ESZTER LAKATOS

Dept. of Mathematical Sciences

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I am a computational biologist passionate about applying quantitative techniques to understand the biological principles governing disease in order improve clinical decision making. I am particularly interested in uncovering how cancers evolve using next-generation sequencing datasets.

RESEARCH

Current research: My research focuses on understanding how the mutation landscape of tumours is shaped by the immune system. I create stochastic models of mutation accumulation and contrast them to sequencing datasets to identify evolutionary processes acting on cancers with different mutation burden and tumour micro-environment. I am also interested in analysing large-scale copy number aberrations to understand and tackle the emergence of therapeutic resistance.

Previous research: I developed modelling and analytical tools for stochastic models to understand biological regulation and uncertainty on the single cell level. I created frameworks for model-based simulation, control and parameter inference of biochemical networks, which I used to uncover p53 dynamics in cancer cells.

EDUCATION

Imperial College London (2013–2017)   **London, United Kingdom**
Ph.D. in Theoretical Systems Biology
Supervisor: Prof Michael P.H. Stumpf

Pázmány Péter Catholic University (2012–2013)   **Budapest, Hungary**
M.Sc. of Infobionics Engineer
Grade: *honours*, Average: 5.0/5.0

Pázmány Péter Catholic University (2008–2012)   **Budapest, Hungary**
B.Sc. in Molecular Bionics
Grade: *honours*, Average: 5.0/5.0

WORK & PROFESSIONAL EXPERIENCE

Assistant Professor at Chalmers University of Technology (2023–)   **Gothenburg, Sweden**
Research focus: developing mathematical models and bioinformatic techniques for understanding disease evolution in cancer

Postdoctoral Researcher at BCI/ICR (2017–2022)   **London, United Kingdom**
Supervisor: Prof Trevor Graham
Project: modelling and analysis of the evolution of cancer genomes in interaction with the immune system and therapy.

MSc Diploma Student at Institute of Biophysics, SU (2012–2013)   **Budapest, Hungary**
Supervisor: Dr Miklós Kellermayer
Project: structural and mechanical examination of vertebrate myosin thick filaments using Atomic Force Microscopy.

Intern at EMBL (June–September 2011)   **Heidelberg, Germany**
Supervisor: Dr Francois Nèdèlec
Project: modelling the contraction mechanism of the cytokinetic ring in yeast cells, in the C++ based simulation environment, cyto**sim**.

Guest Associate Editor for Frontiers in Genetics (2021)
Journal Research Topic: Computational approaches applied to cancer genetics, immunogenomics,

and immuno-oncology

SELECTED PUBLICATIONS

A. Cornish*, **E. Lakatos*** *et al.*: "Whole genome sequencing of 2,023 colorectal cancers reveals mutational landscapes, new driver genes and immune interactions,", *bioRxiv, under review at Nature*, **2023**

Q. Guo, **E. Lakatos**, I. Al Bakir, K. Curtius, T. A. Graham and V. Mustonen: "The mutational signatures of formalin fixation on the human genome," *Nature Communications*, **2022**

J. Househam, T. Heide, G. Cresswell, I. Spiteri, C. Kimberley, L. Zapata, *et al.*: "Phenotypic plasticity limits genetic control in colorectal cancer evolution," *Nature*, **2022**

E. Lakatos, H. Hockings, M. Mossner, W. Huang, M. Lockley and T. A. Graham: "LiquidCNA: tracking subclonal evolution from longitudinal liquid biopsies using somatic copy number alterations," *iScience*, **2021**

H. Kayhanian*, P. Barmpoutis*, **E. Lakatos***, W. C. H. Cross* *et al.*: "Mutation rate evolution drives immune escape in mismatch repair-deficient cancer," *bioRxiv, in revision in Nature Genetics*, **2022**

E. Lakatos *et al.*: "The evolutionary dynamics of neoantigens in growing tumors," *Nature Genetics*, **2020**

R. O. Schenck, **E. Lakatos**, C. Gatenbee, T. A. Graham and A. R. A. Anderson: "NeoPredPipe: High-Throughput Neoantigen Prediction and Recognition Potential Pipeline," *BMC Bioinformatics*, **2019**

E. Lakatos*, R. D. Brackston* and M. P. H. Stumpf: "Transition state characteristics during cell differentiation," *PLOS Computational Biology*, **2018**

E. Lakatos and M. P. H. Stumpf: "Control mechanisms for stochastic biochemical systems via computation of reachable set," *Royal Society Open Science*, **2017**

E. Lakatos*, A. Salehi-Reyhani*, M. Barclay*, M. P. H. Stumpf and D. R. Klug: "Protein degradation rate is the dominant mechanism accounting for the differences in protein abundance of basal p53 in a human breast and colorectal cancer cell line," *PLOS One*, **2017**

E. Lakatos, P. Kirk, A. Ale and M. P. H. Stumpf: "Multivariate moment closure techniques for stochastic kinetic models," *The Journal of Chemical Physics*, **2015**

SUPERVISION & TEACHING

Gerard Llibre (2021)   9-month MSc dissertation
Project: The role post-transcriptional processes in the evolutionary dynamics of frameshift neoantigens in colorectal cancer

Syeda Fatima (2021)   6-month MSc dissertation
Project: The immune landscape of tumours associated with inflammatory bowel disease

Dr Badia Ahmed (2021)   3-month MSc dissertation
Project: The role of mutations affecting antigen presentation in colorectal cancers of the 100,000 Genomes Project

Ziba Niazi (2020)   8-week summer internship
Project: Modelling T-cell expansion in response to tumour growth.

Bryony Coppack (2020)   6-month MSc dissertation
Project: Post-genetic processes shaping the neoantigen landscape of colorectal cancers.

Jatinder Singh Stanley (2019)   3-month MSc dissertation
Project: Evolutionary characteristics of neoantigens in inflammatory bowel disease and colorectal cancer.
Jay received the prize for Best MSc Dissertation.

Sisi Fan, Quentin Geissmann, Saulius Lukauskas   3-month MSc project
Project: Python implementation of moment closure methods for stochastic simulations.

The resulting package has been published in *Bioinformatics*.

Graduate Teaching Assistant (2014–2018)   **ICL, United Kingdom**
Courses taught: Introduction to Python programming; Coding for Medics (python); Introduction to scientific modelling and Matlab language; Introduction to Bioinformatics module; Genome and protein databases
Teaching Assistant (2009–2013)   **PPCU, Hungary**
Courses taught: Digital Signal Processing; Data Mining; Calculus I-II; Linear Algebra and Discrete Mathematics I-II; Cell Biology and Genetics I-II; Physics of Information Technology; Operation of AFM and STM

SKILLS & INTERESTS

Computational skills: R, Python, High Performance Computing clusters, Julia, bash, LaTeX, C++, MATLAB, Microsoft Office
Languages: Hungarian (native speaker), English (fluent), Russian (basic level)
Interests: cycling, indoors climbing, amateur singing, hiking, watercolour

SELECTED AWARDS & ACHIEVEMENTS

Emerging Leaders in Computational Oncology Award for scientific achievement (**2020**)
LIDo Research Experience Placement Award (**2020**)
Life Sciences Initiative, Centre for Computational Biology Showcase Award (**2018 & 2019**)
Prize for Best Lay Summary at Department of Life Sciences Postgraduate Open Day **(2016)**
First prize for best talk at the annual Applied Mathematics and Mathematical Physics day (**2015**)
Schrödinger Scholarship (**2013–2016**)
Grant of the Hungarian Republic (academic years **2011/12 & 2012/13**)
Fifth place at Hungarian National High School Competition in Mathematics (**2008**)