Fritz J. Sedlazeck

Curriculum Vitae

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Personal Information

Date of Birth	January 22, 1983
Place of Birth	Vienna, Austria

Main Research Areas

Sequence Analysis	Method development to analyze Next Generation Sequencing data; Detection of Structural Variations; Assessment of the variability of genomes
High performance computing	Programming on Graphics Cards (CUDA, OpenCL); on CPUs (SSE, AVX); on Grid Engine (SGE, Slurm)

Education

2008–2012	**Dr. rer. nat**, *Bioinformatics*, University of Vienna.
PhD thesis	Benchtop Sequencing on Benchtop Computers
Supervisors	Prof. Dr. Arndt von Haeseler
Reviewers	Prof. Dr. med. Dag Harmsen, University of Münster, Germany
	Prof. Dr. Alexandros Stamatakis, Karlsruhe Institute of Technology, Germany
Core competences	Method development for and analysis of Next Generation Sequencing data, Software development, Programming on parallel and high throughput architectures
2004–2008	**Dipl. Ing. (FH)**, *Bioinformatics*, Upper Austria University of Applied Sciences, Hagenberg.
Diploma thesis	Correlative Cryo-Fluorescence and Cryo-Electron Microscopy
Supervisors	Prof. Dr. Achilleas Frangakis, DI Dr. Werner Backfrieder
Core competences	Software development, Statistics, Machine Learning, Data Engineering, Structural Biology, Image processing, Bioinformatics algorithms, Scripting Languages, Proteomics, Genetics, Cell and Cellular Processes

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Professional Experience

12/14-present	Computational Sci. Analyst I at the Cold Spring Harbor Laboratories - Simons Center for Quantitative Biology, USA
01/13-12/14	PostDoc at the Max F. Perutz Laboratories - Center for Integrative Bioinformatics Vienna (CIBIV), Austria

11/08-12/12	PhD student at the CIBIV, Austria
01/08-06/08	Diploma student at the European Molecular Biology Laboratory (EMBL), Germany
08/07-01/08	Internship at the European Molecular Biology Laboratory (EMBL), Germany
1999-2007	Various temporary summer jobs

Fellowships, Fundings, and Awards

2013	Vienna Biocenter PhD Award
2007	Leonardo da Vinci II Traineeship

Professional Service

Reviewing	Oxford Bioinformatics, PLOS ONE, Molecular Biology and Evolution, PeerJ, International Journal of Computational Science and Engineering (IJCSE)

Teaching Experience

2015	**iPlant Genome Assembly workshop**, *Lecturer*, Cold Spring Harbor.
2013, 2014	**Applied Bioinformatics**, *Lecturer and Tutor*, University of Vienna.
2013	**Lecture Series Bioinformatics**, *Lecturer*, University of Vienna.
2013, 2014	**Introduction to Bioinformatics**, *Lecturer*, Medical University of Vienna.
2013	**Bioinformatics Workshop - Large Scale Data Analysis**, *Lecturer and Tutor*, DARE (Detecting Antibiotic Resistance in Europe).
2009	**Advanced Bioinformatics**, *Tutor*, Medical University of Vienna.

Developed Bioinformatics Tools

BODscore	`cibiv.github.io/BODscore`.
Mummersplit	`github.com/fritzsedlazeck/sge_mummer`.
NextGenMap	`cibiv.github.io/NextGenMap`.
Sniffles	`github.com/fritzsedlazeck/Sniffles`.
SURVIVOR	`github.com/fritzsedlazeck/SURVIVOR`.
Teaser	`github.com/Cibiv/Teaser`, teaser.cibiv.univie.ac.at.

