

CURRICULUM VITAE

RICHARD A. NEHER

ADDRESS

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PERSONAL DATA

Date of birth: 30th of August, 1979
Place of birth: Göttingen, Germany
Nationality: German

EDUCATION

2007/05	PhD in physics. Grade: Summa cum laude University of Munich Thesis advisor: Prof. Ulrich Gerland Thesis title: Dynamics aspects of DNA
2003/11	Diploma in physics. Grade: With distinction University of Munich Thesis advisor: Prof. Herbert Wagner Thesis title: Stochastic Geometry and Percolation
2000–2003	Graduate studies in physics at the University of Munich
07/2000	Prediploma in physics. University of Göttingen
1998–2000	Undergraduate studies in physics at the University of Göttingen

POSITIONS HELD

since 2017	Associate Professor, Biozentrum, University of Basel
2010-2017	Independent Max Planck Research Group Leader
2007-2010	Post-Doctoral Fellow at the Kavli Institute for Theoretical Physics, University of California, Santa Barbara, USA
2004-2007	PhD student at the University of Munich, Germany

FELLOWSHIPS & AWARDS

2017/02	OpenSciencePrize (Phase II winner – with Trevor Bedford)
2016/05	OpenSciencePrize (Phase I finalist – with Trevor Bedford)
2012/12	ARCHES award of the German Secretary of Science and Education
2011/03	ERC Starting Grant
2009/08	Harvey L. Karp Discovery Award
2007-2010	Post-Doctoral Fellow at the Kavli Institute for Theoretical Physics

PROFESSIONAL ACTIVITIES

2020-2022	Member of the Swiss National Science Taskforce (SARS-CoV-2)
summer 2017	Co-Director of the UCSB advanced school of Quantitative Biology
since 2015/09	Associate editor for Virus Evolution
since 2014/08	Reviewing Editor at eLife
summer 2014	Co-organizer of the <i>Drug resistance evolution</i> program a two month meeting at the interface of evolutionary biology, public health, and physics at KITP, UC Santa Barbara
2011-2015	Associate Editor, BMC Evolutionary Biology Reviewer for many journals including Science, Nature, PNAS, Bioinformatics, eLife, PRL, Genetics, MBE, PLoS Genetics, PLoS Pathogens, Trends in Ecology & Evolution Reviewer for grant agencies including ERC, ANR, SNF, HFSP, GIF, NWO.

OUTREACH ACTIVITIES (SINCE 2017)

since 2020	Numerous public lectures and media appearances on the SARS-CoV-2 pandemic
2019/02	Lectures to the general public on viral metagenomics
2018/10	Seminar on data sharing and open access in public health emergencies
2018/03	Lectures to the general public on influenza virus evolution
2018/03	Lecture/course on sequence bioinformatics at XLAB Göttingen.

PUBLICATIONS

See Google Scholar for up-to-date citation statistics.

<http://scholar.google.de/citations?user=dfvXOrMAAAAJ>

80. Estimation and worldwide monitoring of the effective reproductive number of SARS-CoV-2.

Jana S. Huisman, Jeremie Scire, Daniel C. Angst et al.

eLife, in press, 10.1101/2020.11.26.20239368, 2022

79. Evolution, geographic spreading, and demographic distribution of Enterovirus D68.

Emma B. Hodcroft, Robert Dyrdak, Cristina Andres et al.

PLOS Pathogens, 10.1371/journal.ppat.1010515, 2022

78. Nextclade: clade assignment, mutation calling and quality control for viral genomes.

Ivan Aksamentov, Cornelius Roemer, Emma B. Hodcroft and **Richard A. Neher**.

Journal of Open Source Software, 10.21105/joss.03773, 2021

77. SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse.

Frank Konings, Mark D. Perkins, Jens H. Kuhn et al.

Nature Microbiology, 10.1038/s41564-021-00932-w, 2021

76. Spread of a SARS-CoV-2 variant through Europe in the summer of 2020.

Emma B. Hodcroft, Moira Zuber, Sarah Nadeau et al.

Nature, 10.1038/s41586-021-03677-y, 2021

75. Molecular Epidemiology and Evolutionary Trajectory of Emerging Echovirus 30, Europe.

Kimberley S.M. Benschop, Eeva K. Broberg, Emma Hodcroft et al.

Emerging Infectious Diseases, 10.3201/eid2706.203096, 2021

74. Novel SARS-CoV-2 variants: the pandemics within the pandemic.

Erik Boehm, Ilona Kronig, **Richard A. Neher** et al.

