

# Genealogies of Sequential Monte Carlo Algorithms

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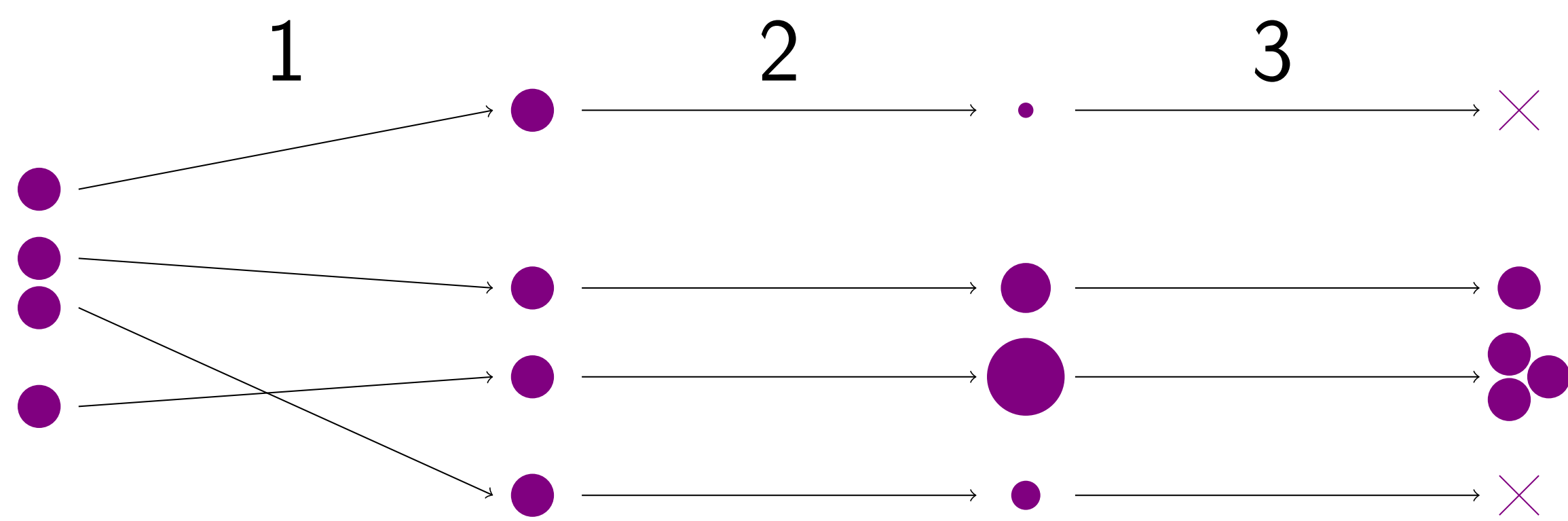
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## Sequential Monte Carlo

