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**EASTBIO DTP Foundation Masterclasses 2021/22 – Set 3**

**Mapping and Modelling your Biological Pathway**

**Masterclass leader**: **Professor Andrew Millar (University of Edinburgh)**

**Date: 16 May 2023, 11:00 - 16:30**

**Location:** Dundee, [Dalhousie Building, room 2S15](https://www.dundee.ac.uk/roombookings/catalogue/dalhousie2s15ils/#!faq-6) (IT suite)

Systems biology aims to integrate data on all components of a biology system into mathematical models that quantitatively recapitulate the data. Studying the models provides a new set of tools to understand complex dynamic behaviors, such as oscillations, and system-level properties, such as robustness. These in turn can be integrated in models at a larger scale: cell-level behaviors into an organ model, for example, in the heart model. From this understanding, systems biologists seek the general principles of operation that distinguish living from non-living systems (to paraphrase Waddington, 1976), or in engineering terms “the design space of evolution” (Kitano, 2007).

The data required for systems biology stretch the best experimental laboratories, extending the requirements of contemporary cell and molecular biology, usually in ways that seem natural to the researchers. Because of the past training of most of the relevant biologists, however, the requirement for mathematical modelling can appear more challenging. Our course aims to illustrate the reasons to model and to demonstrate the methods. We introduce the process of building a dynamic model and exploring its behavior: you can do a lot with one equation. We illustrate the process using free software for graphical models (VANTED and SBGN-ED) and dynamic models (COPASI) in community-standard formats.

We’ll also discuss how these Open resources in systems biology illustrate the benefits of sharing data and resources, especially with community standards and using the FAIR principles (Findable, Accessible, Interoperable, Reusable).

**Learning outcomes**

Participants will:

* Explain the conceptual reasons to use formal modelling in a biological investigation
* Locate biological pathway diagrams and dynamic models in public, online resources
* Manipulate a pathway diagram in the standard, graphical language SBGN, suitable for a Supplementary Figure.
* Distinguish the structure of a small regulatory network from its parameter values, using each concept to understand (explain and predict) a dynamic pattern of biological regulation.
* Obtain timeseries simulation results, from a gene network model in the standard SBML format.

**Requirements**: All participants are requested to use a laptop computer with rights to install applications.

Before the class, it is essential that students install and test COPASI on a laptop that you can bring to Dundee. VANTED is optional, it is a backup to be aware of but we will use the online alternative, Newt. Finding and loading the relevant model files into the software is part of the process we will be learning so that students do not need to do that ahead of time.

COPASI - <http://copasi.org/Download/>

The default download will usually be appropriate for the machine you're using.

If you wish to do some familiarisation in advance, the video tutorials on Basics, Timeseries simulation and Parameter Scanning are here:

<https://www.youtube.com/user/CopasiTutorials>

Optional: VANTED with the SBGN-ED add-on -

<https://www.cls.uni-konstanz.de/software/vanted/download/>

After installing VANTED, install the SBGN-ED Add-on as described here:

<http://kim25.wwwdns.kim.uni-konstanz.de/vanted/addons/sbgn-ed/>

The website has demo files and a video here:

<https://www.cls.uni-konstanz.de/software/vanted/tutorialsexample-files/graph-editor-features/>

FYI, online resources that we’ll use:

[www.reactome.org](http://www.reactome.org)

[www.ebi.ac.uk/biomodels](http://www.ebi.ac.uk/biomodels/)

[newteditor.org](http://newteditor.org/)

**Training web-page:** <http://www.eastscotbiodtp.ac.uk/foundation-masterclasses>

For further queries, email enquiries@eastscotbiodtp.ac.uk.