Recent Progress in Genealogies of Sequential Monte Carlo Algorithms
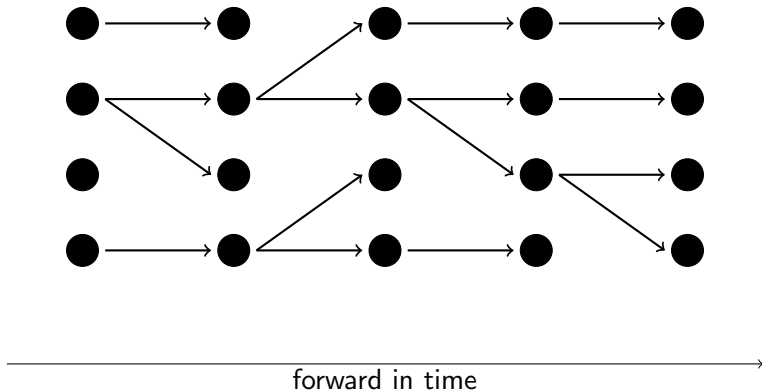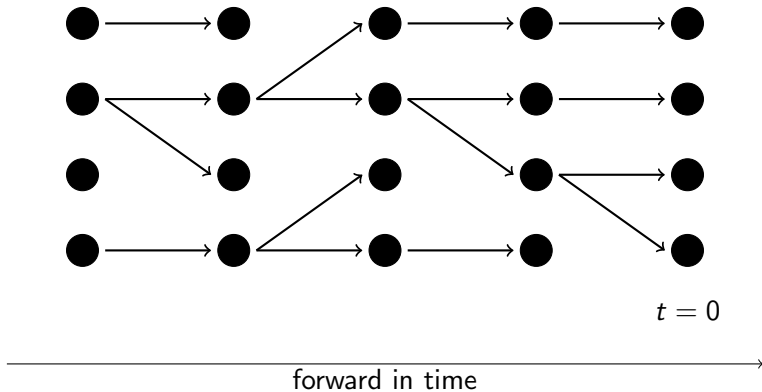
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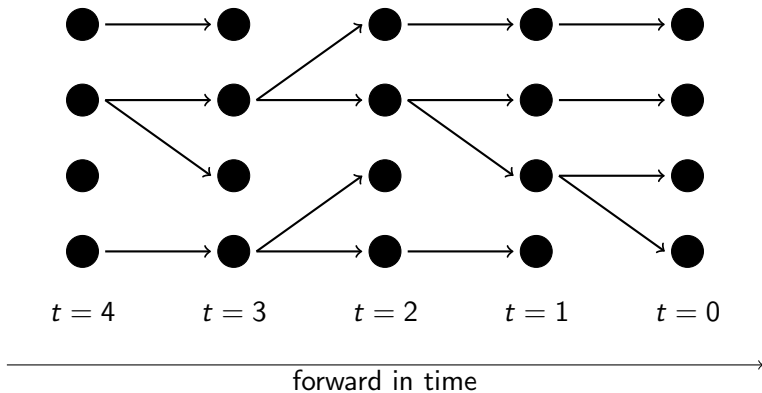
forward in time

Sequential Monte Carlo

$t = 0$

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$t = 4$ $t = 3$ $t = 2$ $t = 1$ $t = 0$

