Berkeley
UNIVERSITY OF CALIFORNIA

Principled Statistical Approaches For Sampling and Inference in High Dimensions

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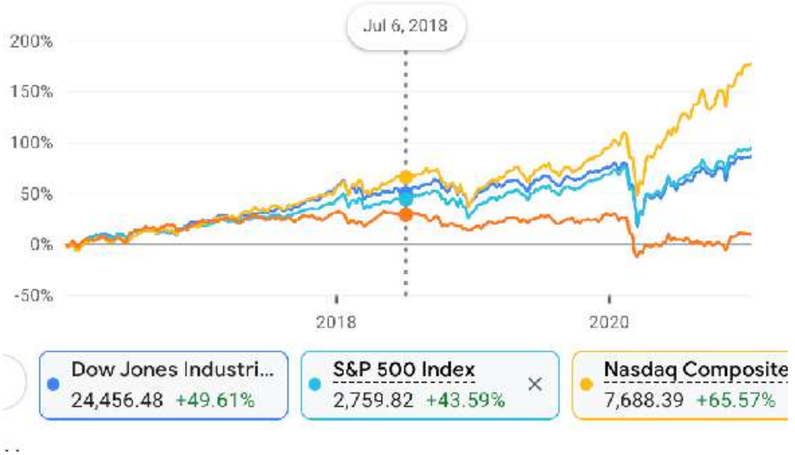
Dissertation Talk
August 11, 2021

Advances of machine learning

The explosion in data abundance and the compute power is fueling the **increase in number of complex ML models and algorithms and the advent of ML in high-stakes domains**

Self-driving car

Financial markets

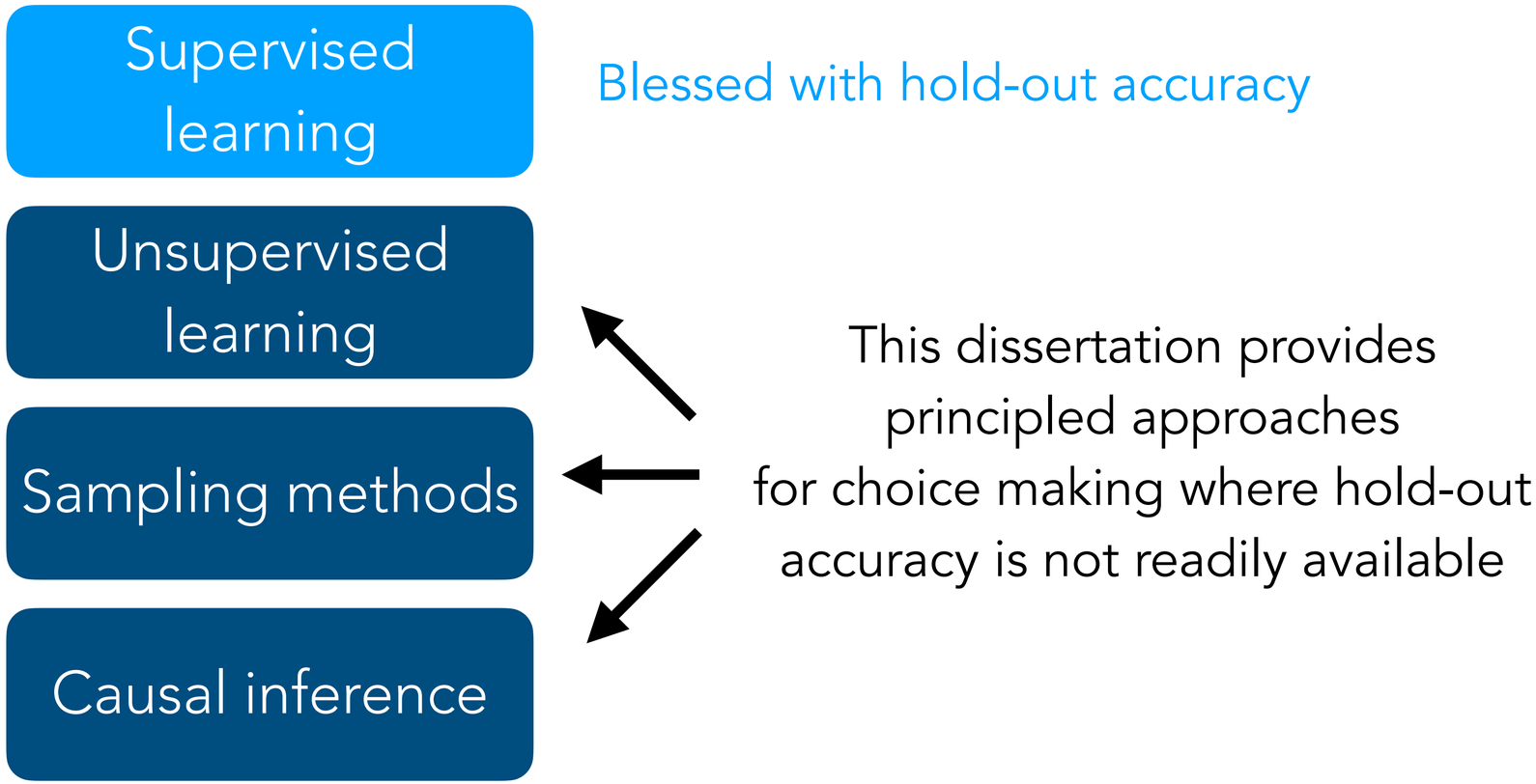


Justice systems

Precision medicine

Which model/algorithm to prefer?

Judgment calls become critical and we need principled approaches to gather empirical and theoretical evidence to inform decision making



Which model/algorithm to prefer?

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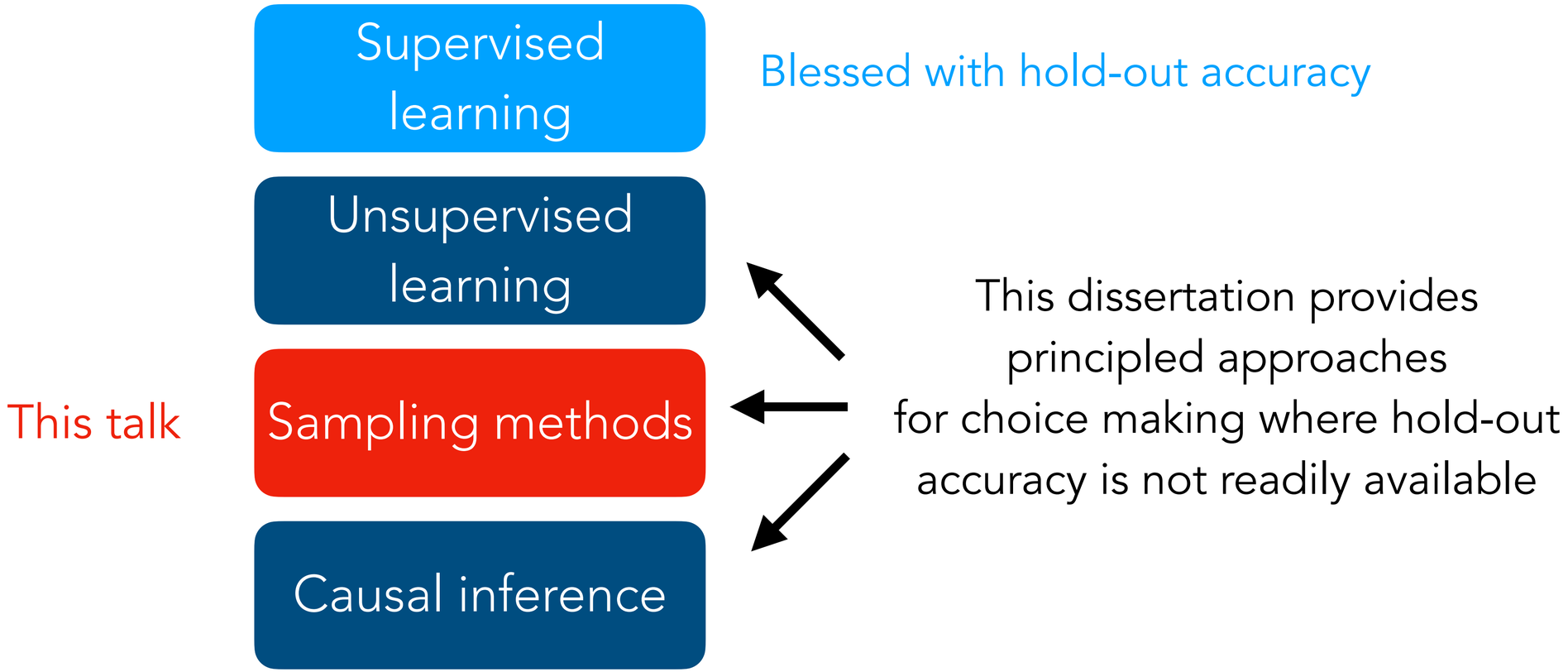
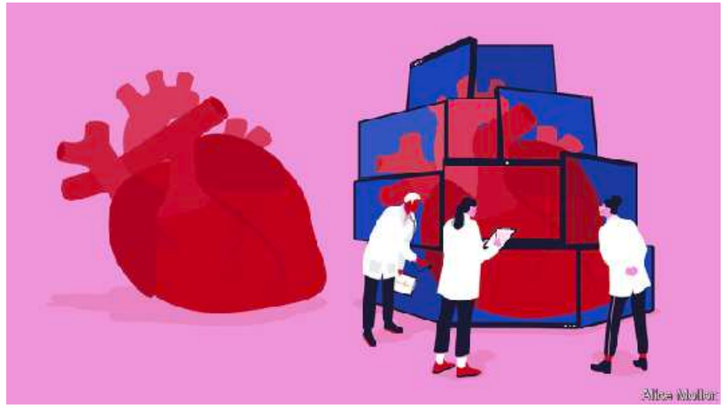
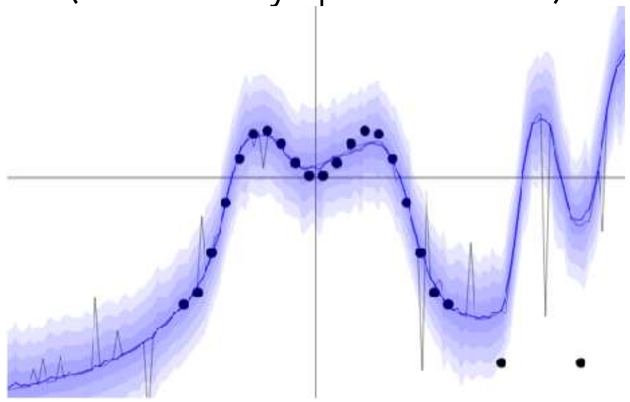


Drawing samples from probability distributions: A fundamental task!

