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The stationary distribution of the ancestral types in the Moran model with mutation and selection

We consider a stochastic model of population genetics, namely, the Moran model with mutation and selection. We use it to trace back the ancestral lines of single individuals, and are interested in the stationary distribution of the corresponding ancestral types. Two approaches to this problem are already available: The one by Fearnhead (2002), which is based on the ancestral selection graph (Krone/Neuhauser 1997), and the one by Taylor (2007), which relies on a description of the full population backward in time by means of a diffusion equation.

In both approaches, the resulting expression for the stationary distribution does not have an obvious interpretation in terms of the graphical representation of the model (i.e. the representation that makes individual lineages and their interactions explicit). In this contribution (which is joint work with Ellen Baake), we use the graphical representation to derive equations for the fixation probabilities of the offspring of all 'fit' individuals (regardless of the offspring's type). In the diffusion limit, this yields Taylor's differential equation - but now with a plausible interpretation attached to it. Furthermore, this also points the way towards a better understanding of the coefficients that define the stationary distribution.