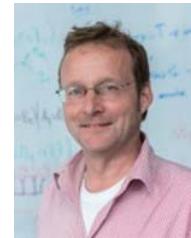## Curriculum Vitae

Name & Address

Arndt Peter von Haeseler - Professor of Bioinformatics

Current Position: Scientific Director of the Center for Integrative Bioinformatics Vienna

Center for Integrative Bioinformatics Vienna (CIBIV), University of Vienna,

Max F. Perutz Laboratories, Campus Vienna Biocenter 5; A-1030 Vienna

Austria

Phone +43-1-4277-74320 (assistant); Fax +43-1-4277-9743

e-mail: arndt.von.haeseler@univie.ac.at ORCID: 0000-0002-3366-4458

Web: www.cibiv.at

Main Research Interests

Molecular Evolution - We develop bioinformatics methods to infer the phylogenetic relationship of contemporary organisms. To this end we develop (1) time and memory efficient algorithm (2) models of sequence evolution and databases to administer the data. The tools are made available to the scientific community. We are also interested in the mathematical structure behind the bioinformatics problems, to understand and improve the heuristics suggested by others. **High Throughput Data** - In close collaboration with wet lab biologists, we analyse all sort of "omics" data, including also whole genome assembly and SNP calling procedures. Moreover, we develop tools to rapidly analyse such data. In the collaboration with the biologists and physicians we often develop new bioinformatics pipelines (including new computer science or statistical approaches) to analyse non-standard data.

Scientific Education & Career History

2010 - date	Full Professor for Bioinformatics at the Center for Molecular Biology and Department for Computer Science (both University of Vienna) and the Department for Medical biochemistry (Medical University of Vienna), Austria
2005 – date	Scientific Director of the Center for Integrative Bioinformatics Vienna (CIBIV)
2005 - 2011	WWTF Science Chair for Bioinformatics and Full Professor for Bioinformatics at the University of Vienna, the Medical University Vienna and the University of Veterinary Medicine, Austria
2002 - 2005	Chairman of Computer Sciences, Heinrich-Heine-University Düsseldorf
2001 - 2004	Research Center Jülich, Group Leader of Bioinformatics Group at the Neumann-Institute for Computing
2001 - 2005	Heinrich-Heine-University Düsseldorf, Full Professor (C4) for Bioinformatics
1999	University of Leipzig, Honorary Professor for Theoretical Biology
1998 - 2001	Max-Planck-Institute for evolutionary Anthropology, Group Leader (C3)
1995 - 1998	University of Munich, Senior scientific lecturer (Hochschulassistent, C2), Biology
1994	University of Munich, State doctorate (Habilitation) in Zoology
1991 - 1995	University of Munich, Scientific lecturer (Hochschulassistent, C1), Biology
1990 - 1991	University of Southern California, Visiting Assistant Professor, Mathematics
1989 - 1990	University of Southern California, Postdoc
1988 - 1989	University of Bielefeld, Postdoc
1988	University of Bielefeld, Ph.D. in Mathematics
1984	Philipps-University Marburg, State examination (1. Staatsexamen) for biology, mathematics, education science
1978	General qualification for university entrance (Abitur)

Visiting Positions (selection of 5 most relevant)

2012 - 2015	Visiting Professor, Division of theoretical Genetics, National Institute for Genetics, Mishima, Japan
9-12/ 2007	Visiting Fellow Isaac Newton Institute Mathematical Sciences, Cambridge, UK
3/2001	Mathematics and Computer Science Department, University Jena

8-9/1993   Mathematics Department, University of Southern California, Los Angeles, USA
10/1991   Instituto Nacional de Investigaciones Agrarias, Madrid, Spain

Experience in Scientific Management and Organization & Student Supervision

2016   Co-Head of studies Computer Sciences (Bioinformatics), Univ. of Vienna

2016   Organizer of the SMBE Symposium: Extracting evolutionary patterns and processes fromgenomic data. Queensland's Gold Coast, Australia

2016   Organizer of the SMBE Satellite meeting on RNA modification and its implication onadaptation and evolution, Valencia, Spain

2015   Minisymposium on Evolutionary Biology, Vienna, Austria

2015   Programm committee member at the SMBE 2015, Vienna, Austria

2015   Head of the curriculum committee for a Master of Science in Bioinformatics

2014   Programme Committee: "German Conference of Bioinformatics", Bielefeld

2014   Organizer of the SMBE 2014 Symposium: "Statistical and Computational Approaches to Evolution, San Juan, Puerto Rico

2013   2nd DARE Bioinformatics Winterschool, Vienna, Austria

2012   RNA Workshop Introduction to R and BioConductor, Vienna, Austria

2012   DARE Bioinformatics Winterschool 2012

2012   Vice Director of the Doctoral Program in Natural Sciences and the PhD Program in Natural Sciences at the University of Vienna.

