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**A mathematical formalism for natural selection with arbitrary spatial and genetic structure.**  
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**Summary:** We define a general class of models representing natural selection between two alleles. The population size and spatial structure are arbitrary, but fixed. Genetics can be haploid, diploid, or otherwise; reproduction can be asexual or sexual. Biological events (e.g. births, deaths, mating, dispersal) depend in arbitrary fashion on the current population state. Our formalism is based on the idea of genetic sites. Each genetic site resides at a particular locus and houses a single allele. Each individual contains a number of sites equal to its ploidy (one for haploids, two for diploids, etc.). Selection occurs via replacement events, in which alleles in some sites are replaced by copies of others. Replacement events depend stochastically on the population state, leading to a Markov chain representation of natural selection. Within this formalism, we define reproductive value, fitness, neutral drift, and fixation probability, and prove relationships among them. We identify four criteria for evaluating which allele is selected and show that these become equivalent in the limit of low mutation. We then formalize the method of weak selection. The power of our formalism is illustrated with applications to evolutionary games on graphs and to selection in a haplodiploid population.

**MSC:**

- [92D10](#) Genetics and epigenetics
- [92D15](#) Problems related to evolution
- [91A22](#) Evolutionary games
- [91A43](#) Games involving graphs
- [60J85](#) Applications of branching processes

**Keywords:**

[evolution](#); [population genetics](#); [fixation probability](#); [spatial structure](#); [weak selection](#); [Markov chain](#)

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