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Morpheus: a user-friendly modeling environment for multicellular systems

In face of the growing amount of data on gene expression as well as microscopy images, mathematical modeling of multicellular systems is increasingly required to understand the regulation of tissue morphogenesis and (dys)function. This typically involves the construction of computational models that couple discrete cell-based modeling methods, representing cell motility and shape, to continuum models that represent intracellular biochemical regulation and reaction/diffusion of extracellular morphogens. Integration of these disparate modeling methods into multiscale simulations is an error-prone and computationally complex challenge. In order to enable scientists with biological rather than computational skills to adopt these methods in biological and biomedical research, there is a growing need for software that facilitates development and simulation of multiscale models of multicellular systems.

Morpheus is a user-friendly modeling environment for the simulation and integration of cell-based models with ordinary differential equations and reaction-diffusion systems [Starruß et al, 2014]. It allows rapid development of multiscale models using a novel domain-specific markup language with biological terminology and mathematical expressions rather than programming code. Similar to the systems biology markup language (SBML), it uses symbolic identifiers and allows the specification of a variety of mathematical expressions (functions, equations, events, differential equations). Integration of discrete and continuous model formalisms is performed automatically, using the network of dependencies between the symbolic identifiers to map spatial data between formalisms and to schedule numerical updates in appropriate and correct order.

The graphical user interface provides tools for creating, editing and simulating models and contains a variety of example use cases that can serve as templates. It also features tools for archiving of models and results, job scheduling of parallel and multithreaded simulations, batch processing and high performance computing.

Morpheus is freely available as an application for Linux, Mac OSX and Windows on the website: <http://imc.zih.tu-dresden.de/wiki/morpheus>.

REFERENCES

- [1] Starruß, J., de Back, W., Brusch, L., and Deutsch, A., 2014. *Bioinformatics*, **30**(9):1331–1332.