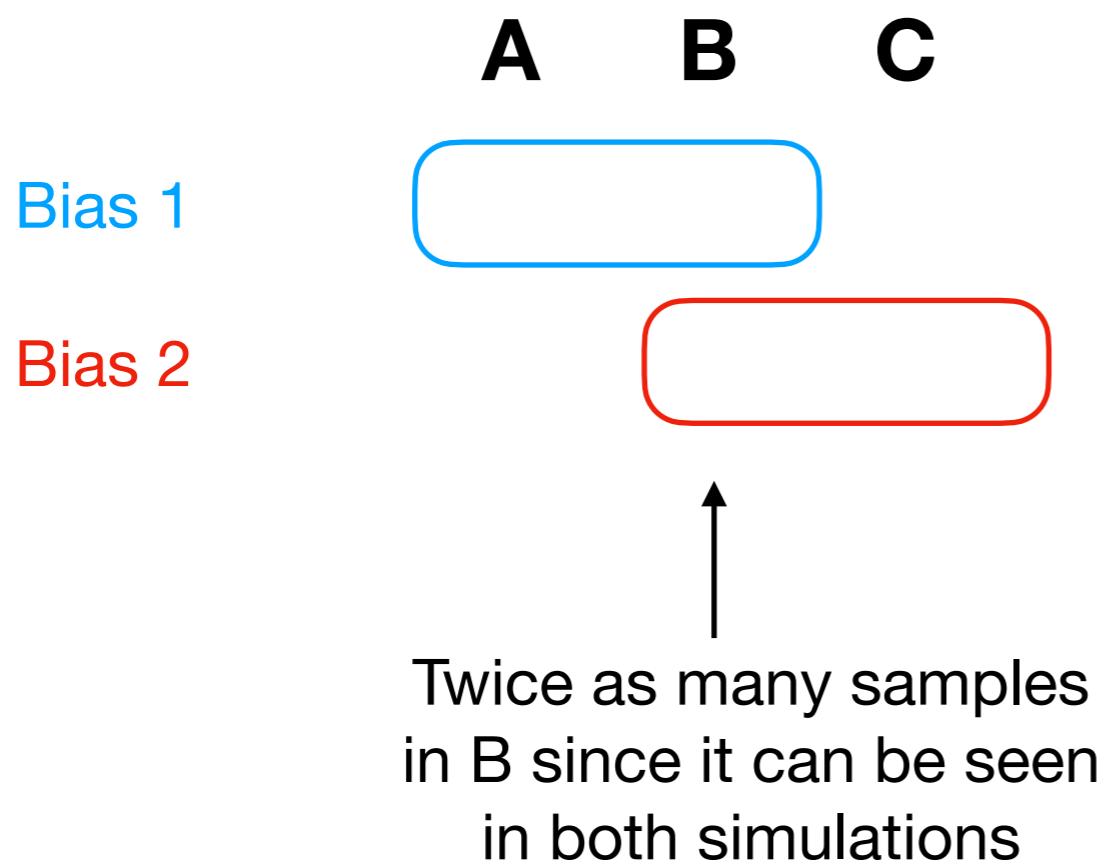
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Self-consistent equations