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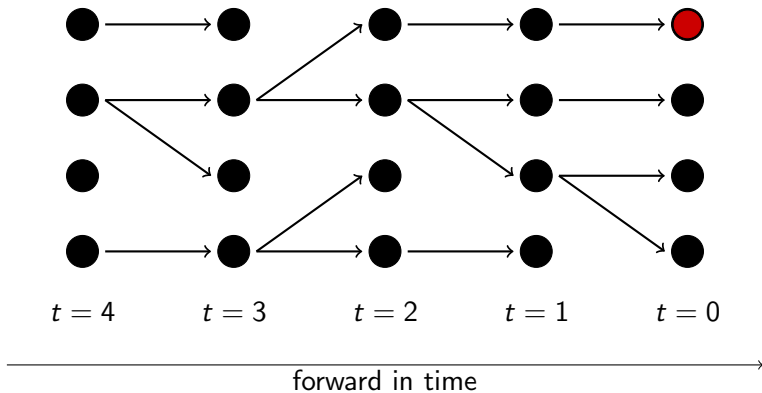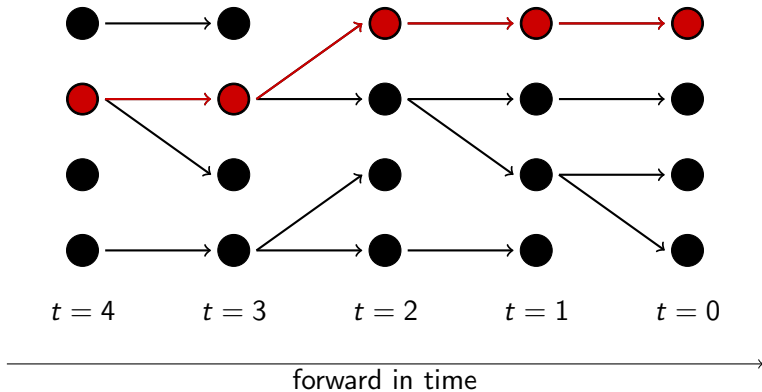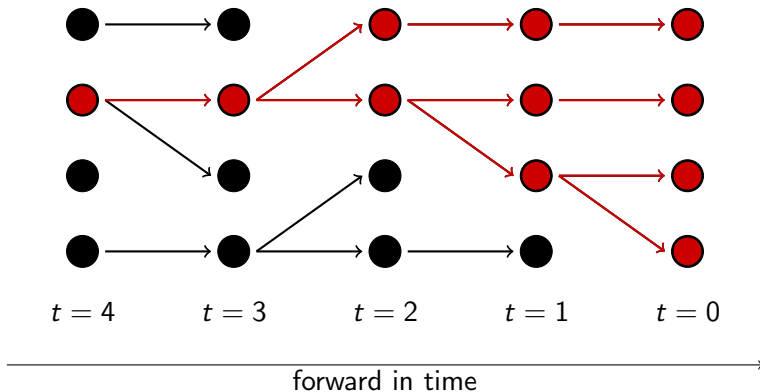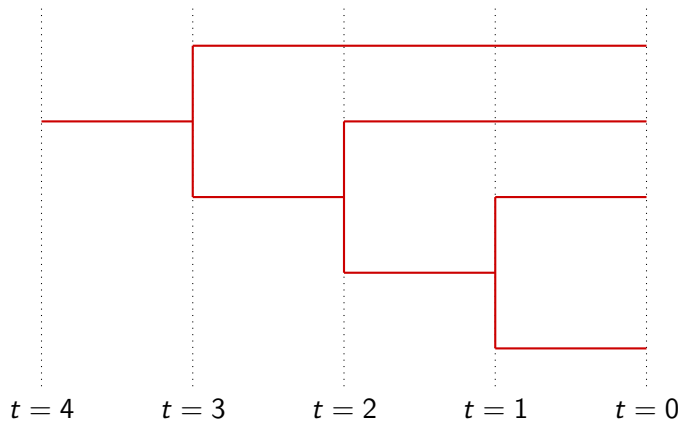
Mathematical formulation

▶ Population of N particles
▶ Sample $n \leq N$ terminal particles

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▶ Describe genealogy by a partition-valued stochastic process $(G_t^{(n,N)})_{t \in \mathbb{N}_0}$

