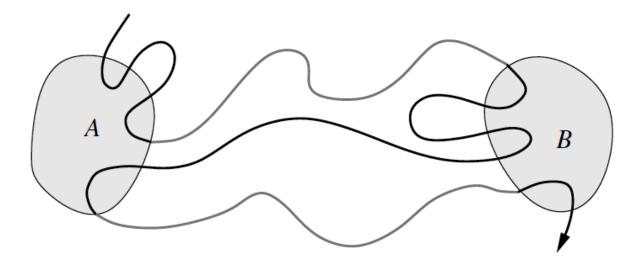
Computing transition-path statistics from short-trajectory data

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> Jonathan Weare New York University

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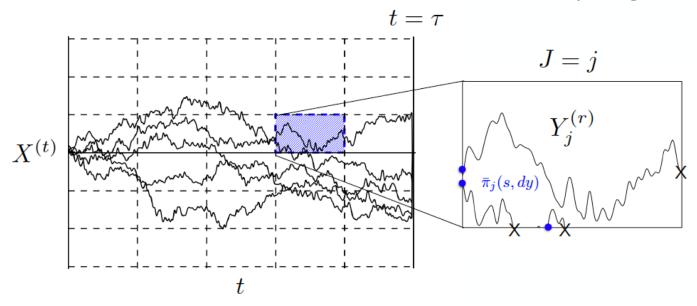
For reactions between two states (A and B), we want to compute committors, mean first passage times, reactive currents, rates, and potentials of mean force.



This is challenging by direct simulation.

picture from Vanden-Eijnden (2006)

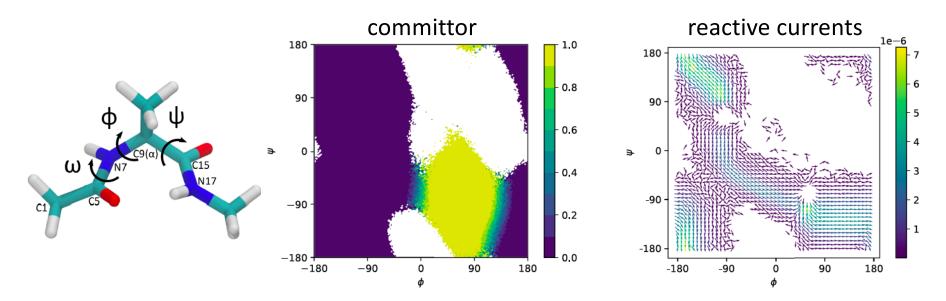
One solution is to use enhanced sampling.



See for example Vani, Weare, and Dinner, J Chem Phys (2022), where we split the ensemble of paths based on their origins and use trajectory stratification (nonequilibrium umbrella sampling) to improve statistics.

This builds on work from our group going back to 2007, and Vanden-Eijnden and Venturoli (2009); see also exact milestoning from Elber.

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See for example Vani, Weare, and Dinner, J Chem Phys (2022), where we split the ensemble of paths based on their origins and use trajectory stratification (nonequilibrium umbrella sampling) to improve statistics.

This builds on work from our group going back to 2007, and Vanden-Eijnden and Venturoli (2009); see also exact milestoning from Elber.

In this talk, we will instead make a Markov assumption and solve operator equations of the form

$$(\mathcal{S}^{ au} - \mathcal{I})u(x) = -\mathbb{E}_{x}\left[\int_{0}^{ au \wedge T} h(X_{s})ds\right] ext{ for } x \in D = (A \cup B)^{c}$$
 $u(x) = g(x) ext{ for } x \notin D$

where S^{τ} is the "stopped" transition operator:

$$\mathcal{S}^{\tau}f(x) = \mathbb{E}_{x}\left[f(X_{\tau \wedge T})\right] = \mathbb{E}\left[f(X_{\tau \wedge T})|X_{0} = x\right]$$

for $T = \inf\{t > 0 : X_t \in A \cup B\}$.

For example, the committor:

$$q_+(x) = \mathbb{P}_x[X_T \in B] = \mathbb{E}_x[\mathbb{1}_B(X_T)]$$

satisfies

$$\mathcal{S}^ au q_+(x) = q_+(x) ext{ for } x \in D$$

 $q_+(x) = \mathbbm{1}_B ext{ for } x
otin D$

The lead time (mean first passage time conditioned on entering *B* before *A*):

$$m_{AB}(x) = \frac{\mathbb{E}_{x}[\mathcal{T}\mathbb{1}_{B}(X_{T})]}{\mathbb{E}_{x}[\mathbb{1}_{B}(X_{T})]}$$
(1)

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satisfies

$$S^{\tau}[m_{AB}q](x) = -\mathbb{E}_{x}\left[\int_{0}^{\tau \wedge T} q(X_{s})ds\right]$$
(2)

 $m_{AB} = 0$ for $x \in A \cup B$.

For the special case of Langevin dynamics

$$\dot{X}(t) = b(X(t)) + \sqrt{2}\sigma(X(t))\eta(t),$$

the Itô formula of stochastic calculus leads to an explicit form for the infinitesimal generator of the transition operator:

$$\mathcal{L}f(x) = \sum_{i=1}^{n} b_i(x) \frac{\partial f}{\partial x_i} + \sum_{i,j=1}^{n} a_{ij}(x) \frac{\partial^2 f}{\partial x_i \partial x_j}.$$

However, in general, we do not know the form of S^{τ} and \mathcal{L} .

This talk is about how we can still solve equations of S^{τ} using partial observations sampled at finite times.

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Outline

- A Galerkin approach
 - Applications to protein dynamics
- A neural-network approach
 - Numerical experiments illustrating key features
 - Application to a model of sudden stratospheric warming

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Addressing the two-trajectory requirement

We want to solve equations of the form

$$(\mathcal{S}^{ au} - \mathcal{I})u(x) = -\mathbb{E}_x \left[\int_0^{ au \wedge T} h(X_s) ds
ight] ext{ for } x \in D = (A \cup B)^c$$
 $u(x) = g(x) ext{ for } x \notin D.$

Expand u(x) in terms of basis functions $\phi_i(x)$:

$$u(\mathbf{x}) \approx \psi(\mathbf{x}) + \sum_{j=1}^{n} v_j \phi_j(\mathbf{x}),$$

where $\psi(x)$ is a guess that homogenizes the boundary conditions.

