Figure S1: Fitting a constant population models: As in Fig. 7, in every run we simulated IBD-sharing between 625 chromosomes of length 150cM picked randomly from an initial sample grid with distance 2 on an overall torus with 90 nodes per axis. We simulated the same demographic scenarios ($n(t) = t, n(t) = 10$ and $n(t) = 200/t$, and Laplace dispersal with $\sigma = 1$). Here, parameters were estimated by (wrongly) fitting a model of constant population density.