Demi-journée thématique Symbiose
Modélisation

Jeudi 25 Mars 2010
13h45-17h30

IRISA, Campus Beaulieu, Rennes
Salle Jersey (au sous-sol du bâtiment IFSIC)

Programme

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Diversity and plasticity of Th cell types predicted from regulatory network modelling

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Alternative cell differentiation pathways are believed to arise from the concerted action of signalling pathways and transcriptional regulatory networks. However, the prediction of mammalian cell differentiation from the knowledge of the presence of specific signals and transcriptional factors is still a daunting challenge. In this respect, the vertebrate hematopoietic system, with its many branching differentiation pathways and cell types, is a compelling case study. In this paper, we propose an integrated, comprehensive model of the regulatory network and signalling pathways controlling Th cell differentiation. Our main aim is to gain insight into the potential heterogeneity and plasticity of late Th cell lineages. As the majority of available data are qualitative, we rely on a logical formalism to perform extensive dynamical analyses. To cope with the size and complexity of the resulting network, we use an original model reduction approach coupled to a stable state identification algorithm. To assess the effects of heterogeneous environments on Th cell differentiation, we have performed a systematic, extensive series of simulations, considering various prototypic environments. Consequently, we have identified stable states corresponding to canonical Th1, Th2, Th17 and Treg subtypes, but these were found to coexist with other transient hybrid cell types that co-express combinations of Th1, Th2, Treg and Th17 markers in an environment-dependent fashion. In the process, our logical analysis highlights the nature of these cell types and their relationships with canonical Th subtypes. Finally, our logical model can be used to explore novel differentiation pathways in silico.

Simple micro-tools to study complex cell behaviors: from yeast morphogenesis to dendritic cell migration and orientation of the mitotic spindle in mammalian cells

Mathieu Piel
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Equipe Biologie cellulaire systémique de la polarité et de la division

Fine control of the micro-environment of single cells is a major improvement for in vitro cell biology studies. But it is important that device fabrication remains the easy part of the experiment, to be compatible with sophisticated biological assays. In the last years, while studying cell polarity, we developed and used simple tools – mainly cell adhesive micro-patterns and micro-channels in the micron range - that turned out to be crucial for answering fundamental cell biology questions. I will first rapidly present a few examples illustrating our recent work, showing how simple micro-fabricated tools enable new questions to be asked in vitro, but also make cell biology more quantitative and open the way to new quantitative cell based assays for complex cell functions. These will include: how fission yeast cells can maintain a rod like shape through growth and division? How can budding yeast cells maintain a private conversation with a single mating partner when surrounded by a crowd of suitors? What is the effect of cell adhesive geometry on cell polarity and cell division axis?
I will then spend some time on a new research program in which our team is involved, whose aim is to understand how leukocytes and invasive cancer cells migrate in confined environments.

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Modeling biological systems: bridging the gap between formalisms and biological contexts.

Damien Eveillard
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Modeling biological systems is a difficult task. By nature, these systems are complex and partially known. Several recent formalisms tackle this problem by focusing on distinct biological features that occur in dynamical living systems. Whereas some focus on qualitative biological behaviors, others analyze times between the events of interest or quantify them. This talk proposes an overview of the modeling techniques at disposal, with a particular emphasis on the conditions of their use, as well as their respective limitations. In particular, we propose to highlight the "user" aspect of modeling systems from different biological fields: from molecular biology to ecology.