

Master assignment BME, Applied Physics, Applied Mathematics

Computational models of signal transduction networks

Supervisor:

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Possible daily supervisors:

Members of the quantitative biology lab headed by dr. Post:

- Lucas Jansen Klomp, PhD student Mathematics of Imaging & AI and Developmental bioengineering, l.f.jansenklomp@utwente.nl
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Background:

Cells respond to cues from their environment via complex signal transduction networks. The change in signaling activity prompts various commands in the cell, for example migration, proliferation, differentiation, etc. In addition, changes in network activity also leads to changes in gene expression which precede the cell differentiation.

We investigate the best way to make cartilage or heart from iPS cells. For this, we generate dynamic models of transcription factor networks. These transcription factors are activated by upstream signaling pathways. In this ma-assignment, we aim to generate a computational model of the upstream signaling pathways that regulate the activity of these transcription factors.

Techniques used in this project:

- Generating computational models using ANIMO
- Matlab or R and / or Python

The project will consist of many steps:

1. Familiarizing oneself with ANIMO or other language of choice
2. Training with other, existing, models in ANIMO
3. Generating a static network diagram of the signal transduction pathways that regulate specific transcription factors
4. Formalizing the network
5. Running simulations
6. Optimizing the network to fit existing (literature) data
7. Incorporating the transcription factor networks
8. Repeat steps 5-7 until time runs out