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A study of evolutionary branching in a logistically regulated population

We are trying to give a mathematical basis to the notion of evolutionary branching introduced by Metz et al. in 1996 in the framework of adaptive dynamics, which studies the long-term evolution of ecologically explicit populations. It is said that evolutionary branching occurs in a population when the evolutionary dynamics drives the population from an (essentially) monotype population to an (essentially) 2-type population. We consider a finite stochastic population with birth, mutation, death and selection due to a logistic-type competition (nonlinearity in the death rates), where individuals are characterized by a finite dimensional phenotypic trait (such as body size, rate of food intake,...). We first consider the combination of the limits of large population and rare mutation, which allows one to simplify the dynamics as a jump process over the trait space describing the successive invasions of mutants, and which is based on a time-scale separation. This process allows transitions from monomorphic populations (with only one trait) to dimorphic populations.

This process is therefore a natural one to study evolutionary branching. In particular, when the size of mutations in the trait space converges to 0, we are able to justify the branching criterion proposed by biologists, to precisely describe the transition from a monomorphic population to a dimorphic one, and to explicitly compute the time-scale of mutation.

This is joint work with Michel Bénaïm, Anton Bovier and Sylvie Méléard.