Ralf Andreas Bundschuh

Contact:

The Ohio State University
191 West Woodruff Avenue
Columbus, OH 43210-1117

Tel: +1 (614) 688-3978
Fax: +1 (614) 292-7557
E-Mail: bundschuh@mps.ohio-state.edu
WWW: http://bioserv.mps.ohio-state.edu/~rbund

Education and academic appointments:

2010–present : **Professor**, Department of Physics, The Ohio State University
2012–present : **Courtesy Professor**, Division of Hematology, Department of Internal Medicine, The Ohio State University
2010–present : **Courtesy Professor**, Department of Chemistry&Biochemistry, The Ohio State University
2006–2010 : **Associate Professor**, Department of Physics, The Ohio State University
2008–2010 : **Courtesy Associate Professor**, Department of Chemistry&Biochemistry, The Ohio State University
2008–2009 : **Visiting Professor**, Institute for theoretical Physics, University of Cologne
2001–2006 : **Assistant Professor**, Department of Physics, The Ohio State University
1997–2001 : **Postdoc**, Physics Department, University of California at San Diego
Supervisor: *T. Hwa*
1996–1997 : **Postdoc**, Institute for theoretical Physics, University of Cologne
Supervisor: *M. Zirnbauer*
1994–1996 : **PhD**, U. of Potsdam and Max–Planck–Institute of Colloids and Interfaces
Supervisor: *R. Lipowksy* Grade: *magna cum laude*
Title: Critical behavior of strings and semi-flexible polymers
1993–1994 : **Research assistant**, Jülich research center (Forschungszentrum Jülich)
Supervisor: *R. Lipowsky*
1993 : **Diplom** (MSc) in physics, University of Cologne
Supervisor: *M. Zirnbauer* Grade: *A with honor*
Title: Ensemble averaging in disordered mesoscopic conductors:
superanalytic coordinate systems and their boundary terms
1989 : **Vordiplom** (BA) in mathematics, University of Cologne (grade: *A*)
1989 : **Vordiplom** (BA) in physics, University of Cologne (grade: *A*)
1987–1993 : Studies of physics and mathematics, University of Cologne

Professional activities:

- Co-director of the Interdisciplinary Biophysics Graduate Program at OSU since 2006
- Chair of the scientific advisory board of the arXiv preprint archive 2013–2015
- Chair of the subject advisory commitee of the arXiv/q-bio preprint archive since 2009
- Associate editor for Physical Review E
- Reviewer for over 20 different journals including Science, Nature, PNAS, Physical Review Letters, Nucleic Acids Research, and Bioinformatics
- frequent member of NSF review panels and ad hoc member of NIH study section
- organizer of several workshops: Rustbelt RNA meeting, OSU workshop on membrane Biophysics, Mathematical Biosciences Institute workshop on gene regulatory networks

Awards:

2015 : ISCB senior member
2013 : Fellow of the American Physical Society
2006,2009,2013: Dr. Elizabeth L. Gross award for faculty excellence
2000 : Best paper by young scientist award at the Fourth Annual International Conference on Computational Molecular Biology (RECOMB 2000)
1999 : Outstanding paper award at the Seventh International Conference on Intelligent Systems for Molecular Biology, Heidelberg
1997 – 1999 : Fellow of the DAAD (German Academic Exchange Service)
1990 – 1993 : Fellow of the Studienstiftung des Deutschen Volkes

Teaching experience:

- Undergraduate freshmen honors, thermal physics, theoretical mechanics, and introduction to biophysics
- Graduate statistical mechanics and classical mechanics
- Graduate mentoring seminar (research ethics, preparation of presentations and fellowship proposals, navigating the academic environment)
- Contributions on Computational Biology and Bioinformatics to various graduate courses
- Supervision of numerous graduate and undergraduate students

Peer-reviewed publications:

(including peer-reviewed Bioinformatics conference proceedings)

103. D.L. Kiss, W.D. Baez, K. Huebner, R. Bundschuh, and D.R. Schoenberg, *Loss of fragile histidine triad Fhit protein expression alters the translation of cancer-associated mRNAs.* BMC Res. Notes 11, 178 (2018).

102. J.A. Killian, T.M. Topiwala, A.R. Pelletier, D.E. Frankhouser, P.S. Yan, and R. Bundschuh, *FuSpot: a web-based tool for visual evaluation of fusion candidates.* BMC Genomics 19, 139 (2018).

101. D.L. Kiss, W. Baez, K. Huebner, R. Bundschuh, and D.R. Schoenberg, *Impact of FHIT loss on the translation of cancer-associated mRNAs.* Mol. Cancer 16, 179 (2017).

100. D. Papaioannou, D. Nicolet, S. Volinia, K. Mrózek, P. Yan, R. Bundschuh, A.J. Carroll, J. Kohlschmidt, W. Blum, B.L. Powell, G.L. Uy, J.E. Kolitz, E.S. Wang, A.-K. Eisfeld, S.J. Orwick, D.M. Lucas, M.A. Caligiuri, R.M. Stone, J.C. Byrd, R. Garzon, and C.D. Bloomfield, *Prognostic and biologic significance of long non-coding RNA profiling in younger adults with cytogenetically normal acute myeloid leukemia.* Haematologica 102, 1391–1400 (2017).

99. C.J. Walker, A.-K. Eisfeld, L.K. Genutis, M. Bainazar, J. Kohlschmidt, K. Mrózek, A.J. Carroll, J.E. Kolitz, B.L. Powell, E.S. Wang, R.M. Stone, R. Bundschuh, A. de la Chapelle, and C.D. Bloomfield, *No evidence for microsatellite instability in acute myeloid leukemia.* Leukemia 31, 1474–1476 (2017).

98. D.L. Kiss, C.E. Waters, I.M. Ouda, J.C. Saldivar, J.R. Karras, Z.A. Amin, S. Mahrous, T. Druck, R. Bundschuh, D.R. Schoenberg, and K. Huebner, *Identification of Fhit as a post-transcriptional effector of Thymidine Kinase 1 expression.* Biochim. Biophys. Acta 1860, 374–382 (2017).

97. M.P. Trimarchi, P. Yan, J. Groden, R. Bundschuh, and P.J. Goodfellow, *Identification of endometrial cancer methylation features using combined methylation analysis methods.* PLoS ONE 12, e0173242 (2017).

96. B. Moreland, K. Oman, J. Curfman, P. Yan, and R. Bundschuh, *Methyl-CpG/MBD2 Interaction Requires Minimum Separation and Exhibits Minimal Sequence Specificity.* Biophys. J. 111, 2551–2561 (2016).

95. K.E. Yoder and R. Bundschuh, *Host Double Strand Break Repair Generates HIV-1 Strains Resistant to CRISPR/Cas9.* Sci. Rep. 6, 29530 (2016).

94. C.J. Walker, M.A. Miranda, M.J. OHern, J.S. Blachly, C.L. Moyer, J. Ivanovich, K.W. Kroll, A.-K. Eisfeld, C.E. Sapp, D.G. Mutch, D.E. Cohn, R. Bundschuh, and P.J. Goodfellow, *MonoSeq Variant Caller Reveals Novel Mononucleotide Run Indel Mutations in Tumors with Defective DNA Mismatch Repair.* Hum. Mutat. 37, 1004–1012 (2016).

