

Dr. Daniel Ziemek

Head of Computational Biology -
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Personal Information

3.6.1975 **born as Daniel Hanisch in Paderborn, Germany.**
Family **married, two children.**
Citizenship **German.**
Residence **USA (Green Card).**

Education

1995–1999 **Graduate Studies in Computer Science, University of Bonn, Germany.**
1997–1998 **Graduate Studies in Computer Science, University of Tennessee, Knoxville, USA.**
Direct exchange scholarship granted by the University of Bonn.
1999 **Diploma (~M.Sc.) in Computer Science, University of Bonn, Germany,**
“ProML - a Protein Markup Language for specification of protein sequences, structures
and families”, supervised by Prof. Thomas Lengauer.
2000–2004 **Research Assistant, Fraunhofer SCAI, St. Augustin, Germany.**
2002–2004 **Graduate Studies in Bioinformatics, Ludwig-Maximilians-Universität, München, Ger-**
many.
2004 **Ph.D. in Bioinformatics, Ludwig-Maximilians-Universität München, Germany,**
“New Analysis Methods for Gene Expression Data via Construction and Incorporation
of Biological Networks”, supervised by Prof. Thomas Lengauer and Prof. Ralf Zimmer.
Grade: With Distinction (*summa cum laude*).

Relevant Experience

since 2011 **Head of Computational Biology - Algorithms and Platforms, Pfizer Inc., Cam-**
bridge, MA, USA.
Responsible for a team of scientists to design, implement, and deliver algorithms and applications
that impact drug development projects.
Received Pfizer's 2012 R&D Award for "extraordinary scientific, operational or decision making
contributions to WRD and Pfizer goals". This prestigious award is only given to up to 10 out
of more than 10,000 R&D employees each year and includes a substantial monetary reward of
\$25,000 as well as a reception with the R&D Leadership team in New York City.
Developed method for discovery of interpretable and predictive biomarkers based on expression
data and prior biological knowledge. Validated on internal clinical data with Oncology Business
Unit.

- 2008–2011 **Senior Principal Scientist, Pfizer Inc., Cambridge, MA, USA.**
 Biological Systems Domain Lead. Design, prototyping, and application of innovative methods across computational biology and chemistry. Managerial responsibility for a direct report, a contractor, and several students.
- Pioneered causal network-based analysis method for rare genetic variants from exome next generation sequencing (in collaboration with Prof. Shamil Sunyaev, Harvard Medical School).
- Proposed and fully executed the design and implementation of a Causal Reasoning Platform for analysis of experimental data. Algorithms for transcriptional data analysis have been published [2, 3, 4]. Included soliciting high-level sponsorship from disease area leads, funding for required data sets and resources. Platform now in repeated use across disease areas.
- Causal Reasoning applied to transcriptomics data led to several prospectively validated predictions for safety and regenerative medicine groups.
- Significantly impacted many analysis projects involving gene expression, common and rare variant sequencing as well as metabolomics data.
- 2004–2005 **Senior Research Scientist (Expatriate Assignment), Sanofi-Aventis, Cambridge, MA, USA.**
 Scientific Lead for enterprise-wide pathway analysis platform. Responsible for quality of algorithms and scalability of solution. In charge of scientific steering committee to align user demands with available resources. Hands-on experience with agile software development and scalable software components resulting in a sophisticated global solution.
- Statistical analysis of microarray (Affymetrix) data using R.
- Achievement award for excellent performance and timely delivery in 2005.
- 2004–2008 **Senior Research Scientist, Sanofi-Aventis, Frankfurt, Germany.**
 Expansion of pathway analysis platform as Scientific Lead through continuous innovation and feature design in response to user needs.
- Application of internal and external analysis platforms to analyze microarray data in several disease areas, e.g. Diabetes, Pain, Osteoarthritis.
- Support of target discovery for cardiac arrhythmias using ODE-based models of cardiac ion channels. Part of this work has been published [7].
- In-depth analysis of high-throughput screening (HTS) results using advanced statistical techniques (mixture models) leading to higher true positive rate in secondary screening.