Clinical Microbiology and Infection, 10.1016/j.cmi.2021.05.022, 2021

73. Investigate the origins of COVID-19.

Jesse D. Bloom, Yujia Alina Chan, Ralph S. Baric et al.

Science, 10.1126/science.abj0016, 2021

72. Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2.

Chantal B. F. Vogels, Mallery I. Breban, Isabel M. Ott et al.

PLOS Biology, 10.1371/journal.pbio.3001236, 2021

71. SARS-CoV-2 N501Y Introductions and Transmissions in Switzerland from Beginning of October 2020 to February 2021—Implementation of Swiss-Wide Diagnostic Screening and Whole Genome Sequencing.

Ana Rita Goncalves Cabecinhas, Tim Roloff, Madlen Stange et al.
Microorganisms, 10.3390/microorganisms9040677, 2021

70. Limited Predictability of Amino Acid Substitutions in Seasonal Influenza Viruses.

Pierre Barrat-Charlaix, John Huddleston, Trevor Bedford and **Richard A Neher**.
Molecular Biology and Evolution, 10.1093/molbev/msab065, 2021

69. Interactions between seasonal human coronaviruses and implications for the SARS-CoV-2 pandemic: A retrospective study in Stockholm, Sweden, 2009-2020.

Robert Dyrdak, Emma B. Hodcroft, Martina Wahlund, **Richard A. Neher** and Jan Albert.
Journal of Clinical Virology, 10.1016/j.jcv.2021.104754, 2021

68. Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens.

John Huddleston, James Hadfield, Thomas R. Sibley et al.
Journal of Open Source Software, 10.21105/joss.02906, 2021

67. Asynchrony between virus diversity and antibody selection limits influenza virus evolution.

Dylan H Morris, Velislava N Petrova, Fernando W Rossine et al.
eLife, 10.7554/eLife.62105, 2020

66. Cryptic transmission of SARS-CoV-2 in Washington state.

Trevor Bedford, Alexander L. Greninger, Pavitra Roychoudhury et al.
Science, 10.1126/science.abc0523, 2020

65. Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution.

John Huddleston, John R Barnes, Thomas Rowe et al.
eLife, 10.7554/eLife.60067, 2020

64. Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020.

Erik Alm, Eeva K. Broberg, Thomas Connor et al.
Eurosurveillance, 10.2807/1560-7917.ES.2020.25.32.2001410, 2020

63. Efficient inference, potential, and limitations of site-specific substitution models.

Vadim Puller, Pavel Sagulenko and **Richard A. Neher**.
Virus Evolution, 10.1093/ve/veaa066, 2020

62. Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable.

Carla Mavian, Sergei Kosakovsky Pond, Simone Marini et al.
Proceedings of the National Academy of Sciences, 10.1073/pnas.2007295117, 2020

61. Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States.

Joseph R. Fauver, Mary E. Petrone, Emma B. Hodcroft et al.
Cell, 10.1016/j.cell.2020.04.021, 2020

60. COVID-19 epidemic in Switzerland: on the importance of testing, contact tracing and isolation.

Marcel Salathe, Christian L. Althaus, Richard Neher et al.
Swiss Medical Weekly, 10.4414/smw.2020.20225, 2020

59. Potential impact of seasonal forcing on a SARS-CoV-2 pandemic.

Richard A. Neher, Robert Dyrdak, Valentin Druelle, Emma B. Hodcroft and Jan Albert.
Swiss Medical Weekly, 10.4414/smw.2020.20224, 2020

58. 2019-novel Coronavirus (2019-nCoV): estimating the case fatality rate – a word of caution.

Manuel Battegay, Richard Kuehl, Sarah Tschudin-Sutter et al.
Swiss Medical Weekly, 10.4414/smw.2020.20203, 2020

57. Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017–2018 influenza season.

Barney I. Potter, Rebecca Kondor, James Hadfield et al.
Virus Evolution, 10.1093/ve/vez046, 2019

56. Phylodynamic theory of persistence, extinction and speciation of rapidly adapting pathogens.

Le Yan, Richard A Neher and Boris I Shraiman.
eLife, 10.7554/eLife.44205, 2019

55. A global surveillance system for crop diseases.

M. Carvajal-Yepes, K. Cardwell, A. Nelson et al.
Science, 10.1126/science.aaw1572, 2019

54. Intra- and interpatient evolution of enterovirus D68 analyzed by whole-genome deep sequencing.

Robert Dyrdak, Monika Mastafa, Emma B. Hodcroft, Richard A. Neher and Jan Albert.
Virus Evolution, 10.1093/ve/vez007, 2019

53. Quantitative contribution of efflux to multi-drug resistance of clinical *Escherichia coli* and *Pseudomonas aeruginosa* strains.