$$\langle A \rangle = \frac{\sum_j A_j w(s_j)}{\sum_j w(s_j)}$$

# Combining multiple simulations: WHAM

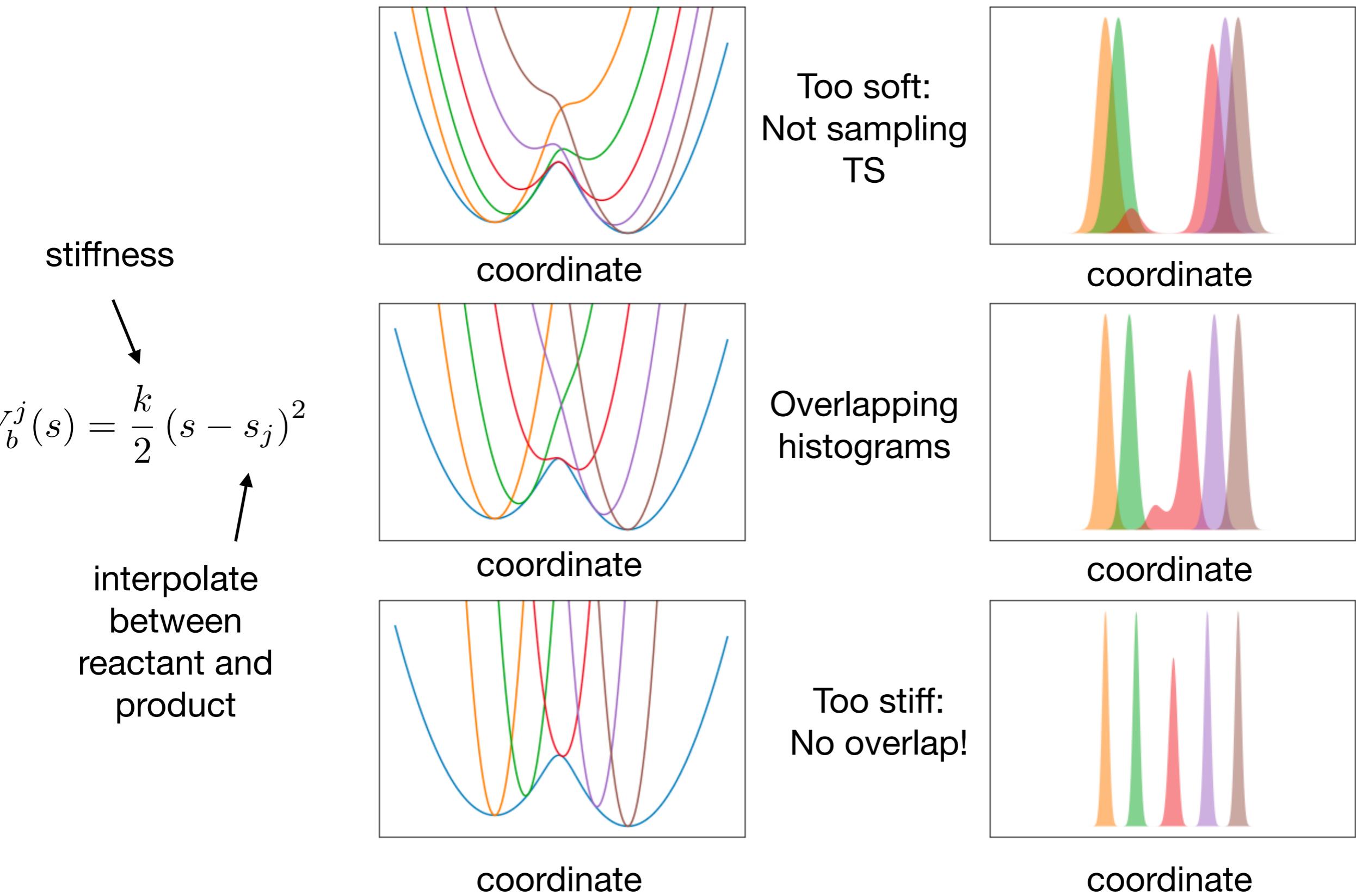


