

File S3. Supporting Figures

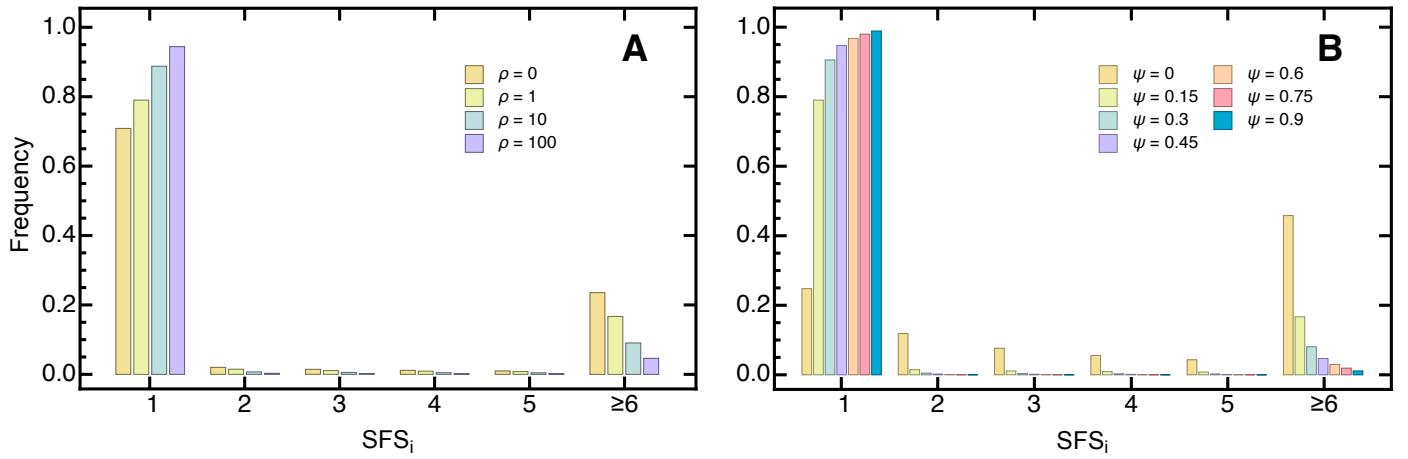


Figure S1 – The normalized expected (lumped) SFS for the psi-coalescent for an exponentially growing population (eq. 18) with sample size  $k = 100$  (A) for different values of  $\rho$  and fixed  $\psi = 0.15$  and (B) for different values of  $\psi$  and fixed  $\rho = 1$ . The sixth entry in the SFS contains the aggregate of the higher frequency classes.

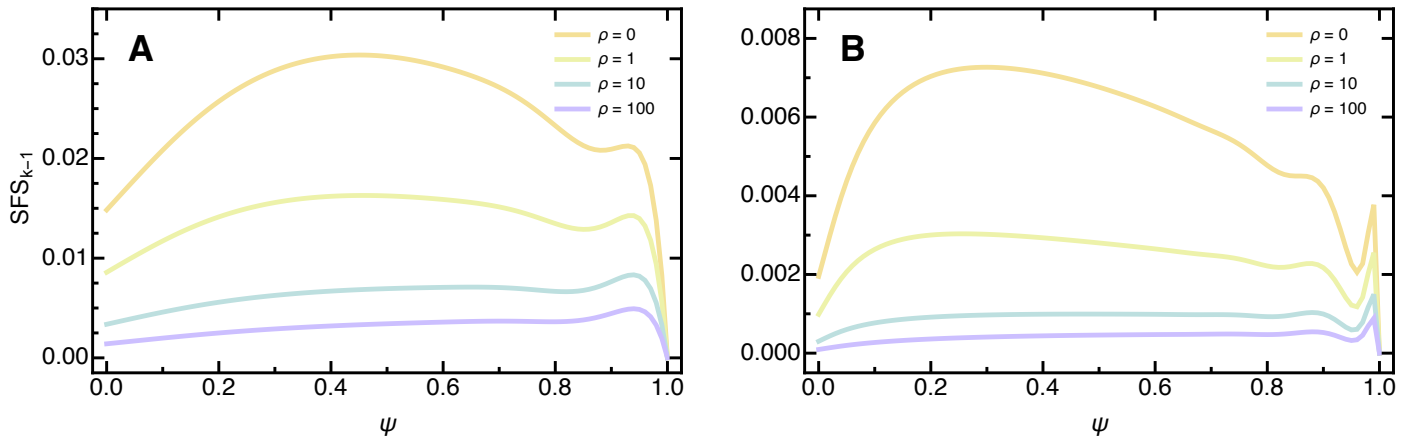


Figure S2 – The normalized expected last entry of the SFS (eq. 18) as a function of  $\psi$  for various values of  $\rho$  with sample size (A)  $k = 20$  and (B)  $k = 100$ .

