Sebastian Höhna

PERSONAL DATA

DATE OF BIRTH:	17 August 1983
PLACE OF BIRTH:	Berlin, Germany
ADDRESS:	Ginsterweg 17, 81377 München, Germany
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SUMMARY

Funding	15 grants/fellowships in 4 countries total ≈ 3.3 Mio €	Supervision	4 PhD students 1 postdoctoral researcher
Publications	31 Journal articles 7 preprints 1 conference proceeding article	Research profiles	Google Scholar Publons Orcid ID
Citations	19,124 (Google Scholar) 13,483 (Web of Science)	H-Index	19 (Google Scholar) 15 (Web of Science)

ACADEMIC POSITIONS

MAR 2020-DEC 2020	50% parental leave (Elternzeit)
JAN 2019-PRESENT	Emmy Noether Research Group Leader, Ludwig-Maximilians-Universität, München, Germany
APR 2017-DEC 2018	Research Group Leader (Akademischer Rat), Ludwig-Maximilians-Universität, München, Germany

Education

Sept 2014-Mar 2017	Miller fellow (Postdoc), University of California, Berkeley, USA Host: John P. Huelsenbeck
Jan 2014-Aug 2014	Postdoc, University of California, Davis, USA Supervisor: Brian R. Moore
Apr 2009-Nov 2013	PhD in Mathematical Statistics, Stockholm University, Sweden PhD Thesis defended on 29th November 2013 Licenciate Thesis presented in December 2011 Supervisors: Tom Britton and Fredrik Ronquist
Oct 2012-Mar 2013	Erasmus Exchange Semester in Mathematics, Technical University Munich, Germany
Mar 2008-Feb 2009	Master of Science in Computer Science, The University of Auckland, New Zealand with First Class Honors Supervisor: Alexei J. Drummond
Mar 2007-Feb 2008	Postgraduate Diploma in Computer Science, The University of Auckland, New Zealand with Distinction
Sept 2003-Aug 2006	Diplom-Engineer in Computer Science, Berlin School of Economics and Law (Berufsakademie Berlin), Germany

Work Experience

Sept 2006 - Jan 2007	Systems Engineer at Bayer-Schering-Pharma AG, Berlin, Germany
Jul 2005 - Sept 2005	Software Engineer at Nihon Schering KK, Osaka, Japan
Sept 2003 - Aug 2006	Software Engineer at Schering AG, Berlin, Germany

TEACHING EXPERIENCE

University Classes:

2021	*Phylogenetics & Macroevolution*	lectures and practicals	LMU München, Germany
2019	*Programming for Bayesian phylogenetics*	lectures and practicals	LMU München, Germany
2018	*Computational Phylogenetics*	practicals	LMU München, Germany
2018	*Evolutionsbiologie*	lectures and practicals	LMU München, Germany
2018	*Phylogenetics & Macroevolution*	lectures and practicals	LMU München, Germany
2017	*Computational Phylogenetics*	practicals	LMU München, Germany
2017	*Evolutionsbiologie*	lectures and practicals	LMU München, Germany
2016	*Phylogeny and Macroevolution*	Guest Lecturer	UC Davis, California, USA
2011	*Bayesian Methods*	lectures and practicals	Stockholm University, Sweden
2009	*Mastering Cyberspace: An introduction to practical computing*	lectures	The University of Auckland, New Zealand
2008	*Computational Biology*	practicals	The University of Auckland, New Zealand
2007	*Algorithms and data structures*	practicals	The University of Auckland, New Zealand

International Workshops:

APR 2021	*Stay-at-Home RevBayes Workshop Spring 2021*	online
FEB 2021	*Mathematical, Inferential, and Computational Phylogenomics*	online
SEPT 2019	*Bayesian phylogenetics and macroevolution in RevBayes*	LMU München, Germany
JULY 2019	*Phylogenomics and Population Genomics: Inference and Applications*	University of Barcelona, Spain
JUNE 2019	*MadPhylo: Madrid Workshop on Phylogenetics*	Royal Botanical Garden, Madrid, Spain
MAY 2019	*Applied Phylogenetics Workshop*	Bodega Bay, California, USA
DEC 2018	*Analysing Macroevolutionary Processes using RevBayes*	Université de Montpellier, France
AUG 2018	*MadPhylo: Madrid Workshop on Phylogenetics*	Royal Botanical Garden, Madrid, Spain
MAY 2018	*Analysing Macroevolutionary Processes using RevBayes*	University of Bristol, UK
APR 2018	*Estimating time-calibrated phylogenies and diversification rates*	MACN, Buenos Aires, Argentina
AUG 2017	*Bayesian phylogenetics using RevBayes*	NIMBioS, Knoxville, Tennessee, USA
MAR 2017	*Applied Phylogenetics Workshop*	Bodega Bay, California, USA
JAN 2017	*Introduction to Bayesian Phylogenetic inference using RevBayes*	SSB Meeting, Baton Rouge, Louisiana, USA
JULY 2016	*Bayesian Phylogenetic inference using RevBayes*	UC Davis, California, USA
MAR 2016	*Bayesian Phylogenetic inference using RevBayes*	UC Irvine, California, USA
SEPT 2015	*Bayesian Phylogenetic inference using RevBayes*	LSU, Louisiana, USA
APR 2015	*Bayesian Phylogenetic inference using RevBayes*	UC Berkeley, California, USA
MAR 2015	*Applied Phylogenetics Workshop*	Bodega Bay, California, USA
FEB 2015	*Molecular Evolution Workshop*	Cesky Krumlov, Czech Republic
AUG 2014	*Bayesian Phylogenetic inference using RevBayes*	NESCent, Durham, NC, USA
MAR 2013	*Bayesian Phylogenetic inference using RevBayes*	University of Groningen, The Netherlands
AUG 2012	*Virus Evolution and Molecular Epidemics*	Belgrade, Serbia

Student & Postdoc Supervision

Dec 2021 – Present	John Clarke, Postdoc (Humboldt Fellowship)
Feb 2020 – Present	Bjørn Tore Kopperud, PhD student
Nov 2019 – Present	Ronja Jessica Billenstein, PhD student
Nov 2019 – Present	Killian Smith, PhD student
Mar 2019 – Present	Luiza Fabreti, PhD student
Mar 2019 – Feb 2021	Allison Hsiang, Postdoc (now independent researcher at Stockholm University)
2009 – Present	supervision of several undergraduate and master-level student projects, including main advisor for 5 bachelor thesis projects and 3 master thesis projects

Visiting Students & Postdocs

postponed due to COVID19	Ignacio Quintero, Postdoc, Marie Curie Secondment, primary host: Hélène Morlon, Ecole Normale Supérieure in Paris
Sept 2019 – Oct 2019	Andrew F. Magee, PhD Student, University of Washington, Seattle, DAAD Fellowship

PUBLICATIONS

Submitted preprints:

[S1] **Höhna S**, Kopperud BT, Magee AF: ACDC: Analysis of Congruent Diversification Classes, *bioRxiv*, doi:10.1101/2022.01.12.476142.

[S2] Borges R, Boussau B, **Höhna S**, Pereira RJ and Carolin Kosiol C: Polymorphism-aware estimation of species trees and evolutionary forces from genomic sequences with RevBayes, *bioRxiv*, doi:10.1101/2021.12.15.472751.

[S3] **Höhna S**, Lower SE, Duchen P and Catalán A: A Time-calibrated Firefly (Coleoptera: Lampyridae) Phylogeny: Using Genomic Data for Divergence Time Estimation, *bioRxiv*, doi:10.1101/2021.11.19.469195.

[S4] Juravel K, Porras L, **Höhna S**, Pisani D and Wörheide G: Improved resolution of recalcitrant nodes in the animal phylogeny through the analysis of genome gene content and morphology, *bioRxiv*, doi:10.1101/2021.11.19.469253.