2011   Head of Bioinformatics and Computational Research Group, Faculty of Computer Science, Univ. of Vienna

2011   Organizer MASAMB "Mathematical and Statistical Aspects of Molecular Biology" Conference Vienna

2011   Programme Committee: "European Conference on Complex Systems", Vienna

2009   Programme Committee: "German Conference on Bioinformatics", Halle, Germany

2008   Programme Committee:"BIRD: Bioinformatics in Research & Development", Vienna

2008   Programme Committee:"RECOMB2008", Singapore

2007   Programme Committee "German Conference on Bioinformatics, Potsdam, Germany

2007   Workshop "Bioinformatics, Evolution and Databases", FEBS2007, Vienna

2007   Conference: "Computational Biology as Driving Force for Discovery in Life Sciences", Brno, Czech (jointly with Frank Eisenhaber, Jaroslav Koca)

2007   Programme Committee: "BIRD: Bioinformatics in Research & Development", Berlin

2006   Organizing Committee: "Evolution of Biomolecular Structure" A Symposium on current topics at the interface of molecular and computational biology and bioinformatics, Vienna

2006   Workshop "Ontologies and Grid Computing", Univ. Leipzig (jointly with E. Rahm)

2001-2005 Chairman of Computer Science, Heinrich-Heine University Düsseldorf.

Supervision of Doctoral (PhD) Thesis Students (past five years – 34 since 1995)

Tina Köstler – MFPL PhD Student - 2008 – 2012
"Domains, Proteins, and Evolution"
Fritz Sedlazeck – MFPL PhD Student - 2008 – 2012
"Benchtop sequencing on benchtop computers
Stefanie Tauber – MFPL PhD Student - 2010 – 2013
"Exploring the transcriptome "
Mikhail Okun – MFPL PhD Student - 2010 – 2014
"Molecular Phylogeny and Taxonomy of the Physarum notabile Species Complex (Myxomycetes)"
Lam Tung Nguyen – MFPL PhD Student - 2011 – 2016
"Computational methods for fast and accurate phylogenetic inference"
Dinh Quang Huy – MFPL PhD Student - 2011 – 2012

"Bioinformatic tools for analyzing epigenomic profiling data"

Olga Chernomor – MFPL PhD Student - 2011 – 2015
"Phylogenomics: theory, algorithms and applications"
Milica Krunic – MFPL PhD Student - 2011 – ongoing
"Bioinformatic analysis of medically relevant NGS data"
Philipp Rescheneder – MFPL PhD Student - 2012 – ongoing
"Analysis of next-generation-sequencing data with high mismatch rates"
Celine Prakash – MFPL PhD Student - 2012 – ongoing
"An Enumerative Combinatorics Model for Fragmentation Patterns in RNA Sequencing Provides Insights into the Expected Coverage Profile"
Konstantina Kyriakouli – MFPL PhD Student - 2013 – ongoing
"Detection of polymorphisms from NGS data with focus on NKRs and their ligands"
Luis Paulin Paz – MFPL PhD Student - 2014 – ongoing
"Understanding the sampling properties of high throuput sequencing technologies"
Philip Stevens – MFPL PhD Student - 2014 – 2017
"Establishment of a quantitative score for liquid biopsy in sepsis diagnostics"
Florian Pflug – MFPL PhD Student - 2015– ongoing
"Model-based bias correction and accuracy improvent for quantitative NGS experiments "

Invited Conference Presentations (5 recent selected)

2016 - Annual Meeting of the Soc. Molecular Biology and EvolutionGold Coast, Australia
2016 - "Pacific meets Plateau" 20th Ann Phylogenomics Meeting, New Zealand
2015 - 7th UTAS Theoretical Phylogenetics Conference, Univ. Tasmania, Hobart, Australia
2015 - German Conference on Bioinformatics - University Alliance Ruhr, Dortmund
2013 - Annual Meeting of the Society for Evolutionary Studies, Tsukuba, Japan

Honors & Awards

2015	Corresponding member of the Austrian Academy of Science
2005	Award of WWTF Science Chair, Vienna
1999	Honorary Professor for Theoretical Biology, Univ. Leipzig, Germany
1985 - 1988	PhD scholarship Studienstiftung des Deutschen Volkes