$$c_k = \frac{1}{\sum_j e^{-\beta V_b^k(s_j)} w(s_j)}$$

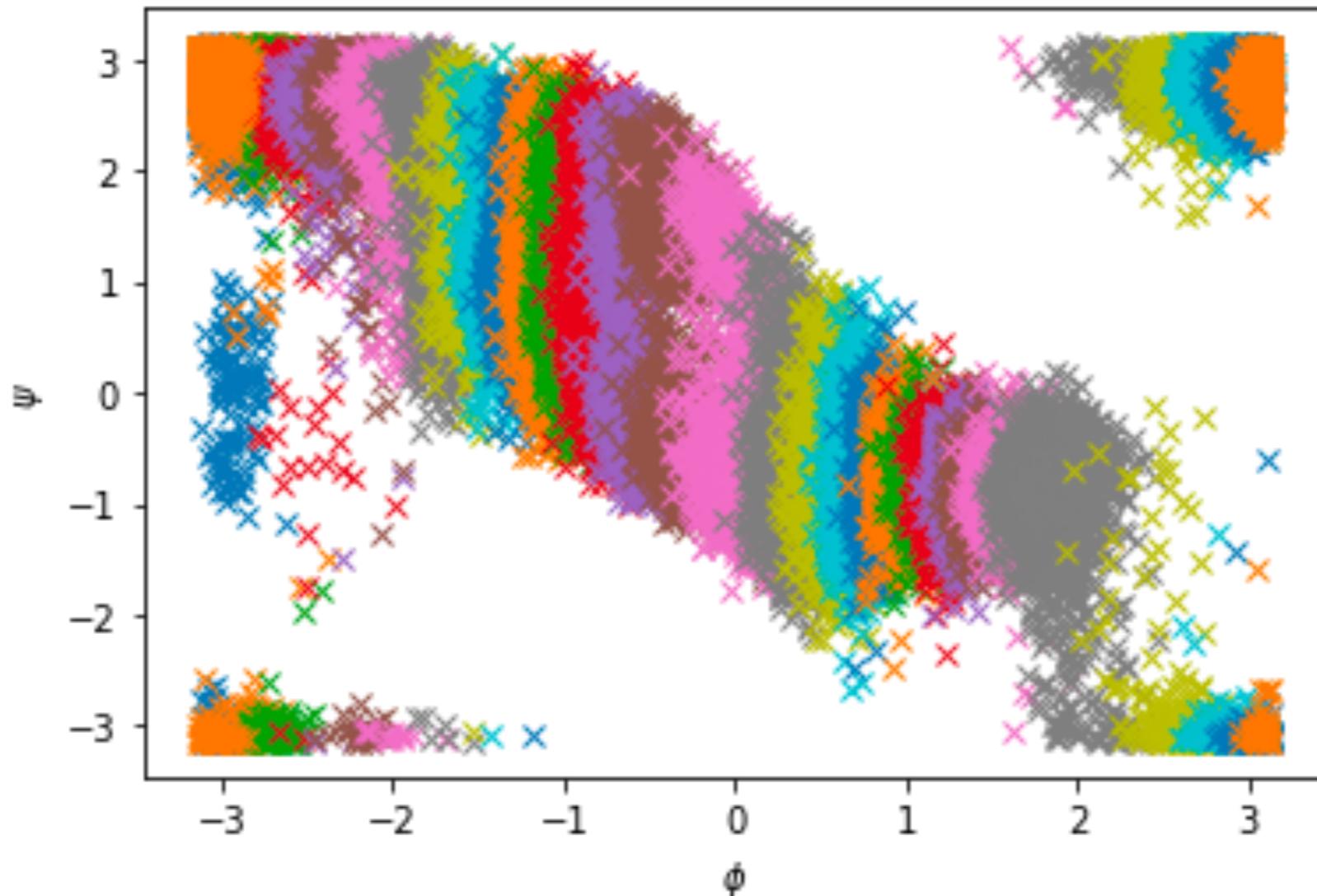
$$w(s) \propto \frac{1}{\sum_k c_k e^{-\beta V_b^k(s)}}$$

