Curriculum Vitae

Florian P. Breitwieser, PhD

Position:	Post-doctoral research fellow Steven Salzberg lab	**Address:** Center for Computational Biology Johns Hopkins University Welch Medical Library, Room 101 1900 E. Monument St. Baltimore, MD 21205, USA
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EDUCATION

2009-2014	**PhD** at CeMM Center for Molecular Medicine / Medical University of Vienna, Austria. Doctoral thesis: 'Computational approaches to quantifying protein and post-translational modification changes'. Thesis advisor: Jacques Colinge
2003-2007	**DI (FH) [equiv MSc] in Bioinformatics** at Upper Austrian University of Applied Sciences Diploma thesis: 'Genetic Variation In Protein Biomarkers' at University of New South Wales, Sydney. Graduated w/ first class honors. Thesis advisor: Marc Wilkins

WORK EXPERIENCE

since Feb 2015
Postdoctoral fellow at Johns Hopkins University, MD, US Computational metagenomics and microbiomics research.

10/2009 - 10/2014
Predoctoral fellow at CeMM, Austria Developed algorithms, statistical methods and software tools for the analysis of quantitative proteomics data. Contributed the proteomics analysis for several publications.

09/2008 - 09/2014
Bioinformatician at CeMM, Austria Developed tools, databases and websites for the analysis of large-scale proteomics datasets. Contributed in the analysis of diverse biological datasets. Responsible for the institute's mass spectrometry computational analysis pipeline.

09/2007 - 05/2008
Web developer at CIAT, Colombia (Centro International de Agricultura Tropical) Engineered a web platform for project management using Apache Tapestry, Java JCR / Apache Jackrabbit, and MySQL; and a repository for sharing of scientific documents.

09/2006 - 06/2007
Diploma thesis at University of New South Wales, Australia. Research on transcriptome of proteins reported as cancer markers: Analysis of heritability and inter-individual variation of gene expression. Set-up of biomarker proteins database. Supervisor: Marc Wilkins.

academic year 2005 - 2006
Project manager of study project for biotech startup Anagnostics (www.anagnostics.com). Oversaw the development of HybWiz, a scripting tool for the control of a novel biological analysis machine.

academic year 2004 - 2005
Software engineer for study project for the University Hospital Salzburg. Helped in the development of a software tool for sequence analysis and other bioinformatics tasks termed Insilico Sequence Analysis (ISA).

PUBLICATIONS

SUBMITTED

1 **F. P. Breitwieser**, C. A. Pardo, and S. L. Salzberg (*awaiting review*). “Re-analysis of metagenomic sequences from acute flaccid myelitis patients reveals alternatives to enterovirus D68 infection”. In: *F1000 Research*

FIRST AUTHORED, PEER-REVIEWED PUBLICATIONS

2 **F. P. Breitwieser** and J. Colinge (2013). “Isobar(PTM): a software tool for the quantitative analysis of post-translationally modified proteins.” In: *J Proteomics*

1 **F. P. Breitwieser**, A. Müller, L. Dayon, T. Köcher, A. Hainard, P. Pichler, U. Schmidt-Erfurth, G. Superti-Furga, J.-C. Sanchez, K. Mechtler, K. L. Bennett, and J. Colinge (2011). “General statistical modeling of data from protein relative expression isobaric tags.” In: *J Proteome Res*

Plus 14 co-authored publications in Nature Immunology, Nature Chemical Biology, Journal of Proteome Research, Analytical Chemistry, Oncogene, Journal of Proteomics, BMC Systems Biology, PLoS Computational Biology, Proteomics, and Leukemia (PubMed link).

BOOK CHAPTERS

F. P. Breitwieser and J. Colinge (2012). “Analysis of Labeled Quantitative Mass Spectrometry Proteomics Data”. In: *Computational Medicine.* Ed. by Z. Trajanoski. Springer Vienna

CONFERENCE PRESENTATIONS

4 **F. P. Breitwieser** and J. Colinge (2012). “isobar: Quantifying changes of the proteome and its post-translational modifications”. Presented at the 9th Siena Meeting: From Genome to Proteome. Siena, Italy

3 **F. P. Breitwieser** (2012). “Statistical Modeling of Post-translational Protein Regulation Dynamics”. Presented at the Young Investigators Day. Faculty of Computational Life Sciences, University of Vienna

2 **F. P. Breitwieser** and J. Colinge (2012). “isobar R package for the analysis of quantitative proteomics data”. Presented at the 12th Annual Bioinformatics Open Source Conference. Vienna, Austria

1 **F. P. Breitwieser**, A. Müller, G. Superti-Furga, K. L. Bennett, and J. Colinge (2010). “Statistical Models for Quantitative Proteomics using Isobaric Tags”. Presented at the 4th Central and Eastern European Proteomics Conference. Vienna, Austria

ACHIEVEMENTS

FWF grant for doctoral thesis project (2012)

Full AUPA grant for FEBS summer school on high performance proteomics (2012)

Student travel fellowship for BOSC conference (2011)

First class honors at graduation at Upper Austrian University of Applied Sciences (2007)

Best bioinformatics student scholarship in academic year 2003/2004 at Upper Austrian University of Applied Sciences (2004)

SKILLS

SOFT SKILLS

Interacted with many researchers from diverse fields for co-authored research work. Delivered presentations of research works at several conferences, at group and institute-wide meetings, and in front of the institute’s scientific advisory board.

Software Engineering

Operating systems	Proficient in Linux/Unix, Microsoft Windows 3.1 - XP, DOS
Programming languages	R, Perl, Java, C++, LaTeX
Databases	PostgreSQL, MySQL, JCR. Database programming in plSQL and plPerl
Software technologies	Apache Tapestry 5, Apache JackRabbit, Java Enterprise APIs, Microsoft .NET Framework

Bioinformatics

Applications	Extensive working knowledge in analysis of metagenomics and mass spectrometry/proteomics data using R/Bioconductor, Perl and Linux shell scripting. Design and usage of biological databases.
Statistics	Good understanding of biostatistical methodology and tools.
Laboratory skills	Basic training in gel electrophresis, crystallisation, western blot, ELISA, DNA extraction, yeast 2 hybrid

Languages

German (mother tongue), English (very good), Spanish (conversational), French (basic)

Contacts for References

Prof Steven Salzberg, PhD (postdoc supervisor)	Director of the Center of Computation Biology, Johns Hopkins University. Maryland, USA Tel: +1 410-614-6112 - Email salzberg@jhu.edu
Jacques Colinge, PhD, Univ.-Doz. (PhD supervisor)	Head of Bioinformatics, Research Center for Molecular Medicine of the Austrian Academy of Sciences Tel: +43 1 40160-70 020 - Email: jcolinge@cemm.oeaw.ac.at
Prof Marc Wilkins, PhD (diploma thesis supervisor)	Head of Systems Biology Lab, School of Biotechnology and Biomolecular Sciences, University of New South Wales Tel: +61 9385 3633 - Email: m.wilkins@unsw.edu.au
Dipl.-Ing. Dr. Karin Proell (professor and diploma thesis supervisor)	Head of Bioinformatics, Upper Austrian University of Applied Sciences Tel: +43 7236 3888 2700 - Email: karin.proell@fh-hagenberg.at
Dipl.-Ing. Norbert Niederhauser (supervisor in Colombia)	Information and Communication Engineer, CIAT Tel: +57 2 445 0000 3285 - Email: n.niederhauser@cgiar.org

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