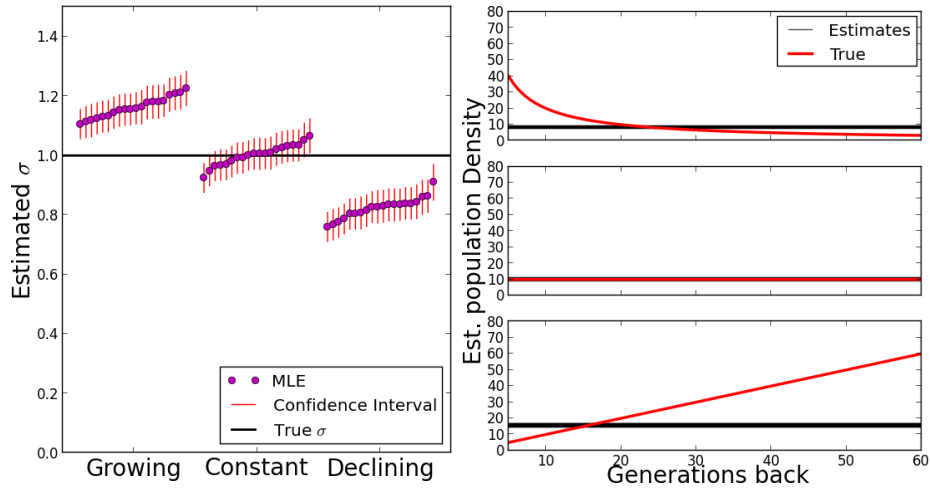
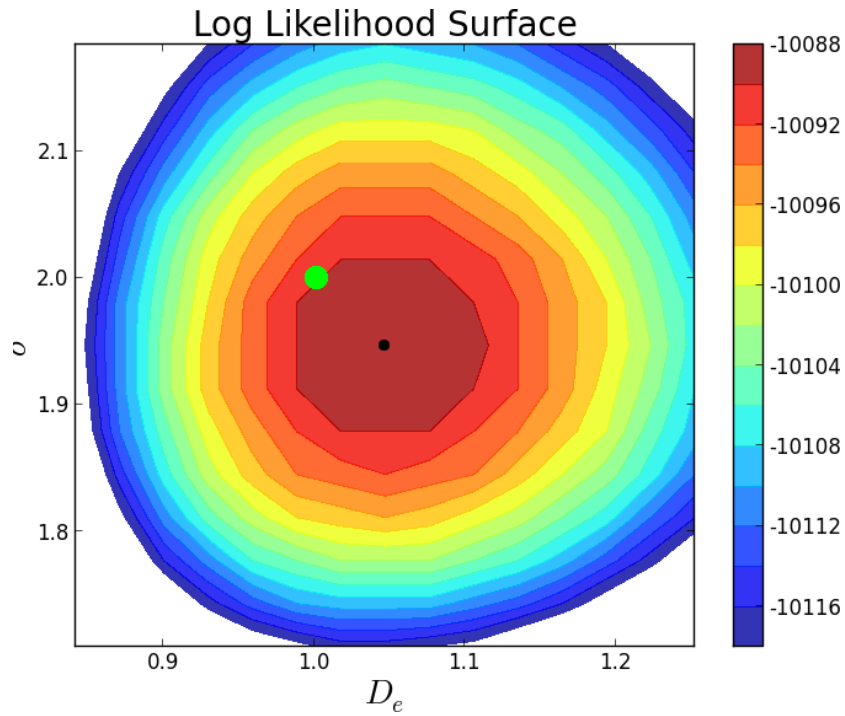


