

### 07-Factors and mechanisms affecting spatial heterogeneity of insect populations

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1. The spatial distribution of populations is affected by the dispersal abilities of the species, interactions among individuals, or habitat selection. Linking these ecological processes to spatial patterns is of primary importance for understanding and prediction purposes.
2. We review both statistical and mechanistic methods for studying the spatial distribution of populations. Statistical methods, such as spatial indexes and nearest-neighbour analyses help characterizing the spatial pattern. They allow testing the effect of environmental variables on spatial patterns using regression analyses.
3. Mechanistic modelling can be used to analyse the effect of mechanisms underlying the spatial pattern. We review mechanistic models (e.g. metapopulation, individual-based and cellular automaton models) devoted to represent dispersal abilities, interactions among individuals and habitat selection.
4. We illustrate each method by works on insects, which cover a broad range of spatial patterns. Strengths and limitations of methods are discussed according to the process and type of data set.
5. Scientists can use statistical or mechanistic methods in an iterative manner to infer process from spatial pattern. New approaches such as ‘pattern-oriented modelling’ or ‘space as a surrogate framework’ determine whether alternative models reproduce an observed pattern. It allows selection of the process that best explain the observed pattern.

### 08-Use of population genetics to choose between vector control strategies: the example of tsetse in West-Africa

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In sub-Saharan Africa, tsetse transmitted Trypanosomiasis have an enormous impact on human health and economic development. Both the World Health Organisation and African countries through the Pan African Tsetse and Trypanosomiasis Eradication Campaign (PATTEC) have recently asserted their determination to rid the sub-continent of these diseases, and it is increasingly recognised that vector control should play an important role. This review mainly focuses on population genetics of tsetse of the *palpalis* group, the main vectors of sleeping sickness, and reports recent results on tsetse population structure and on measures of gene flow between populations. Implications of these studies for large-scale tsetse control programmes being undertaken in West Africa are important, particularly regarding control strategies (suppression or eradication).