



Métaprogramme DIGIT-BIO
X Axe 1 : Multiscale deciphering of living functions
 Axe 2 : Prediction of phenotypes
 Axe 3 : Transfer and generalisation

Exploratory project
(June 2022 – May 2024)

Project Coordination
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Partnership
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TEMPLATE - inTEractive siMulations to exPlore pLant pATHogEns interactions

Introduction/ Context - The plant immune response differs from that of animals in that **all plant cells are spatially fixed and immunocompetent**, i.e. they have the same capacity to respond to pathogen attack. These specificities have two consequences: the **regulation of immunity is central for resistance phenotype**, and the **plant immune response is highly spatially structured**. Studying these two properties and their impact on disease development is crucial to link gene expression and resistance phenotype at the scale of organism and **identify genes and signaling pathways regulating immunity**.

Objectives

The project aims at **developing a simulation model of plant/fungus interaction** at the cellular scale to study the spatiotemporal processes involved in the quantitative defense of the plant. This model will attempt to represent the progression of a mycelium colony of the pathogenic fungus *Sclerotinia sclerotiorum* in an *Arabidopsis thaliana* leaf.

The biological question at the heart of this project will **concern the formation of patterns of immune response self-organized in time and space** and **associated with transcriptomic reprogramming**.

Results and methods

We propose to use **Irritator**, a DEVS discrete event formalism which is known for its reproducibility, modularity and multi-formalism modeling approach.

We develop a computer environment allowing **interactive modeling and simulation, to help biologists** in their experimental explorations, in an interactive approach linking the experimenter, the biological object and the numerical model.

Expected impact and perspectives

This project will allow:

- To further understand the **spatiotemporal regulation of plant immune response**
- To provide an **integrative simulation tool** to the plant pathology community
- a more relevant **analysis of data from single cell transcriptomic** studies which is a major challenge for biology in the next ten years.