[S5] Magee AF, **Höhna S**: Impact of K-Pg Mass Extinction Event on Crocodylomorpha Inferred from Phylogeny of Extinct and Extant Taxa, *bioRxiv*, doi:10.1101/2021.01.14.426715.

[S6] **Höhna S**, Hsiang AY: Stepwise Bayesian Phylogenetic Inference, *bioRxiv*, doi:10.1101/2020.11.11.376459.

[S7] Catalán A, **Höhna S**, Lower SE, Duchen P: On the inference of a southern origin of the North American firefly Photinus pyralis, *bioRxiv*, doi:10.1101/851139.

[S8] **Höhna S**, Freyman WA, Nolen Z, Huelsenbeck JP, May MR and Moore BR: A Bayesian Approach for Estimating Branch-Specific Speciation and Extinction Rates, *bioRxiv*, doi:10.1101/463174.

Publications in peer reviewed journals (three most important indicated with *):

[J1] Barido-Sottani J, Justison JA, Borges R, Brown JM, Dismukes W, Petrucci BR, Fabreti L, **Höhna S**, Landis MJ, Lewis, PO, May MR, Mendes FK, Pett W, Redelings BD, Tribble CM, Wright AM, Zenil-Ferguson R and Heath TA: Lessons learned from organizing and teaching virtual phylogenetics workshops. *The Bulletin of the Society of Systematic Biologists*, 2022, in press.

[J2] Szöllősi GJ, **Höhna S**, Williams TA, Schrempf D, Daubin V, Boussau B: Relative time constraints improve molecular dating, *Systematic Biology*, 2022, in press, doi:10.1093/sysbio/syab084.

[J3] Palazzesi L, Hidalgo O, Barreda V. D, Forest F, and **Höhna S**: The rise of grasslands is linked to atmospheric CO_2 decline in the late paleogene. *Nature Communications*, 2022, 13, 293, doi:110.1038/s41467-021-27897-y.

[J4] Tribble CM, Freyman WA, Landis MJ, Lim JY, Barido-Sottani J, Kopperud BT, **Höhna S**, May MR: RevGadgets: an R Package for visualizing Bayesian phylogenetic analyses from RevBayes, *Methods in Ecology and Evolution*, 2022, 13:314–323, doi:10.1111/2041-210X.13750.

[J5] Fabreti L, **Höhna S**: Convergence assessment for bayesian phylogenetic analysis using mcmc simulation, *Methods in Ecology and Evolution*, 2022, 13:77–90, doi:10.1111/2041-210X.13727.

[J6] **Höhna S**, Landis MJ and Huelsenbeck JP: Parallel power posterior analyses for fast computation of Bayes factors in phylogenetics, *PeerJ*, 2021, 9:e12438, doi:10.7717/peerj.12438.

[J7] Orsi WD, Magritsch T, Vargas S, Coskun ÖK, Vuillemin A, **Höhna S**, Wörheide G, D'Hondt S, Shapiro BJ, Carini P: Genome evolution in bacteria isolated from million-year-old subseafloor sediment, *mBio*, 2021, 12:e01150-21, doi:10.1101/10.1128/mBio.01150-21.

[J8] Magee AF, **Höhna S**, Vasylyeva TI, Leaché AD, and Minin VN: Locally adaptive Bayesian birth-death model successfully detects slow and rapid rate shifts, *PLoS Comput Biol*, 2020, 16(10): e1007999, 2020, doi:10.1371/journal.pcbi.1007999.

[J9] Catalán A, Briscoe A and **Höhna S**: Drift and directional selection are the evolutionary forces driving gene expression divergence in eye and brain tissue of Heliconius butterflies, *Genetics*, 2019, 213 (2), 581–594, doi:10.1534/genetics.119.302493.

