Workshop 2017
September 19-20, 2017, Amsterdam

Marie-France Sagot (Inria) and Leen Stougie (CWI)
ERABLE research team

Title: « Modules of ERABLE and of Metabolic Networks »

Abstract:
In the first part of the lecture, we will present a brief overview of the work of the INRIA European Research Team ERABLE. We start by introducing the team. We then give some examples from the research done by the team.

The second part of the lecture is about a result we obtained on Flux balance analysis (FBA). It is aimed at finding the optimal way in which a cell produces biomass, given some nutrient source. It is one of the most often applied methods on genome-scale metabolic networks and can be solved by Linear Programming. Although FBA uniquely determines the optimal yield, the pathway, that is the set of reaction-fluxes, that achieves this is usually not unique.

The analysis of the optimal-yield flux space has been an open challenge in systems bioinformatics. This space is a polyhedron again and we are interested in its extreme points. Enumerating them is not useful due to their enormous number.

Our discovery was that we can decompose the space of optimal-yield fluxes into modules. These decompositions allow a much easier but still comprehensive analysis of the optimal-yield flux space. A module has a crystal clear definition in matroid theory. It allows us to compute the decomposition into modules in a few seconds for genome-scale networks. Hence, we expect the new method to replace flux variability analysis in the pipelines for metabolic networks.

In a follow-up project we are extending the notion of module, allowing us to enumerate vertices of polytopes efficiently in some specific sense.

The second part of the lecture is joint work with Steven Kelk, Arne Reimers, Brett Olivier, Frank Bruggeman and Marie-France Sagot.