

Experience and Qualifications

- 09/2011 – present** **Research Associate**
Luxembourg Centre for Systems Biomedicine,
Bioinformatics Core Unit, Esch-sur-Alzette, Luxembourg
Team leader: Dr. Reinhard Schneider
- 05/2011 – 09/2011** **Fellowship by the German Academic Exchange Service (DAAD)**
European Molecular Biology Laboratory, Heidelberg, Germany
Data Integration and Knowledge Management Group
Team leader: Dr. Reinhard Schneider
- 10/2007 – 05/2011** **PhD in Computer Science**

University of Nottingham, United Kingdom
Supervisors: Prof. Natalio Krasnogor and Dr. Jonathan Garibaldi

Including the following doctoral fellowship periods:
2007 - 2009 **Marie Curie Research Fellow**
2009 - 2010 **EPSRC Bridging the Gaps Research Fellow**

Doctoral thesis: “Analysing functional genomics data using novel ensemble, consensus and data fusion techniques”
- 06/2006 – 10/2007** **MSc. in Computational Molecular Biology (Honours Degree)**
Saarland University, Saarbrücken, Germany

Grade: 1.0 (A) [best possible grade]

Modules studied include:
 - Bioinformatics lectures: Bioinformatics III (Biological Network Analysis), Membrane Bioinformatics, Docking, Computer-Aided Drug Design, Drug Discovery, Computational Immunology
 - Life sciences and biomedical sciences: Biotechnology, Biopharmacy and Drug Delivery, Human Genome and Genetic Diseases, Functional Genomics and Metabolic Engineering
 - Mathematics and Computer Science: Statistical Learning I and II, Image Analysis and Computer Vision, Computer Graphics, Geometric Modelling, Artificial Intelligence
 - 8 weeks laboratory internship
Master thesis: “Methods for Comparative Molecular Field Analysis in the Biochemical Algorithms Library (BALL)” (under Prof. Hans-Peter Lenhof)
- 10/2003 – 06/2006** **BSc. in Computational Molecular Biology**
Saarland University, Saarbrücken, Germany

Grade: 1.1 (A)

Modules studied include:
 - Bioinformatics lectures: Bioinformatics I (Sequence Analysis), Bioinformatics II (Structural and Functional Protein Analysis)
 - Life sciences and biomedical sciences: Molecular Biology, Microbiology, Genetics, Biophysics, Inorganic Chemistry, Computational Chemistry, Medical Chemistry, Biochemistry, Physical Chemistry
 - Mathematics and Computer Science: Mathematics for Computer Scientists I and II, Programming I and II, Theoretical Computer Science
 - 6 weeks practical software engineering and programming project

Bachelor Thesis: “On the predictability of CpG methylation in human tissue at single base pair resolution” (under Prof. Thomas Lengauer)

08/2003 - 09/2003 **Mathematics Preparatory Course for Natural Science Students**
Saarland University, Saarbrücken, Germany

08/2002 – 06/2003 **Civilian Service**
Federal Office of Civilian Service, Frankfurt, Germany

08/1993 – 06/2002 **Secondary Education**
Goethe-Gymnasium, Frankfurt, Germany

Degrees:

- Abitur (grade: 1.0 – best possible grade)
- International Baccalaureate Diploma (53 out of 55 points)
- AP International Diploma (AP Scholar with Honour Award)

