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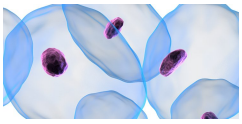

Modelling transcriptional changes in response to plant developmental programs

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Type of thesis: Computational

Required competences: Programming knowledge in R, MATLAB and/or Python, particularly useful if you have followed SSB20306 or SSB30306. Mathematical modelling knowledge will also be required in the project, e.g. from SSB30806 or BCT20306.

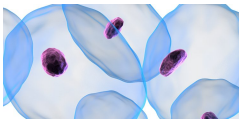
Acquired competences: Data analysis of omics datasets, combined with developing mathematical models of biological systems.

Date: 25-06-21

Description

In higher plants, ARF proteins function as integrators in a signalling network induced by the hormone auxin and resulting in transcriptional regulation of developmental pathways. However, even in the classic model plant *Arabidopsis thaliana*, the large size of the involved protein families makes it difficult to understand the key process underlying a plants response to auxin. Recently, experimental work in *Marchantia polymorpha* – that possesses a far simpler auxin network – has shown that stoichiometric balance between different members of the ARF protein family is a key determinant in a plants response to auxin signals. An overview of the ARF system in Marchantia can be found in Das et al.

In a previous thesis project we constructed a mathematical model of ARF protein dynamics and their control of two transcriptional targets as Marchantia is released from a dormant state to a growth phase. We now have time-dependent RNA-seq (transcriptomic) data available to investigate how mRNA in Marchantia changes more widely during this developmental switch. Using clustering methods (e.g. maSigPro; Conesa et al.) we want to understand if patterns in mRNA regulation emerge. For example, is there a fast and a slow transcriptional response? Can this response time be correlated



with genes that contain an ARF binding site in their promoter (implying that they are directly regulated by the ARF proteins)?

Based on these mRNA clusters, we can then extend our mathematical model of ARF protein dynamics to quantify the ARFs role in regulating mRNA levels (an example from a similar system can be seen in Seaton, Smith et al.). This will allow us to further our understanding of Marchantia development regulated by the ARF proteins – including how long it takes for ARF proteins to regulate targets and whether ARF hetero-dimers play a role in regulating a subset of transcriptional targets.

References

Das et al. (2021) 'Auxin response by the numbers', *Trends in Plant Science,* doi: 10.1016/j.tplants.2020.12.017

Conesa et al. (2006) 'maSigPro: a method to identify significantly differential expression profiles in time-course microarray experiments', *Bioinformatics,* doi: 10.1093/bioinformatics/btl056

Seaton, Smith et al. (2015) 'Linked circadian outputs control elongation growth and flowering in response to photoperiod and temperature', *Molecular Systems Biology*, doi: 10.15252/msb.20145766