Olivier Cunrath, Dominik M. Meinel, Pauline Maturana et al.
EBioMedicine, 10.1016/j.ebiom.2019.02.061, 2019

52. Evaluation of two workflows for whole genome sequencing-based typing of influenza A viruses.

Daniel Wuthrich, Daniela Lang, Nicola F. Muller et al.
Journal of Virological Methods, 10.1016/j.jviromet.2019.01.009, 2019

51. Improving the quality and workflow of bacterial genome sequencing and analysis: paving the way for a Switzerland-wide molecular epidemiological surveillance platform.

Adrian Egli, Dominique S. Blanc, Gilbert Greub et al.
Swiss Medical Weekly, 10.4414/smw.2018.14693, 2019

50. Real-Time Analysis and Visualization of Pathogen Sequence Data.

Richard A. Neher and Trevor Bedford.
Journal of Clinical Microbiology, 10.1128/JCM.00480-18, 2018

49. Colistin susceptibility test evaluation of multiple-resistance-level *Pseudomonas aeruginosa* isolates generated in a morbidostat device.

Mumina Javed, Viola Ueltzhoeffer, Maximilian Heinrich et al.
Journal of Antimicrobial Chemotherapy, 10.1093/jac/dky337, 2018

48. *Arabidopsis thaliana* and *Pseudomonas* Pathogens Exhibit Stable Associations over Evolutionary Timescales.

Talia L. Karasov, Juliana Almario, Claudia Friedemann et al.
Cell Host & Microbe, 10.1016/j.chom.2018.06.011, 2018

47. Nextstrain: real-time tracking of pathogen evolution.

James Hadfield, Colin Megill, Sidney M. Bell et al.
Bioinformatics, 10.1093/bioinformatics/bty407, 2018

46. Incomplete inhibition of HIV infection results in more HIV infected lymph node cells by reducing cell death.

Laurelle Jackson, Jessica Hunter, Sandile Cele et al.
eLife, 10.7554/eLife.30134, 2018

45. TreeTime: Maximum-likelihood phylodynamic analysis.

Pavel Sagulenko, Vadim Puller and Richard A. Neher.
Virus Evolution, 10.1093/ve/vex042, 2017

44. Predictive Modeling of Influenza Shows the Promise of Applied Evolutionary Biology.

Dylan H. Morris, Katelyn M. Gostic, Simone Pompei et al.
Trends in Microbiology, 10.1016/j.tim.2017.09.004, 2017

43. panX: pan-genome analysis and exploration.

Wei Ding, Franz Baumdicker and Richard A. Neher.
Nucleic Acids Research, 10.1093/nar/gkx977, 2017

42. Estimating time of HIV-1 infection from next-generation sequence diversity.

Vadim Puller, Richard Neher and Jan Albert.
PLOS Computational Biology, 10.1371/journal.pcbi.1005775, 2017

41. Rapid and consistent evolution of colistin resistance in XDR *Pseudomonas aeruginosa* during morbidostat culture.

Bianca Doesselmann, Matthias Willmann, Matthias Steglich et al.
Antimicrobial Agents and Chemotherapy, 10.1128/AAC.00043-17, 2017

