Polymorphic trait substitution sequence and evolutionary branching

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Joint work with Nicolas Champagnat

We are interested in the study of models describing the evolution of a polymorphic population with mutation and selection in the specific scales of the biological framework of adaptive dynamics. The population size is assumed to be large and the mutation rate small. We prove that under a good combination of these two scales, the population process is approximated in the long time scale of mutations by a Markov pure jump process describing the successive trait equilibria of the population. This process, which generalizes the so-called trait substitution sequence, is called polymorphic evolution sequence. Then we introduce a scaling of the size of mutations and we study the polymorphic evolution sequence in the limit of small mutations. From this study in the neighborhood of evolutionary singularities, we obtain a full mathematical justification of a heuristic criterion for the phenomenon of evolutionary branching. To this end we finely analyze the asymptotic behavior of 3-dimensional competitive Lotka-Volterra systems.