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From organism to tissue level modelling: extending a time-dependent system to include spatial effects of ARF proteins

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Type of thesis: Computational

Required competences: Programming knowledge in MATLAB and/or Python. Mathematical modelling knowledge will also be required in the project, e.g. from SSB30806, SSB31806 or BCT20306.

Acquired competences: Construction and analysis of mathematical models that change with time and space (partial differential equations).

Date: 27-06-21

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 time-dependent mathematical model of ARF protein dynamics as Marchantia development switches from a dormant to growth stage. However this model ignored spatial changes in ARF dynamics across the Marchantia tissue. For example, we know from data that some cell-types express ARF proteins to a higher level than other parts of the organism. Likewise, we know from

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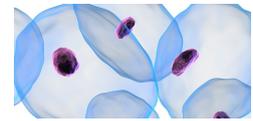
Arabidopsis studies that auxin, a key regulator of ARF activity, is not equally abundant across the entire tissue. Once we have constructed a model that can describe the spatial changes of ARF levels (adapting the modelling methodology from Balkunde, Deneer et al.), we would like to quantify the growth rate of the different cell types as a consequence of ARF dynamics. This would allow us to determine which cell types drive growth of Marchantia tissue as it exits the dormant developmental stage.

References

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

Balkunde, Deneer et al. (2020) `Identification of the trichome patterning core network using data from weak *ttg1* alleles to constrain the model space', *Cell Reports*, doi: 10.1016/j.celrep.2020.108497