

New analysis uses network theory to model speciation

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The diversity of the biological world is astounding. How do new species arise? In the traditional view, most speciation events occur under special circumstances, when a physical barrier arises and divides a population into groups that can no longer interbreed. The populations diverge genetically and eventually can't interbreed even if the barrier disappears.

In new research NECSI has explained why barriers are not needed for speciation to occur. They modeled the mating interactions as an influence network, mathematically mapping the dynamics of evolution onto a model they have studied before in a wide range of contexts.

NECSI researchers have previously shown that populations that are distributed across space spontaneously break up into species, even without physical barriers. It is enough that individuals travel only limited distances to find a mate and only mate with genetically similar individuals. This work, published in Nature in 2009, also found that patterns of diversity predicted by this model match remarkably well the diversity found in nature.

The new NECSI research, published March 8 on the Arxiv, analytically derives an expression for the conditions under which speciation is expected to occur. The research finds that speciation results from the influence of two opposing forces:

- Geographically localized mating increases diversity as mutants mate with each other and mutations become fixed in sub-populations.

- Mating with genetically similar individuals (assortative mating) reduces diversity by limiting the genetic variation within a mating [population](#).

These opposing forces together produce speciation through the formation of patches of individuals with localized [mating](#) patterns, that are genetically similar among themselves and increasingly differ from other patches.

The new results strengthen those of the earlier work, showing that speciation can occur under the “ordinary” circumstances of individuals distributed across space, and clarifying the processes that give rise to it. The analytic derivation also provides a quantitative formula in terms of the mutation rate, genome length, and density of the organisms that agrees with simulation results and can be compared with observations.

In this work, researchers treated natural populations as networks of connected individuals, an innovative application of NECSI’s Network Influence Model, the same model NECSI used to model and predict market crashes. The model is a quite general model of conformity and diversity and therefore also described the forces that drive genetic conformity and diversity in evolution. Many other applications are possible, for example to describe and predict behaviors of ideological or economic groups in sociopolitical settings.

More information: arxiv.org/abs/1012.3913

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