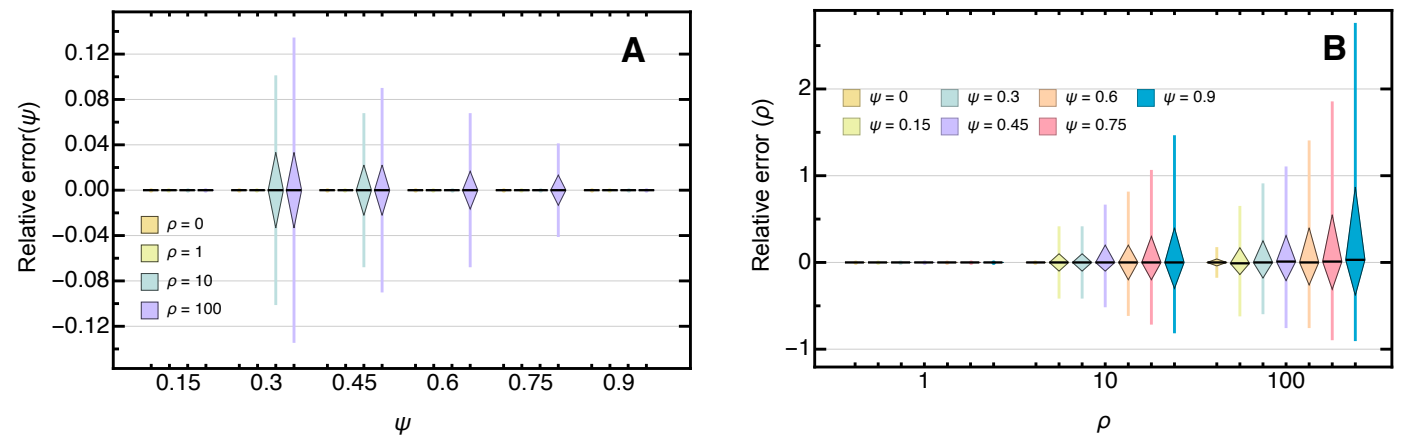


Figure S3 – Boxplot of the relative error of the maximum likelihood estimate from the true (A)  $\psi$  and (B)  $\rho$  for 10,000 data sets assuming independent sites with  $k = 100$  and  $\theta$  (eq. 45) with  $s = 10,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.

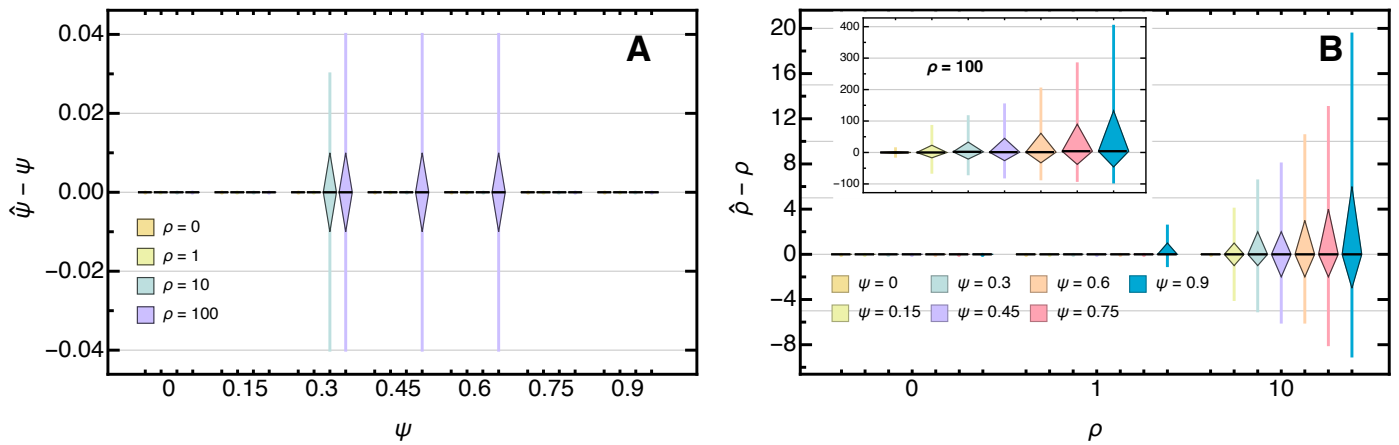


Figure S4 – Boxplot of the deviation of the maximum likelihood estimate from the true (A)  $\psi$  and (B)  $\rho$  for 10,000 data sets assuming independent sites with  $k = 200$  and  $\theta$  (eq. 45) with  $s = 10,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.

