

## Research Interests and Experience

### Bioinformatics and biomedical data science

- Bioinformatics analysis of high-dimensional next-generation sequencing data
- Precision medicine drug recommendation systems with machine learning
- Prediction of disease-causing genomic variants with machine learning

### Deep learning and computer vision

- Deep learning and computer vision for precision aquaculture
- Graph neural networks for pharmaceutical discovery

## Education

2011–2015

### Doctor of Philosophy



Institute for Integrated and Intelligent Systems, Griffith University, Australia  
NICTA – Australia's ICT Research Centre of Excellence, Australia

Advisers: Prof Bela Stantic, Prof Yaoqi Zhou, Prof Abdul Sattar

Thesis: **Predicting stability and functional changes induced by protein mutations with a machine learning approach**

Awards: Three-Minutes Thesis competition finalist

2007–2010

### Master's Degree in Informatics



Faculty of Informatics, Masaryk University, Czech Republic

Thesis: **Neighbour-based intrusion detection in wireless sensor networks**

Awards: Dean's awards for excellent study results and outstanding thesis

2004–2007

### Bachelor's Degree in Applied Informatics



Faculty of Informatics, Masaryk University, Czech Republic

Thesis: **The use of a power analysis for influencing PIN verification on cryptographic smart cards**

Awards: Average grade ranked within the best 2% of 2006/2007 graduates

## Professional Experience

Nov 2022–

### Research Fellow

now



Big Data and Smart Analytics Lab, Institute for Integrated and Intelligent Systems  
Coastal and Marine Research Centre, Australian Rivers Institute, Griffith University

Mentors: Prof Kylie Pitt, Prof Bela Stantic

Project: **Deep learning and computer vision for underwater object detection**

I am developing deep learning and computer vision algorithms for longitudinal fish health and welfare monitoring. These methods will be deployed to salmon farms operated by our three industry partners. Main objective is achieving accurate, real-time, production-scale monitoring of hundreds of fish pens.

Jul 2018–

### Postdoctoral Researcher

Oct 2022

Institute for Artificial Intelligence, Medical University of Vienna, Austria (since May 2022)  
CeMM Research Center for Molecular Medicine, Austrian Academy of Sciences




Ce-M-M-

Mentor: Prof Christoph Bock (<https://www.bocklab.org>)

Projects: **Bioinformatics and machine learning for molecular medicine**


I was the lead bioinformatician of a clinical trial for which I designed and conducted bioinformatics and machine-learning analysis of ATAC-seq, single-cell RNA-seq, and immunophenotyping data. My additional projects focused on graph neural networks for pharmaceutical discovery and explainable deep learning for single-cell RNA-seq.

- Jun 2016–  
Jun 2018** **Postdoctoral Researcher**  
Department of Biosystems Science and Engineering, ETH Zurich, Switzerland  
**ETH** zürich Mentor: Prof Karsten Borgwardt (<https://bsse.ethz.ch/mlcb>)  
Project: **Machine learning for precision medicine drug recommendation systems**  
In this precision medicine project we developed a novel approach to recommend cancer treatments based on high-dimensional transcriptomics profiles of cancer cell lines. Our data-driven learning-to-rank approach achieved high clinical relevance compared to other regression-based methods. This work received two best poster awards at premiere national and international conferences.
- Mar 2015–  
Mar 2016** **Visiting Researcher**  
Institute for Integrated and Intelligent Systems, Griffith University, Australia  
 Adviser: Prof Yaoqi Zhou (<https://sparks-lab.org>)  
Project: **Machine learning for prediction of disease-causing genomic variants**  
Capitalising on research from my doctoral thesis, we developed a machine-learning method for predicting disease-causing synonymous variants, which are particularly challenging as the protein sequence remain unchanged despite a variant occurring at the DNA level. The accuracy of our model superseded all other available methods.
- Mar 2010–  
Jul 2010** **Software Developer and Consultant**  
ARTIN, Czech Republic

