



# pyABC: Efficient and robust easy-to-use approximate Bayesian computation

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Inverse Problems Summer School, HCM Bonn 2022-08-26



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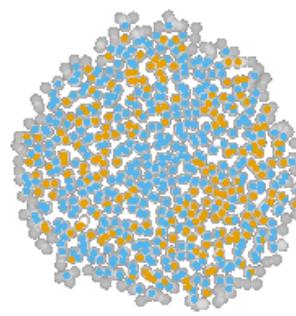
# WHY?

# MODEL TYPES

	Boolean / Petri net models	Constraint-based models	Markov chain models	SDE models	ODE models	PDE models	Agent-based models
<b>whole-heart</b> (tissue and fluid mechanics, signaling)							Hunter and Borg, <i>Nature Reviews Molecular Cell Biology</i> , 4(3):237-243, 2003
<b>cancer growth</b> (signaling, cell division and death, angiogenesis, tissue remodeling)							Anderson and Quaranta, <i>Nature Reviews Cancer</i> , 8(3):227-234. 2008
<b>liver lobule</b> (cell division and cell death, tissue mechanics)							Hoehme et al., <i>PNAS</i> , 107(23):10371-10376, 2010
<b>glucose-insulin-glucagon regulation</b> (blood and interstitial flow, organ uptake, signaling)							Schaller et al., <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2:e65, 2013
<b>whole-cell</b> (transcription, translation, DNA replication, metabolism, replication)							Karr et al., <i>Cell</i> , 150(2):389-401, 2012

# EXAMPLE: TUMOR GROWTH MULTI-SCALE MODEL

based on Jagiella et al., Cell Systems 2017



- cells modeled as interacting stochastic agents, dynamics of extracellular substances by PDEs
- simulate up to  $10^6$  cells
- 10s - 1h for one forward simulation

## WHAT WE TRIED

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- multi-start local methods
  - deterministic gradient descent
    - Levenberg-Marquardt
    - interior-point
    - trust-region
  - stochastic gradient descent
  - Bayesian optimization
- global methods
  - simulated annealing
  - > 20 particle methods
  - enhanced scatter search

## FAILED

## WORKED

---

- multi-start local methods
  - deterministic gradient descent
    - Levenberg-Marquardt
    - interior-point
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- global methods
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# WHAT?

# ABC

likelihood-free approximate Bayesian computation

$$\pi(\theta|\bar{y}_{\text{obs}}) \propto \cancel{\pi(\bar{y}_{\text{obs}}|\theta)\pi(\theta)}$$

posterior

likelihood prior

$$\bar{y} \sim \pi(\bar{y}|\theta)$$

✓

```
graph TD; A[posterior] --> B["pi(theta|bar{y}_obs)"]; C[prior] --> D["pi(theta)"]; E[likelihood] --> F["pi取消(bar{y}_obs|theta)"]; G["pi(theta|bar{y}_obs) proportional to pi取消(bar{y}_obs|theta)pi(theta)"]; H["bar{y} ~ pi(bar{y}|theta)"] --> I["✓"];
```

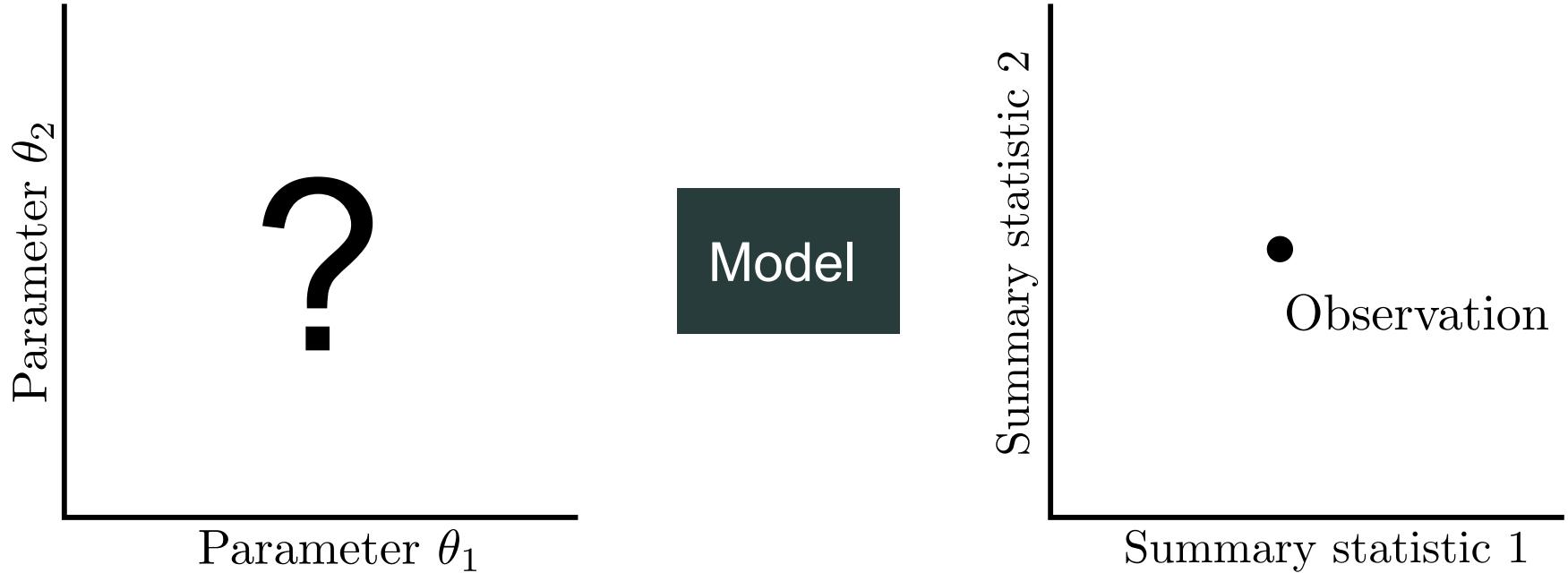
# ABC

likelihood-free approximate Bayesian computation

Model

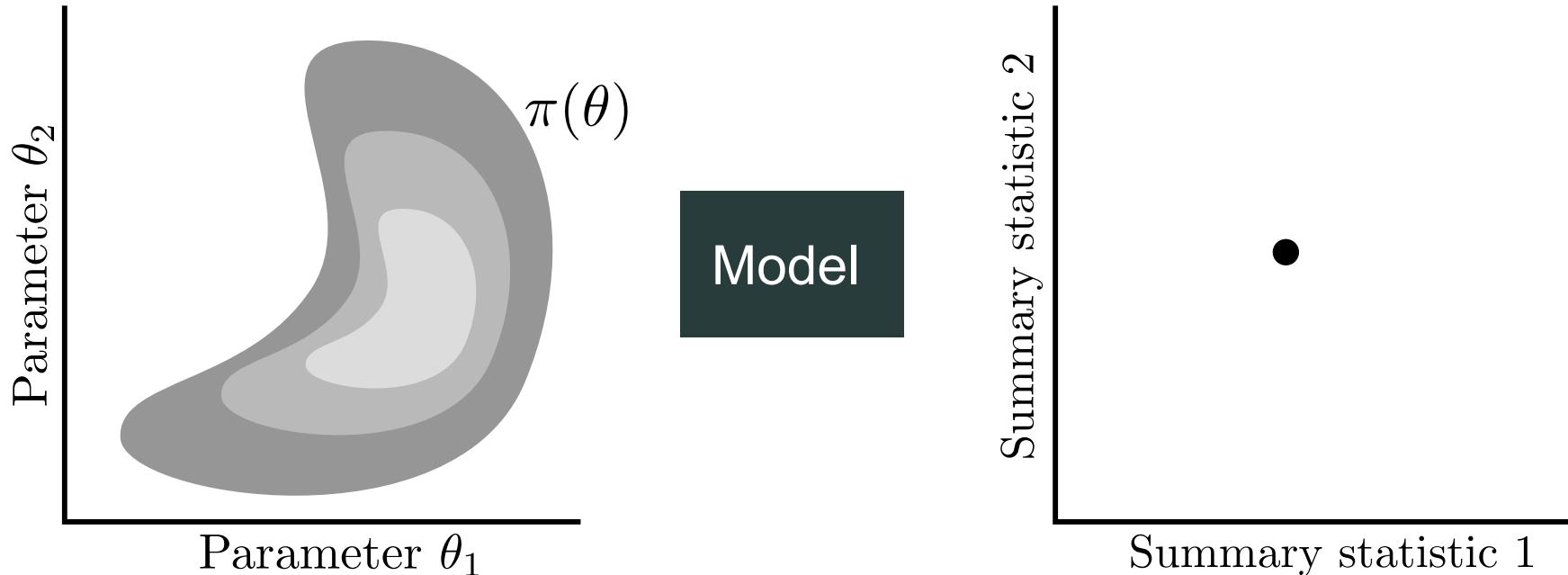
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likelihood-free approximate Bayesian computation



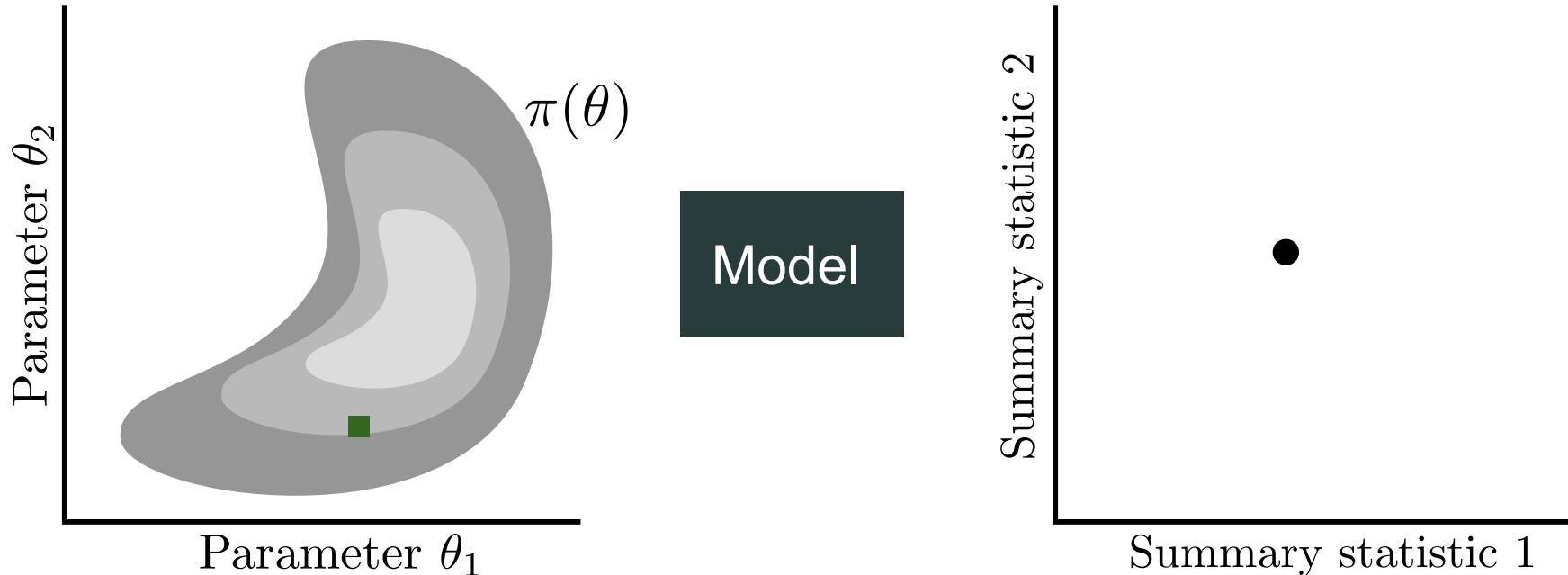
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likelihood-free approximate Bayesian computation



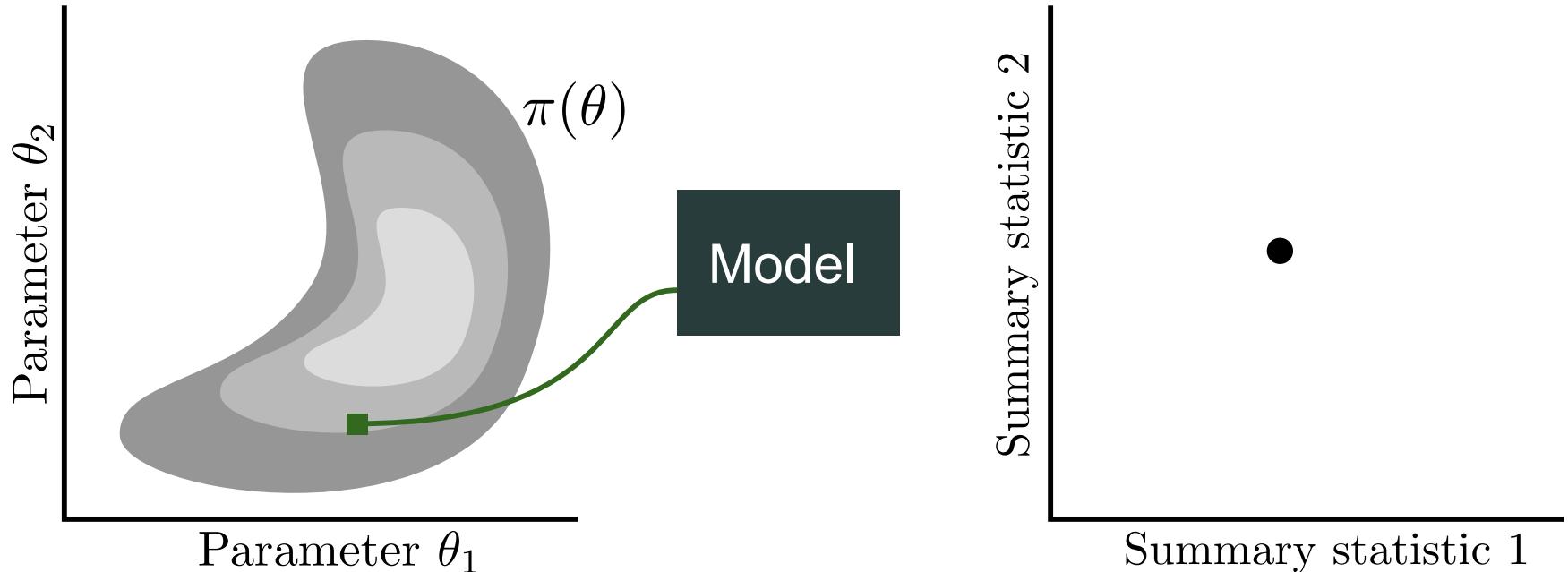
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likelihood-free approximate Bayesian computation