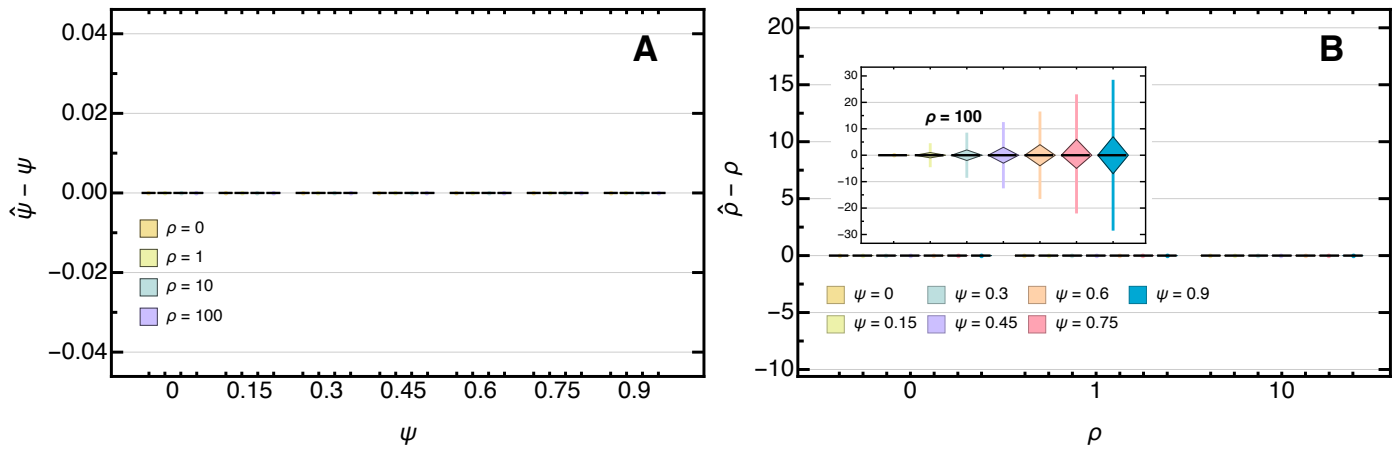


Figure S5 – Boxplot of the deviation of the maximum likelihood estimate from the true (A)  $\psi$  and (B)  $\rho$  for 10,000 data sets assuming independent sites with  $k = 200$  and  $\theta$  (eq. 45) with  $s = 1,000,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range. As the number of segregating sites  $s$  increases the variance of the estimator decreases and approaches its true underlying value.

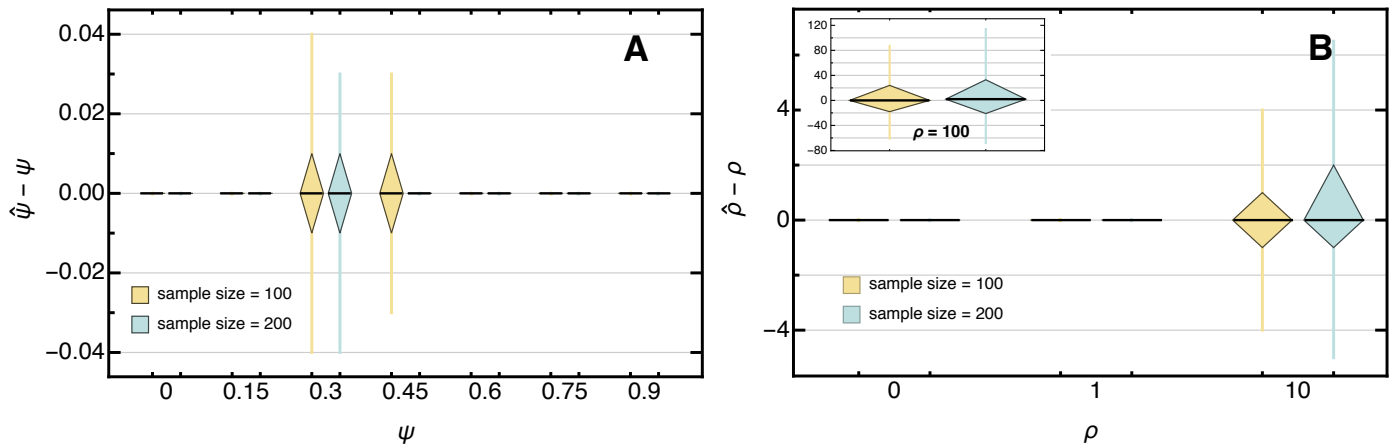


Figure S6 – Boxplot of the deviation of the maximum likelihood estimate from the true (A)  $\psi$  and fixed  $\rho = 10$ , and (B)  $\rho$  and fixed  $\psi = 0.3$  for 10,000 data sets assuming independent sites for different sample sizes  $k$  and  $\theta$  (eq. 45) with  $s = 10,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.