#### Funding

- 2019–2021** **Marie Skłodowska-Curie Actions Individual Fellowship** (186,000 EUR)  
Success rate of 12.4%; competitive fellowship sponsored by the European Commission
- 2011–2014** NICTA Project Award Scholarship (28,000 AUD)
- 2011–2014** Griffith University Postgraduate Research Scholarship (74,000 AUD + tuition fee waiver)
- Dec 2010** NICTA Summer Research Scholarship (5,000 AUD)













#### Awards


- Jan 2024** “Multi-omics analysis of innate and adaptive responses to BCG vaccination reveals epigenetic cell states that predict trained immunity” was selected for *Nature Research Highlights* 
- Sep 2017** Online Poster Award (1st place) at [BC]<sup>2</sup> Basel Computational Biology Conference 2017 for “Kernelized rank learning for personalized drug recommendation”, Basel, Switzerland
- Jul 2017** F1000Research Poster Award at the international conference ISMB/ECCB 2017 for “Kernelized rank learning for personalized drug recommendation”, Prague, Czech Rep.
- Jun 2014** Winner of the Three-Minutes Thesis competition, School of ICT, Griffith University
- Apr 2014** Gold Coast Association of Postgraduates Conference Funding Award, Griffith University
- Jan 2013** Griffith University Conference Travel Grant, Griffith University
- Dec 2010** 2nd best paper in the workshop Keymaker 2010, Brno, Czech Rep.
- May 2010** 2nd place in Czech and Slovak university research competition, Ostrava, Czech Rep.
- Mar 2010** Dean's award for outstanding thesis, Faculty of Informatics, Masaryk University
- Mar 2010** Dean's award for excellent study results, Faculty of Informatics, Masaryk University


## Publications


# These authors contributed equally and they are equal “first” authors.


Impact factors were sourced from the 2022 journal impact factor report.


- Folkman L, Pitt KA, Stantic B: “A framework for combating domain shift in underwater object detection with image enhancement”. *Applied Intelligence* (2024), [accepted](#), **impact factor 5.3**.
- Moorlag<sup>#</sup> SJCFM, Folkman<sup>#</sup> L, ter Horst<sup>#</sup> R, Krausgruber<sup>#</sup> T, ..., Netea\* MG, Bock\* C: “Multi-omics analysis of human population variation in immune function and *in vivo* response to BCG vaccination”. *Immunity* (2024), 57(1), 171–187, **impact factor 32.4**. 
- Teufel LU, Matzaraki V, Folkman L, ter Horst R, Moorlag SJCFM, Mulders-Manders CM, Netea MG, Krausgruber T, Joosten LAB, Arts RJW: “Insights into the multifaceted role of interleukin-37 on human immune cell regulation”. *Clinical Immunology* (2024), 268(1), 110368, **impact factor 4.5**. 
- Turina<sup>#</sup> P, Cortivo<sup>#</sup> GD, ..., Folkman L, ..., Dell’Orco\* D, Capriotti\* E: “Assessing the predicted impact of single amino acid substitutions in calmodulin for CAGI6 challenges”. *Human Genetics* (2024), [accepted](#), **impact factor 5.3**.
- Turina<sup>#</sup> P, Petrosino<sup>#</sup> M, ..., Folkman L, ..., Chiaraluce\* R, Consalvi\* V, Capriotti\* E: “Assessing the predicted impact of single amino acid substitution in MAPK proteins for CAGI6 challenges”. *Human Genetics* (2024), [accepted](#), **impact factor 5.3**.
- The Critical Assessment of Genome Interpretation Consortium: “CAGI, the Critical Assessment of Genome Interpretation, establishes progress and prospects for computational genetic variant interpretation methods”. *Genome Biology* (2024), 25, 53, **impact factor 12.3**. 
- de Bree<sup>#</sup> LCJ, Mourits<sup>#</sup> VP, ..., Folkman L, ..., Netea MG: “Circadian rhythm influences induction of trained immunity by BCG vaccination”. *The Journal of Clinical Investigation* (2020), 130(10), 5603–5617, **impact factor 15.9**. 
- Pejaver V, Babbi G, Casadio R, Folkman L, ..., Bromberg Y: “Assessment of methods for predicting the effects of PTEN and TPMT protein variants”. *Human Mutation* (2019), 40(9), 1495–1506, **impact factor 3.9**. 
- Savojardo<sup>#</sup> C, Petrosino<sup>#</sup> M, ..., Folkman L, ..., Capriotti E: “Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge”. *Human Mutation* (2019), 40(9), 1392–1399, **impact factor 3.9**. 
- Clark WT, ..., Folkman L, ..., LeBowitz JH: “Assessment of predicted enzymatic activity of alpha-N-acetyl-glucosaminidase (NAGLU) variants of unknown significance for CAGI 2016”. *Human Mutation* (2019) 40(9), 1519–1529, **impact factor 3.9**. 
- He<sup>#</sup> X, Folkman<sup>#</sup> L, Borgwardt K: “Kernelized rank learning for personalized drug recommendation”. *Bioinformatics* (2018), 34(16), 2808–2816, **impact factor 5.8**. 
- Livingstone<sup>#</sup> M, Folkman<sup>#</sup> L, Yang Y, Zhang P, Mort M, Cooper DN, Liu Y, Stantic B, Zhou Y: “Investigating DNA-, RNA-, and protein-based features as a means to discriminate pathogenic synonymous variants”. *Human Mutation* (2017), 38(10), 1336–1347, **impact factor 3.9**. 
- Folkman L, Stantic B, Sattar A, Zhou Y: “EASE-MM: sequence-based prediction of mutation-induced stability changes with feature-based multiple models”. *Journal of Molecular Biology* (2016), 428(6), 1394–1405, **impact factor 5.6**. 
- Folkman L, Yang Y, Li Z, Stantic B, Sattar B, Mort M, Cooper DN, Liu Y, Zhou Y: “DDIG-in: detecting disease-causing genetic variations due to frameshifting indels and nonsense mutations by sequence and structural properties at nucleotide and protein levels”. *Bioinformatics* (2015) 31(10), 1599–1606, **impact factor 5.8**. 
- Folkman L, Stantic B, Sattar A: “Feature-based multiple models improve classification of mutation-induced stability changes”. *BMC Genomics* (2014) 15(Suppl 4), S6, **impact factor 4.4**. 

