

Supporting Information

File S3: Simulations with MaCS

We use MaCS (Chen et al., 2009) for all our simulations with the following code lines:

Constant population size:

```
./macs2 300000 -t 1.0 -T -r .005 -h 1 (SEED: 1420480396)
./macs20 3000000 -t 1.0 -T -r .0002 -h 1 (SEED: 1399175725)
./macs100 3000000 -t 1.0 -T -r .0002 -h 1 (SEED: 1400528079)
```

Exponential growth and constant:

```
./macs2 300000 -t 1.0 -eG .1 10 -T -r .02 -h 1 (SEED: 1419985269)
./macs20 300000 -t 4.0 -eG .1 10 -T -r .002 -h 1 (SEED: 1420040333)
./macs100 300000 -t 1.0 -eG .1 10 -T -r .0002 -h 1 (SEED: 1401855826)
```

Bottleneck:

```
./macs2 300000 -t 4.0 -eN 0 1 -eN 0.3 0.1 -eN 0.5 1 -T -r .01 -h 1 (SEED: 1420824821)
./macs20 300000 -t 4.0 -eN 0 1 -eN 0.3 0.1 -eN 0.5 1 -T -r .002 -h 1 (SEED: 1420826310)
./macs100 300000 -t 4.0 -eN 0 1 -eN 0.3 0.1 -eN 0.5 1 -T -r .001 -h 1 (SEED: 1420826409)
```

References

Chen, G. K., Marjoram, P., and Wall, J. D. (2009). Fast and flexible simulation of DNA sequence data. *Genome Research*, 19(1):136–142.