93. S. Liyanarachchi, W. Li, P. Yan, R. Bundschuh, P. Brock, L. Senter, M.D. Ringel, A. de la Chapelle, and H. He, *Genome-wide expression screening discloses long noncoding RNAs involved in thyroid carcinogenesis.* J. Clin. Endocrinol. Metab., jc20161991 (2016).

92. D.L. Kiss, K.M. Oman, J.A. Dougherty, C. Mukherjee, R. Bundschuh, and D.R. Schoenberg, *Cap homeostasis is independent of poly(A) tail length.* Nucleic Acids Res. 44, 394–314 (2016).

91. D.N. Ayyala, D.E. Frankhouser, J.O. Ganbat, G. Marcucci, R. Bundschuh, P. Yan, and S. Lin, *Statistical Methods for Detecting Differentially Methylated Regions Based on MethylCap-Seq Data.* Brief. Bioinformatics 17, 926–937 (2016).

90. P. Schaap, I. Barrantes, P. Minx, N. Sasaki, R.W. Anderson, M. Bénard, K.K. Biggar, N.E. Buchler, R. Bundschuh, X. Chen, C. Fronick, L. Fulton, G. Golderer, N. Jahn, V. Knoop, L.F. Landweber, C. Maric, D. Miller, A.A. Noegel, R. Peace, G. Pierron, T. Sasaki, M. Schallenberg-Rüdinger, M. Schleicher, R. Singh, T. Spaller, K.B. Storey, T. Suzuki, C. Tomlinson, J.J. Tyson, W.C. Warren, E.R. Werner, G. Werner-Felmayer, R.K. Wilson, T. Winckler, J.M. Gott, G. Glöckner, and W. Marwan, *The Physarum polycephalum Genome Reveals Extensive Use of Prokaryotic Two-Component and Metazoan-Type Tyrosine Kinase Signaling.* Genome Biol. Evol. 8, 109–125 (2015).

89. C.J. Walker, M.A. Miranda, M.J. O'Hern, J.P. McElroy, K.R. Coombes, R. Bundschuh, D.E. Cohn, D.G. Mutch, and P.J. Goodfellow, *Patterns of CTCF and ZFHX3 Mutation and Associated Outcomes in Endometrial Cancer.* J. Natl. Cancer Inst. 107, djv249 (2015).

88. D.L. Kiss, K. Oman, R. Bundschuh, and D.R. Schoenberg, *Uncapped 5' ends of mRNAs targeted by cytoplasmic capping map to the vicinity of downstream CAGE tags.* FEBS Lett. 589, 279-284 (2015).

87. C. Niederwieser, J. Kohlschmidt, S. Volinia, S.P. Whitman, K.H. Metzeler, A.K. Eisfeld, K. Maharry, P. Yan, D. Frankhouser, H. Becker, S. Schwind, A.J. Carroll, D. Nicolet, J.H. Mendler, J.P. Curfman, Y.Z. Wu, M.R. Baer, B.L. Powell, J.E. Kolitz, J.O. Moore, T.H. Carter, R. Bundschuh, R.A. Larson, R.M. Stone, K. Mrzek, G. Marcucci, and C.D. Bloomfield, *Prognostic and biologic significance of DNMT3B expression in older patients with cytogenetically normal primary acute myeloid leukemia* Leukemia 29, 567-75 (2015).

86. Y.-H. Lin and R. Bundschuh, *RNA structure generates natural cooperativity between single-stranded RNA binding proteins targeting 5' and 3'UTRs* Nucleic Acids Res. 43, 1160-1160 (2015).

85. R. Balakrishnan, K. Oman, S. Shoji, R. Bundschuh, and K. Fredrick, *The conserved GTPase LepA contributes mainly to translation initiation in Escherichia coli.* Nucleic Acids Res. 42, 13370-13383 (2014).

84. D.E. Frankhouser, M. Murphy, J.S. Blachly, J. Park, M.W. Zoller, J. Ganbat, J. Curfman, J.C. Byrd, S. Lin, G. Marcucci, P. Yan, and R. Bundschuh, *PrEMeR-CG: Inferring Nucleotide Level DNA Methylation Values from MethylCap-Seq Data.* Bioinformatics 30, 3567-3574 (2014).

83. C. Niederwieser, J. Kohlschmidt, S. Volinia, S.P. Whitman, K.H. Metzeler, A.K. Eisfeld, K. Maharry, P. Yan, D. Frankhouser, H. Becker, S. Schwind, A.J. Carroll, D. Nicolet, J.H. Mendler, J.P. Curfman, Y.Z. Wu, M.R. Baer, B.L. Powell, J.E. Kolitz, J. Moore, T.H. Carter, R. Bundschuh, R.A. Larson, R.M. Stone, K. Mrózek, G. Marcucci, and C.D. Bloomfield, *Prognostic and biologic significance of DNMT3B expression in older patients with cytogenetically normal primary acute myeloid leukemia.* Leukemia doi:10.1038/leu.2014.267 [Epub ahead of print].

82. K.W. Kroll, N.E. Mokaram, A.R. Pelletier, D.E. Frankhouser, M.S. Westphal, P.A. Stump, C.L. Stump, R. Bundschuh, J.S. Blachly, and P. Yan, *Quality Control for RNA-Seq (QuaCRS): An Integrated Quality Control Pipeline.* Cancer Inform. 13(Suppl 3), 7-14 (2014).

81. R. Bundschuh, *Unified approach to partition functions of RNA secondary structures.* J Math. Biol. 69, 1129-1150 (2014).

80. C. Chen and R. Bundschuh, *Quantitative models for accelerated protein dissociation from nucleosomal DNA.* Nucleic Acids Res. 42, 9753-60 (2014).

79. B.R. Madina, V. Kumar, R. Metz, B.H.M. Mooers, R. Bundschuh, and J. Cruz-Reyes, *Native mitochondrial RNA-binding complexes in kinetoplastid RNA editing differ in guide RNA composition.* RNA 20, 1142-52 (2014).

78. G.R. Bennett, R. Peters, X.-H. Wang, J. Hanne, R.W. Sobol, R. Bundschuh, R. Fishel, and K.E. Yoder, *Repair of Oxidative DNA Base Damage in the Host Genome Influences the HIV Integration Site Sequence Preference.* PLoS ONE 9, e103164 (2014).

77. G. Marcucci, P. Yan, K. Maharry, D. Frankhouser, D. Nicolet, K.H. Metzeler, J. Kohlschmidt, K. Mrózek, Y.-Z. Wu, D. Bucci, J.P. Curfman, S.P. Whitman, A.-K. Eisfeld, J.H. Mendler, S. Schwind, H. Becker, C. Bär, A.J. Carroll, M.R. Baer, M. Wetzler, T.H. Carter, B.L. Powell, J.E. Kolitz, J.C. Byrd, C. Plass, R. Garzon, M.A. Caligiuri, R.M. Stone, S. Volinia, R. Bundschuh, and C.D. Bloomfield, *Epigenetics meets genetics in acute myeloid leukemia: clinical impact of a novel seven-gene score.* J. Clin. Oncol. 32, 548-56 (2014).

76. R.A. Fodah, J.B. Scott, H.-H. Tam, P. Yan, T.L. Pfeffer, R. Bundschuh, and J.M. Warawa *Correlation of Klebsiella pneumoniae Comparative Genetic Analyses with Virulence Profiles in a Murine Respiratory Disease Model.* PLoS ONE 9, e107394 (2014).