Self-consistent equations

# Pay attention to stiffness



# Checking for overlap

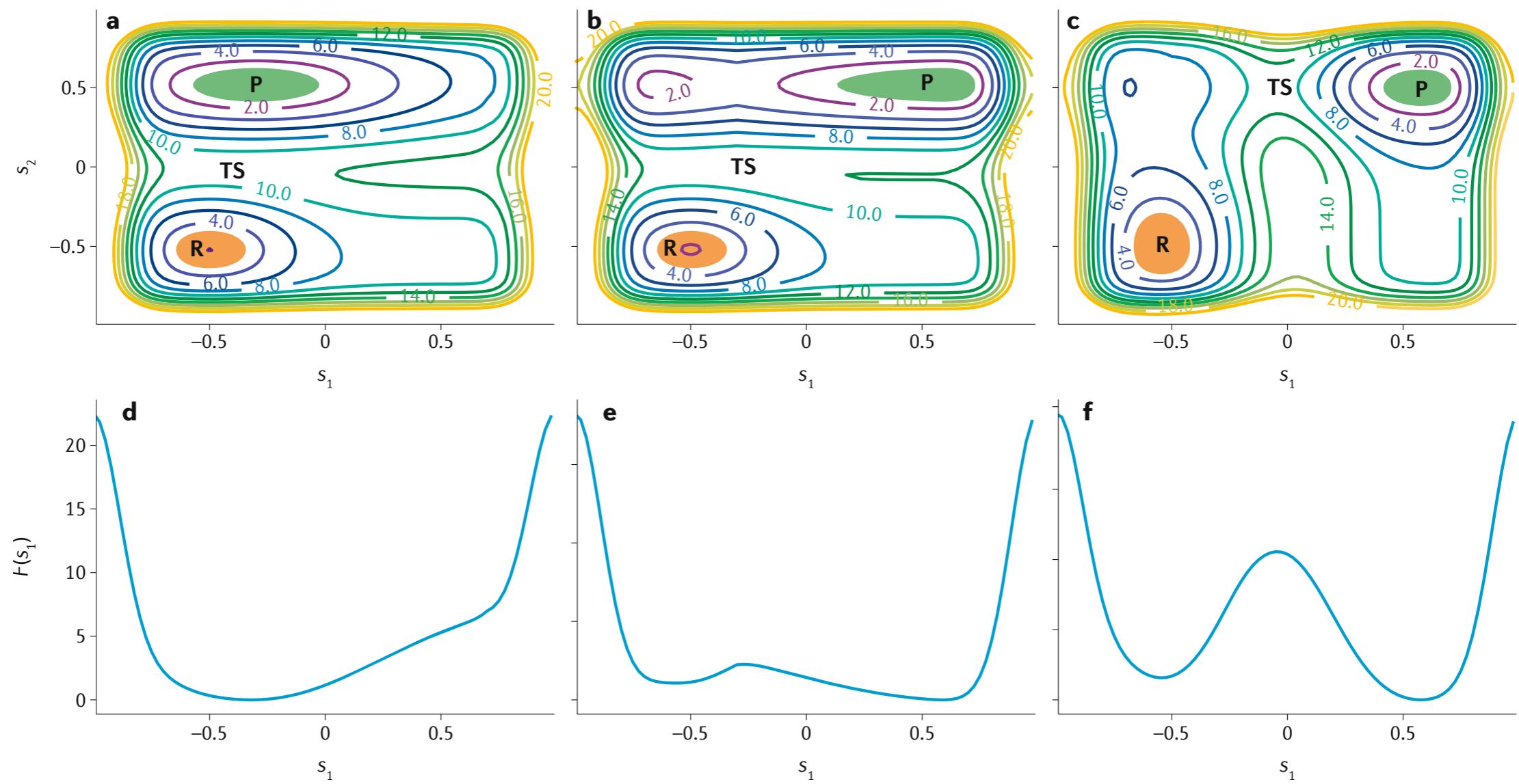


Simulations should overlap also in not-biased degrees of freedom

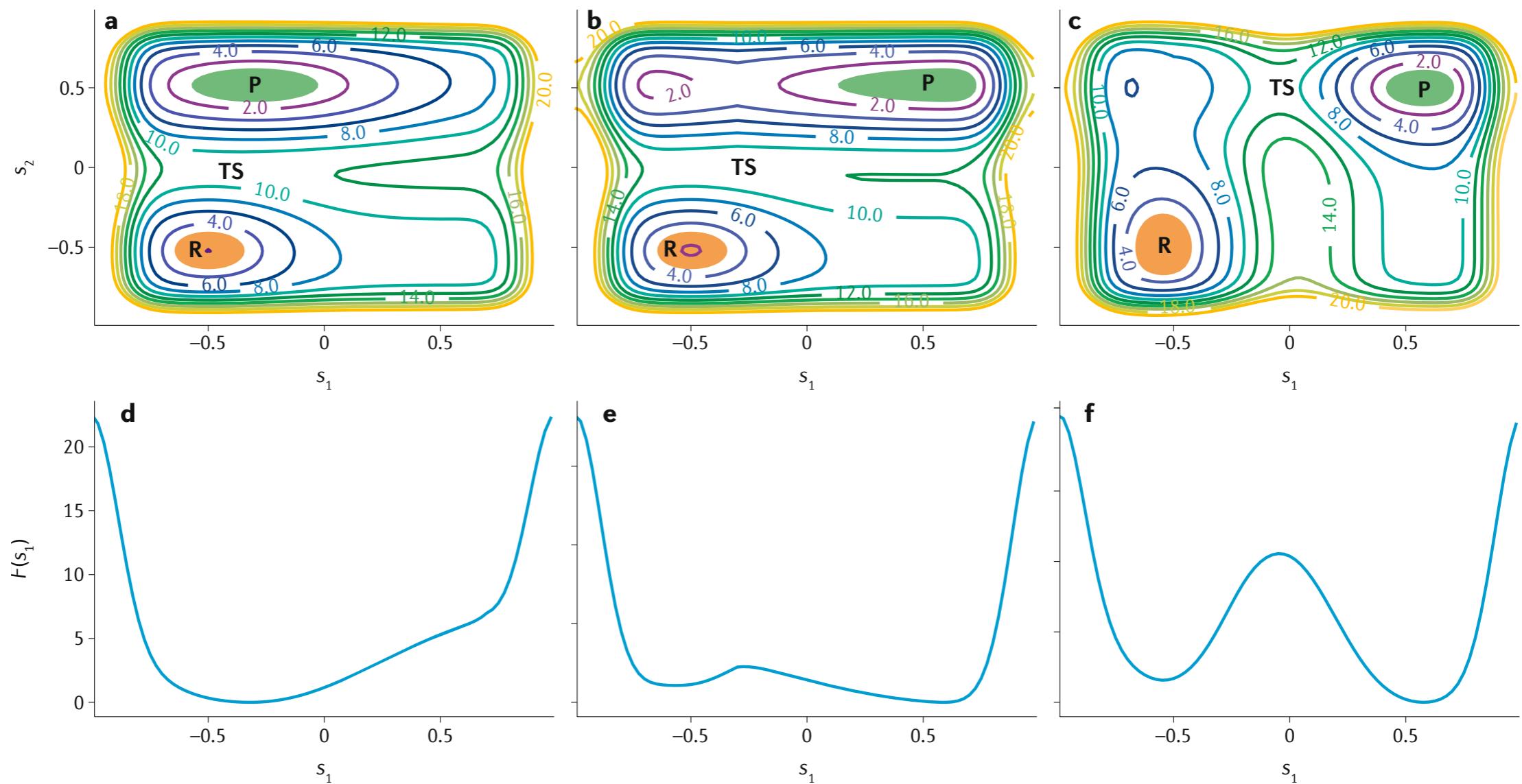
Very difficult to check without doing replica exchange (come to masterclass 4!)

A minimal check: compare results initialising in R vs P

