

Genealogies of sequential Monte Carlo algorithms

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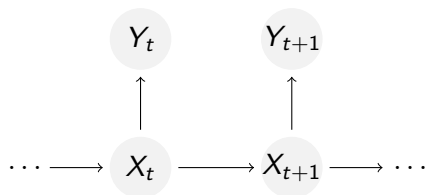
Outline

1. Sequential Monte Carlo
2. Resampling and degeneracy
3. Genealogies

Sequential Monte Carlo

- ▶ Want to sample from a sequence of intractable target distributions
- ▶ Typical settings: dimension of target increases in time, strong dependence between consecutive targets (so MCMC is impractical)
- ▶ SMC can obtain exact draws, and thus approximate expectations

State space models



$$X_0 \sim \mu(\cdot)$$

$$X_{t+1} \mid (X_t = x_t) \sim f_t(\cdot \mid x_t)$$

$$Y_t \mid (X_t = x_t) \sim g_t(\cdot \mid x_t)$$

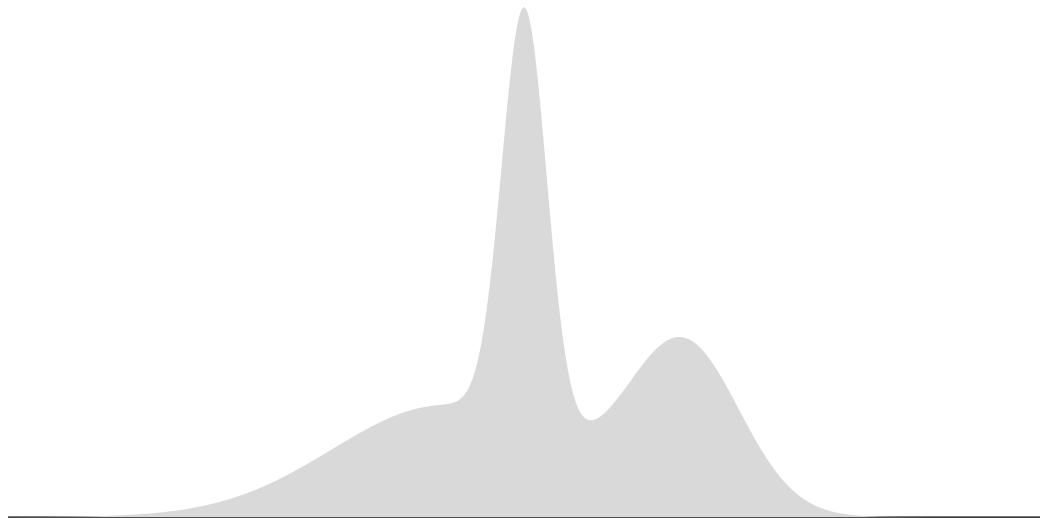
May want to infer ($t < T$):

$$p(x_{1:T} \mid y_{1:t}) \quad \text{"prediction"}$$

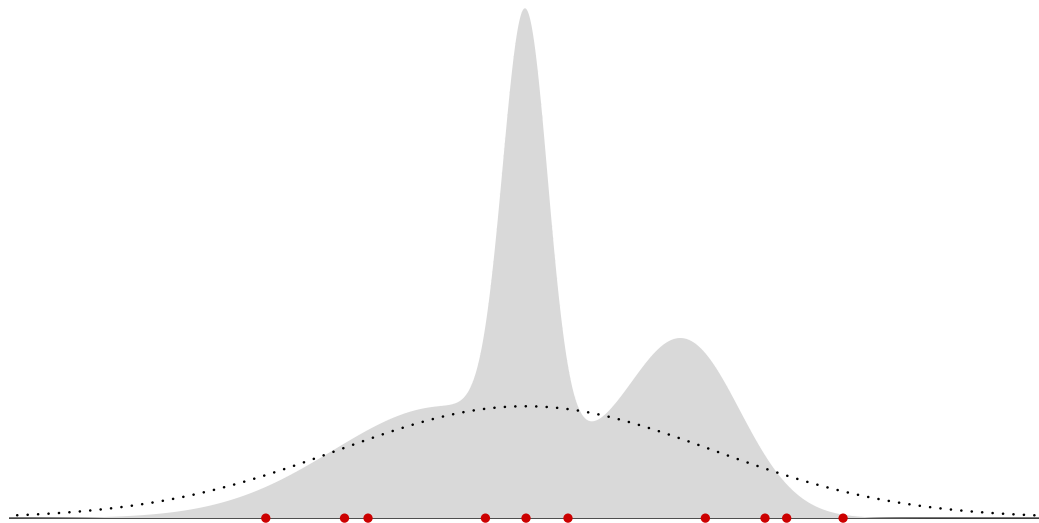
$$p(x_{1:t} \mid y_{1:t}) \quad \text{"filtering"}$$

