Mathematical modelling breakout session during ATTRACT virtual symposium June 2020

We will run a mathematical modelling and data analysis breakout session during the virtual ATTRACT symposium on 16-18 June. The objective is bringing together method developers and potential new users to begin work on a particular new data analysis task hopefully leading to follow-up work and collaboration after the symposium.

This document contains a short summary of modelling capabilities by some of the ATTRACT teams. We are now seeking input from two different groups of people: a) method developers that would like to present their methods for general ATTRACT use (adding a new tool to this list), b) people with datasets that could benefit from the analysis tools presented. Please send your questions and input to Wolfgang (wolfgang.giese@mdc-berlin.de).

Tool 1: Multidimensional analysis of cell movement (Andre, Wolfgang MDC)

We developed a data analysis pipeline that extends from data extraction, curation, correlation and statistical inference to deduce the properties of single and collective migration of cells in several models. This pipeline serves as a platform for data collection and archiving for fasten the translation from bench to in silico models and vice-versa. One key element of this process is the organization experimental by using a data catalogue that allows painless exploration of the data set in a systematic way. Our goal is to establish this protocol as a tool to standardize the libraries of metadata from all projects with focus on cell dynamics to collaborators with hands on in the execution chain of command-line tools and/or custom scripts for data exploration based on python and R. The workflow will be exemplified for endothelial cell movement in Zebrafish, mouse retina vessel networks and cell culture.

Tool 2: Force driven agent-based migration models (Lowell UoE)

We have developed a new agent-based model of cell migration that captures many aspects of flow-mediated and collective migration. This model can be applied towards the numerous experimental assays utilised within the research group: mouse retinal networks, zebrafish vasculature, and EC monolayers (wound scratch, flow chamber, etc). Our goal is to open up the following projects related to this model within our research network: 1) explore the parameter space to identify which aspects of force transmission between migrating ECs have the biggest effect on remodelling outcome; 2) use experimental cell trajectory data from live imaging as input for the model to measure force transmission between cells both in vitro and in vivo; 3) simulate full-scale network complexity in the mouse retina and explore conditions in which AVMs arise while informed by Alk1-MT mouse models.
Tool 3: PolNet (Miguel UoE)

PolNet [1] is an open-source software tool for the study of blood flow and cell-level biological activity during vessel morphogenesis. We provide an image acquisition, segmentation, and analysis protocol to quantify endothelial cell polarity in entire in vivo vascular networks. In combination, we use computational fluid dynamics to characterize the hemodynamics of the vascular networks under study. The tool enables, to our knowledge for the first time, a network-level analysis of polarity and flow for individual endothelial cells. To date, PolNet has proven invaluable for the study of endothelial cell polarization and migration during vascular patterning, as demonstrated by two recent publications. Additionally, the tool can be easily extended to correlate blood flow with other experimental observations at the cellular/molecular level.