Publications

- K. A. Fujita, M. Ostaszewski, Y. Matsuoka, S. Ghosh, E. Glaab, C. Trefois, I. Crespo, T. M. Perumal, W. Jurkowski, P. M. A. Antony, N. Diederich, M. Buttini, A. Kodama, V. P. Satagopam, S. Eifes, A. del Sol, R. Schneider, H. Kitano, R. Balling, *Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map*, Molecular Neurobiology (in press, DOI: 10.1007/s12035-013-8489-4)
- S. Ballereau, E. Glaab, A. Kolodkin, A. Chaiboonchoe, M. Biryukov, N. Vlassis, H. Ahmed, J. Pellet, N. Baliga, L. Hood, R. Schneider, R. Balling, C. Auffray, *Functional genomics and bioinformatics for systems biology*. Springer book in Systems Biology, Vol.1: Systems Biology: Integrative Biology and Simulation Tools (2013), Springer (book chapter, in press)
- A. Chaiboonchoe, W. Jurkowski, J. Pellet, E. Glaab, A. Kolodkin, A. Raussel, A. Le Béhec, L. Meyniel, S. Ballereau, I. Crespo, H. Ahmed, V. Volpert, V. Lotteau, N. Baliga, L. Hood, A. del Sol, R. Balling, C. Auffray, *Network analysis for systems biology*, Springer book in Systems Biology, Vol.1: Systems Biology: Integrative Biology and Simulation Tools (2013), Springer (book chapter, in press)
- E. Muller, E. Glaab, P. May, N. Vlassis, P. Wilmes, *Condensing the omics fog of microbial communities*, Trends in Microbiology (2013) (in press)
- E. Glaab, A. Baudot, N. Krasnogor, R. Schneider, A. Valencia, *EnrichNet: network-based gene set enrichment analysis*, Bioinformatics (Proceedings of the European Conference on Computational Biology, ECCB 2012), Vol. 28, No. 18, pp. i451 (acceptance rate: 14%)
- E. Glaab, R. Schneider, *PathVar: analysis of gene and protein expression variance in cellular pathways using microarray data*, Bioinformatics (2012), Vol. 28, No. 3, pp. 446
- E. Glaab, J. Bacardit, J. M. Garibaldi, N. Krasnogor, *Using rule-based machine learning for candidate disease gene prioritization and sample classification of cancer gene expression data*, PLoS ONE (2012), Vol. 7, No. 7, e39932
- G. W. Bassel, H. Lan, E. Glaab, D. J. Gibbs, T. Gerjets, N. Krasnogor, A. J. Bonner, M. J. Holdsworth, N. J. Provart, *A genome-wide network model capturing seed germination reveals co-ordinated regulation of plant cellular phase transitions*, Proceedings of the National Academy of Sciences USA 2011, 108(23):9709
- E. Glaab, *Analysing functional genomics data using novel ensemble, consensus and data fusion techniques*, Doctoral thesis, University of Nottingham, March 2011
- G. W. Bassel, E. Glaab, J. Marquez, M. J. Holdsworth, J. Bacardit, *Functional Network Construction in Arabidopsis Using Rule-Based Machine Learning on Large-Scale Data Sets*, Plant Cell 2011, 23(9):3101
- E. Glaab, A. Baudot, N. Krasnogor, A. Valencia. *Extending pathways and processes using molecular interaction networks to analyse cancer genome data*, BMC Bioinformatics 2010 (RECOMB Computational Cancer Biology, Oslo, Norway), 11(1):597 (received designation “highly accessed” from BioMed Central)
- E. Glaab, A. Baudot, N. Krasnogor, A. Valencia. *TopoGSA: network topological gene set analysis*, Bioinformatics 2010, 26(9):1271
- E. Glaab, J. M. Garibaldi, N. Krasnogor. *Learning pathway-based decision rules to classify microarray cancer samples*, German Conference on Bioinformatics 2010, Lecture Notes in Informatics (LNI), 173:123-134
- H. O. Habashy, D. G. Powe, E. Glaab, N. Krasnogor, J. M. Garibaldi, E. A. Rakha, G. Ball, A. R. Green, C. Caldas, I. O. Ellis. *REG (Ras-related and oestrogen-regulated growth-inhibitor) expression in breast cancer: A marker of ER-positive luminal-like subtype*, Breast Cancer Research and Treatment 2011, 128(2):315-326
- E. Glaab, J. M. Garibaldi and N. Krasnogor. *VRMLGen: An R-package for 3D Data Visualization on the Web*, Journal of Statistical Software 2010, 36(8):1-18
- E. Glaab, J. M. Garibaldi and N. Krasnogor. *ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization*, BMC Bioinformatics 2009, 10:358