75. K.M. Bernot, R.F. Siebenaler, S.P. Whitman, N.A. Zorko, G.G. Marcucci, R. Santhanam, E.H. Ahmed, M. Ngangana, K.K. McConnell, J.S. Nemer, D.L. Brook, S.K. Kulp, C.S. Chen, D. Frankhouser, P. Yan, R. Bundschuh, X. Zhang, A.M. Dorrance, K.E. Dickerson, D. Jarjoura, W. Blum, G. Marcucci, and M.A. Caligiuri, *Toward personalized therapy in AML: in vivo benefit of targeting aberrant epigenetics in MLL-PTD-associated AML.* Leukemia 27, 2379-82 (2013).

74. Y.-H. Lin and R. Bundschuh, *Interplay between single-stranded binding proteins on RNA secondary structure*, Phys Rev E 88, 052707 (2013).

73. M. Trimarchi, M. Murphy, D. Frankhouser, B. Rodriguez, J. Curfman, G. Marcucci, P. Yan, and R. Bundschuh, *Enrichment-based DNA methylation analysis using next-generation sequencing: sample exclusion, estimating changes in global methylation, and the contribution of replicate lanes*, BMC Genomics 13(Suppl 8), S6 (2012).

72. C. Chen and R. Bundschuh, *Systematic investigation of insertional and deletional RNA-DNA differences in the human transcriptome*, BMC Genomics 13, 616 (2012).

71. B. Rodriguez, H.-H. Tam, D. Frankhouser, M. Trimarchi, M. Murphy, C. Kuo, D. Parikh, B. Ball, J. Curfman, W. Blum, G. Marcucci, P. Yan, and R. Bundschuh, *Methods for high-throughput MethylCap-Seq data analysis*, BMC Genomics 13(Suppl 6), S14 (2012).

70. J.A. North, J.C. Shimko, S. Javaid, A.M. Mooney, M.A. Shoffner, S.D. Rose, R. Bundschuh, R. Fishel, J.J. Ottesen, and M.G. Poirier. *Regulation of the nucleosome unwrapping rate controls DNA accessibility*, Nucleic Acids Res. 40, 10215-27 (2012).

69. C. Mukherjee, D.P. Patil, B.A. Kennedy, B. Bakthavachalu, R. Bundschuh, and D.R. Schoenberg. *Identification of cytoplasmic capping targets reveals a role for cap homeostasis in translation and mRNA stability*, Cell Rep. 2, 674-84 (2012).

68. P. Yan, D. Frankhouser, M. Murphy, H.-H. Tam, B. Rodriguez, J. Curfman, M. Trimarchi, S. Geyer, Y.-Z. Wu, S.P. Whitman, K. Metzeler, A. Walker, R. Klisovic, S. Jacob, M.R. Grever, J.C. Byrd, C.D. Bloomfield, R. Garzon, W. Blum, M.A. Caligiuri, R. Bundschuh, and G. Marcucci. *Genome-wide methylation profiling in decitabine-treated patients with acute myeloid leukemia*, Blood 120, 2466-74 (2012).

67. D.M. Bornman, M.E. Hester, J.M. Schuetter, M.D. Kasoji, A. Minard-Smith, C.A. Barden, S.C. Nelson, G.D. Godbold, C.H. Baker, B. Yang, J.E. Walther, I.E. Tornes, P.S. Yan, B. Rodriguez, R. Bundschuh, M.L. Dickens, B.A. Young, and S.A. Faith. *Short-read, high-throughput sequencing technology for STR genotyping*, BioTechniques 1-6 (2012).

66. M.P. Trimarchi, M. Murphy, D. Frankhouser, B.A.T. Rodrigues, J. Curfman, G. Marcucci, P. Yan, and R. Bundschuh. *Next-generation Sequencing-based Analysis of DNA Methylation using MethylCap-seq: Sample Exclusion, Validation, and the Contribution of Replicate Lanes*, proceedings of the international conference on intelligent Biology and Medicine (ICIBM 2012).

65. R. Amunugama, Y. He, S. Willcox, R.A. Forties, K.-S. Shim, R. Bundschuh, Y. Luo, J. Griffith, and R. Fishel, *The RAD51 ATP Cap Regulates Nucleoprotein Filament Stability*, Journal Biol. Chem. **287** 8724–8736 (2012).

64. C. Chen, D. Frankhouser, and R. Bundschuh, *Comparison of insertional RNA editing in Myxomycetes*, PLoS Comp. Biol. **8**, e1002400 (2012).

63. B. Rodriguez, H.-H. Tam, D. Frankhouser, M. Trimarchi, M. Murphy, C. Kuo, D. Parikh, B. Ball, J. Curfman, W. Blum, G. Marcucci, P. Yan, and R. Bundschuh, *A Scalable, Flexible Workflow for MethylCap-Sequencing Data Analysis*, proceedings of the IEEE International Workshop on Genomic Signal Processing and Statistics (2011).

62. R.A. Forties, J. North, S. Javaid, O. Tabbaa, R. Fishel, M. Poirier, and R. Bundschuh, *A quantitative model of nucleosome dynamics*, Nucleic Acids Res. **39**, 8306–8313 (2011).

61. R. Bundschuh, J. Altmüller, C. Becker, P. Nürnberg, and J. Gott, *Complete characterization of the edited transcriptome of the mitochondrion of Physarum polycephalum using deep sequencing of RNA*, Nucleic Acids Res. **39**, 6044–6055 (2011).

60. Y. Li, N. Chia, M. Lauria, and R. Bundschuh, *A performance enhanced PSI-BLAST based on hybrid alignment*, Bioinformatics **27**, 31–37 (2011).

59. R. Bundschuh and P. Bundschuh, *Distribution of Fibonacci and Lucas numbers modulo* 3^k, Fibonacci Quart. **49**, 201–210 (2011).

58. R.A. Forties and R. Bundschuh, *Modeling the interplay of single-stranded binding proteins and nucleic acid secondary structure*, Bioinformatics **26**, 61–67 (2010).

57. P. Bundschuh and R. Bundschuh, *The sequence of Lucas numbers is not stable modulo 2 and 5*, Uniform Dist. Theory **5**, 113–130 (2010).

56. R.A. Forties, R. Bundschuh, and M.G. Poirier, *The flexibility of locally melted DNA*, Nucleic Acids Res. **37**, 4580–4586 (2009).

55. S. Shoji, N. Abdi, R. Bundschuh, and K. Fredrick, *Contribution of ribosomal residues to P-site tRNA binding*, Nucleic Acids Res. **37**, 4033–4042 (2009).

54. M.M. Lee, M. Chan, and R. Bundschuh, *SIB-BLAST: a web server for improved delineation of true and false positives in PSI-BLAST searches*, Nucleic Acids Res. **37**, W53–W56 (2009).

53. M. McCauley, R. Forties, U. Gerland, and R. Bundschuh, *Anomalous scaling in nanopore translocation of structured heteropolymers*, Physical biology **6**, 036006 (2009).

52. C. Beargie, T. Liu, M. Corriveau, H.Y. Lee, J. Gott, and R. Bundschuh, *Genome annotation in the presence of RNA editing*, Bioinformatics **24**, 2571–2578 (2008).

51. M. Lee, M. Chan, and R. Bundschuh, *Simple is beautiful: a straightforward approach to improve the delineation of true and false positives in PSI-BLAST searches*, Bioinformatics **24**, 1339–1343 (2008).

50. M. Djordjevich and R. Bundschuh, *Formation of the Open Complex by Bacterial RNA Polymerase — a Quantitative Model*, Biophys. J. **94**, 4233–4248 (2008).