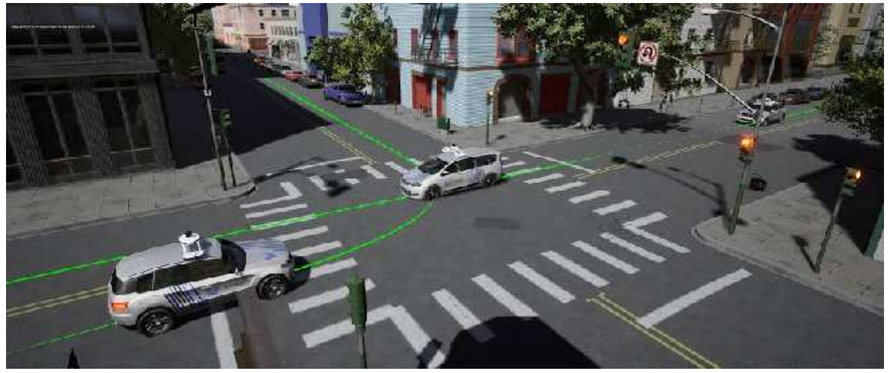
Monte Carlo simulation
(Digital Heart Experiments)



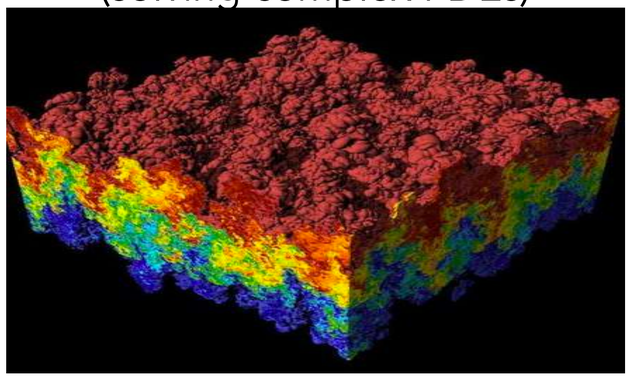
Bayesian inference
(Uncertainty quantification)



Generative modeling
(generating natural scenarios)



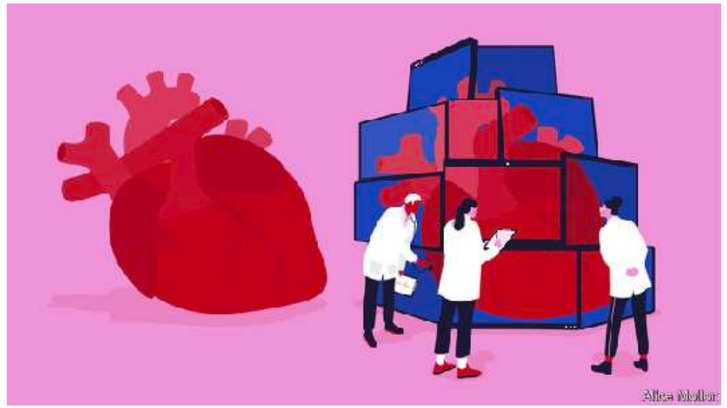
Numerical integration
(solving complex PDEs)



Digital heart experiments in computational cardiology

- Digital *twin* heart experiments try to simulate patient's response to various therapies in a non-invasive way

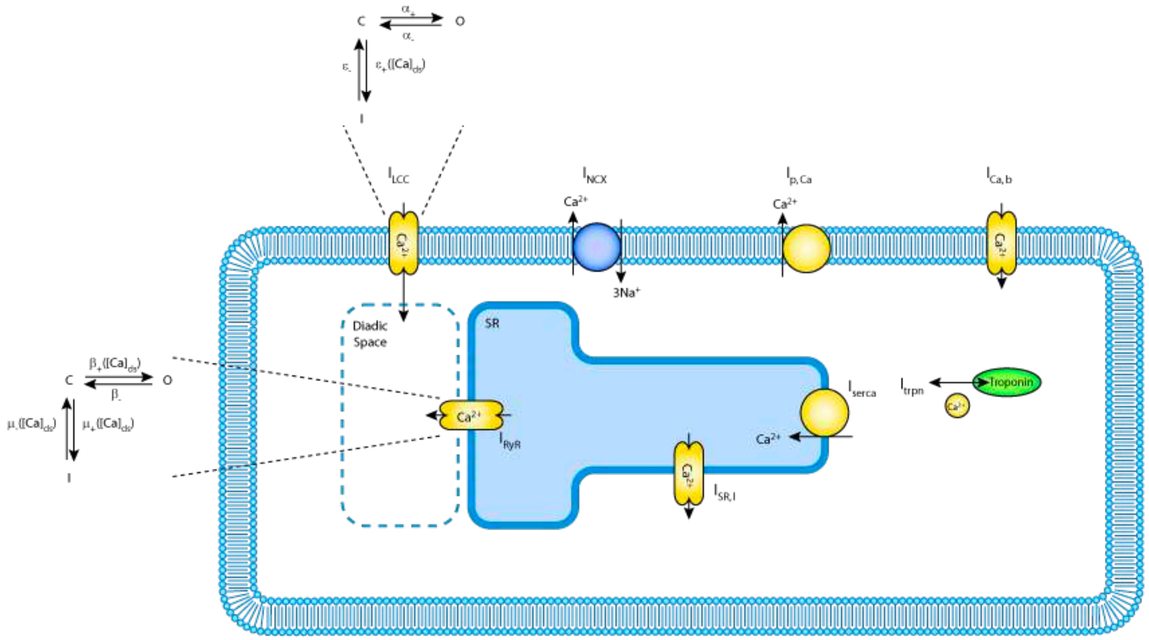
- Single-cell calcium signaling model a building block for the tissue- and heart-level models

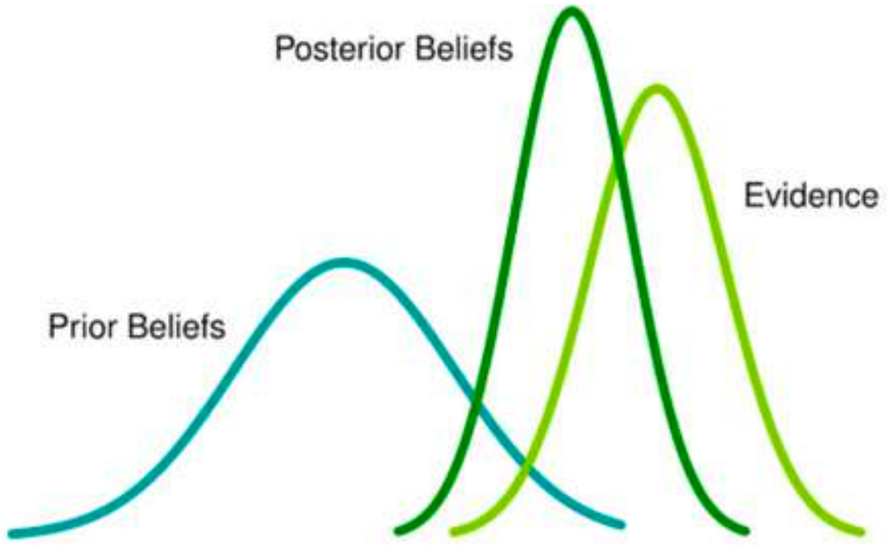


*Picture credits: Google

Single-cell model

- Single-cell calcium signaling modeled via ODEs, and unknown parameters inferred from observed data using a Bayesian set-up

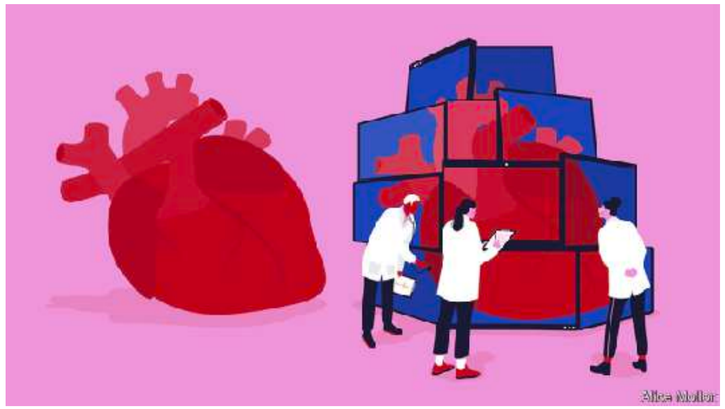


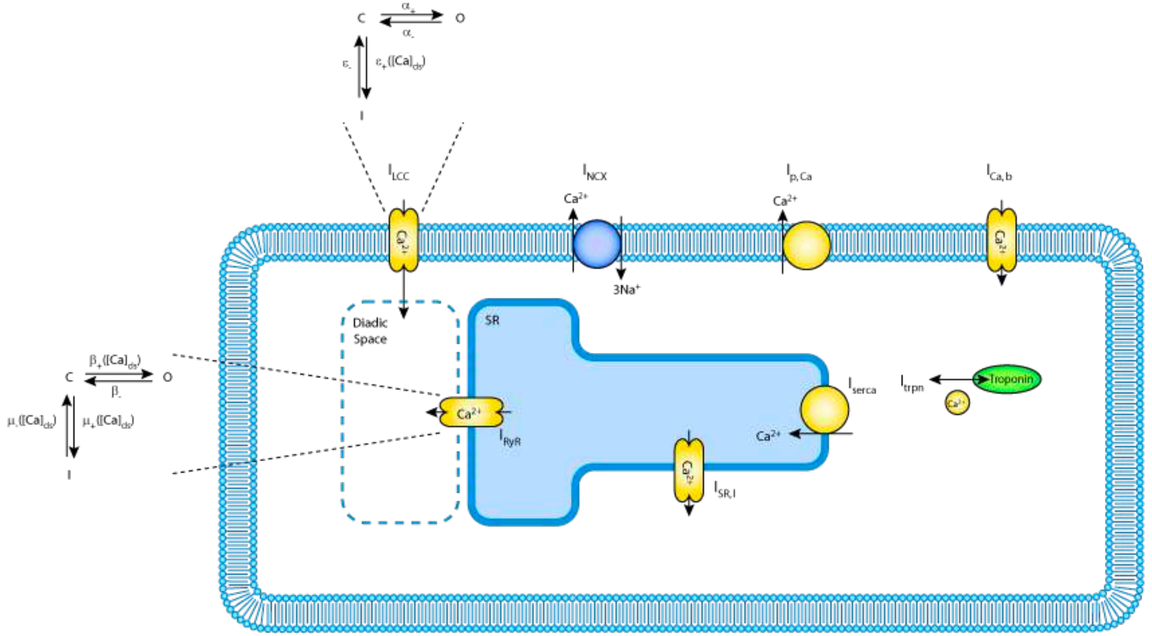


*Picture credits: Google, Hinch et al. 2004

Organ-level modeling

- Single-cell model then passed to various tissue and organ-level simulators that take **1000s of CPU hours** for single computation