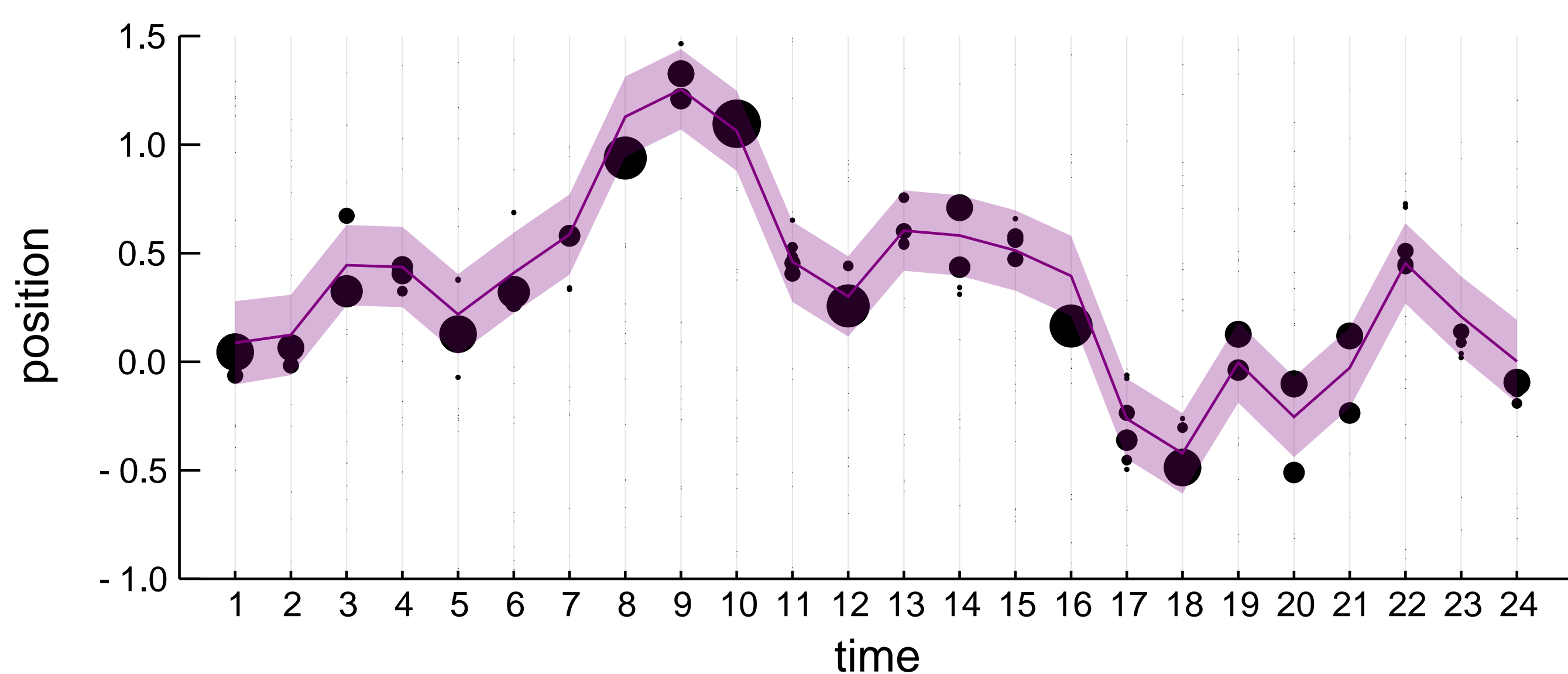
SMC<sup>1</sup> is an effective Monte Carlo method for models with strong correlation between parameters. For example, inferring a sequence of underlying parameters from an autocorrelated time series.

We approximate distributions by samples of “particles”. The algorithm starts with  $N$  equally-weighted particles and repeats the steps:



1. **Propagate:** update particle positions for the next parameter
2. **Weight:** weight particles according to a potential function
3. **Resample:** duplicate high-weight particles and kill off low-weight particles to obtain a new sample of  $N$  particles.

The figure shows a particle approximation for a tractable model. The exact posterior mode and 95% high posterior density set are obtained with the Kalman filter.