49. R. Bundschuh and R. Bruinsma, *Melting of Branched RNA Molecules*, Phys. Rev. Lett. **100**, 148101/1–148101/4 (2008).

48. M. Lee, R. Bundschuh, and M. Chan, *Distant homology detection using a LEngth and STructure-based sequence Alignment Tool (LESTAT)*, Proteins **71**, 1409–1419 (2008).

47. A. Itaya, R. Bundschuh, A.J. Archual, J.-G. Joung, Z. Fei, X. Dai, P.X. Zhao, Y. Tang, R.S. Nelson, and B. Ding, *Small RNAs in tomato fruit and leaf development*, Biochim. Biophy. Act. - Gene Reg. Mech. **1779**, 99–107 (2008).

46. R. Bundschuh, *Computational approaches to insertional RNA editing*, Meth. Enzym. **424**, 173–195 (2007).

45. F. Habib, A.D. Johnson, R. Bundschuh, and D. Janies, *Large scale genotype-phenotype correlation analysis based on phylogenetic trees*, Bioinformatics **23**, 785–788 (2007).

44. A. Itaya, X. Zhong, R. Bundschuh, Y. Qi, Y.Wang, R. Takeda, A.R. Harris, C. Molina, R.S. Nelson, and B. Ding, *A structured viroid RNA is substrate for dicer-like cleavage to produce biologically active small RNAs but is resistant to RISC-mediated degradation*, J. Virol. **91**, 2980–2994 (2007).

43. P. Messer, R. Bundschuh, M. Vingron, and P. Arndt, *Alignment Statistics for Long-Range Correlated Genomic Sequences*, Proceedings of the Tenth Annual International Conference on Computational Molecular Biology (RECOMB2006) (Lecture Notes in Computer Science **3909**), (Springer, Berlin, 2006), 426–440 (2006).

42. R. Bundschuh and U. Gerland, *A puzzle in DNA biophysics*, Europ. Phys. J. E **19**, 347–350 (2006).

41. R. Bundschuh and U. Gerland, *Dynamics of intramolecular recognition: Base-pairing in DNA/ RNA near and far from equilibrium*, Europ. Phys. J. E **19**, 319–330 (2006).

40. V. Guttal and R. Bundschuh, *Model for folding and aggregation in RNA secondary structures*, Phys. Rev. Lett. **96**, 018105/1–018105/4 (2006).

39. R. Bundschuh and U. Gerland, *Coupled dynamics of RNA folding and nanopore translocation*, Phys. Rev. Lett. **95**, 208104/1–208104/4 (2005).

38. J.M. Gott, N. Parimi, and R. Bundschuh, *Discovery of new genes and deletion editing in Physarum mitochondria enabled by a novel algorithm for finding edited mRNAs*, Nucleic Acids Res. **33**, 5063–5072 (2005).

37. T. Liu and R. Bundschuh, *Quantification of the differences between quenched and annealed averaging for RNA secondary structures*, Phys. Rev. E **72**, 061905/1–061905/9 (2005).

36. N. Chia and R. Bundschuh, *Numerical Method for Assessing the Universality of the Scaling Function for a Multi-Particle Discrete Time Asymmetric Exclusion Process*, Phys. Rev. E **72**, 051102/1–051102/7 (2005).

35. Y. Li, M. Lauria, and R. Bundschuh, *Suboptimal Alignments Improve the Detection of Weak Homologs in Sequence Database Searches*, Proceedings of BIBE05, 153–160 (2005).

34. F. Habib and R. Bundschuh, *Modeling DNA unzipping in the presence of bound proteins*, Phys. Rev. E **72**, 031906/1–031906/6 (2005).

33. T. Liu and R. Bundschuh, *A model for codon position bias in RNA editing*, Phys. Rev. Lett. **95**, 088101/1–088101/4 (2005).

32. N. Chia and R. Bundschuh, *A Practical Approach to Significance Assessment in Alignment with Gaps*, Proceedings of the Ninth Annual International Conference on Computational Molecular Biology (RECOMB2005), (Springer, Berlin, 2005), 474–488 and J. Comp. Biol. **13**, 429–441 (2006).

31. D.M. Layton and R. Bundschuh, *A Statistical Analysis of RNA Folding Algorithms Through Thermodynamic Parameter Perturbation*, Nucleic Acids Res. **33**, 519–524 (2005).

30. N. Chia and R. Bundschuh, *Finite Width Model Sequence Comparison*, Phys. Rev. E **70**, 021906/1–021906/9 (2004).

29. R. Bundschuh, *Computational prediction of RNA editing sites*, Bioinformatics **20**, 3214–3220 (2004).

28. T. Liu and R. Bundschuh, *Analytical description of finite size effects for RNA secondary structures*, Phys. Rev. E **69** 061912/1–061912/10 (2004).

27. U. Gerland, R. Bundschuh, and T. Hwa, *Translocation of structured polynucleotides through nanopores*, Phys. Biol. **1**, 19–26 (2004).

26. U. Gerland, R. Bundschuh, and T. Hwa, *Mechanically probing the folding pathway of single RNA molecules*, Biophys. J. **84**, 2831–2840 (2003).

25. Y. Li, M. Lauria, and R. Bundschuh, *Using Hybrid Alignment for Iterative Sequence Database Searches*, Proceedings of HICOMB 2003 (IEEE CS press, Los Alamitos, CA, 2003) and *Concurr. Comp. Pract. Exp.* **16**, 841–853 (2004).

24. R. Bundschuh, F. Hayot, and C. Jayaprakash, *Fluctuations and slow variables in genetic networks*, Biophys. J. **84**, 1606–1615 (2003).

23. R. Bundschuh, F. Hayot, and C. Jayaprakash, *The role of dimerization in noise reduction of simple genetic networks*, J. Theor. Biol. **220**, 261–269 (2003).

22. R. Bundschuh and T. Hwa, *Phases of the secondary structures of RNA sequences*, Europhys. Lett. **59**, 903–909 (2002).

21. R. Bundschuh and M. Lässig, *Delocalization transitions of semi-flexible manifolds*, Phys. Rev. E **65**, 061502/1–061502/7 (2002).

20. Y.-K. Yu, R. Bundschuh, and T. Hwa, *Statistical Significance and Extremal Ensemble of Gapped Local Hybrid Alignment*, Biological Evolution and Statistical Physics, M. Lässig and A. Valeriani eds., (Springer, Berlin, Germany, 2002), pp. 3–22.

19. Y.-K. Yu, R. Bundschuh, and T. Hwa, *Hybrid Alignment: High Performance with Universal Statistics*, Bioinformatics **18**, 864–872 (2002).

18. R. Bundschuh and T. Hwa, *Statistical mechanics of secondary structures formed by random RNA sequences*, Phys. Rev. E. **65**, 031903/1–031903/22 (2002).

17. R. Bundschuh, *Asymmetric Exclusion Process and Extremal Statistics of Random Sequences*, Phys. Rev. E **65**, 031911/1–031911/19 (2002).

16. R. Bundschuh, *High precision simulations of the longest common subsequence problem*, Europ. Phys. J. B **22**, 533–541 (2001).

15. U. Gerland, R. Bundschuh, and T. Hwa, *Force-induced denaturation of RNA*, Biophys. J. **81**, 1324–1332 (2001).

14. R. Bundschuh, *Rapid Significance Estimation in Local Sequence Alignment with Gaps*, J. Comp. Biol. **9**, 243–260 (2002), and Proceedings of the Fifth Annual International Conference on Computational Molecular Biology (RECOMB2001), (ACM press, New York, NY, 2001).