Member of Reviewing Panels, Editorial Boards, Scientific Organizations (5 selected)

2015	Scientific Advisory Board Biology Department, Univ. Munich, Germany
2013	Editorial Board member PLoS One
2012	Senior Editor for Molecular Biology and Evolution
2011	Associate Editor Statistical Applications in Genetics and Molecular Biology
2010	Section Editor for BMC Evolutionary Biology

Most Important Research Funding (selection of most relevant in past 5 years)

2016 – 2019	FWF-FLIP - Future Likelihood Interferences for Phylogenetic,	215 k€
2014 – 2017	FWF-DK-W1207: RNA Biology Regulation of Transcriptome	145 k€
2013 – 2016	EU MC-ITN : Naturimmun Natural Killer Cell-based anti-Cancer Immunnotherapies 193 k€	
2011 – 2014	Research Cluster Microbial Infections & Host Immune Response, Cooperation University of Vienna and Medical University,	158 k€
2011 – 2014	IK Computational Science University of Vienna,	627 k€

Key International Collaborators (selection of 5 with joint publications since 2012)

Alexandros Stamatakis   Heidelberg Inst. for Theor. Studies Alexandros.Stamatakis@h-its.org
Karl-Erich Jäger   University Düsseldorf Karl-Erich.jaeger@fz-juelich.de
Enrico Schleiff   University Frankfur schleiff@bio.uni-frankfurt.de
Kai Sohn   Fraunhofer IGB Institute kai.sohn@igb.fraunhofer.de

Steffen Klaere Univeristy of Auckland, New Zealand steffen.klaere@gmail.com

List of Publications (2012 - 2016)

Overall more than **130** papers. Based on Google Scholar, publications received more >17,300 citations with a life-time Hirsch **h Index** of **57**.

1. Prakash, C., and **A. von Haeseler** (2016) An Enumerative Combinatorics Model for Fragmentation Patterns in RNA Sequencing Provides Insights into Non-uniformity of the Expected Fragment Starting Point and Coverage Profile. **J. Comp. Bio.** In press.

2. Kaiser, T., B. Poehn, D. Szkiba, M. Preussner, F.J. Sedlazeck, A. Zrim, T. Neumann, L.-T. Nguyen, A.J. Betancourt, T. Hummel, H. Vogel, S. Dorner, F. Heyd, **A. von Haeseler**, and K. Tessmar-Raible. The Genomic Basis of Circadian and Circalunar timing Adaptations in a Midge. Nature, 2016. 540,69-73.

3. Chernomor, O., **A. von Haeseler**, and B.Q. Minh, Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. **Syst Biol**, 2016. 65,997-1008.

4. Gesson, K*, P. Rescheneder*, M.P. Skoruppa, **A. von Haeseler**, T. Dechat, and R. Foisner, A-type lamins bind both hetero- and euchromatin, the latter being regulated by lamina-associated polypeptide 2 alpha. **Genome Res**, 2016. 26(4): p. 462-73. (* equal contribution).

5. Grumaz, S.*, P. Stevens*, C. Grumaz, S. Decker, M. Weigand, S. Hofer, T. Brenner, **A. von Haeseler**, and K. Sohn, Next generation sequencing diagnostics of bacteremia in septic patients. **Genome Med.**, 8:73. (* equal contribution).

6. Jagut, M., P. Hamminger, A. Woglar, S. Millonigg, L. Paulin, M. Mikl, M.R. Dello Stritto, L. Tang, C. Habacher, A. Tam, M. Gallach, **A. von Haeseler**, A.M. Villeneuve, and V. Jantsch, Separable Roles for a Caenorhabditis elegans RMI1 Homolog in Promoting and Antagonizing Meiotic Crossovers Ensure Faithful Chromosome Inheritance. **PLoS Biol**, 2016. 14(3): p. e1002412.

7. Schrempf, D., B.Q. Minh, N. De Maio, **A. von Haeseler**, and C. Kosiol (2016) Reversible polymorphism-awere phylogenetic models and their application to tree inference. **J. Theor. Biol.**, 407,362-370.

8. Trifinopoulos, J., L.T. Nguyen, **A. von Haeseler**, and B.Q. Minh, W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Res, 2016. 44, W232-W235.

9. Smolka, M., P. Rescheneder, M.C. Schatz, **A. von Haeseler**, and F.J. Sedlazeck, Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. **Genome Biol**, 2015. 16: p. 235.