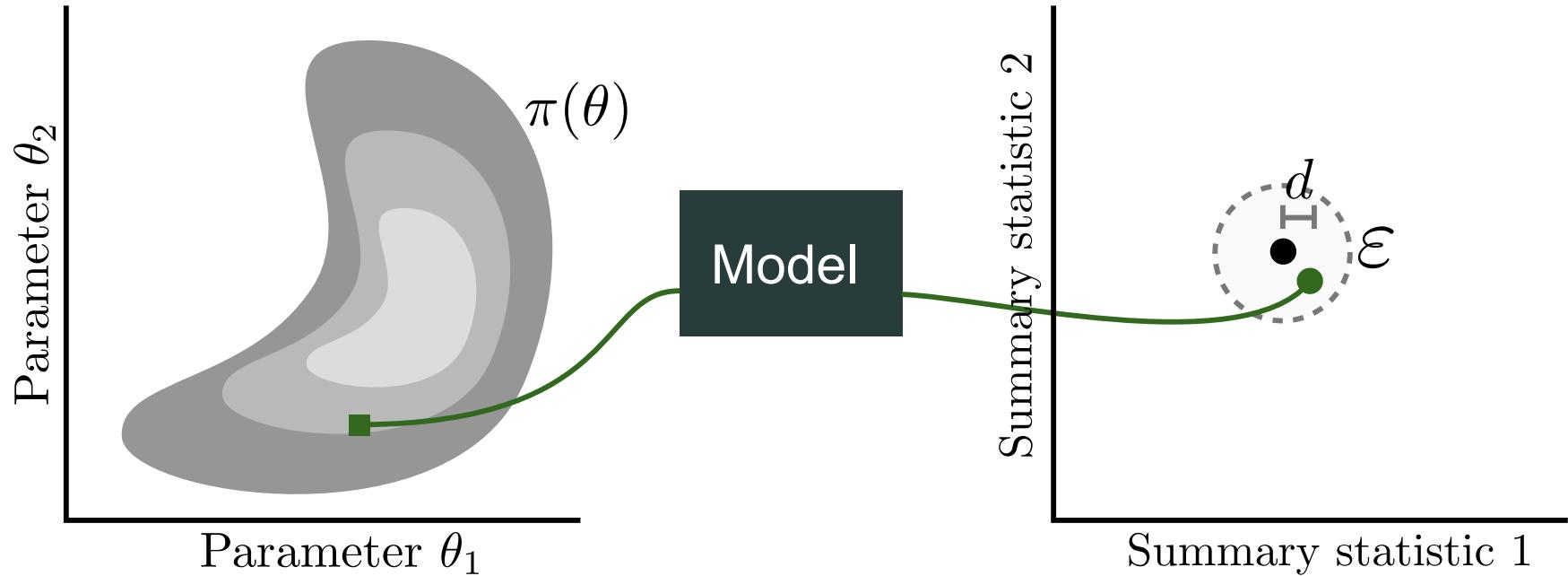
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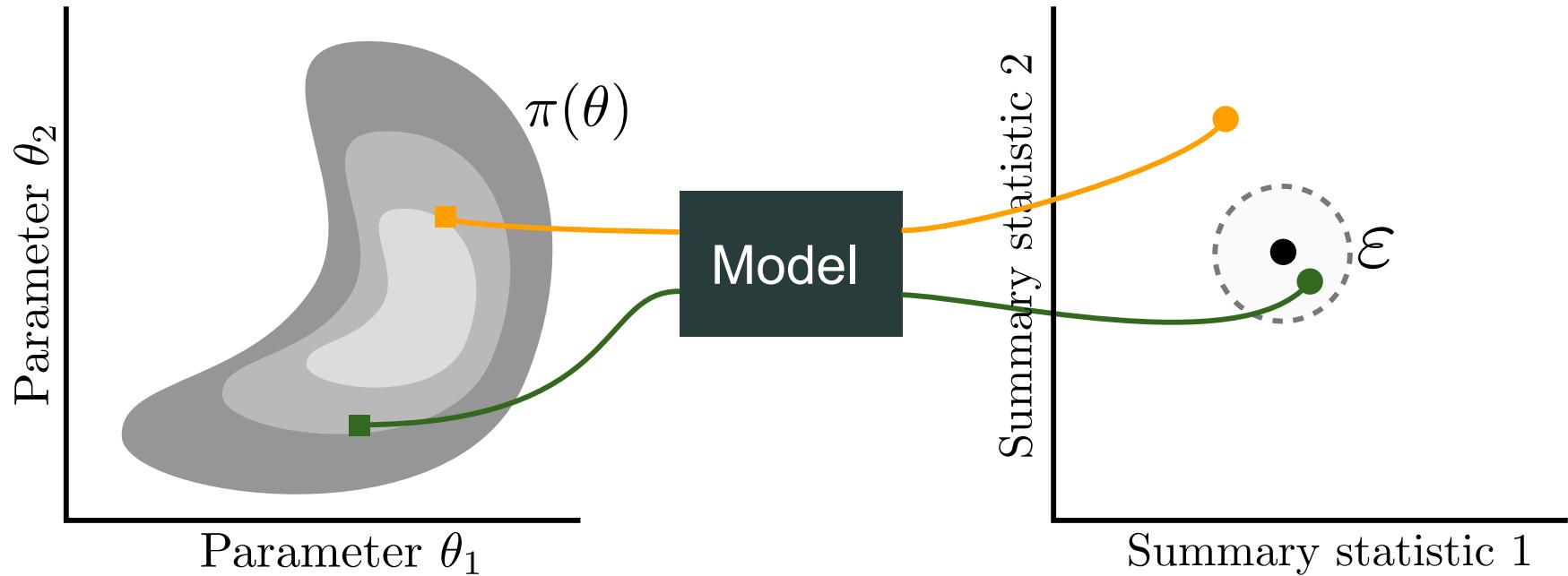
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likelihood-free approximate Bayesian computation



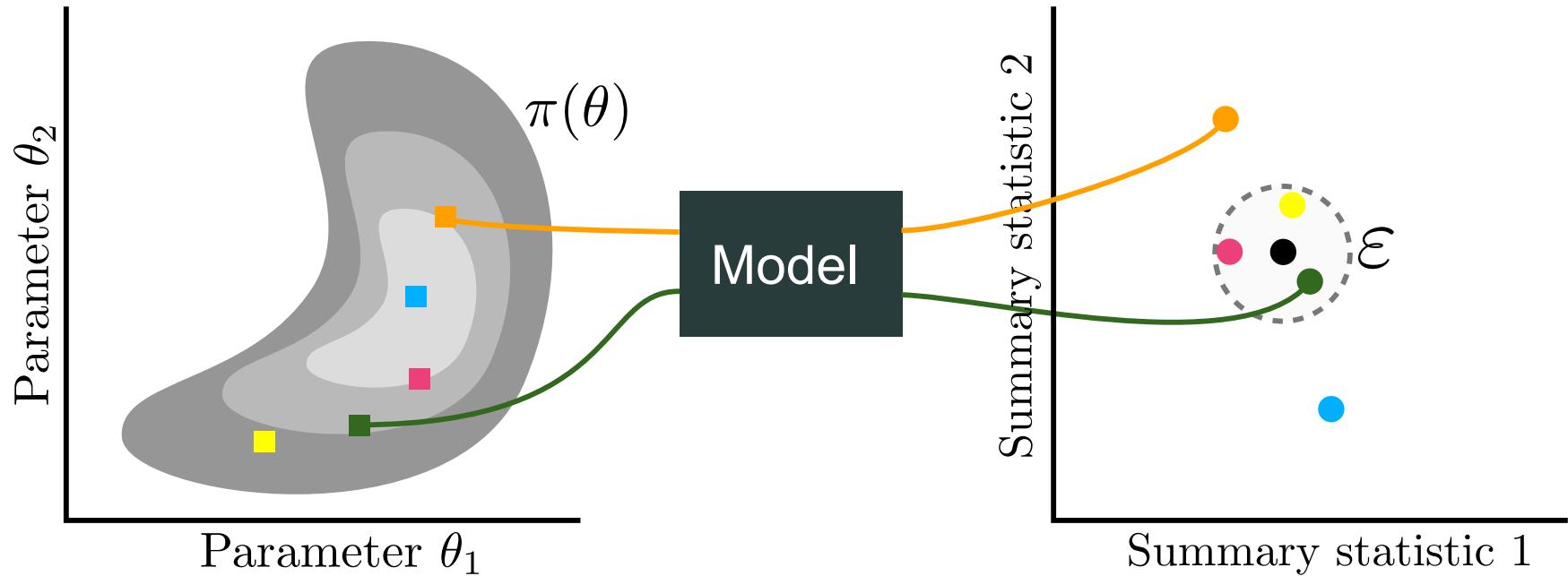
# ABC

likelihood-free approximate Bayesian computation



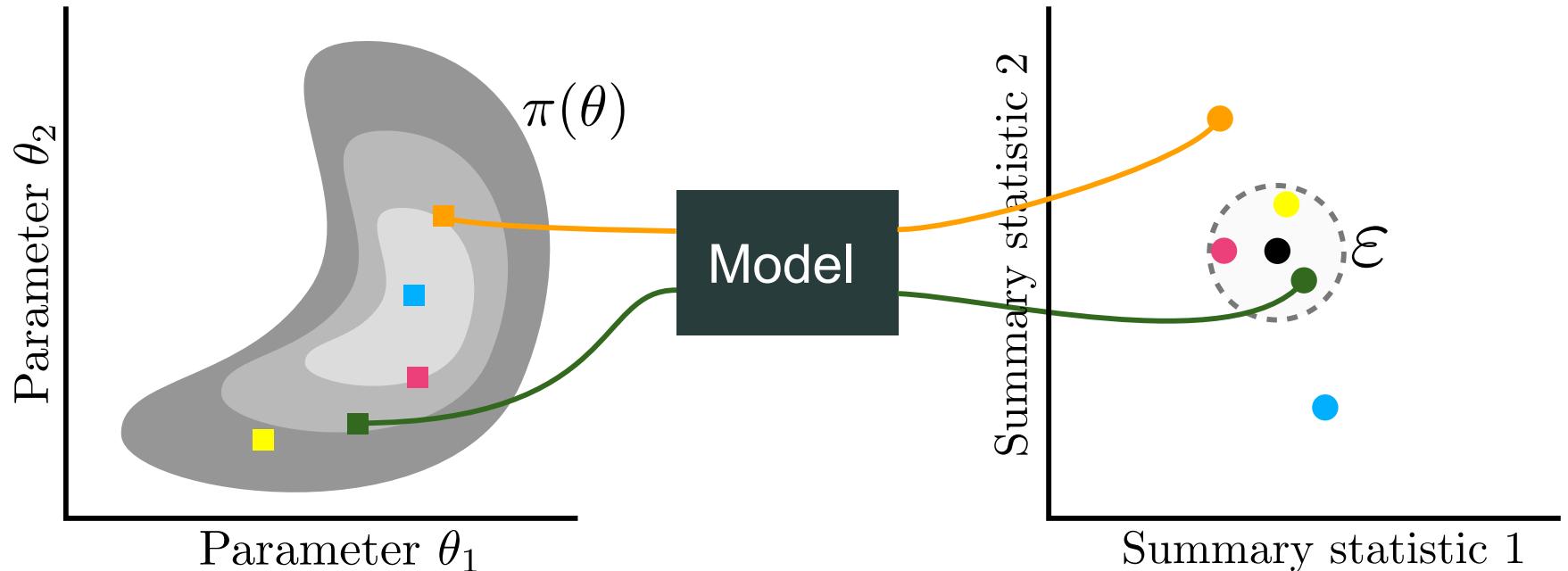
# ABC

likelihood-free approximate Bayesian computation



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likelihood-free approximate Bayesian computation

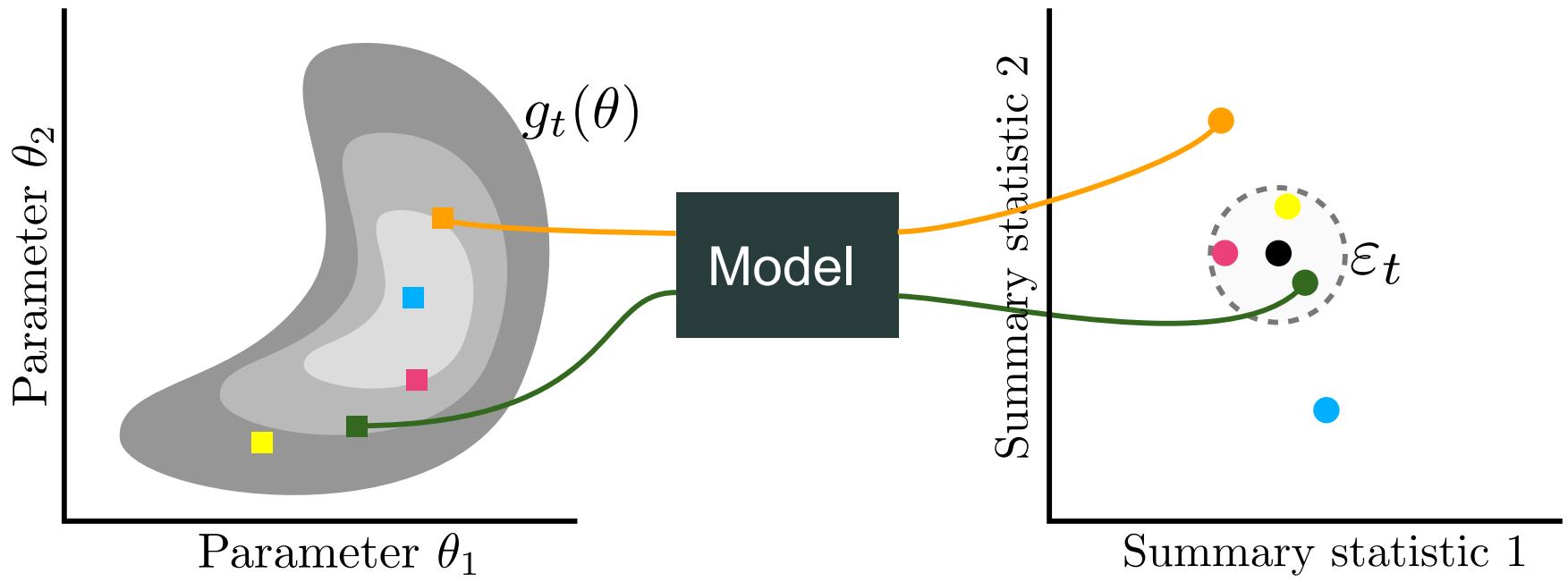


conflicting goals:

- reduce approximation error  $\varepsilon$
- keep high acceptance rates

# ABC-SMC

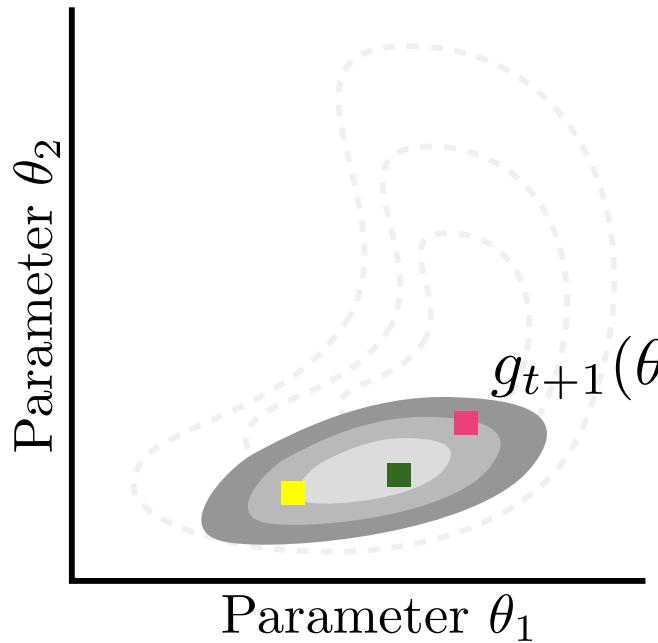
combine with a sequential Monte-Carlo scheme



similar to Toni et al., JRS 2009

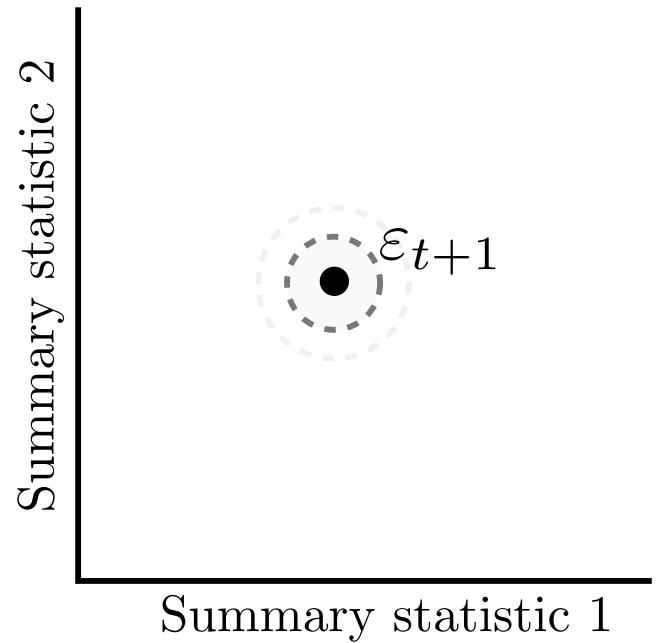
# ABC-SMC

combine with a sequential Monte-Carlo scheme



$$w_t(\theta) \propto \frac{\pi(\theta)}{g_t(\theta)}$$

similar to Toni et al., JRS 2009



## ABC

With distance  $d$ , threshold  $\varepsilon > 0$ , summary statistics  $s$ :

until  $N$  acceptances:

1. sample  $\theta \sim g(\theta)$
2. simulate data  $y \sim \pi(y|\theta)$
3. accept  $\theta$  if  $d(s(y), s(y_{\text{obs}})) \leq \varepsilon$

## A "DERIVATION"

## REJECTION SAMPLING

Background: Want to sample from  $f$ , but can only sample from  $g \gg f$ .

until  $N$  acceptances:

1. sample  $\theta \sim g(\theta)$
2. accept  $\theta$  with probability  $\propto \frac{f(\theta)}{g(\theta)}$

Accepted  $\theta$  are independent samples from  $f(\theta)$ .