[J10] * Freyman WA and **Höhna S**: Stochastic Character Mapping of State-Dependent Diversification Reveals the Tempo of Evolutionary Decline in Self-Compatible Onagraceae Lineages, *Systematic Biology*, 2019, 68 (3), 505–519, doi:10.1093/sysbio/syy078.

[J11] Silvestro D, Tejedor MF, Serrano-Serrano ML, Loiseau O, Rossier V, Rolland J, Zizka A, **Höhna S**, Antonelli A and Salamin N: Early Arrival and Climatically-Linked Geographic Expansion of New World Monkeys from Tiny African Ancestors, *Systematic Biology*, 2019, 68 (1), 78–92, doi:10.1093/sysbio/syy046.

[J12] Condamine FL, Rolland J, **Höhna S**, Sperling FAH and Sanmartín I: Testing the Role of the Red Queen and Court Jester as Drivers of the Macroevolution of Apollo Butterflies, *Systematic Biology*, 2018, 67 (6), 940–964, doi:10.1093/sysbio/syy009.

[J13] Martin CH and **Höhna S**: New evidence for the recent divergence of Devil's Hole pupfish and the plausibility of elevated mutation rates in endangered taxa, *Molecular Ecology*, 2018, 27 (4), 831–838, doi:10.1111/mec.14404.

[J14] **Höhna S**, Coghill LM, Mount G, Thomson R and Brown JM: P^3: Phylogenetic Posterior Prediction in RevBayes, *Molecular Biology and Evolution*, 2018, 35 (4), 1028–1034, doi:10.1093/molbev/msx286.

[J15] Freyman WA and **Höhna S**: Cladogenetic and Anagenetic Models of Chromosome Number Evolution: a Bayesian Model Averaging Approach, *Systematic Biology*, 2018, 67 (2), 195–215 doi:10.1093/sysbio/syx065.

[J16] Martin CH☯, **Höhna S**☯, Crawford JE, Turner BJ, Richards EJ and Simons LH: The complex effects of demographic history on the estimation of substitution rate: concatenated analysis results in no more than 2-fold overestimation, *Proceedings of the Royal Society B*, 2017, 284: 20170537, doi:10.1098/rspb.2017.0537.

[J17] **Höhna S**, Landis MJ and Heath TA: Phylogenetic Inference using RevBayes, *Current Protocols in Bioinformatics*, 2017, 57:6.16.1-6.16.34, doi:10.1002/cpbi.22.

[J18] Moore BR, **Höhna S**, May MR, Rannala B and Huelsenbeck JP: Critically evaluating the theory and performance of Bayesian analysis of macroevolutionary mixtures. Proceedings of the National Academy of Sciences, 2016, 113, 9569–9574, doi:10.1073/pnas.1518659113.

[J19] * **Höhna S**, Landis MJ, Heath TA, Boussau B, Moore BR, Lartillot N, Huelsenbeck JP and Ronquist F: RevBayes: Bayesian Phylogenetic Inference Using Graphical Models and an Interactive Model-Specification Language, *Systematic Biology*, 2016, 65 (4), 726–736 doi:10.1093/sysbio/syw021.

[J20] May MR☯, **Höhna S**☯ and Moore BR: A Bayesian Approach for Detecting the Impact of Mass-Extinction Events on Molecular Phylogenies When Rates of Lineage Diversification May Vary, *Methods in Ecology and Evolution*, 2016, doi:10.1111/2041-210X.12563.

[J21] Conroy CR, Patton JL, Lim M, Phuong M, Parmenter B and **Höhna S**: Following the rivers: historical reconstruction of California voles (Microtus californicus, Muridae, Rodentia) in the deserts of eastern California, *Biological Journal of the Linnean Society*, 2016, 119, 80-98 doi:10.1111/bij.12808.