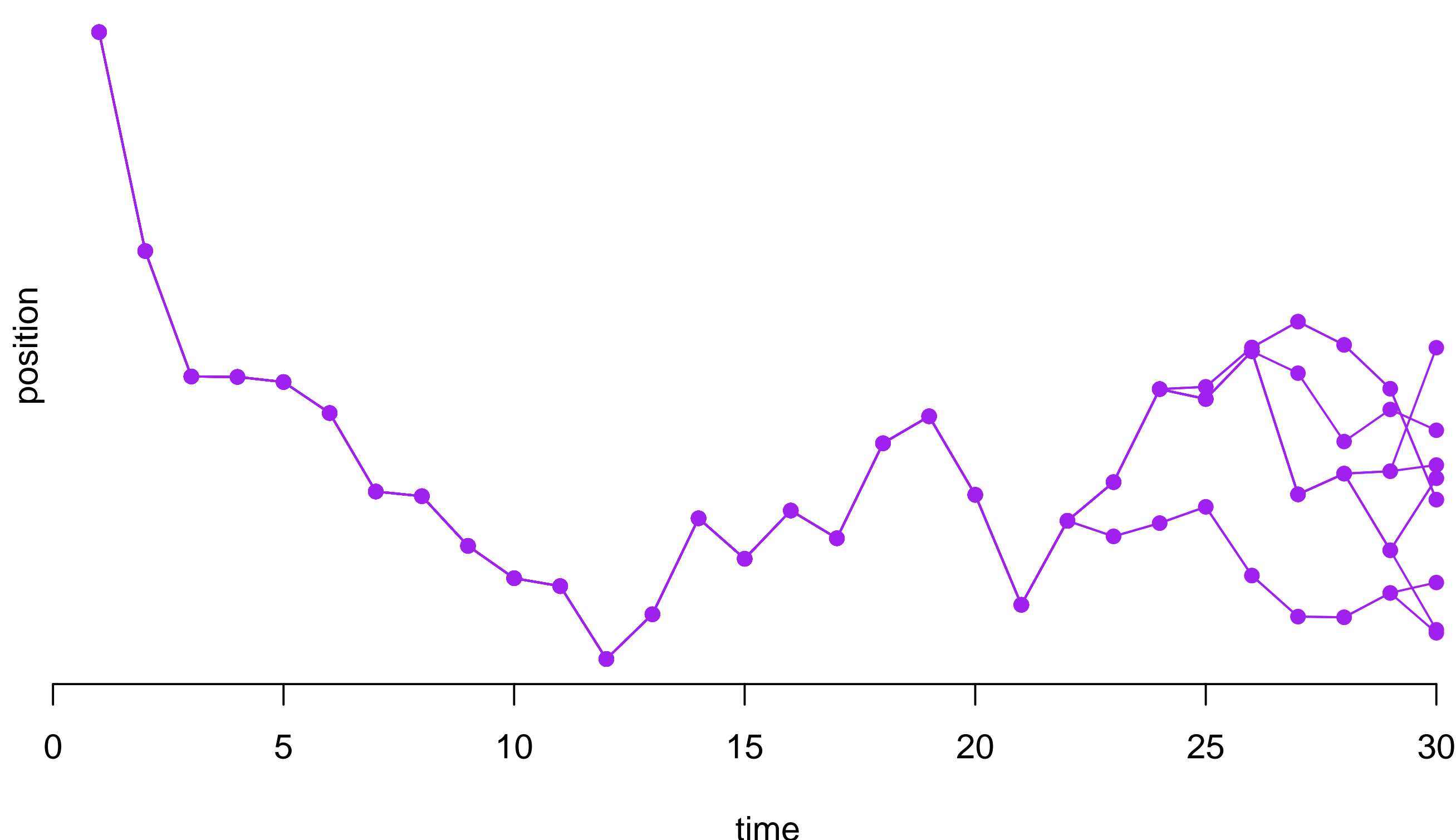


**Figure:** Exact posterior (purple) and weighted SMC particles before resampling (black) for a linear Gaussian HMM.

## Ancestral Degeneracy

For some applications, we want to approximate the *joint* distribution over all parameters. We can approximate this distribution by the “trajectories” of each of the  $N$  particles.

However, due to resampling these trajectories overlap, coalescing backwards in time. At some point all the trajectories coalesce, and we approximate that parameter’s distribution with just one point!