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▶ Population of N particles
▶ Sample $n \leq N$ terminal particles
▶ Describe genealogy by a partition-valued stochastic process $(G_t^{(n,N)})_{t \in \mathbb{N}_0}$
▶ Elements i, j are in the same block of the partition $G_t^{(n,N)}$ iff particles i and j share a common ancestor at time t
▶ At time 0, the partition of $\{1, \ldots, n\}$ consisting of singletons: $G_0^{(n,N)} = \{\{1\}, \ldots, \{n\}\}$
▶ The only possible non-identity transitions are those that merge blocks

Example

$t = 0$

$\{1\}, \{2\}, \{3\}, \{4\}$

$t = 1$

$\{1\}, \{2\}, \{3, 4\}$

$t = 2$

$\{1\}, \{2, 3, 4\}$

$t = 3$

$\{1, 2, 3, 4\}$
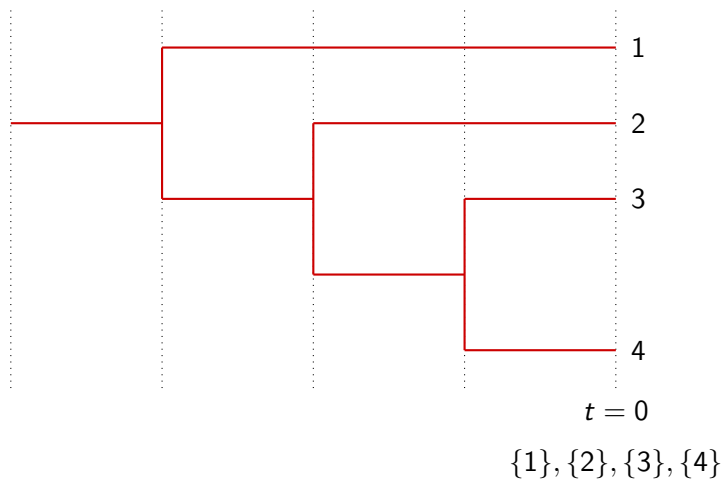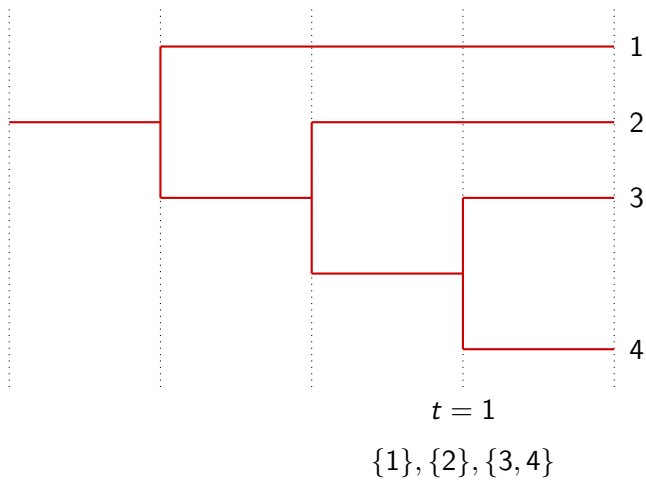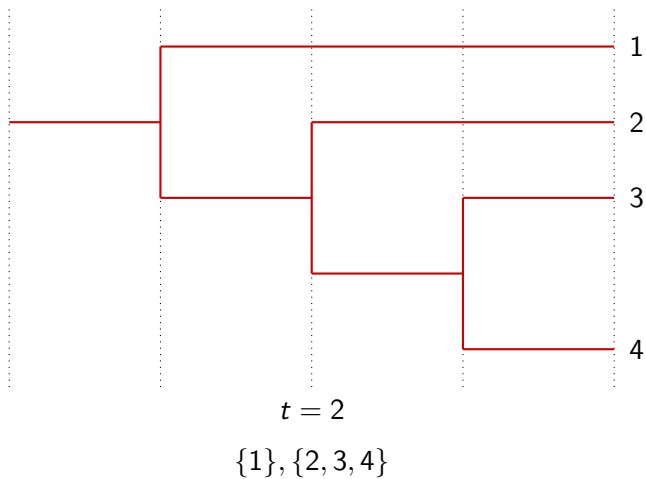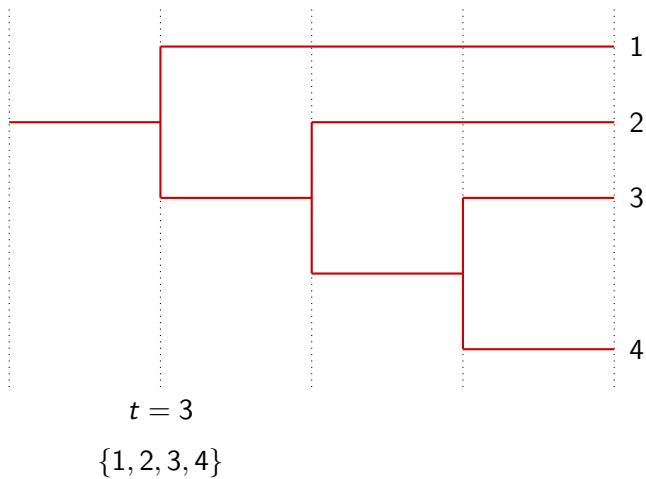
Kingman's *n*-coalescent