[J22] * **Höhna S**, May MR and Moore BR: `TESS`: An R package for efficiently simulating phylogenetic trees and performing Bayesian inference of lineage diversification rates, *Bioinformatics*, 2016, 32 (5): 789–791. doi:10.1093/bioinformatics/btv651

[J23] Janzen T, **Höhna S**, Etienne RS: Approximate Bayesian Computation of diversification rates from molecular phylogenies: introducing a new efficient summary statistic, the nLTT, *Methods in Ecology and Evolution*, 2015, 61 (1): 1–11. doi:10.1111/2041-210X.12350

[J24] **Höhna S**: The time-dependent reconstructed evolutionary process with a key-role for mass-extinction events, *Journal of Theoretical Biology* 2015, 380, 321–331. doi:10.1016/j.jtbi.2015.06.005

[J25] **Höhna S**, Heath TA, Boussau B, Landis MJ, Ronquist F and Huelsenbeck JP: Graphical Model Representation in Phylogenetics, *Systematic Biology*, 2014, 63 (5): 753–771. doi:10.1093/sysbio/syu039

[J26] **Höhna S**: Likelihood Inference of non-constant Diversification Rates with Incomplete Taxon Sampling, *PLoS One*, 2014; 9(1): e84184, doi:10.1371/journal.pone.0084184

[J27] **Höhna S**: Fast simulation of reconstructed phylogenies under global time-dependent birth-death processes, Bioinformatics, 2013, 29 (11), 1367–1374, doi:10.1093/bioinformatics/btt153

[J28] * Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, **Höhna S**, Larget B, Liu L, Suchard MA and Huelsenbeck JP: `MrBayes` 3.2: Efficient Bayesian MCMC Inference and Model Choice Across a Large Model Space, Systematic Biology, 2012, 61 (3): 539-542. doi: 10.1093/sysbio/sys029

[J29] **Höhna S** and Drummond AJ: Guided Tree Topology Proposals for Bayesian Phylogenetic Inference, Systematic Biology, 2012, 61 (1): 1-11. //doi:10.1093/sysbio/syr074

[J30] Alström P, **Höhna S**, Gelang M, Ericson P and Olsson U: Non-monophyly and intricate morphological evolution within the avian family Cettiidae revealed by multilocus analysis of a taxonomically densely sampled dataset, BMC Evolutionary Biology 11 (1), 352, doi:10.1186/1471-2148-11-352

[J31] * **Höhna S**, Stadler T, Ronquist F, Britton T: Inferring speciation and extinction rates under different sampling schemes, Molecular Biology and Evolution, 2011, 28(9): 2577-2589, doi:10.1093/molbev/msr095

Publications in conference proceedings:

[P1] **Höhna S**, Defoin-Platel M, Drummond AJ: Clock-constrained Tree Proposal Operators in Bayesian Phylogenetic Inference, 8th IEEE International Conference on BioInformatics and BioEngineering, Athens, September 2008

Scientific Presentations

Contributed Scientific Presentations at conferences and workshops:

Jan 2020	SSB Meetings, Gainesville, USA
May 2019	Phyloseminar (webcast)
Aug 2018	Evolution Meetings, Montpellier, France
Jul 2018	SMBE Meetings, Oklahoma, Japan
Jan 2017	SSB Meetings, Baton Rouge, USA
Jun 2015	Evolution Meetings, Sao Paolo, Brazil
Jun 2013	Evolution Meetings (Ernst Mayr Award Symposium), Snowbird, USA
Jun 2012	SMBE Meetings, Dublin, Ireland
Feb 2012	Phyloseminar (webcast)
Aug 2011	ESEB Meetings, Tübingen, Germany
Jun 2011	iEvoBio, Oklahoma, USA
Jun 2011	Evolution Meetings, Oklahoma, USA
Aug 2010	IMS, Gothenburg
Jul 2010	SMBE Meetings, Lyon, France
Jun 2010	Evolution Meetings (Ernst Mayr Award Symposium), Portland
Jan 2010	Workshop on Molecular Evolution, Cesky Krumlov
Oct 2008	BIBE, Athens
Mar 2008	NZCRSC, Christchurch