13. S. Altschul, R. Bundschuh, R. Olsen, and T. Hwa, *The Estimation of Statistical Parameters for Local Alignment Score Distributions*, Nucleic Acids Research **29**, 351–361 (2001).

12. R. Bundschuh, M. Lässig, and R. Lipowsky, *Semi-flexible polymers with attractive interactions*, Europ. Phys. J. E **3**, 295–306 (2000).
11. R. Bundschuh, *An Analytic Approach to Significance Assessment in Local Sequence Alignment with Gaps*, Proceedings of the Fourth Annual International Conference on Computational Molecular Biology (RECOMB 2000), 86–95 (ACM press, New York, NY, 2000).
10. R. Bundschuh and T. Hwa, *An analytic study of the phase transition line in local sequence alignment with gaps*, Disc. Appl. Math. **104**, 113–142 (2000).
9. R. Bundschuh and T. Hwa, *RNA secondary structure formation: a solvable model of heteropolymer folding*, Phys. Rev. Lett. **83**, 1479–1482 (1999).
8. R. Olsen, R. Bundschuh, and T. Hwa, *Rapid Assessment of Extremal Statistics for Local Alignment with Gaps*, Proceedings of the Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB '99), 211–222 (AAAI Press, Menlo Park, CA, 1999).
7. R. Bundschuh and T. Hwa, *An analytic study of the phase transition line in local sequence alignment with gaps*, Proceedings of the Third Annual International Conference on Computational Molecular Biology (RECOMB'99), 70–76 (ACM press, New York, NY, 1999).
6. R. Bundschuh, C. Cassanello, D. Serban, and M. Zirnbauer, *Weak localization of disordered quasiparticles in the mixed superconducting state*, Phys. Rev. B **59**, 4382–4389 (1999).
5. R. Bundschuh, C. Cassanello, D. Serban, and M. Zirnbauer, *Localization of quasiparticles in a disordered vortex*, Nucl. Phys. B **532**, 689–732 (1998).
4. R. Bundschuh, and M. Lässig, *Comment on 'Simplest possible self-organized critical system'*, Phys. Rev. Lett. **77**, 4273 (1996).
3. R. Bundschuh, and M. Lässig, *Directed polymers in high dimensions*, Phys. Rev. E **54**, 304–320 (1996).
2. R. Everaers, R. Bundschuh, and K. Kremer, *Fluctuations and stiffness of double-stranded polymers: railway-track model*, Europhys. Lett. **29**, 263–268 (1995)
1. U. Fastenrath, G. Adams, R. Bundschuh, T. Hermes, B. Raab, I. Schlosser, T. Wehner, and T. Wichmann, *Universality in the 2D localization problem*, Physica A **172**, 302–308 (1991).

Other publications:

2. R. Bundschuh, *Book review: Physical Biology of the Cell*, Physics Today **62**, 44 (2009).
1. R. Bundschuh, *Book review: Mathematics of genome analysis*, Physics Today **56**, 65 (2003).

Invited conference presentations (presenter in bold):

41. **R. Bundschuh**, *Nucleosome unwrapping may be easier than you think*, March Meeting of the American Physical Society, Los Angeles, CA, 3/5/18-3/9/18
40. **R. Bundschuh**, *FuSpot and SMaSH: Tools for fusion and sample identification in genomics data*, 1st International Conference on Computational Genomics and Proteomics, Guanacaste, Costa Rica, 10/18/16-10/22/16

39. **R. Bundschuh**, *Quantifying genome-wide DNA methylation from MethylCap-Seq data and its applications in cancer*, Belgrade Bioinformatics Conference BELBi 2016, 6/20/16-6/24/16
38. **R. Bundschuh**, *The effect of RNA secondary structure on RNA-protein interactions*, 3rd International Conference on Protein and RNA Structure Prediction, Punta Cana, Dominican Republic, 12/14/15-12/18/15
37. **R. Bundschuh**, *The search for the determinants of insertional RNA editing in Physarum polycephalum mitochondrial RNAs*, PhysNet Worshop, New York, NY, 12/3/15-12/5/15
36. **R. Bundschuh**, *Quantitative modeling of nucleic-acid protein interactions*, Mathematical Biosciences Institute Workshop on Geometric and Topological Modeling of Biomolecules, Columbus, OH, 9/28/15-10/2/15
35. **R. Bundschuh**, *Quantitative modeling of nucleic-acid protein interactions*, presentation as invited participant at workshop on RNA, Benasque, Spain, 7/19/15-7/31/15
34. **R. Bundschuh**, *Dynamics of the Competition Between Nucleosome Unwrapping and DNA Binding Proteins*, March Meeting of the American Physical Society, San Antonio, TX, 3/2/15-3/6/15
33. **R. Bundschuh**, *Phase transitions in homopolymer models of RNA*, PIMS Analytic RNA Combinatorics, Vancouver, Canada, 4/15/14-4/16/14
32. **R. Bundschuh**, RNA structure mediated cooperativity in RNA-protein interactions Zing conference on protein and RNA structure prediction, Xcaret, Mexico, 12/1/13-12/5/13
31. **R. Bundschuh**, *Biophysics of protein-nucleic acid interactions*, Symposium “From Soft Matter to Bio-Systems”, Potsdam, Germany, 11/21/13-11/22/13
30. **R. Bundschuh**, *Genome-wide DNA methylation profiling in cancer*, Zing conference on Mathematical and Computational Medicine, Xcaret, Mexico, 12/1/12-12/5/12
29. **R. Bundschuh**, *Fitness and structure landscapes for pre-miRNA processing*, *Incorporating RNA-Protein Interactions into RNA Secondary Structure Prediction*, presentations as invited participant at workshop on RNA, Benasque, Spain, 7/22/12-8/3/12
28. **R. Bundschuh**, *Statistical Physics of Sequence Analysis*, March Meeting of the American Physical Society, Boston, MA, 2/27/12-3/2/12
27. **R. Bundschuh**, *Incorporating Biophysicsal Observables and RNA-Protein Interactions into RNA Secondary Structure Prediction*, Zing conference on protein and RNA structure prediction, Xcaret, Mexico, 12/3/11-12/7/11
26. **R. Bundschuh**, J. de Meaux, and M. Lässig, *Fitness and structure landscapes for pre-miRNA processing*, SFB 680 Conference on Molecular Basis of Evolutionary Innovations, Marche-en-Famenne, Belgium, 7/1/10-7/3/10
25. **R. Forties** and R. Bundschuh, *RNA Secondary Structure Prediction in the Presence of Single-Stranded Binding Proteins*, Ohio Collaborative Conference on Bioinformatics 2009, Cleveland, OH, 6/15/09-5/17/09
24. **R. Bundschuh**, *An evolutionary hypothesis and computational identification of insertional RNA editing sites*, 435th WE Heraeus Seminar: Physics of Biological Function, Bad Honnef, Germany, 6/21/09-6/25/09