By standard means, we can convert the operator equation into a linear algebra problem:

$$(C^{\tau}-C^0)v=r^{\tau},$$

where

$$egin{aligned} & C^{m{s}}_{ij} = \langle \phi_i, \mathcal{S}^{m{s}} \phi_j
angle_\mu & ext{for} \quad m{s} = m{0}, au \ & \mathbf{r}^{ au}_i = \langle \phi_i, \psi(m{x}) - \mathcal{S}^{ au} \psi(m{x})
angle_\mu, \end{aligned}$$

and the inner product is over an *arbitrary* initial density $\mu(x)$:

$$\langle \alpha(\mathbf{x}), \beta(\mathbf{x}) \rangle = \int \alpha(\mathbf{x}) \beta(\mathbf{x}) \mu(\mathbf{x}) d\mathbf{x}.$$

In practice, cover the space with initial points and run (short) simulations.

The fact that μ is arbitrary enables us to choose the initial points so as to maximize the sampling efficiency.

Compute

$$\overline{\langle \phi_i, \mathcal{S}^{\tau} \phi_j \rangle} = \frac{1}{N} \sum_{n=1}^N \phi_i(X_0^{(n)}) \phi_j(X_{\tau \wedge T}^{(n)})$$

and similarly for the inner products involving ψ .

Solve $(C^{\tau} - C^0)v = r^{\tau}$ by standard linear algebra methods, and use *v* to construct *u*.

Benchmark system: Trp-cage folding

Fast-folding miniprotein extensively studied both experimentally and computationally (Zhou, Berne, Roitberg, Hagen, Bohuis, Garcia, Laio, Piana, Shaw, Dror, Mukamel, Wang, Dickson, Brooks, Zuckerman, Levy, Kevrekidis, Debenedetti, Ferguson, others).

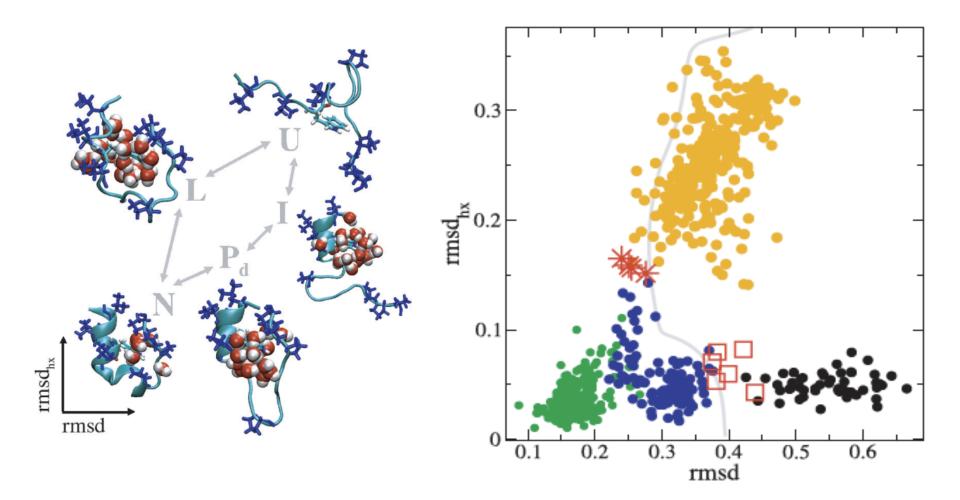
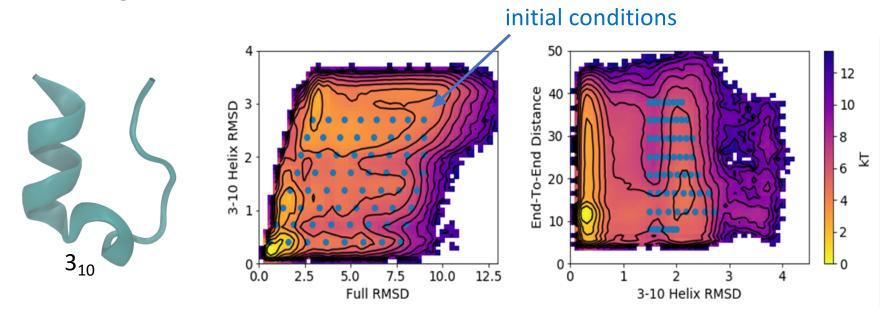


Figure from Juraszek and Bolhuis, PNAS 103, 15859-15864 (2006).

