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Homogenization of a model of propagation of a fungal disease in a heterogenous crop field

For production purpose, crop fields usually display a high degree of periodic spatial structure: vineyards are made of vine rows, orchards of regularly spaced trees...

To model this, we introduce a small parameter $\varepsilon > 0$. The crop field, assumed to be large, is described by a domain $\Omega \subset \mathbb{R}^N$, $N = 1, 2$ or 3 . Let $Y = [0, 1]^N$ the reference cell, and $Y_1 \subset Y$. The set Y_1 describes the part of Y occupied by the crop. The domain Ω is then equal to $\Omega_1^\varepsilon \cup \Omega_2^\varepsilon$ where

$$\Omega_1^\varepsilon = \{x \in \Omega, \chi_{Y_1}(x/\varepsilon) = 1\}, \quad \Omega_2^\varepsilon = \{x \in \Omega, \chi_{Y_1}(x/\varepsilon) = 0\}.$$

For example, in a orchard or in a vineyard, each cell Y could contain a single tree or vine stock. For a vineyard, each cell Y could also contain an entire row of vine stocks. This modeling formalism also applies to the case of cultivar mixture fields that could be used for disease control [2].

We study the propagation of a fungal disease over this field. The following model is a simplified version of the one in [1]. The vectors of the propagation of the disease are the spores produced by the fungus lesions. We assume that these spores disperse according to a Fickian diffusion process. Moreover they may disperse at the cell range, hence the diffusion coefficient will be of order ε^2 , or at long range. A very simple model for this is given by the following system of partial differential equations that describe the spores production and dispersal, coupled with an ordinary differential equation of SI type that describes the inoculation of the crop by the fungus:

$$\begin{cases} \frac{\partial S_S^\varepsilon(t, x)}{\partial t} - \varepsilon^2 \nabla \cdot (d_S(x, x/\varepsilon) \nabla S_S^\varepsilon(t, x)) + S_S^\varepsilon(t, x) = (1 - P(t, x, x/\varepsilon)) I^\varepsilon(t, x), \\ \frac{\partial S_L^\varepsilon(t, x)}{\partial t} - \Delta S_L^\varepsilon(t, x) + S_L^\varepsilon(t, x) = P(t, x, x/\varepsilon) I^\varepsilon(t, x), \\ \frac{\partial I^\varepsilon(t, x)}{\partial t} = \chi_{Y_1} \left(\frac{x}{\varepsilon} \right) (S_S^\varepsilon(t, x) + S_L^\varepsilon(t, x)) (1 - I^\varepsilon(t, x)) \end{cases}$$

for $t > 0$ and $x \in \Omega$ a regular bounded open subset of \mathbb{R}^N , supplemented with Neumann boundary conditions

$$\partial_\nu S_S^\varepsilon(t, x) = \partial_\nu S_L^\varepsilon(t, x) = 0, \quad \forall t > 0 \text{ and } x \in \partial\Omega$$

and with some initial data.

The state variables are: S_S^ε the short range spores density, S_L^ε the long range spores density and I^ε the diseased foliar surface density. The ode describing the evolution of I^ε is non trivial only if $x \in Y_1$.

Now we are able to show that as ε tend to 0, up to a subsequence, the solution of this model converges towards the solution of a homogenized problem. This homogenized problem is a coupled system of equations at the macroscopic scale (in Ω) and at the microscopic one (in Y). To prove this result, we use standard results from homogeneization theory, see e.g. [3]. The benefit from this homogeneization process is that the numerical computation of the solution of the homogenized problem is easier than the original one.

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