- 40. Temporal dynamics of gene expression and histone marks at the Arabidopsis shoot meristem during flowering.**
Yuan You, Aneta Sawikowska, Manuela Neumann et al.
Nature Communications, 10.1038/ncomms15120, 2017
- 39. In vivo mutation rates and the landscape of fitness costs of HIV-1.**
Fabio Zanini, Vadim Puller, Johanna Brodin, Jan Albert and **Richard A. Neher**.
Virus Evol, 10.1093/ve/vex003, 2017
- 38. Error rates, PCR recombination, and sampling depth in HIV-1 Whole Genome Deep Sequencing..**
Fabio Zanini, Johanna Brodin, Jan Albert and **Richard A. Neher**.
Virus research, 10.1016/j.virusres.2016.12.009, 2016
- 37. Establishment and stability of the latent HIV-1 DNA reservoir..**
Johanna Brodin, Fabio Zanini, Lina Thebo et al.
eLife, 10.7554/eLife.18889, 2016
- 36. HIV Cell-to-Cell Spread Results in Earlier Onset of Viral Gene Expression by Multiple Infections per Cell..**
Mikael Boule, Thorsten G. Muller, Sabrina Dahling et al.
PLoS pathogens, 10.1371/journal.ppat.1005964, 2016
- 35. Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses..**
Richard A. Neher, Trevor Bedford, Rodney S. Daniels, Colin A. Russell and Boris I. Shraiman.
Proceedings of the National Academy of Sciences of the United States of America, 10.1073/pnas.1525578113, 2016
- 34. Revisiting adult neurogenesis and the role of erythropoietin for neuronal and oligodendroglial differentiation in the hippocampus..**
I. Hassouna, C. Ott, L. Wustefeld et al.
Molecular psychiatry, 10.1038/mp.2015.212, 2016
- 33. Population genomics of inpatient HIV-1 evolution..**
Fabio Zanini, Johanna Brodin, Lina Thebo et al.
eLife, 10.7554/eLife.11282, 2015
- 32. nextflu: real-time tracking of seasonal influenza virus evolution in humans..**
Richard A. Neher and Trevor Bedford.
Bioinformatics (Oxford, England), 10.1093/bioinformatics/btv381, 2015
- 31. Challenges with using primer IDs to improve accuracy of next generation sequencing..**
Johanna Brodin, Charlotte Hedskog, Alexander Heddini et al.
PloS one, 10.1371/journal.pone.0119123, 2015
- 30. Predicting evolution from the shape of genealogical trees..**
Richard A. Neher, Colin A. Russell and Boris I. Shraiman.
eLife, 10.7554/eLife.03568, 2014

- 29. Characterization of genetic diversity in the nematode *Pristionchus pacificus* from population-scale resequencing data..**
Christian Rodelsperger, **Richard A. Neher**, Andreas M. Weller et al.
Genetics, 10.1534/genetics.113.159855, 2014
- 28. Genetic diversity in the interference selection limit..**
Benjamin H. Good, Aleksandra M. Walczak, **Richard A. Neher** and Michael M. Desai.
PLoS genetics, 10.1371/journal.pgen.1004222, 2014
- 27. Genetic Draft, Selective Interference, and Population Genetics of Rapid Adaptation.**
Richard A. Neher.
Annual Review of Ecology, Evolution, and Systematics, 10.1146/annurev-ecolsys-110512-135920, 2013
- 26. Inferring HIV Escape Rates from Multi-Locus Genotype Data..**
Taylor A. Kessinger, Alan S. Perelson and **Richard A. Neher.**
Frontiers in immunology, 10.3389/fimmu.2013.00252, 2013
- 25. Coalescence and genetic diversity in sexual populations under selection..**
Richard A. Neher, Taylor A. Kessinger and Boris I. Shraiman.
Proceedings of the National Academy of Sciences of the United States of America, 10.1073/pnas.1309697110, 2013
- 24. Quantifying selection against synonymous mutations in HIV-1 env evolution..**
Fabio Zanini and **Richard A. Neher.**
Journal of virology, 10.1128/JVI.01529-13, 2013
- 23. Quantifying the range of a lipid phosphate signal in vivo..**
Amrita Mukherjee, **Richard A. Neher** and Andrew D. Renault.
Journal of cell science, 10.1242/jcs.136176, 2013
- 22. Emergence of clones in sexual populations.**
Richard A. Neher, Marija Vucelja, Mark Mezard and Boris I. Shraiman.
Journal of Statistical Mechanics: Theory and Experiment, 10.1088/1742-5468/2013/01/P01008, 2013
- 21. Mathematical modeling of escape of HIV from cytotoxic T lymphocyte responses..**
Vitaly V. Ganusov, **Richard A. Neher** and Alan S. Perelson.
Journal of statistical mechanics (Online), 10.1088/1742-5468/2013/01/P01010, 2013
- 20. Genealogies of rapidly adapting populations..**
Richard A. Neher and Oskar Hallatschek.
Proceedings of the National Academy of Sciences of the United States of America, 10.1073/pnas.1213113110, 2013
- 19. FFPopSim: an efficient forward simulation package for the evolution of large populations..**
Fabio Zanini and **Richard A. Neher.**
Bioinformatics (Oxford, England), 10.1093/bioinformatics/bts633, 2012