Personal Skills and Competences

Informatics	C++ (OpenMP, P-threads, CUDA, OpenCL), Java, Perl, Python, Shell, R, Matlab, SQL, XML
Analytical skills	Analytical thinking, Effective collaboration and communication skills, Creative ideas, Independence, Flexibility
Languages	German - first language, English - fluent, Latin - basic knowledge

References

-**Associate Prof. Dr. Michael C. Schatz**, Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA

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-**Prof. Dr Arndt von Haeseler**, Center for Integrative Bioinformatics Vienna (CIBIV), Max F. Perutz Laboratories, Dr. Bohr Gasse 9, A-1130 Vienna, Austria

arndt.von.haeseler@univie.ac.at, 0043 1 4277-24007

-**Prof. Dr. Christophe Dessimoz**, Dept. of Ecology and Evolution & Center for Integrative Genomics, University of Lausanne, Biophore 4309, 1015 Lausanne, Switzerland

Christophe.Dessimoz@unil.ch, 0041 21 692 4155

List of Publications

Journal Articles

[1] **R. Ming, R. VanBuren, C.M. Wai, H. Tang, M.C. Schatz, J.E. Bowers, E. Lyons, M. Wang, J. Chen, E. Biggers, J. Zhang, L. Huang, L. Zhang, W. Miao, J. Zhang, Z. Ye, C. Miao, Z. Lin, H. Wang, H. Zhou, W.C. Yim, H.D. Priest, C. Zheng, M. Woodhouse, P.P. Edger, R. Guyot, H. Guo, H. Guo, G. Zheng, R. Singh, A. Sharma, X. Min, Y. Zheng, H. Lee, J. Gurtowski, F.J. Sedlazeck, A. Harkess, M.R. McKain, Z. Liao, J. Fang, J. Liu, X. Zhang, Q. Zhang, W. Hu, Y. Qin, K. Wang, L. Chen, N. Shirley, Y. Lin, L. Liu, A.G. Hernandez, C.L. Wright, V. Bulone, G.A. Tuskan, K. Heath, F. Zee, P.H. Moore, R. Sunkar, J. H. Leebens-Mack, T. Mockler, J.L. Bennetzen, M. Freeling, D. Sankoff, A.H. Paterson, X. Zhu, X. Yang, J.A.C. Smith, J.C. Cushman, R.E. Paull, Q. Yu (2015)**, The pineapple genome and the evolution of CAM photosynthesis, *Nature Genetics*.
DOI:10.1038/ng.3435

[2] **M. Smolka, P. Rescheneder, M.C. Schatz, A. von Haeseler, F.J. Sedlazeck (2015)**, Teaser: Individualized benchmarking and optimization of read mapping results for NGS data, *Genome Biology*.
DOI:10.1186/s13059-015-0803-1

[3] **M. Tscherner, F. Zwolanek, S. Jenull, F.J. Sedlazeck, I.E. Frohner, N. Chauhan, A. von Haeseler and K. Kuchler (2015)**, The Candida albicans Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways, *PLOS Pathogen*.
DOI: 10.1371/journal.ppat.1005218

[4] **J. Cheng, <u>F.J. Sedlazeck</u>, J. Altmüller, A.W. Nolte (2015)**, Ectodysplasin signalling genes and phenotypic evolution in sculpins (Cottus), *Proceedings B*.
DOI: 10.1098/rspb.2015.0746

[5] **M. Krunice, R. Ertle, B. Hagen, <u>F.J. Sedlazeck</u>, R. Hofmann-Lehmann, A. von Haeseler and D. Klein (2015)**, Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study., *BMC Vet. Res.*, 11, 90.
DOI: 10.1186/s12917-015-0378-9

[6] **C. Vesely, S. Tauber, <u>F.J. Sedlazeck</u>, M. Tajaddod,A. von Haeseler, M.F. Jantsch (2014)**, ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain, *Nucleic Acids Research*, 42, 2155-12168.
DOI: 10.1093/nar/gku844

[7] **<u>F.J. Sedlazeck</u>*, P. Rescheneder*, and A. von Haeseler (2013)**, NextGenMap: fast and accurate read mapping in highly polymorphic genomes, *Bioinformatics*, 29, 2790-2791.
DOI: 10.1093/bioinformatics/btt468

