

Supplementary Materials

Polymer physics of structural evolution in synthetic yeast chromosomes

Giovanni Stracquadanio^{1,*}, Kun Yang², Jef D. Boeke^{3,4}, Romain Koszul⁵, and Joel S. Bader^{2,*}

¹School of Biological Sciences, The University of Edinburgh, Edinburgh EH9 3BF, United Kingdom

²Department of Biomedical Engineering, Johns Hopkins University, USA

³Institute for Systems Genetics and Department of Biochemistry and Molecular Pharmacology, NYU Langone University School of Medicine, USA 10016

⁴Department of Biomedical Engineering, NYU Tandon School of Engineering, Brooklyn NY 11201

⁵Institut Pasteur, CNRS UMR3525, Université de Paris, Unité Régulation Spatiale des Génomes, F-75015 Paris, France

*Corresponding author. Email: giovanni.stracquadanio@ed.ac.uk;joel.bader@jhu.edu

List of Tables

1	synIXR genomic structure. For each segment in the chromosome, we report its numeric id, its length and the type, being either essential, non-essential or auxotrophic marker.	2
2	Parameters settings used for SPI simulations.	2
3	Parameter estimation. For each model, we report the log-likelihood value, the best estimate for each parameter, with 95% confidence intervals within brackets.	3

List of Figures

1	Structural analysis of simulated genomes using a uniform recombination event probability model. A) Analysis of genome length and B) Deletion frequency of each segment compared to the one observed in SCRaMbLE genomes.	4
2	Histogram reweighting performance analysis. For each persistence length setting, we report the log-likelihood estimates of the model parameters computed by rejection sampling and histogram reweighting.	5

Tables

Id	Length (bp)	Type	Id	Length (bp)	Type
1	15761	non essential	23	135	non essential
2	689	essential	24	1421	non essential
3	1306	non essential	25	4156	non essential
4	5550	non essential	26	1497	non essential
5	1629	non essential	27	229	non essential
6	850	non essential	28	1009	non essential
7	5112	essential	29	2049	non essential
8	2547	non essential	30	4476	non essential
9	1896	essential	31	177	non essential
10	5186	essential	32	1445	aux. marker(<i>LYS1</i>)
11	1836	non essential	33	1082	non essential
12	1645	essential	34	1586	non essential
13	158	non essential	35	217	non essential
14	1831	aux. marker (<i>MET28</i>)	36	2429	non essential
15	245	non essential	37	4102	non essential
16	4042	non essential	38	2925	non essential
17	4717	non essential	39	955	non essential
18	945	non essential	40	998	non essential
19	3260	non essential	41	1804	non essential
20	4338	essential	42	985	non essential
21	179	non essential	43	1006	non essential
22	1965	non essential			

Table 1: synIXR genomic structure. For each segment in the chromosome, we report its numeric id, its length and the type, being either essential, non-essential or auxotrophic marker.

Model parameter	Rejection sampling parameters grid (step size)	Histogram reweighting parameters grid (step size)
Expected number of recombination events (λ)	[4, ..., 13](+1)	9
Scaling exponent (ν)	[0.3, ..., 0.7](+0.05)	[0.45, ..., 0.6](+0.01)
Persistence length (b)	[50bp, ..., 300bp](+50bp)	[150bp, ..., 250bp](+10bp)

Table 2: Parameters settings used for SPI simulations.

Model	Log-likelihood	λ	ν	b
Rejection sampling	-178.713	9 (6, 13)	0.55 (0.45, 0.6)	200 (150, 250)
Histogram reweighting	-179.295	9 (-)	0.55 (0.45, 0.6)	200 (150, 210)
Null (random uniform)	-385.237	12 (-)	0 (-)	0 (-)

Table 3: Parameter estimation. For each model, we report the log-likelihood value, the best estimate for each parameter, with 95% confidence intervals within brackets.

