

ネイマン・スコットクラスター一点過程の 平衡及び非定常への拡張

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It has been increasingly recognized that common ideas such as neutrality, stochastic drift, coalescence, dispersal kernel, distance-decay similarity play an essential role both in community ecology, population genetics and spatial molecular ecology (Hubbell 2001, Chave 2002, Shimatani 2002, Hardy and Sonke 2004, Etienne 2004). Spatially limited seed dispersal causes spatially clustering individual distribution, and contributes to forming spatial genetic structure (isolation by distance, Wright 1943). Clustering reproductive system around mothers can be modeled by the Neyman-Scott process (Neyman and Scott 1958, Stoyan and Stoyan 1994, Penttinen and Stoyan 2002). Its replicated, genetic versions provide basic null models of spatial population dynamics controlled by neutral seed dispersal and allows us to examine spatial individual distribution and spatial genetic structure comprehensively (Shimatani 2002, Shimatani and Takahashi 2003). Even though, unlike frequent applications of point process models in spatial ecology (e.g. Penttinen et al. 1992, Batista and Maguire 1998, Shimatani and Kubota 2004, Weigand et al. 2007, Morlon et al. 2008, Tanaka et al. 2008), theoretical spatial genetics studies rarely considered spatial individual distributions (Doligez et al. 1998). Instead, spatial genetics models first assumed random individual distribution on a plane (in the coalescence model, Malécot (194), Chave (2002)) or individuals on lattice points (in many of simulation studies such as Hardy and Vekemans 1999), then their parentage was assigned according to a given spatially regulated reproductive process (here I call them “fixed-distribution” assumption). An exception was Doligez et al. (1999) that conducted simulations on the context of the Neyman-Scott process and reached similar conclusions with previous studies. Although the reproductive systems given by the Neyman-Scott process (definitions are given below) and the fixed-distribution sound like essentially equivalent, Shimatani (2002) showed that there exist significant differences between the two:

1. Spatial individual distribution gives significant effects of spatial genetic structure, as opposed to Doligez et al. (1998), “the presence of strong clumping leads to a slight increase in spatial autocorrelations compared with uniformly distributed populations”.

2. The degree of genetic clustering decreases over generations, as opposed to the increasing genetic structures shown in almost all the previous papers (e.g. Hardy and Vakeman, 1999)

In the genetic Neyman-Scott process in Shimatani (2002), the fundamental parameters are seed dispersal kernel, the density of parents and the number of offspring produced, and did not incorporate pollen flow. In other words, all pollen were assumed to be immigrants and the process is repeated on an infinite plane with infinite number of individuals. The first object is to compliment this simplified assumption by simulating the genetic Neyman-Scott process with spatially limited pollen flow on a finite region. This elucidated the essential role of reducing number of ancestral parents over generations in addition to the spatially limited dispersal.

The second object is to extend the process to incorporate immigration. This released us from the classical problem: the individual clustering is accumulated and diverges, thus does not reach an equilibrium state, which was first pointed out by Felesenstein (1975) and showed again in the point process formulation in Shimatani (2002).

Third, the expected number of offspring does not solely affect the spatial genetic structure. Instead, the relative magnitude between the expected value and the variance is essential and we need to consider the probability distribution for the numbers of offspring. I briefly mentioned some published papers that wrongly discussed this point (Asuka et al. (2005).

The fourth object is to extend the genetic Neyman-Scott formulae to generation overlapping, and the fifth is to more general functions, a sum of the normal distributions. This extension is clearly applicable to the two-component dispersal kernel (Goto et al. 2007), and to the t -distribution kernel that can be expressed by the infinite sum of the normal distributions (Clark et al.1999). More importantly, the extended formula can demonstrate the effects of high mortality near mothers on spatial structure, that is the point process model of the Janzen-Connell hypothesis (Janzen 1970, Connell 1971). It is then shown that high mortality near a mother also involves a clustering distribution, as opposed to “a repulsive interaction between seedlings and their parent trees could result in spacing of congeneric trees, driving the spatial patterns towards regularity (Forget et al. 1999).

The sixth object is applications of the theory to real spatial genetic data.