[8] **S. Jünemann, <u>F.J. Sedlazeck</u>, K. Prior, A. Albersmeier, U. John, J. Kalinowski, A. Mellmann, A. Goesmann, A. von Haeseler, J. Stoye, and D. Harmsen (2013)**, Update on "Performance comparison of benchtop high-throughput sequencing platforms", *Nature Biotechnology*, 31, 294-296.
DOI: 10.1038/nbt.2522

[9] **<u>F.J. Sedlazeck</u>, P. Talloji, A. von Haeseler, and A. Bachmair (2013)**, Benefit-of-doubt (BOD) scoring: a sequencing-based method for SNP candidate assessment from high to medium read number data sets, *Genomics*, 101, 204-209.
DOI: 10.1016/j.ygeno.2012.12.001

[10] **H.Q. Dinh, M. Dubin*, <u>F.J. Sedlazeck</u>*, N. Lettner, O. Mittelsten Scheid, and A. von Haeseler (2012)**, Advanced Methylome Analysis after Bisulfite Deep Sequencing: an Example in Arabidopsis, *PLoS ONE*, 7, e41528.
DOI: 10.1371/journal.pone.0041528

[11] **P. Rescheneder, A. von Haeseler, and <u>F.J. Sedlazeck</u> (2012)**, MASon: Million Alignments In Seconds - A Platform Independent Pairwise Sequence Alignment Library for Next Generation Sequencing Data, *Proceedings of the International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2012)*, 195-201, SciTePress, Setubal, Portugal.
DOI: 10.5220/0003775701950201

[12] **C. Vesely**[*]**, S. Tauber**[*]**, <u>F.J. Sedlazeck</u>, A. von Haeseler, and M.F. Jantsch (2012)**, Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs, *Genome Research*, 22, 1468-1476.
DOI: 10.1101/gr.133025.111

Submitted/ In Preparation

[1] **T.S. Kaiser, B. Poehn, D. Szkiba, M. Preussner, <u>F.J. Sedlazeck</u>, A. Zrim, T. Neumann, L.T. Nguyen, A.J. Betancourt, T. Hummel, H. Vogel, S. Dorner, F. Heyd, A. von Haeseler, K. Tessmar-Raible** Insight into the adaptive evolution of circadian and circalunar timing from the genome of a marine insect. *submitted: Nature*

[2] **D.C. Jeffares, C. Jolly, M. Hoti, D. Speed, C. Rallis, C. Dessimoz, J. Bähler, <u>F.J. Sedlazeck</u>,** Meta-stable structural variants alter gene expression and quantitative traits in the fission yeast. *In preparation*

[3] **<u>F.J. Sedlazeck</u>, J. Cheng, J. Altmüller, A. von Haeseler, A.W. Nolte,** Emerging genome wide signatures of hybrid speciation in invasive sculpins(Cottus). *In preparation*

[4] **<u>F.J. Sedlazeck</u>, N. Osada, A. von Haeseler, M.C. Schatz,** Impact of highly polymorphic regions on the analysis of high throughput sequencing data. *In preparation*

[5] **<u>F.J. Sedlazeck</u>, P. Rescheneder, M. Nattestad, M.C. Schatz,** Detection of complex SV using third generation sequencing. *In preparation*

[6] **G. Vurture**[*], **<u>F.J. Sedlazeck</u>**[*]**, M. Nattestad, C. Underwood, J. Gurtowski, M.C. Schatz,** Fast genome-wide heterozygosity analysis from unassembled short reads. *In preparation*

[7] **M. Nattestad, K. Ng, S. Goodwin, T. Baslan, <u>F.J. Sedlazeck</u>, J. Gurtowski, E. Hutton, M. Alford, E. Tseng,J. Chin, T. Beck, Y. Sundaravadanam, M. Kramer, E. Antoniou, J. McPherson, J. Hicks, M.C. Schatz, W.R. McCombie,** Comprehensive Genome and Transcriptome Structural Analysis of a Breast Cancer Cell Line using PacBio Long Read Sequencing. *In preparation*

[*]: equally contributed

Invited Talks

[1] **NextGenMap: How to accurately map 150,000 reads per second and why should we care.**, *Cold Spring Harbor Laboratory*, Cold Spring Harbor, USA, 8 April, 2015.