10. Tscherner, M., F. Zwolanek, S. Jenull, F.J. Sedlazeck, A. Petryshyn, I.E. Frohner, J. Mavrianos, N. Chauhan, **A. von Haeseler**, and K. Kuchler, The Candida albicans Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways. PLoS Pathog, 2015. 11(10): p. e1005218.

11. Chernomor, O., B.Q. Minh, and **A. von Haeseler**, Consequences of Common Topological Rearrangements for Partition Trees in Phylogenomic Inference. **J Comput Biol**, 2015. 22(12): p. 1129-42.

12. Chernomor, O., B.Q. Minh, F. Forest, S. Klaere, T. Ingram, M. Henzinger, and **A. von Haeseler**, Split diversity in constrained conservation prioritization using integer linear programming. **Methods Ecol Evol**, 2015. 6(1): p. 83-91.

13. Krunic, M., R. Ertl, B. Hagen, F.J. Sedlazeck, R. Hofmann-Lehmann, **A. von Haeseler**, and D. Klein, Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study. **BMC Vet Res**, 2015. 11: p. 90.

14. Fieber, C., M. Janos, T. Koestler, N. Gratz, X.D. Li, V. Castiglia, M. Aberle, M. Sauert, M. Wegner, L. Alexopoulou, C.J. Kirschning, Z.J. Chen, **A. von Haeseler**, and P. Kovarik, Innate immune response to Streptococcus pyogenes depends on the combined activation of TLR13 and TLR2. **PLoS One**, 2015. 10(3): p. e0119727.

15. Nguyen, L.T., H.A. Schmidt, A. von Haeseler, and B.Q. Minh, IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. **Mol Biol Evol**, 2015. 32(1): p. 268-74.

16. Flouri, T., F. Izquierdo-Carrasco, D. Darriba, A.J. Aberer, L.T. Nguyen, B.Q. Minh, **A. von Haeseler**, and A. Stamatakis, The phylogenetic likelihood library. **Syst Biol**, 2015. 64(2): p. 356-62.

17. Chipman, A.D., D.E. Ferrier, C. Brena, J. Qu, D.S. Hughes, R. Schroder, M. Torres-Oliva, N. Znassi, H. Jiang, F.C. Almeida, C.R. Alonso, Z. Apostolou, P. Aqrawi, W. Arthur, J.C. Barna, K.P. Blankenburg, D. Brites, S. Capella-Gutierrez, M. Coyle, P.K. Dearden, L. Du Pasquier, E.J. Duncan, D. Ebert, C. Eibner, G. Erikson, P.D. Evans, C.G. Extavour, L. Francisco, T. Gabaldon, W.J. Gillis, E.A. Goodwin-Horn, J.E. Green, S. Griffiths-Jones, C.J. Grimmelikhuijzen, S. Gubbala, R. Guigo, Y. Han, F. Hauser, P. Havlak, L. Hayden, S. Helbing, M. Holder, J.H. Hui, J.P. Hunn, V.S. Hunnekuhl, L. Jackson, M. Javaid, S.N. Jhangiani, F.M. Jiggins, T.E. Jones, T.S. Kaiser, D. Kalra, N.J. Kenny, V. Korchina, C.L. Kovar, F.B. Kraus, F. Lapraz, S.L. Lee, J. Lv, C. Mandapat, G. Manning, M. Mariotti, R. Mata, T. Mathew, T. Neumann, I. Newsham, D.N. Ngo, M. Ninova, G. Okwuonu, F. Ongeri, W.J. Palmer, S. Patil, P. Patraquim, C. Pham, L.L. Pu, N.H. Putman, C. Rabouille, O.M. Ramos, A.C. Rhodes, H.E. Robertson, H.M. Robertson, M. Ronshaugen, J. Rozas, N. Saada, A. Sanchez-Gracia, S.E. Scherer, A.M. Schurko, K.W. Siggens, D. Simmons, A. Stief, E. Stolle, M.J. Telford, K. Tessmar-Raible, R. Thornton, M. van der Zee, **A. von Haeseler**, J.M. Williams, J.H. Willis, Y. Wu, X. Zou, D. Lawson, D.M. Muzny, K.C. Worley, R.A. Gibbs, M. Akam and S. Richards, The first myriapod genome sequence reveals conservative arthropod gene content and genome organisation in the centipede Strigamia maritima. **PLoS Biol**, 2014. 12(11): p. e1002005.