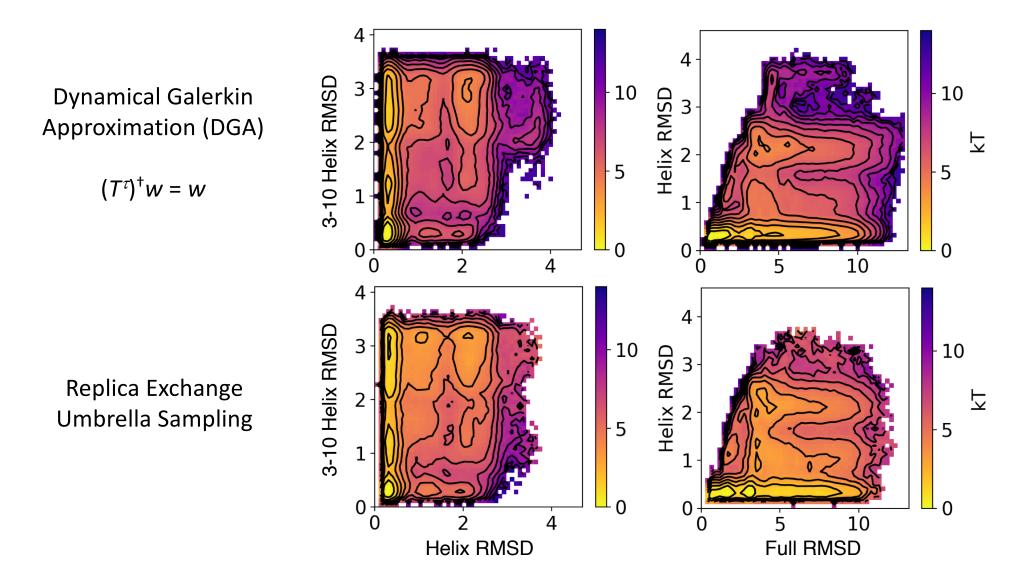
Generating the data set



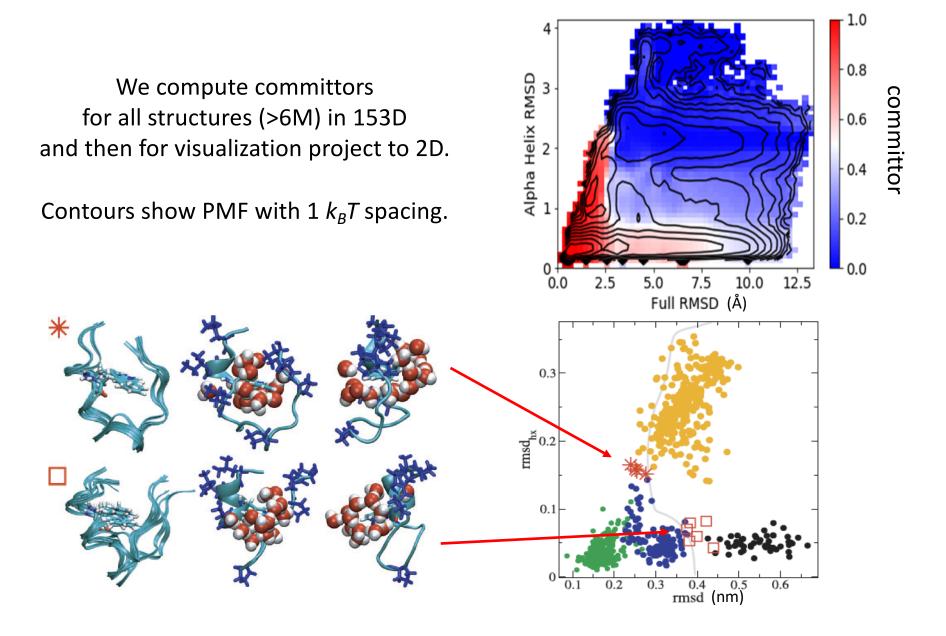
- Represent system with CHARMM36m force field;
- Distribute initial points in RMSD and 3-10 helix RMSD space;
- Launch 14 independent 30 ns trajectories from each of the points.
- Based on comparison with umbrella sampling, add 2 more 30 ns trajectories from points in α helix RMSD and end-to-end distance space;
- 1024 trajectories for a total of $30 \ \mu s$

Strahan, Antoszewski, Lorpaiboon, Vani, Weare, Dinner (2021) JCTC 17, 2948-2963

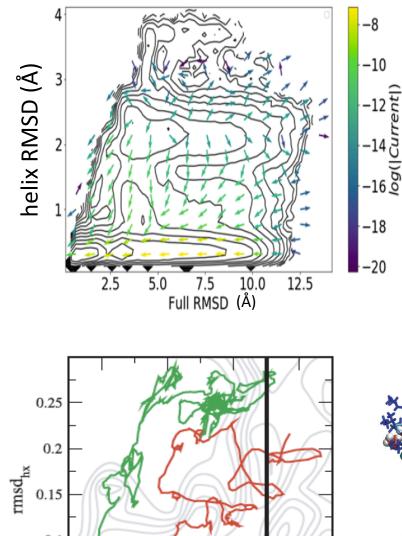
Our Galerkin method gives good agreement with independent simulations.



Comparison of committors to transition states identified by Juraszek and Bolhuis, PNAS 103, 15859-15864 (2006)



Reactive currents for trp-cage folding

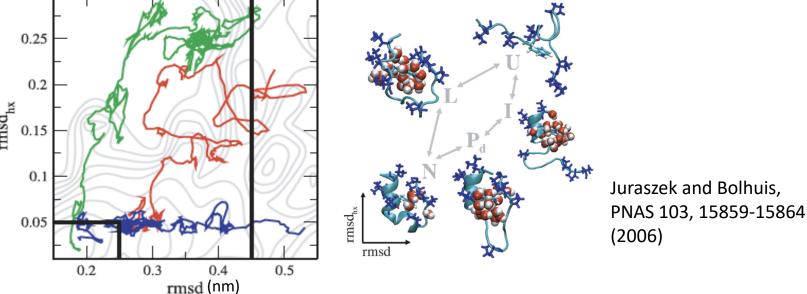


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(color scale shows magnitude of the current, contours show PMF with $1 k_B T$ spacing)

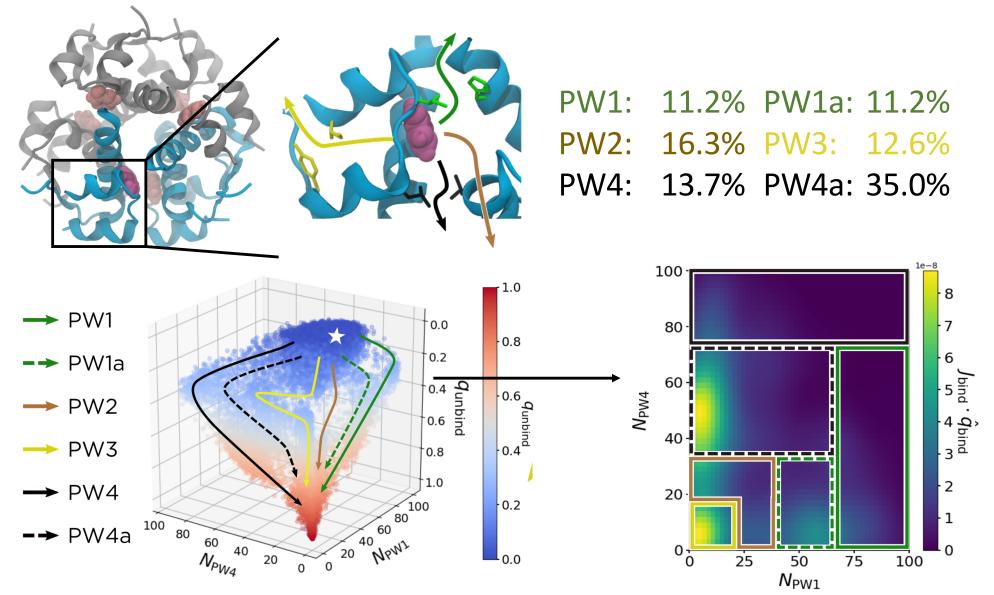
$$R_{AB} = \{\mathbf{1}_{C}(x)\mathcal{L}[\mathbf{1}_{C^{c}}q_{+}](x) - \mathbf{1}_{C^{c}}(x)\mathcal{L}[\mathbf{1}_{C}q_{+}](x)\} q_{-}(x)\pi(x)dx$$
$$= \int_{\partial C} J_{AB}(x) \cdot n_{C}(x)d\sigma_{C} = \int_{\partial C^{\theta}} J_{AB}^{\theta}(s) \cdot n_{C^{\theta}}d\sigma_{C^{\theta}}$$

The first calculation of this key TPT quantity for a molecular simulation clearly shows the two pathways and allows quantification of their contributions.