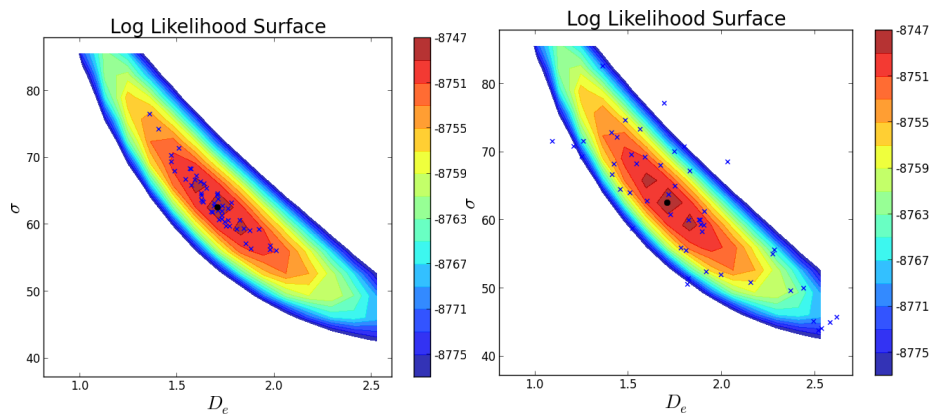
## Supplementary figures



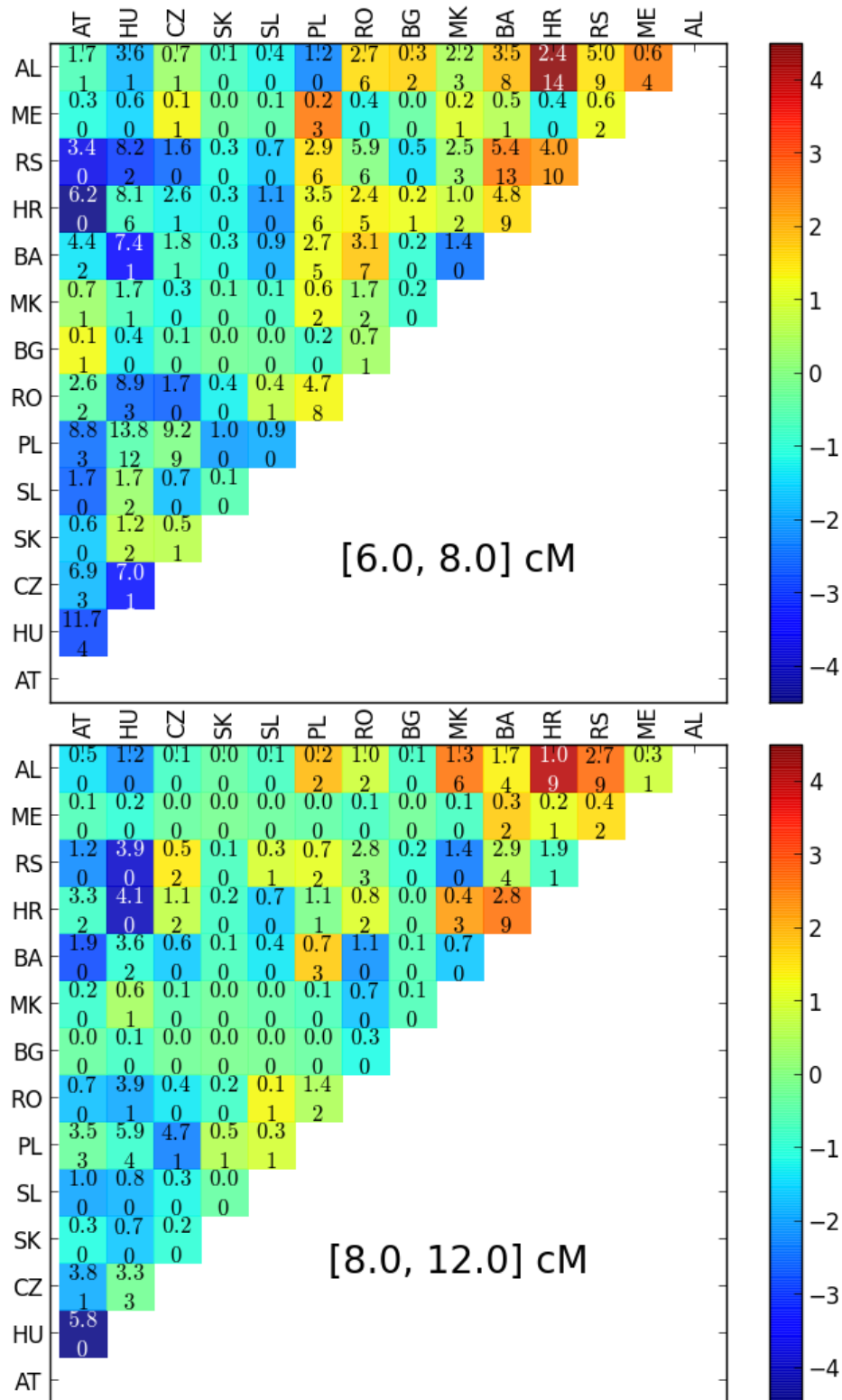
**Figure S1:** Fitting a constant population models: As in Fig. 7, in every run we simulated IBD-sharing between 625 chromosomes of length 150cM picked randomly from an initial sample grid with distance 2 on an overall torus with 90 nodes per axis. We simulated the same demographic scenarios ( $n(t)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



**Figure S2:** Likelihood surface: The likelihood surface based on block-sharing data from a random single simulation run as described in Fig. 6 with 625 samples of 150 cM chromosomes. Every color represents two Log-Likelihoods.



**Figure S3:** Bootstrapping POPRES-data: 50 bootstraps of the model of quick growth ( $D(t) = \frac{1}{t}$ ) plotted against the inferred likelihood surface of this model. Left: Bootstrap over blocks - every block was resampled Poisson with mean 1. Right: Bootstrap over country pairs - data from whole country pairs resampled Poisson with mean 1.



**Figure S4:** Residual of best fit: As described in Fig. 10, residuals of the best fit for blocks of length 6 – 8 cm and 8 – 12 cm. AT: Austria, HU: Hungary, CZ: Czech Republic, SK: Slovakia, SL: Slovenia, PL: Poland, RO: Romania, BG: Bulgaria, MK: Macedonia, BA: Bosnia, HR: Croatia, RS: Serbia, ME: Montenegro, AL: Albania