18. Vesely, C., S. Tauber, F.J. Sedlazeck, M. Tajaddod, **A. von Haeseler**, and M.F. Jantsch, ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. **Nucleic Acids Res**, 2014. 42(19): p. 12155-68.

19. Sengoelge, G., W. Winnicki, A. Kupczok, **A. von Haeseler**, M. Schuster, W. Pfaller, P. Jennings, A. Weltermann, S. Blake, and G. Sunder-Plassmann, A SAGE based approach to human glomerular endothelium: defining the transcriptome, finding a novel molecule and highlighting endothelial diversity. **BMC Genomics**, 2014. 15: p. 725.

20. Kaschner, M., A. Loeschcke, J. Krause, B.Q. Minh, A. Heck, S. Endres, V. Svensson, A. Wirtz, **A. von Haeseler**, K.E. Jaeger, T. Drepper, and U. Krauss, Discovery of the first lightdependent protochlorophyllide oxidoreductase in anoxygenic phototrophic bacteria. **Mol Microbiol**, 2014. 93(5): p. 1066-78.

21. Szkiba, D., M. Kapun, **A. von Haeseler**, and M. Gallach, SNP2GO: functional analysis of genome-wide association studies. **Genetics**, 2014. 197(1): p. 285-9.

22. Ebersberger, I., S. Simm, M.S. Leisegang, P. Schmitzberger, O. Mirus, **A. von Haeseler**, M.T. Bohnsack, and E. Schleiff, The evolution of the ribosome biogenesis pathway from a yeast perspective. **Nucleic Acids Res**, 2014. 42(3): p. 1509-23.

23. Dell'Ampio, E., K. Meusemann, N.U. Szucsich, R.S. Peters, B. Meyer, J. Borner, M. Petersen, A.J. Aberer, A. Stamatakis, M.G. Walzl, B.Q. Minh, **A. von Haeseler**, I. Ebersberger, G. Pass, and B. Misof, Decisive data sets in phylogenomics: lessons from studies on the phylogenetic relationships of primarily wingless insects. **Mol Biol Evol**, 2014. 31(1): p. 239-49.

24. Sedlazeck, F.J., P. Rescheneder, and **A. von Haeseler**, NextGenMap: fast and accurate read mapping in highly polymorphic genomes. **Bioinformatics**, 2013. 29(21): p. 2790-1.

25. Anisimova, M., D.A. Liberles, H. Philippe, J. Provan, T. Pupko, and **A. von Haeseler**, State-of the art methodologies dictate new standards for phylogenetic analysis. BMC Evol Biol, 2013. 13: p. 161.

26. Tauber, S. and **A. von Haeseler**, Exploring the sampling universe of RNA-seq. **Stat Appl Genet Mol Biol**, 2013. 12(2): p. 175-88.

27. Junemann, S., F.J. Sedlazeck, K. Prior, A. Albersmeier, U. John, J. Kalinowski, A. Mellmann, A. Goesmann, A. **von Haeseler**, J. Stoye, and D. Harmsen, Updating benchtop sequencing performance comparison. **Nat Biotechnol**, 2013. 31(4): p. 294-6.

28. Minh, B.Q., M.A. Nguyen, and **A. von Haeseler**, Ultrafast approximation for phylogenetic bootstrap. **Mol Biol Evol**, 2013. 30(5): p. 1188-95.

29. Sedlazeck, F.J., P. Talloji, **A. von Haeseler**, and A. Bachmair, Benefit-of-doubt (BOD) scoring: a sequencing-based method for SNP candidate assessment from high to medium read number data sets. **Genomics**, 2013. 101(3): p. 204-9.

30. Popitsch, N. and A. **von Haeseler**, NGC: lossless and lossy compression of aligned highthroughput sequencing data. **Nucleic Acids Res**, 2013. 41(1): p. e27.

31. **von Haeseler, A.**, Do we still need supertrees? **BMC Biol**, 2012. 10: p. 13.

32. Fischer, M., S. Klaere, M.A. Thi Nguyen, and **A. von Haeseler**, On the group theoretical background of assigning stepwise mutations onto phylogenies. **Algorithms Mol Biol**, 2012. 7(1): p. 36.

33. Dinh, H.Q., M. Dubin, F.J. Sedlazeck, N. Lettner, O. Mittelsten Scheid, and **A. von Haeseler**, Advanced methylome analysis after bisulfite deep sequencing: an example in Arabidopsis. **PLoS One**, 2012. 7(7): p. e41528.

34. Laubach, T., **A. von Haeseler**, and M.J. Lercher, TreeSnatcher plus: capturing phylogenetic trees from images. **BMC Bioinformatics**, 2012. 13: p. 110.