[2] **Impact of highly polymorphic regions on HTS analysis**, *University College London*, London, UK, 25 September, 2014.

[3] **NextGenMap: Fast and accurate read mapping independent of evolutionary distance**, *Max Planck Institute for Evolutionary Biology*, Plön, Germany, 6 March, 2013.

[4] **Comprehensive Evaluation of NGS Mapping Programs**, *Austrian Agency for Health and Food Safety (AGES)*, Vienna, Austria, 28 April, 2011.

[5] **Whole Genome Sequencing: Possibilities, Perspectives and Problems for the Analysis**, *Research Institute of Molecular Pathology (IMP)* , Vienna, Austria, 2 December, 2010.

[6] **NextGenMap: Using high throughput hardware for high throughput sequencing**, *Research Institute of Molecular Pathology (IMP)* , Vienna, Austria, 10 November, 2009.

Conferences

Conference Talks

[1] **Methods for improved SV detection and interpretation**, *Genome in a bottle workshop*, Gaithersburg, USA, 27-28 August, 2015.

[2] **NextGenMap: Fast and accurate read mapping independent of evolutionary distance**, *MASAMB 2013*, London, United Kingdom, 11-12 April, 2013.

[3] **MASon: Million Alignments In Seconds - A Platform Independent Pairwise Sequence Alignment Library for Next Generation Sequencing Data**, *BIOINFORMATICS 2012*, Vilamoura, Portugal, 1-4 February, 2012.

[4] **Identifying wrongly mapped reads via majority vote of several scoring schemata**, *European Science Foundation - COST action: StatSeq meeting on RNA-Seq*, Vienna, Austria, 24-26 March, 2011.

Conference Posters

[1] **Detection of Structural Variants using third generation sequencing**, *Genome Informatics*, Cold Spring Harbor, USA, 28 October-31 October, 2015.

[2] **The impact of highly polymorhic regions on HTS related studies.**, *Probabilistic Modeling in Genomics*, Cold Spring Harbor, USA, 14 October-17 October, 2015.

[3] **The impact of highly polymorhic regions on HTS related studies.**, *Biology of Genomes*, Cold Spring Harbor, USA, 5 May-9 May, 2015.

[4] **Impact of highly polymorphic regions on HTS analysis**, *Genome Informatics*, Cambridge, UK, 21 September-24 September, 2014.

[5] **Improving de novo Genome Assemblies**, *Genome Informatics*, Cold Spring Harbor, USA, 30 October-2 November, 2013.

[6] **MONTY: On the accuracy of high throughput sequencing technology**, *Genome Informatics*, Cambridge, UK, 6-9 September, 2012.

[7] **Identifying wrongly mapped reads via different scoring schemata**, *Genome Informatics*, Cold Spring Harbor, USA, 2-5 November, 2011.

[8] **Comprehensive Analysis of Next Generation Sequencing Programs**, *10th International Conference on Systems Biology(ICSB 2010)*, Edinburgh, Scotland, 10-16 October, 2010.

[9] **NextGenMap: Using high throughput hardware for high throughput sequencing**, *Genome Informatics*, Hinxton, UK, 15-19 September, 2010.

━━ Press releases

[1] **Introducing Teaser: Optimization of read mapping results over a coffee break.**, *http://blogs.biomedcentral.com/on-biology/2015/10/28/introducing-teaser-optimization-read-mapping-results-coffee-break/*, BioMed Central Blogs, 28 October 2015.

[2] **Bioinformaticians are becoming more important.**, *http://sciencev1.orf.at/science/news/156344*, Science ORF Online, 22 July 2009.

East Northport, November 30, 2015