Kingman's *n*-coalescent

- ▶ *n* terminal particles
- ▶ Continuous time
- ▶ Each pair of lineages coalesces at rate 1
- ▶ No other ($>$ pair) mergers allowed

Notation

- $w_t^{(i)}$ = weight of particle i in generation t
- family size $v_t^{(i)}$ = number of offspring of particle i in generation t
- pair merger rate $c_N(t) = \frac{1}{(N)_2} \sum_{i=1}^N (v_t^{(i)})_2$
- time scale $\tau_N(t)$ = inverse of $c_N(t)$

A convergence theorem[1]

Suppose:

$$\mathbb{E}[c_N(t)] \to 0, \tag{1}$$

$$\mathbb{E}\left[\sum_{r=\tau_N(s)+1}^{\tau_N(t)} D_N(r)\right] \to 0, \tag{2}$$

$$\mathbb{E}\left[\sum_{r=\tau_N(s)+1}^{\tau_N(t)} c_N(r)^2\right] \to 0, \tag{3}$$

$$\mathbb{E}[\tau_N(t) - \tau_N(s)] \leq C_{t,s}N; \tag{4}$$

Then the rescaled genealogical process $(G_{\tau_N(t)}^{(n,N)})_{t\geq 0}$ converges to Kingman's coalescent in the sense of finite-dimensional distributions as $N \to \infty$.

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[1]Koskela, Jenkins, Johansen, Spanò. *Ann Stat,* to appear.

A simplified statement

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Suppose there exists a deterministic sequence $(b_N)_{N \in \mathbb{N}}$ uniform in $t \geq 1$ such that $b_N \to 0$.

$$\frac{1}{(N)_3} \sum_{i=1}^{N} \mathbb{E}_t[(v_t^{(i)})_3] \leq b_N \frac{1}{(N)_2} \sum_{i=1}^{N} \mathbb{E}_t[(v_t^{(i)})_2] \qquad (5)$$

Then the rescaled genealogical process $(G_{\tau_N(t)}^{(n,N)})_{t \geq 0}$ converges to Kingman's coalescent in the sense of finite-dimensional distributions as $N \to \infty$.

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▶ We remove (2) and (3), which contain awkward mixed moments
▶ We can verify the new condition in more complicated cases...

Problem : map weights $(w_t^{(1)}, \ldots, w_t^{(N)})$ to family sizes $(v_t^{(1)}, \ldots, v_t^{(N)})$.

