

MACIEJ DOBRZYŃSKI

A computational biologist and a mathematical modeller with 10+ years of experience in academia and industry, focusing on data analysis and visualisation. Superb at building pipelines for diverse biological data that provide actionable insights through interactive visualisations. An interdisciplinary mind with organisational skills to conduct and lead computational biology projects under tight deadlines. Strong science communicator with a proven track record of designing and teaching courses, training the staff, publishing in scientific journals.



View this CV online with links at macdoby.net/cv/

EDUCATION

2009
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2004

PhD., Mathematics & Computer Science

Centre for Mathematics and Computer Science (CWI)
📍 Amsterdam, The Netherlands

- Thesis: [A theoretical study of noise in gene expression and cell signalling](#)

2003
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1997

M.Sc., Physics, Theoretical Biophysics

Faculty of Physics, Warsaw University 📍 Warsaw, Poland

- Thesis: [Particle-based algorithm for modelling of biochemical networks](#)
- Erasmus Scholarship at Vrije Universiteit Amsterdam

EXPERIENCE

current
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2016

Postdoctoral Researcher

Cellular Dynamics Lab, Institute of Cell Biology, University of Bern
📍 Bern, Switzerland

- Developed an [R/Shiny app](#) to explore and cluster time series
- Developed a [web portal](#) to visualise drug screen imaging data
- Set up a computational cluster and developed pipelines to process data from high-content screening and time-lapse microscopy experiments.

2018
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2014

Data Scientist

TickerFit (start-up) 📍 Dublin, Ireland

- Consulted and analysed in R patient activity during cardiac rehabilitation

2016
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2015

Data Scientist

AstraZeneca Discovery Sciences 📍 Cambridge, UK

- Used CellProfiler/R to analyse single-cell data from high-content screens
- Used Matlab/Mathematica to develop a mathematical model of cell-cell heterogeneity in a mitogenic signalling pathway

CONTACT

✉ info@macdoby.net

🌐 [Homepage](#)

🐙 [GitHub](#)

🏛️ [ORCID](#)

🌐 [LinkedIn](#)

🐦 [Twitter](#)

CODING SKILLS

R/Shiny

Python

Mathematica

Matlab

C/C++

Bash

AWK

Last updated on 2022-03-04.

2015
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2010

Postdoctoral Researcher

Systems Biology Ireland, University College Dublin  Dublin, Ireland

- Developed deterministic and stochastic models of oncogenic signalling
- Performed wet-lab experiments: flow cytometry and live cell imaging
- Programmed in Python, Matlab, Mathematica, R

2009

Research Assistant

Institute of Theoretical Biology, Humboldt University  Berlin, Germany

- Studied the robustness of a bacterial chemotactic network

2004
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2003

Undergraduate Researcher

Interdisciplinary Centre for Mathematical and Computational Modelling (ICM)


 Warsaw, Poland

- Vectorized a [gene sequence alignment algorithm](#) on Cray X1 architecture
- Programmed in C/C++, Perl, MPI

2002

Undergraduate Researcher

FOM Institute for Atomic and Molecular Physics (AMOLF)

 Amsterdam, The Netherlands

- Developed a [method for simulation](#) of biochemical networks
- Programmed in C/C++, Fortran 77 & 95

I have bridged academia and industry, have worked in interdisciplinary, fast-paced, collaborative R&D environments.

TEACHING EXPERIENCE

2021

Course: Imaging statistics

Microscopy Imaging Center

 Bern, Switzerland

- Held a lecture & practicals on data analysis for microscopy

2020

Course: Modern data analysis in R/RStudio

Microscopy Imaging Center


 Bern, Switzerland

- Held a workshop on advanced topics of data analysis in R

2019

Course: Analysis on microscopy images with CellProfiler

Microscopy Imaging Center


 Bern, Switzerland

- Assisted a workshop on image analysis with CellProfiler

2019

Processing data from single-cell time-lapse microscopy

Quantitative Biology Workshop

 Fiesch, Switzerland

- Held a workshop on analysis of data from time-lapse microscopy

2019

Semi-advanced R programming tricks

BernR MeetUp

 Bern, Switzerland

- Held a lecture on advanced topics in R programming

I have held numerous invited lectures and workshops about biological image processing, statistical analysis, and visualisation of experimental data.

