

## IT-767 : Computational Systems Biology (Sysbio)

**Objective:** A wealth of biological data has become available in recent years. In the post-genomic era, sequence information is routine and proteomics and metabolomic data on a wide variety of organisms under a range of physical conditions is accessible. In these circumstances, a more quantitative approach to analyzing molecular biological data is possible and indeed necessary. The quantitative approach needs also to go beyond enumerating the various components or constituent molecules: one needs to understand how they interact spatially and mechanistically, and how the entire machinery of a living cell operates. Methods of physics, techniques from mathematics, statistics and computer science, bioinformatics, modeling techniques, all contribute in the systems approach. Cutting edge applications of quantitative biology are already beginning to have an impact in medical areas. A course on systems biology therefore needs to build background and expertise in diverse areas.

### Syllabus:

**Introduction to systems biology:** Terms and definitions. Biochemical kinetics and pathways.

Genome regulation, expressions, switches and microRNA regulations.

**Classification of enzymes and metabolic pathways:** KEGG database. Genome annotation through knowledge of metabolic pathways. Organism specific metabolic pathways. Comparison of metabolic pathways. Engineering of metabolic pathways.

**Pathways databases:** pathway inference, visualization tools: DAVID, Gene Ontologies, Pathway Miner and similar software. Applications in chemical kinetics and metabolic pathways analysis (model E. Coli), Metabolic control analysis and Flux balance analysis

**Dynamical systems:** linear stability and bifurcation analysis. Limit cycles, attractors

**Genetic and biochemical networks:** Deterministic and stochastic descriptions. Other network types. Regulatory (e.g.fly), signal transduction (e.g. MAP kinase cascade in yeast), neural, mechanical etc.

**Software for systems biology:** SBML and open source programs. Ecell, Virtual Cell, StochSim, BioNets etc.

**Quantitative models for E. Coll:** lac operon and lambda switch. The chemotactic module in E. Coli.

### Suggested readings:

1. Mark Ptashne, The Genetic Switch, CSI-IL Press
2. Horoaki Kitano, ed Foundations of Systems Biology, MIT Press 2001
3. JM Bower and H Bolouri eds. Computational modeling of genetic and biochemical networks, MIT Press 2001
4. GB Benedek and FMH Villars, Physics with illustrative examples from medicine and biology Vol 1, Mechanics 2nd ed Springer 2000.