

Curriculum Vitae DI(FH) Dr. Stephan Pabinger

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 Austria
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Telephone +43 660 683 77 87
Languages German/English (fluent)

Career history

12/2013 - ongoing **AIT - Austrian Institute of Technology, Health & Environment, Molecular Diagnostics, Vienna.** Bioinformatics Scientist.

03/2013 - 11/2013 **Section for Bioinformatics, Biocenter, Innsbruck Medical University.** Analysis and tool development for NGS sequencing data; Translational Bioinformatics.

09/2012 - 03/2013 **McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University - School of Medicine, Baltimore, USA.** De novo genome assembly; Genome assembly evaluation.

05/2010 - 09/2012 **Section for Bioinformatics, Biocenter, Innsbruck Medical University.** Analysis and tool development for NGS sequencing data; Data integration using metabolic models.

09/2006 - 04/2010 **Institute for Genomics and Bioinformatics, University of Technology, Graz.** Design and implementation of a bioinformatics platform for metabolic model development.

09/2005 - 06/2006 **Institute for Genomics and Bioinformatics, University of Technology, Graz.** Development of a web-based application for managing and analyzing real-time qPCR experiments.

Education

2006 - 2010 **PhD Study of Electrical Engineering (focus on Bioinformatics)**, graduated with excellence, University of Technology, Graz, Austria.

2002 - 2006

Graduate Study of Bioinformatics, graduated with excellence, Upper Austrian University of Applied Sciences Hagenberg, Austria.

Technical Skills

- Linux, Microsoft, MasOS
- Python, R, Java, JEE, JSF, Perl, PHP, HTML, L^AT_EX, ...
- PostgreSQL, MySQL, Oracle

Research interests

- Analysis of high-throughput biological data - especially next-generation sequencing data
- Development of bioinformatics methods and tools (NGS, Assembly, QPCR, ...)
- Cancer data analysis
- Integration of heterogeneous high-throughput data
- Multivariate data analysis

Publications

- [1] Ram Vinay Pandey, Walter Pulverer, Rainer Kallmeyer, Gabriel Beikirchner, Stephan Pabinger, Albert Kriegner, and Andreas Weinhäusel. MSP-HTPrimer: a high-throughput primer design tool to improve assay design for DNA methylation analysis in epigenetics. *Clin Epigenetics*, 2016 Sep 21;8., 2016.
- [2] Stephan Pabinger, Karina Ernst, Walter Pulverer, Rainer Kallmeyer, Ana Valdes, Sarah Metrustry, Denis Katic, Angelo Nuzzo, Albert Kriegner, Klemens Vierlinger, and Andreas Weinhäusel. Analysis and Visualization Tool for Targeted Amplicon Bisulfite Sequencing on Ion Torrent Sequencers. *PLoS One*, 2016 July 28;11(7), 2016.
- [3] Ram Vinay Pandey, Walter Pulverer, Rainer Kallmeyer, Gabriel Beikirchner, Stephan Pabinger, Albert Kriegner, and Andreas Weinhäusel. MSRE-HTPrimer: a high-throughput and genome-wide primer design pipeline optimized for epigenetic research. *Clin Epigenetics*, 2016 Mar 5;8:26, 2016.
- [4] Ram Vinay Pandey, Stephan Pabinger, Albert Kriegner, and Andreas Weinhäusel. MutAid: Sanger and NGS Based Integrated Pipeline for Mutation Identification, Validation and Annotation in Human Molecular Genetics. *PLoS One*, 2016, Feb 3;11(2), 2016.

