

Curriculum Vitae DI(FH) Dr. Stephan Pabinger

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Webpage <http://pabinger.site44.com>
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, LATEX, ...
- 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 Maghuly F, **Pabinger S**, Krainer J, Laimer M .
The Pattern and Distribution of Induced Mutations in J. curcas Using Reduced Representation Sequencing.
Front Plant Sci 2018
- 2 Hendling M, **Pabinger S**, Peters K, Wolff N, Conzemius R, Barišić I .
Oli2go: an automated multiplex oligonucleotide design tool.
Nucleic Acids Res. 2018
- 3 Gencay M, Seffner A, **Pabinger S**, Gautier J, Gohl P, Weizenegger M, Neofytos D, Batrla R, Woeste A, Kim HS, Westergaard G, Reinsch C, Brill E, Thuy PTT, Hoang BH, Sonderup M, Spearman CW, Brancaccio G, Fasano M, Gaeta GB, Santantonio T, Kaminski WE .
Detection of in vivo hepatitis B virus surface antigen mutations-A comparison of four routine screening assays.
J. Viral Hepat. 2018
- 4 Kim HS, Chen X, Xu M, Yan C, Liu Y, Deng H, Hoang BH, Thuy PTT, Wang T, Yan Y, Zeng Z, Gencay M, Westergaard G, **Pabinger S**, Kriegner A, Nauck M, Seffner A, Gohl P, Hübner K, Kaminski WE .
Frequency of hepatitis B surface antigen variants (HBsAg) in hepatitis B virus genotype B and C infected East- and Southeast Asian patients: Detection by the Elecsys[®] HBsAg II assay.
J. Clin. Virol. 2018
- 5 Gencay M, Vermeulen M, Neofytos D, Westergaard G, **Pabinger S**, Kriegner A, Seffner A, Gohl P, Huebner K, Nauck M, Kaminski WE .
Substantial variation in the hepatitis B surface antigen (HBsAg) in hepatitis B virus (HBV)-positive patients from South Africa: Reliable detection of HBV by the Elecsys HBsAg II assay.
J. Clin. Virol. 2018
- 6 Gencay M, Hübner K, Gohl P, Seffner A, Weizenegger M, Neofytos D, Batrla R, Woeste A, Kim HS, Westergaard G, Reinsch C, Brill E, Thu Thuy PT, Hoang BH, Sonderup M, Spearman CW, **Pabinger S**, Gautier J, Brancaccio G, Fasano M, Santantonio T, Gaeta GB, Nauck M, Kaminski WE .
Ultra-deep sequencing reveals high prevalence and broad structural diversity of hepatitis B surface antigen mutations in a global population.
PLoS ONE 2017
- 7 Pandey RV, **Pabinger S**, Kriegner A, Weinhäusel A .
DaMold: A data-mining platform for variant annotation and visualization in molecular diagnostics research.
Hum. Mutat. 2017