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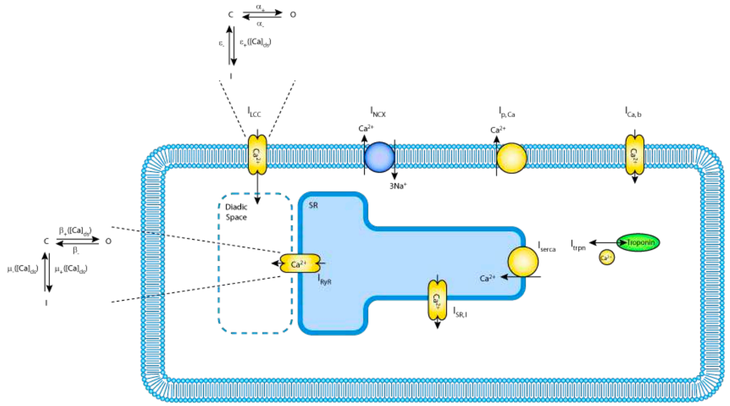
Estimate single-cell model parameters



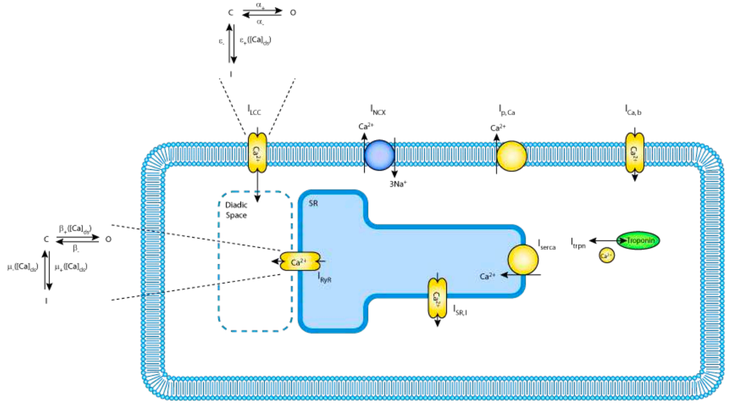
How to draw random samples from the posterior?

$$\theta_1, \theta_2, \ldots, \theta_n \sim p^\star$$

(θ = single cell parameters)

Sampling methods

Estimate single-cell model parameters



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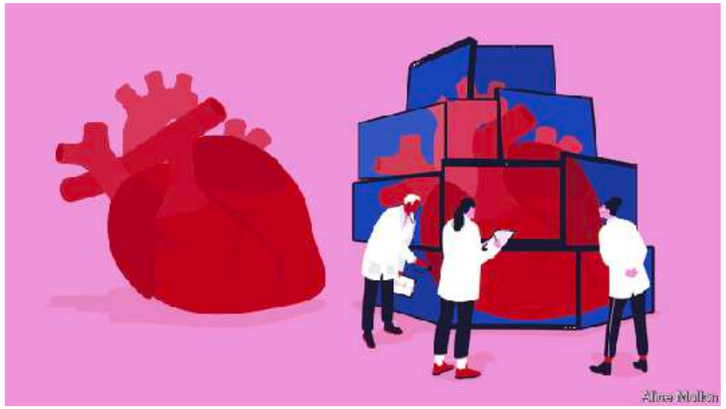
Estimate effect of therapy at organ-level



$$\mathbb{E}[g(\theta)] = \int g(\theta) p^\star(\theta) d\theta \approx \frac{1}{n} \sum_{i=1}^{n} g(\theta_i)$$

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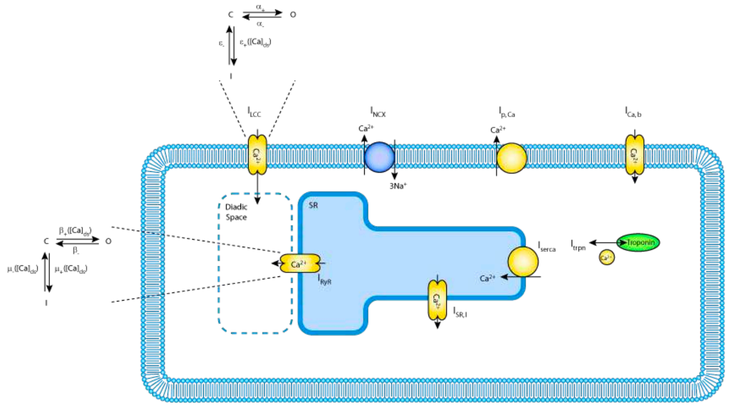

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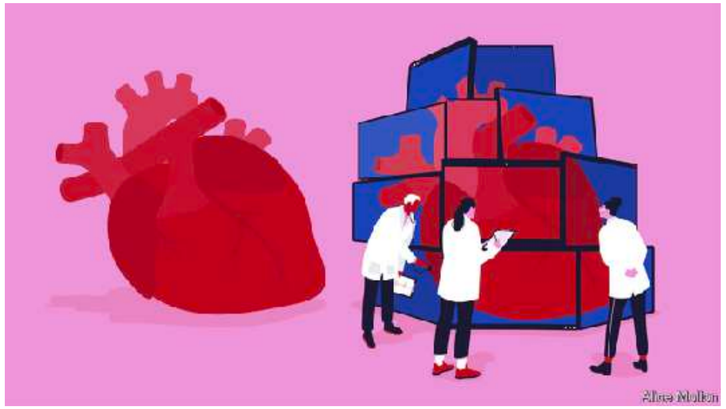

$$\mathbb{E}[g(\theta)] = \int g(\theta) p^\star(\theta) d\theta \approx \frac{1}{n} \sum_{i=1}^{n} g(\theta_i)$$

g = Heart simulator takes 1000s of hours

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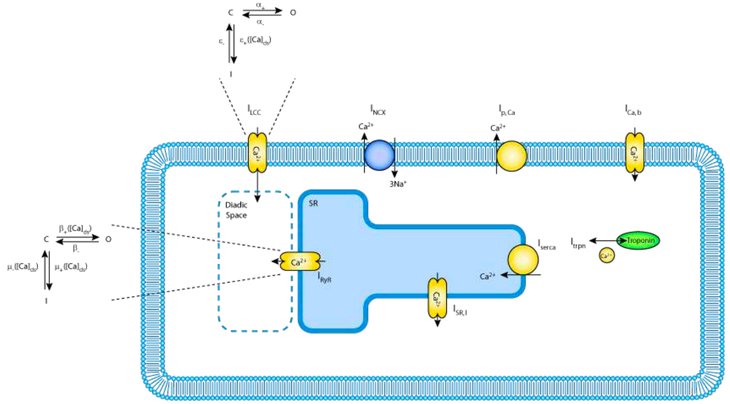

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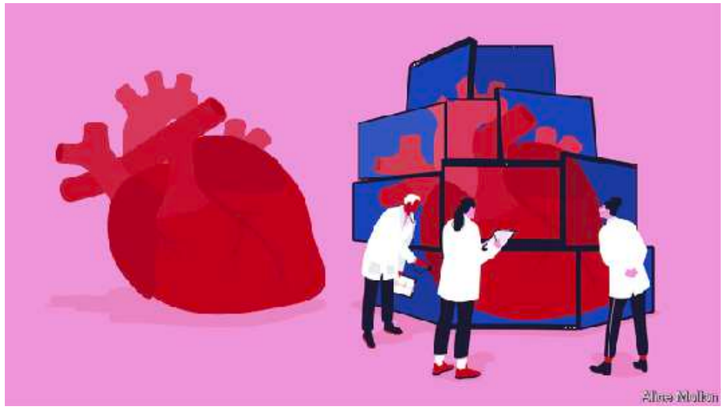


$$\mathbb{E}[g(\theta)] = \int g(\theta) p^\star(\theta) d\theta \approx \frac{1}{n} \sum_{i=1}^{n} g(\theta_i)$$

g = Heart simulator takes 1000s of hours

How to compress the points to size $t \ll n$ while ensuring $\frac{1}{n} \sum_{i=1}^{n} g(\theta_i) \approx \frac{1}{t} \sum_{j=1}^{t} g(\tilde{\theta}_j)$?