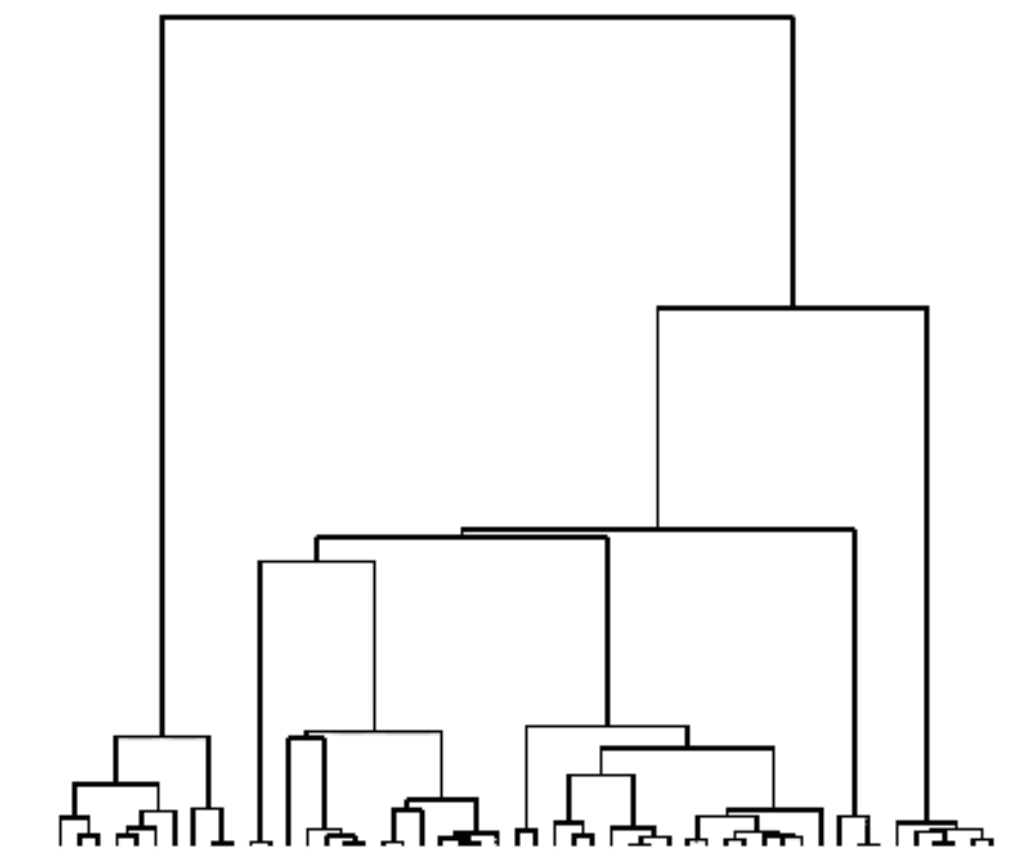


**Figure:** Trajectories from a sample of  $N=10$  particles. At most points there are just one or two distinct samples.

This phenomenon is known as *ancestral degeneracy*<sup>2</sup>, since the joint structure of the trajectories can be viewed as a *genealogy* of particles. It is one of the main issues with SMC, so we would like to analyse it.

## The Kingman Coalescent<sup>3</sup>

Kingman’s  $n$ -coalescent is the coalescent process on a sample of  $n$  individuals from a population of size  $N$  in which each pair of lineages merges with unit rate. It describes the limiting genealogies for a large class of population models when  $N \rightarrow \infty$ .



**A realisation of the 50-coalescent.**

Source: Wikimedia Commons

## SMC Genealogies

The genealogy depends on the number of offspring of each particle upon resampling at each time  $t$ , denoted  $(\nu_t^{(1)}, \dots, \nu_t^{(N)})$ . A key quantity in the asymptotic analysis is the coalescence rate

