

Professional experience

since 04/2019 Postdoctoral Research Fellow
MacRae Lab & One Brave Idea Initiative
Brigham and Women's Hospital
Harvard Medical School








Development of **machine learning algorithms** for the analysis of biomedical data from multiple modalities such as blood cytometry, electrocardiogram recordings and medical notes. **Genetic association studies** using novel phenotypes, blood cell perturbation responses and deep learning-derived cardiac traits in biobank-scale cohorts. Integrative analyses of **sequencing, metabolomic and proteomic data** in human and animal models.

09/2018-02/2019 Postdoctoral Research Associate
Troyanskaya Lab
Lewis-Sigler Institute for Integrative Genomics
Princeton University

Education

- 2018 PhD Computer Science, Princeton University
Thesis: "Network-Based Prioritization of Disease Genes, Animal Models, and Drug Targets"
Adviser: Dr. Olga Troyanskaya
- 2014 MA Computer Science, Princeton University
- 2011 MPhil Computational Biology, University of Cambridge
Thesis: "Bootstrap Aggregating for Phylogenetic Inference"
Adviser: Dr. Florian Markowetz
- 2009 BSc Bioinformatics, Free University of Berlin
Thesis: "Supertree Heuristics on Reduced Sets of Triplets"
Adviser: Dr. Oliver Eulenstein

Selected publications

- Deep phenotyping, GWAS, polygenic scores. **Homilius M***, Zhu W*, ..., MacRae CA and Deo RC. "Perturbational phenotyping of human blood cells reveals genetically determined latent traits associated with subsets of common diseases". *Nature Genetics* 10.1038/s41588-023-01600-x, 2023.  
- Multimodal & contrastive training, medical notes, diagnostic codes. Kailas P*, **Homilius M***, Deo RC, MacRae CA. "Contrastive Language-Diagnostic Pretraining for automated adjudication of medical notes". *Machine Learning for Health Symposium, Proceedings of Machine Learning Research* 225:201–216, 2023.  
- Transformers, medical notes, PHI. Kailas P*, **Homilius M***, Goto S*, ..., MacRae CA, Deo RC. "Robust de-identification of medical notes using transformer architectures, sentence context and recall thresholding". Submitted. 
- Federated learning, CNNs, ECG & Echo. Goto S, Solanki D, John JE, Yagi R, **Homilius M**, Ichihara G, Katsumata Y, Gaggin HK, Itabashi Y, MacRae CA and Deo RC. "Multinational Federated Learning Approach to Train ECG and Echocardiogram Models for Hypertrophic Cardiomyopathy Detection.", *Circulation* 146(10), 755-769, 2022.  
- CNN-LSTMs, medical notes, blood cytometry, risk prediction. Truslow JG, Goto S, **Homilius M**, Mow C, Higgins JM, MacRae CA, Deo RC. "Cardiovascular Risk Assessment Using Artificial Intelligence-Enabled Event Adjudication and Hematologic

Deep phenotyping, automated imaging.	Predictors.”, <i>Circulation Cardiovascular Quality and Outcomes</i> 15(6):e008007, 2022.
	Zhu W, Guo S, Homilius M , ..., Flaumenhaft R, Deo RC, MacRae CA. “PIEZO1 mediates a mechanothrombotic pathway in diabetes.”, <i>Science Translational Medicine</i> 14(626):p.eabk1707, 2022.
CNNs, Echo & PET, GWAS.	Goto S, Werdich AA, Homilius M , John JE, Gan L, MacRae CA, DiCarli MF, Deo RC. “Discovery of cardiac imaging biomarkers by training neural network models across diagnostic modalities”. Preprint medRxiv:2021.02.07.21251025, 2021.
CNN-LSTMs, medical notes, survival models.	Goto S*, Homilius M* , ..., MacRae CA, Deo RC. “Artificial intelligence-enabled event adjudication: estimating delayed cardiovascular effects of respiratory viruses”. Preprint medRxiv:2020.11.12.20230706, 2020.
Functional gene networks.	Goya J, Wong AK, Yao V, Krishnan A, Homilius M , Troyanskaya OG. “FNTM: a server for predicting functional networks of tissues in mouse.”, <i>Nucleic Acids Research</i> 43 (W1): W182-W187, 2015.
Drug interactions.	Bansal M, ..., NCI-DREAM Community . “A Community computational challenge to predict the activity of pairs of compounds.”, <i>Nature Biotechnology</i> 32, 1213–1222, 2014.
Protein interaction networks.	Yosef N, Zalckvar E, Rubinstein A, Homilius M , ..., Ruppin E, Sharan R “ANAT: a tool for constructing and analyzing functional protein networks.” <i>Science Signaling</i> 196, p11, 2011.
Evolution, protein domains.	Homilius M , Wiedenhoeft J, Thieme S, Standfuß C, Kel I, Krause R. “Cocos: Constructing multi-domain protein phylogenies.” <i>PLoS Currents</i> 3:RRN1240, 2011.

Previous research and teaching positions

9/2012-6/2013	<i>Assistant in instruction</i> , Princeton University Integrated Science Curriculum (General Computer Science I/II) Prepared exercises and exams for introductory computer science courses with a focus on scientific computing. Wrote automated grading scripts for programming exercises.
3/2010-9/2010	<i>Research assistant</i> , Max Planck Institute of Molecular Genetics Dr. Martin Vingron and Dr. Roland Krause, Research Advisers Design and implementation of a program for the inference of the joint phylogeny of multi-domain proteins.
11/2008-12/2008	<i>Undergraduate researcher</i> , Max Planck Institute of Molecular Genetics Dr. Hans Lehrach and Dr. Lukas Chavez, Research Advisers Statistical analysis of DNA methylation data.
08/2008-10/2008	<i>Undergraduate researcher</i> , Tel Aviv University Dr. Roded Sharan and Dr. Nir Yosef, Research Advisers Implementation of a program for the generation, analysis and refinement of functional sub-networks in protein interaction networks.

Honors and awards

2022-2023	Drs. Tobia and Morton Mower Fellow
2010-2011	German Academic Scholarship Foundation Study Abroad Stipend (University of Cambridge)
2008-2011	German Academic Scholarship Foundation Fellow
2008	German Academic Exchange Service Travel Award (Tel Aviv University)