- 8 Pandey RV, Pulverer W, Kallmeyer R, Beikircher G, **Pabinger S**, Kriegner A, Weinhäusel A .
MSP-HTPrimer: a high-throughput primer design tool to improve assay design for DNA methylation analysis in epigenetics.
Clin Epigenetics 2016
- 9 **Pabinger S**, Ernst K, Pulverer W, Kallmeyer R, Valdes AM, Metrustry S, Katic D, Nuzzo A, Kriegner A, Vierlinger K, Weinhäusel A .
Analysis and Visualization Tool for Targeted Amplicon Bisulfite Sequencing on Ion Torrent Sequencers.
PLoS ONE 2016
- 10 Pandey RV, Pulverer W, Kallmeyer R, Beikircher G, **Pabinger S**, Kriegner A, Weinhäusel A .
MSRE-HTPrimer: a high-throughput and genome-wide primer design pipeline optimized for epigenetic research.
Clin Epigenetics 2016
- 11 Pandey RV, **Pabinger S**, Kriegner A, Weinhäusel A .
MutAid: Sanger and NGS Based Integrated Pipeline for Mutation Identification, Validation and Annotation in Human Molecular Genetics.
PLoS ONE 2016
- 12 Pandey RV, **Pabinger S**, Kriegner A, Weinhäusel A .
ClinQC: a tool for quality control and cleaning of Sanger and NGS data in clinical research.
BMC Bioinformatics 2016
- 13 Friedrich V, **Pabinger S**, Chen T, Messner P, Dewhirst FE, Schäffer C .
Draft Genome Sequence of Tannerella forsythia Type Strain ATCC 43037.
Genome Announc 2015
- 14 Friedrich V, Gruber C, Nimeth I, **Pabinger S**, Sekot G, Posch G, Altmann F, Messner P, Andrukhov O, Schäffer C .
Outer membrane vesicles of Tannerella forsythia: biogenesis, composition, and virulence.
Mol Oral Microbiol 2015
- 15 Maghuly F, Jankowicz-Cieslak J, **Pabinger S**, Till BJ, Laimer M .
Geographic origin is not supported by the genetic variability found in a large living collection of Jatropha curcas with accessions from three continents.
Biotechnol J 2015
- 16 **Pabinger S**, Rödiger S, Kriegner A, Vierlinger K, Weinhäusel A .
A survey of tools for the analysis of quantitative PCR (qPCR) data.
Biomol Detect Quantif 2014
- 17 Dander A, Baldauf M, Sperk M, **Pabinger S**, Hiltspolt B, Trajanoski Z .
Personalized Oncology Suite: integrating next-generation sequencing data and whole-slide bioimages.
BMC Bioinformatics 2014
- 18 Schweiger D, Trajanoski Z, **Pabinger S** .
SPARQLGraph: a web-based platform for graphically querying biological Semantic Web databases.
BMC Bioinformatics 2014
- 19 **Pabinger S**, Snajder R, Hardiman T, Willi M, Dander A, Trajanoski Z .
MEMOSys 2.0: an update of the bioinformatics database for genome-scale models and genomic data.
Database (Oxford) 2014

- 20 Dander A, **Pabinger S**, Sperk M, Fischer M, Stocker G, Trajanoski Z .
SeqBench: integrated solution for the management and analysis of exome sequencing data.
BMC Res Notes 2014
- 21 Dander A, Mueller LA, Gallasch R, **Pabinger S**, Emmert-Streib F, Graber A, Dehmer M .
ICOMMODEI a large-scale database of molecular descriptors using compounds from Pub-Chem.
Source Code Biol Med 2013
- 22 Magoc T, **Pabinger S**, Canzar S, Liu X, Su Q, Puiu D, Tallon LJ, Salzberg SL .
GAGE-B: an evaluation of genome assemblers for bacterial organisms.
Bioinformatics 2013
- 23 **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
- 24 **Pabinger S**, Trajanoski Z .
Genome-scale model management and comparison.
Methods Mol. Biol. 2013
- 25 Fischer M, Snajder R, **Pabinger S**, Dander A, Schossig A, Zschocke J, Trajanoski Z, Stocker G .
SIMPLEX: cloud-enabled pipeline for the comprehensive analysis of exome sequencing data.
PLoS ONE 2012
- 26 Schossig A, Wolf NI, Fischer C, Fischer M, Stocker G, **Pabinger S**, Dander A, Steiner B, Tönz O, Kotzot D, Haberlandt E, Amberger A, Burwinkel B, Wimmer K, Fauth C, Grond-Ginsbach C, Koch MJ, Deichmann A, von Kalle C, Bartram CR, Kohlschütter A, Trajanoski Z, Zschocke J .
Mutations in ROGD1 Cause Kohlschütter-Tönz Syndrome.
Am. J. Hum. Genet. 2012
- 27 **Pabinger S**, Rader R, Agren R, Nielsen J, Trajanoski Z .
MEMOSys: Bioinformatics platform for genome-scale metabolic models.
BMC Syst Biol 2011
- 28 **Pabinger S**, Thallinger GG, Snajder R, Eichhorn H, Rader R, Trajanoski Z .
QPCR: Application for real-time PCR data management and analysis.
BMC Bioinformatics 2009
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