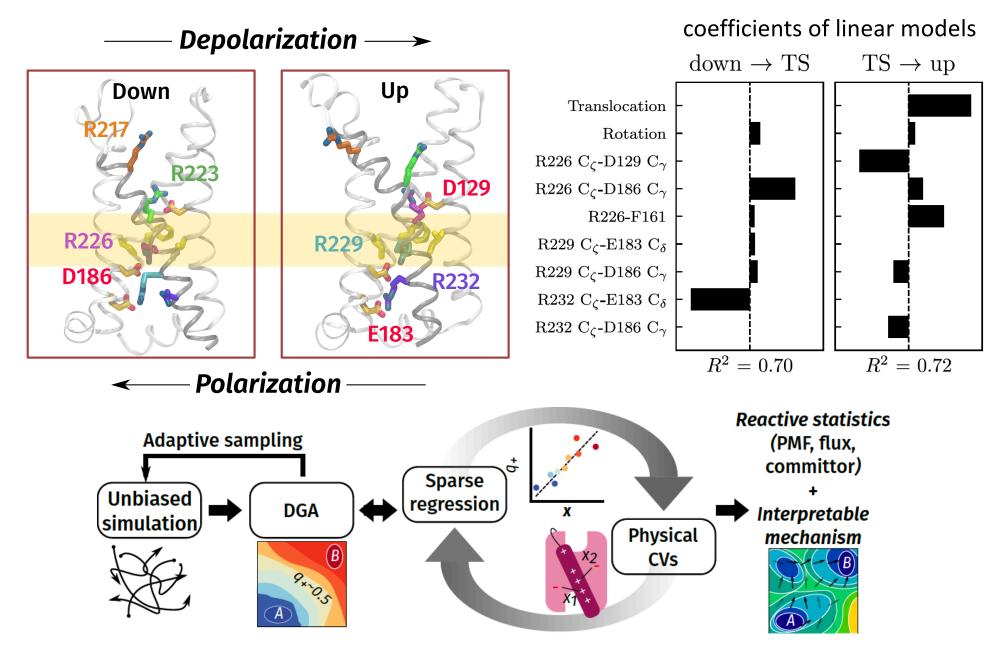
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DGA enables us to compute the relative fluxes through six pathways of phenol release from the insulin hexamer.



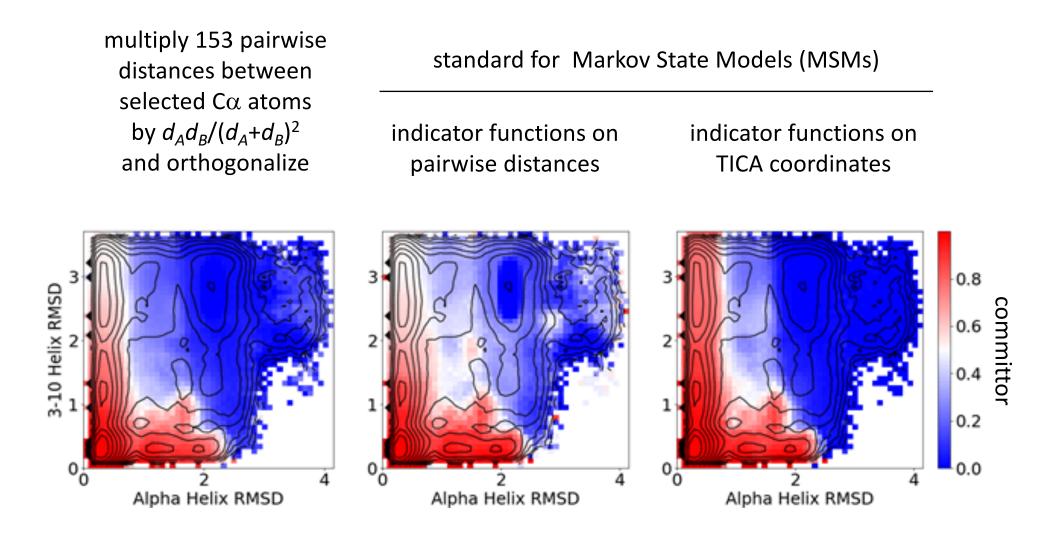
Antoszewski, Lorpaiboon, Strahan, Dinner, J Phys Chem B 125, 11637–11649 (2021) See also Lorpaiboon, Weare, Dinner, J Chem Phys 157, 094115 (2022) for an augmented TPT.

DGA reveals a stepwise mechanism for voltage sensing.



Guo, Shen, Roux, Dinner, biorxiv.org (2022)

The choice of basis matters.



trp-cage committors computed for all structures (>6M) and then projected to 2D (color scale shows committors, contours show PMF with 1 k_BT spacing)

Outline

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Addressing the two-trajectory requirement

