Supplementary Information 2: Simulation details

Parameters values

Given the formula $\frac{1}{2D_e} := \int_{\mathrm{R}^2} \nu(\mathbf{x}) d\mathbf{x}$ (Appendix A) for the effective density, it is straightforward to calculate the effective density D_e for the here used models to simulate IBD-block sharing.

First, in the case of the described grid model, where every node occupied by a single diploid individual is separated by one distance unit, $\nu(\mathbf{x})$ is simply the chance of changing pairwise distance by $-\mathbf{x}$ multiplied with a factor $\frac{1}{2}$. Summing $2\sum \nu(\mathbf{x})$ over all pairwise distances therefore is simply the sum over all probabilities of moving distance $\mathbf{x}$. This trivially sums to 1, independent of the exact shape of the dispersal kernel. Therefore, the effective density is given by $D_e = 1$. When modeling multiple individual per node, such as in a stepping stone model, an analogous calculation shows that D_e is given by the number of diploid individuals per node.

For the `DISCSIM` model, two lineages coalesce when they are hit by the same event and both lineages jump to the same ancestral chromosome. Therefore, $\nu(\mathbf{x})$ is the integrated rate of all those events affecting two individuals at distance x. Exchange the order of integrals in the full integral then yields $\nu(\mathbf{x}) = \frac{1}{2}u^2R^4\pi^2$. Normalizing with the rate by which an individual gets hit by an event gives the rate in generation times: $\frac{1}{2}R^2\pi u$ and therefore $D_e = \frac{1}{R^2\pi u}$.

The dispersal rate σ^2 in the deme and grid model is simply given by the axial variance of the single generation dispersal kernel. In the `DISCSIM` model, in every migration event a lineage jumps from a random point within a circle of radius R to another random point, the average squared distance of such jumps can be calculated to be R^2. This is two times the axial variance, and thus $\sigma^2 = \frac{R^2}{2}$.

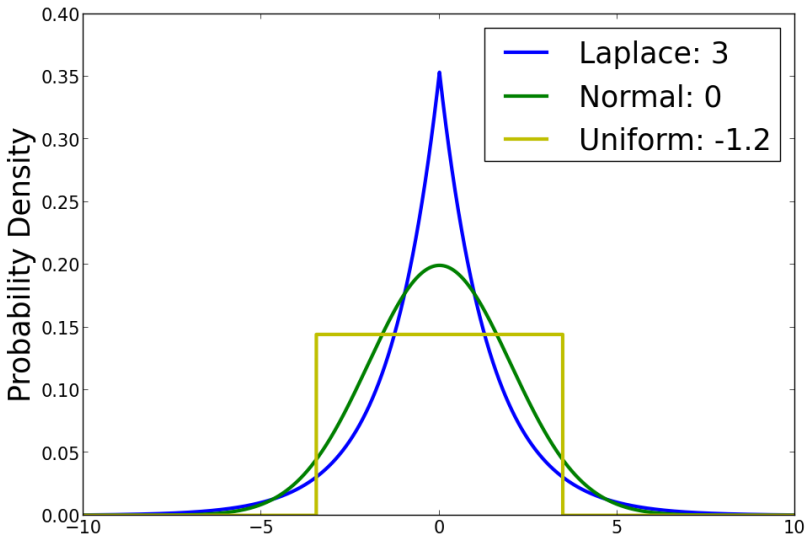
Simulation parameters

Here we give the simulation parameters used for generating the pictures above. Since we used discretized dispersal kernels for the simulations on grids, throughout the paper we always adjusted the parameters to draw from the continuous dispersal kernels (Laplace, Normal, Uniform) such that the empirical single generation axial σ^2 matched the target value on a simulated very large number of discretized random draws.

For the simulations used to generate Fig. 3, we used the following parameters:

Parameter	Value
Torus Size (Axis)	180
Sample Distance (Axis)	2
Chromosome length	150 cM
Locus Nr. (DISCSIM)	1500
σ (axial, per generation)	2
u (DISCSIM)	$\frac{1}{8\pi}$
R (DISCSIM)	$\sqrt{2} \cdot 2$
Deme Size (Axis, deme model)	5
t_{Max} (in generations)	200

Visualisation of axial dispersal kernels with $\sigma^2 = 2$, value on right top gives excess kurtosis:



Comparison Confidence Intervals

Here we compare the empirical 95% confidence interval from Fig. 6 to the mean length of the estimated confidence intervals, which shows that the estimates from the curvature of the likelihood surface capture parameter uncertainties rather well. This indicates that IBD-blocks originate from mostly independent events in the here simulated scenarios. We also give the correlation of σ and D based on 100 replicate runs for each sample size.

Sample Size	σ		D_e		Correlation
	Emp. CI	Est. CI	Emp. CI	Est. CI	(MLE-estimates)
100	0.967	1.12	1.24	1.07	0.1
270	0.304	0.390	0.350	0.332	-0.16
440	0.258	0.239	0.219	0.200	- 0.10
625	0.209	0.166	0.186	0.140	-0.20