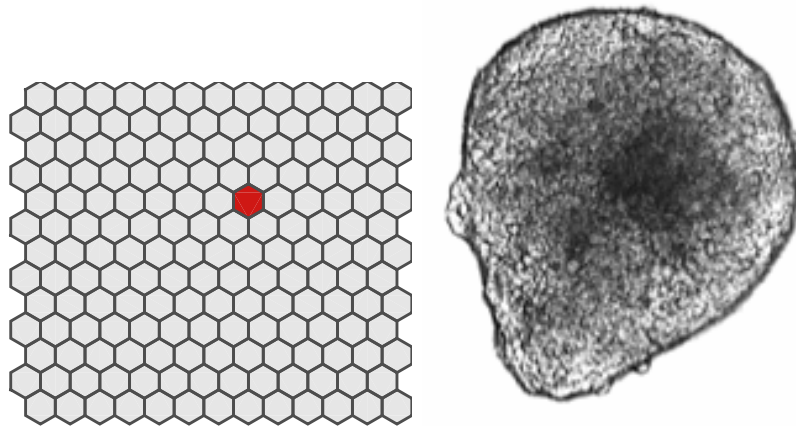


# COMPUTATIONAL MODELING OF AVASCULAR TUMORS: TOWARDS MULTISCALE HYBRID MODELS

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## EFFECTIVE SUMMARY

Correctly bridging single cell descriptions with models of a large interacting cell population is a challenge due to the vast scale separation in both time and space. Research in the biosciences has now advanced to the stage where sophisticated predictive models of single cell processes may be formed. However, a range of emerging Life science applications require models consisting on the order of millions of living cells.

In this project we target this modeling gap in two intertwined sub-projects with the specific application of computational models for avascular tumors:

- (1) Mesoscopic models and boundary conditions: this part aims to investigate the effect of tumor boundary conditions. Once correctly understood, one should be able to, given a requested tumor size, deduce suitable parameters and boundary conditions for this tumor size to be realized.
- (2) Macroscopic models: towards hybrid simulation. This part will investigate a more direct, if possible less accurate. PDE-based approach. What are the trade-offs and possibilities for bridging this scale with the mesoscopic scale?

## BACKGROUND

This project deals with computational modeling of processes taking place inside and among living cells. The concrete *aim* is to be able to accurately and consistently simulate large multicellular systems. The multiscale challenge is that models of cells at the population level take place on a different temporal and spatial scale compared to the single cell dynamics. Another outstanding difficulty is the issue with model calibration in the presence of process noise, and, importantly, understanding the inherent limitations with such parametrization techniques. These challenges call for novel fast multiscale simulation algorithms equipped with a consistent analysis and supported by sound parametrization procedures.

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