Let  $f = \pi(\theta|y_{\text{obs}})$ ,  $g = \pi(\theta) \Rightarrow \frac{\pi(\theta|y_{\text{obs}})}{\pi(\theta)} \propto \pi(y_{\text{obs}}|\theta)$

- not available
- idea: **circumvent likelihood evaluation by simulating data** and matching them to the observed data

## LIKELIHOOD-FREE REJECTION SAMPLING

until  $N$  acceptances:

1. sample  $\theta \sim \pi(\theta)$
2. simulate data  $y \sim \pi(y|\theta)$
3. accept  $\theta$  if  $y = y_{\text{obs}}$

- Acceptance probability:  $\mathbb{P}[y_{\text{obs}}]$
- can be small in particular for continuous data
- idea: accept simulations that are **similar** to  $y_{\text{obs}}$

## ABC-REJECTION

With distance  $d$ , threshold  $\varepsilon > 0$ :

until  $N$  acceptances:

1. sample  $\theta \sim \pi(\theta)$
2. simulate data  $y \sim \pi(y|\theta)$
3. accept  $\theta$  if  $d(y, y_{\text{obs}}) \leq \varepsilon$

- **curse of dimensionality:** if the data are too high-dimensional, the probability of simulating similar data sets is small
- idea: create an informative lower-dimensional representation via **summary statistics**
- ideally minimal sufficient statistics

# APPROXIMATE BAYESIAN POSTERIOR

We want:

$$\pi(\theta | y_{\text{obs}}) \propto p(y_{\text{obs}} | \theta) \pi(\theta)$$

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$$\pi(\theta | y_{\text{obs}}) \propto p(y_{\text{obs}} | \theta) \pi(\theta)$$

We get:

$$\pi_{ABC}(\theta | s(y_{\text{obs}})) \propto \int I(\{d(s(y), s(y_{\text{obs}})) \leq \varepsilon\}) p(y | \theta) dy \pi(\theta) \approx \frac{1}{N} \sum_{i=1}^N \delta_{\theta^{(i)}}(\theta)$$

with distance  $d$ , threshold  $\varepsilon > 0$ , and summary statistics  $s$

## SOURCES OF APPROXIMATION ERRORS IN ABC

- model error (as for every model of reality)
- Monte-Carlo error (as for sampling in general)
- summary statistics
- epsilon threshold

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- summary statistics
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*Far better an approximate answer to the right question, which is often vague, than an exact answer to the wrong question, which can always be made precise.*

John Tukey 1962

# HOW?



[github.com/icb-dcm/pyabc](https://github.com/icb-dcm/pyabc)

Klinger et al., Bioinformatics 2018 and Schälte et al., JOSS 2022



flexible

modular  
configure  
extend



user-friendly

documented  
self-tuning  
robust



scalable

1 to 1,000s cores  
efficient  
tested

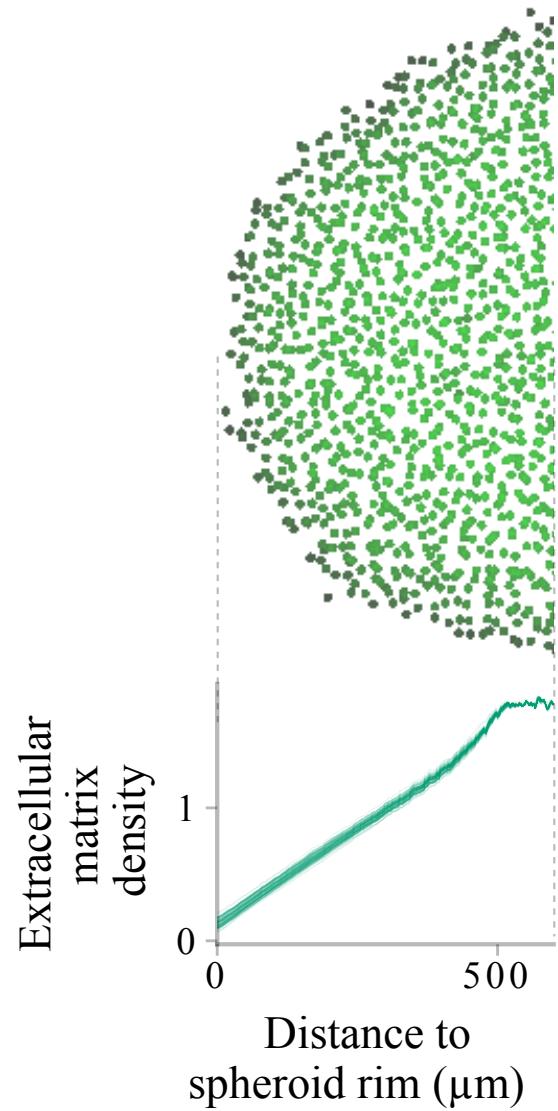
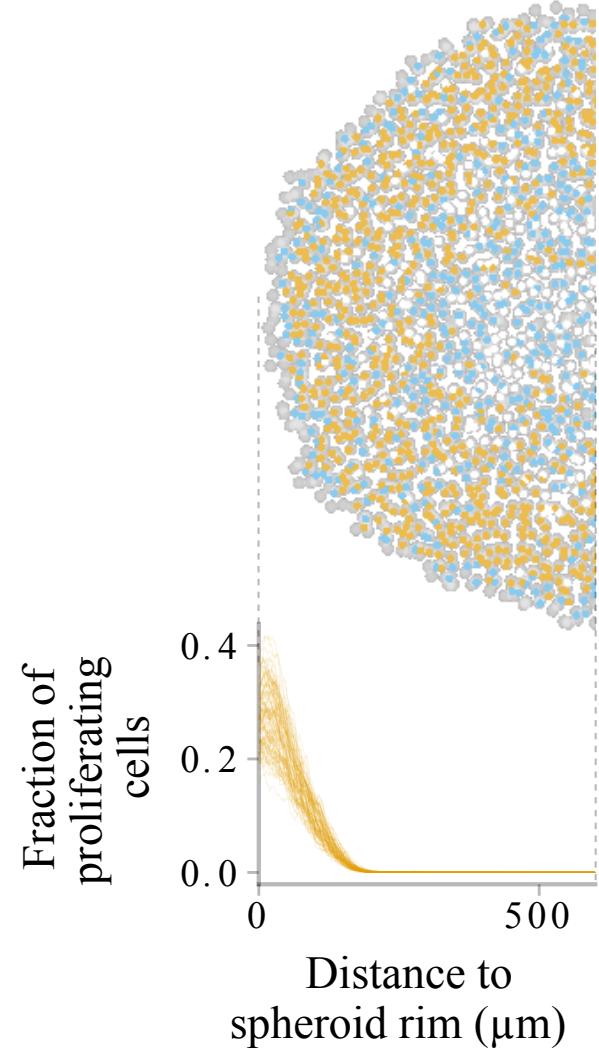
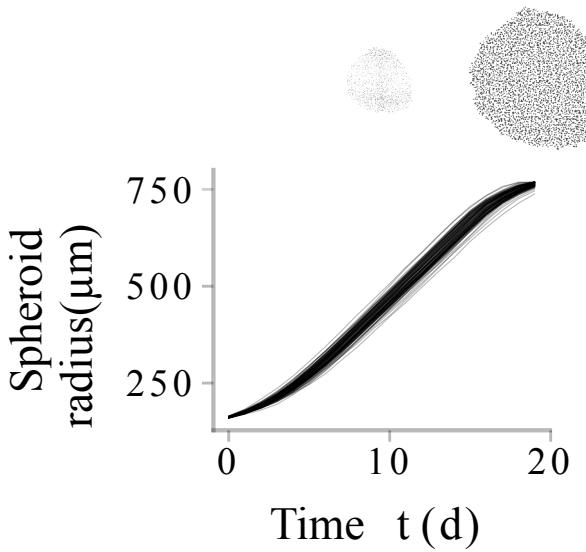
# EASY TO USE

```
1 # define problem
2 abc = pyabc.ABCSMC(model, prior, distance)
3
4 # pass data
5 abc.new(database, observation)
6
7 # run it
8 abc.run()
```

# EXAMPLE: TUMOR GROWTH MODEL

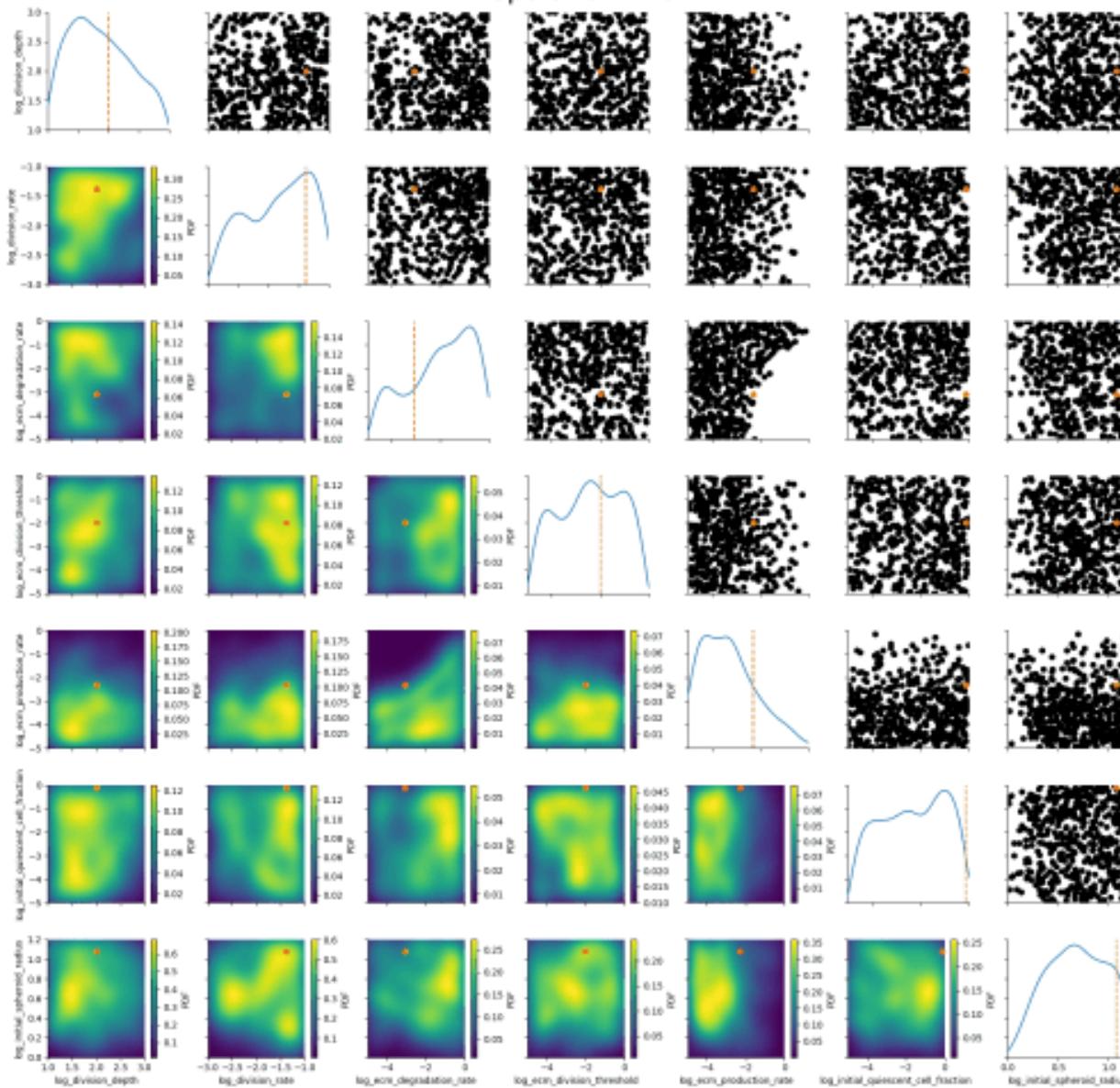
based on Jagiella et al., Cell Systems 2017

# DEFINE SUMMARY STATISTICS



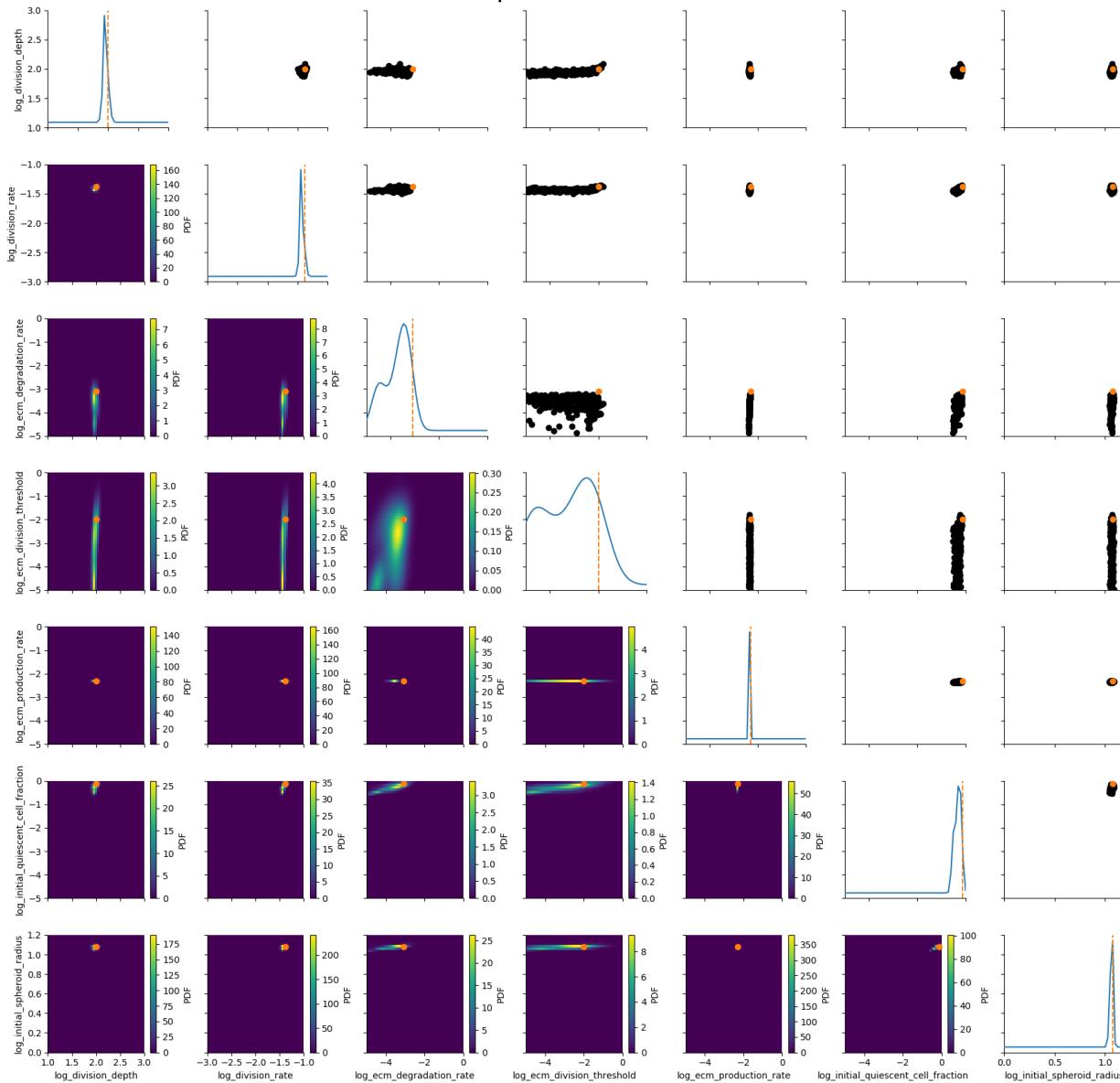
- 
- A photograph of a dense server rack filled with Dell PowerEdge server units. The servers are arranged in a grid pattern, with many blue indicator lights visible on their front panels. The rack has a dark frame and is set against a light-colored wall.
- 400 cores
  - 2 days
  - 1.8e6 simulations

Population t=0

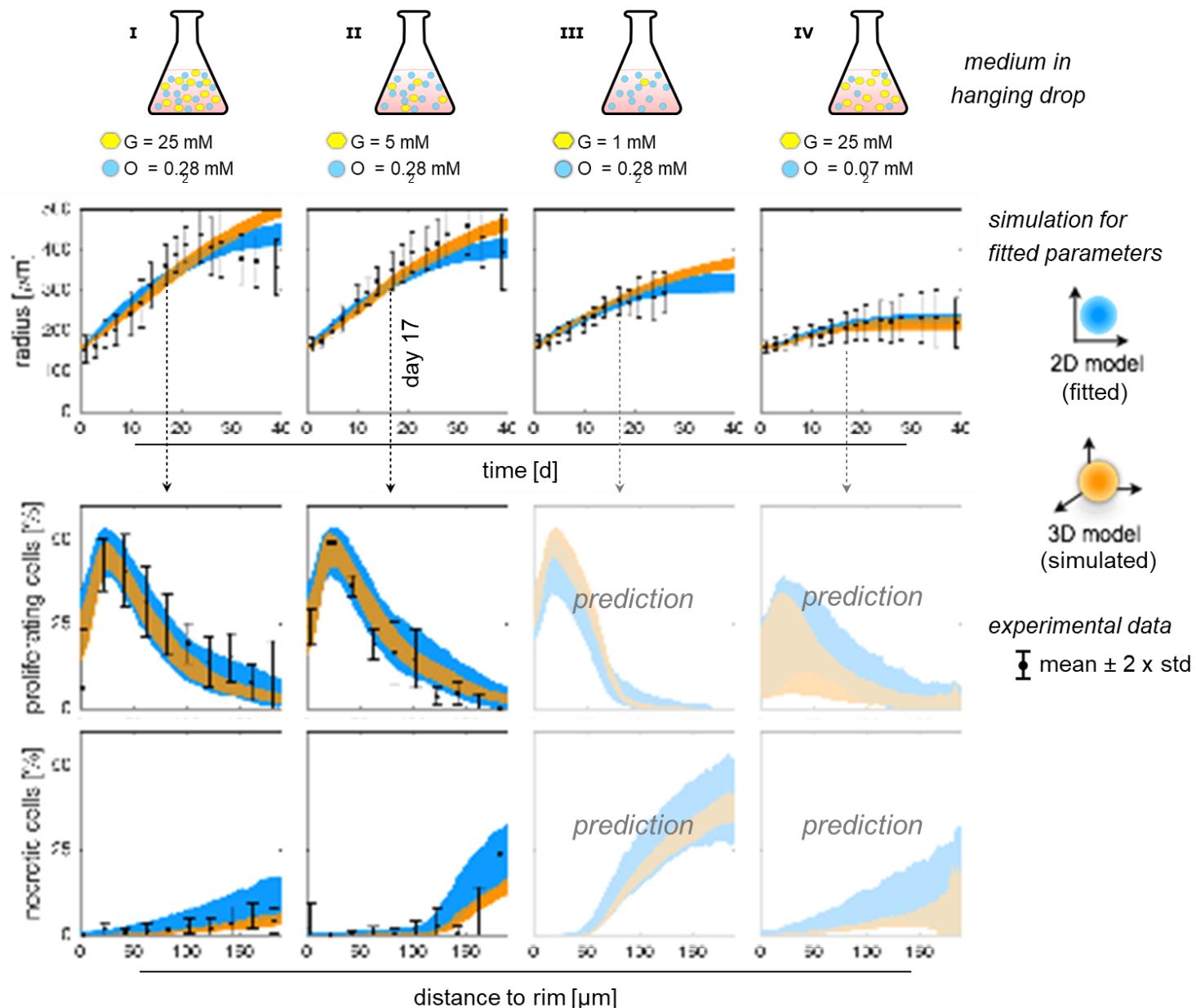


ABC worked where many other methods had failed.