Recent Participation in Research Projects

- *EpiPGX: Epilepsy Pharmacogenomics: delivering biomarkers for clinical use*, EU FP7 (279062)
- *CoGIE: Complex genetics of idiopathic epilepsies (EuroEpinomics)*, Deutsche Forschungsgemeinschaft, DFG (<http://www.euroepinomics.org>)
- *Beta-JUDO: Beta-cell function in juvenile diabetes and obesity*, EU FP7, (HEALTH.2011.2.4.3-2)
- *MUST: Diabetes Multiplex Family Study*, Luxembourg Personalized Medicine Consortium (PMC)
- *BioMAGNet: Bioinformatics and modeling: from genomes to networks*, Belgian Federal Science Policy Office (Interuniversity Attraction Poles IAP-VII)
- *COMBIOMED: Cooperative Thematic Research Network on Computational Biomedicine*, Instituto de Salud Carlos III, Spain (grant RD07/0067/0014)
- *Functions for Gene Sets*, Spanish Ministry of Education and Science, Science and Innovation (MICINN) grant (BIO2007-66855)
- *SynBioNT: A Synthetic Biology Network for Modelling and Programming Cell-Cell Interactions*, Biotechnology and Biological Sciences Research Council (grant BB/F01855X/1)
- *(Semi)Formal Artificial Life Through P-systems & Learning Classifier Systems: An Investigation into InfoBiotics*, UK Engineering and Physical Sciences Research Council (grant EP/E017215/1)
- *BIOPTRAIN: Marie Curie Early Stage Training Network in Bioinformatics Optimisation*, EU FP6 (grant MEST-CT-2004-007597)

Scholarships and Awards

- Poster prize award at the Benelux Bioinformatics Conference, Nijmegen, Netherlands (2012)
- Short-term fellowship by the German Academic Exchange Service (DAAD), EMBL, Heidelberg, Germany (2011)
- ECCB 2010 Travel Fellowship Award to attend the European Conference on Computational Biology 2010, Ghent, Belgium
- Nottingham University Graduate School Travel Prize to attend the German Conference on Bioinformatics 2010
- Stipend "Bridging the Gaps Research Fellowship" (2009) funded by the Engineering and Physical Sciences Research Council (EPSRC)
- Peer Review Poster Award at Graduate School Poster Prize event (May 2009, Nottingham)
- Marie Curie Early Stage Training Research Fellowship (as part of the "Marie Curie Actions" programme by the European Union, 2007)
- Member of the German National Merit Foundation (Studienstiftung des Deutschen Volkes) during undergraduate and graduate education in Germany (monthly book allowance)
- Scholarship from the Chair of Bioinformatics at Saarland University (1000 € stipend for the students with the three best results in the Bioinformatics I exam)
- Member of the Honours Program for Graduate Students in Computer Science and Bioinformatics at Saarland University
- Winner of the national competition "Jugend forscht" ("Youth Researches") in the category Mathematics/Computer Science (2001, while attending high school)
- Winner of the "Konrad Zuse Youth Prize" for Computer Science awarded by the Eduard-Rhein Trust (2001, while attending high school)

Community-related Activities / Student supervision and tutoring

- Tutor and guest lecturer in multiple bioinformatics courses for Computer Science students at Saarland University and Nottingham University, and for biotechnology students at the University of Luxembourg
- Supervision of a Master student's bioinformatics project at the University of Luxembourg in 2012, reviewer for a Master thesis in Integrative Systems Biology in 2013
- Peer reviewer for the journals *Bioinformatics* (8 times), *Nucleic Acids Research*, *BMC Bioinformatics*, *BMC Systems Biology*, *Transactions on Evolutionary Computation*, *FEBS Journal*, *Journal of Heuristics*, *PeerJ*, *PLoS ONE* and *Journal of Artificial Evolution and Applications*
- In charge of the research group's internal source code repository and software collection (Nottingham University)
- Member of the International Society for Computational Biology (ISCB), the ISCB Student Council and the Bioinformatics Open Student Society (BIMATICS)