Dr.-Ing. Debdas Paul

computer science engineer

computational systems biologist

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RESEARCH EXPERIENCE

09/2020 – present **Computational biologist/Bioinformatician** Hans-Knöll-Institut, Jena, Germany

- providing bio-informatic solutions to the on going projects that involve analysis of NGS data
- supervise and manage undergraduate and post-graduate students
- responsible for setting-up bioinformatic facilities in the lab
- undertake new projects involving machine learning, bio informatics, modeling, and simulations

bioinformatics / single-cell technologies / immunology

06/2020 – 08/2022 **Postdoctoral researcher** University Hospital, Tübingen, Germany

- developed computational framework for the integrative analysis of multi-omics single cell data with a goal of finding novel associations between cell subsets across patients.
- Developed computational pipeline to analyse mass cytometry data using machine learning approaches as a part of a collaboration to find cellular immune signatures in pediatric systemic lupus erythematosus and lupus nephritis.

machine learning / single-cell data, multi-omics integration / biomarker discovery / immunotherapy / cancer / autoimmune disease

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.

MCMC / Bayesian inference / mass spectrometry / immunology

07/2017 – 10/2017 **Visiting researcher** Harvard Medical School, USA

- Developed a rule-based modelling approach based on the kappa-language framework for gene regulation.

Python / Kappa - a rule-based language / stochastic simulation

11/2014 – 12/2018 **Doctoral researcher** Institute for Systems Theory and Automatic Control, University of Stuttgart, Germany

- characterization of robustness in biological signaling networks as well as in gene regulation using mechanistic and rule-based modelling approaches.
- Thesis: Understanding the mechanisms of robustness in intracellular protein signalling cascades and gene expression [PDF]

MATLAB / Systems & control theory / Systems biology / Mathematical modeling

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** Computer Science & Engineering, First class	**Jadavpur University, India**
2005 – 2009	**Bachelor of Technology** Computer Science & Engineering, First class	**West Bengal University of Technology, India**

KEY PROGRAMMING SKILLS & DL/ML FRAMEWORKS

- Python, MATLAB, R, TensorFlow, scikit-learn

HONORS & AWARDS

- **European Union's - Erasmus Mundus Fellowship (EU equivalent of Fullbright)** - EUR 48K (2012-14)
- **Bilateral Mobility Grant, Govt. of Republic of Slovenia** - 2011

INVITED TALKS

- Comparison between combinatorial and spectral approaches in identifying the largest bipartite subgraphs of a graph
  - at Workshop on Graph Spectra, Combinatorics and Optimization – WGSCO 2018, Aveiro, Portugal. [PDF]
- Stochastic sequestration dynamics can act as intrinsic noise filter in signaling network motifs
  - at Inria Saclay - Île-de-France research centre, 2018. [PDF]

SERVICE AND LEADERSHIP

- Organized MATLAB course for bachelor students in the faculty of Engineering at the University of Stuttgart, Germany.

ACADEMIC COLLABORATORS

- **Prof. Jeremy Gunawardena** - Harvard Medical School, Boston, USA
- **Prof. Elena Hsieh, MD** - University of Colorado, School of Medicine, USA
- **Prof. Dragan Stevanovic** - Mathematical Institute, Serbia
- **Prof. Steve Kirkland** - University of Manitoba, Canada

LANGUAGES

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

REFERENCES

Prof. Jeremy Gunawardena
Harvard Medical School, USA
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Prof. Elena Hsieh, MD
University of Colorado Anschutz School of Medicine, USA
Email: Elena.Hsieh@cuanschutz.edu

Prof. Dr. rer. nat. Nicole Radde
University of Stuttgart, Germany
Email: nicole.radde@simtech.uni-stuttgart.de

Prof. Dr Manfred Claassen
University Hospital, Tübingen, Germany
Email: Manfred.Claassen@med.uni-tuebingen.de

Manuscript in preparation

Machine learning, mass cytometry, auto-immune disease

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. Distinct cellular immune signatures in pediatric systemic lupus erythematosus and lupus nephritis**.** ***In preparation***.

Publications (Peer-reviewed)

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

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.

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

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

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

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

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%).

Immune-peptidomics, Bayesian inference, MCMC

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***.

Translation

University of Stuttgart

The University of Stuttgart confers upon the decision of the Doctoral Committee of the Stuttgart Centre for Simulation Science involving the Faculty of Engineering Design, Production Engineering and Automotive Engineering on

Mr.

Debdas Paul, M.Sc. M.Eng.

born October 20, 1986

the academic degree

Doktor-Ingenieur (Dr.-Ing.)

The scientific qualification was demonstrated – in accordance with the regulations for a doctorate – with the dissertation

"Understanding the Mechanisms of Robustness in Intracellular Protein Signalling Cascades and Gene Expression"

The scientific qualification was further demonstrated with the collaboration of
Professor Dr. rer. nat. Nicole Radde as examiner and
Professor Dr.-Ing. habil. Manfred Bischoff as co-examiner as well as
Professor Ph.D. Jeremy Gunawardena (Harvard Medical School) by the oral examination of April 30, 2019.

Mr. Paul earned his doctorate with an overall rating of **"magna cum laude"**.

Stuttgart, April 30, 2019

University of Stuttgart
Disclaimer:

Informative translation. Only German original has legal status.

Seal of the University of Stuttgart