## Population t=37



ABC worked where many other methods had failed.



Uncertainty-aware predictions, easy data integration.

# ALGORITHMIC DETAILS

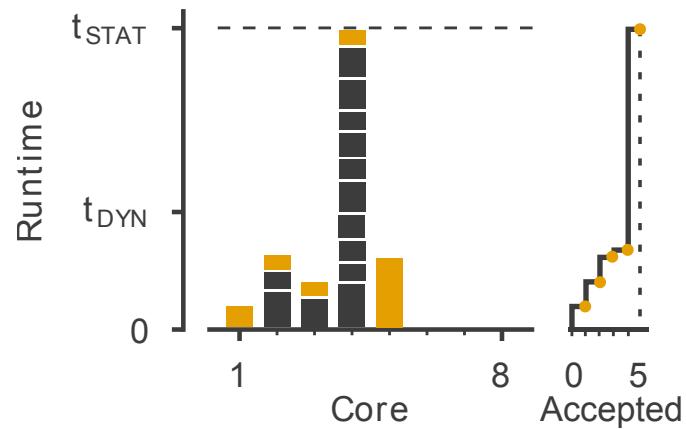
# PARALLEL BACKENDS: 1 TO 1,000S CORES



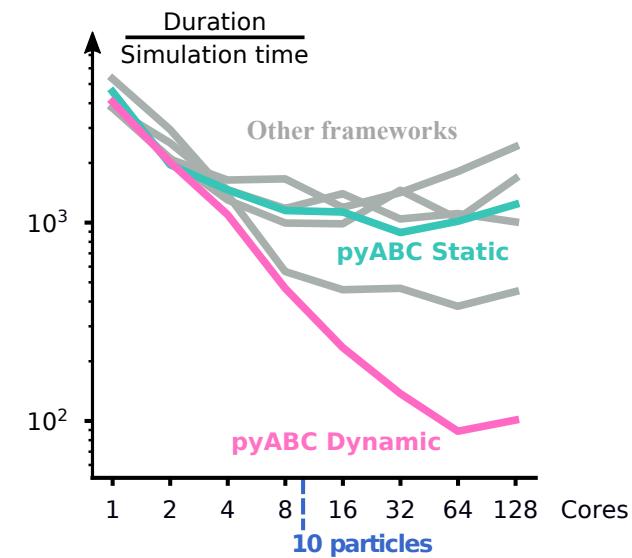
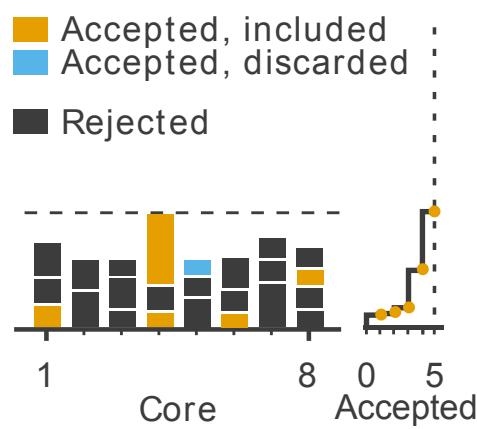
# PARALLELIZATION STRATEGIES

Klinger et al., CMSB Proceedings 2017

Static Scheduling

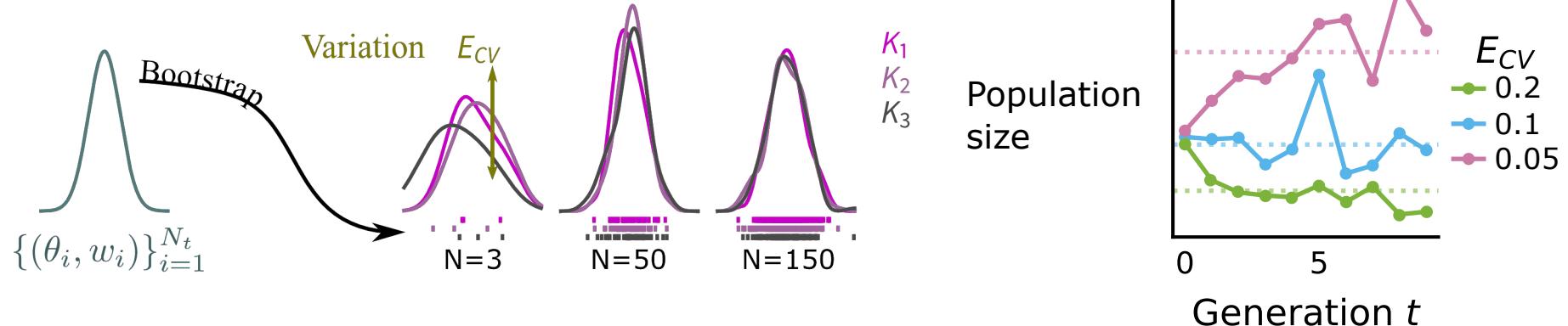


Dynamic Scheduling



# ADAPTIVE POPULATION SIZES

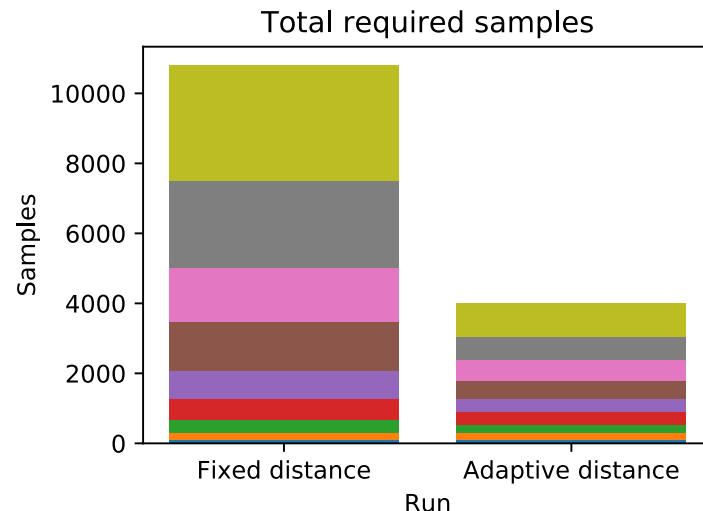
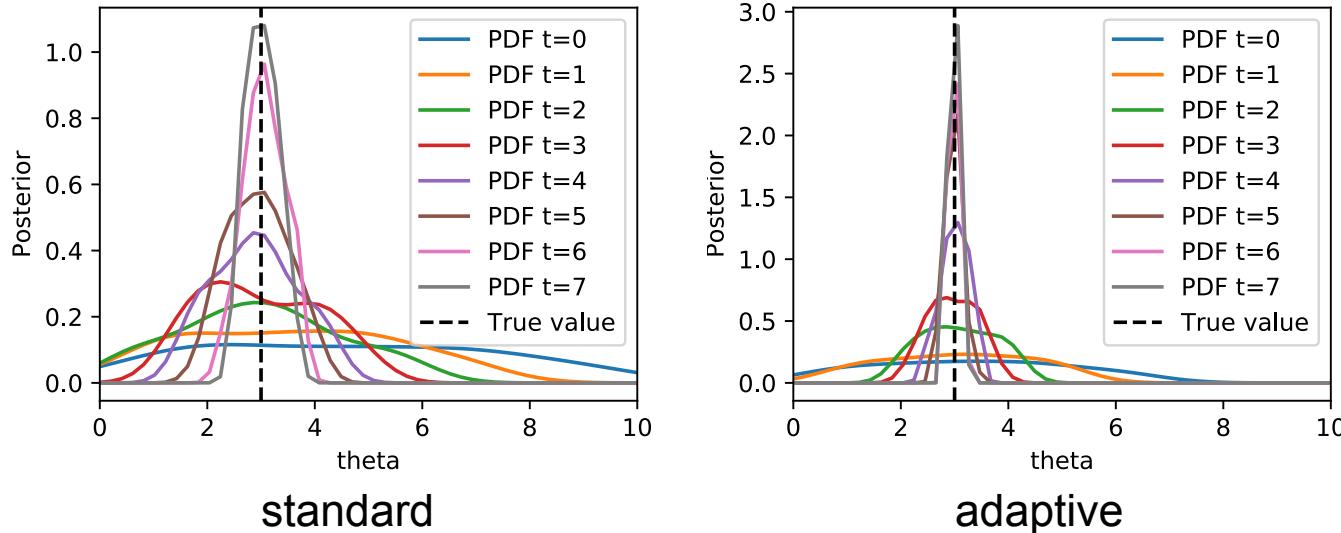
Klinger et al., CMSB Proceedings 2017



idea: adapt population size trying to match a target accuracy

# SELF-TUNING DISTANCE FUNCTIONS

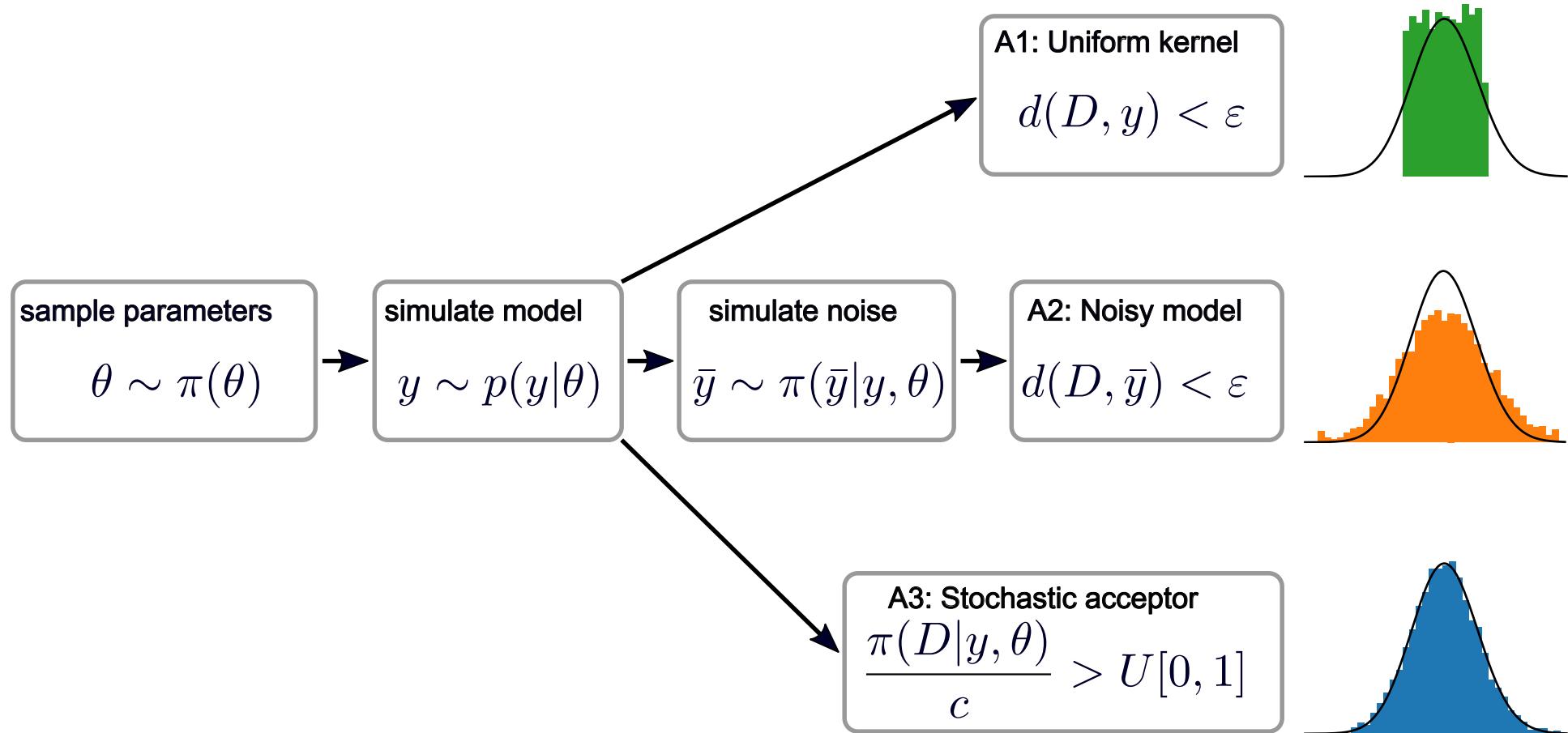
based on Prangle, Bayesian Analysis 2015



# MEASUREMENT NOISE

Schälte et al., Bioinformatics 2020

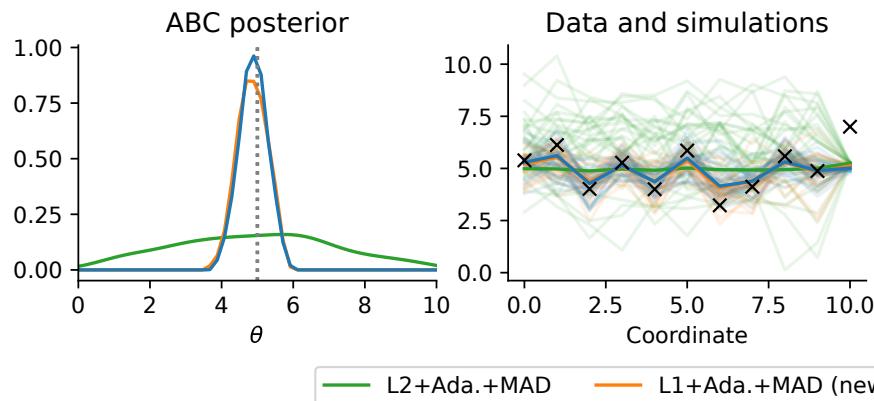
How to efficiently account for measurement noise in ABC?