Motivated by the equations we want to solve

$$(\mathcal{S}^{\tau} - \mathcal{I})u(x) = -\mathbb{E}_{x}\left[\int_{0}^{\tau \wedge T} h(X_{s})ds\right] \text{ for } x \in D = (A \cup B)^{c}$$

u(x) = g(x) for $x \notin D$

we consider the loss functions

$$egin{aligned} \mathcal{C}_{ ext{FKE}} &= \left\| \left((\mathcal{S}^ au - \mathcal{I}) u_ heta + \mathbb{E}_x \left[\int_0^{ au \wedge T} h(X_s) ds
ight]
ight) \mathbbm{1}_D
ight\|_\mu^2 \ \mathcal{C}_{ ext{BC}} &= \left\| (u_ heta - g) \mathbbm{1}_{D^c}
ight\|_\mu^2. \end{aligned}$$

and seek

$$\theta^* = \arg\min_{\theta} [C_{\text{FKE}} + \lambda C_{\text{BC}}].$$

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Because there are terms that are quadratic in $S^{\tau}u_{\theta}$, we need two trajectories from each initial point for unbiased estimates:

$$\begin{split} \bar{C}_{\text{FKE}} &= \frac{1}{n} \sum_{i=1}^{n} \left(u_{\theta}(X_{k^{i,1}\Delta}^{i,1}) - u_{\theta}(X_{0}^{i}) - \Delta \sum_{s=0}^{k^{i,1}} h(X_{s\Delta}^{i,1}) \right) \\ & \times \left(u_{\theta}(X_{k^{i,2}\Delta}^{i,2}) - u_{\theta}(X_{0}^{i}) - \Delta \sum_{s=0}^{k^{i,2}} h(X_{s\Delta}^{i,2}) \right) \mathbb{1}_{D}(X_{0}^{i}) \\ \bar{C}_{\text{BC}} &= \frac{1}{n} \sum_{i=1}^{n} \left(u_{\theta}(X_{0}^{i}) - g(X_{0}^{i}) \right)^{2} \mathbb{1}_{D^{c}}(X_{0}^{i}). \end{split}$$

We represent u_{θ} by a neural network and minimize

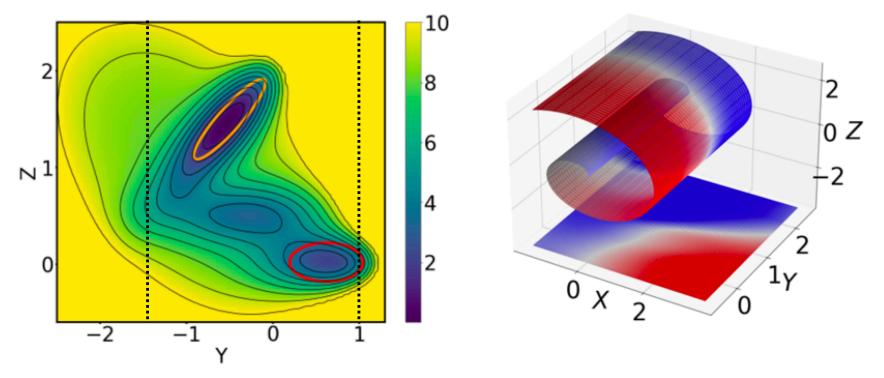
$$\bar{C} = \bar{C}_{FKE} + \lambda \bar{C}_{BC}$$

Our loss has several advantages over previous ones:

- it allows computation of any statistic that can be cast in Feynman-Kac form;
- it does not require explicit knowledge of the model;
- it does not require microscopic reversibility;
- it allows for use of arbitrary lag times;
- it allows use of an arbitrary sampling distribution.

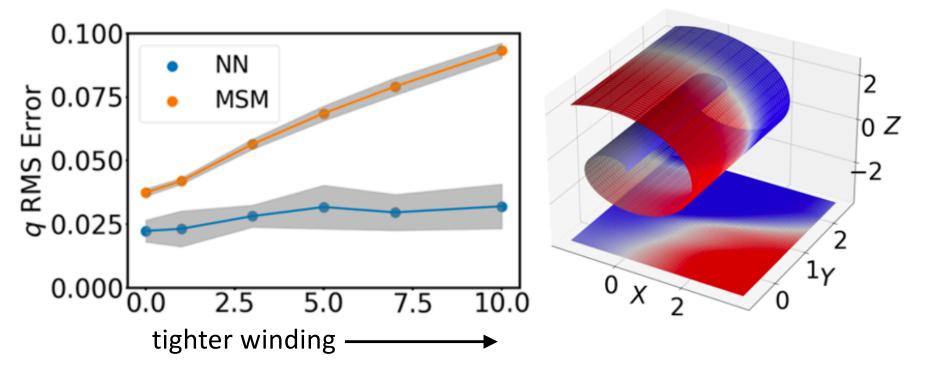
Strahan, Finkel, Dinner, Weare, arxiv:2208.01717 (2022)

To illustrate these advantages, we consider dynamics on the Müller-Brown potential mapped to the Swiss roll.



- Overdamped Langevin dynamics initiated from 30,000 points drawn uniformly from between the dashed lines.
- Map the trajectories onto the Swiss Roll so the algorithm must learn the manifold of the dynamics.
- Compare a 3-input, 3 30-sigmoid hidden layers, 1-sigmoid output neural network with a 300 state MSM and a grid-based reference.

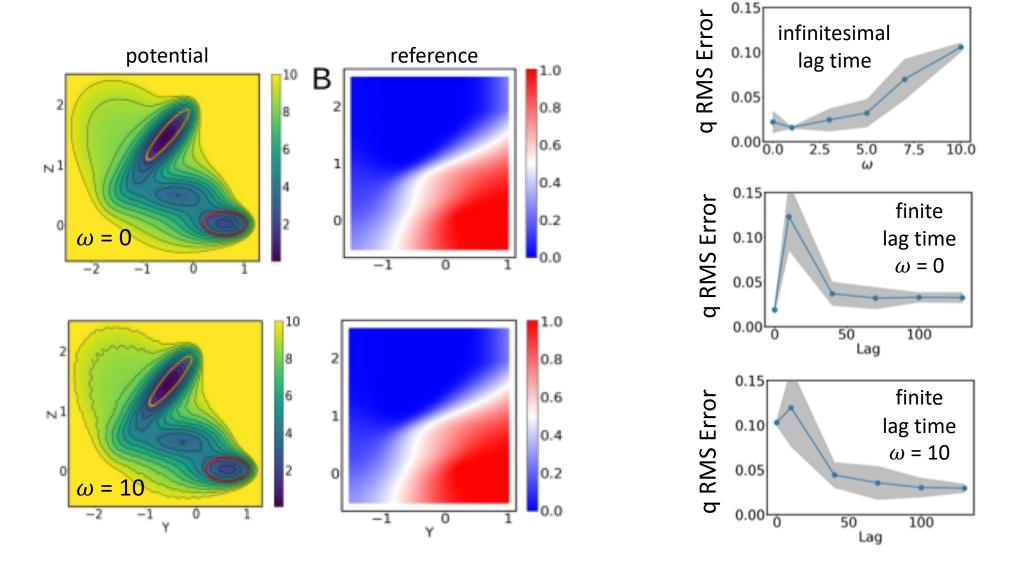
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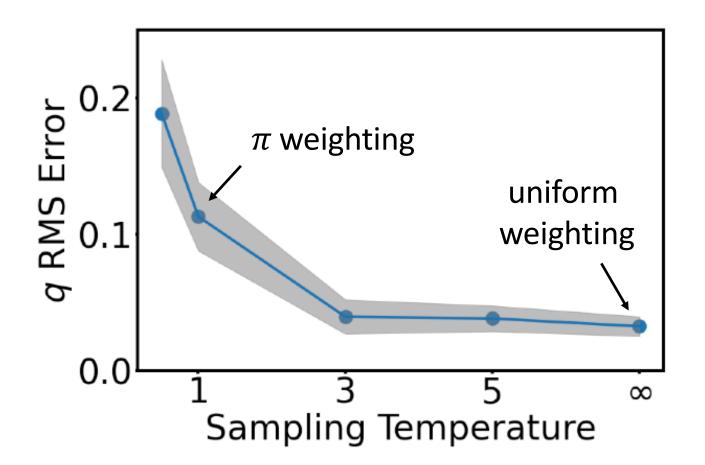
Infinitesimal (or short) vs finite (or long) lag time

