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A structured growth model for hairy roots of beetroot (*Beta vulgaris*)

Secondary metabolites produced by plant in vitro cultures such as Betanin (red-dye in beetroot) are nowadays in the main focus within the branch of White Biotechnology. Cells genetically altered using *Agrobacterium rhizogenes* form hairy roots which can be cultivated in hormone free media in modern bioreactors.

In order to improve the cultivation process (higher yield, shorter cultivation time) and the bioreactor design (bubble column vs. stirred) a structured growth model with consequent simulations and visualization is necessary. While the growth of these tissue cultures on agar plates, in shaking flasks or bioreactors for industrial use has been heavily investigated experimentally only limited theoretical descriptions of the growth processes exist. The gained knowledge can be used by other scientists to improve their cultivation protocols and to simulate growth of their own cultures by amending the parameters of the model.

The hairy roots of beetroot (*Beta vulgaris*) have been chosen for modeling the growth morphology of hairy roots also with respect to the distribution of secondary metabolites such as the red dye Betanin. A matrix based approach is used for the proposed model which consists of a 2-dimensional model matrix for agar plates containing information about the condition of each cell forming the organ complex. Conditions are position, age, nutrient concentration inside the cell as well as concentration of secondary metabolites. A second matrix contains nutrient concentrations such as carbon source and oxygen in the media.

The simulation process begins with a given start state of a small organ complex which is recalculated recursively for a defined time step. The growth processes involved such as elongation and branching through cell division as well as secondary thickening of already existing cells are described using differential equations. After each growth step the organ matrix and the nutrient matrix with the involved diffusion processes are calculated using partial differential equations (PDE). The newly formed matrices are used for the next calculation step. Experimental results of cultivations of *B. vulgaris* are compared with the results of simulations.