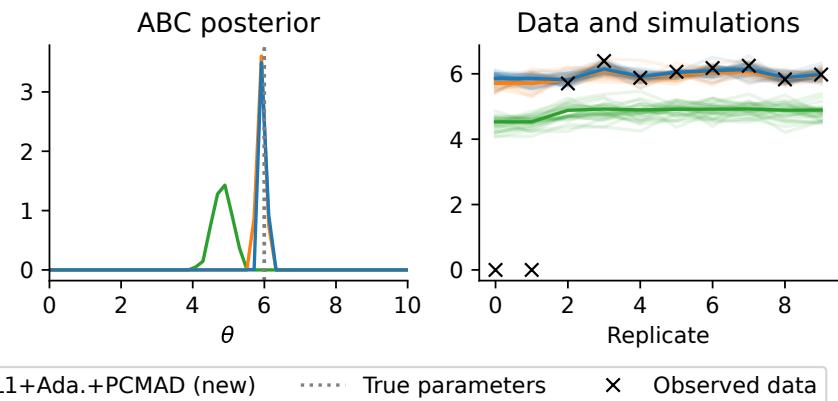
# ROBUSTNESS TO OUTLIERS

Schälte et al., bioRxiv 2021

Model M1: Uninformative outlier

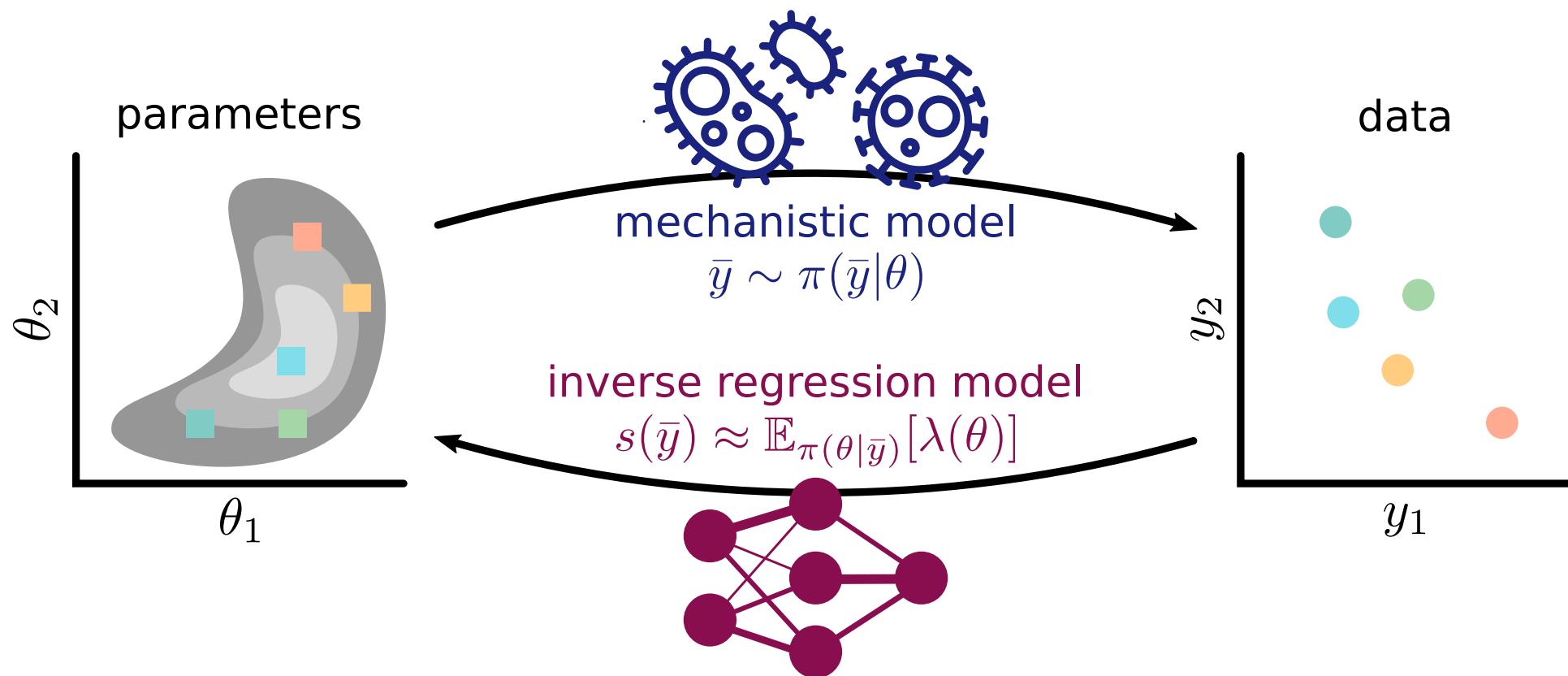


Model M2: Conflicting replicate outliers



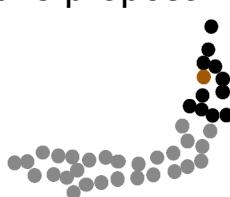
# ASSESS DATA INFORMATIVENESS

based on Fearnhead and Prangle, RSS B 2012  
Schälte and Hasenauer, bioRxiv 2022



# AND ...

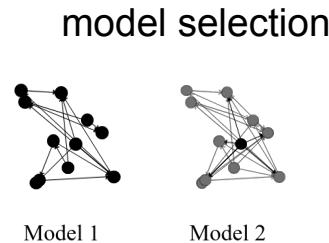
adaptive proposal kernels



adaptive epsilon schedules


$$\varepsilon$$

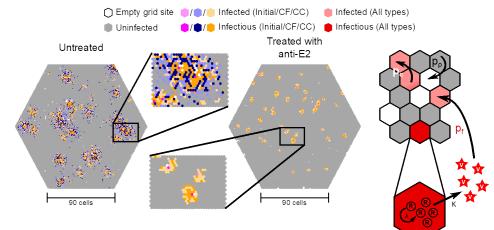
early rejection

$$\sum_i d_i < \varepsilon$$


speaks python, R and julia



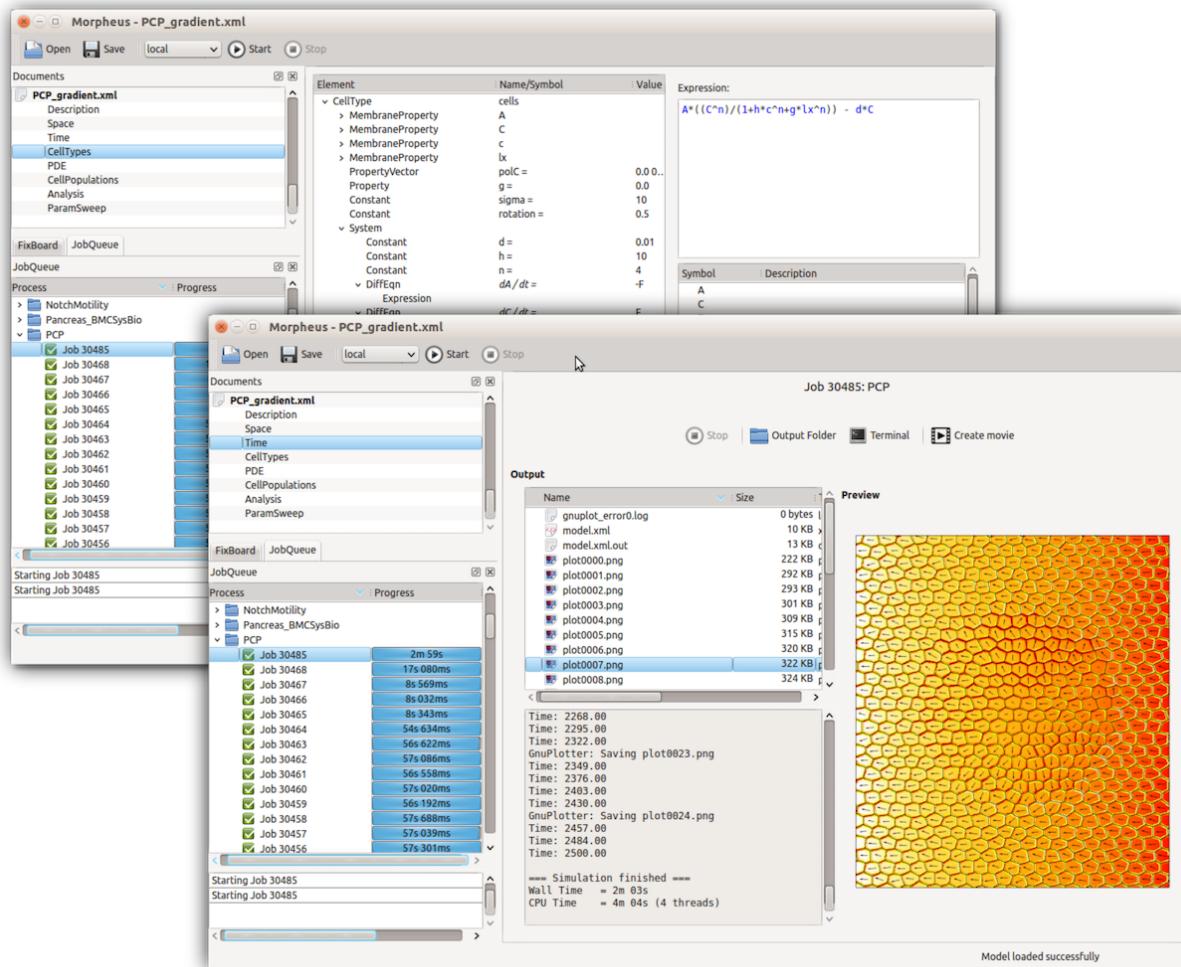
applications



...



Joint initiative to perform inference for multi-cellular models



Morpheus toolbox: Staruß et al., Bioinformatics 2014

# EFFICIENT EXACT ABC WITH NOISE

## THE PROBLEM: (BIOLOGICAL) DATA ARE NOISY

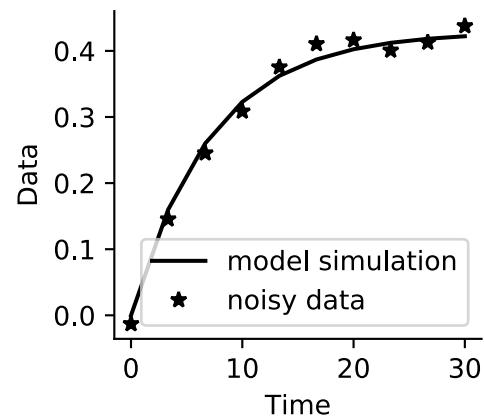


# WHAT HAPPENS WHEN IGNORING NOISE IN ABC?

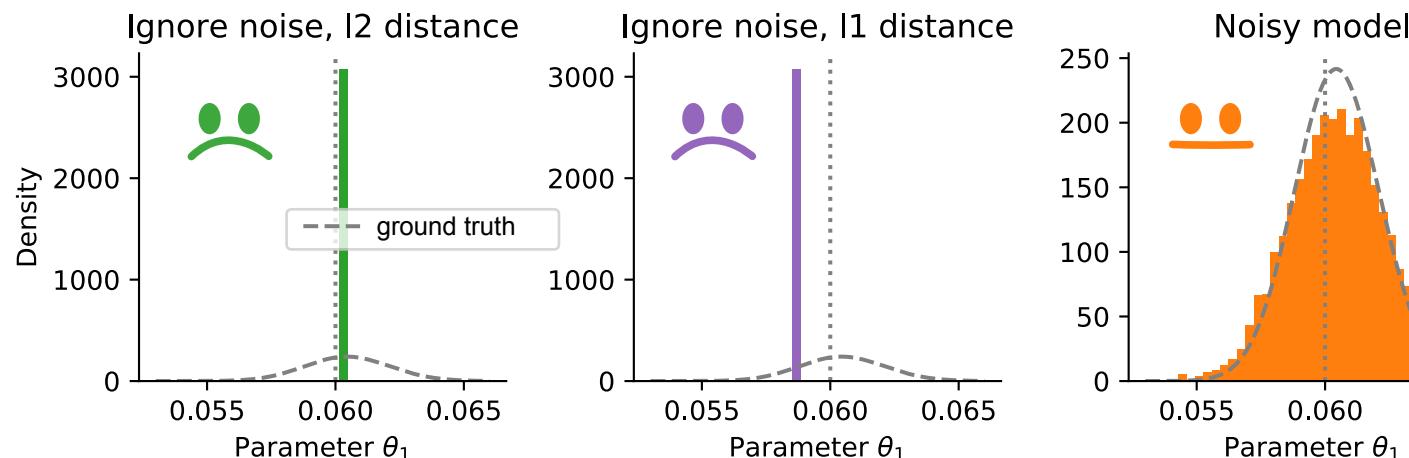
Assume: Model  $y \sim \pi(y|\theta)$  does not account for noise.

But: Measurements are noisy,  $\bar{y}_{\text{obs}} \sim \pi(\bar{y}|y, \theta)$ .

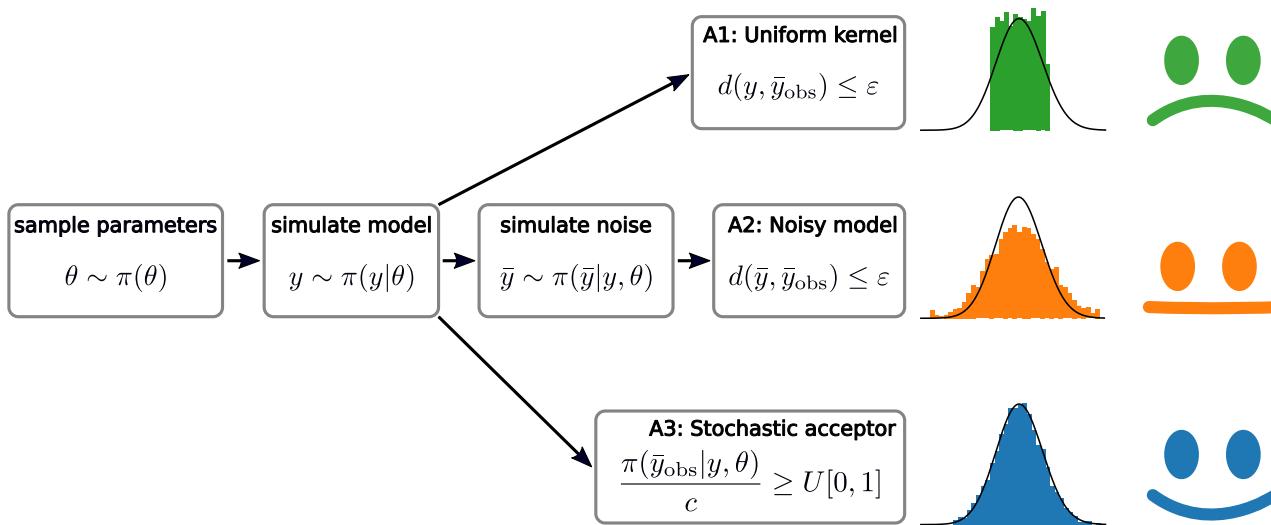
data and simulations



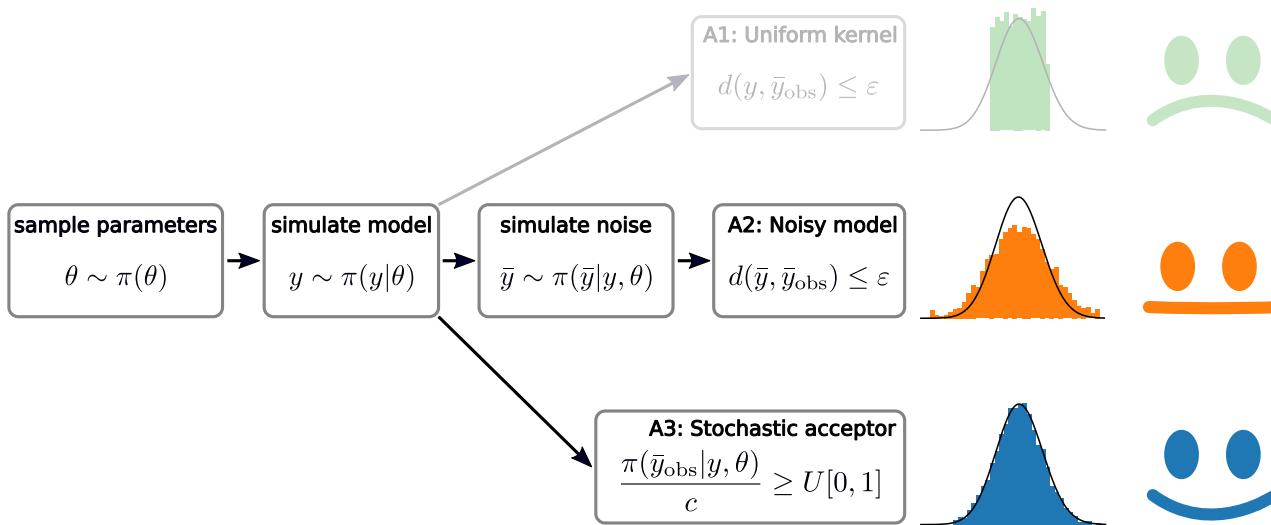
different ABC posteriors



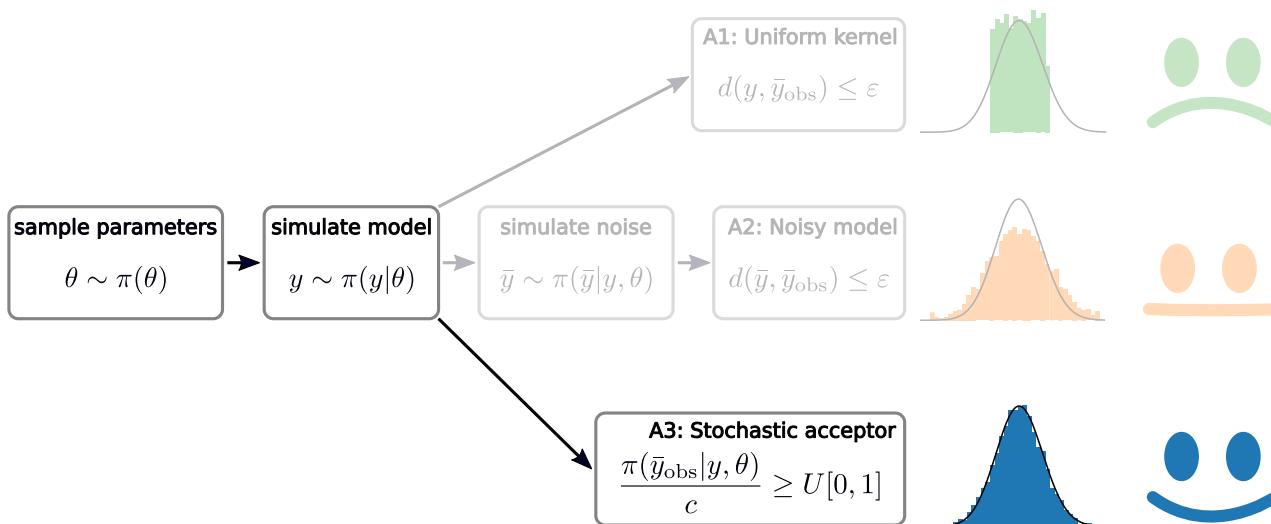
# HOW TO ACCOUNT FOR NOISE?



