University of Basel

Department
Biozentrum

SIB
Swiss Institute of Bioinformatics

BIOZENTRUM
The Center for
Molecular Life Sciences

Basel Computational Biology Seminar

Robert Noble

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London, UK

Explaining the modes of tumour evolution

Understanding the nature of tumour evolution underpins accurate prognosis and the design of effective treatment strategies. Whereas selective sweeps are prevalent during early tumour growth, later stages exhibit either sparse branching or effectively neutral evolution. I will present new insights into the causes and consequences of these different patterns based on mathematical analysis, computational models, and analysis of clinical data. I will show that, within biologically relevant parameter ranges, different spatial structures can generate distinct tumour evolutionary modes. These model predictions are moreover consistent with data for cancer types with corresponding spatial structures. Surprisingly simple mathematical expressions can be derived to explain why selective sweeps are rare except when tumours are relatively very small. I will further introduce indices for categorising evolutionary modes, including a new class of robust, universal tree balance indices. Although my work is motivated by questions in cancer research, many of these results are readily applicable to other systems.

Date:	Monday, October 25, 2021
Time:	16:15 h – 17:30h
Location:	Online via Zoom
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