

Machine Learning techniques for risk assessment: identifying new proxies of *Xylella fastidiosa*

Location

INRAE Avignon, Biostatistics and Spatial Processes unit
<https://informatique-mia.inrae.fr/biosp/accueil>

Supervisors

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Duration 4 to 6 months

Mission

Invasive plant pathogens cause serious environmental and ecological damages with major economic impacts. *Xylella fastidiosa* is one of them, causing serious diseases in a wide range of plants such as grapevine and olive trees. Designing efficient surveillance of invasive pathogens relies on the knowledge of risk factors and their interactions. Martinetti and Soubeyrand (2018) proposed a risk-based surveillance strategy, based on a combination of machine learning techniques and network analysis, for understanding the main abiotic drivers of infections caused by *Xylella fastidiosa* and producing risk maps. Their predictors for explaining the presence of *Xylella fastidiosa* are mainly related to climate variables (precipitation seasonality, temperature in winter, solar radiation in summer...).

Recent works, see e.g. Del Coco et al. (2020), reveal significant differences in soil and leaf ionome composition between safe areas and in presence of *Xylella fastidiosa*. **The aim is to develop predictive models on the basis of such new variables, using them as proxies of *Xylella fastidiosa* presence.** The main steps will be:

- to use several machine learning techniques (e.g. random forest, regression and decision-trees algorithms, ...) and feature selection strategies to select a set of predictors that better correlates with the presence of *Xylella fastidiosa* and to identify new proxies.
- to compare the predictions to the ones of Martinetti and Soubeyrand (2018).

Del Coco L et al. (2020) Soil and Leaf Ionome Heterogeneity in *Xylella fastidiosa* Subsp. Pauca-Infected, Non-Infected and Treated Olive Groves in Apulia, Italy. *Plants*, 9(6), 760.

Martinetti D and Soubeyrand S (2018) Identifying Lookouts for Epidemio-Surveillance: Application to the Emergence of *Xylella fastidiosa* in France. *Phytopathology*, 109(2):265–76.

Profile

Strong understanding of machine learning concepts; Good coding skill in R; Interest for reading research papers; Interest for applied mathematics and epidemiology.

Application

Please send your CV, cover letter and a copy of your M1 and M2 transcripts to edith.gabrie@inrae.fr, dino.ienco@inrae.fr and eric.verdin@inrae.fr **before 14 March 2021**.

Ph.D opportunity: yes