Genetic diversity in an expanding population

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Why is an allele common in an area ?

Hypotheses

- locally large spatially structured population
- one allele is present and abundant only in a specific area

Example : Flower species present in all Europe.
In France, only blue flowers. Elsewhere, other colors abundantly present.

Why is an allele common ?

- *Explanation 1 :* selective advantage

- *Explanation 2 :* genetic hitchhiking
  The allele is next to another bearing a selective advantage
  See e.g "Genetic hitchhiking", N. Barton,Philosophical Transactions of the Royal Society of London, 2000 and references therein

- *Explanation 3 :* genetic drift $+$ past expansion
  During the expansion, the population is not locally large everywhere.

O. Hallatschek's experiment
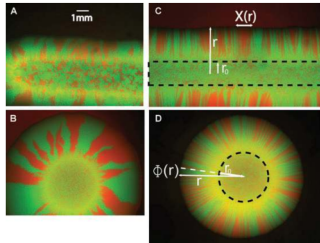
Figure 1: Sectorisation observed in populations of bacteria or yeasts, differing only by the colour of their fluorescence (green or red), which is selectively neutral.

Reference : *"Life at the front of an expanding population"*, O. Hallatschek, D. R Nelson, Evolution : International Journal of Organic Evolution, 2010

$\longrightarrow$ but no theoretical framework predicting the apparition of these sectors and their characteristics

Why is a mathematical framework interesting ?

- basis to do statistics using the number and shape of patters

- difference between the footprints on genetic diversity of expansion and selection

- new theoretical results on the genetic diversity in an expanding population

- beautiful mathematics involved

What I am trying to do

1. *2D, continuous space* : obtain the results of O. Hallatschek theorically

2. *1/2D, discrete space (patches), plants* : design a model in order to study the impact of seed bank and disturbance of the environment on the speed of expansion and patters of genetic diversity
Example : tree bases in a city

Thank you for your attention !

How to study genetic diversity in an expanding population from a mathematical viewpoint ?

2 parts (which are connected) :

1. how to study genetic diversity ? $\longrightarrow$ *using coalescent theory*

2. how to model an expanding population ? $\longrightarrow$ *adding "ghost" individuals to fill completely the space*

Simplifying assumptions

- haploid population

- no mutations occuring (but different alleles are already present)

How to study genetic diversity ?

Main idea : two individuals sharing a common ancestor have the same alleles
Since individuals are haploid and no mutations occur.

Studying genetic diversity looking at common ancestors is called *coalescent theory*, and was first introduced in the 80s by J.F.C. Kingman.

"The coalescent", J. F. C Kingman, Stoch. Process. Appl., 1982
"On the genealogy of large populations", J. F. C Kingman, J. Appl. Probab., 1982

Here, we also have to take into account the structuration in space of the population.

How to model an expanding population ?

Main idea : Add "ghost" individuals which can reproduce as well, but with a selective disadvantage.
The total number of individuals (real individuals + ghosts) is an analog of the carrying capacity.

This idea is for instance used in *"Genealogies in expanding populations"*, R. Durrett, WTL. Fan, The Annals of Applied probability, 2016.