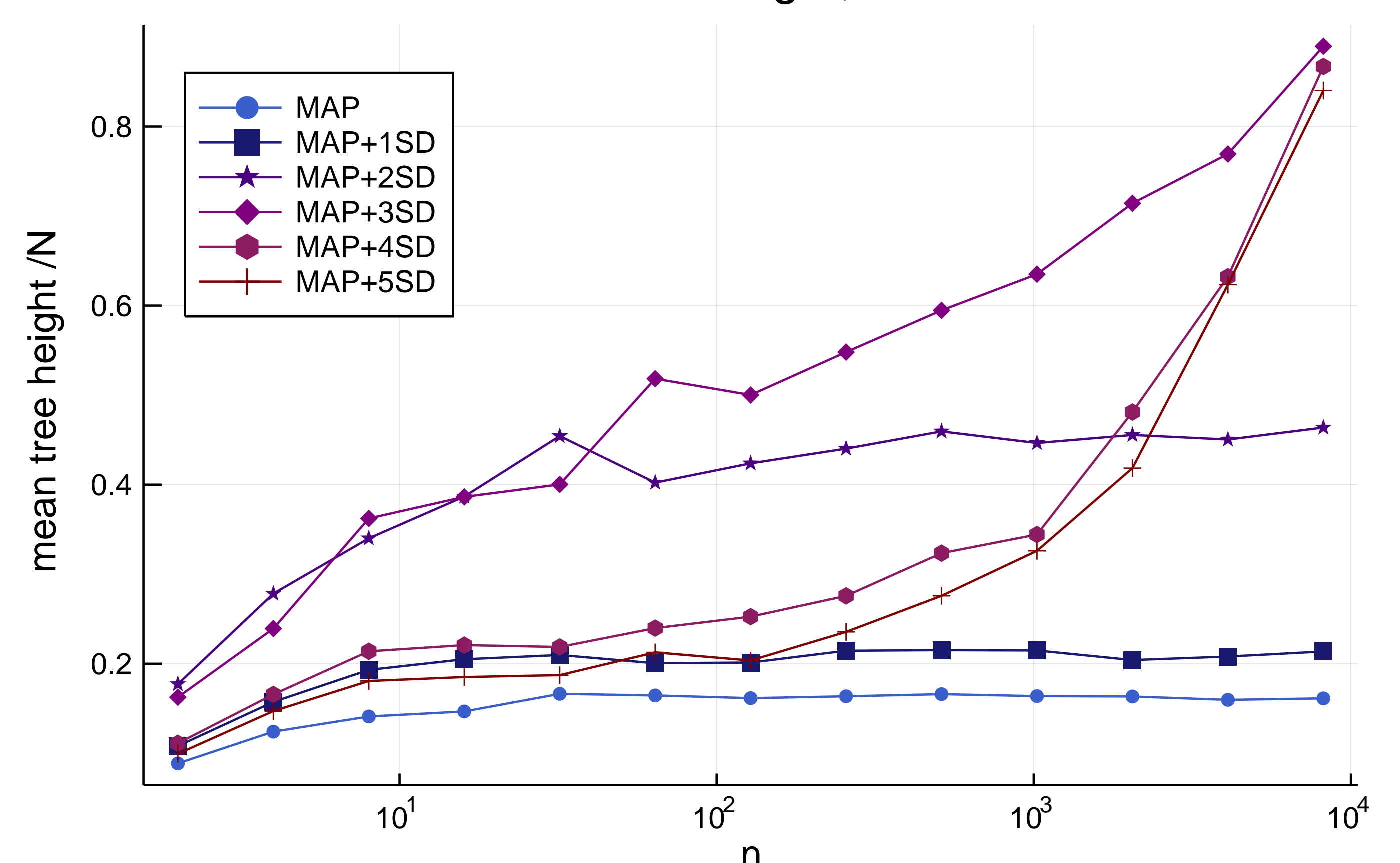
$$c_N(t) := \frac{1}{(N)_2} \sum_{i=1}^N \nu_t^{(i)} (\nu_t^{(i)} - 1).$$

To obtain convergence to the Kingman coalescent, we rescale time by the inverse coalescence rate to achieve the required unit rate.

It has been shown that, under such a rescaling and some standard assumptions, genealogies induced by multinomial resampling converge (in the sense of finite-dimensional distributions) to the Kingman coalescent<sup>4</sup>. Simulations show the same structure even for finite  $N$ .

We have since extended this result to cover conditional SMC<sup>5</sup> with multinomial resampling. In this algorithm, a certain “immortal trajectory” is conditioned to survive all the resampling steps. This still admits the Kingman coalescent as its limiting genealogy, but simulations show different behaviour for  $N < \infty$ .

CSMC treeheight,  $N=8192$



**Figure:** Average height of subtrees with  $n$  randomly chosen nodes, for different choices of immortal trajectory.

We conjecture that the process undergoes a phase transition when the immortal trajectory is particularly “unlikely” and  $n$  approaches  $N$ .

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