# Reaction coordinates: good ones vs bad ones



# Reaction coordinates: good ones vs bad ones



	$R \approx P$	$R \approx TS \neq P$ or vice versa	$R \neq TS \neq P$
Analysis	😢	😊	😊
Enhanced sampling	😢	😢	😊

# Error calculations



# Error calculations



analysis  
A



# Error calculations



bootstrap samples

0 5 0 5 2 8 8 4 9 0 1

1 1 9 8 1 9 5 9 4 6 1

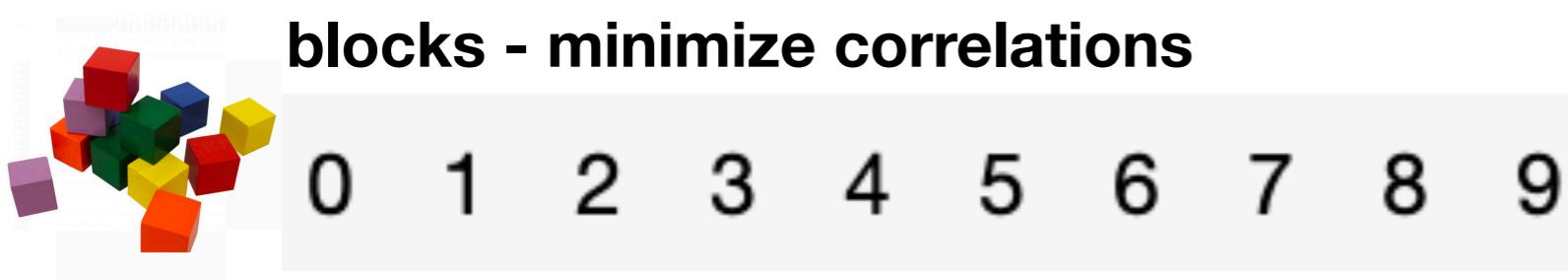
2 7 2 4 2 3 9 4 8 8 4

... ... ... ... ... ... ... ...

