

## **Bacterial biofilms – towards ‘hybrid’ modelling**

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# Population dynamics

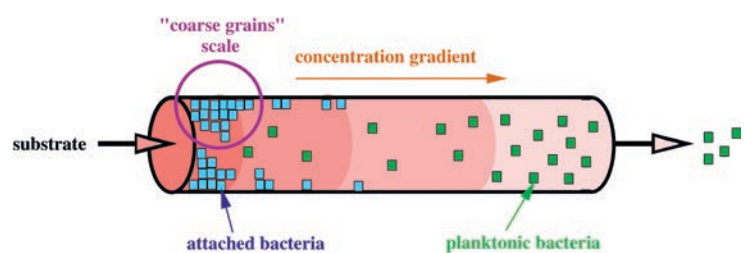
## Bacterial biofilms – towards ‘hybrid’ modelling

Biofilms—which are found in many natural ecosystems—are assemblies of bacteria and their secreted adherent matrix. They consist of billions of microorganisms belonging to hundreds or even thousands of species, and can form various 3D structures. A biofilm is generally a complex system, i.e. composed of a very high number of individuals whose interactions depend on the spatial structure of the biofilm and the bacterial diversity. Biofilms contribute to the functioning of recent water treatment systems by improving the bacterial treatment efficiency in bioreactors. Functional biofilm models must encompass both biodiversity and spatial structure, while including realistic assumptions about the interplay between bacteria and the polymer matrix they produce. An effective macroscopic description is therefore insufficient. The models commonly used are stochastic and individual-based, i.e. each bacterium is simulated with its plethora of behaviours, which can become very time-consuming for large populations. We propose to generate reduced versions of these individual-based models through homogenization and approximations of the first moments, in order to acquire the most statistically robust properties of these computational models in terms of more synthetic mathematical models. The consideration of hybrid, stochastic or deterministic multiscale dynamics according to population size has yielded

striking and generic results: a study of ‘macroscopic’ models obtained by scaling from pure jump models at the microscopic level has revealed areas in the state space that are sensitive to the population size. A major finding is that more individuals than expected occur within the size range of ‘small populations’, for which stochastic terms cannot be neglected.

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**For further information:** research carried out as part of the ANR DISCO project, <https://sites.google.com/site/anrdisco>



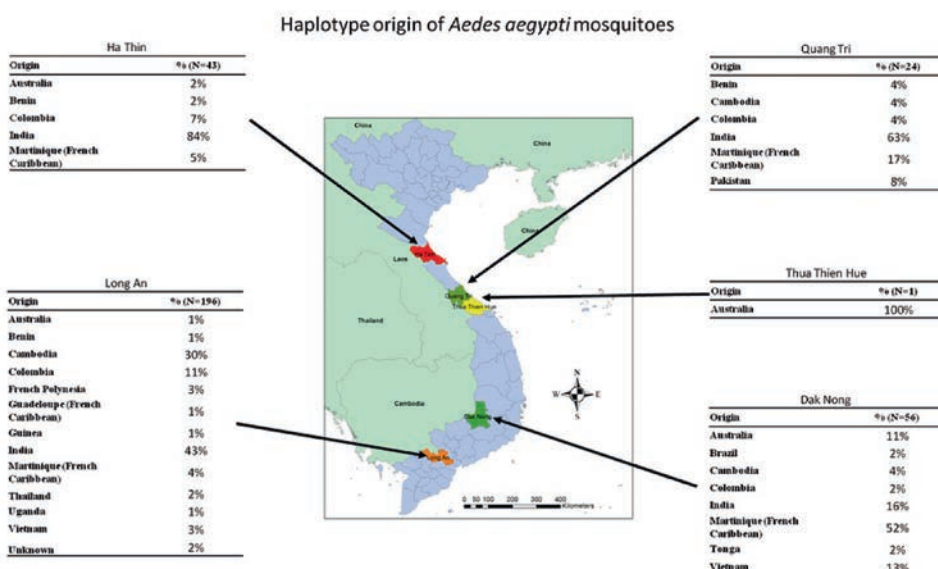
▲ *Diagram of a piston-type bioreactor.*  
From Deygout et al. *Ecological Modelling*. 250:15 (2013).

## Eco-evolutive parameters of communicable disease emergence

The emergence or re-emergence of communicable diseases in a species or population is the outcome of increasingly complex and understood processes. However, despite theoretical advances, models fail to pre-empt these outbreaks. Data must be integrated at different biological (gene, genome, population, metapopulation), spatial (local, regional and global) and temporal (short- and long-term) scales when studying disease outbreaks. ISEM and its partners\* are investigating the epidemic and evolutionary dynamics of different pathogens in host populations in an effort to get a clearer understanding and prevent the emergence of new pathogens and epidemic outbreaks. ISEM works mainly on so-called vectorial diseases (transmitted by blood-sucking arthropods). The multidisciplinary and interdisciplinary approach used is based on renowned expertise in parasite ecology, evolution and coevolution, public and veterinary health, analysis of complex biological data, etc. The dengue fever pathogen, for instance,

although pivotal, is not the main determinant of the onset and maintenance of outbreaks. The vector mosquito species present in a given geographical area (mainly *Aedes aegypti* and *A. albopictus*, the Asian tiger mosquito) are equally important. Beyond the species, different lines of each species may have different disease transmission capacities (vectorial capacity) and thus influence the disease dynamics. An analysis of vector lines carried out in Vietnam between 2012 and 2014 (see figure below) revealed that: (i) the main vector species vary in different geographical areas, (ii) virus-carrying lines are systematically lines that have already been detected in other geographical areas (Africa, Oceania, South America or even Europe) and (iii) the total population density of a mosquito species is not a major contributory factor in outbreaks.

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◀ *Distribution of haplotypes of *A. aegypti* mosquito populations in Vietnam.*  
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