Special Skills

In my experience, personal leadership, scientific curiosity, the will to deliver on time, as well as an understanding of team dynamics (how to motivate, when to delegate, etc.) are key ingredients to impacting scientific discovery.

- Drug Discovery Successfully contributed to projects along the drug discovery pipeline, e.g. target finding and validation, safety assessments, biomarker discovery, HTS analysis.
- Computational Biology First-hand experience in generating testable hypotheses from data of different modalities, e.g. transcriptomics, common and rare variant genetics, metabolomics.
- Algorithms and Statistics Proficient in many aspects of algorithm development (esp. networks / graphs). Expert working knowledge in applied machine learning methods, and a variety of statistical techniques.
- Software Engineering Lead in agile development projects. Expert working knowledge of JAVA, R. Good working knowledge of Perl, Ruby, Matlab. Following innovative trends, e.g. noSQL database systems such as Neo4j.

Line and Project Management	Managerial responsibility for PhD-level scientists with diverse backgrounds including biochemistry, applied mathematics, and computer science. Participated in managerial training courses on situational leadership and project management. Involved in budgetary planning decisions for the department.
Customer Service	Experienced in interfacing with customers, understanding their underlying problems and delivering solutions (<i>Beyond the voice of the customer</i>).
Collaboration	Initiated collaborations with academic partners at Harvard Medical School and University of Denver, Colorado. Participated in several internal and external collaborations with academic partners and biotech companies.

Scientific Excellence

Publications	Published 20 peer-reviewed articles that have been cited >620 times.
Presentations	Invited external presentation on Causal Reasoning at SIBS 2011, Boston University and M.I.T. Numerous internal presentations at all organizational levels.
Reviewer	Bioinformatics, BMC Bioinformatics.
Committees	Member of Phd Thesis Committees for students at Boston University and Georgia Tech.
Innovation	Recipient of Pfizer's prestigious \$25,000 WRD award for "extraordinary scientific, operational or decision making contributions to WRD and Pfizer goals" in 2012. Recipient of the Pfizer CoE Innovation Award for design and implementation of the Causal Reasoning Platform in 2010.

Publications

- [1] Wanida Ruangsiriluk, Shaun E Grosskurth, Daniel Ziemek, Max Kuhn, Shelly G des Etages, and Omar L Francone. Silencing of enzymes involved in ceramide biosynthesis causes distinct global alterations of lipid homeostasis and gene expression. *Journal of lipid research*, May 2012.
- [2] Leonid Chindelevitch, Po-Ru Loh, Ahmed Enayetallah, Bonnie Berger, and Daniel Ziemek. Assessing statistical significance in causal graphs. *BMC Bioinformatics*, 13(1):35, Feb 2012.
- [3] Leonid Chindelevitch, Daniel Ziemek, Ahmed Enayetallah, Ranjit Randhawa, Ben Sidders, Christoph Brockel, and Enoch Huang. Causal reasoning on biological networks: Interpreting transcriptional changes. *Bioinformatics*, Feb 2012.
- [4] Ahmed E Enayetallah, Daniel Ziemek, Michael T Leininger, Ranjit Randhawa, Jianxin Yang, Tara B Manion, Dawn E Mather, William J Zavadski, Max Kuhn, Judith L Treadway, Shelly Ann G des Etages, E Michael Gibbs, Nigel Greene, and Claire M Stepan. Modeling the mechanism of action of a dgat1 inhibitor using a causal reasoning platform. *PLoS ONE*, 6(11):e27009, Jan 2011.
- [5] Leonid Chindelevitch, Daniel Ziemek, Ahmed Enayetallah, Ranjit Randhawa, Ben Sidders, Christoph Brockel, and Enoch Huang. Causal reasoning on biological networks: Interpreting transcriptional changes. In Vineet Bafna and S. Sahinalp, editors, *Research in Computational Molecular Biology*, volume 6577 of *Lecture Notes in Computer Science*, pages 34–37. Springer Berlin / Heidelberg, 2011.
- [6] Daniel Ziemek and Christoph Brockel. Network-driven analysis methods and their application to drug discovery. In Limin Angela Liu, Donqing Wei, Yixue Li, and Huimin Lei, editors, *Handbook of Research on Computational and Systems Biology: Interdisciplinary Applications*, volume 1, pages 294–315. Hershey: IGI Global, 2011.
- [7] Joachim R Ehrlich, Hellen Ocholla, Daniel Ziemek, Hartmut Rütten, Stefan H Hohnloser, and Heinz Gögelein. Characterization of human cardiac kv1.5 inhibition by the novel atrial-selective antiarrhythmic compound ave1231. *J Cardiovasc Pharmacol*, 51(4):380–7, Apr 2008.

