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In silico evolution of biochemical networks

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We use computational evolution to select models of genetic networks that can be built from a predefined set of parts to achieve a certain behavior. Selection is made with the help of a fitness defining biological functions in a quantitative way. This fitness has to be specific to a process, but general enough to find processes common to many species. Computational evolution favors models that can be built by incremental improvements in fitness rather than via multiple neutral steps or transitions through less fit intermediates. With the help of these simulations, we propose a kinetic view of evolution, where networks are rapidly selected along a fitness gradient. This mathematics recapitulates Darwin's original insight that small changes in fitness can rapidly lead to the evolution of complex structures such as the eye, and explain the phenomenon of convergent/parallel evolution of similar structures in independent lineages. We will illustrate these ideas with networks implicated in embryonic development and patterning of vertebrates and primitive insects.