Thinning methods

Random sampling

$$\theta_1, \theta_2, \ldots, \theta_n \sim p^\star$$

- Numerous sampling algorithms proposed, Markov chain Monte Carlo (MCMC) being the most popular

- MCMC method = Set up a Markov chain that converges to the target distribution $p^\star$ as number of steps go to ∞

1. How many steps do we need to simulate the chain for?

2. How do we tune the Markov chain for fast convergence?

Thinning/compression

$$\frac{1}{n}\sum_{i=1}^{n} g(\theta_i) \approx \frac{1}{t}\sum_{j=1}^{t} g(\tilde{\theta}_j) \text{ for } t \ll n$$

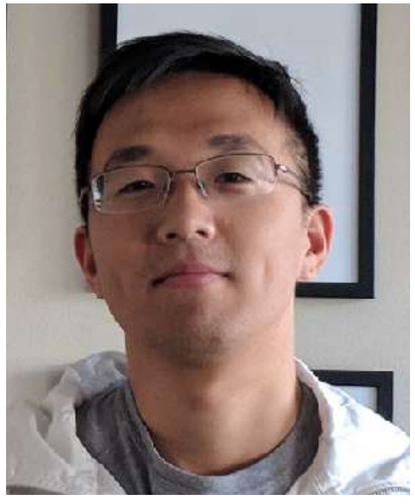
- Commonly used: Standard thinning—-choose t points uniformly at random, but approximation error gets worse quickly as t reduces
- Other fancier methods: Do not apply to general enough function class

1. How to thin without losing information?
2. How to ensure validity for rich enough function class?

Explicit user-friendly guarantees for MCMC methods

Joint work with

Yuansi Chen



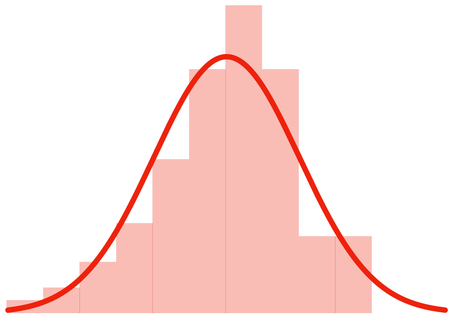
Martin Wainwright

Bin Yu

Sampling versus optimization

- Draw samples from the density

$$X \sim p^\star \propto e^{-f}$$

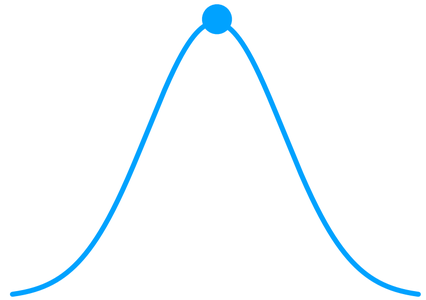


- Unadjusted Langevin algorithm (ULA)

$$X_k = X_{k-1} - h\nabla f(X_{k-1}) + \sqrt{2h}\xi_k$$
$$\xi_k \sim \mathcal{N}(0, I_d)$$

- Find mode of the density (or MAP)

$$x^\star \leftarrow \arg\max p^\star = \arg\min f$$



- Gradient descent

$$x_k = x_{k-1} - h\nabla f(x_{k-1})$$

’81 Parisi ’94 Grenander-Miller, ’96 Roberts-Tweedie

Langevin algorithms: Origin

- Langevin diffusion

$$dX_t = -\nabla f(X_t)dt + \sqrt{2}dB_t$$

- Under mild assumptions, diffusion converges to desired distribution

$$\|\mathbf{P}(X_t) - \mathbf{P}^\star\|_{\mathrm{tv}} \to 0 \text{ as } t \to \infty \ (p^\star \propto e^{-f})$$

- Unadjusted Langevin algorithm: Euler discretization of Langevin diffusion

$$X_k = X_{k-1} - h\nabla f(X_{k-1}) + \sqrt{2h}\xi_k$$

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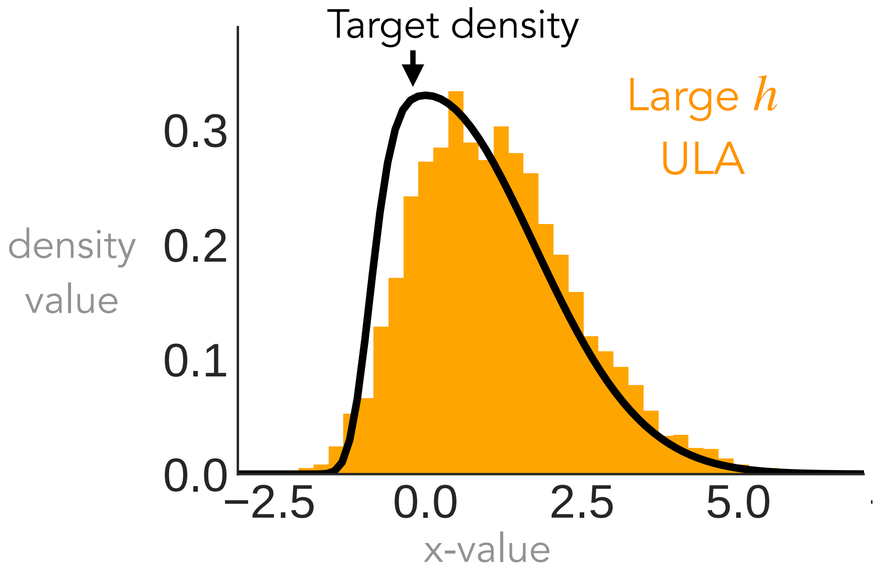
How to choose h?

How many steps to take?

Langevin simulation: Trade-offs on convergence

Histogram of iterates upon convergence



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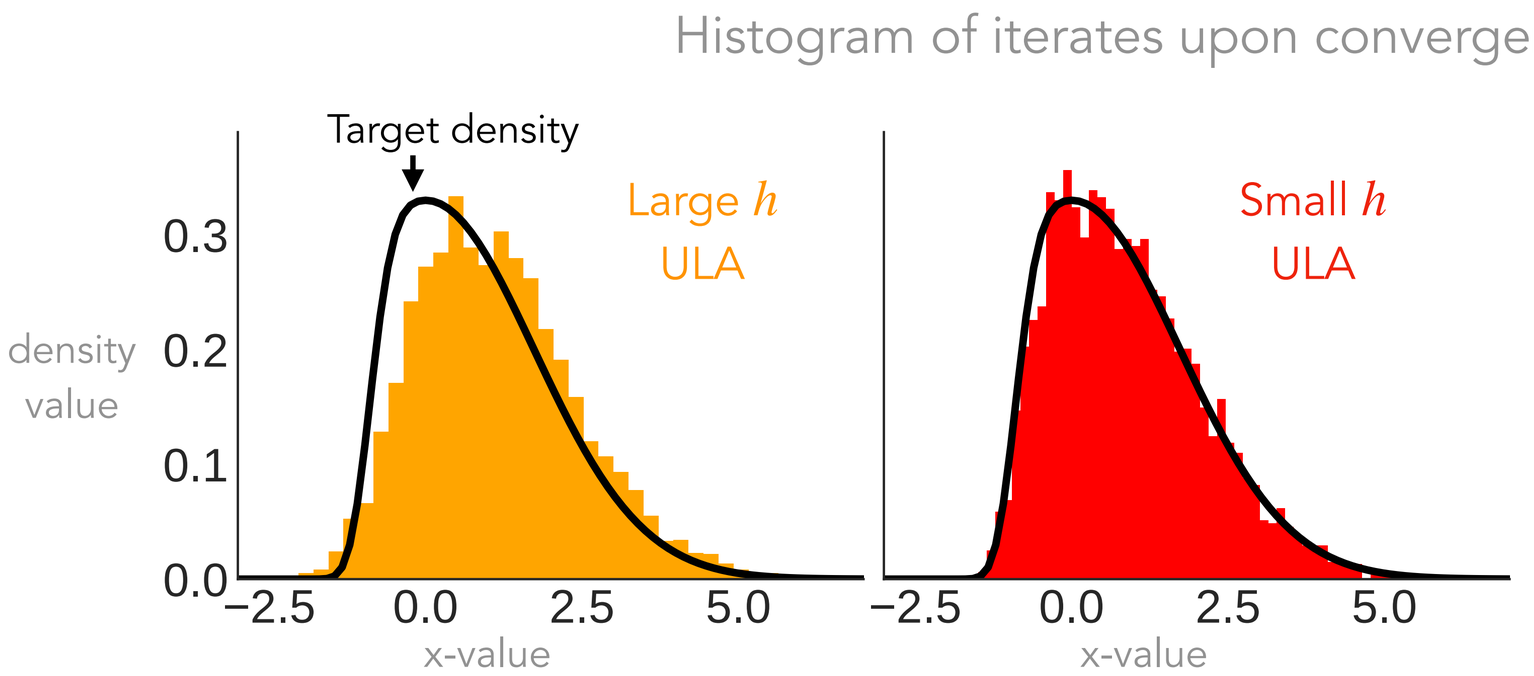

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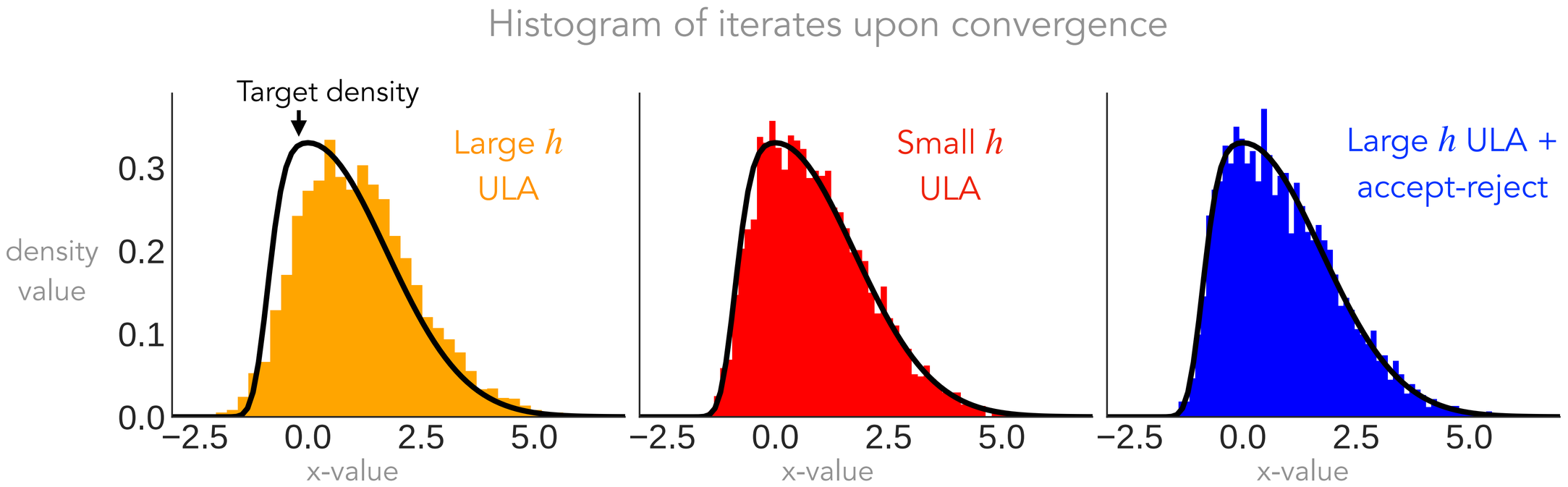

