

Dr.-Ing. Debdas Paul

Machine learning | Mathematical modeling | Computational & systems biology

I am particularly interested in developing framework for integration (esp. diagonal integration, unmatched pairs) of multi-modal omics data. Apart from that, I have long standing interest in understanding biological robustness using concepts from control and systems theory.



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RESEARCH EXPERIENCE

- 06/2020 – present **Postdoctoral researcher** [University Hospital, Tübingen, Germany](#)
- developing machine and deep learning based approaches to integrate single cell flow-cytometry and radiomics data to identify and monitor cancer-immunotherapy responses.
 - Group leader: Prof. Dr. Manfred Claassen
- Deep & machine learning / Flow cytometry / Radiomics / cancer immunotherapy / Biomarker discovery
- 02/2019 – 05/2020 **Postdoctoral researcher** [The Max Planck Institute for Biophysical Chemistry, Göttingen, Germany](#)
- Contributed to the development of [QPuB](#) - a tool that employs Bayesian statistical inference based on MCMC sampling to learn the posterior distributions of the conversion factors for the peptide products without further experimentation.
 - Group leader: Dr. Juliane Liepe
- R / MCMC / Bayesian inference / Mass spectrometry / Immunology
- 07/2017 – 10/2017 **Visiting researcher** [Harvard Medical School](#)
- Developed a rule-based modelling approach based on the [kappa-language](#) framework for gene regulation.
 - Collaborator: Prof. Jeremy Gunawardena
- Python / Kappa - a rule-based language / stochastic simulation
- 11/2014 – 12/2018 **Doctoral researcher** [Institute for Systems Theory and Automatic Control](#)
- explored the origin of robustness and its characterization in biological signaling networks as well as in gene regulation using mechanistic modeling, stochastic simulation and rule-based modelling approach.
 - Supervisor: Prof. Dr. rer. nat. Nicole Radde
- MATLAB / Systems & control theory / Systems biology / Mathematical modeling & Stochastic simulation

EDUCATION

- 2014 – 2019 **Dr.-Ing.** [University of Stuttgart, Germany](#)
Systems theory, Systems Biology, Magna cum Laude
- 2012 – 2014 **Master of Science & Master of Science (Technology)** [KTH, Sweden & Aalto University, Finland](#)
Computational Systems Biology, Distinction
- 2009 – 2011 **Master of Engineering** [Jadavpur University, India](#)
Computer Science & Engineering, First class
- 2005 – 2009 **Bachelor of Technology** [West Bengal University of Technology, India](#)
Computer Science & Engineering, First class

KEY PROGRAMMING SKILLS



MACHINE LEARNING FRAMEWORKS



COMPUTATIONAL INFRASTRUCTURES



HONORS & AWARDS

- European Union's - Erasmus Mundus Fellowship (EU equivalent of Fullbright)
- Bilateral Mobility Grant, Govt. of Republic of Slovenia

ACADEMIC COLLABORATORS

- [Prof. Elena Hsieh, MD](#) - University of Colorado Anschutz School of Medicine, USA • [Prof. Jeremy Gunawardena](#) - HMS, USA
- [Prof. Dragan Stevanovic](#) - Mathematical Institute, Serbia • [Prof. Steve Kirkland](#) - University of Manitoba, Canada

LANGUAGES

- German - A1 (Goethe-Zertifikat) [98/100] • English - full working proficiency • Bengali - native

Publications

Mathematical modeling, systems biology, systems theory, stochastic simulation, biomimetics

[The role of stochastic sequestration dynamics for intrinsic noise filtering in signaling network motifs](#)

Paul, D., and Radde, N., 2018. The role of stochastic sequestration dynamics for intrinsic noise filtering in signaling network motifs. *Journal of Theoretical Biology* 455, pp.86-96.

[Robustness and filtering properties of ubiquitous signaling network motifs](#)

Paul, D., and Radde, N., 2016. Robustness and filtering properties of ubiquitous signaling network motifs. *IFAC-PapersOnLine* 49(26), pp.120-127

[Structural Design with Biological Methods: Optimality, Multi-functionality and Robustness](#)

Paul, D., Dehkordi, L.K.F., von Scheven, M., Bischoff, M. and Radde, N., 2016. Structural Design with Biological Methods: Optimality, Multi-functionality and Robustness. *In Biomimetic Research for Architecture and Building Construction* pp. 341-360. Springer, Cham.

spectral graph theory, complex networks

[Eigenvector-based identification of bipartite subgraphs](#)

Paul, D. and Stevanović, D., 2019. Eigenvector-based identification of bipartite subgraphs. *Discrete Applied Mathematics* 269, pp.146-158.

[Bipartite subgraphs and the signless Laplacian matrix](#)

Kirkland, S. and **Paul, D.**, 2011. Bipartite subgraphs and the signless Laplacian matrix. *Applicable Analysis and Discrete Mathematics* 5(1), pp.1-13.

structural bioinformatics, computational geometry

[A volumetric method for representing and comparing regions of electrostatic focusing in molecular structure](#)

Chen, B.Y. and **Paul, D.**, 2012. A volumetric method for representing and comparing regions of electrostatic focusing in molecular structure. *In Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine* pp.242-249 (Acceptance rate: 20.7%).

immunoepitidomics, Bayesian inference, MCMC

[An in silico -in vitro pipeline identifying an HLA-A*02:01+ KRAS G12V+ spliced epitope candidate for a broad tumor-immune response in cancer patients](#)

Mishto, M., Mansurkhodzhaev, A., Ying, G., Bitra, A., Cordfunke, A R., Henze, S., **Paul, D.**, Sidney, J., Urlaub, H., Neefjes, J., Sette, A., Dirk, Z., Liepe, J., 2019. An in silico-in vitro pipeline identifying an HLA-A*02:01+ KRAS G12V+spliced epitope candidate for a broad tumor-immune response in cancer patients. *Frontiers Immunology*.