

Figure S1 Comparison of the true LRS distribution to the χ^2 distribution with 1 df. Panels show comparisons for different values of the population size N and the number of sampled time points L , as indicated on the left and on top. Notations are as in Figure 1. Parameter values: $T = 100$, $\Delta = 20$, $v_0 = 0.5$; the number of Wright-Fisher simulations was 10^6 .

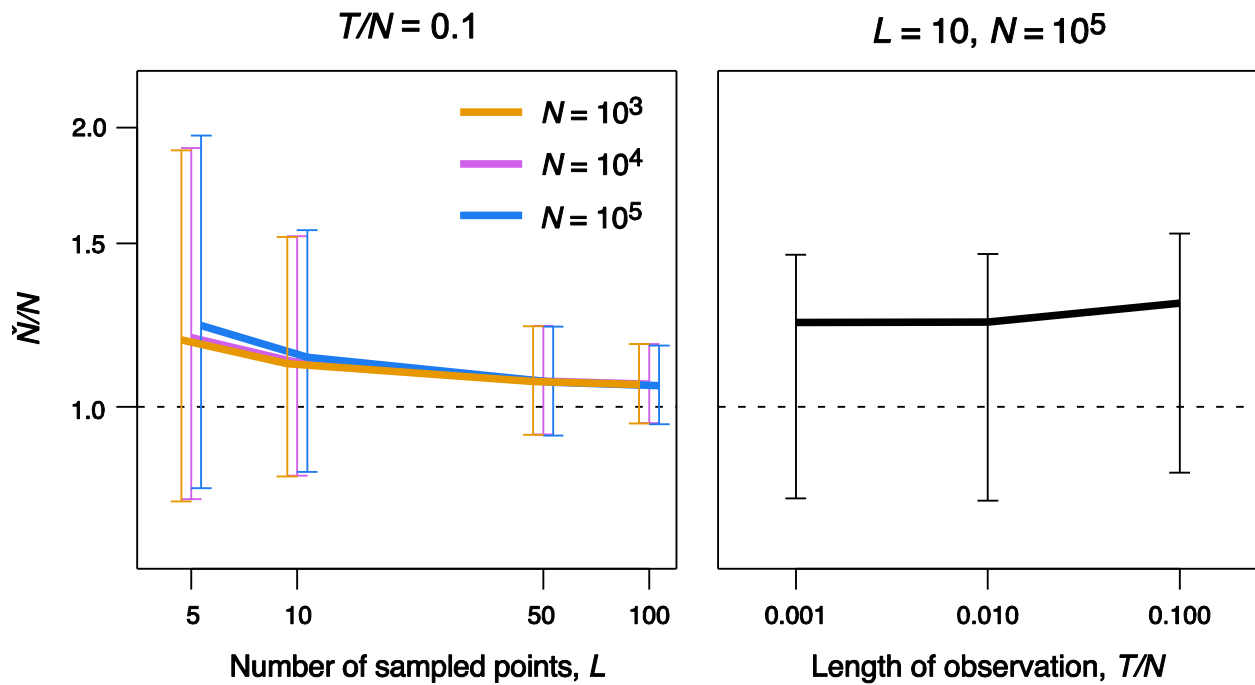


Figure S2 Bias in the maximum-likelihood estimate of population size under neutrality. The figure shows the ratio of the most-likely population size under neutrality, \tilde{N} , to the true population size, N , as a function of the number of sampled points L (left panel) and as a function of the length of the observed time series T (right panel). Whiskers indicate quartiles of the distribution of \tilde{N}/N . In the right panel, curves for different population sizes are slightly shifted along the x-axis for clarity. Bias in \tilde{N} decreases as the number of sampled time points increases. The bias is nearly independent of N and of the length of the sampling period. The number of Wright-Fisher simulations was 10^5 .