23. **R. Bundschuh**, *Statistical Physics of RNA*, Workshop on Disorder and Localization Phenomena: from Theory to Applications, Paris, France, 3/17/08-3/19/08
22. **R. Bundschuh**, *Statistical Physics of RNA folding*, Summer School Non-equilibrium in Physics and in Biology, St Etienne de Tineé, France, 8/13/07-10/8/07
21. **R. Bundschuh**, *Computational and physical models of RNA structure*, Workshop on Computational Models in Biomolecular Structures and Interaction Networks, Singapore, Singapore, 7/9/07-8/3/07
20. **R. Bundschuh**, *Quantitative models of RNA single molecule experiments*, International Workshop Physical and Chemical Foundations of Bioinformatics Methods, Dresden, Germany, 6/18/07-6/22/07
19. **R. Bundschuh**, *Aggregation and folding phase transitions of RNA molecules*, Workshop on Physics Inspired by Biology, Minneapolis, MN, 5/4/07-5/6/07
18. **R. Bundschuh**, *Aggregation and folding phase transitions of RNA molecules*, March Meeting of the American Physical Society 2007, Denver, CO, 3/5/07-3/9/07
17. **R. Bundschuh**, *Structure prediction with force*, *Insertional RNA editing*, and *Translocation through Nanopores*, presentations as invited participant at workshop on Computational approaches to functional and regulatory RNAs, Benasque, Spain, 7/16/06-7/28/06
16. **R. Bundschuh**, *Kinetic modeling of RNA single-molecule experiments*, Canadian Association of Physicists yearly meeting, St. Catherines, ON, 6/11/06-6/14/06
15. **R. Bundschuh**, *Computational Approaches to the Prediction of RNA Editing Sites*, Ohio Collaborative Conference on Bioinformatics, Athens, OH, 6/28/06-6/30/06
14. **R. Bundschuh**, *Modeling the translocation of structured RNA molecules through a nanopore*, Electronic Recognition of Bio-molecules meeting, Urbana, IL, 9/7/05-9/9/05
13. **R. Bundschuh**, *Kinetics of RNA translocation through a nanopore*, March Meeting of the American Physical Society 2005, Los Angeles, CA, 3/20/05-3/25/05
12. **R. Bundschuh**, *Statistical Physics of RNA Secondary Structures*, March meeting (Frühjahrstagung) of the German Physical Society, Regensburg, Germany, 3/8/04-3/12/04
11. **R. Bundschuh**, *Glassiness in RNA secondary structures*, Cecam workshop Statistical Mechanics of Random Copolymers, Lyon, France, 9/22/03-9/26/03
10. **R. Bundschuh**, *Statistical mechanics of secondary structures formed by random RNA sequences*, March Meeting of the American Physical Society 2003, Austin, TX, 3/03/03-3/07/03
9. **R. Bundschuh**, *RNA secondary structure: Statistical physics and quantitative modeling*, Cell Systems Biology workshop, Berlin, Germany, 11/21/02-11/23/02
8. **R. Bundschuh**, *Modeling single molecule RNA force extension experiments*, Satellite meeting to ECCB02 on bioinformatics and statistical physics, Saarbrücken, Germany, 10/6/02-10/11/02
7. **R. Bundschuh**, *Sequence Alignment and Statistical Physics*, 7th Claude Itzykson meeting, Gif-sur-Yvette, France, 6/19/02-6/21/02.

6. **R. Bundschuh**, *The role of disorder in RNA folding*, Statistical Physics and Biological Information program at the Institute for Theoretical Physics, Santa Barbara, CA, 1/31/01
5. **R. Bundschuh**, *Tutorial on RNA secondary structure*, Statistical Physics and Biological Information program at the Institute for Theoretical Physics, Santa Barbara, CA, 1/31/01
4. **R. Bundschuh**, *Sequence Alignment, Directed Polymers, and the Asymmetric Exclusion Process*, Statistical Physics and Biological Information program at the Institute for Theoretical Physics, Santa Barbara, CA, 1/24/01
3. **R. Bundschuh**, *Large-score Statistics for Sequence Alignment with Gaps*, Stochastics in sequence alignment and population biology workshop, Frankfurt, Germany, 10/12/00-10/14/00
2. **R. Bundschuh**, U. Gerland, and T. Hwa, *The Stability of RNA Secondary Structures*, International Workshop on Biological Evolution and Statistical Physics, Dresden, Germany, 5/10/00-5/14/00
1. **R. Bundschuh** and T. Hwa, *Sequence Alignment, Extremal Distribution, and the Asymmetric Exclusion Process*, Nordita Workshop on Non Equilibrium Physics, Copenhagen, Denmark, 9/23/99-9/25/99

Invited seminars and colloquia:

64. *Quantitative modeling of nucleic-acid protein interactions*, Center for Theoretical Biological Physics Seminar, Rice University, Houston, TX 2/23/16
63. *Quantitative modeling of nucleosome dynamics*, Physics colloquium, Kent State University, Kent, OH, 9/25/14
62. *Quantitative modeling of nucleic-acid protein interactions*, Biophysics seminar, Simon Fraser University, Vancouver, Canada, 4/16/14
61. *Quantitative modeling of nucleic-acid protein interactions*, Center for Biological Physics seminar, UCLA, CA, 3/14/14
60. *Gene discovery in the presence of RNA editing*, Biochemistry seminar, Texas A&M University, College Station, TX, 9/25/13
59. *Biophysical modeling of RNA structures*, Biophysics lecture, Xavier University, OH, 4/10/13
58. *From the Ising Model to Biological Sequence Analysis*, Colloquium of the center for synthetic microbiology, Marburg, Germany, 6/19/12
57. *Quantitative modeling of nucleosome dynamics*, Special seminar, University of California at Riverside, Riverside, CA, 1/3/12
56. *Quantitative Modeling of Nucleosome Dynamics*, Biophysics seminar, Arizona State University, Tempe, AZ, 9/7/11
55. *Fitness and structure landscapes for pre-miRNA processing*, Biophysics seminar, Princeton University, Princeton, NJ, 4/4/11
54. *Flexibility of short DNA*, BioMaPS seminar, Rutgers University, Piscataway, NJ, 3/3/10

53. *From the Ising Model to Biological Sequence Analysis*, Physics Colloquium, Ohio State University, Columbus, OH, 11/10/09
52. *From the Ising Model to Biological Sequence Analysis*, Physics Colloquium, University of Waterloo, Waterloo, ON, 10/22/09
51. *Flexibility of short DNA*, Physics Colloquium, McMaster University, Hamilton, ON, 10/21/09
50. *Gene discovery in the presence of RNA editing*, chemistry and biochemistry seminar, Northern Arizona University, Flagstaff, AZ, 9/25/09
49. *From the Ising Model to Biological Sequence Analysis*, Physics Colloquium, Carnegie Mellon University, Pittsburgh, PA, 9/21/09
48. *Vom Ising-Modell zur biologischen Sequenzanalyse*, Physics colloquium at the Universität des Saarlandes, Saarbrücken, Germany, 7/16/09
47. *Aggregation and folding phase transitions of RNA molecules*, Seminar of the Laboratoire de Physique Théorique, Ecole Normale Supérieure, Paris, France, 3/30/09
46. *Quantitative modeling of RNA single-molecule experiments*, Soft condensed matter theory group seminar, Institute for condensed matter research, Forschungszentrum Jülich, Jülich, Germany, 1/29/09
45. *From the Ising Model to Biological Sequence Analysis*, Colloquium for theoretical Physics, Universität zu Köln, Köln, Germany, 10/24/08
44. *Vom Ising-Modell zur biologischen Sequenzanalyse*, Physics colloquium, Universität Duisburg-Essen, Duisburg, Germany, 10/15/08
43. *From the Ising Model to Biological Sequence Analysis*, Physics Colloquium, University of California at Riverside, Riverside, CA, 5/08/08
42. *Computational Prediction of Insertional RNA Editing*, Mathematical Biosciences Institute seminar, Ohio State University, Columbus, OH, 4/15/08
41. *Quantitative modeling of RNA single-molecule experiments*, Departmental seminar of the department of Biophysics and Biochemistry, University of Rochester, Rochester, NY, 9/12/07
40. *An Evolutionary Hypothesis and Computational Identification of Insertional RNA Editing Sites*, Evolution of Molecular Networks program at the Kavli Institute for Theoretical Physics, Santa Barbara, CA, 1/25/07
39. *Gene discovery in the presence of RNA editing*, biochemistry seminar, The Ohio State University, Columbus, OH, 10/10/06
38. *Quantitative modeling of RNA single-molecule experiments*, condensed matter seminar, Ohio University, Athens, OH, 6/1/06.
37. *A practical approach to significance assessment in alignment with gaps*, postdoc seminar of the Mathematical Biosciences Institute, The Ohio State University, Columbus, OH, 1/19/06
36. *Quantitative modeling of RNA single-molecule experiments*, condensed matter seminar, Case Western Reserve University, Cleveland, OH, 11/28/05