**Folkman L**, Stantic B, Sattar A: “Towards sequence-based prediction of mutation-induced stability changes in unseen non-homologous proteins”.  
*BMC Genomics* (2014) 15(Suppl 1), S4, **impact factor 4.4**. 

**Folkman L**, Stantic B, Sattar, A: “Sequence-only evolutionary and predicted structural features for the prediction of stability changes in protein mutants”.  
*BMC Bioinformatics* (2013) 14(Suppl 2), S6, **impact factor 3.0**. 

Higgs T, **Folkman L**, Stantic B: “Combining protein fragment feature-based resampling and local optimisation”. in ‘IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB)’, Vol. 7986 of *LNCS*, pp. 114–125, Springer, 2013. 

**Folkman L**, Pullan W, Stantic B: “Generic parallel genetic algorithm framework for protein optimisation”. in ‘Algorithms and architectures for parallel processing (ICA3PP)’, Vol. 7017 of *LNCS*, pp. 64–73, Springer, 2011. 

Stetsko A, **Folkman L**, Matyas V: “Neighbor-based intrusion detection in wireless sensor networks”. in ‘Wireless and Mobile Communications (ICWMC)’, pp. 420–425, IEEE, 2010. 

## Teaching

2022



### Teaching Assistant

Medical University of Vienna, Austria

- *Biomedical Informatics and Genomic Medicine* (master’s degree course)
  - Developed and delivered practical sessions on biomedical data science

2022



### Lecturer

University of Applied Sciences Technikum Vienna, Austria

- *Special Topics of Artificial Intelligence* (master’s degree course)
  - Developed and delivered two lectures on deep learning in biomedicine

2021



### Guest Lecturer

Medical University of Vienna, Austria

- *Biomedical Informatics and Genomic Medicine* (master’s degree course)
  - Developed and delivered a lecture and a practical session on machine learning

2020–2021

Ce-M-M-

### Guest Lecturer

CeMM Research Center for Molecular Medicine, Austrian Academy of Sciences

- *Machine-learning workshop for biomedical PhD students*
  - Developed and delivered a lecture and a practical session on machine learning

