Estimation of the Dispersal of Flavescence Dorée Using Multi-Annual, Landscape-scale Plant-to-Plant Surveys with Detection Delays

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CONTEXT

- **Flavescence dorée** (FD) is a severe grapevine disease transmitted by the leafhopper ***Scaphoideus titanus***
- In EU it is a **quarantine** disease with mandatory prospection & removal of infected plants *and* insecticide treatment
- **Detection delays** in prospection surveys can occur for: **(1)** delay in symptoms **(2)** efficiency in detection

Objectives

- Improvement of our (limited) knowledge of the dispersal of FD, and ultimately, the prospection strategies
- Methodological development accounting for detection delays, relevant across human, animal and plant epidemiology

DATA

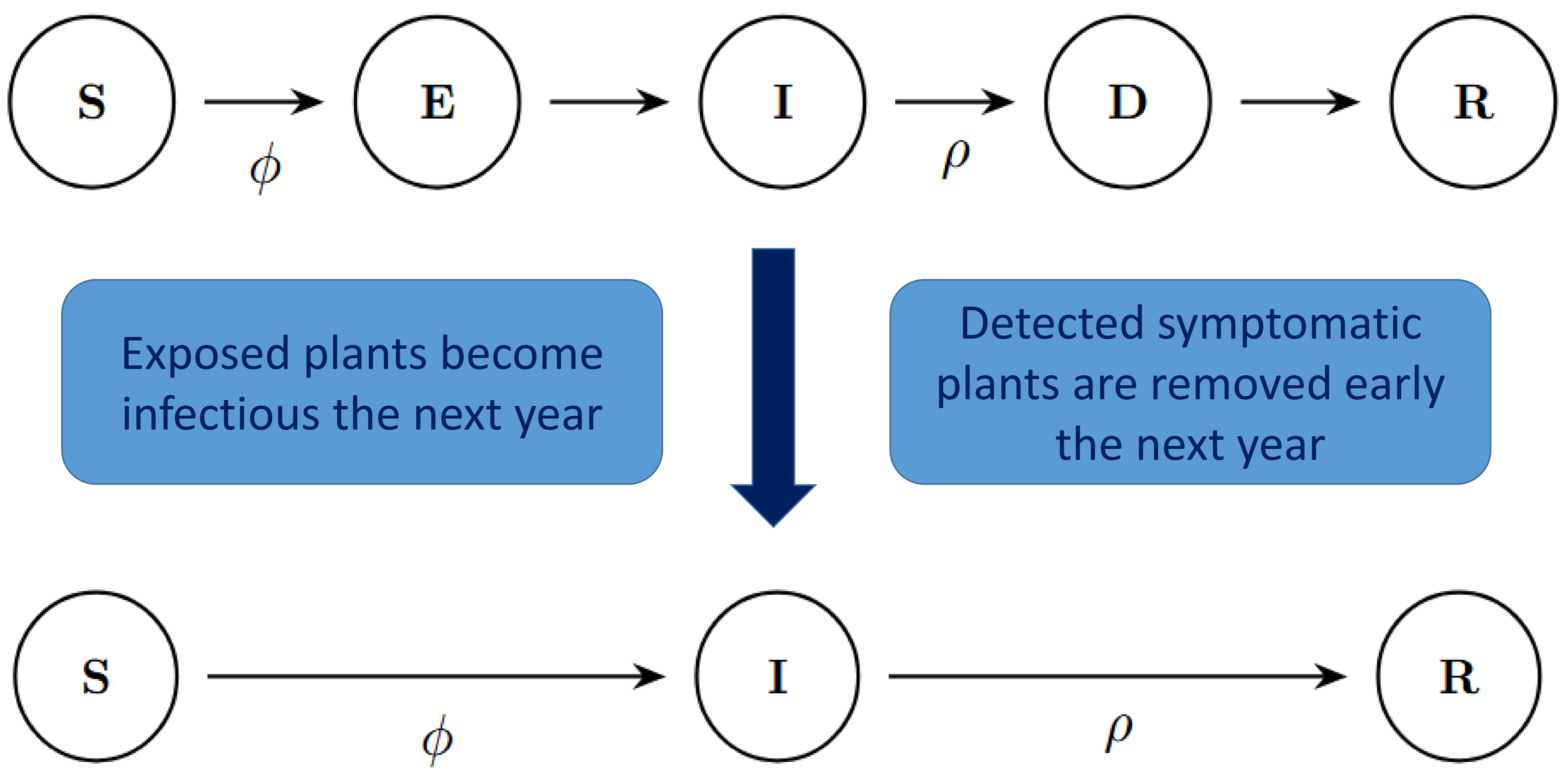
Survey by CIVC in Champagne vineyard in France

