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A rigorous model for adaptive dynamics of Mendelian diploids

Adaptive dynamics so far has been put on a rigorous footing only for clonal inheritance. We extend this to sexually reproducing diploids, although admittedly still under the restriction of an unstructured population with Lotka-Volterra-like dynamics and single locus genetics (as in Kimura's infinite allele model). We prove under the usual smoothness assumptions that when advantageous mutations are rare and mutational steps are not too large the population behaves on the mutational time scale (the "long" time scale of the literature on the genetical foundations of ESS theory) as a jump process moving between homozygous states (the trait substitution sequence of the adaptive dynamics literature). Essential technical ingredients are an individual-based stochastic (birth and death) process with mutation and selection, a rigorous, geometric singular perturbation theory based, invasion implies substitution theorem and estimates for the probability of invasion in a dynamical diploid population. In the small mutational steps limit this process gives rise to a differential equation in allele or in phenotype space of a type referred to in the adaptive dynamics literature as 'canonical equation'.

(joint work with P. Collet and J.A.J. Metz)