



FIGURE S3.— The 95th percentile for (A) the ω_{MAX} and (B) Λ_{MAX} based on the $F\theta$ (full circles), the FS procedure (open circles) and the $F\theta S$ approach (crosses). Bottleneck simulations have been performed for a 50-kb genomic segment and 12 sequences ($h_n \approx 3$). We have used the demographic scenario inferred by LI and STEPHAN (2006) that describes the history of the European population of *D. melanogaster*. Recombination rate is 0.05/bp. For a given number of segregating sites (x-axis) simulations were performed by (i) fixing the number of segregating sites S_n (open circles), (ii) using $\theta_{\text{NEU}} = \hat{\theta} = \frac{2S_n}{E(T_c)}$, where $E(T_c)$ is the expected total length of the coalescent of n sequences (ZIVKOVIC and WIEHE, 2008) (filled circles). In this case simulations generate on average S_n segregating sites. (iii) Under the $F\theta S$ process (crosses) we used the same $\theta_{\text{NEU}} = \hat{\theta}$, but only the realizations that produced S_n segregating sites).