2016

ETH zürich

### Teaching Assistant

Department of Biosystems Science and Engineering, ETH Zurich, Switzerland

- *Data Mining I* (master’s degree course)
  - Co-developed and delivered practical sessions, marked homework and exam

2012–2013



### Teaching Assistant

School of Information and Communication Technology, Griffith University, Australia

- *Database Systems and Administration* (bachelor’s degree course) offered in conjunction with *Database Technology* (master’s degree course)
  - Developed and delivered tutorial workshops and quizzes
  - Received a mean **score of 4.78 (out of 5)** and 5 award nominations: “Lukas was also an excellent tutor. He explains things so clearly and breaks up complex subjects into something simple which helped me understand topics better.”
- *Introduction to Programming* (bachelor’s degree course)
  - Delivered practical sessions and assessment sessions
- *Object-Oriented Programming* (bachelor’s degree course)
  - Delivered practical sessions and assessment sessions

## Supervision and Mentoring

- 2022–now** Quynh Le Khanh Vo, **PhD candidate** (Griffith University, Gold Coast, Australia)  
My role: **co-supervisor**  
Project: Advanced monitoring to maximise fish welfare in offshore aquaculture
- 2024** Karlo Siljeg, **Honours project student** (Griffith University, Gold Coast, Australia)  
My role: **supervisor** of Karlo's *Advanced Topics* project  
Project: Dynamic copy-paste data augmentation for underwater object detection
- 2020–2022** Stephan Reichl, **PhD candidate** (CeMM and Medical University of Vienna, Austria)  
My role: **mentor**, a co-authored paper currently under review  
Project: Statistical and bioinformatics analysis of high-dimensional molecular data
- 2017** Elli Tzini, **Master's degree student** (ETH Zurich, Basel, Switzerland)  
My role: **co-supervisor (to a successful completion)**  
Project: Machine learning for personalised drug recommendation systems  
*Elli continued her career as a machine-learning engineer.*
- 2016–2017** Udo Gieraths, **PhD candidate** (ETH Zurich, Basel, Switzerland)  
My role: **co-supervisor**  
Project: Machine learning for prediction of disease-linked genes  
*Udo continued his career as a data scientist.*
- 2016** Caroline Weis, **Master's degree student** (ETH Zurich, Basel, Switzerland)  
My role: **co-supervisor (to a successful completion)**  
Project: Machine learning for prediction of disease-causing genomic variants  
*Caroline continued her research as a PhD candidate at ETH Zurich.*
- 2013** Mark Livingstone, **Honours student** (Griffith University, Gold Coast, Australia)  
My role: **mentor**, co-authored a paper with Mark  
Project: Impact of single amino acid change upon protein structure  
*Mark continued his research as a PhD candidate at Griffith University.*

## Institutional Service

- 2020–2022** Data ambassador and manager, part of a working group for implementing and enforcing institute-wide "FAIR" (findable, accessible, inter-operable, and reusable) data principles
- 2017** Contributed to the conceptualisation and presentation of a video game to popularise machine learning for medicine at the Swiss national scientific outreach event Scientifica
- 2012–2013** Founding chair of the IIS/ICT Higher-Degree-Research Student Community

## Academic Service

- Peer-review** Bioinformatics (impact factor 5.8)  
eLife (served as a Reviewing Editor, impact factor 7.7)  
Bioinformatics Advances (impact factor 2.4)  
Journal of Machine Learning Research (A\*-ranked by CORE)  
European Conference on Machine Learning (A-ranked by CORE)  
Journal of Molecular Biology (impact factor 5.6)  
Scientific Reports (impact factor 4.6)

## Skills and Competencies

- Soft Skills\*** Academic writing, public speaking, time management, project management, supervising Master and PhD projects (\*including formal training via workshops)
- Programming** Python (including PyTorch, Scikit-Learn, Pandas, Statsmodels, NumPy, SciPy), R (including LIMMA for RNA-seq analysis), Unix systems, bash, Java, C, C++
- Languages** English – fluent, Czech – fluent, German – beginner, Slovak – native