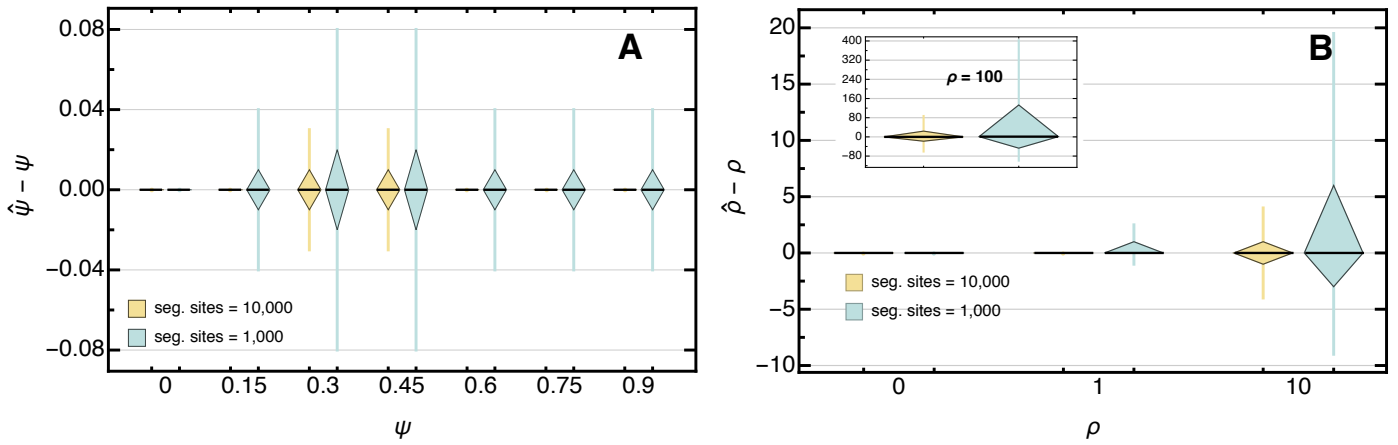


Figure S7 – Boxplot of the deviation of the maximum likelihood estimate from the true (A)  $\psi$  and fixed  $\rho = 10$ , and (B)  $\rho$  and fixed  $\psi = 0.3$  for 10,000 data sets assuming independent sites for different segregating sites  $s$  with  $k = 100$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.

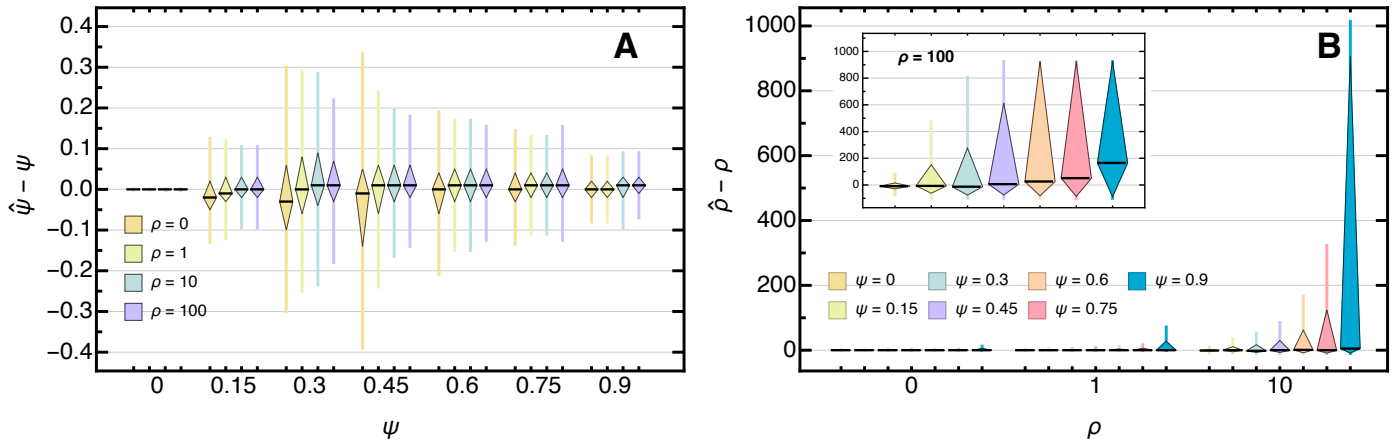


Figure S8 – Boxplot of the deviation of the maximum likelihood estimate from the true (A)  $\psi$  and (B)  $\rho$  for 10,000 whole-genome data sets with  $\ell = 1, k = 100, \gamma = 1.5$ , and  $\theta$  (eq. 45) with  $s = 100,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range. Coalescent parameters (A) and growth rates (B) estimates inferred from a single locus only, display a huge variance, in particular when the true underlying growth rate is large. Note that growth rate estimates are limited by the maximum grid point considered (i.e., 1024).

