

Professional experience

since 04/2019 Postdoctoral Research Fellow
Brigham and Women's Hospital
Harvard Medical School

Development of **machine learning algorithms** for the analysis of biomedical data from modalities such as blood cytometry, electrocardiogram recordings, medical notes and wearable device sensors. **Genetic association studies** using novel phenotypes, such as 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, including metagenomic analyses of gut microbiome data.

09/2018-02/2019 Postdoctoral Research Associate
Troyanskaya Laboratory
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

Publications and presentations

Articles

- Homilius M***, Zhu W*, Eddy S, Thompson P, Zheng H, Xuan L, Kim D, Nsubuga C, Strecker Z, Cho J, Evans C, Howie M, Thaler AA, Wilson E, Gupta P, Cupelo M, Smith C, Nascimben J, Sridaran S, Lunati G, Folks H, Rheinstein C, Pettit C, Ghosal A, Truslow J, Wollison B, Goto S, Warren C, Vandenwijngaert S, MacRae CA and Deo RC. "Perturbational phenotyping of human blood cells reveals genetically determined latent traits associated with subsets of common diseases". *Nat Genet* 10.1038/s41588-023-01600-x, 2023.
- Kailas P*, **Homilius M***, Deo RC, MacRae CA. "Contrastive Language-Diagnostic Pretraining for automated adjudication of medical notes". *Machine Learning for Health, Proceedings of Machine Learning Research* 225:201–216, 2023.
- Kailas P*, **Homilius M***, Goto S*, Nascimben J, Smith C, Cupelo M, MacRae CA, Deo RC. "Robust de-identification of medical notes using transformer architectures, sentence context and recall thresholding". Submitted.
- 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.
- 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 Predictors.”, *Circ Cardiovasc Qual Outcomes* 15(6):e008007, 2022.
- Zhu W, Guo S, **Homilius M**, Nsubuga C, Wright SH, Quan D, Kc A, Eddy SS, Victorio RA, Beerens M, Flaumenhaft R, Deo RC, MacRae CA. “PIEZO1 mediates a mechanothrombotic pathway in diabetes.”, *Sci Transl Med* 14(626):p.eabk1707, 2022.
- 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.
- Goto S*, **Homilius M***, John JE, Truslow JG, Werdich AA, Blood AJ, Park BH, MacRae CA, Deo RC. “Artificial intelligence-enabled event adjudication: estimating delayed cardiovascular effects of respiratory viruses”. Preprint [medRxiv:2020.11.12.20230706], 2020.
- Goya J, Wong AK, Yao V, Krishnan A, **Homilius M**, Troyanskaya OG. “FNTM: a server for predicting functional networks of tissues in mouse.”, *Nucleic Acids Research* 43 (W1): W182-W187, 2015.
- Bansal M, ..., **NCI-DREAM Community**. “A Community computational challenge to predict the activity of pairs of compounds.”, *Nature Biotechnology* 32, 1213–1222, 2014.
- Yosef N, Zalcikvar E, Rubinstein A, **Homilius M**, Atias N, Vardi L, Berman I, Zur H, Kimchi A, Ruppin E, Sharan R “ANAT: a tool for constructing and analyzing functional protein networks.” *Science Signaling* 196, p11, 2011.
- Homilius M**, Wiedenhoeft J, Thieme S, Standfuß C, Kel I, Krause R. “Cocos: Constructing multi-domain protein phylogenies.” *PLoS Currents* 3:RRN1240, 2011.

Manuscripts in preparation

- Saha K, **Homilius M**, MacRae CA. “Hypoxia pathway contributes to cyanide resistance in developing zebrafish embryos”.
- Yagi R, **Homilius M***, Katsumata Y, MacRae CA, Goto S, Deo RC. “Using artificial intelligence to identify key electrocardiographic features for detecting left ventricular systolic dysfunction”.
- Homilius M**, Ricciotti E, Grosser T, FitzGerald GA, Troyanskaya OG. “A network-based approach to detect drug mode-of-action at therapeutic doses”.
- Homilius M**, Krishnan A, MacRae CA, Troyanskaya OG. “Prioritizing animal models for human diseases using genome-wide functional networks”.
- Homilius M**, Troyanskaya OG. “Tissue-specific multi-label prediction of human disease genes”.

Conference proceedings and posters

- 2019 **Homilius M**, Blood AJ, Park BH, Yazdi D, Veytsman JN, MacRae CA, Deo RC. “Automated Disease Detection Using Document Classification Outperforms Encounter-Level Diagnostic Codes for Cardiovascular Diseases”, American Heart Association Scientific Sessions, Philadelphia, Nov 16-18, 2019.
- 2018 **Homilius M**, Ricciotti E, Krishnan A, MacRae C, Grosser T, FitzGerald G, Troyanskaya O. “Prioritizing animal models and drug targets using functional networks”, CIFAR Genetic Networks Program Meeting, Toronto, June 02, 2018.
- 2016 **Homilius M**, Ricciotti E, Krishnan A, Grosser T, Troyanskaya O. “A network-based approach to detect drug mode-of-action at therapeutic doses”, New York Area meeting on Computational and Statistical Genomics, Cold Spring Harbor Laboratory, July 20, 2016.
- 2015 **Homilius M**, Krishnan A, MacRae C, Troyanskaya O. “Prioritizing animal models for human diseases using genome-wide functional networks”, RECOMB/ISCB Conference on Regulatory and Systems Genomics, Philadelphia, Nov 15-18, 2015.
- 2010 **Homilius M**, Burleigh G, Eulenstein O. “Triplet-supertrees constructed from minimum triplet presentations”, BICoB 2010, 127-132.

Teaching

- 9/2012-1/2013 Assistant in Instruction, Integrated Science Curriculum (General Computer Science I)
Princeton University
- 2/2013-6/2013 Assistant in Instruction, Integrated Science Curriculum (General Computer Science II)
Princeton University

Previous research positions

- 3/2010-9/2010 *Research assistant*, 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 *Undergraduate researcher*, 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 *Undergraduate researcher*, 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)

Service

- 2018-2023 Peer review, *Journal of Computational Biology*
- 2020 Peer review, *Pacific Symposium on Biocomputing*
- 2016 Peer review, *RECOMB/ISCB Conference on Regulatory and Systems Genomics*
- 2015, 2018 Peer review, *Circulation: Cardiovascular Genetics*

References

- Prof. Calum MacRae, Postdoc Research Adviser
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- Prof. Rahul Deo, Postdoc Research Adviser
rdeo@bwh.harvard.edu
- Prof. Olga Troyanskaya, PhD Research Adviser
ogt@genomics.princeton.edu
- Prof. Mona Singh, PhD Thesis Committee Member
msingh@cs.princeton.edu