

P018 Network modelling of *Arabidopsis* root epidermis patterning

Natasha S. Savage and Nicholas A. M. Monk

Computational Systems Biology Group, Kroto Research Institute, University of Sheffield

The *Arabidopsis* root epidermis provides an ideal system in which to explore the molecular mechanisms that drive the special patterning of cell fates during development. Assignment of epidermal cells to either the hair (trichoblast) or non-hair (atri-choblast) fate depends on a network of transcription factors that mediate interactions both within and between cells. We have developed a mathematical model of this network based on the known functional interactions and intercellular movements of the components. We adopt a probabilistic Boolean formalism in which local rules control the probabilities of gene expression. This modification of the classic Boolean formalism allows us to study the balance between WER and CPC, which plays a central role in differentiation of epidermal cells.

Our model does not take into account putative positional bias deriving from the cortical cells that underlie the epidermis, but can nonetheless generate a pattern of cell fate reflecting that of wild type epidermis cells. We have shown that this pattern emerges only if we incorporate logical assumptions about specific interactions within the network. These modelling assumptions relate directly to predictions about the nature of network interactions and possible forms of cortical bias, and these are currently being explored experimentally.