CellSys: Modular software for physics-based tissue modelling in 3D

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The task of testing biophysical hypotheses about tissue growth, degeneration, and regeneration generally involves the modelling of processes on many scales ranging from the molecule up to the whole organ level. Advanced imaging methods often reveal characteristic spatial patterns emerging from an interplay involving molecules, cells, functional tissue units, or even central control instances. As it is often not feasible to simultaneously access the different components, the processes underlying the patterns can often not be clarified.
CellSys is a software simulation tool to test hypotheses on monolayers, multi-cellular spheroids, and complex tissues at histological scales that involves the interplay of components on many scales. CellSys combines an image processing and analysis component with a modelling environment. A graphical user interface (GUI) makes setup and execution of model simulations more accessible for non-experts.
One feature of CellSys is that it permits passing statistical information acquired from imaging data directly to the modelling engine, thus models can directly be generated from images. The centre of the modelling engine is an agent-based simulation framework for off-lattice, physics-based tissue models.
Since the spatial and temporal scales involved may span many levels, the resulting simulation code can have an enormous complexity. The software toolkit of CellSys addresses the variety of models by facilitating the programming of new models with existing modules. The software focuses on extensibility of existing models by developers, as well as on reducing the effort to integrate user-interaction with models in a GUI by providing pre-defined tools and data structures. CellSys' software modules are engineered for re-use with newly developed elements such as new cell types, so that models with new elements are quickly integrated.
While CellSys primarily has been developed to implement off-lattice physics- and centre-based models as those for liver regeneration [1] it is now being extended to feature a module for cells with more resolved surfaces, as well as flows in tissues.

[1] Hoehme, S., Brulport, M., Bauer, A., Bedawy, E., Schormann, W., Gebhardt, R., Zellmer, S., Schwarz, M., Bockamp, E., Timmel, T.G., Hengstler, J.G., and Drasdo, D. (2010) Prediction and validation of cell alignment along microvessels as order principle to restore tissue architecture in liver regeneration. *Proc. Natl. Acad. Sci.* (USA), 107(23), 10371-10376.