Contribution ID: **166** Type: **Oral Presentation**

Grab Your Glasses! Modelling Cancer Immunology in 3D

Thursday, 12 July 2018 12:00 (30 minutes)

Immune responses to cancer-including innate responses and immunotherapy-involve complex biochemical and biomechanical interactions between tumour cells and many types of immune cells. To date, most modelling has not focused on the spatial and mechanical effects of these interactions. In this talk, we will adapt PhysiCell (an open source platform for 3-D multicellular systems biology [1]) to simulate individual immune cells as they respond to tumour-secreted immunostimulatory signals, adhere to cells, test immunogenicity, and induce apoptosis before repeating their search for new immunogenic targets. We will examine the key roles played by random motility and spatial geometry in the success or failure of an immune response. We will show ongoing work to bridge molecular and multicellular systems biology in 3-D multiscale simulations (e.g., [2]). Lastly, we will discuss and demonstrate the potential for high-throughput multicellular systems biology, where large parameter investigations can be run on supercomputers to efficiently explore 3-D multicellular dynamics under many sets of hypotheses [3], with examples in cancer immunology. With HPC-deployed versions of PhysiCell, we can complete a year's worth of mechanistic computational investigations in a little over a day. In the future, we believe that high-throughput mathematical model investigations will help drive biological discovery and even engineering of the immune system and other complex multicellular systems.

[1] Ghaffarizadeh *et al.*, "PhysiCell: An open source physics-based cell simulator for 3-D multicellular systems," PLoS Comput Biol (2018), http://dx.plos.org/10.1371/journal.pcbi.1005991
[2] Letort *et al.*, "PhysiBoSS: a multi-scale agent based modelling framework integrating physical dimension and cell signalling," bioRxiv 267070 (2018), https://doi.org/10.1101/267070
[3] Ozik *et al.*, "High-throughput cancer hypothesis testing with an integrated PhysiCell-EMEWS workflow", bioRxiv 196709 (2017), https://doi.org/10.1101/196709

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Session Classification: Immunobiology and infection subgroup

Track Classification: Minisymposium: Immunology and Infection Subgroup