

# A framework for the simulation of 3D physiologically structured population models.

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The PSP modelling approach allows to model biological/pharmacological behaviour by combining micro-scale ordinary differential equation (ODE) models with macro-scale ODE models and their bi-directional interaction. E.g.: based on the model of a single cell, billions of cells can be simulated to get the response of an entire organ (also incorporating the organ to cell reaction). The PSP approach allows to simulate this in a mathematically efficient way by characterising different cells by a set of physiologically relevant quantities [1][2].

Our framework is capable of taking into account up to 3 physiological parameters resulting in a 3D structure for which a partial differential equation (PDE) should be solved. We achieve considerable speed-up by using a semi-Lagrangian PDE solver that allows big and stable time stepping. Combining this with a low level C-language implementation, we achieve exceptional efficient usage of the computing processing unit (CPU). For ease of use, a PSP description language is constructed to allow straightforward input of the different models. The simulator should empower future computational/mathematical biologists to create and evaluate more detailed models than currently is common practice.

## References

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