$$p(x_{1:t} \mid y_{1:T}) \quad \text{"smoothing"}$$

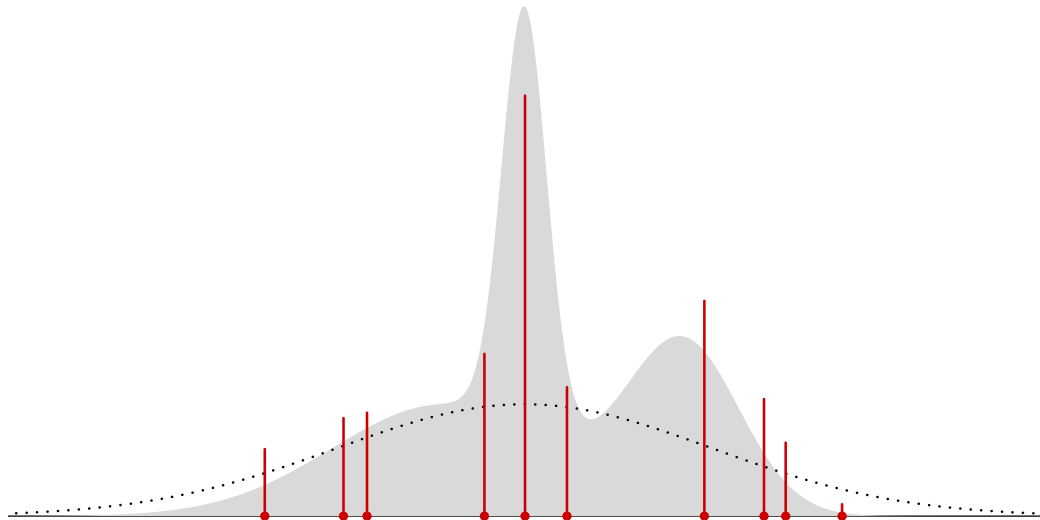
Importance sampling



Importance sampling



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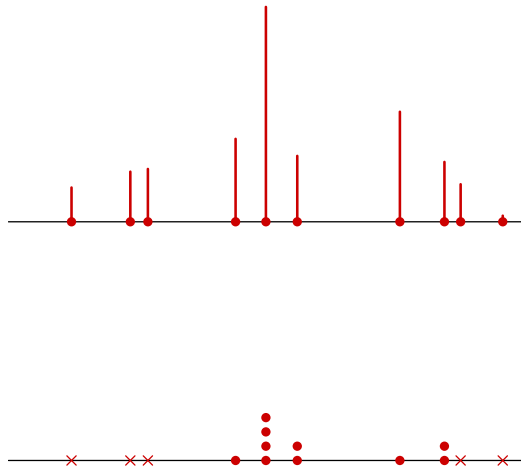


Sequential importance sampling

- ▶ Idea: use weighted samples from one time step to construct a proposal for the next step
- ▶ Multiplying weights over time causes *weight degeneracy*
- ▶ Can avoid this problem by resampling (weights are reset at each step)

Resampling

- ▶ Want to transform continuous weights to discrete offspring counts
- ▶ For example, sample counts from Multinomial distribution