Compare with $\|\mathcal{L}q\|_{\mu}^2$, which gives rise to $\|\nabla q\|_{\pi}^2$ and $\|q(\tau) - q(0)\|_{\pi}^2$ for overdamped reversible dynamics



Choice of sampling distribution (arbitrary μ vs. π)

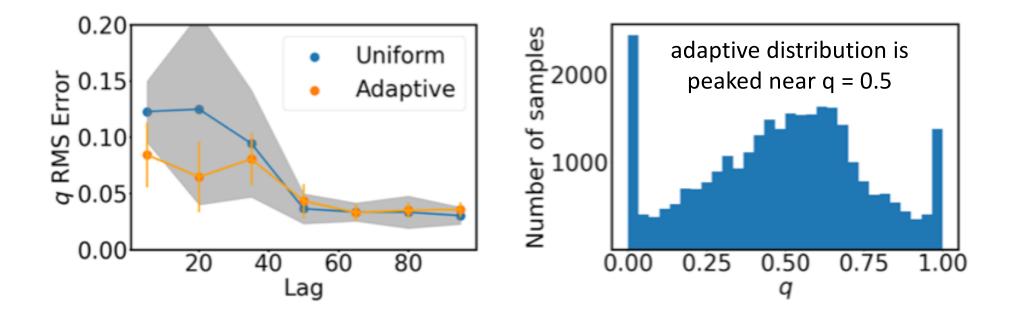
A uniform distribution of initial points is better than the stationary distribution.



Choice of sampling distribution (arbitrary μ vs. π)

Adaptively sample with probability

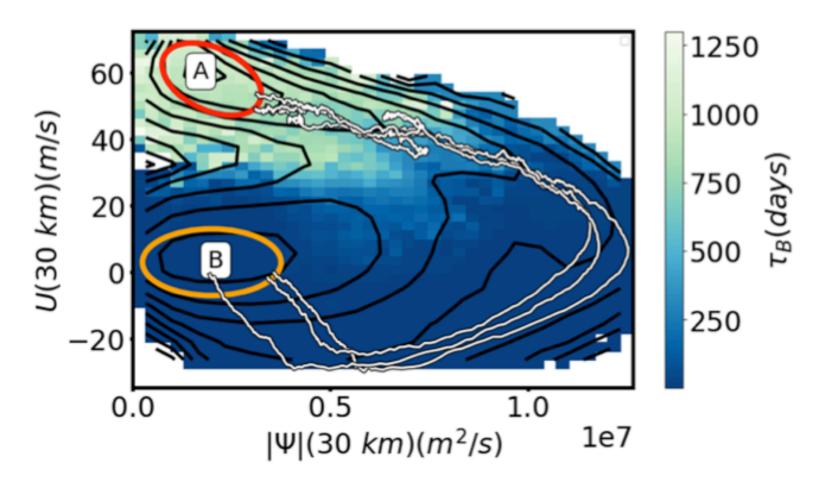
$$P_{\ell} = \frac{\int \left((\mathcal{T}_{D^c}^{\tau} - \mathcal{I}) u_{\theta}(x) - \mathbb{E}_x \left[\int_0^{\tau \wedge T} h(X_s) ds \right] \right)^2 \mathbb{1}_{S_{\ell}} (u_{\theta}(x)) \mu(x) dx}{\int \mathbb{1}_{S_{\ell}} (u_{\theta}(x)) \mu(x) dx}$$



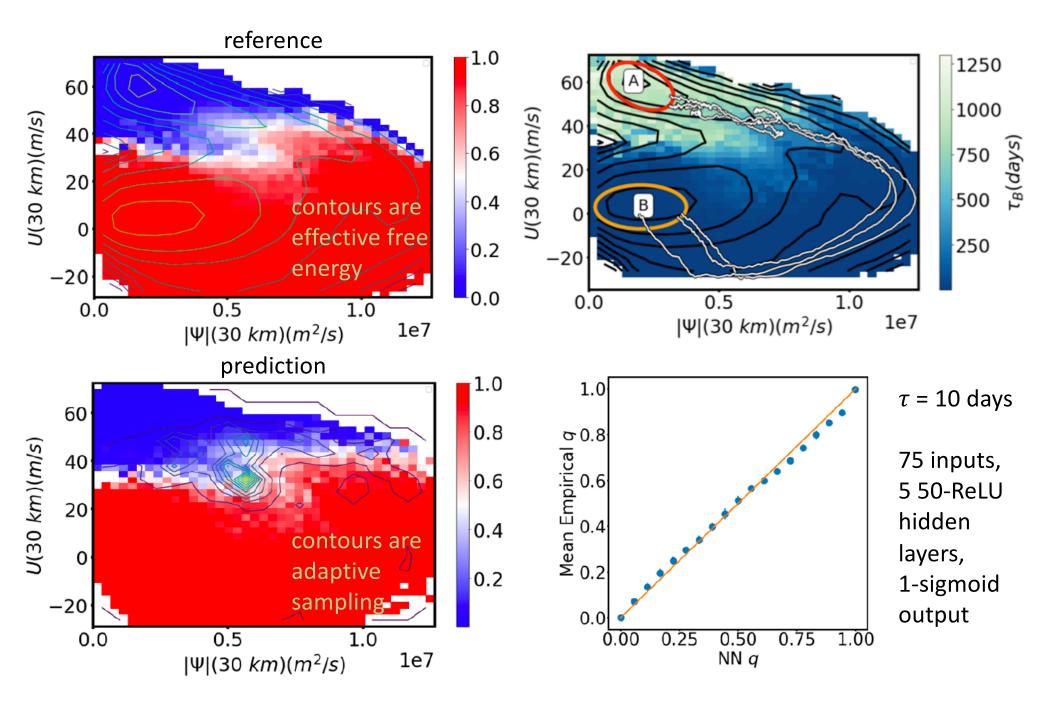
The Holton-Mass model describes stratospheric flow in terms of the interaction of two fields:

- the mean flow \overline{u} ;
- the perturbation streamfunction ψ' .

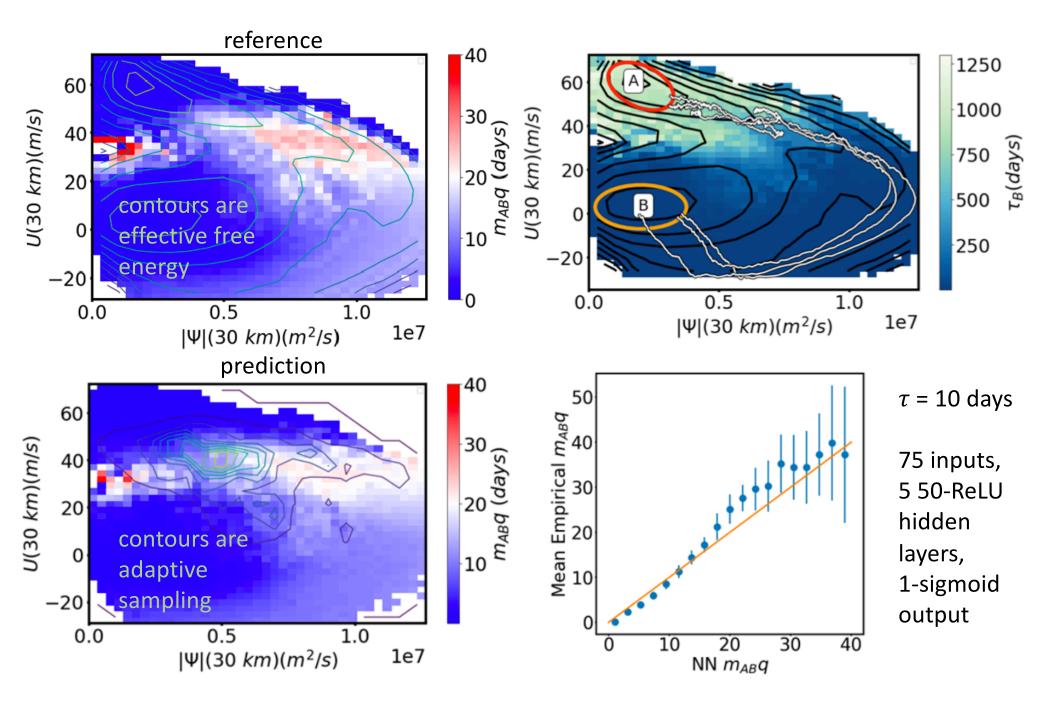
These fields are spatially discretized, resulting in a 75-dimensional state space.



Holton-Mass model committor



Holton-Mass model lead time



Our loss has several advantages over previous ones:

- it allows computation of any statistic that can be cast in Feynman-Kac form;
- it does not require explicit knowledge of the model;
- it does not require microscopic reversibility;
- it allows for use of arbitrary lag times;
- ▶ it allows use of an arbitrary sampling distribution.

But it requires two trajectories from each initial condition.

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Addressing the two-trajectory requirement

The gradient of our norm is

$$\langle (\mathcal{I} - \mathcal{S}^{\tau}) u_{\theta} - r, \nabla_{\theta} u_{\theta} \rangle_{\mu} - \langle (\mathcal{I} - \mathcal{S}^{\tau}) u_{\theta} - r, \mathcal{S}^{\tau} \nabla_{\theta} u_{\theta} \rangle_{\mu},$$
where $r(x) = -\mathbb{E}_{x} \left[\int_{0}^{\tau \wedge T} h(X^{s}) ds \right].$

In TD methods for reinforcement learning, a "semigradient" descent is often used (i.e., the second term is dropped).

Notice that the first term is the exact gradient of the loss

$$\frac{1}{2}\|u_{\theta'}-\mathcal{S}^{\tau}u_{\theta}-r\|_{\mu}^{2}$$

evaluated at $\theta' = \theta$. This suggests the (Richardson) iteration

$$U_{\theta^{s+1}} \approx S^{\tau} U_{\theta^s} + r.$$

Müller-Brown committor (2D)

0.100

U.075 BWS 0.050 W2 0.02!