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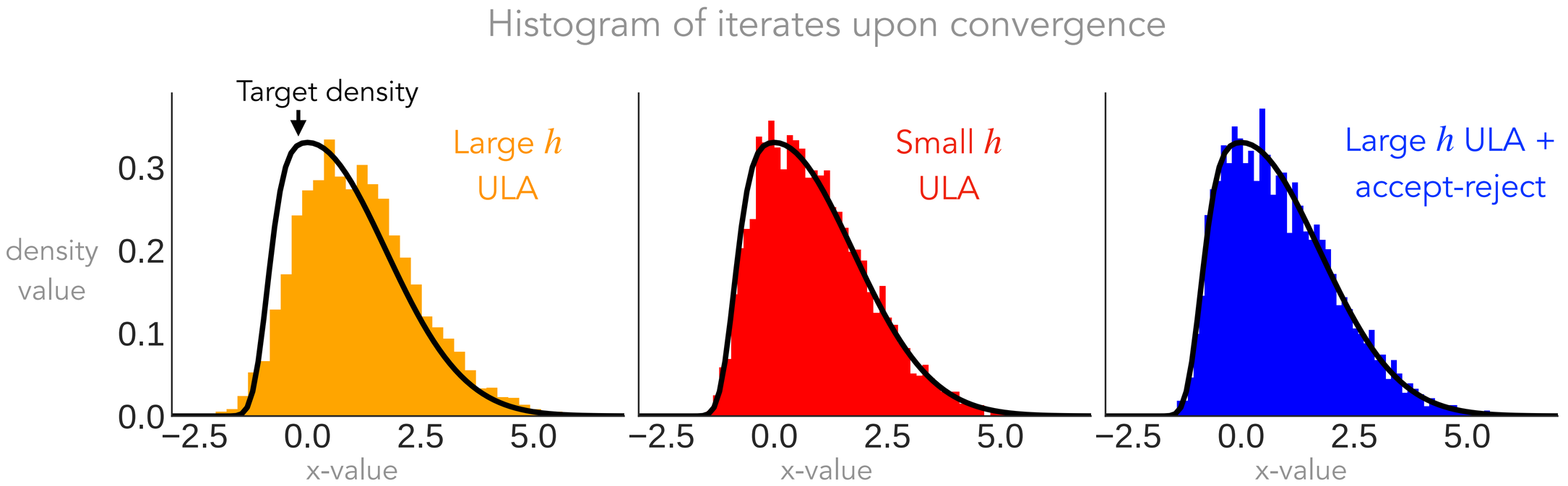
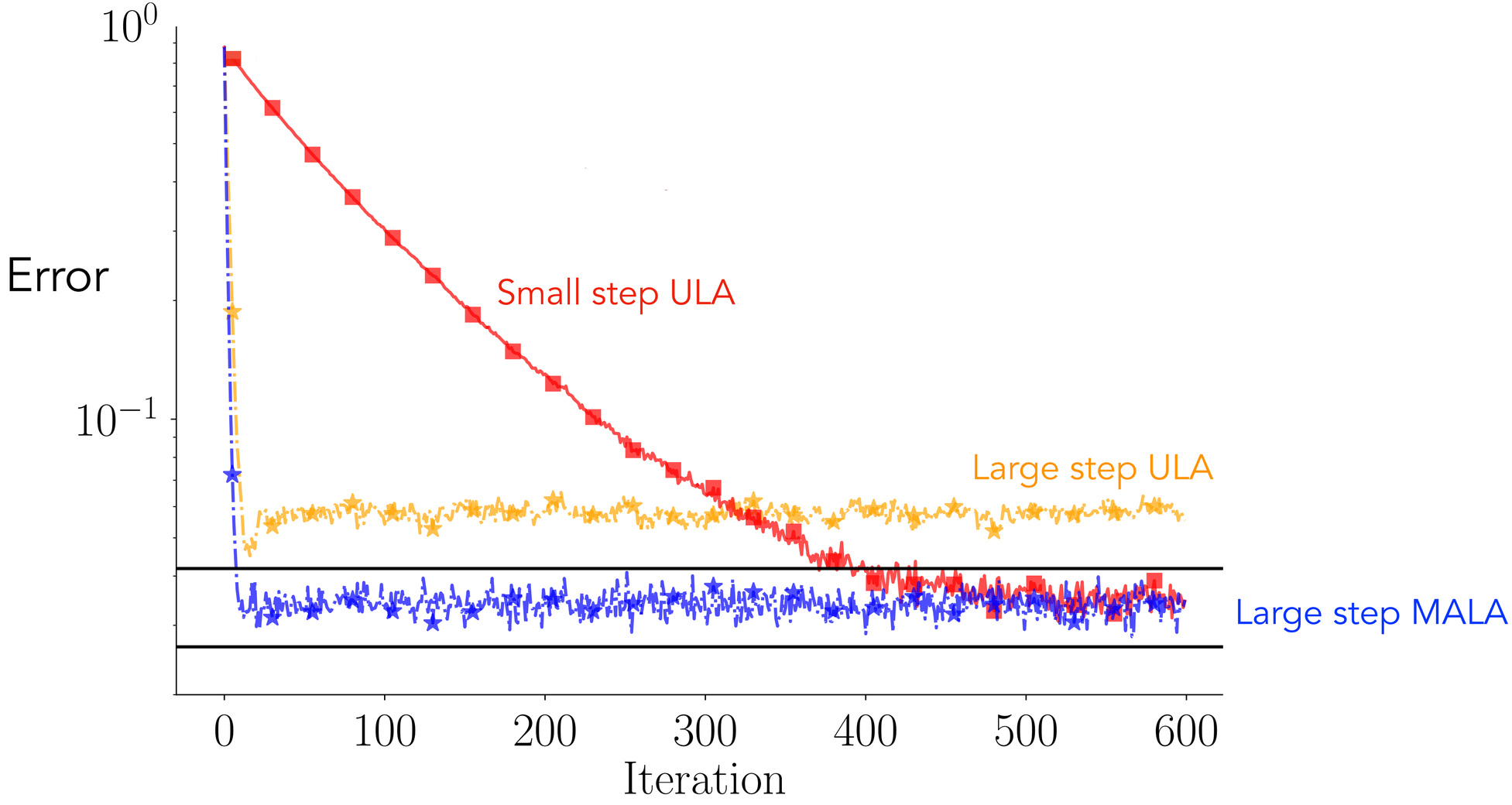


Metropolis-adjusted Langevin algorithm (MALA)

1. Proposal step: $z = x - h\nabla f(x) + \sqrt{2h}\xi$
2. Accept-reject step: Accept z with probability $\min\left\{1, \frac{e^{-f(z)} \cdot \mathbf{P}_h(z \to x)}{e^{-f(x)} \cdot \mathbf{P}_h(x \to z)}\right\}$

Langevin simulation: Trade-offs for mixing



Several asymptotic and non-explicit guarantees

- Existence, Harris recurrence
  ['95 Meyn-Tweedie, '96 Roberts-Rosenthal, '00 Diaconis-Holmes-Neal,…]

- Weak convergence and diffusion limits as $d \to \infty$
  ['98 Roberts-Rosenthal, '12 Pillai et al., '10 Beskos et al.,…]

- Geometric and uniform ergodicity, Lyapunov coupling
  ['96 Roberts-Tweedie, '04 Roberts-Rosenthal, '09 Bou-Rabee-Hairer, '16 Livingstone et al.,…]

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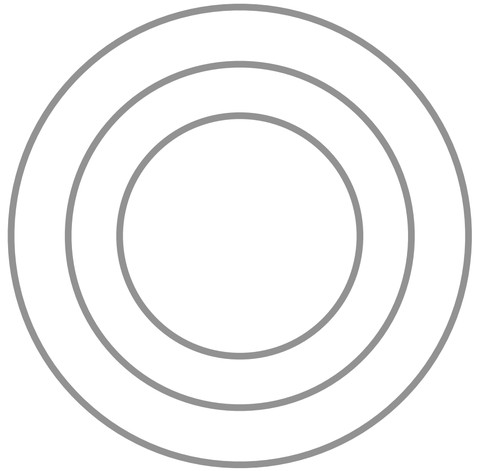
Asymptotic convergence and geometric ergodicity do not immediately reveal user-friendly mixing time bounds in high-dimensions.

Can we characterize dominance of MALA over ULA in a non-asymptotic sense?

