

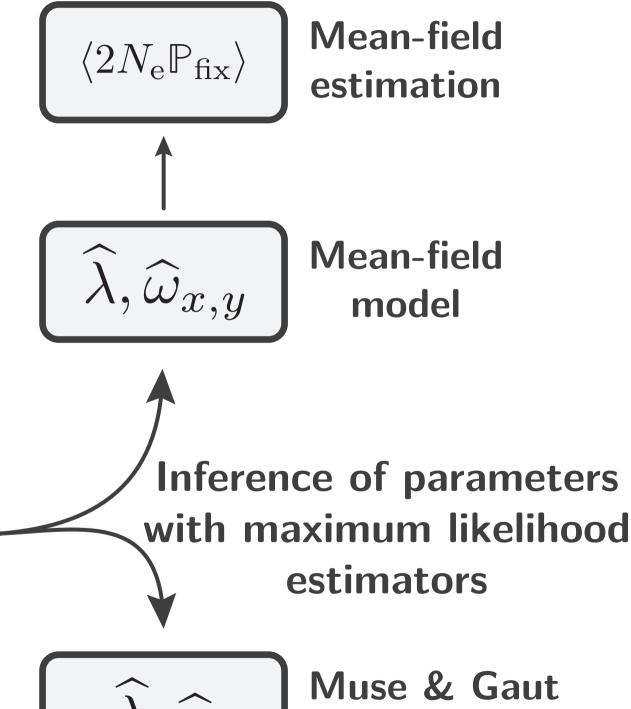
 $\langle 2N_e\mathbb{P}_{\rm fix}\rangle$ is the mean scaled fixation probability of non-synonymous mutations.

 $\langle 2N_{\rm e}\mathbb{P}_{\rm fix}\left(x\to y\right)\rangle$ is between pairs of amino acids.

 $\langle 2N_{\rm e}\mathbb{P}_{\rm fix}\left({\rm GC} \to {\rm AT}\right)\rangle$ is from strong to weak nucleotides.

 $\langle 2N_{\rm e}\mathbb{P}_{\rm fix}\left({\rm AT}\to{\rm GC}\right)\rangle$ is from weak to strong nucleotides.

ATG|GGA|TCC|ATG|CTA|CGA|TCG
ATG|CGA|TCC|ATG|GTA|CGA|TCG
ATG|CGA|TCG|AAG|CTT|CGA|TCC
ATG|CGA|TAG|AAG|CTT|CGA|TCG
ATG|CGA|TCG|ATC|CAT|CGA|TCG
Alignment of coding sequence



model