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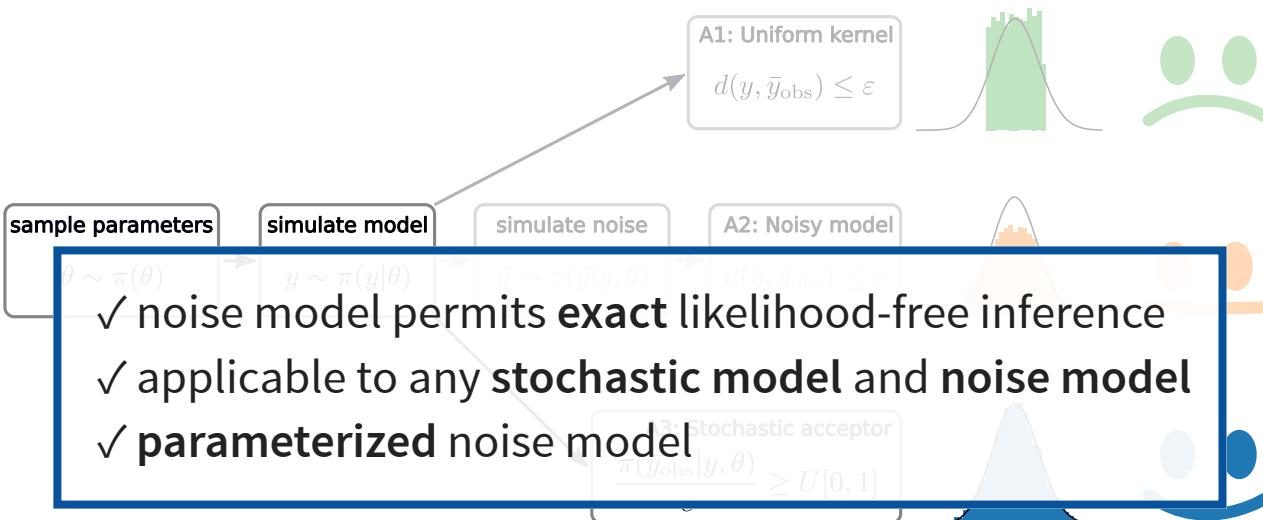
# HOW TO ACCOUNT FOR NOISE?



*“ABC gives exact inference for the wrong model”*

*Richard Wilkinson, Stat. App. Gen. Mol. Bio. 2013*

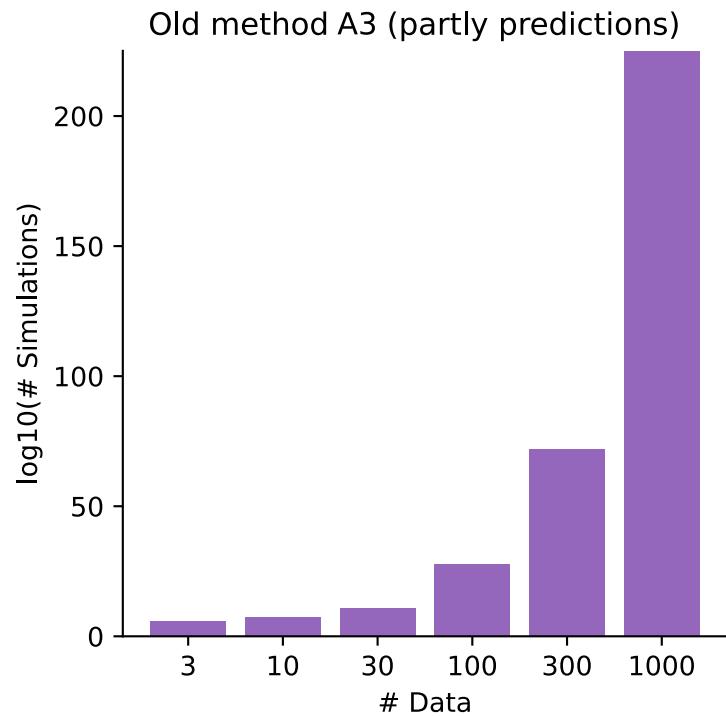
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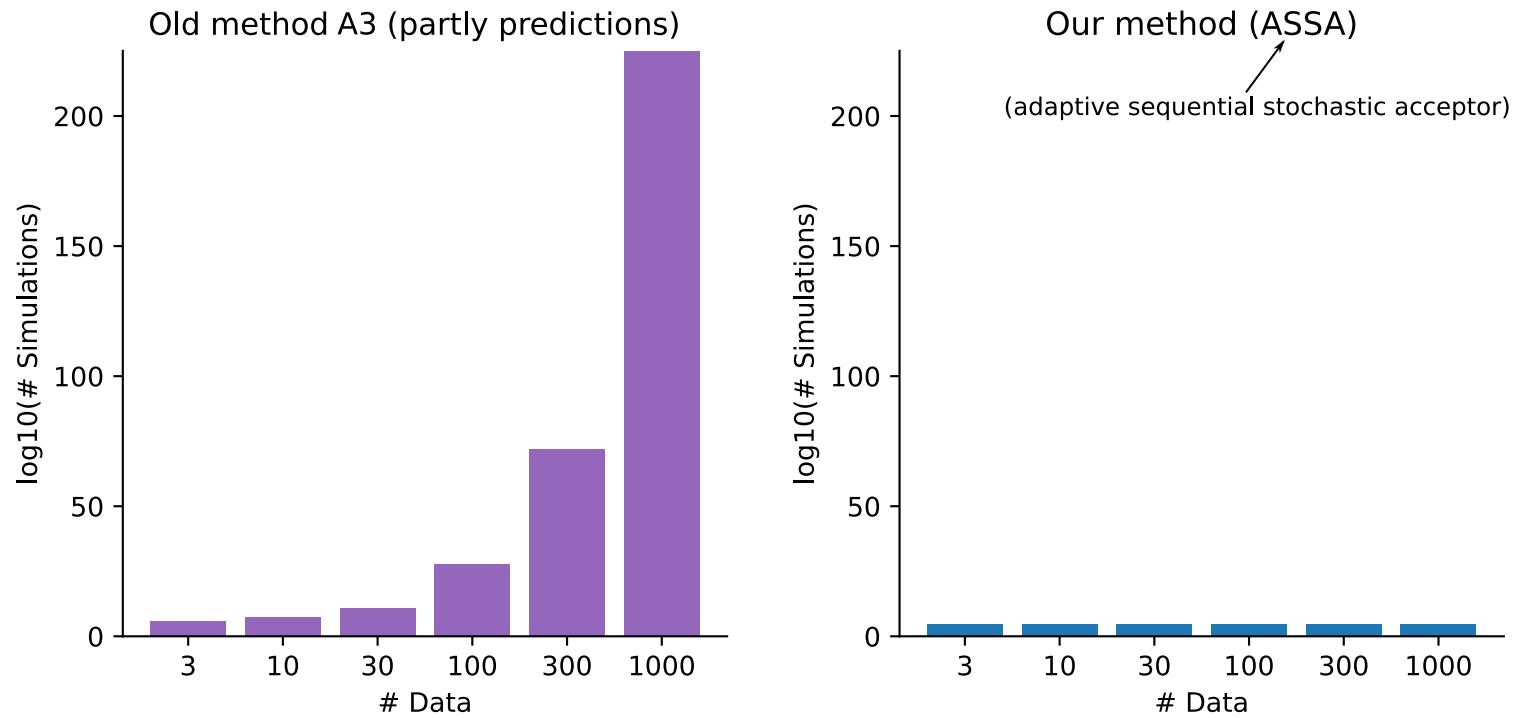
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# PROBLEM: EXISTING METHODS DO NOT SCALE IN PRACTICE



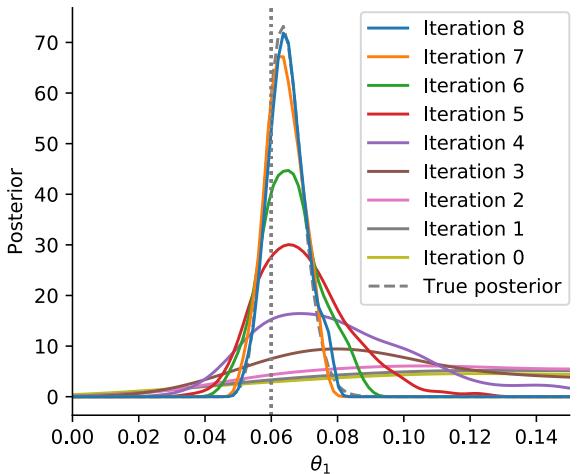
# PROBLEM: EXISTING METHODS DO NOT SCALE IN PRACTICE



# CAN WE MAKE IT MORE EFFICIENT?



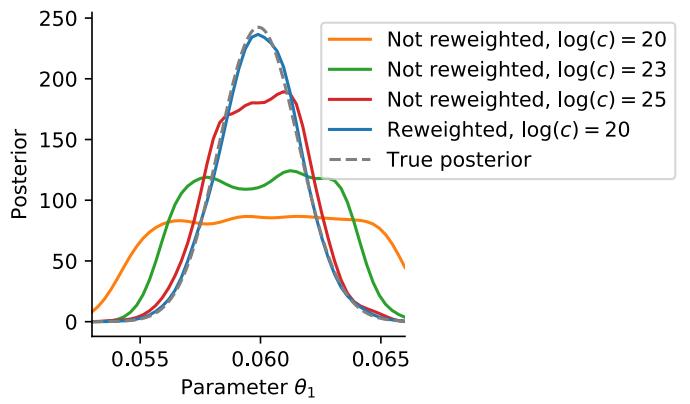
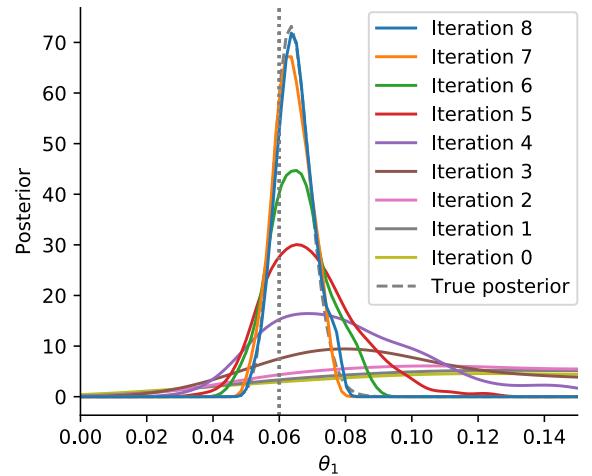
# CAN WE MAKE IT MORE EFFICIENT?



- How to propose parameters?

⇝ integrate in **SMC** via **tempering**,  $\pi(\bar{y}_{\text{obs}} | y, \theta)^{1/T_t}$ .

# CAN WE MAKE IT MORE EFFICIENT?



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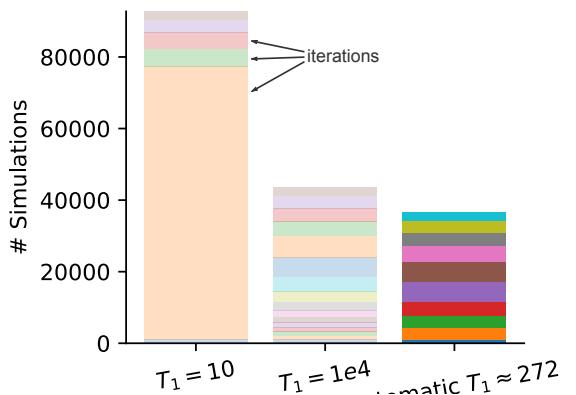
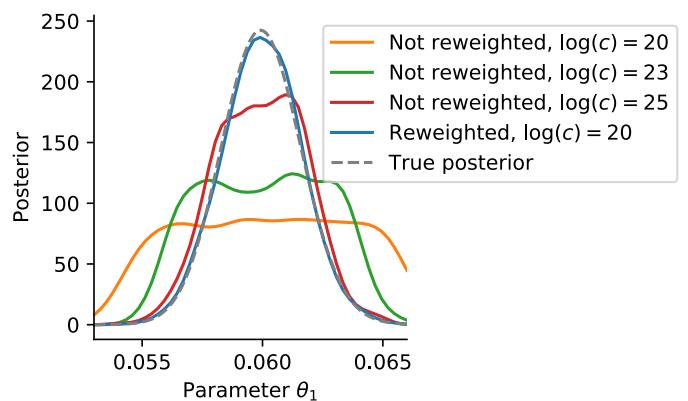
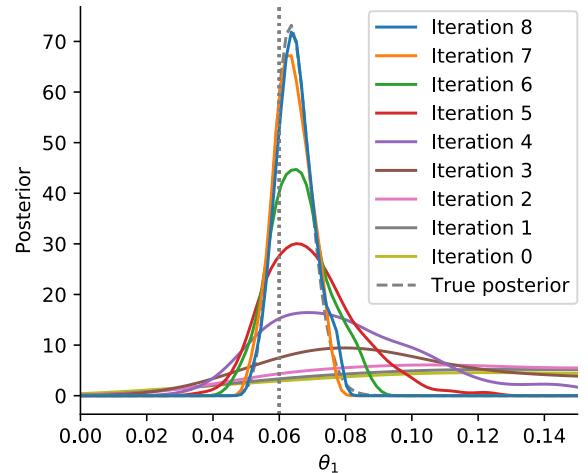
⇝ integrate in SMC via **tempering**,  $\pi(\bar{y}_{\text{obs}}|y, \theta)^{1/T_t}$ .

- How to choose the *normalization c*?

⇝ based on **previous samples**, and avoid decapitation via **reweighting**

$$\tilde{w} := \frac{\left( \frac{\pi(\bar{y}_{\text{obs}}|y, \theta)}{c_t} \right)^{1/T_t}}{\min \left[ \frac{\pi(\bar{y}_{\text{obs}}|y, \theta)}{c_t}, 1 \right]^{1/T_t}} \cdot \frac{\pi(\theta)}{g_t(\theta)}$$

# CAN WE MAKE IT MORE EFFICIENT?



- How to propose parameters?

⇝ integrate in SMC via **tempering**,  $\pi(\bar{y}_{\text{obs}}|y, \theta)^{1/T_t}$ .