198 5 2 3 2 4 5 0 6 8 5

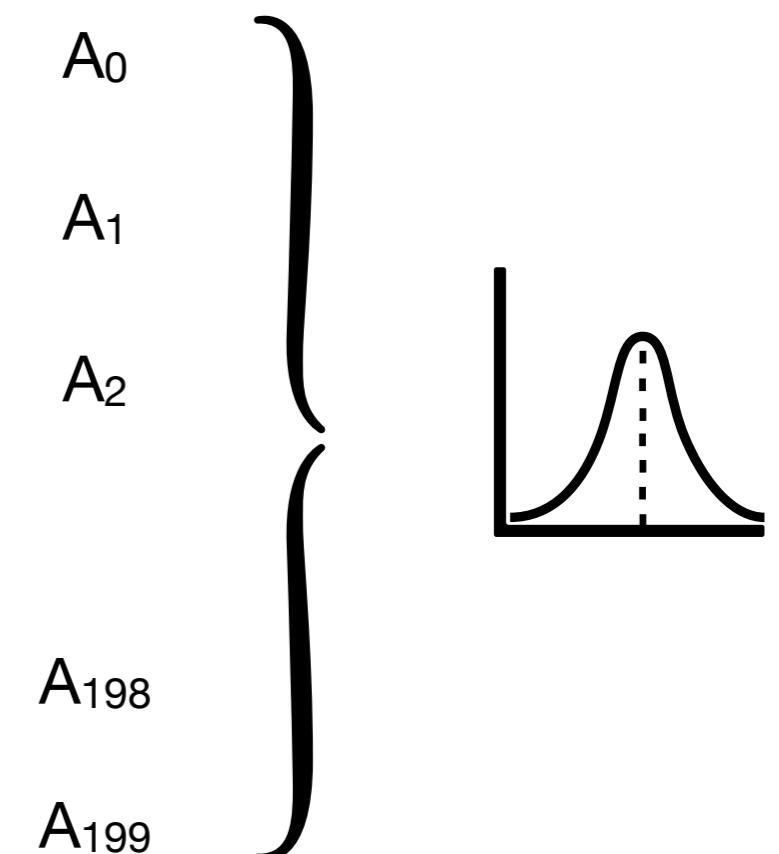
199 6 5 6 6 2 5 3 2 5 2

# Error calculations



bootstrap samples

0	5	0	5	2	8	8	4	9	0	1	$A_0$
1	1	9	8	1	9	5	9	4	6	1	$A_1$
2	7	2	4	2	3	9	4	8	8	4	$A_2$
...	...	...	...	...	...	...	...	...	...	...	
198	5	2	3	2	4	5	0	6	8	5	$A_{198}$
199	6	5	6	6	2	5	3	2	5	2	$A_{199}$



# Useful references on WHAM

Ferrenberg and Swendsen, PRL (1989)

Initial formulation

Kumar et al JCC (1992)

First example in biomolecular simulations

Souaille and Roux CPC (2001)

Weights for individual frames

Shirts and Chodera JCP (2008)

