



**S4 Figure. Number of IBD segments between pairs of individuals versus total length of shared IBD segments, under the Gutenkunst et. al. (2009) [1] out-of-Africa model.** 22 chromosomes of realistic lengths, simulated under Wright-Fisher model (top) and coalescent (bottom), compared to the analytical expectation under Eqs (1) and (2) of S3 Appendix. The African, European, and Asian populations had 1000 haploid samples each.

## References

- [1] R. N. Gutenkunst, R. D. Hernandez, S. H. Williamson, and C. D. Bustamante. “Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data”. In: *PLoS Genetics* 5.10 (2009).