- 18. Dynamic mutation-selection balance as an evolutionary attractor..**
Sidhartha Goyal, Daniel J. Balick, Elizabeth R. Jerison et al.
Genetics, 10.1534/genetics.112.141291, 2012
- 17. Estimating the strength of selective sweeps from deep population diversity data..**
Philipp W. Messer and **Richard A. Neher**.
Genetics, 10.1534/genetics.112.138461, 2012
- 16. Target search on a dynamic DNA molecule..**
Thomas Schotz, **Richard A. Neher** and Ulrich Gerland.
Physical review. E, Statistical, nonlinear, and soft matter physics, 10.1103/PhysRevE.84.051911, 2011
- 15. Statistical genetics and evolution of quantitative traits.**
Richard A. Neher and Boris I. Shraiman.
Reviews of Modern Physics, 10.1103/RevModPhys.83.1283, 2011
- 14. Genetic draft and quasi-neutrality in large facultatively sexual populations..**
R. A. Neher and B. I. Shraiman.
Genetics, 10.1534/genetics.111.128876, 2011
- 13. Correlated evolution of nearby residues in Drosophilid proteins..**
Benjamin Callahan, **Richard A. Neher**, Doris Bachtrog, Peter Andolfatto and Boris I. Shraiman.
PLoS genetics, 10.1371/journal.pgen.1001315, 2011
- 12. Rate of adaptation in large sexual populations..**
R. A. Neher, B. I. Shraiman and D. S. Fisher.
Genetics, 10.1534/genetics.109.109009, 2010
- 11. Recombination rate and selection strength in HIV intra-patient evolution..**
Richard A. Neher and Thomas Leitner.
PLoS computational biology, 10.1371/journal.pcbi.1000660, 2010
- 10. Blind source separation techniques for the decomposition of multiply labeled fluorescence images..**
Richard A. Neher, Miso Mitkovski, Frank Kirchhoff et al.
Biophysical journal, 10.1016/j.bpj.2008.10.068, 2009
- 9. Competition between recombination and epistasis can cause a transition from allele to genotype selection..**
Richard A. Neher and Boris I. Shraiman.
Proceedings of the National Academy of Sciences of the United States of America, 10.1073/pnas.0812560106, 2009
- 8. Optimal flexibility for conformational transitions in macromolecules..**
Richard A. Neher, Wolfram Mobius, Erwin Frey and Ulrich Gerland.
Physical review letters, 10.1103/PhysRevLett.99.178101, 2007
- 7. Force-induced DNA slippage..**
Ferdinand Kuhner, Julia Morfill, **Richard A. Neher**, Kerstin Blank and Hermann E. Gaub.
Biophysical journal, 10.1529/biophysj.106.095836, 2007

- 6. Kinetic accessibility of buried DNA sites in nucleosomes..**
Wolfram Mobius, **Richard A. Neher** and Ulrich Gerland.
Physical review letters, 10.1103/PhysRevLett.97.208102, 2006

- 5. Intermediate phase in DNA melting..**
Richard A. Neher and Ulrich Gerland.
Physical review. E, Statistical, nonlinear, and soft matter physics, 10.1103/PhysRevE.73.030902, 2006

- 4. DNA as a programmable viscoelastic nanoelement..**
Richard A. Neher and Ulrich Gerland.
Biophysical journal, 10.1529/biophysj.105.068866, 2005

- 3. Applying spectral fingerprinting to the analysis of FRET images..**
Richard A. Neher and **Erwin Neher**.
Microscopy research and technique, 10.1002/jemt.20078, 2004

- 2. Dynamics of force-induced DNA slippage..**
Richard A. Neher and Ulrich Gerland.
Physical review letters, 10.1103/PhysRevLett.93.198102, 2004

- 1. Optimizing imaging parameters for the separation of multiple labels in a fluorescence image.**
R. Neher and **E. Neher**.
Journal of Microscopy, 10.1111/j.1365-2818.2004.01262.x, 2004

