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A CUTFEM METHOD FOR A SPATIALLY RESOLVED ENERGY METABOLISM MODEL IN COMPLEX CELLULAR GEOMETRIES

Sofia Farina[1], Susanne Claus[2], Jack S. Hale [3], Niko Komin[4], Alexander Skupin[5] and Stéphane P.A. Bordas[6]

[1] University of Luxembourg, sofia.farina@uni.lu
[2] Onera, 91120 Palaiseau, France, susanne.claus@web.de
[3] University of Luxembourg, jack.hale@uni.lu
[4] LCSB- Luxembourg Centre for Systems Biomedicine, niko.komin@uni.lu
[5] LCSB- Luxembourg Centre for Systems Biomedicine, alexander.skupin@uni.lu
[6] University of Luxembourg, stephane.bordas@uni.lu

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Computational techniques have been widely used to tackle problems in the biological sciences. A compromise between high quality simulations and simple but accurate models can help to understand unknown aspects of this field.
In this work, we will show how the Cut Finite Element Method (CutFEM) [1] can be a powerful tool to solve a reaction diffusion PDE system that models the energy metabolism of a cell. The main difficulty to approach this problem is dealing with the morphology of the cell that can have sharp edges and evolves over time. While classical FEM requires the mesh conform to the domain boundary, CutFEM allows a non-conforming discretisation of the domain, and thus is especially suited for modeling complex and evolving cellular geometries.
First, we introduce our simplified model for metabolic pathways taking place in a region small enough to consider the material property as homogeneous. The results obtained with FEM (FENICS Project [2][3]) and CutFEM suggest that the two methods are equivalent. This allows us to use CutFEM to increase the complexity of the domain, from a spherical shaped cell to an irregular astrocyte.
We conclude that CutFEM is a robust method for tackling biological problems with complex geometries, opening the possibility to extend the complexity of our mathematical model including more features and to consider real cellular shapes that evolve in time in future work.

REFERENCES

[1] Erik Burman, Susanne Claus, Peter Hansbo, Mats G Larson, and André Massing. Cutfem: discretizing geometry and partial differential equations. *International Journal for Numerical Methods in Engineering*, 104(7):472–501, 2015.

[2] Anders Logg, Kent-Andre Mardal, and Garth Wells. *Automated solution of differential equations by the finite element method: The FEniCS book*, volume 84. Springer Science & Business Media, 2012.

[3] Martin S Alnæs, Jan Blechta, Johan Hake, August Johansson, Benjamin Kehlet, Anders Logg, Chris Richardson, Johannes Ring, Marie E Rognes, and Garth N Wells. The fenics project version 1.5. *Archive of Numerical Software*, 3(100):9–23, 2015.