Sampling analog of convex optimization

- **Assumption**: Log-concave target density $p^\star \propto e^{-f}$ in $\mathbb{R}^d$ with f strongly convex and smooth

$$m\mathbb{I}_d \preceq \nabla^2 f \preceq L\mathbb{I}_d; \;\; \kappa = L/m$$

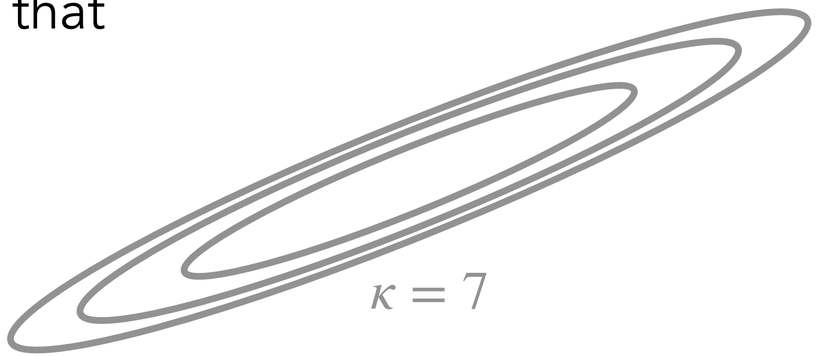


Contour of target distribution

$\kappa = 1$

- **Mixing-time guarantee**: Bound on iterations T with dimension d, conditioning κ, error δ such that

$$\|\mathbf{P}^\star - \mathbf{P}(X_T)\|_{\mathrm{tv}} \leq \delta$$



$\kappa = 7$

Non-asymptotic mixing time for Langevin algorithms

$$\|\mathbf{P}^\star - \mathbf{P}(X_T)\|_{\mathrm{tv}} \le \delta$$

$$p^\star \propto e^{-f} \text{ with } f : \mathbb{R}^d \to \mathbb{R} \text{ convex}$$

$$m\mathbb{I}_d \le \nabla^2 f \le L\mathbb{I}_d; \;\; \kappa = L/m$$

	ULA ['15 Dalalyan]	
Mixing time	$d\kappa^2 \dfrac{\log(1/\delta)}{\delta^2}$	

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Accept-reject helps

- Exponentially better dependence on δ
- Better dependence on κ

Non-asymptotic mixing time for Langevin algorithms

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	ULA ['15 Dalalyan]	MALA [Our work]
Mixing time	$d\kappa^2 \frac{\log(1/\delta)}{\delta^2}$	$d\kappa \log(1/\delta)$
Step size	$\frac{\delta^2}{d\kappa L}$	$\frac{1}{dL}$

Accept-reject helps

- Exponentially better dependence on δ
- Better dependence on κ

step size limited by bias in ULA, and by accept-reject step in MALA

Next: How does gradient information help?

$$\|\mathbf{P}^\star - \mathbf{P}(X_T)\|_{\mathrm{tv}} \le \delta$$

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		Metropolis-adjusted Langevin algorithm (MALA)	
Proposal step		$z = x - h\nabla f(x) + \sqrt{2h}\xi$ one gradient step	
Mixing time		$d\kappa \log(1/\delta)$	
Step size		$\frac{1}{dL}$	

MRW: No gradient leads to slower mixing

$$\|\mathbf{P}^\star - \mathbf{P}(X_T)\|_{\mathrm{tv}} \le \delta$$

$$p^\star \propto e^{-f} \text{ with } f : \mathbb{R}^d \to \mathbb{R} \text{ convex}$$

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	Metropolis random walk (MRW)	Metropolis-adjusted Langevin algorithm (MALA)	
Proposal step	$z = x + \sqrt{2h}\xi$ no gradient	$z = x - h\nabla f(x) + \sqrt{2h}\xi$ one gradient step	
Mixing time	$d\kappa^2 \log(1/\delta)$	$d\kappa \log(1/\delta)$	
Step size	$\frac{1}{d\kappa L}$	$\frac{1}{dL}$	

HMC: Multiple gradient steps help mix faster

$$\|\mathbf{P}^\star - \mathbf{P}(X_T)\|_{\mathrm{tv}} \le \delta$$

$$p^\star \propto e^{-f} \text{ with } f : \mathbb{R}^d \to \mathbb{R} \text{ convex}$$

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	Metropolis random walk (MRW)	Metropolis-adjusted Langevin algorithm (MALA)	Metropolis-adjusted Hamiltonian Monte Carlo (HMC)
Proposal step	$z = x + \sqrt{2h}\xi$ no gradient	$z = x - h\nabla f(x) + \sqrt{2h}\xi$ one gradient step	Hamiltonian dynamics with K gradients per step (non-Gaussian proposal)
Mixing time	$d\kappa^2 \log(1/\delta)$	$d\kappa \log(1/\delta)$	$d^{\frac{2}{3}}\kappa \log(1/\delta)$
Step size	$\frac{1}{d\kappa L}$	$\frac{1}{dL}$	$\frac{1}{d^{\frac{7}{12}}L^{\frac{1}{2}}}$ $(K = d^{\frac{1}{4}})$

Total #gradients = $d^{\frac{11}{12}}\kappa \log(1/\delta)$

HMC: Multiple gradient steps help mix faster

$$\|\mathbf{P}^\star - \mathbf{P}(X_T)\|_{\mathrm{tv}} \le \delta$$

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Mixing time	$d\kappa^2 \log(1/\delta)$	$d\kappa \log(1/\delta)$	$d^{\frac{2}{3}}\kappa \log(1/\delta)$
Step size	$\frac{1}{d\kappa L}$	$\frac{1}{dL}$	$\frac{1}{d^{\frac{7}{12}}L^{\frac{1}{2}}}$ $(K = d^{\frac{1}{4}})$

Total #gradients = $d^{\frac{11}{12}}\kappa \log(1/\delta)$

Previous HMC bounds either worse than MALA or had $1/\delta^2$ dependence due to no accept-reject step

How do the guarantees depend on where you start?

- Distance of initial distribution: $M = \sup_x \frac{p_0(x)}{p_\star(x)}$

- Previous mixing bounds scale $\mathcal{O}(\log M)$

$M = \mathcal{O}(e^d)$ quite common $\Rightarrow$ Extra d factor in mixing time bounds

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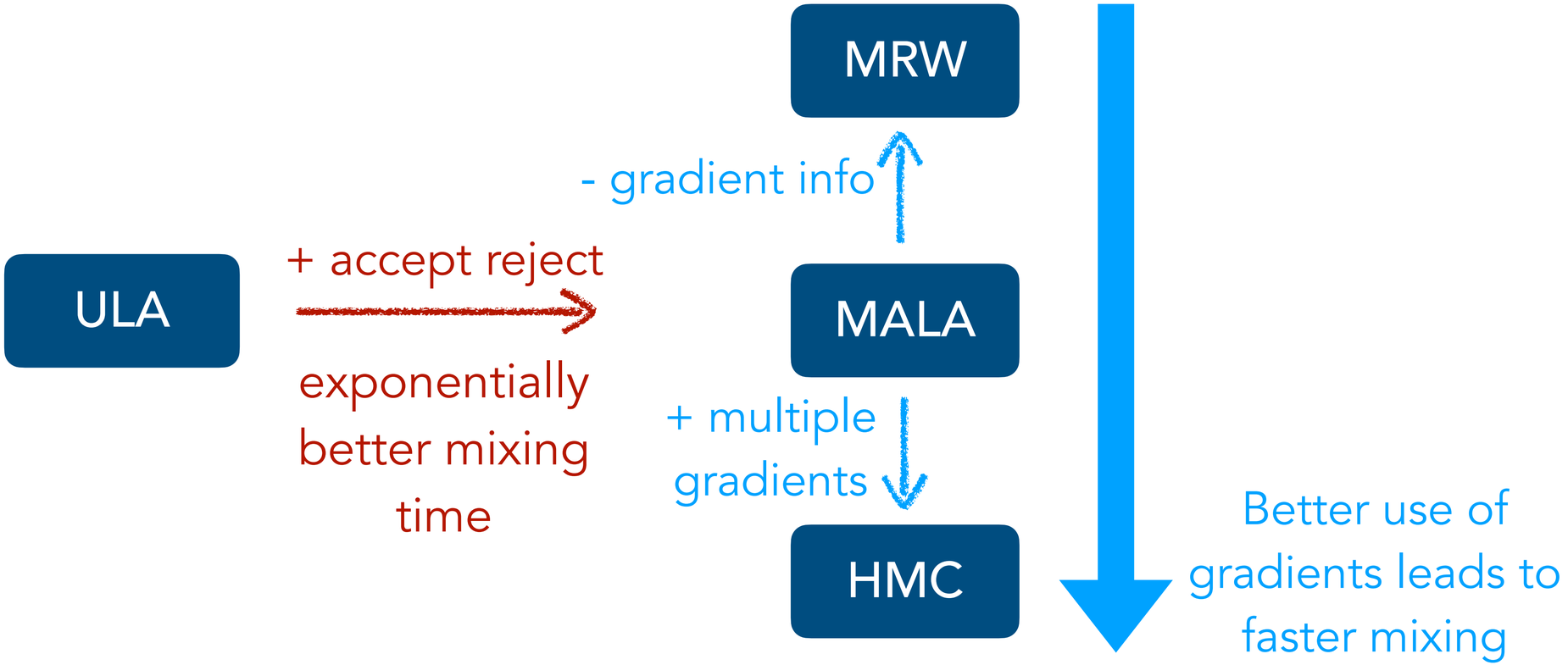
  $M = \mathcal{O}(e^d)$ quite common ⇒ Extra d factor in mixing time bounds

- We provide an exponential improvement

  $\mathcal{O}\left(\log\log M\right)$ scaling ⇒ Starting point doesn't affect much

Overview of MCMC guarantees



Refs: **1.** Log-concave sampling: Metropolis-Hastings algorithms are fast
[**Dwivedi***-Chen*-Wainwright-Yu, '19 JMLR]
2. Fast mixing of Metropolized Hamiltonian Monte Carlo: Benefits of multi-step gradients
[Chen-**Dwivedi**-Wainwright-Yu, '20 JMLR]

Thinning without losing

1. How to thin without losing information?
2. How to ensure validity for rich enough function class?

Recall: Motivation

- Long runs of MCMC often simulated to ensure convergence and mixing

$$\mathbb{P}^\star g := \int g(\theta) p^\star(\theta) d\theta \approx \frac{1}{n} \sum_{i=1}^{n} g(\theta_i) =: \mathbb{P}_n g \quad \text{for } x_i\text{'s from Markov Chain}$$

- When evaluating g expensive, samples often compressed/thinned to save computation

Standard Thinning

$$x_1, x_2, \ldots, x_n \in \mathbb{R}^d$$

$$\mathbb{P}_{in} := \frac{1}{n} \sum_{i=1}^{n} \delta_{x_i}$$

Standard-m Thinning

Uniform subsample

of size n/m

$$y_1, \ldots, y_{n/m}$$

$$\mathbb{P}_{out} := \frac{1}{n/m} \sum_{i=1}^{n/m} \delta_{y_i}$$

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$$\sup_{\|g\| \leq 1} |\mathbb{P}_{in} g - \mathbb{P}_{out} g| \lesssim \sqrt{\frac{m}{n}}$$

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Monte Carlo guarantee:

(Input = n iid or fast mixing MCMC points)

$$\sup_{\|g\|\leq 1} |\mathbb{P}_{in} g - \mathbb{P}^{\star} g| \lesssim \sqrt{\frac{1}{n}}$$

Standard Thinning: Can not compress too much

$$x_1, x_2, \ldots, x_n \in \mathbb{R}^d$$

$$\mathbb{P}_{in} := \frac{1}{n}\sum_{i=1}^{n} \delta_{x_i}$$

→ **Standard-m Thinning** →

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Monte Carlo guarantee:

(Input = n iid or fast mixing MCMC points)

$$\sup_{\|g\|\leq 1} |\mathbb{P}_{in} g - \mathbb{P}^{\star} g| \lesssim \sqrt{\frac{1}{n}}$$

m has to be a constant to have $n^{-1/2}$ accuracy after thinning

How can we **provably and practically compress much more** while keeping $n^{-1/2}$ accuracy?