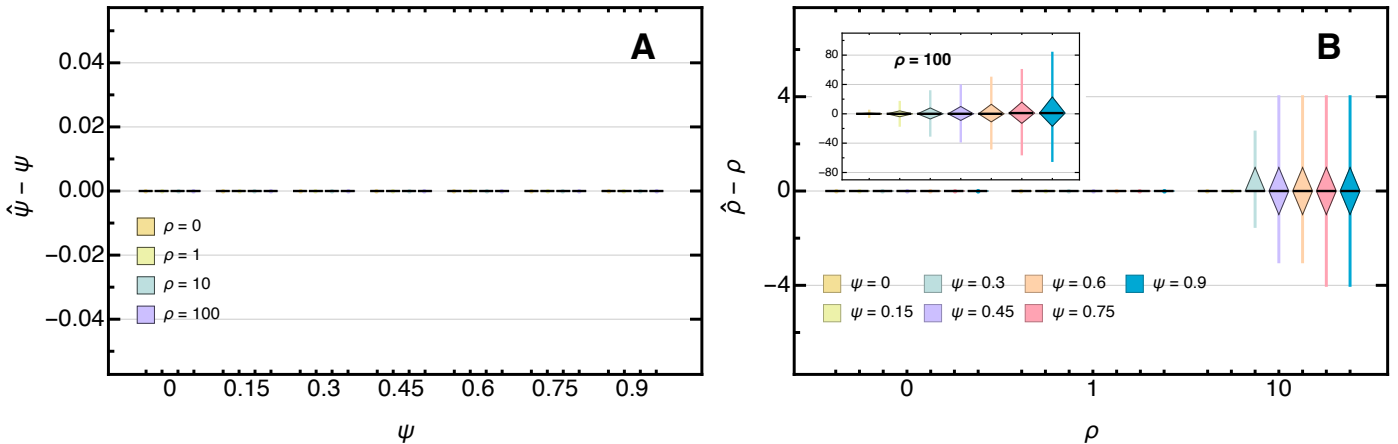


Figure S9 – Boxplot of the deviation of the maximum likelihood estimate from the true (A)  $\psi$  and (B)  $\rho$  for 10,000 whole-genome data sets with  $\ell = 1,000, k = 100, \gamma = 1.5$ , and  $\theta$  (eq. 45) with  $s = 100$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range. The variance in the coalescent parameter (A) and growth rate (B) estimates decreases dramatically as the number of independent loci increases (even when the number of segregating sites is held constant; for comparison see Fig. 8).

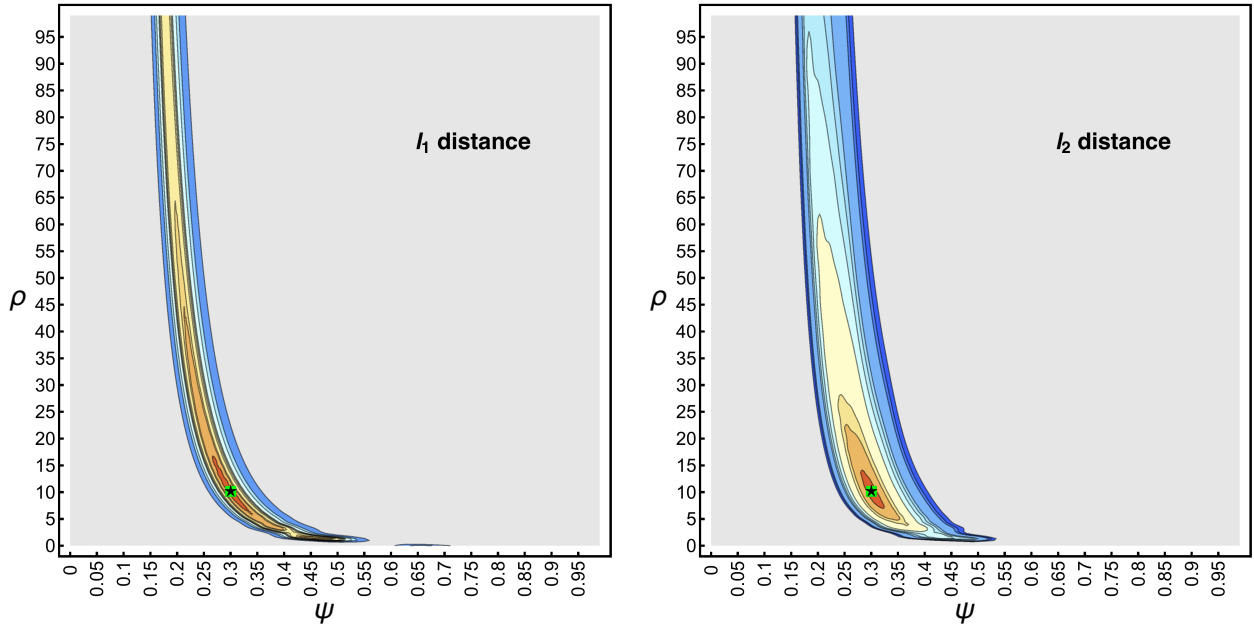


Figure S10 – Surface of the  $l_1$  (left) and the  $l_2$  (right) distance of the idealized SFS with  $k = 100$ ,  $\psi = 0.3$ ,  $\rho = 10$  and  $s = 10,000$ . Contours show the 0.95, 0.9675, 0.975, 0.99, 0.99225, 0.9945, 0.99675, 0.999, 0.99945 and 0.9999 quantiles. Distances below the 0.95 quantile are uniformly colored in gray. The green square shows the true  $\psi$  and  $\rho$ . The black star shows the minimum distance estimates  $\hat{\psi}$  and  $\hat{\rho}$ .

