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Isolation by distance patterns arising from short range and long range dispersal

Abstract : The spatial structure of genetic diversity is mainly shaped by the way individuals move around and disperse their offspring in space. Since shared ancestry translates (at least partially) into shared genetic material, some genealogical information can be recovered from observed or simulated patterns of genetic diversity. Using a model introduced by N. Barton, A. Etheridge and A. Véber, I will study these patterns under two very different dispersal assumptions: limited (short-range) dispersal and unlimited (long-range) dispersal. I will present a functional central limit theorem for measure-valued processes under a space-time rescaling and I will show how one can recover genealogical information from this result. In particular one obtains a natural generalisation of the Wright-Malécot formula under long-range dispersal.