35. Reitter-Pfoertner, S., **A. von Haeseler**, B. Horvath, R. Sunder-Plassmann, V. Tiedje, I. Pabinger, and C. Mannhalter, Identification of an ancient haemophilia A splice site mutation. **Thromb Res**, 2012. 130(3): p. 445-50.

36. Koestler, T., **A. von Haeseler**, and I. Ebersberger, REvolver: modeling sequence evolution under domain constraints. **Mol Biol Evol**, 2012. 29(9): p. 2133-45.

37. Vesely, C., S. Tauber, F.J. Sedlazeck, **A. von Haeseler**, and M.F. Jantsch, Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. **Genome Res**, 2012. 22(8): p. 1468-76.

38. Ebersberger, I., R. de Matos Simoes, A. Kupczok, M. Gube, E. Kothe, K. Voigt, and **A. von Haeseler**, A consistent phylogenetic backbone for the fungi. **Mol Biol Evol**, 2012. 29(5): p. 1319-34.

39. Thi Nguyen, M.A., T. Gesell, and **A. von Haeseler**, ImOSM: intermittent evolution and robustness of phylogenetic methods. **Mol Biol Evol**, 2012. 29(2): p. 663-73.

40. Salzburger, W., G.B. Ewing, and **A. von Haeseler**, The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. Mol Ecol, 2011. 20(9): p. 1952-63.

41. Vinh le, S., A. Fuehrer, and **A. von Haeseler**, Random Tree-Puzzle leads to the Yule-Harding distribution. **Mol Biol Evol**, 2011. 28(2): p. 873-7.

42. Nguyen, M.A., S. Klaere, and **A. von Haeseler**, MISFITS: evaluating the goodness of fit between a phylogenetic model and an alignment. Mol Biol Evol, 2011. 28(1): p. 143-52.

Patent

2015 *"Method and device for nucleic acid based diagnostic approaches including the determination of a deviant condition, especially a health condition and/or pathogenic condition of a sample".* Inventors: K. Sohn, S. Grumaz, P. Stevens, **A. von Haeseler**. Patent application #EP 15184688.8-1404.

10 Most Important Career Publications

1. Strimmer, K. and **A. von Haeseler**, Quartet puzzling: A quartet maximum likelihood method for reconstructing tree topologies. **Mol Biol Evol**, 1996. 13(7): p. 964-969.

2. Strimmer, K. and **A. von Haeseler**, Likelihood-mapping: a simple method to visualize phylogenetic content of a sequence alignment. **Proc Natl Acad Sci U S A**, 1997. 94(13): p. 6815-9.

3. Weiss, G. and **A. von Haeseler**, Inference of population history using a likelihood approach. **Genetics**, 1998. 149(3): p. 1539-46

4. Meyer, S., G. Weiss, and **A. von Haeseler**, Pattern of nucleotide substitution and rate heterogeneity in the hypervariable regions I and II of human mtDNA. **Genetics**, 1999. 152(3): p. 1103-10.

5. Schmidt, H.A., K. Strimmer, M. Vingron, and **A. von Haeseler**, TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. **Bioinformatics**, 2002. 18(3): p. 502-4.

6. Minh, B.Q., M.A. Nguyen, and A**. von Haeseler**, Ultrafast approximation for phylogenetic bootstrap. **Mol Biol Evol**, 2013. 30(5): p. 1188-95.

7. Junemann, S., F.J. Sedlazeck, K. Prior, A. Albersmeier, U. John, J. Kalinowski, A. Mellmann, A. Goesmann, **A. von Haeseler**, J. Stoye, and D. Harmsen, Updating benchtop sequencing performance comparison. **Nat Biotechnol**, 2013. 31(4): p. 294-6.

8. Sedlazeck, F.J., P. Rescheneder, and **A. von Haeseler**, NextGenMap: fast and accurate read mapping in highly polymorphic genomes. **Bioinformatics**, 2013. 29(21): p. 2790-1.

9. Nguyen, L.T., H.A. Schmidt, **A. von Haeseler**, and B.Q. Minh, IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. **Mol Biol Evol**, 2015. 32(1): p. 268-74.

10. Prakash, C., and **A. von Haeseler** (2016) An Enumerative Combinatorics Model for Fragmentation Patterns in RNA Sequencing Provides Insights into Non-uniformity of the Expected Fragment Starting Point and Coverage Profile. **J. Comp. Bio.** 2017, 24(3):200-212