INVITED CONFERENCE CONTRIBUTIONS

- 2022/04 Quantitative Viral Dynamics Across Scales. PSI-Qlife, Paris.
- 2022/04 Biological systems – from first principles to data-driven modelling and back. Monte Verita, Ascona.
- 2021/09 Keynote speaker, BC2, Basel.
- 2020/07 ISMB 2020.
- 2020/04 COVID-19 Keynote speaker, TAGC 2020.
- 2020/01 Digital ID, Basel.
- 2019/03 American Physical Society March Meeting, Boston, USA.
- 2019/02 Lausanne Genomics Days 2019, Switzerland.
- 2019/01 HIV reservoirs and evolution, St Lucia, South Africa.
- 2018/10 International Conference on Clinical Metagenomics, Geneva.
- 2018/10 The Graduate Center, NYC. Symposium on the Physics of Biological Function.
- 2018/07 SMBE 2018, Yokohama. Intra-host evolution symposium.
- 2018/02 2nd International Meeting on Respiratory Pathogens, Singapore
- 2017/10 Rapporteur at the 27th Solvay Conference on Physics, Brussels
- 2017/10 DFG Priority Program 1590 Probabilistic Structures in Evolution, Freiburg
- 2017/10 EPFL Computational Biology Symposium 2017, Lausanne
- 2017/10 PCCMI 2017, Boston
- 2017/10 Session keynote at the 2nd ASM Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines, Washington DC
- 2017/09 Keynote at German Conference on Bioinformatics, Tübingen
- 2017/09 Swiss Society of Microbiology, Basel
- 2017/09 Symposium on Open-Data at EMBO BaselLife, Basel
- 2017/02 Keynote at the ‘Young Compare’ meeting, Rotterdam
- 2016/07 “Exploring Predictive Models for Improving Influenza Vaccine Virus Selection”, Princeton
- 2016/07 “Statistical-physics methods in biology and computer science”, Paris
- 2016/06 Keynote at Mathematical and Computational, Evolutionary Biology Conference, Montepellier
- 2015/07 “Forecasting Evolution”. Instituto Gulbenkian, Lisbon
- 2015/06 “Probability and Biological Evolution”. CIRM, Luminy
- 2015/05 “Next generation sequencing of viruses”. Institute Pasteur, Paris

2014/06	Heraeus-Seminar on “Mechanisms, Strategies, and Evolution of Microbial Systems”, Bad Honnef, Germany
2014/05	Molecular Frontiers in Ecology and Evolution, Tübingen, Germany
2014/02	Physics of Evolution, Regulation and Signaling, Munich, Germany
2013/08	European Society for Evolutionary Biology, Lisbon, Portugal
2012/12	KITP program on “Quantitative Immunology”, Santa Barbara, CA, USA
2012/05	Selection in Population Genetics, Radcliffe Institute, Harvard University, MA, USA
2012/02	Cologne Spring Meeting (Satellite meeting on viral evolution)
2011/12	Population Genetics, ENS, Paris, France
2011/09	Mind the Gap 2011, Cologne, Germany
2011/03	Kavli Future Conference: Evolution of Novelty, Aspen, CO, USA
2011/03	KITP program on “Viral and Microbial Evolution”, Santa Barbara, CA, USA
2010/03	American Physical Society Annual Meeting: Symposium on evolutionary dynamics, Portland, OR, USA
2010/01	Aspen Center for Physics: Populations, Evolution, and Physics, Aspen, CO, USA
2009/06	DIMACS Workshop: Identifying genetic signatures for the evolution of complex phenotypes, Rutgers, USA

INVITED TALKS & SEMINARS (SELECTION)

2022/05	Colloquium, Department of Physics, University of Cologne.
2022/05	Mössbauer Colloquium, MPI for medical research, Heidelberg.
2021/06	Physics of Life Seminar series, EPFL, Lausanne.
2020/10	Center for studies in Physics and Biology, Rockefeller University, NYC.
2019/03	DBMI Seminar. Harvard Medical School, Boston, USA.
2018/09	Colloquium, Paul-Ehrlich Institute, Langen.
2017/06	Robert Koch Colloquium ”Digital Epidemiology”, RKI, Berlin
2017/05	Bethe Colloquium, Bonn.
2017/04	Simons Foundation Lecture, New York.
2016/05	Cambridge University
2016/02	MIT, Boston, Biophysics Seminar Series
2016/01	KRITH, Durban, South Africa, Biophysics Seminar Series
2015/11	CIDID Seminar, Fred Hutchinson Cancer Research Center, Seattle

2015/02 Pacific Center for Emerging Infectious Diseases. University of Hawai'i
2014/11 CeNS Colloquium, LMU Munich, Germany
2014/04 BioQuant Seminar, Heidelberg, Germany
2013/12 Virological Colloquium, Medical School Tübingen, Germany
2013/05 Seminar at the Institute for Molecular Virology, University Ulm, Germany
2012/01 Transregio Seminar, University Duisburg-Essen, Germany
2011/04 Colloquium, Max-Planck Institute for Dynamics and Self-Organization, Göttingen, Germany
2010/07 T6 Seminar, Los Alamos National Lab, Los Alamos, NM, USA
2009/07 SFB 680 Colloquium, Institute for Genetics, University of Cologne, Germany