35. *Quantitative modeling of RNA single-molecule experiments*, biophysics seminar, Rice University, Houston, TX, 11/18/05
34. *Gene discovery in the presence of RNA editing*, biology seminar, NYU, New York, NY, 9/19/05
33. *Quantitative modeling of single molecule RNA force-extension experiments*, special physics seminar, Universität Bielefeld, Bielefeld, Germany, 6/15/05
32. *Statistical Assessment of Sequence Alignments*, seminar of the MPIMG, Max Planck Institute for molecular genetics, Berlin, Germany, 6/14/05
31. *A Practical Approach to Significance Assessment in Alignments with Gaps*, Graduiertenkolleg Strukturbildungsprozesse colloquium, Universität Bielefeld, Bielefeld, Germany, 6/9/05
30. *Quantitative modeling of RNA single-molecule experiments*, AG Praktische Informatik seminar, Universität Bielefeld, Bielefeld, Germany, 6/6/05
29. *Statistical Assessment of Sequence Alignments*, CeBiTec colloquium, Universität Bielefeld, Bielefeld, Germany, 5/30/05
28. *Significance assessment in local sequence alignment with gaps*, Physics colloquium, Virginia Tech, Blacksburg, VA, 4/29/05
27. *Quantitative modeling of single-molecule RNA force-extension experiments*, Condensed matter seminar, University of Cincinnati, Cincinnati, OH, 4/13/05
26. *Statistical Assessment of Sequence Alignments*, Department of Chemistry and Center for Photochemical Sciences seminar, Bowling Green University, Bowling Green, OH, 1/28/04
25. *Significance assessment in local sequence alignment with gaps*, Biophysics program seminar, The Ohio State University, Columbus, OH, 12/4/03
24. *Quantitative modeling of single-molecule RNA force-extension experiments*, Center for Physics and Biology seminar, Rockefeller University, New York, NY, 11/18/03
23. *Quantitative modeling of single-molecule RNA force-extension experiments*, Condensed matter and applied physics colloquium, Harvard University, Cambridge, MA, 11/14/03
22. *Directed Polymers and Sequence Comparison*, Alumni meeting of the Max-Planck institute for colloid and interface research, Potsdam, Germany, 6/20/03
21. *Statistical Physics of Biological Sequences*, Physics colloquium at Ohio University, Athens, OH, 10/25/02
20. *Rare events and statistical physics of biological sequences*, Biological physics seminar of the Max-Planck-Institute for Physics of Complex Systems, Dresden, Germany, 6/17/02.
19. *Statistical Assessment of Sequence Alignments*, Molecular and microbiology seminar at Case Western Reserve University, Cleveland, OH, 5/13/02
18. *Large Score Statistics for Sequence Alignment with Gaps*, Applied mathematics seminar of The Ohio State University, Columbus, OH, 2/28/02
17. *Statistical Physics of Biological Sequences*, Physics colloquium of The Ohio State University, Columbus, OH, 11/6/01

16. *Statistics of RNA secondary structures and what we can learn from single-molecule experiments*, RNA group seminar of The Ohio State University, Columbus, OH, 10/10/01
15. *Statistical Physics of RNA folding*, Condensed matter physics seminar of the University of Cincinnati, Cincinnati, 2/14/01
14. *Biopolymers - Information Carriers and Structural Building Blocks*, ITP blackboard lunch, Santa Barbara, CA, 2/5/01
13. *Rare events and statistical physics of sequence alignments*, Condensed matter theory seminar of The Ohio State University, Columbus, OH, 11/20/00
12. *Statistical physics of sequence alignment*, Career issues seminar of the University of Michigan, Ann Arbor, MI, 11/9/00
11. *Statistical Physics of RNA folding*, Physics colloquium, George Washington University, Washington, DC, 3/28/00
10. *Statistical Physics of RNA folding*, Special physics colloqium, University of Wisconsin at Milwaukee, Milwaukee, WI, 3/9/00
9. *Statistical Physics of RNA folding*, Special condensed matter physics seminar, Ohio State University, Columbus, OH, 3/7/00
8. *Bioinformatics: Overview and Perspectives*, Special bioengineering seminar, University of Illinois at Chicago, Bioengineering department, Chicago, IL, 2/29/00
7. *Statistical Assessment of Sequence Alignments*, Special bioengineering seminar, University of Illinois at Chicago, Bioengineering department, Chicago, IL, 2/28/00
6. *Statistical Physics of RNA folding*, Special physics seminar, Iowa State University, Department of Physics and Astronomy, Ames, Iowa, 2/25/00
5. *Statistical Physics of RNA folding*, Special condensed matter seminar, MIT Physics department, Cambridge, MA, 2/10/00
4. *Statistical Assessment of Sequence Alignments*, Special seminar, MIT Biology department, Cambridge, MA, 2/9/00
3. *Statistical Physics of RNA folding*, Condensed matter seminar, Harvard, Cambridge, MA, 2/3/00
2. *Statistical Assessment of Sequence Alignments*, National Center for Biotechnology Information seminar, Bethesda, MD, 10/4/99
1. *RNA secondary structure formation: a solvable model of heteropolymer folding*, Complex dynamical systems seminar at UCSD, La Jolla, 5/3/99

Contributed conference talks and posters (presenter in bold):

76. **L.A. Walker**, M.G. Sovic, C.-L. Chiang, E. Hu, J.K. Denninger, X. Chen, E.D. Kirby, J.C. Byrd, N. Muthusamy, R. Bundschuh, and P. Yan, *CLEAR: Coverage-based Limiting-cell Experiment Analysis for RNA-seq*, contributed poster at the 2018 Asia Pacific Society for Biology and Medical Sciences annual meeting, 7/20/18-7/23/18

75. **L.A. Walker**, R. Bundschuh, and P. Yan, *Oversight: A Fast and Nimble Utility to Evaluate RNA-Seq Data Quality*, contributed poster at the 2018 Asia Pacific Society for Biology and Medical Sciences annual meeting, 7/20/18-7/23/18

74. **L.A. Walker**, M.G. Sovic, N.C. Chiang, E. Hu, M.B. Broe, J.C. Byrd, N. Muthusamy, R. Bundschuh, and P. Yan, *Gene Expression Analysis at the Ultralow RNA Input Levels*, contributed poster at the 2017 Cancer Systems Biology Consortium Annual Meeting, 10/2/17-10/3/17