Figures

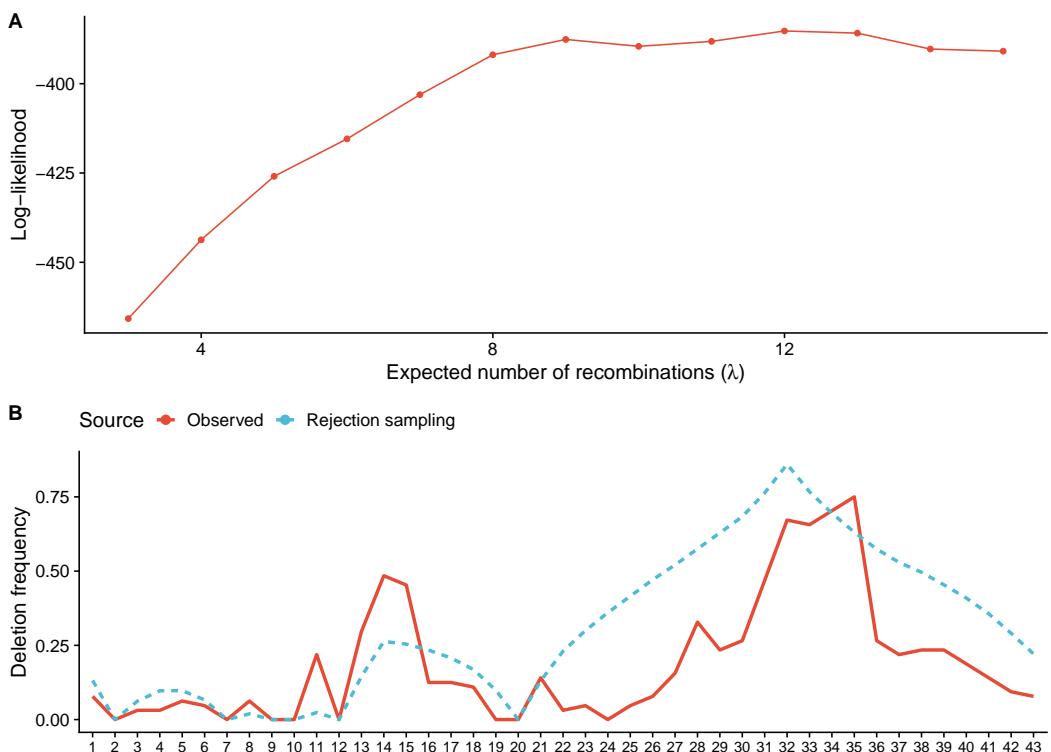


Figure 1: Structural analysis of simulated genomes using a uniform recombination event probability model. A) Analysis of genome length and B) Deletion frequency of each segment compared to the one observed in SCRaMbLE genomes.

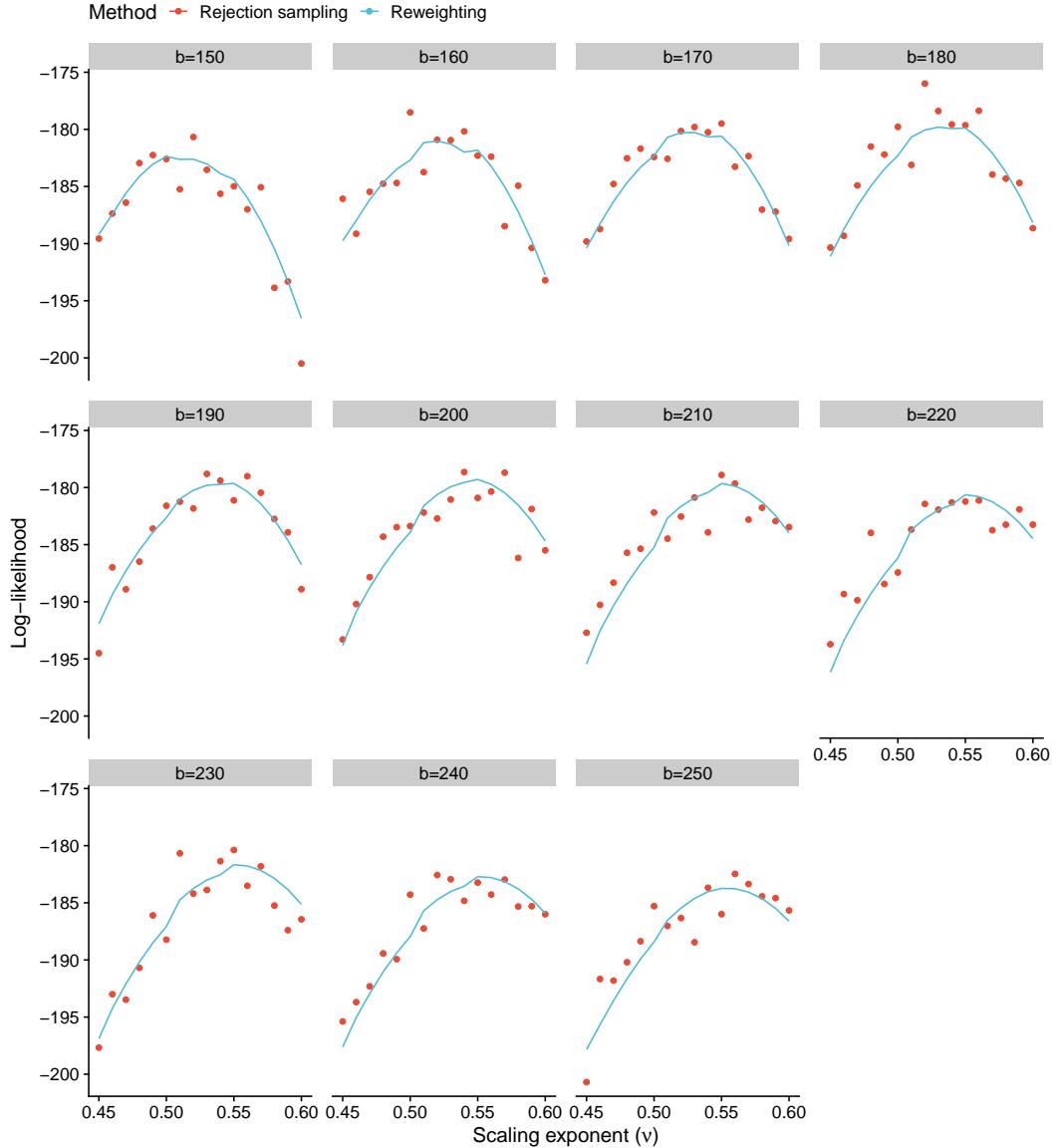


Figure 2: Histogram reweighting performance analysis. For each persistence length setting, we report the log-likelihood estimates of the model parameters computed by rejection sampling and histogram reweighting.