Resampling schemes

Problem : map weights $(w_t^{(1)}, \ldots, w_t^{(N)})$ to family sizes $(v_t^{(1)}, \ldots, v_t^{(N)})$.
Desirable properties:

▶ constant population size $\sum_{i=1}^{N} v_t^{(i)} = N$

▶ equal weights after resampling $w_{t+}^{(i)} = 1/N$

▶ unbiased $\mathbb{E}[v_t^{(i)}|w_t^{(i)}] = N w_t^{(i)}$

Corollary: multinomial resampling

Consider an SMC algorithm with potential g and transition density q, satisfying

$$\frac{1}{a} \leq g_t(x, x') \leq a \tag{6}$$

$$\varepsilon h(x') \leq q_t(x, x') \leq \frac{1}{\varepsilon} h(x') \tag{7}$$

for constants $0 < \varepsilon \leq 1 \leq a < \infty$, and probablity distribution $h(\cdot)$.

Under multinomial resampling, the rescaled genealogies converge to Kingman's coalescent.

Stochastic roundings

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Let $X \geq 0$.
$Y : \mathbb{R}_+ \to \mathbb{N}$ is a *stochastic rounding* of X if Y takes the values

$$Y \mid X = \begin{cases} \lfloor X \rfloor & \text{with probability } 1 - X + \lfloor X \rfloor \\ \lfloor X \rfloor + 1 & \text{with probability } X - \lfloor X \rfloor \end{cases}$$

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Can generalise to multivariate case, with marginals $Y_i \mid X_i$ as above.

Stochastic roundings

- $X_i = N w_t^{(i)}$
- $v_t^{(i)} = Y_i$
- Constraint $Y_1 + \cdots + Y_N = N$

[2]Gerber, Whiteley, Chopin. *Ann Stat,* 2019.

Stochastic roundings

- $X_i = N w_t^{(i)}$
- $v_t^{(i)} = Y_i$
- Constraint $Y_1 + \cdots + Y_N = N$
- Examples: systematic resampling, residual-stratified resampling, SSP resampling[2],...

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[2]Gerber, Whiteley, Chopin. *Ann Stat,* 2019.

Corollary: stochastic rounding -based resampling

Consider an SMC algorithm with potential g and transition density q, satisfying

$$\frac{1}{a} \leq g_t(x, x') \leq a \tag{8}$$

$$\varepsilon h(x') \leq q_t(x, x') \leq \frac{1}{\varepsilon} h(x') \tag{9}$$

for constants $0 < \varepsilon \leq 1 \leq a < \infty$, and probablity distribution $h(\cdot)$.

Under stochastic rounding -based resampling, the rescaled genealogies converge to Kingman's coalescent.

Conditional SMC

- Used for SMC updates in particle MCMC[3]
- Given a fixed "immortal trajectory", conditioned to survive all transition and resampling steps

[3]Andrieu, Doucet, Holenstein. *JRSSB*, 2010.

Corollary: conditional SMC

Consider a conditional SMC algorithm with potential g and transition density q, satisfying

$$\frac{1}{a} \leq g_t(x, x') \leq a \tag{10}$$

$$\varepsilon h(x') \leq q_t(x, x') \leq \frac{1}{\varepsilon} h(x') \tag{11}$$

for constants $0 < \varepsilon \leq 1 \leq a < \infty$, and probablity distribution $h(\cdot)$.

Under multinomial resampling, the rescaled genealogies converge to Kingman's coalescent.

What about finite N?

- As $N \to \infty$ but sample size n fixed, probability of sampling immortal line vanishes, so its effect isn't seen in the limit
- For finite N we have more interesting behaviour
- Depends how "close" the immortal line is to other trajectories

Summary

▶ Genealogies can provide insight into performance of SMC algorithms
▶ We provide simple conditions for asymptotically Kingman genealogies
▶ Satisfied by stochastic rounding -based resampling
▶ Satisfied by conditional SMC with multinomial resampling...
▶ ... but this hides some interesting pre-limiting behaviour