The spreading of evolutionary novelties across populations is the central element of adaptation. Models of evolutionary spread have been limited, until quite recently, to the infinite population size limit ignoring number fluctuations. Using microbial evolution experiments and simulations, I show that these mean-field models generically fail to predict genealogical relationships, and break down entirely when rare long-range jumps are involved. I present novel modeling approaches to account for number fluctuations in these non-linear spatio-temporal problems that can explain observed patterns of genetic diversity, spatial spread and adaptation in microbial populations, and that make novel predictions about epidemic spread on a global scale.

Monday, November 17, 4:00 PM
Technological Institute M416

For further information see http://www.esam.northwestern.edu

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