Tutorial: mEPN and yEd: a Graphical and Computational Modelling Platform for Biological Pathways

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Aim of tutorial

To introduce our biologist-friendly graphical and computational modelling approach1-3. This combines three elements, a sophisticated but easy to use language for depicting biological events at the molecular level, a Petri net-based flow simulation algorithm, and a powerful visualisation engine with which to observe the dynamics of the system being modelled. The modified Edinburgh Pathway Notation (mEPN) language facilitates the construction of detailed network diagrams, summarising the components of a biological pathway (such as proteins, biochemicals etc.) and how they interact. Once constructed, these diagrams can then be used to simulate activity flow through a pathway, thereby modelling system dynamics.

Tools/methods

The workshop will involve discussion and hands on experience of the four stages of modelling using this approach: (1) assembly of network diagrams using the mEPN scheme and yEd network editing software using pathway information obtained from published literature and databases of molecular interaction data; (2) parameterisation of the pathway model within yEd through the placement of 'tokens' based on the known or imputed amount or activity of a component; (3) model testing through visualization and quantitative analysis of the movement of tokens through the pathway using network analysis tool Graphia Professional; (4) optimisation of model parameterisation and experimentation. The tutorial requires no prior experience of modelling.

Summary

Depending on a model's complexity and the availability of information, its construction can take days to months, and, with refinement, possibly years. However, once assembled and parameterised, a simulation run, even on a large model, typically takes only seconds. Models constructed using this approach provide a means of knowledge management, information exchange, and through the computation simulation of their dynamic activity, a means to generate and test hypotheses, and predict a system's behaviour when perturbed.

References:

1. O'Hara et al., Modelling the Structure and Dynamics of Biological Pathways. PLoS Biol. 14(8): e1002530 (2016).
2. Livigni et al., A graphical and computational modelling platform for biological pathways. Nature Protocols 4: 705 (2018).
3. www.virtuallyimmune.org