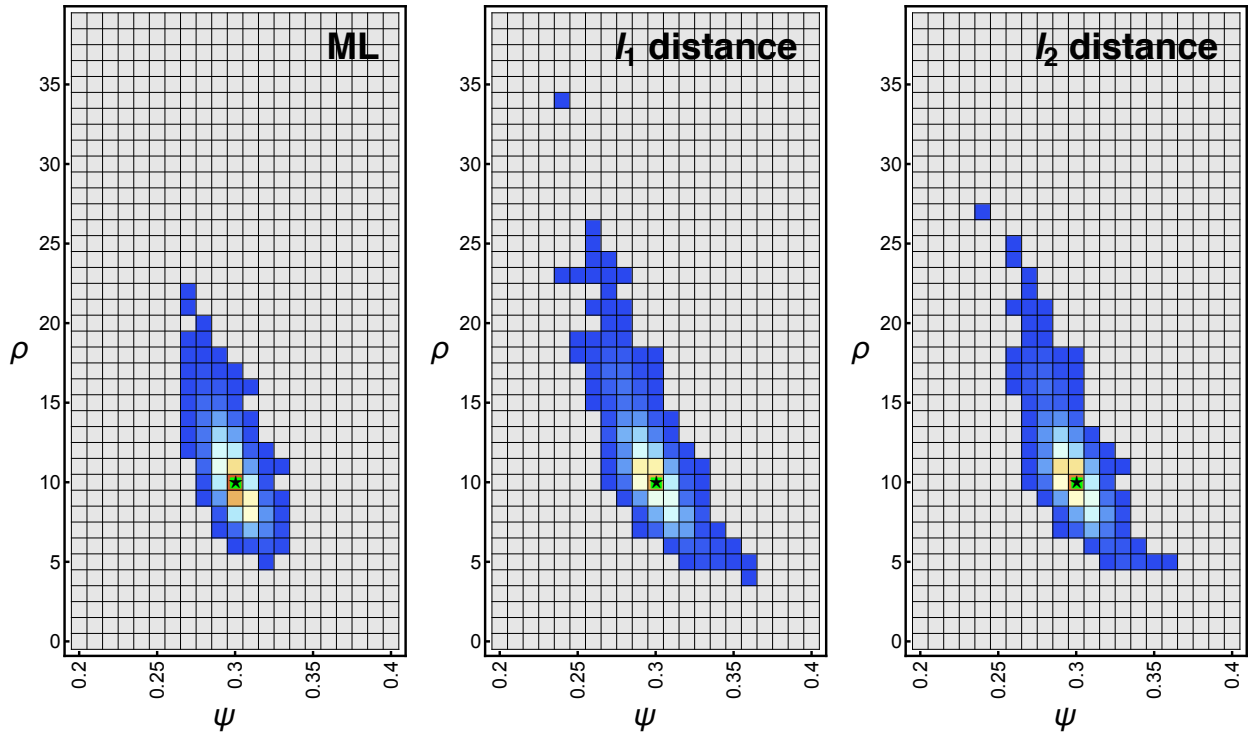


Figure S11 – Heatplot of the frequency of the maximum likelihood estimates (left), the  $l_1$  distance (middle), and the  $l_2$  distance (right) for 10,000 data sets assuming independent sites with  $k = 100$ ,  $\psi = 0.3$ ,  $\rho = 10$  and  $s = 10,000$ . Counts increase from blue to red with grey squares showing zero counts. The green square shows the true  $\psi$  and  $\rho$ . The black star shows the median (and mean) of the maximum likelihood respectively the minimum distance estimates  $\hat{\psi}$  and  $\hat{\rho}$ .

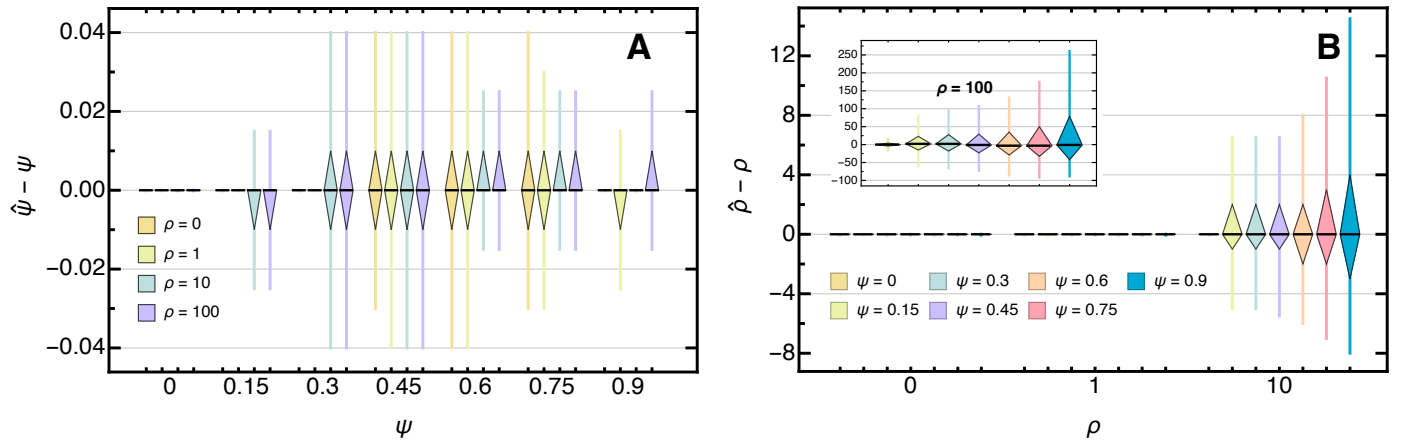


Figure S12 – Boxplot of the deviation of the L1-distance estimate from the true (A)  $\psi$  and fixed  $\rho = 10$ , and (B)  $\rho$  and fixed  $\psi = 0.3$  for 10,000 data sets assuming independent sites with  $k = 100$  and  $\theta$  (eq. 45) with  $s = 10,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.

