The spreading dynamics of genetic information plays a key role in evolution of spatially structured populations. As with chemical reactions, diffusive populations (which experience short-ranged migration or dispersal behavior) exhibit spatiotemporal patterns of genetic variation which differ markedly from well-mixed populations (where each individual interacts with all others over the population range). Between these two extremes lies the situation of populations experiencing long-range dispersal, with migration events drawn at random from a broad probability distribution (akin to Lévy flights). Although long-range dispersal is ubiquitous in nature (plants whose seeds and pollen are spread wide by wind, water, or animals; pathogens riding on jet setting humans), its evolutionary consequences are still being uncovered. I'll talk about recent work that uses simulations and theory to elucidate the patterns left behind by multiple genetic variants during adaptation and expansion events driven by stochastic long-range dispersal.

By studying a class of models in which the dispersal distribution is systematically broadened by varying a parameter, I'll show how stochastic effects accumulate to give rise to qualitatively different phases and counterintuitive effects on both local and population-wide genetic diversity.