

Curriculum Vitae DI(FH) Dr. Stephan Pabinger

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Webpage <http://pabinger.site44.com>
Languages German/English (fluent)

Career history

10/2019 - ongoing **HOFER KG - International Supply Chain Management**; Data analysis and tool/method development; Supply Chain Modelling
12/2013 - 10/2019 **AIT - Austrian Institute of Technology, Health & Bioresources, Molecular Diagnostics, Vienna**. Bioinformatics Scientist; Data analysis and tool/method development; Project acquisition.
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

- Proficient in Python, R, HTML, Java, Javascript, LATEX
- Basic skills in C++, Perl
- PostgreSQL, MySQL, Oracle
- Linux, Microsoft, MacOS

Research interests

- Development of bioinformatics methods and tools
- Analysis of high-throughput biological data
- Machine learning
- Reproducible research
- Supply Chain Modelling

Work related

- Reviewer on several international journals
- Program committee member of the German Conference on Bioinformatics 2018
- Teaching: University Vienna, FH Campus Wien, UMIT, University Innsbruck, TU Graz, EMBL Bioinformatics Course

Publications (selected)

- 1 Gemmell NJ, Rutherford K, Prost S, Tollis M, Winter D, Macey JR, Adelson DL, Suh A, Bertozzi T, Grau JH, Organ C, Gardner PP, Muffato M, Patricio M, Billis K, Martin FJ, Flicek P, Petersen B, Kang L, Michalak P, Buckley TR, Wilson M, Cheng Y, Miller H, Schott RK, Jordan MD, Newcomb RD, Arroyo JI, Valenzuela N, Hore TA, Renart J, Peona V, Peart CR, Warmuth VM, Zeng L, Kortschak RD, Raison JM, Zapata VV, Wu Z, Santesmases D, Mariotti M, Guigó R, Rupp SM, Twort VG, Dussex N, Taylor H, Abe H, Bond DM, Paterson JM, Mulcahy DG, Gonzalez VL, Barbieri CG, DeMeo DP, **Pabinger S**, Van Stijn T, Clarke S, Ryder O, Edwards SV, Salzberg SL, Anderson L, Nelson N, Stone C .
The tuatara genome reveals ancient features of amniote evolution.
Nature 2020
 - 2 Krainer J, Weinhäusel A, Hanak K, Pulverer W, Özen S, Vierlinger K, **Pabinger S** .
EPIC-TABSAT: analysis tool for targeted bisulfite sequencing experiments and array-based methylation studies.
Nucleic Acids Res. 2019
 - 3 Hendling M, **Pabinger S**, Peters K, Wolff N, Conzemius R, Barišić I .
Oli2go: an automated multiplex oligonucleotide design tool.
Nucleic Acids Res. 2018
 - 4 **Pabinger S**, Ernst K, Pulverer W, Kallmeyer R, Valdes AM, Metrustry S, Katic D, Nuzzo A, Kriegner A, Vierlinger K, Weinhaeusel A .
Analysis and Visualization Tool for Targeted Amplicon Bisulfite Sequencing on Ion Torrent Sequencers.
PLoS ONE 2016
 - 5 **Pabinger S**, Dander A, Fischer M, Snajder R, Sperk M, Efremova M, Krabichler B, Speicher MR, Zschocke J, Trajanoski Z .
A survey of tools for variant analysis of next-generation genome sequencing data.
Brief. Bioinformatics 2014
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Austria, May 2, 2021