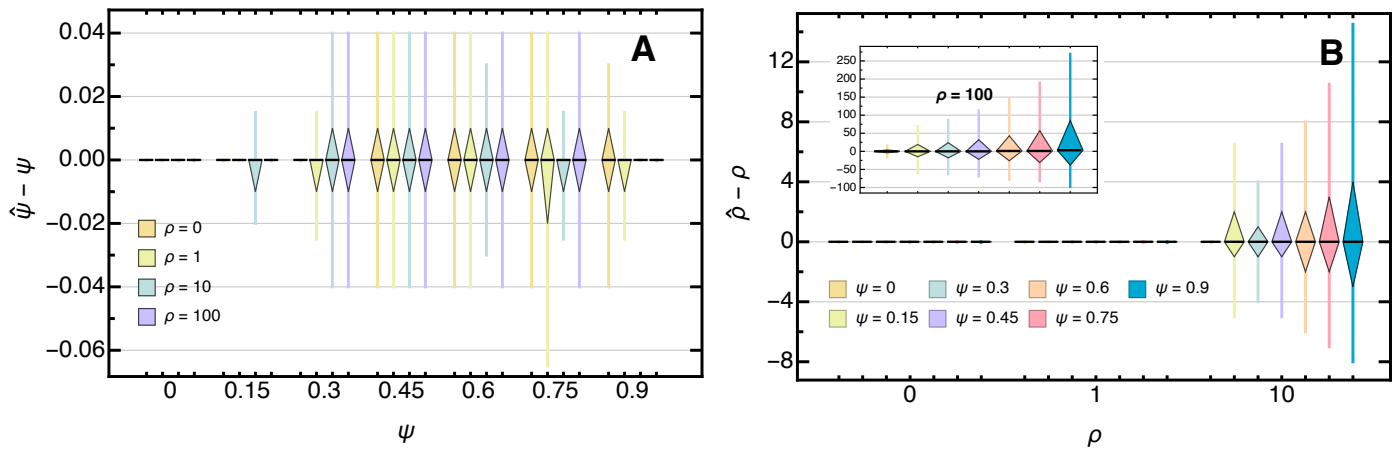


Figure S13 – Boxplot of the deviation of the L2-distance estimate from the true (A)  $\psi$  and fixed  $\rho = 10$ , and (B)  $\rho$  and fixed  $\psi = 0.3$  for 10,000 data sets assuming independent sites with  $k = 100$  and  $\theta$  (eq. 45) with  $s = 10,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.

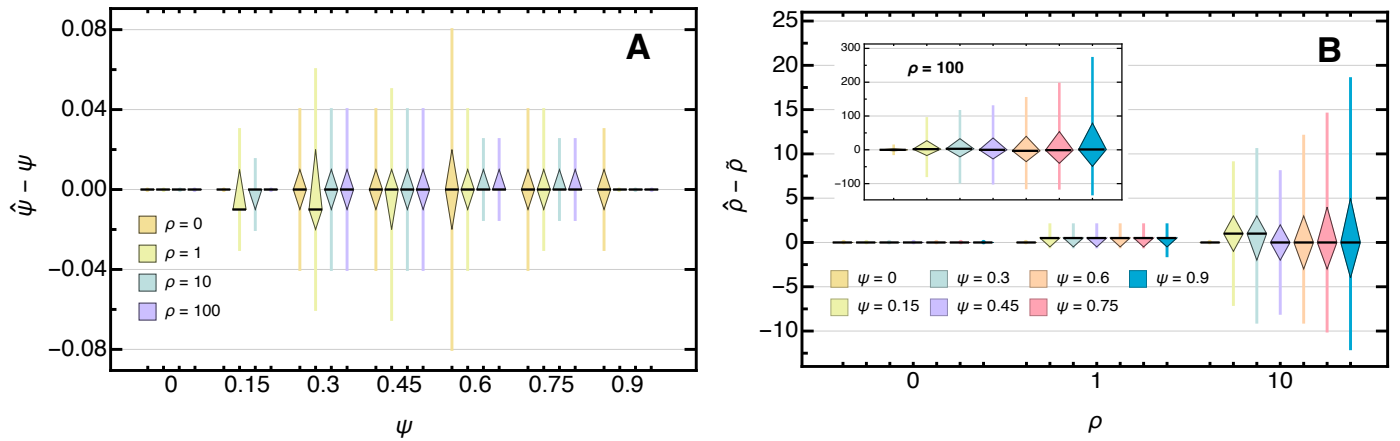


Figure S14 – Boxplot of the deviation of the  $I_1$  distance estimate from the true (A)  $\psi$  and (B)  $\rho$  for 10,000 whole-genome data sets with  $\ell = 100, k = 100, \gamma = 1.5$ , and  $\theta$  (eq. 45) with  $s = 1,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.

