**Development of a tool to analyze experimental data, simulate its interaction network and integrate logic-based models**

Aging-related processes such as cellular senescence are believed to underlie the accumulation of diseases in time, causing (co-)morbidity, including cancer, thromboembolism and stroke. Intervening into these processes may delay, stop or reverse morbidity. To study the link between (co-)morbidity and aging, we will integrate omics data with disease network which will subsequently be simulated with systems dynamic theory using suitable mathematical model.

Logic-based models are getting popular for the analysis of large scale biological systems because they do not require detailed kinetic parameters. Like other models, logic-based models are also trained/calibrated with data, to decide about “AND” or “OR” logic in logical functions, to represent biological reality as good as possible. To automatize this process can make model construction quicker and less prone to mistakes in comparison to manual process.

Tasks:

* analysis and cleaning of experimental data
* Identify the valid reactions
* Model construction of disease comorbidity from literature
* Simulate interaction Network from experimental data
* Development of a tool for logic-based model training/calibration with fold-change expression data
* Identification of disease signature using sensitivity analysis
* Model validation using machine learning algorithm