- [8] Daniel Hanisch, Katrin Fundel, Heinz-Theodor Mevissen, Ralf Zimmer, and Juliane Fluck. Prominer: rule-based protein and gene entity recognition. *BMC Bioinformatics*, 6 Suppl 1:S14, Jan 2005.
- [9] Florian Sohler, Daniel Hanisch, and Ralf Zimmer. New methods for joint analysis of biological networks and expression data. *Bioinformatics*, 20(10):1517–21, Jul 2004.
- [10] Daniel Hanisch, Florian Sohler, and Ralf Zimmer. Topnet—an application for interactive analysis of expression data and biological networks. *Bioinformatics*, 20(9):1470–1, Jun 2004.
- [11] Dong-Yup Lee, Ralf Zimmer, Sang-Yup Lee, Daniel Hanisch, and Sunwon Park. Knowledge representation model for systems-level analysis of signal transduction networks. *Genome Inform*, 15(2):234–43, Jan 2004.
- [12] C. Gieger, D. Hanisch, J. Fluck, H.T. Mevissen, A. Tresch, and H. Deneke. S26. 2: Using text mining networks for the context specific interpretation of gene expression data. *Biometrical Journal*, 46(S1):56–56, 2004.
- [13] D. Hanisch. *New analysis methods for gene expression data via construction and incorporation of biological networks*. Fraunhofer series in information and communication technology. Shaker, 2004.
- [14] Thomas Aigner, Alexander Zien, Daniel Hanisch, and Ralf Zimmer. Gene expression in chondrocytes assessed with use of microarrays. *J Bone Joint Surg Am*, 85-A Suppl 2:117–23, Jan 2003.
- [15] Daniel Hanisch, Juliane Fluck, Heinz-Theodor Mevissen, and Ralf Zimmer. Playing biology's name game: identifying protein names in scientific text. *Pac Symp Biocomput*, pages 403–14, Jan 2003.
- [16] Mario Albrecht, Daniel Hanisch, Ralf Zimmer, and Thomas Lengauer. Improving fold recognition of protein threading by experimental distance constraints. *In Silico Biol (Gedruckt)*, 2(3):325–37, Jan 2002.
- [17] Jan Freudenberg, Ralf Zimmer, Daniel Hanisch, and Thomas Lengauer. A hypergraph-based method for unification of existing protein structure- and sequence-families. *In Silico Biol (Gedruckt)*, 2(3):339–49, Jan 2002.
- [18] Daniel Hanisch, Alexander Zien, Ralf Zimmer, and Thomas Lengauer. Co-clustering of biological networks and gene expression data. *Bioinformatics*, 18 Suppl 1:S145–54, Jan 2002.
- [19] Daniel Hanisch, Ralf Zimmer, and Thomas Lengauer. Proml—the protein markup language for specification of protein sequences, structures and families. *In Silico Biol (Gedruckt)*, 2(3):313–24, Jan 2002.
- [20] Daniel Hoffmann, Volker Schnaible, Stephan Wefing, Mario Albrecht, Daniel Hanisch, and Ralf Zimmer. A new method for the fast solution of protein-3D-structures, combining experiments and bioinformatics. In Karl-Heinz Hoffmann, editor, *Coupling of Biological and Electronic Systems: Proceedings of the 2nd Caesarium, Bonn, 1-3 November 2000*, pages 59–78, Bonn, Germany, 2002. Springer.