

Supporting Information for “A genetics-style document using RMarkdown”

Aaron P. Ragsdale

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The diffusion equation and moment system for the two-locus sampling distribution

The two-locus diffusion equation with additive selection was first described by Kimura (1955) and studied extensively in the 1960s and 70s (e.g., Ohta and Kimura 1969).

Supplementary Tables

Table S1: Thousand Genomes Project population descriptions for populations used in this study.

Code	Description	Region
ESN	Esan in Nigeria	Africa
GWD	Gambian in Western Divisions in the Gambia	Africa
LWK	Luhya in Webuye, Kenya	Africa
MSL	Mende in Sierra Leone	Africa
YRI	Yoruba in Ibadan, Nigeria	Africa
CEU	Utah Residents (CEPH) with Northern and Western European Ancestry	Europe
GBR	British in England and Scotland	Europe
FIN	Finnish in Finland	Europe
IBS	Iberian Population in Spain	Europe
TSI	Toscani in Italia	Europe
CDX	Chinese Dai in Xishuangbanna, China	East Asia
CHB	Han Chinese in Beijing, China	East Asia
CHS	Southern Han Chinese	East Asia
JPT	Japanese in Tokyo, Japan	East Asia
KHV	Kinh in Ho Chi Minh City, Vietnam	East Asia

Table S2: DFEs inferred for missense and loss-of-function variants in MSL for varying values of h . General patterns are consistent across different chosen values of h , although $h = 0$ results in poorer fits for both missense and LOF variants. Columns to the right of the log-likelihood (LL) column show proportions of new mutations with $|s|$ in each given bin.

Class	h	shape	scale	LL	$[0, 10^{-5})$	$[10^{-5}, 10^{-4})$	$[10^{-4}, 10^{-3})$	$[10^{-3}, 10^{-2})$	$[10^{-2}, \infty)$
Missense	0.0	0.093	768505	-678.2	0.260	0.062	0.077	0.096	0.505
	0.2	0.138	6660	-416.7	0.260	0.098	0.134	0.182	0.327
	0.5	0.147	2117	-392.0	0.282	0.114	0.159	0.214	0.231
LOF	0.0	0.132	99999054	-248.3	0.077	0.028	0.037	0.051	0.807
	0.2	0.177	477994	-226.7	0.083	0.042	0.063	0.095	0.717
	0.5	0.188	121419	-224.2	0.092	0.050	0.077	0.119	0.662

Supplementary Figures

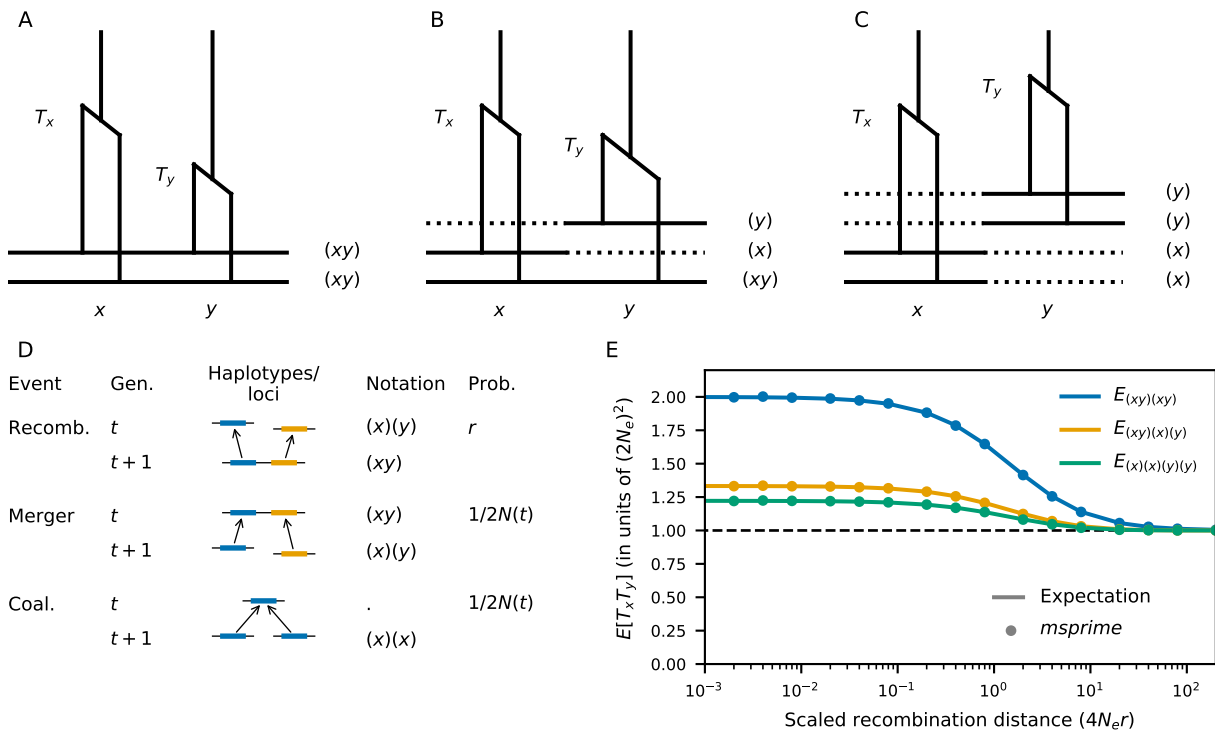


Figure S1: The distribution at stationarity of AB haplotype counts in a sample size of 30, in which we observe 10 *A* alleles at the left locus, and 10 *B* alleles at the right locus.

References

- Kimura, Motoo. 1955. "Random Genetic Drift in Multi-Allelic Locus." *Evolution* 9 (4): 419–35.
- Ohta, T, and M Kimura. 1969. "Linkage Disequilibrium at Steady State Determined by Random Genetic Drift and Recurrent Mutation." *Genetics* 63 (1): 229–38.