Via Kernel Thinning!

Joint work with

Lester Mackey

Kernel Thinning: Compress to $\sqrt{n}$ points

$x_1, x_2, \ldots, x_n \in \mathbb{R}^d$

suitable kernels

$$\mathbb{P}_{in} := \frac{1}{n} \sum_{i=1}^{n} \delta_{x_i}$$

→ **Kernel Thinning (KT)** →

Non-uniform sample of size $\sqrt{n}$

$$y_1, \ldots, y_{\sqrt{n}}$$

$$\mathbb{P}_{KT} := \frac{1}{\sqrt{n}} \sum_{i=1}^{\sqrt{n}} \delta_{y_i}$$

Kernel Thinning: Compress to $\sqrt{n}$ points with $n^{-1/2}$ error

$x_1, x_2, \ldots, x_n \in \mathbb{R}^d$

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$$\mathbb{P}_{in} := \frac{1}{n} \sum_{i=1}^{n} \delta_{x_i}$$

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$$\mathbb{P}_{KT} := \frac{1}{\sqrt{n}} \sum_{i=1}^{\sqrt{n}} \delta_{y_i}$$

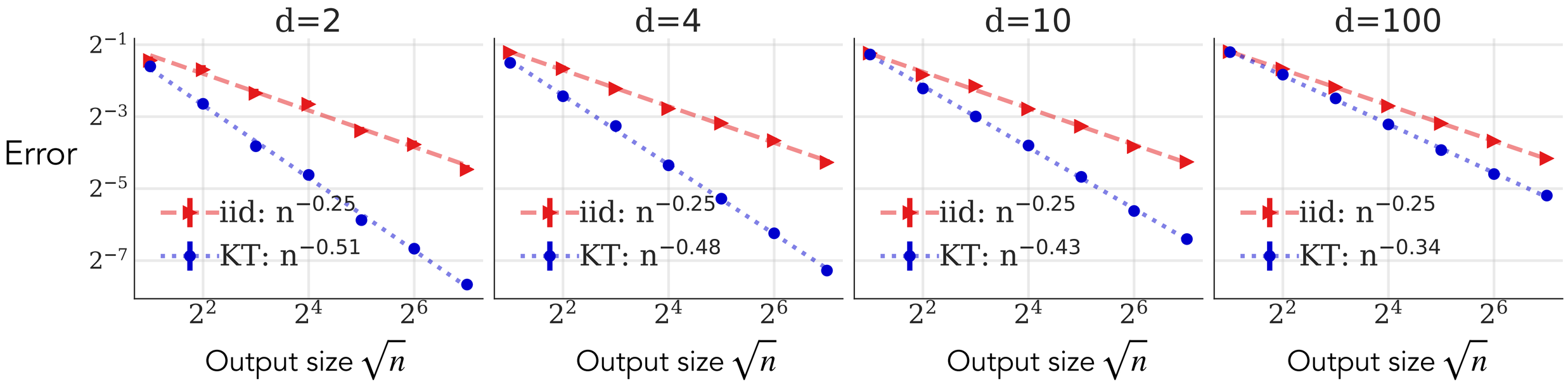
$$\sup_{\|g\|_{\mathbf{k}} \leq 1} |\mathbb{P}_{in} g - \mathbb{P}_{KT} g| \precsim_d \begin{cases} n^{-1/2} \sqrt{\log n} & \text{(Compactly supported)} \\ n^{-1/2} \sqrt{\log^{d+1} n \log\log n} & \text{(Sub-exponential tails)} \end{cases}$$

Highlights of kernel thinning

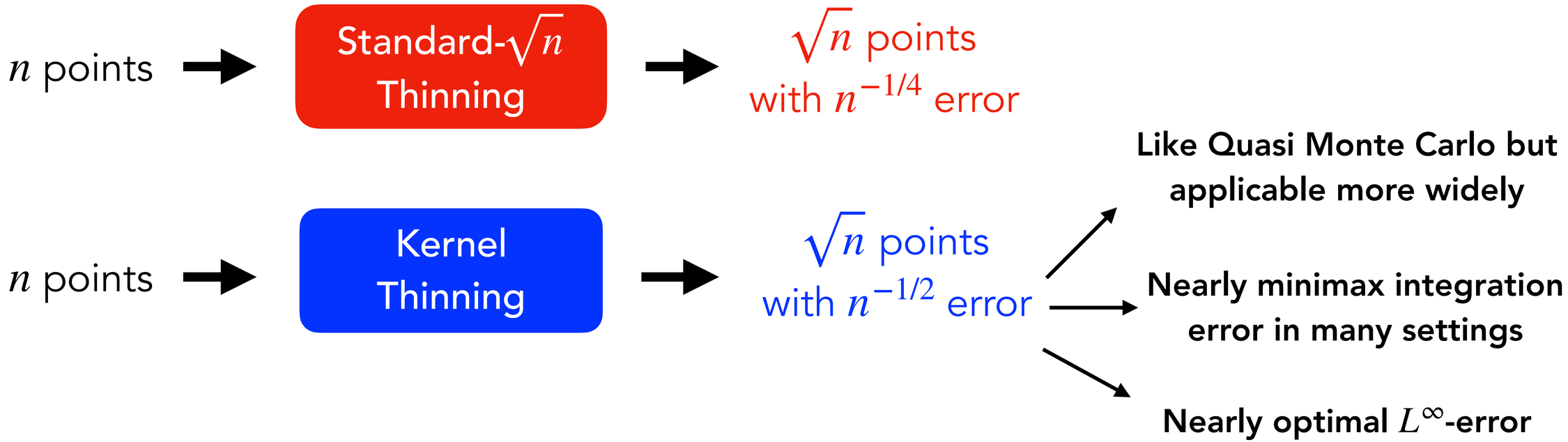
- KT guarantees $n^{-1/2}$ error with $\sqrt{n}$ points, which
  - is significantly superior to $n^{-1/4}$ rates from Standard-$\sqrt{n}$ Thinning
  - applies to arbitrary functions in infinite-dimensional reproducing kernel Hilbert spaces (RKHS), and fairly generic input points (including MCMC points)
- The algorithm requires only kernel evaluations for implementation

Effect of high dimensions on KT

IID input, Gaussian target distribution with Gaussian kernel



Summary: Thinning a lot without losing!

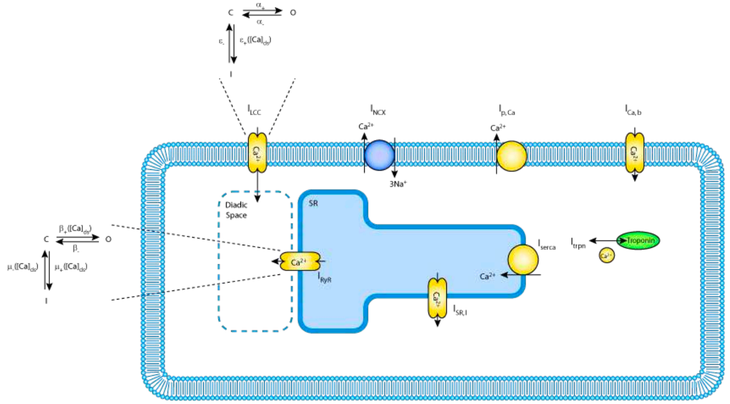


python™ `pip install kernelthinning`

Refs: **Kernel Thinning** [**Dwivedi**-Mackey, '21 COLT]

Going back to the cardiac experiments

Estimate single-cell model parameters

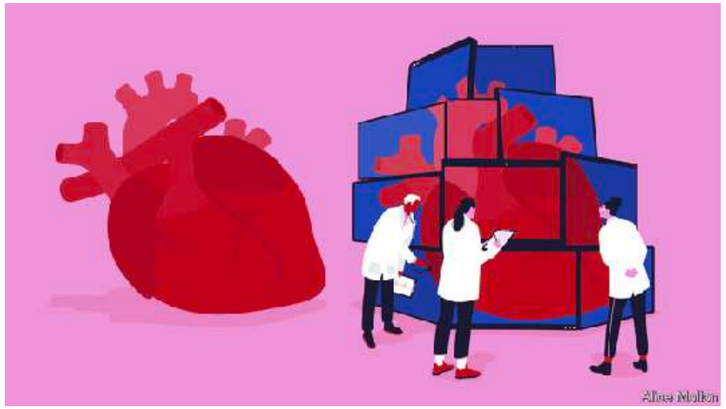


How to draw random samples from the posterior?

$\theta_1, \theta_2, \ldots, \theta_n \sim p^\star$ (38-dimensional)

(θ = single cell parameters)

Estimate effect of therapy at organ-level

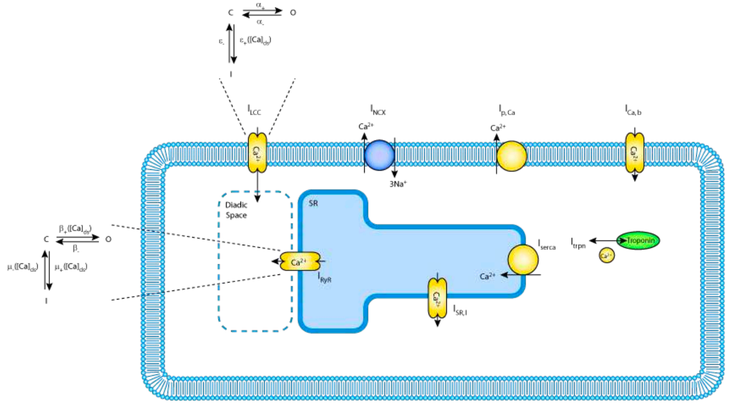


$$\mathbb{E}[g(\theta)] = \int g(\theta) p^\star(\theta) d\theta \approx \frac{1}{n} \sum_{i=1}^{n} g(\theta_i)$$

g = Heart simulator takes 1000s of hours

How to compress the points to size $t \ll n$ while ensuring $\frac{1}{n} \sum_{i=1}^{n} g(\theta_i) \approx \frac{1}{t} \sum_{j=1}^{t} g(\tilde{\theta}_j)$?