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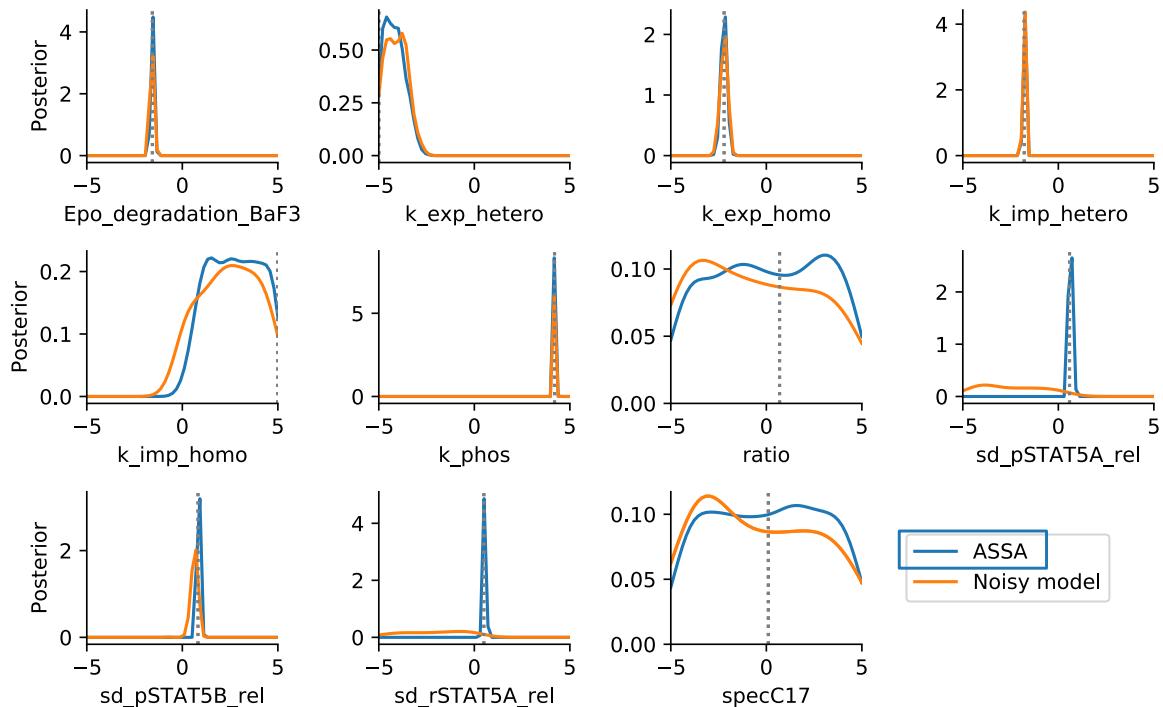
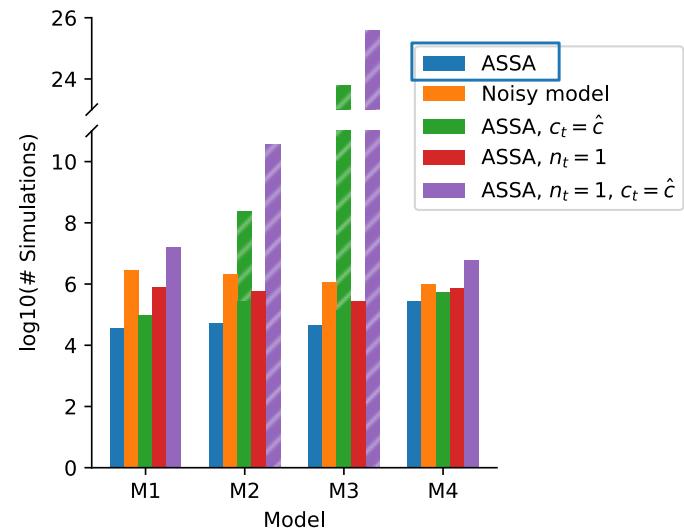
$$\tilde{w} := \frac{\left( \frac{\pi(\bar{y}_{\text{obs}}|y, \theta)}{c_t} \right)^{1/T_t}}{\min \left[ \frac{\pi(\bar{y}_{\text{obs}}|y, \theta)}{c_t}, 1 \right]^{1/T_t}} \cdot \frac{\pi(\theta)}{g_t(\theta)}$$

- How to choose the temperatures  $T_p, t = 1, \dots, n_t$ ?
  - ⇝ **predict the acceptance rate**

$$\gamma = \int \left( \int \min \left[ \left( \frac{\pi(\bar{y}_{\text{obs}}|y, \theta)}{c_t} \right)^{1/T}, 1 \right] \pi(y|\theta) dy \right) g_t(\theta) d\theta$$

(esp. allows choosing  $T_1$ )

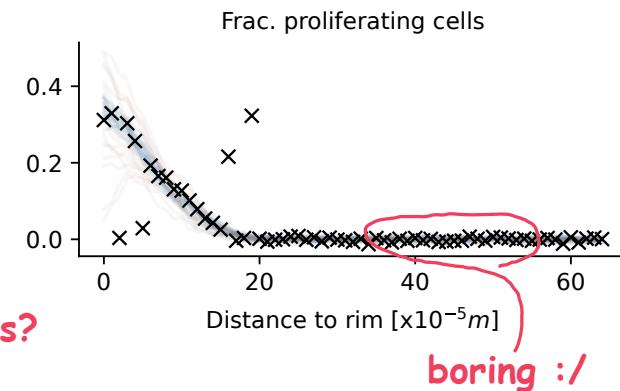
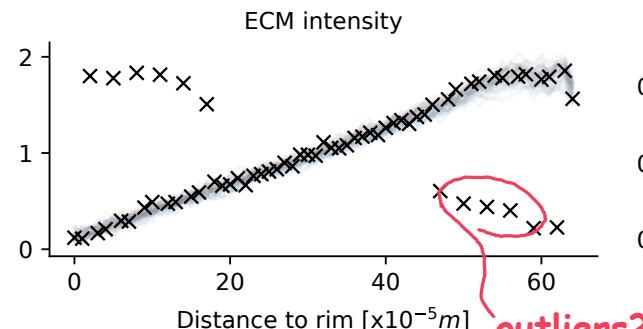
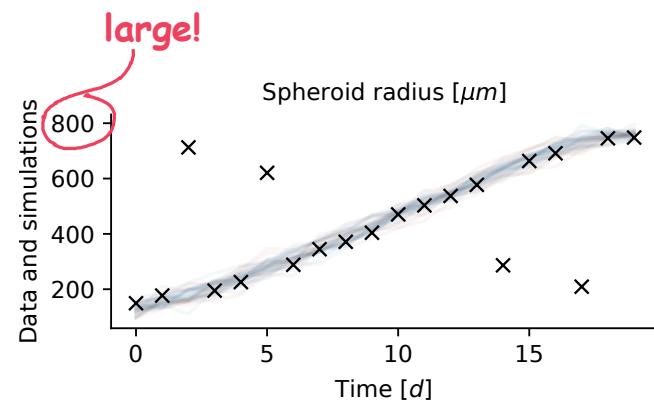
# EVALUATION



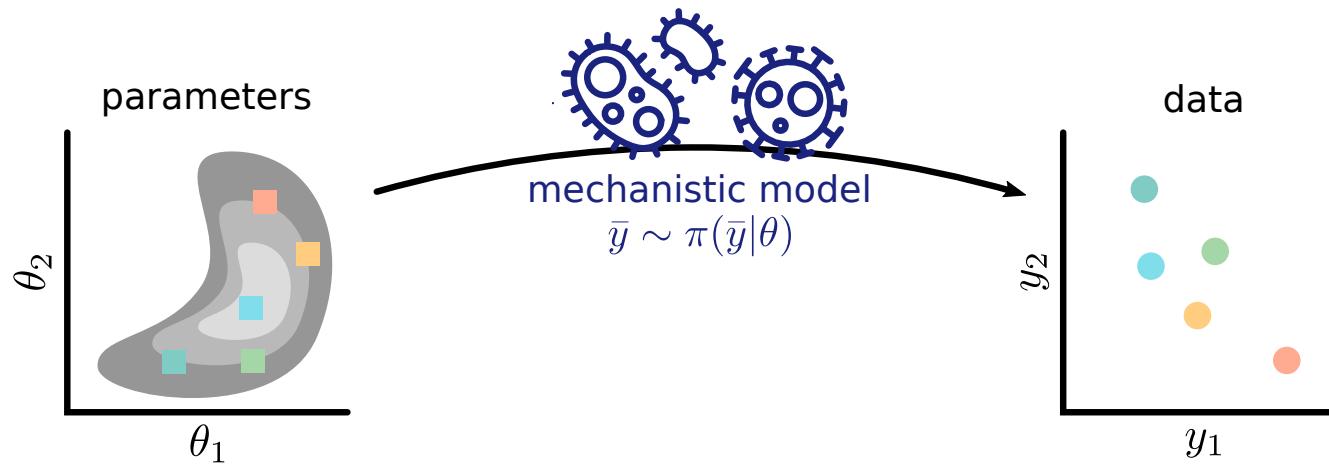
- ✓ Applicable to **various model and noise model types**
- ✓ orders of magnitude **speed-up**
- ✓ **scales** to challenging application problems

# ROBUST AND EFFICIENT ABC VIA INVERSE MACHINE LEARNING MODELS

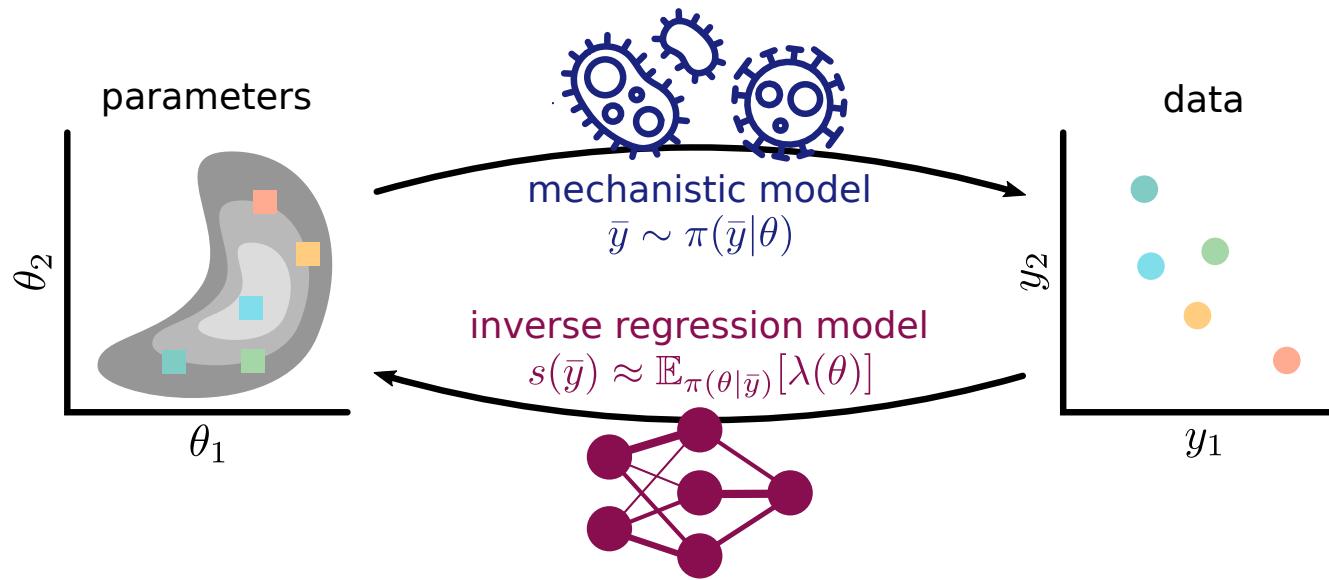
# THE PROBLEM: FITTING HETEROGENEOUS DATA



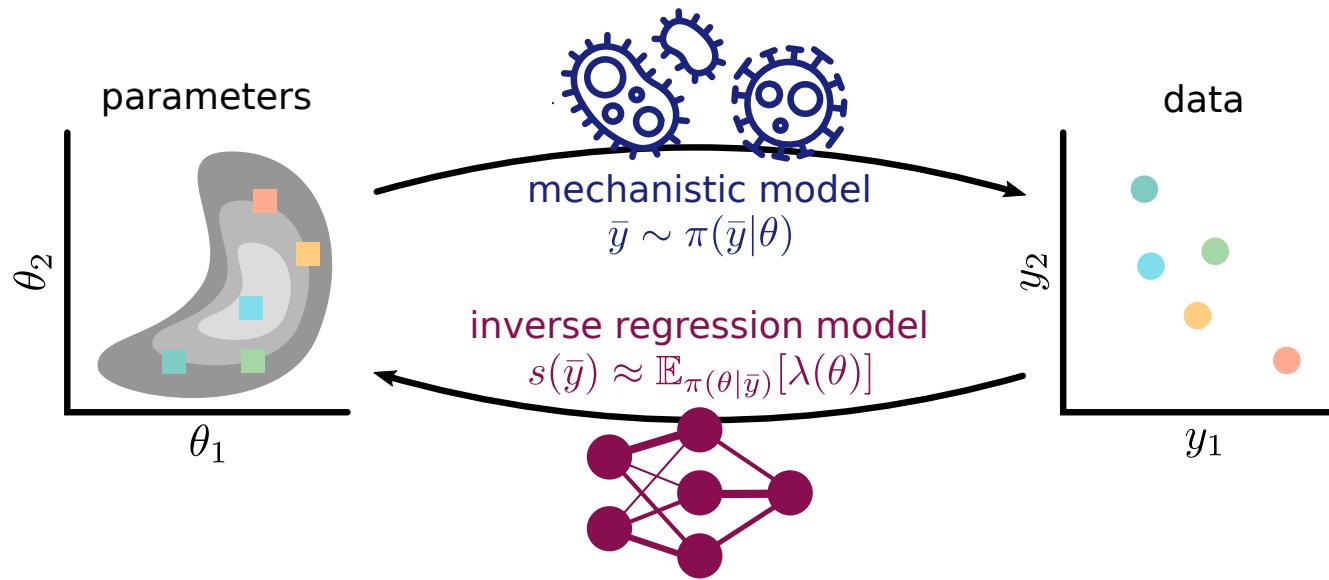
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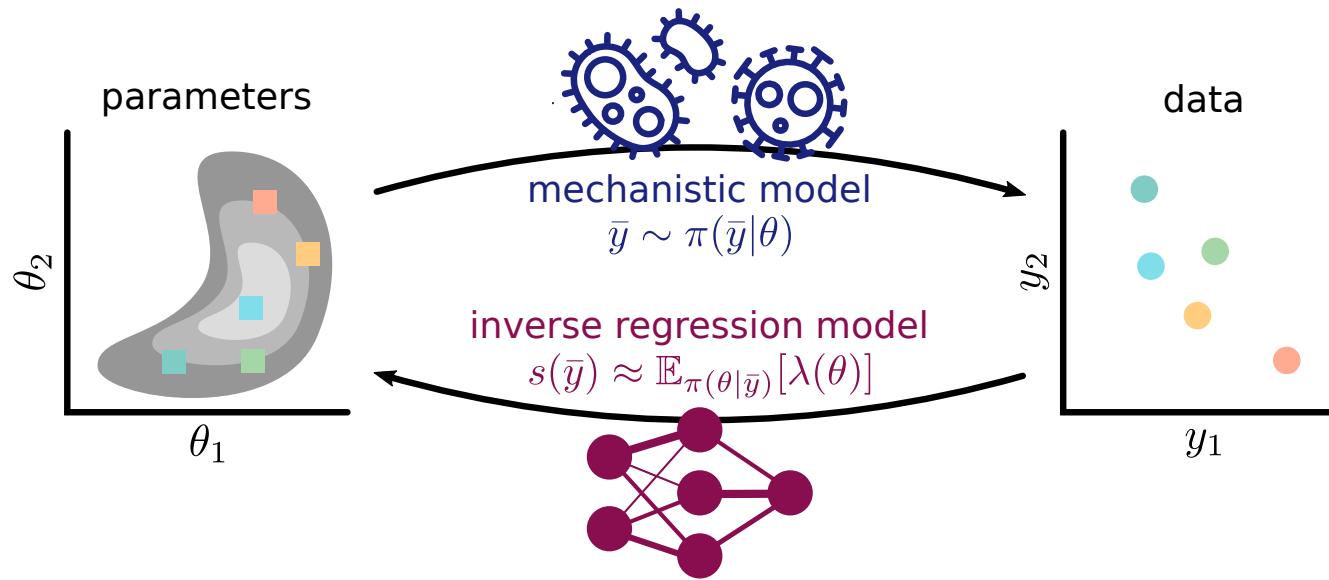


# HOW TO ACCOUNT FOR DATA INFORMATIVENESS?



- construct low-dimensional **summary statistics** (see Fearnhead & Prangle, JRSS 2012)