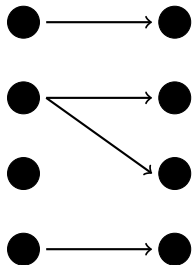


Sequential Monte Carlo algorithm

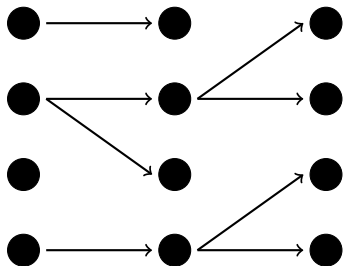
Iterate these steps:

1. Mutate: move particle positions (according to f_t)
2. Weight: Calculate importance weights for each particle
3. Resample: Duplicate/kill particles according to weights, reset weights to $1/N$

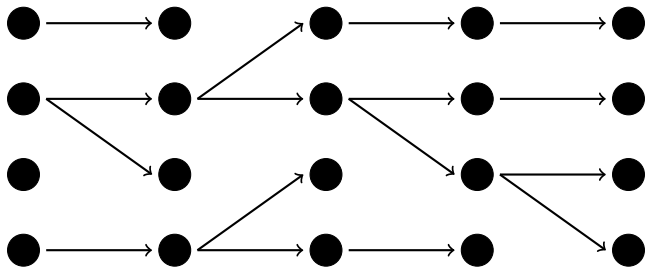
Ancestral degeneracy



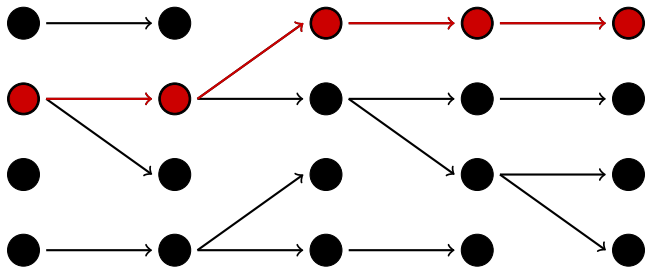
Ancestral degeneracy



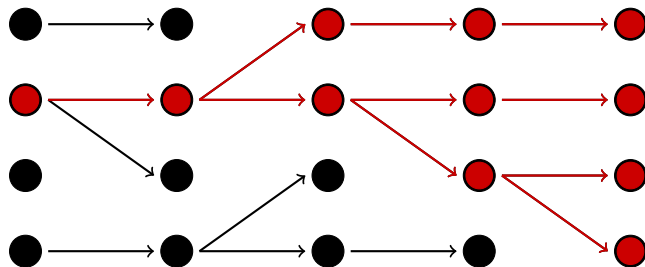
Ancestral degeneracy



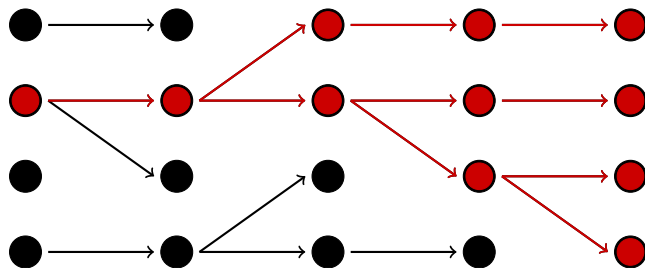
Ancestral degeneracy



Ancestral degeneracy



Ancestral degeneracy



For $t \ll T$, $p(x_{1:t}|y_{1:T})$ is approximated by very few distinct points!

Ancestral degeneracy

- ▶ In smoothing applications, ancestral degeneracy can seriously limit the performance of SMC
- ▶ Can be mitigated by resampling less often (e.g. only when variance of weights gets too big — “adaptive resampling”)
- ▶ Can also use low-variance resampling schemes
- ▶ If we knew how bad ancestral degeneracy would be, we could tune parameters to limit it (e.g. number of particles, threshold for adaptive resampling)
- ▶ Our aim: quantify ancestral degeneracy by analysing the induced genealogy

Coalescence Probability

Definition

The probability that a randomly chosen pair of particles at generation t share a common ancestor at generation $(t - 1)$, conditional on offspring counts

$$c_N = \frac{1}{N(N-1)} \sum_{i=1}^N v_i(v_i - 1)$$

THE END