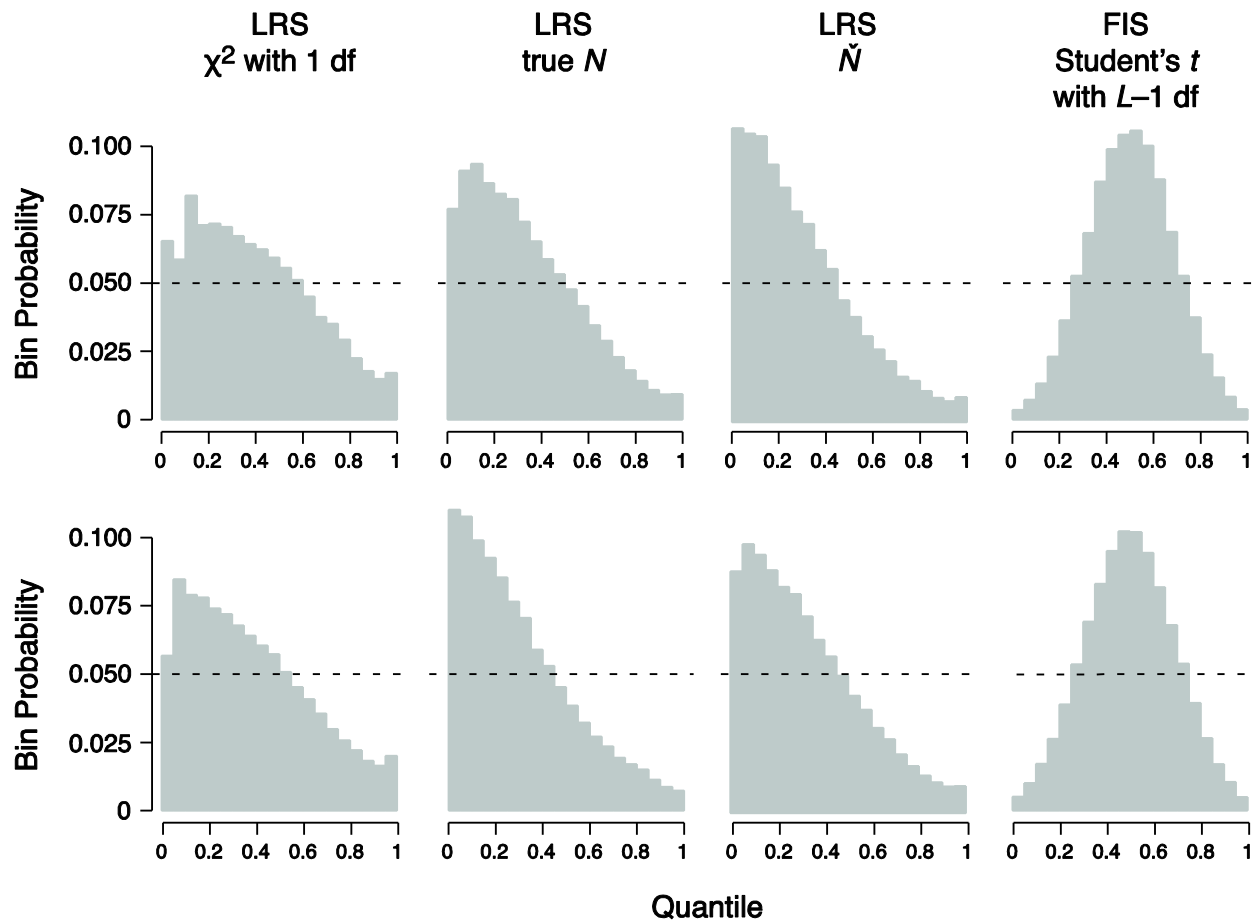


Figure S3 Distributions of various test statistics under the neutral null hypothesis, when allele frequencies are sampled with noise. Top row, $n = 50$. Bottom row, $n = 100$. Notations as in Figure 1. Parameter values: $N = 10^3$, $T = 10$, $\Delta = 2$, $L = 5$, $\nu_0 = 0.5$; the number of Wright-Fisher simulations was 10^5 .

Table S1 Deviation of the distribution of LRS from the χ^2 distribution for different initial allele frequencies