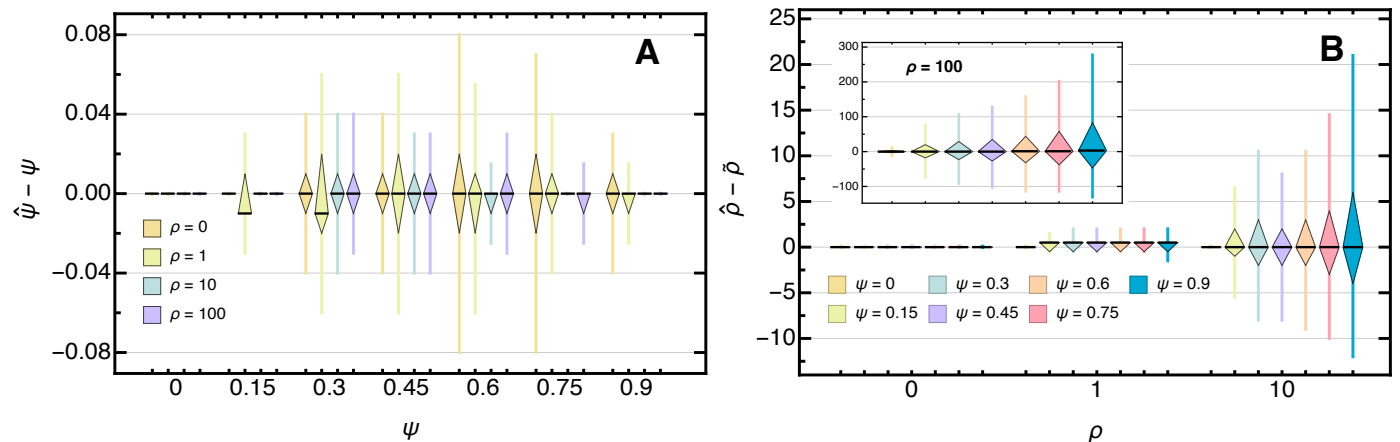
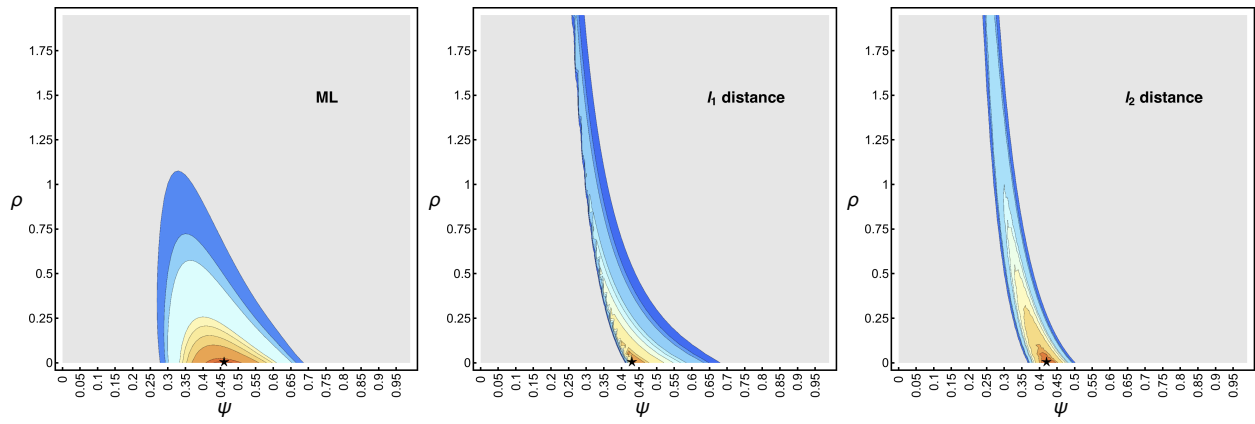


Figure S15 – Boxplot of the deviation of the  $I_2$  distance estimate from the true (A)  $\psi$  and (B)  $\rho$  for 10,000 whole-genome data sets with  $\ell = 100, k = 100, \gamma = 1.5$ , and  $\theta$  (eq. 45) with  $s = 1,000$ . Boxes represent the interquartile range (i.e., the 50% C.I.) and whiskers extend to the highest/lowest data point within the box  $\pm 1.5$  times the interquartile range.



**Figure S16** – Likelihood (left),  $I_1$  distance, and  $I_2$  distance surface of the unfolded SFS (given the ML rooted tree) of the sardine mtDNA sequences with  $k = 106$  and  $s = 81$ . Contours show the corresponding 0.95, 0.9675, 0.975, 0.99, 0.99225, 0.9945, 0.99675, 0.999, 0.99945 and 0.9999 quantiles. Likelihoods respectively distances below their corresponding 0.95 quantile are uniformly colored in gray. The black star shows the maximum likelihood respectively minimum distance estimates:  $\hat{\psi}_{ML} = 0.46$  and  $\hat{\rho}_{ML} = 0$ ,  $\hat{\psi}_{I_1} = 0.43$  and  $\hat{\rho}_{I_1} = 0$ , and  $\hat{\psi}_{I_2} = 0.42$  and  $\hat{\rho}_{I_2} = 0$ .