- [5] Ram Vinay Pandey, Stephan Pabinger, Albert Kriegner, and Andreas Weinhäusel. ClinQC: a tool for quality control and cleaning of Sanger and NGS data in clinical research. *BMC Bioinformatics*, 2016, Feb 2;17(1):56., 2016.
- [6] Valentin Friedrich, Stephan Pabinger, Tsute Chen, Paul Messner, Floyd E. Dewhirst, and Christina Schäffer. Draft Genome Sequence of *Tannerella forsythia* Type Strain ATCC 43037. *Genome Announcements*, 2015, Jun 11 3(3), 2015.
- [7] Valentin Friedrich, Clemens Gruber, Irene Nimeth, Stephan Pabinger, Gerhard Sekot, Gerald Posch, Friedrich Altmann, Paul Messner, Oleh Andrukhov, and Christina Schäffer. Outer membrane vesicles of *Tannerella forsythia*: biogenesis, composition, and virulence. *Molecular Oral Microbiology*, 2015, 2015.
- [8] Fatemeh Maghuly, Joanna Jankowicz-Cieslak, Stephan Pabinger, Bradley J. Till, and Margit Laimer. Geographic origin is not supported by the genetic variability found in a large living collection of *Jatropha curcas* with accessions from three continents. *Biotechnology Journal*, 2014.
- [9] Matthias Baldauf, Andreas Dander, Michael Sperk, Stephan Pabinger, and Zlatko Trajanoski. Integration of NGS Data and Images of Tissue Sections for Personalized Oncology. *UMIT - Lecture Notes in Biomedical Computer Science and Mechatronics*, 4, 2014.
- [10] Stephan Pabinger, Stefan Rödiger, Albert Kriegner, Klemens Vierlinger, and Andreas Weinhäusel. A survey of tools for the analysis of quantitative PCR (qPCR) data. *Biomolecular Detection and Quantification*, 1 (2014) 23-33, 2014.
- [11] Andreas Dander, Matthias Baldauf, Michael Sperk, Stephan Pabinger, Benjamin Hiltolt, and Zlatko Trajanoski. Personalized oncology suite: integrating next-generation sequencing data and whole-slide bioimages. *BMC Bioinformatics*, 2014, 15:306., 2014.
- [12] Dominik Schweiger, Zlatko Trajanoski, and Stephan Pabinger. SPARQLGraph: a web-based platform for graphically querying biological semantic web databases. *BMC Bioinformatics*, 2014, 15:279, 2014.
- [13] Stephan Pabinger, Rene Snajder, Timo Hardiman, Michaela Willi, Andreas Dander, and Zlatko Trajanoski. MEMOSys 2.0: an update of the bioinformatics database for genome-scale models and genomic data. *Database (Oxford)*, bau004, 2014.
- [14] Andreas Dander, Stephan Pabinger, Michael Sperk, Maria Fischer, Gernot Stocker, and Zlatko Trajanoski. SeqBench: Integrated solution for the management and analysis of exome sequencing data. *BMC Research Notes*, 7:43, 2014.
- [15] Andreas Dander, Laurin AJ Mueller, Ralf Gallasch, Stephan Pabinger, Frank Emmert-Streib, Armin Graber, and Matthias Dehmer. [COMMODE] a large-scale database of molecular descriptors using compounds from pubchem. *Source Code for Biology and Medicine*, 8:22, 2013.

- [16] Tanja Magoc, Stephan Pabinger, Stefan Canzar, Xinyue Liu, Qi Su, Daniela Puiu, Luke J. Tal-lon, and Steven L. Salzberg. GAGE-B: An evaluation of genome assemblers for bacterial organisms. *Bioinformatics*, May 10, 2013.
- [17] Stephan Pabinger and Zlatko Trajanoski. MEMOSys. *Encyclopedia of Metagenomics*, in print, 2013.
- [18] Stephan Pabinger, Andreas Dander, Maria Fischer, Rene Snajder, Michael Sperk, Mirjana Efremova, Birgit Krabichler, Michael R Speicher, Johannes Zschocke, Michael Speicher, and Zlatko Trajanoski. A survey of tools for variant analysis of next-generation genome sequencing data. *Brief Bioinform*, Jan 21, 2013.
- [19] Stephan Pabinger and Zlatko Trajanoski. Genome-scale model management and comparison. *Methods Mol Biol*, Vol. 985:3–16, 2013.
- [20] Maria Fischer, Rene Snajder, Stephan Pabinger, Andreas Dander, Zlatko Trajanoski, and Gernot Stocker. SIMPLEX: cloud-enabled pipeline for the comprehensive analysis of exome sequencing data. *PLoS ONE*, 2012;7(8), 2012.
- [21] Anna Schossig, Nicole I Wolf, Christine Fischer, Maria Fischer, Gernot Stocker, Stephan Pabinger, Andreas Dander, Bernhard Steiner, Otmar Tönz, Dieter Kotzot, Edda Haberlandt, Albert Amberger, Barbara Burwinkel, Katharina Wimmer, Christine Fauth, Caspar Grond-Ginsbach, Martin J Koch, Annette Deichmann, Christof von Kalle, Claus R Bartram, Alfried Kohlschütter, Zlatko Trajanoski, and Johannes Zschocke. Mutations in ROGDI Cause Kohlschütter-Tönz Syndrome. *Am J Hum Genet*, 90(4):701–707, Apr 2012.
- [22] Stephan Pabinger, Robert Rader, Rasmus Agren, Jens Nielsen, and Zlatko Trajanoski. MEMOSys: Bioinformatics platform for genome-scale metabolic models. *BMC Syst Biol*, 5:20, 2011.
- [23] Stephan Pabinger, Gerhard G Thallinger, Rene Snajder, Heiko Eichhorn, Robert Rader, and Zlatko Trajanoski. QPCR: Application for real-time PCR data management and analysis. *BMC Bioinformatics*, 10:268, 2009.

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