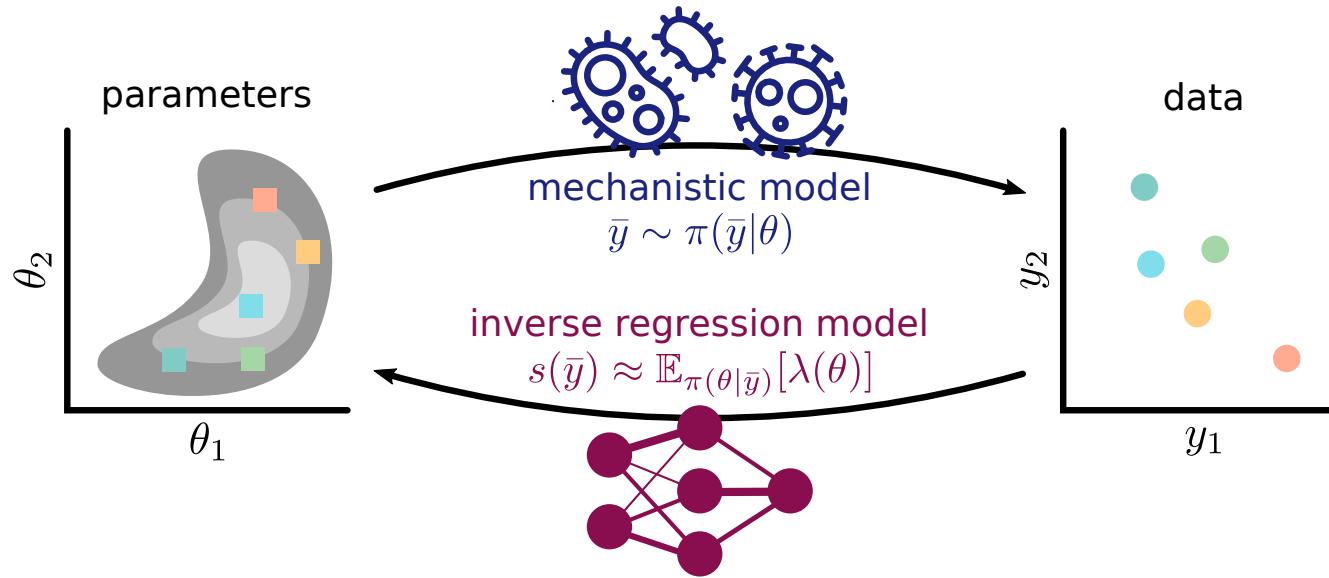
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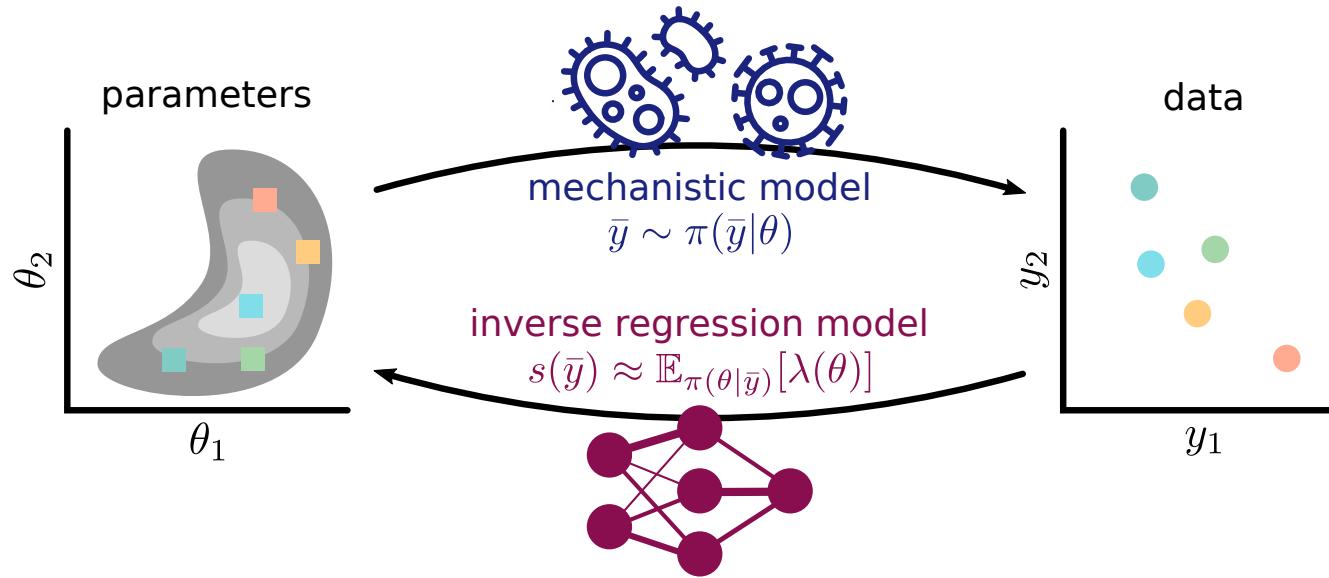
- or: define **sensitivity weights** via the sensitivity matrix  $S = \nabla_{\bar{y}} s(\bar{y}_{\text{obs}})$ ,  $q_{i_y} = \sum_{i_\theta=1}^{n_\theta} \frac{|S_{i_y i_\theta}|}{\sum_{j_y=1}^{n_y} |S_{j_y i_\theta}|}$

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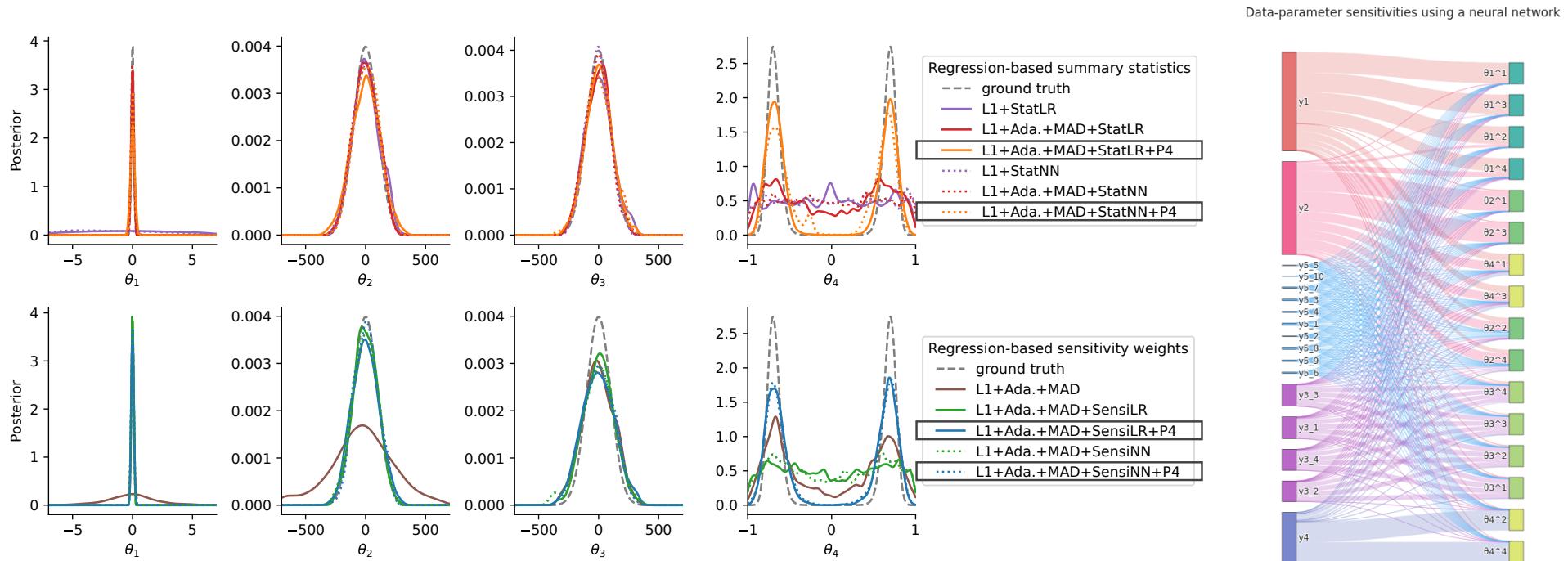
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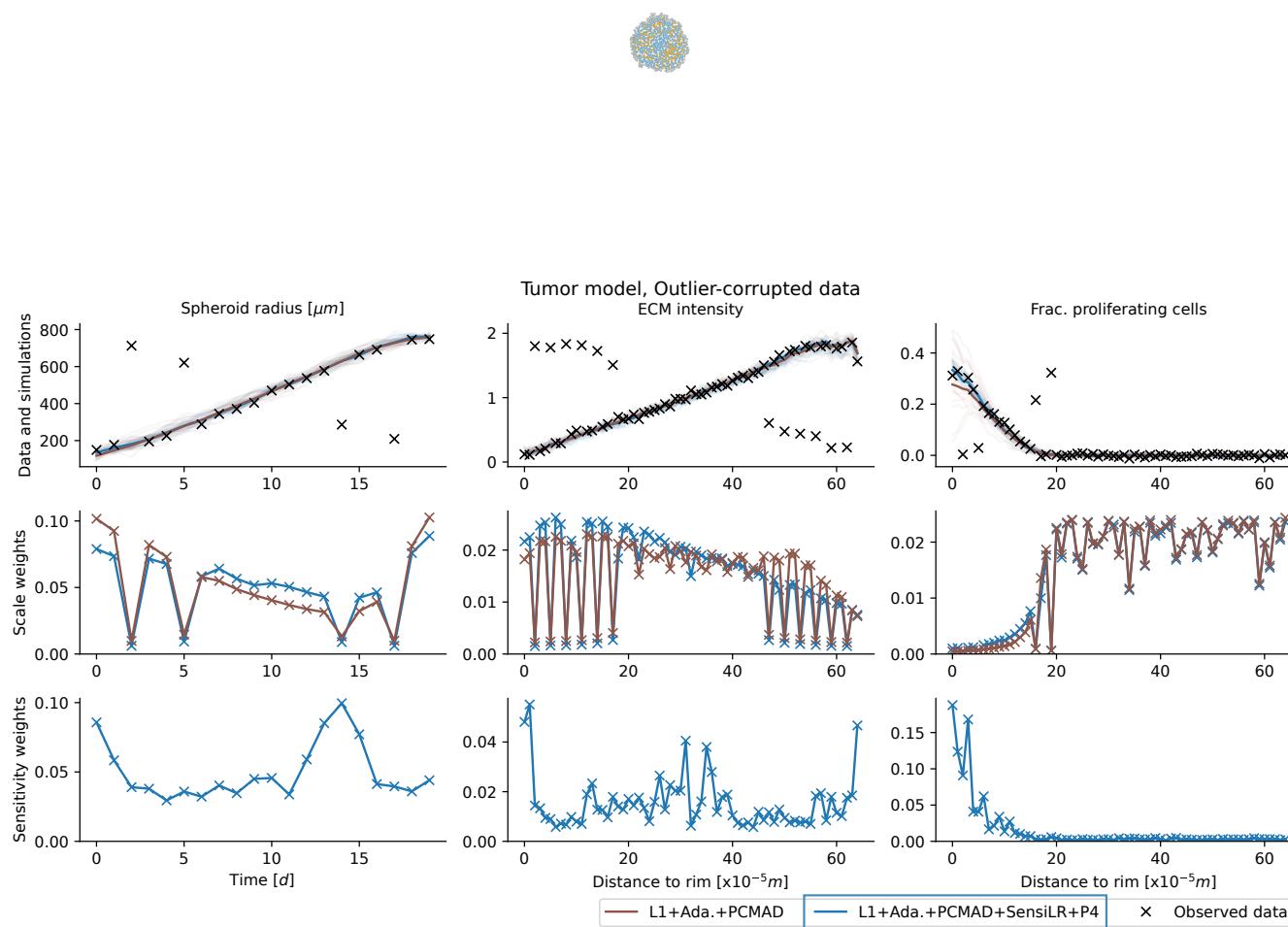
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- **combine** with scale normalization and outlier correction via **adaptive weighting** in an **SMC** framework
- learn functions of parameters  $\lambda(\theta)$  to capture **higher-order moments**

# EVALUATION: SIMPLE TEST MODEL



- ✓ only **combination** of scale normalization, informativeness assessment, and regression target augmentation permits accurate inference
- ✓ sensitivity weights give further **insights**

# EVALUATION: AGENT-BASED TUMOR SPHEROID MODEL



✓ can via sensitivity weighting in **complex application** simultaneously account for informativeness and outliers

# LIVE DEMO

The screenshot shows a web browser displaying the pyABC documentation at [pyabc.readthedocs.io/en/latest/examples/parameter\\_inference.html](https://pyabc.readthedocs.io/en/latest/examples/parameter_inference.html). The page title is "Parameter inference". The left sidebar contains a navigation menu with sections like "USER'S GUIDE", "Examples", "Algorithms and features", "ABOUT", etc. The main content area shows a code snippet for installing the package:

```
[1]: # install if not done yet  
!pip install pyabc --quiet
```

Below the code, there is a note: "Let's start by importing the necessary packages:" followed by another code snippet:

```
[2]: import os  
import tempfile  
  
import matplotlib.pyplot as plt  
import numpy as np  
  
import pyabc  
  
pyabc.settings.set_figure_params('pyabc') # for beautified plots
```

At the bottom of the page, there are navigation links for "Previous" and "Next".

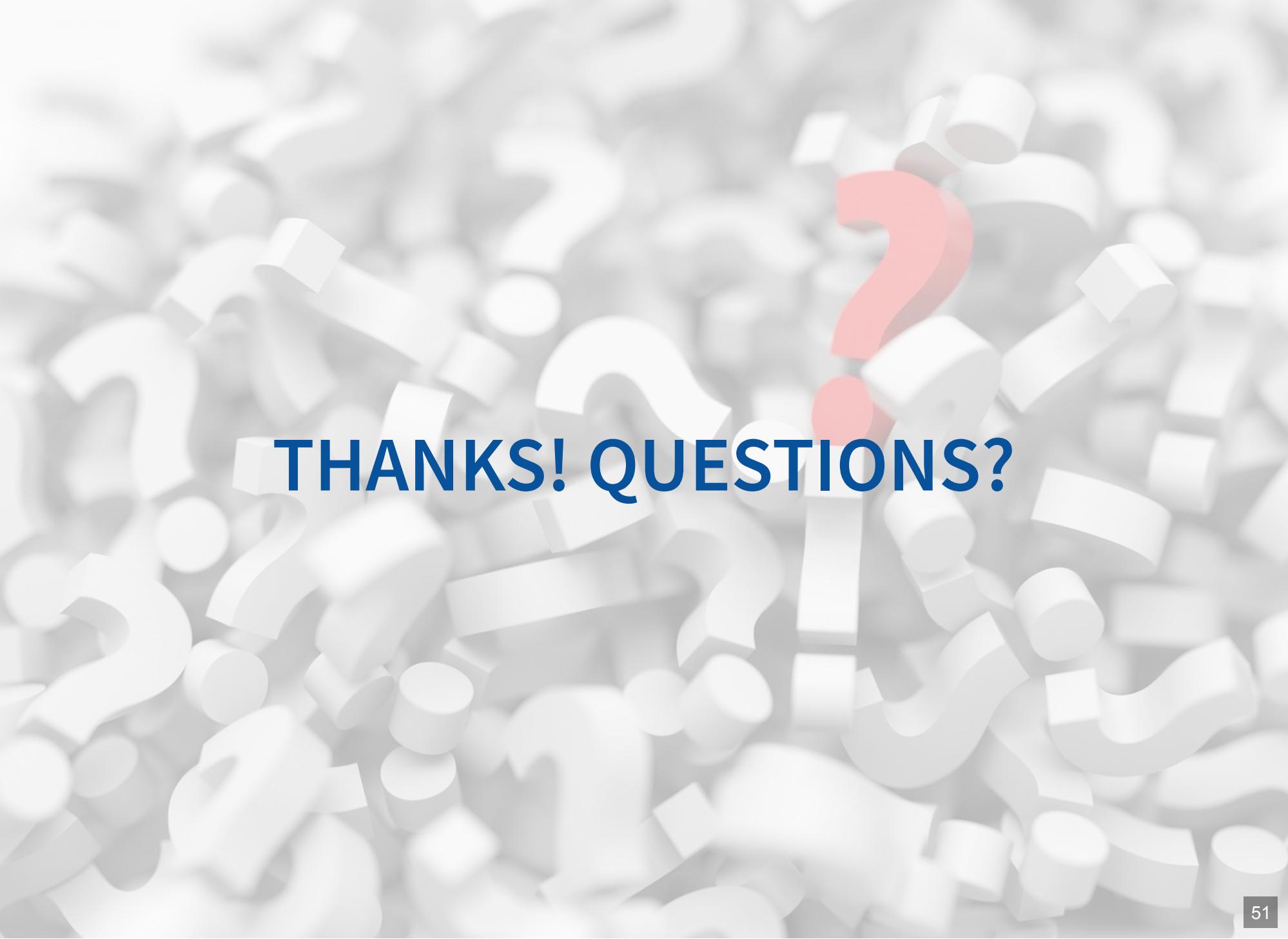
# SUMMARY

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- parameter estimation when we cannot evaluate the likelihood is challenging
- ABC allows for reliable statistical inference
- pyABC provides an easy-to-use framework



Not everything is a nail.



**THANKS! QUESTIONS?**