

Dr.-Ing. Debdas Paul

Computational biology | AI in Health care

I am computational systems biologist and a computer science engineer. I am looking forward to work with a cross-functional, international, and interdisciplinary team to translate knowledge into products for social good, in particular making a positive impact in the lives of patients. Besides, I have a long-standing interest in understanding cellular decision-making processes.



📍 Tübingen, Germany
🇮🇳 Indian
☎ +49 176 217 444 21
in [debdas@Linkedin](#)
🌐 [debdas@HomePage](#)
🐙 [debdas@Github](#)
@ [paul.debdas@gmail.com](#)

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. (Doctoral degree in Engineering)** [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



DEEP AND MACHINE LEARNING FRAMEWORKS AND TOOLS



COMPUTATIONAL INFRASTRUCTURES



HONORS & AWARDS

- European Union's - Erasmus Mundus Fellowship (EU equivalent of Fullbright) - EUR 48K
- Bilateral Mobility Grant, Govt. of Republic of Slovenia

ACADEMIC COLLABORATORS

- [Prof. Elena Hsieh, MD](#) - University of Colorado, School of Medicine, USA • [Prof. Jeremy Gunawardena](#) - Harvard Medical School
- [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

Manuscript in preparation

Machine learning, mass cytometry, auto-immune disease

Distinct cellular immune signatures in pediatric systemic lupus erythematosus and lupus nephritis

Ryan Baxter, Christine Wang, Pratyadipta Rudra, **Debdas Paul**, Tusharkanti Ghosh, Daniel Kong, Josselyn Garcia-Perez, Brianne Coleman, Manfred Claassen, Debashis Ghosh, Jennifer Cooper, Mia Smith, Elena Hsieh., 2022, *In preparation*.

- **Question:** What makes the systemic lupus erythematosus patients with Lupus nephritis so distinct than the one without it? Can we propose an effective targeted therapy based on cell subsets identified using machine learning approaches?

Publications (Peer-reviewed)

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.

- **Question:** How (biological) signaling networks filter out noise in a stochastic environment?

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

- **Question:** Why some (biological) signaling architectures are inherently robust?

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.

- **Question:** Is it possible to transfer the design principles of nature/natural systems to load-bearing structures, at least at a conceptual level?

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.

- **Question:** How can we use eigenvectors of a simple connected graph to identify its largest bipartition?

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.

- **Question:** Under which conditions, we can possibly identify induced bipartite subgraphs from signless Laplacian matrix?

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%).

- **Question:** How electrostatic focusing influences molecular recognition?

Immune-peptidomics, 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*.

- **Question:** Can we propose a framework identifying proteasome catalyzed spliced peptides that constitute a set of effective candidates for adoptive T cell therapy and other anti-cancer immunotherapies?