CEMRACS PROJECT PROPOSAL
Organizers: C. Etchegaray, N. Meunier and L. Navoret
Title: Mathematical modelling of collective and individual cell migration

Cell migration plays a key role in many physiological processes, such as embryogenesis, wound repair, or metastasis formation. Cell migration is the result of a complex activity. It involves many different time and space scales, which makes it difficult to understand. The aim is to develop a model to accurately predict cell migration at the individual cell level.
We will start by studying cell crawling for cells located on a 2D adhesive plane. A recent study [Maiuri et al] has highlighted a universal process through which the structures responsible for migration reinforce cell polarization, which favours a ballistic displacement. This positive loop passes through a molecular marker, which is transported by the cell cytoskeleton. Its inhomogeneous distribution characterises a polarized state [Muller et al]. Then we will enrich the model introduced in [Etchegaray et al] in order to consider other migration mechanisms such as confined cell migration (dendritic cells e.g.). In a second step we will study cell migration for a population of cells.

Maiuri P., et al. (2015), "Actin flows mediate a universal coupling between cell speed and cell persistence", *Cell* **161**, 374– 386.

Muller, N., et al (2016), "A predictive model for yeast cell polarization submitted to pheromone gradients", *PLOS Compt. Biol..*, **14**(12).

Etchegaray, C., et al (2017), "Analysis of a non-local and non-linear Fokker-Planck model for cell crawling migration", *SIAP*.