MBAR, can be shown to be equivalent to binless WHAM

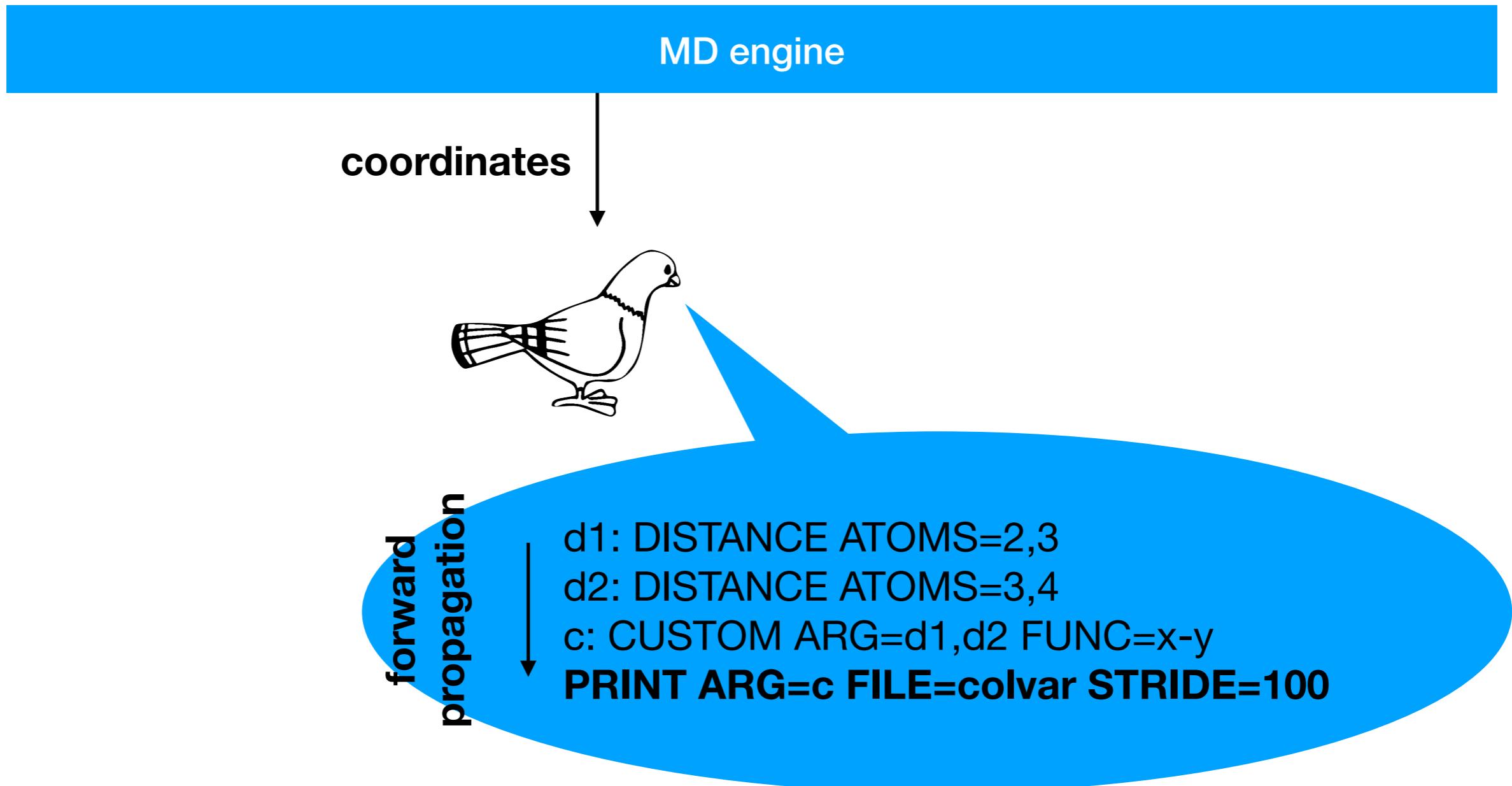
Hub et al, JCTC (2010)