Simulation parameters		Sampling parameters			Absorption probability	\check{N}/N	α			
v_0	N	T	L	Δ			0.05	0.01	0.001	0.0001
0.1	10^4	10	10	1	8×10^{-5}	1.3	1.4	1.8	2.3	3.7
	10^4	100	10	10	2.5×10^{-4}	1.3	1.6	2.2	3.6	5.9
	10^4	1000	10	100	0.067	1.5	2.2	4.4	14.3	51.8
	10^3	100	10	10	0.123	1.5	1.9	3.2	7.9	20.9
	10^4	1000	10	100	0.067	1.5	2.2	4.4	14.3	51.8
	10^5	10000	10	1000	6.6×10^{-4}	1.2	0.2	0.4	0.9	1.9
	10^4	100	5	20	2.3×10^{-4}	1.7	2.2	3.4	6.3	11.5
	10^4	100	10	10	2.5×10^{-4}	1.3	1.6	2.2	3.6	5.9
	10^4	100	100	1	2.4×10^{-4}	1.1	1.2	1.6	2.5	4.9
0.2	10^4	10	10	1	9.8×10^{-5}	1.3	1.4	1.7	2.4	3.4
	10^4	100	10	10	3.4×10^{-4}	1.3	1.5	1.9	2.7	3.8
	10^4	1000	10	100	6.9×10^{-3}	1.4	2.2	4.0	11.4	35.7
	10^3	100	10	10	0.014	1.4	2.2	4.0	10.5	29.8
	10^4	1000	10	100	6.9×10^{-3}	1.4	2.2	4.0	11.4	35.7
	10^5	10000	10	1000	1.3×10^{-3}	1.3	0.5	0.7	1.6	3.5
	10^4	100	5	20	3.2×10^{-4}	1.7	2.0	3.1	5.5	9.5
	10^4	100	10	10	3.4×10^{-4}	1.3	1.5	1.9	2.7	3.8
	10^4	100	100	1	3.5×10^{-4}	1.0	1.1	1.2	1.6	1.8
0.3	10^4	10	10	1	1.0×10^{-4}	1.3	1.4	1.7	2.3	3.2
	10^4	100	10	10	4.3×10^{-4}	1.3	1.4	1.8	2.5	3.5
	10^4	1000	10	100	1.6×10^{-3}	1.3	1.9	3.1	7.0	17.4
	10^3	100	10	10	1.3×10^{-3}	1.3	2.0	3.2	7.5	18.7
	10^4	1000	10	100	1.6×10^{-3}	1.3	1.9	3.1	7.0	17.4
	10^5	10000	10	1000	0.012	1.3	1.3	1.7	2.7	4.5
	10^4	100	5	20	3.5×10^{-4}	1.7	2.0	3.0	5.2	8.6
	10^4	100	10	10	4.3×10^{-4}	1.3	1.4	1.8	2.5	3.5
	10^4	100	100	1	3.7×10^{-4}	1.0	1.1	1.1	1.2	1.5
0.4	10^4	10	10	1	1.1×10^{-4}	1.3	1.4	1.7	2.4	3.1
	10^4	100	10	10	4.1×10^{-4}	1.3	1.4	1.8	2.3	3.0
	10^4	1000	10	100	1.3×10^{-3}	1.3	1.7	2.5	4.9	9.8
	10^3	100	10	10	2.6×10^{-4}	1.3	1.8	2.6	5.2	10.0
	10^4	1000	10	100	1.3×10^{-3}	1.3	1.7	2.5	4.9	9.8
	10^5	10000	10	1000	0.013	1.3	1.2	1.6	2.4	3.9
	10^4	100	5	20	6.2×10^{-4}	1.7	2.0	3.0	5.3	8.5
	10^4	100	10	10	4.1×10^{-4}	1.3	1.4	1.8	2.3	3.0
	10^4	100	100	1	4.1×10^{-4}	1.0	1.1	1.1	1.1	1.2
0.5	10^4	10	10	1	2.6×10^{-3}	1.3	1.4	1.7	2.3	3.3
	10^4	100	10	10	7.9×10^{-4}	1.3	1.4	1.7	2.3	2.9
	10^4	1000	10	100	1.2×10^{-3}	1.3	1.6	2.4	4.3	8.1
	10^3	100	10	10	2.2×10^{-3}	1.3	1.7	2.5	4.5	8.3
	10^4	1000	10	100	1.2×10^{-3}	1.3	1.6	2.4	4.3	8.1
	10^5	10000	10	1000	1.3×10^{-2}	1.3	1.2	1.5	2.3	3.6
	10^4	100	5	20	7.7×10^{-4}	1.7	2.0	2.9	5.2	8.5
	10^4	100	10	10	7.9×10^{-4}	1.3	1.4	1.7	2.3	2.9
	10^4	100	100	1	8.0×10^{-4}	1.0	1.1	1.1	1.2	1.4

Table S2 Mutant allele frequencies in yeast data from Lang et al, 2013 and the application of ELRT and FIT

Line	Gene	Amino acid change	Time in generations ^a								ELRT ^b						FIT		
			415	505	585	665	745	825	910	1000	\tilde{N}	\hat{N}	$\hat{s},\%$	P_{obs}	$P\text{-val bound}$	Cond $P\text{-val}$	t_{FI}	df	$P\text{-val}$
RMB2-F01	STE11	D579Y	n/a	n/a	n/a	n/a	3	9	24	32	181	1.2×10^5	1.7	0.977	0.983	0.261	18.1	1	0.018
			n/a	n/a	n/a	n/a	67	69	60	68									
RMS1-D12	IRA1	Y822*	8	34	84	73	98	97	97	n/a	3338	6.7×10^4	1.6	0.048	0.049	0.001	5.9	2	0.014
			115	64	102	93	105	99	98	n/a									
BYS2-D06	IRA2	A2698T	n/a	2	1	51	64	79	119	n/a	539	850	2.0	0.440	0.557	0.209	2.3	2	0.074
			n/a	154	147	150	152	93	125	n/a									

^aFor each mutation, top row shows the number of reads with the mutant allele and the bottom row shows the total coverage at that site. Data points that give the lowest FIT P -value for each mutation are in bold.

^bFor ELRT, we show the parameter values that maximize likelihood functions (9) and (10) under the Gaussian approximation, the probability P_{obs} of an absorption event during the sampling period in the neutral Wright-Fisher trials with \tilde{N} , an upper bound on the ELRT P -value given by the fraction of trials that have a higher than observed LRS among all trials, and the conditional P -value given by the fraction of trials that have a higher than observed LRS among trials without an absorption event.

Tables S3 and S4 are available for download as Excel files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.158220/-/DC1>.

Table S3 Results of FIT applied to data from yeast populations evolved at different population sizes

Table S4 Raw flow cytometry counts for yeast populations evolved at different population sizes