- 2019

Shiny from basics to awesome in 26 minutes
[BernR MeetUp](#) 📍 Bern, Switzerland

 - Held a lecture on R/Shiny programming

- 2018
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2017

Image analysis with ImageJ and CellProfiler
 Institute of Cell Biology, University of Bern 📍 Bern, Switzerland

 - Held a lecture for undergraduate students

- 2016

Course: Introduction to modelling of signalling networks
[2nd Porto Meeting in Mathematics and Biology](#) 📍 Porto, Portugal

 - Invited lecture series on cell-cell heterogeneity in signalling networks

- 2015
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2013

Course: Introduction to Systems Biology
[Systems Biology Ireland](#), University College Dublin 📍 Dublin, Ireland

 - Gave a lecture series to (under-)graduate students

- 2004

Course: Principles of Object-Oriented Programming in Java
[Faculty of Physics](#), Warsaw University 📍 Warsaw, Poland

 - Teaching assistant



SELECTED PEER-REVIEWED PUBLICATIONS

- 2022

High-Content Screening Pipeline for Natural Products Targeting Oncogenic Signaling in Melanoma
[Journal of Natural Products](#)

 - Analysed and visualised HCS data

- 2021

CODEX, a neural network approach to explore signaling dynamics landscapes
[Molecular Systems Biology](#)

 - Supervised the project
 - R/Python coding by MA Jacques, a PhD student in the lab

- 2021

Collective ERK/Akt activity waves orchestrate epithelial homeostasis by driving apoptosis-induced survival
[Developmental Cell](#)

 - Analysed single-cell ERK/Akt activity waves that induce survival in neighbouring cells of the epithelium
 - Developed an [R package](#) to quantify collective signalling

I design and perform image/data analysis and ensure statistical rigour during results dissemination.

- 2020 **Mining single-cell time-series datasets with Time-Course Inspector**
Bioinformatics
- Developed an R/Shiny app to interactively process, visualise, and cluster time series
- 2019 **Temporal perturbation of Erk dynamics reveals network architecture of FGF2-MAPK signaling**
Molecular Systems Biology
- Modelled the FGF2-MAPK network
 - Analysed single-cell time series data in R and Matlab
- 2017 **Automated Comparative Metabolite Profiling of Large LC-ESIMS Data Sets in an ACD/MS Workbook Suite Add-in, and Data Clustering on a New Open-Source Web Platform FreeClust**
Analytical Chemistry
- Developed an R/Shiny web application to cluster LC-MS data
- 2016 **Stabilization of C-RAF:KSR1 complex by DiRas3 reduces availability of C-RAF for dimerization with B-RAF**
Cellular Signalling
- Performed image and statistical analysis
- 2015 **Frequency modulation of ERK activation dynamics rewires cell fate**
Molecular Systems Biology
- Studied cell fate determination by ERK signalling dynamics
 - Analysed single-cell time series data in R and Matlab
- 2014 **Nonlinear signalling networks and cell-to-cell variability transform external signals into broadly distributed or bimodal responses**
Journal of the Royal Society Interface
- Studied the emergence of cell-cell heterogeneity in signalling pathways
 - Developed a model in Wolfram Mathematica
- 2009 **Elongation dynamics shape bursty transcription and translation**
Proceedings of the National Academy of Sciences of the USA
- Studied stochasticity during mRNA transcription and protein translation
 - Wrote code in C, Matlab, R
- 2007 **Computational methods for diffusion-influenced biochemical reactions**
Bioinformatics
- Evaluated methods for simulating cell signalling in space and time
 - Wrote code in Python and C

SELECTED PRESS (BY)

2015

The Era of Personalised Medicine

[Spider's Web](#)

- Leveraging personalised data to improve health
- Spider's Web is a Polish technology portal with ~4M monthly users

2015

Solving the Human Brain

[Spider's Web](#)

- The state of computational neurology and brain simulations

2012

Healing with a computer

[Polityka](#)

- How computational biology helps to predict new treatments
- Polityka is Poland's biggest selling weekly magazine

I write popular science articles about the role of computational biology in knowledge discovery.

SELECTED PRESS (ABOUT)

2009

Math replaces lab animals

[Experiment NL: Science in The Netherlands](#)

- A feature about my PhD research and how mathematical modelling can help to alleviate animal testing of drugs