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# Noise Up Your ABC

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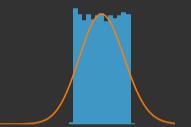
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## Graphical abstract

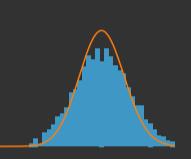
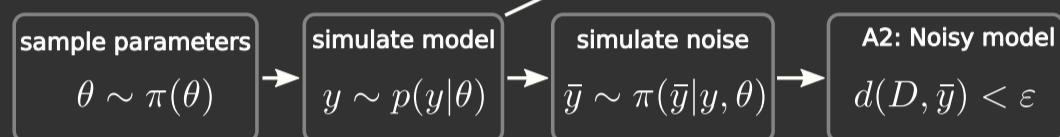
the problem



A1: Uniform kernel  
 $d(D, y) < \varepsilon$



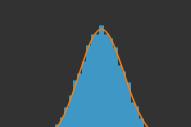
the solutions



make it efficient



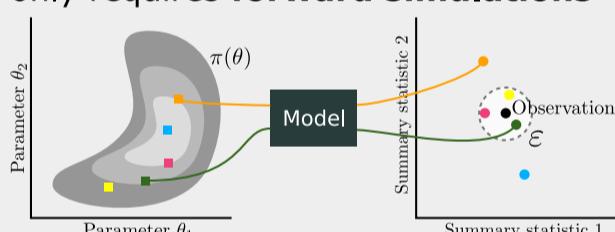
A3: Stochastic acceptor  
 $\frac{\pi(D|y, \theta)}{c} > U[0, 1]$



ABC + noise  
= exact

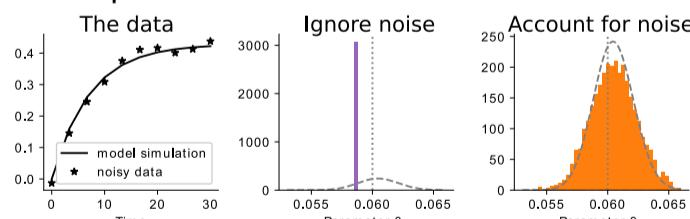
## Mini-Intro: Rejection ABC

- Approximate Bayesian Computation enables **likelihood-free inference**
- only requires **forward simulations**



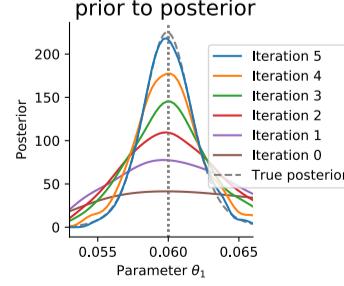
## Measurement noise in ABC

- experimental data usually noise corrupted
- easy to ignore → **wrong estimates**
- **modified acceptor** (A3) yields **exact likelihood-free inference** from the true posterior



## Integrate in sequential ABC

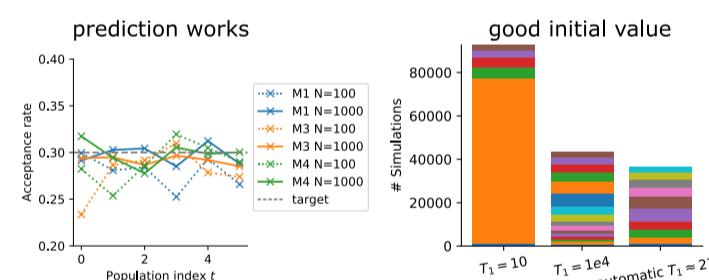
- problem: Rejection ABC **inefficient**  
→ use ABC-SMC (Sequential Monte Carlo)
- instead of  $\varepsilon$ , **temperate** via  $T_t \downarrow 1$



$$\pi_{ABC,t}(\theta|D) \propto \int \pi(D|y, \theta)^{1/T_t} p(y|\theta) dy \cdot \pi(\theta)$$

## Choose temperatures

- problem: **sensitive** to initial temperature
- idea: **predict** the next population's **acceptance rate**
- choose  $T_t$  (esp.  $T_1$ ) to match a **target rate**



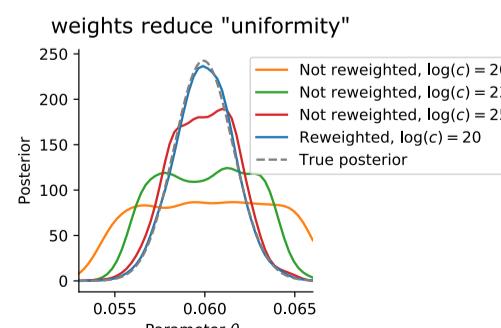
## Automatically find a good $c$

- problem: normalization constant  $c$  **affects acceptance rate**
- idea: **update**  $c$  after each iteration
- **avoid bias**: accept with probability

$$\min \left[ \frac{\pi(D|y, \theta)}{c_t}, 1 \right]^{1/T_t}$$

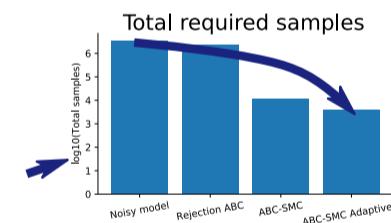
and **re-weight** by

$$w(y, \theta) \propto \frac{\pi(D|y, \theta)^{1/T_t}}{\min \left[ \left( \frac{\pi(D|y, \theta)}{c_t} \right)^{1/T_t}, 1 \right]} \cdot \frac{\pi(\theta)}{g_t(\theta)}$$



## (More) Results

- applied to various model types (ODEs, SDEs, MJPs, ABMs)
- with Gaussian, Laplace, Binomial noise
- orders of magnitude speedups, enabling exact inference for the first time



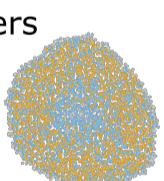
- can estimate noise parameters
- hardly any tuning necessary
- scales to expensive multi-scale models

► scalable, modular implementation in the toolbox pyABC



<https://github.com/icb-dcm/pyabc>

- manuscript: <https://doi.org/10.1093/bioinformatics/btaa397>
- further info: [https://yannikschaelte.github.io/pres\\_ismb2020](https://yannikschaelte.github.io/pres_ismb2020)



## Future

- model selection via thermodynamic integration
- directly target distribution scale parameters
- optimize temperature scheme
- applied in FitMultiCell projects