The hyperbolic diffusion [BN78] is the solution of the SDE
\[ dx(t) = \frac{X(t)}{\sqrt{1 + X(t)^2}} \, dt + \sigma \, dW(t). \] (2)
Its transition probabilities are intractable, but its stationary distribution is known:
\[ \pi(x) = \frac{1}{2\pi \sqrt{1 + x^2}}. \] (3)
where \( X \) is the modified Bessel function of the second kind. We estimate the hitting probability of a level \( \lambda > 0 \) before returning to 0, given \( X_0 = 0 \).

The sets defining the problem are
\[ I = 0], \quad T = \{ \theta \}. \quad \mathcal{R} = (-\infty, \infty). \]
We consider a discretisation (2) and use the Euler scheme with grid spacing \( \Delta \) to define the family of transition densities:
\[ P_{\Delta}(x, y) = \frac{1}{2\pi \Delta} \exp \left( -\frac{1}{2\Delta} (x - y)^2 \right). \] (4)

We use (4) and (3) to define a discretised reverse-time proposal:
\[ P_{\Delta}(x, y) = \frac{1}{2\pi \Delta} \exp \left( -\frac{1}{2\Delta} (x - y)^2 \right) \] (5)
which can be normalised numerically and sampled by proposing \( x \sim \pi(x) \) from the \( \mathcal{N}(\Delta, \Delta) \) proposal distribution, solved for \( x \) and accepting with probability \( \varepsilon = \frac{1}{1 + \varepsilon} \).

The coalescent dynamics depicted in Figure 4 can be viewed as a particle system growing from the most recent common ancestor [VW15]. The likelihood of an observed configuration of types \( \lambda = \{1, \ldots, m\} \) at locations \( c \) corresponds to the probability of the particle system hitting the observed data: an ideal problem for the reverse time algorithm since the terminal state is a null set. The sets defining the problem are
\[ I = \{(c, j) \in \mathcal{C} \times \{2\ldots, m\} \}, \quad T = \{\{c\} \times \{2\ldots, m\}\}, \quad \mathcal{R} = \{\mathcal{C} \times \{1\} \}, \]
and the CSDs can be approximated using standard heuristics [KS116].

Efficient sequential Monte Carlo sampling of rare trajectories in reverse time

The spatial L-coalescent [BEV10] is a model of the genetic ancestry of a population in a continuous geography. Individuals line up occupancies fixed positions \( x_i \in \mathbb{R} \), and evolution is driven by a Poisson process \( \Pi \) of extinction-recolonisation events occurring on \( \mathbb{R} \times \mathbb{T} \) at rate \( \nu(t) \). At each event \( t \in \mathbb{N} \), every lineage with \( x_i \in \mathbb{R} \), i.e. within distance \( \delta > 0 \) of the event location \( c_i \), participates in the event with probability \( \alpha(\cdot) \). Participating lineages coalesce to a common ancestor whose location is sampled uniformly from \( \{c_i\} \).

A one-dimensional example is shown in Figure 4.

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The ATM network [GHSZ99] consists of \( n \) sources which are either on or off. Sources which are on do nothing, while sources which are on each generate packets at rate \( \mu \). Packets are serviced by a common server with rate \( \mu \) using the first-in-first-out policy. Off sources turn on at rate \( \nu \) and on sources turn off at rate \( \omega \). The state of the system is assigned as \( (i, j) \) and \( i + \frac{\omega}{\nu} \) drifts with \( \frac{\nu}{\mu} \). The system is simulated to exhibit a mutation process with probability \( \frac{\omega}{\nu} \) before emptying with exactly \( j \) sources on at the hitting time.

The sets defining the problem are
\[ I = \{(c, j) \in \mathcal{C} \times \{2\ldots, m\} \}, \quad T = \{\{c\} \times \{2\ldots, m\}\}, \quad \mathcal{R} = \{\mathcal{C} \times \{1\} \}, \]
and the CSDs can be approximated using standard heuristics [KS116].


[VW15] A. Véber and A. Wakolbinger. Once the most recent Lambda-Fleming-Waïs process has been reached, a mutation process on a space state \( N \) can be run along the edges of the realised tree. For concreteness we assume that there are finitely many types identified with \( [N] \in \{1, \ldots, m\} \), a mutation rate \( \lambda > 0 \) and a transition matrix \( M \) on \( \{1, \ldots, m\} \) with a unique stationary distribution \( \pi \). Then the type of the most recent common ancestor is sampled from \( \mu \), and mutations take place along ancestral edges with rate \( \lambda \) and transitions in type sampled from \( M \).

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Design of proposal distributions

The reverse-time dynamics in (1) will be a highly efficient proposal distribution if they could be simulated, and if \( \Pi \) could be evaluated. However, the Green’s function is typically at least as difficult to compute as the probability of interest. Progress can be made by approximating \( \Pi \) and defining a proposal based on the approximated Green’s function \( G \). This can also lead to a convenient reduction in dimensionality.

Let \( \nu \) denote the hitting time of a set \( A \), and consider a transition of \( X \) from \( x \sim \pi(x) \) to \( y \sim \pi(y) \). Assume that the conditional distribution (CSD)
\[ \pi(x|y) = \mathbb{P}(X = x | Z = y) \]
is independent of \( y \in \mathcal{Y} \) for \( \mathcal{Y} \) almost every \( y \). Then the ratio of Green’s functions in (1) cancels to the ratio of CSDs:
\[ \frac{1}{\nu} \mathbb{E} \left[ \frac{1}{\nu} \pi(x|y) \right] = \frac{1}{\nu} \mathbb{E} \left[ \frac{1}{\nu} \pi(y|x) \right] \]
CSDs can be substantially lower dimension than \( G \), indeed \( \nu(x|y) \) can be even be a one dimensional family if the dynamics of \( X \) only update one coordinate at a time. However, \( \pi(x|y) \) is still typically intractable. Introducing an application-specific, low dimensional approximation \( \tilde{\pi}(x|y) \) yields an implementable algorithm. Note that the independence assumption above does not have to hold: it is possible to define a proposal distribution via a ratio of CSDs regardless, albeit at a cost in loss of computational efficiency.