Estimate single-cell model parameters



How to draw random samples from the posterior?

Metropolis random walk

$\theta_1, \theta_2, \ldots, \theta_n \sim p^\star$ (38-dimensional)

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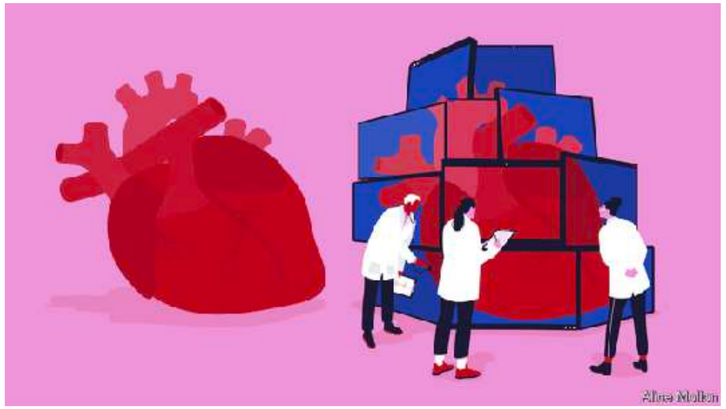
Estimate effect of therapy at organ-level



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Kernel Thinning

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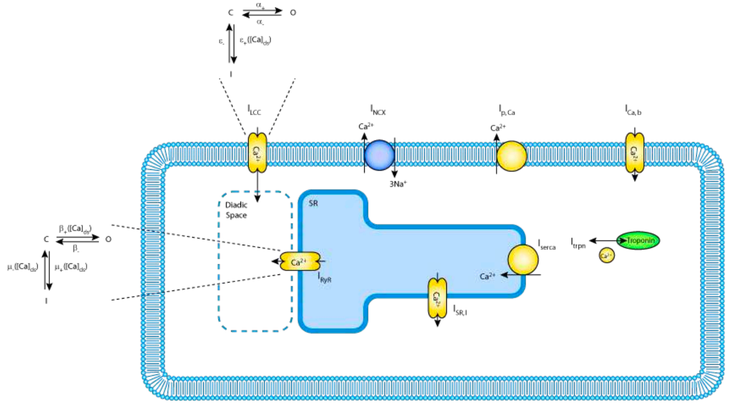

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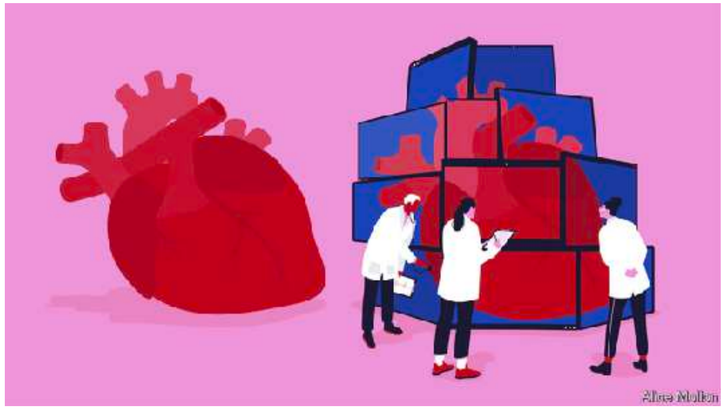
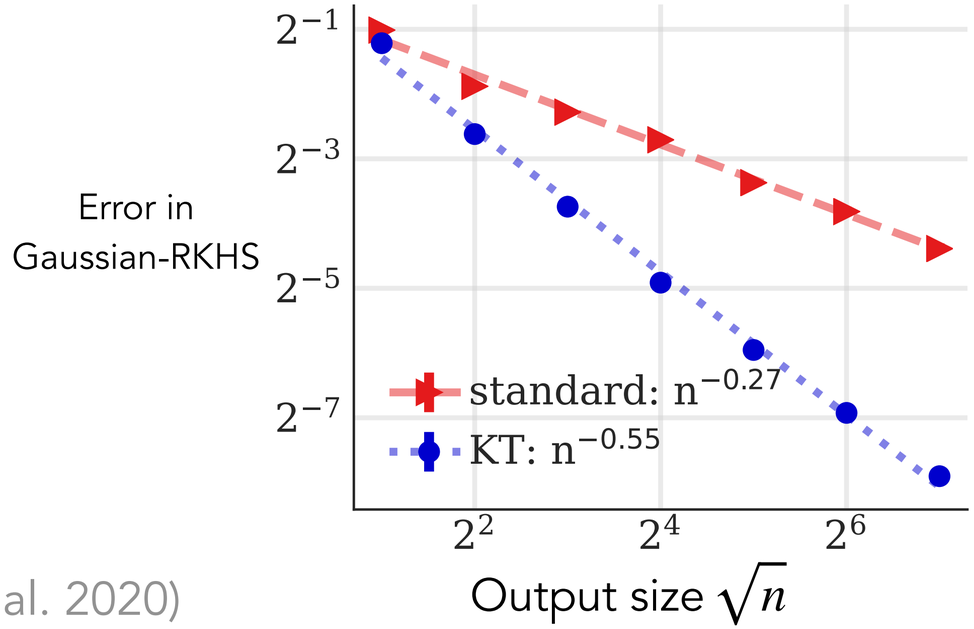
Metropolis random walk

MCMC samples fed to thinning methods





Kernel Thinning

(*MCMC samples taken from Riabiz et al. 2020)

Summary: Generating and thinning MCMC samples

- Guarantees for MCMC sampling:
    - finite time benefits of accept-reject step, and gradients
    - *Not covered*: Sampling under constraints

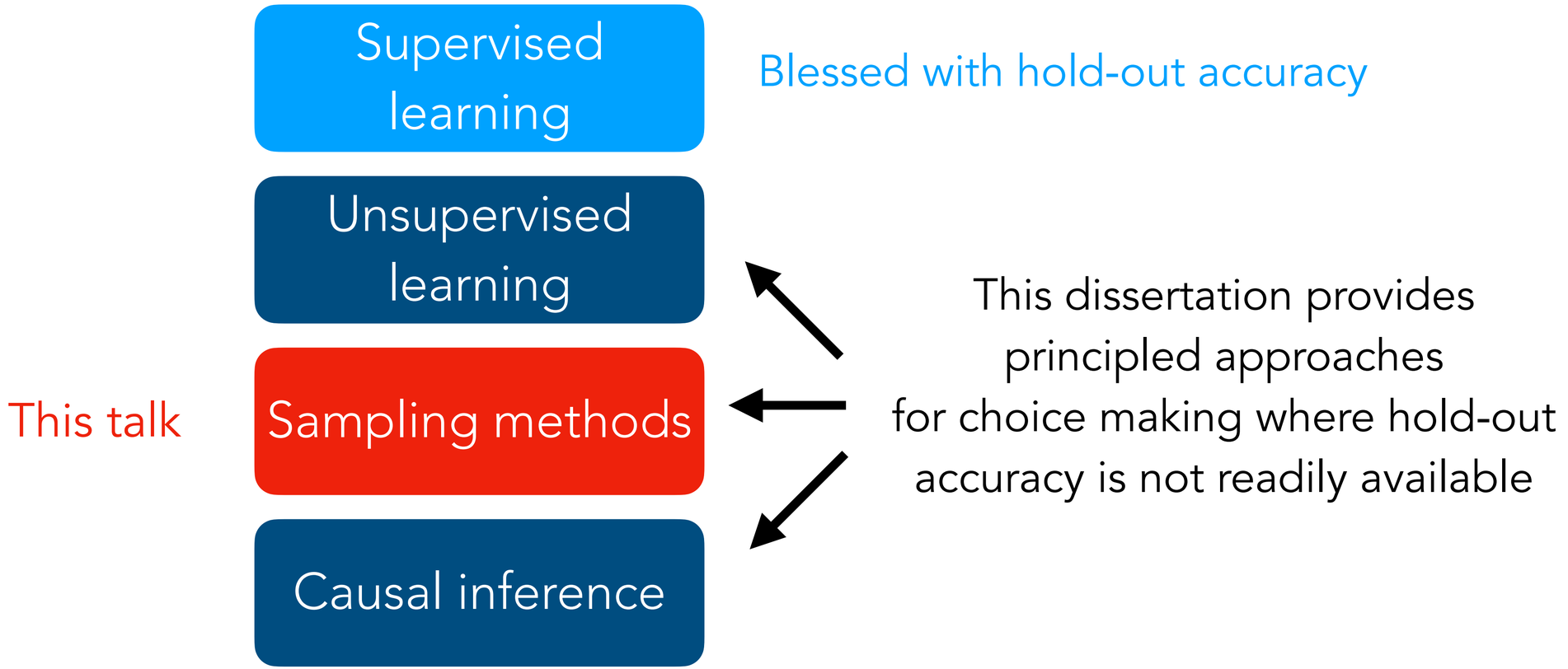
Ref: **Fast MCMC sampling on polytopes**
[Chen*-**Dwivedi***-Wainwright-Yu, '18 JMLR]

- New thinning methods that discard samples effectively:
    - without losing information for rich function classes
    - *Not covered:* Thin a little, and gain a lot

Ref: **The power of online thinning in reducing discrepancy**
[**Dwivedi**-Feldheim-Gurevich-Ramdas, '19 PTRF]

Which model/algorithm to prefer?

Judgment calls become critical and we need principled approaches to gather empirical and theoretical evidence to inform decision making



Acknowledgments