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Genealogies of Sequential Monte Carlo Algorithms



Jere Koskela

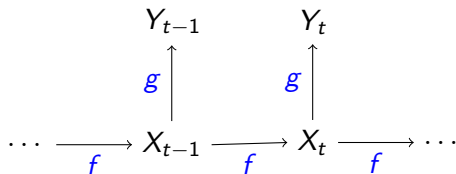


Adam Johansen



Paul Jenkins

Hidden Markov model



- ▶ $\{X_1, X_2, \dots\}$ hidden Markov states
- ▶ Y_i noisy observation of X_i
- ▶ Markov transition kernel f
- ▶ 'emission distribution' g

Inference on a HMM

- ▶ **filtering distribution** $p(x_T \mid y_{1:T})$
'current state'
- ▶ **smoothing distribution** $p(x_{1:T} \mid y_{1:T})$
'trajectory of all previous states'

Sequential Monte Carlo

- ▶ Approximate these distributions using N particles
- ▶ Initialise, then iterate the steps:
 1. **propagate:** update positions of particles by applying the Markov kernel f
 2. **calculate weights:** weight the particles according to how well they agree with the observations
 3. **resample** resample particles proportionally to their weights ('good' particles multiply, 'bad' particles die out)

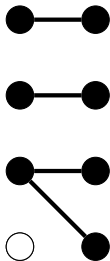
Genealogical interpretation

- ▶ Resampling step induces a genealogical (family tree) structure
- ▶ **Ancestral degeneracy:** genealogies of all current particles necessarily coalesce at some past time step
- ▶ Bad news for estimating smoothing distribution!

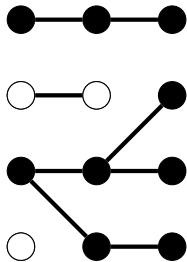
Genealogical interpretation



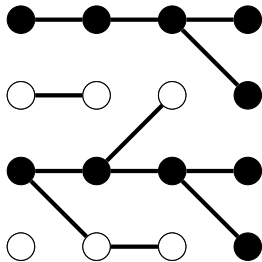
Genealogical interpretation



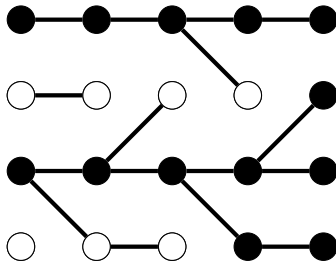
Genealogical interpretation



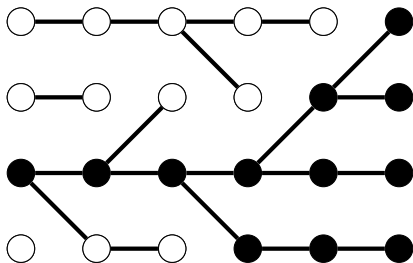
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- ▶ How many particles do I need to ensure n distinct lineages remain in generation $T - t$ with probability greater than $1 - \alpha$?

Genealogical interpretation

- ▶ How many particles do I need to ensure n distinct lineages remain in generation $T - t$ with probability greater than $1 - \alpha$?
- ▶ Easiest case (multinomial resampling) addressed in Koskela, Jere, et al. "Asymptotic genealogies of interacting particle systems with an application to sequential Monte Carlo." arXiv preprint arXiv:1804.01811 (2018).
- ▶ **Next:** relax assumptions, generalise to other resampling schemes and conditional SMC