0.025

0.000

0.1

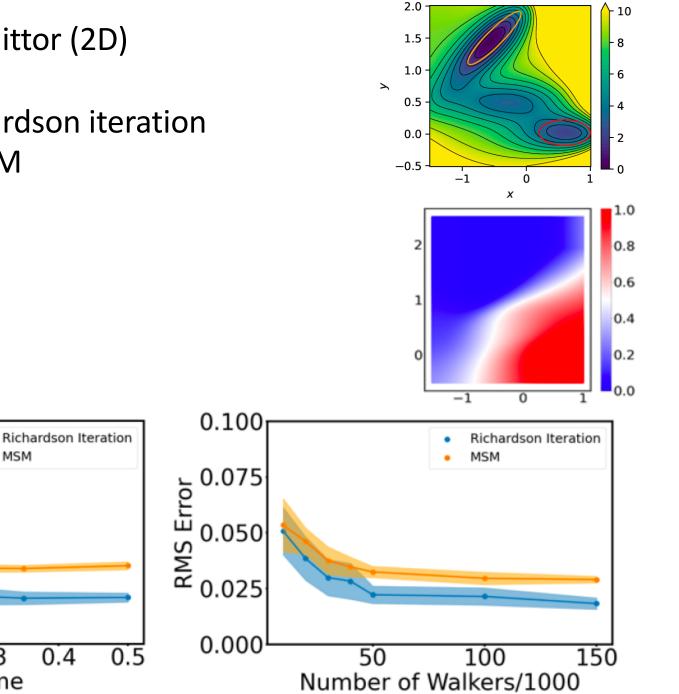
0.2

Comparison of Richardson iteration with a 400-state MSM

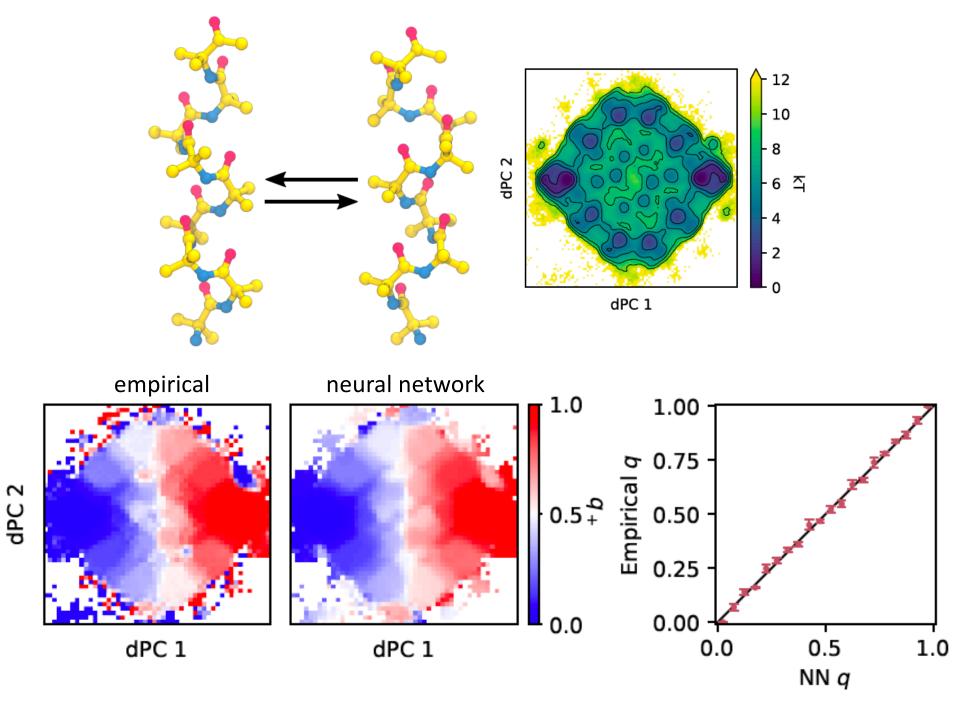
MSM

0.3

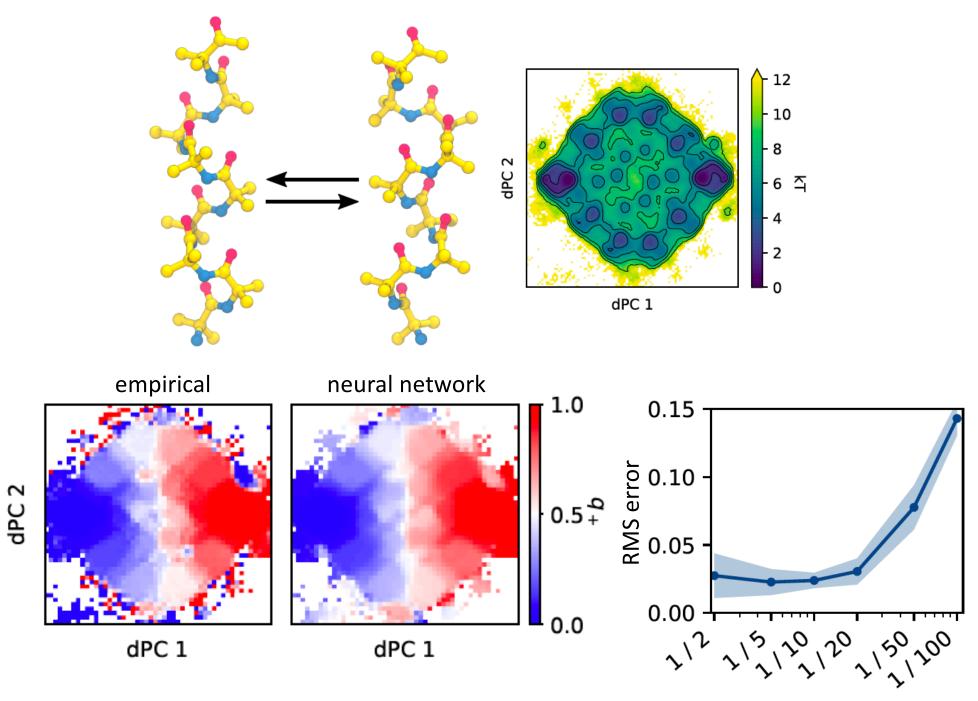
Lag Time



Committor for a peptide of 9 α -aminoisobutyric acids



Committor for a peptide of 9 α -aminoisobutyric acids



Summary

We can obtain rare-event statistics by solving equations of the transition operator.

We have used both Galerkin approximation (basis expansion) and variational approaches based on neural networks to solve these equations.

Our methods can be applied to trajectories sampled at finite lag times, without knowledge of the underlying model or its dynamics (which can be irreversible).

Dynamical Galerkin Approximation

- Thiede, Giannakis, Dinner, Weare, JCP 150, 244111 (2019)
- Strahan, Antoszewski, Lorpaiboon, Vani, Weare, Dinner, JCTC 17, 2948 (2021)

Applications

- Antoszewski, Lorpaiboon, Strahan, Dinner JPC B 125, 11637-11649 (2021)
- Guo, Shen, Roux, Dinner, biorxiv.org (2022)

Neural networks

- Strahan, Finkel, Dinner, Weare, arxiv:2208.01717 (2022)
- Strahan, Guo, Dinner, Weare, in preparation.