Estimating error using bootstrap

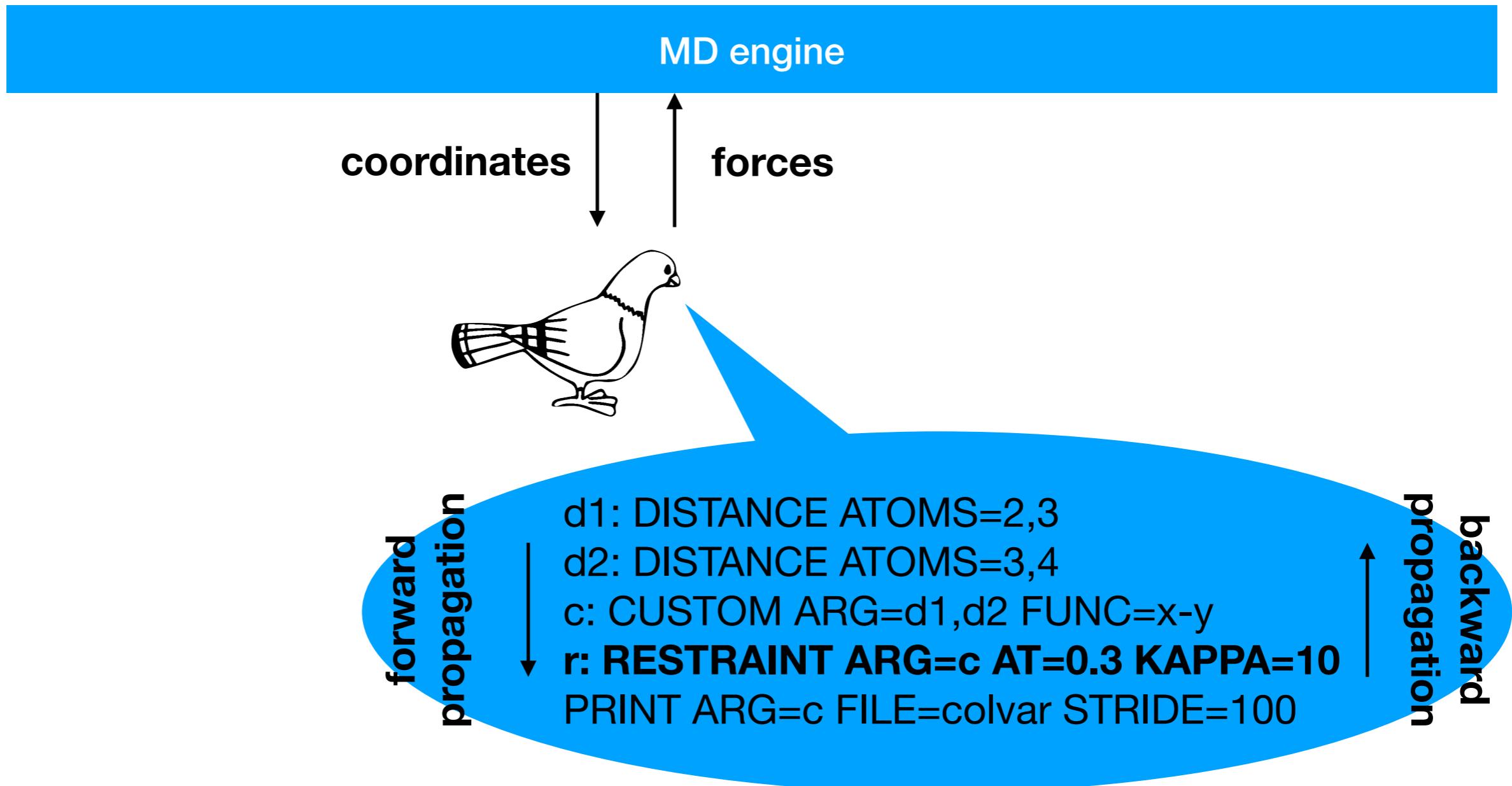
Tan, Gallicchio, Lapeosa, and Levy JCP (2012)

Show that WHAM can be used in a binless fashion

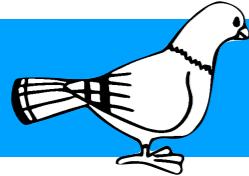
# Using PLUMED for on-the-fly analysis



# Using PLUMED to bias a simulation

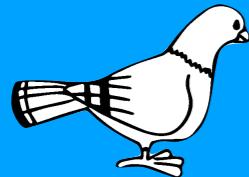


# Using PLUMED for WHAM analysis



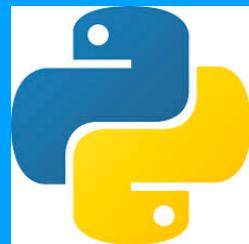
PLUMED driver on concatenated trajectory

+



**REWEIGHT\_WHAM action**  
(integrated with PLUMED)

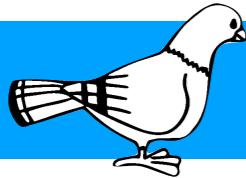
Or



An external python tool, wham.py  
(allow more flexibility for bootstrapping)

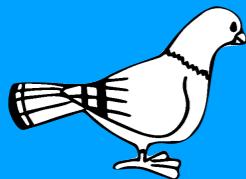
Note: both approaches are bin-less, and allow arbitrary bias potentials to be used in all replicas (i.e., not just a series of restraints on the same variable)

# Using PLUMED for WHAM analysis



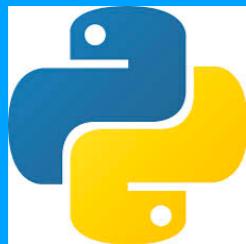
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# Instructions



**PLUMED**  
The community-developed PLUGin for MolEcular Dynamics

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1. Go to [www.plumed.org](http://www.plumed.org)
2. Click on the **Masterclass** tab
3. Click on the **Topic** of class 21.3
4. 1 week to complete the exercises
5. Questions/discussions on Slack channel [masterclass-21-3](#)
6. Lecture I and II available on [YouTube](#)