Master 2 Internship - Applied Mathematics, biological models
Applied Maths Laboratory of Compiègne (LMAC)
Université de Technologie de Compiègne (UTC)

Numerical methods and learning-based surrogates for a model of intestinal cell dynamics

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Location: LMAC, Université de Technologie de Compiègne, Compiègne, France

Academic partner: INRAE project team *MaIAGE*

Profile of the successful candidate: applied maths, PDEs, nonlinear equation, computational methods, finite volumes, numerical analysis, biological models, reduced-order models

How to apply: please sent the following informations to A. Zurek and F. De Vuyst: CV, motivation letter, references

Duration: 4 months

Starting date: flexible, preferably april 2024

Financial rewards: 650€/month

In this internship, a study of the dynamics of cells in intestinal crypts is proposed. The intestinal epithelium is a layer of cells that plays an important role in nutriment absorption and protection against pathogens. The intestinal epithelium is made of lots of folds with crypts. A recent mathematical model of crypt cell dynamics involving multiple cell populations [1] has been proposed. The model is composed of several coupled partial differential equations of cross-diffusion type including source terms modeling growth and differentiation process during time. The goal of this internship is to propose suitable numerical approaches able to deal with the degenerate parabolic feature of the system as well as the source terms. As a first step, the student will deal with simplified models in order to handle the several difficult aspects of the system in a progressive way.

The internship will be organized into two main milestones:

1. Development and implementation of various numerical schemes for the intestinal crypt model. The goal is to compare both accuracy and stability of the different schemes

(full explicit, full implicit, IMEX, ...). According to the skills of the recruited student, a numerical analysis study could be proposed (positivity aspect, a priori estimates, bounds, convergence).

2. This model is also difficult to analyze because of its dependency on multiple biological parameters. Its calibration w.r.t. biological measurements is a challenging problem (context of inverse problems). In this internship, a sensitivity analysis of the different parameters will be considered. A practical way to do that is to derive parametrized reduced-order models (ROMs) of the initial (full-order) one. There are at least two main families of ROMs: projection-based ones and data-driven ones. The first family performs a Galerkin projection of the system of equations on a suitable low-order vector space (intrusive methods). The second family considers computational result data from a high-fidelity solutions of the biological model; then a data-driven model is identified and tries to reproduce the dynamics of the system from a learning process. This approach is closely related to the Machine Learning (ML) topic. Both approaches could be investigated and compared in the internship. Physics-informed ML approaches could also be investigated.

Perspectives: According to the results obtained, the research could evolve toward a PhD work on mathematical analysis and efficient computational approaches for general nonlinear cross-diffusion systems with source terms.

About the University of Technology: UTC is both a French national University and an engineering school, with autonomous training and pedagogy and an innovation-intensive, interdisciplinary technological research program. The UTC trains its students for engineering, Master's degree, PhD and continuing education degrees, to better understand the interactions of technology with man and Society. Compiègne is 80 kms far from Paris (about 40 mins by train).

References

[1] L. Darrigade, M. Haghebaert, C. Cherbuy, S. Labarthe, and B. Laroche. A PDMP model of the epithelial cell turn-over in the intestinal crypt including microbiota-derived regulations. *J. Math. Biol.*, 84(7):60, 2022.