- **Period:** 2021-2024 (sept., oct.)
- **Plots:** 4 cultivars
  - **Meunier**, **Chardonnay**, **Pinot Noir**, **Pinot Blanc**
  - Possibly varying susceptibility to FD
- **Size:** 20 hectares, $\mathbf{n_p = 3 \times 10^5}$ plants
- Individual plants were monitored for FD symptoms
- 1-5 plant samples pooled to confirm FD infection by PCR
- Infectious plants removed before next year vector cycle

Data: Removal years $y_i^R \in \{1, 2, .., n\}$, for i=1,2,..,n_p and n=4

COMITÉ CHAMPAGNE

EPIDEMIOLOGICAL MODEL



- **ρ : Probability of detecting** a FD infected plant
- **ϕ_i(y) : Force of infection** exerted on plant **i** on year **y**

$$\phi_i(y) = \underbrace{\beta_0(y)}_{\text{External infection force}} + \underbrace{\beta g(N_y)}_{\text{Effect of insecticide treatment}} \sum_{j \in \mathbf{I}_{y-1}} \underbrace{c_j}_{\text{Effect of cultivar of plant j}} \underbrace{K(r_{ij}, \alpha)}_{\text{Effect of the distance } r_{ij} \text{ through dispersal kernel } K}$$

LIKELIHOOD BASED INFERENCE

$$\sum_{\substack{\mathcal{I} \subset \{1,\dots,n_p\} \\ y_i^{\mathrm{I}} \in \{1,\dots,n\}: i \in \mathcal{I}}} \mathbb{P}\Big(\overbrace{Y_i^{\mathrm{R}} = y_i^{\mathrm{R}} : i \in \mathcal{R}}^{\text{Year of removal } \mathbf{Y}_i^R \text{ for observed period}}; \overbrace{Y_i^{\mathrm{R}} > n+1 : i \in \mathcal{R}^c}^{\text{Year of removal } \mathbf{Y}_i^R \text{ for right censored period}}; \underbrace{Y_i^{\mathrm{I}} = y_i^{\mathrm{I}} : i \in \mathcal{I}}_{\text{Year of infection } \mathbf{Y}_i^I \text{ for observed period}}; \underbrace{Y_i^{\mathrm{I}} > n : i \in \mathcal{I}^c}_{\text{Year of infection } \mathbf{Y}_i^I \text{ for right censored period}}\Big)$$

The true years of infection $\boldsymbol{y}_i^I$ are unknown due to (potential) detection delay

- $\mathcal{R}$ (resp. $\mathcal{R}^c$) denote the set of plants **removed** during $2 \le y \le n+1$ ($y > n+1$).
- $\mathcal{I}$ (resp. $\mathcal{I}^c$) denotes the set of plants that are **infected** during $1 \le y \le n$ ($y > n$).

(1.1) Likelihood: treating $\boldsymbol{y}_i^I$ as latent variables
(1.2) Pesudo likelihood: $\boldsymbol{y}_i^I = \max\{1, \boldsymbol{y}_i^R - \boldsymbol{\delta}\}$
(1.3) Partial likelihood: for fixed values of **ρ**

(2) Parameter estimation

- Maximum likelihood approach
- Bayesian MCMC approach

Reference:

Adrakey et al. (2024). *Bayesian inference for spatio-temporal stochastic transmission of plant disease in the presence of roguing: A case study to characterise the dispersal of flavescence dorée.* PLOS Computational Biology.

PLAN NATIONAL DÉPÉRISSEMENT DU VIGNOBLE

CATIE

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