Invited Scientific Seminars at Universities:

Dec 2019	Natural History Museum, Oslo
Oct 2019	Swedish Museum of Natural History, Stockholm
May 2019	23andMe, Mountain View
Dec 2018	Université de Montpellier, Montpellier
Jul 2016	EES, Ludwig-Maximilians-University, Munich
Apr 2016	EEB, University of Rochester
Mar 2016	EDG, University of British Columbia
Nov 2015	LBBE, Universite Claude Bernard Lyon 1
Oct 2015	Department of Biological Sciences, Louisiana State University
Sep 2015	CTEG, UC Berkeley
Nov 2014	Biostatistics, UC Davis
Oct 2014	Center for Population Biology, UC Davis
Oct 2014	Neyman Seminar (Statistics), UC Berkeley
Sep 2014	CTEG, UC Berkeley
Mar 2014	Evolution, ETH Zurich
Jun 2013	LBBE, Universite Claude Bernard Lyon 1
Feb 2013	EBC, Uppsala University
Sep 2012	Department of Mathematics, Stockholm University
Aug 2011	RevBayes Workshop, UC Berkeley
Aug 2011	Bayesian Phylogenetic Inference Symposium, UC Berkeley
May 2011	Stockholm-Uppsala Mathematical Statistics Symposium, Uppsala
May 2010	Department of Mathematics, Stockholm University
Apr 2009	Department of Mathematics, Stockholm University
Mar 2009	Department of Computer Science, University of Auckland

Posters presented:

June 2012	Mathematical and Computational Evolutionary Biology, Montpellier
June 2009	ISMB/ECCB, Stockholm

RESEARCH GRANTS, SCHOLARSHIPS AND AWARDS

2022 – 2026	1.5 Mio €	ERC Starting Grant
2020 – 2023	145,500 €	DFG SPP-1991 TaxonOMICS (with Dr. Ana Catalán), Gepris
2019 – 2023	1.4 Mio €	Emmy Noether Program, DFG, Gepris
2019 – 2020	50,000 €	LMU Junior Research Fund
2019 – 2020	50,000 €	KONWIHR-Förderprogram (with Prof. Gert Wörheide)
2018	4,600 €	BayLat Research Collaboration Initiation Grant
2014 – 2017	219,000 $	Miller Fellowship, Miller Institute for Basic Research in Science, Berkeley
2015 – 2016	10,000 $	XSEDE Cluster Allocation
2013	20,000 SEK	The G.S. Magnusson Foundation, Travel Award, Swedish Royal Academy of Sciences
2012	2,400 €	Erasmus Study Scholarship
2012	20,000 SEK	The G.S. Magnusson Foundation, Travel Award, Swedish Royal Academy of Sciences
2011	20,000 SEK	The G.S. Magnusson Foundation, Travel Award, Swedish Royal Academy of Sciences
2010	20,000 SEK	The G.S. Magnusson Foundation, Travel Award, Swedish Royal Academy of Sciences
2010	2,000 €	Graduate Student Travel Award, Society of Molecular Biology and Evolution
2008	3,000 NZD	Faculty of Science Masters Award, University of Auckland, Auckland
2007	-	New Zealand Programming Champion

MISCELLANEOUS

Local Host: Applied Probability Society Conference, Stockholm, 2011.

Associate Editor: Systematic Biology

Reviewer for (Journals): Bayesian Analysis, BMC Evolutionary Biology, Bioinformatics, Evolution, Evolution Letters, Journal of Theoretical Biology, Methods in Ecology and Evolution, Molecular Biology and Evolution, Nature Communications, New Phytologist, PeerJ, PNAS, Proceedings of the Royal Society B, Systematic Biology

Reviewer for (Grants): Austrian Science Fund (FWF), Research Council KU Leuven, Society for Systematic Biology (SSB), Swiss National Science Foundation (SNF)