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Quantitative modeling of gene expression in Arabidopsis flowers

Flowers have a complex structure in which tissues and organs obtain their identities and arrangements in a very special way. According to the so-called ABC(DE) model [1], the different floral organs in Arabidopsis are specified by the expression of five types of MADS box genes. During development, the floral meristem gets divided into four concentric areas (whorls) in which different combinations of MADS gene expressions are observed: A+E in the sepal whorl, A+B+E in the petal whorl, B+C+E in the stamen whorl, and C+E in the carpel whorl.

In [2] we proposed an ODE model for the interactions of the gene regulatory network that underlies the development of the MADS domain proteins. We showed that this model type is well suited for testing hypotheses on formation and functioning of higher order complexes, transcription activation and DNA binding.

For the predictive power of such a model, accurate estimation of parameter values plays an essential role. To this end, we developed a spatiotemporal data set of in vivo protein concentrations, using a state of the art protein tagging procedure. We used a novel image analysis technique to estimate relative protein concentrations from the resulting confocal images [3].

We also developed a novel parameter estimation procedure that explicitly incorporates the temporal expression development, as well as the measured standard deviations. The estimation results will give a direct feedback on the proposed hypotheses, and they will be presented at the conference.

REFERENCES

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