73. **C. Shipps**, and R. Bundschuh, *Determining the dominant secondary structures of a RNA molecule during contranscriptional folding dynamics by grouping similar dominant structures*, contributed poster at the 2016 RustBelt RNA meeting, Cleveland, OH, 10/14/16-10/15/16

72. **L. Walker**, D. Frankhouser, M.B. Broe, J.A. Muszynski, P. Yan, and R. Bundschuh, *Using patient-derived data to customize smRNA-seq databases*, contributed poster at the 2016 RustBelt RNA meeting, Cleveland, OH, 10/14/16-10/15/16

71. **B. Moreland**, S. Dodbele, S. Gardner, J. Jackman, and R. Bundschuh, *Applications of 5-end sequence analysis of small RNA: Nucleotide addition by Thg1/BtTLP and TSS annotations in S. cerevisiae*, contributed poster at the 2016 RustBelt RNA meeting, Cleveland, OH, 10/14/16-10/15/16

70. **D.E. Frankhouser**, M. Westphal, A. Pelletier, A. Urdaneta, P. Stump, P. Shields, P. Yan, H. He , A. de la Chapelle, C. Sonzone, and R. Bundschuh, *MetaComb: Meta-Transcriptomic Alignment with a Combined Genome*, contributed poster at the 2016 RustBelt RNA meeting, Cleveland, OH, 10/14/16-10/15/16

69. **J. Killian**, T. Topiwala, A. Pelletier, D. Frankhouser, P. Yan, and R. Bundschuh, *A tool for fusion detector post-analysis coverage visualization of chimeric RNA-seq data*, contributed poster at the 2016 RustBelt RNA meeting, Cleveland, OH, 10/14/16-10/15/16.

68. **B. Moreland**, K. Oman, J. Curfman, P. Yan, and R. Bundschuh, *Characterization of DNA-protein interactions using high-throughput sequencing data from pulldown experiments*, contributed talk at the 2016 March Meeting of the American Physical Society, Baltimore, MD, 3/14/16-3/18/16

67. **W. Baez**, K. Wiese, and R. Bundschuh, *Characterization of the full base pairing probability distribution in RNA secondary structure folding*, contributed talk at the 2016 March Meeting of the American Physical Society, Baltimore, MD, 3/14/16-3/18/16

66. **C. Chen** and R. Bundschuh, *A-to-I editing is cancer subtype specific*, contributed poster at the 2014 RustBelt RNA meeting, Pittsburgh, PA, 10/17/14-10/18/14

65. **Y.-H. Lin** and R. Bundschuh, *Structure-mediated cooperativity between single-stranded RNA binding partners on 5' and 3'UTRs*, contributed poster at the 2014 RustBelt RNA meeting, Pittsburgh, PA, 10/17/14-10/18/14

64. **W. Baez** and R. Bundschuh, *RNA secondary structure critical exponents of random sequences near the glass transition*, contributed talk at the 2014 March Meeting of the American Physical Society, Denver, CO, 5/3/14-5/7/14

63. **Y.-H. Lin** and R. Bundschuh, *Loop cost in RNA secondary structures and the long-range cooperativity between RNA-binding proteins*, contributed talk at the 2014 March Meeting of the American Physical Society, Denver, CO, 5/3/14-5/7/14

62. **R. Bundschuh**, P. Klajner, J. Hanne, B.M. Britton, J. Liu, J. Park, J.-B. Lee, and R. Fishel, *The DNA mismatch repair protein MutS forms a one-dimensional Tonks gas on DNA*, contributed talk at the 2014 March Meeting of the American Physical Society, Denver, CO, 5/3/14-5/7/14

61. **C. Chen** and R. Bundschuh, *Transcriptome-wide RNA editing can be used in cancer subtype discrimination*, contributed poster at the 2013 RustBelt RNA meeting, Cleveland, OH, 10/18/13-10/19/13

60. **Y.-H. Lin** and R. Bundschuh, *Cooperativity between single-stranded binding proteins on RNA secondary structure*, contributed poster at the 2013 RustBelt RNA meeting, Cleveland, OH, 10/18/13-10/19/13

59. **K. Oman**, K. Fredrick, D. Schoenberg, and R. Bundschuh, *Computational methods for the analysis of high throughput sequencing data in RNA biology*, contributed poster at the 2013 RustBelt RNA meeting, Cleveland, OH, 10/18/13-10/19/13

58. **R. Bundschuh** and C. Chen, *Mechanisms for enhanced protein dissociation driven by nucleosomes*, contributed talk at the 2013 March Meeting of the American Physical Society, Baltimore, MD, 18/3/13-22/3/13

57. **Y.-H.** Lin and R. Bundschuh, *The interplay between single-stranded binding proteins on RNA secondary structure*, contributed talk at the 2013 March Meeting of the American Physical Society, Baltimore, MD, 18/3/13-22/3/13

56. **W. Baez** and R. Bundschuh, *Localizing the critical point of random RNA secondary structures*, contributed talk at the 2013 March Meeting of the American Physical Society, Baltimore, MD, 18/3/13-22/3/13

55. **C. Chen** and R. Bundschuh, *Systematic investigation of insertional and deletional RNA-DNA differences in the human transcriptome*, contributed talk at the 2012 RustBelt RNA meeting, Dayton, OH, 10/19/12-10/20/12

54. **C. Chen**, D. Frankhouser, and R. Bundschuh, *Comparison of insertional RNA editing in Myxomycetes*, contributed poster at the 2011 RustBelt RNA meeting, Dayton, OH, 10/21/11-10/22/11

53. H.-H. Tam, S. Faith, D. Bornman, S. Nelson, P. Yan, B. Young, and **R. Bundschuh**, *Identifying STRs in next generation sequencing data*, contributed poster at the twenty-second international symposium on human identification, National Harbor, MD, 10/3/11-10/6/11

52. **R. Bundschuh**, J. de Meaux, and M. Lässig, *Fitness and structure landscapes for pre-miRNA processing*, contributed talk at the 2011 March meeting of the American Physical Society, Dallas, TX, 3/21/11-3/25/11

51. **R. Forties**, J. North, S. Javaid, O. Tabaa, R. Fishel, M. Poirier, and R. Bundschuh, *A quantitative model of nucleosome dynamics*, contributed talk at the 2011 March meeting of the American Physical Society, Dallas, TX, 3/21/11-3/25/11
50. **R. Bundschuh**, J. Altmüller, C. Becker, P. Nürnberg, and J. Gott, *Complete characterization of the edited transcriptome of the mitochondrion of Physarum polycephalum using deep sequencing of RNA*, contributed poster at Gordon conference on Editing and Modification of RNA and DNA, Galveston, TX, 1/9/11-1/14/11
49. **C. Chen** and R. Bundschuh, *Comparative sequence analysis in insertional RNA editing*, contributed poster at the 2010 Rustbelt RNA meeting, Cleveland, OH, 10/21/10-10/22/10
48. **R. Bundschuh**, J. de Meaux, and M. Lässig, *Fitness and structure landscapes for pre-miRNA processing*, contributed talk at SMBE2010, Lyon, France, 7/4/10-7/8/10
47. **R. Bundschuh**, J. de Meaux, and M. Lässig, *Fitness and structure landscapes for pre-miRNA processing*, poster at Cold Spring Harbor meeting on Biology of Genomes, Cold Spring Harbor, NY, 5/11/10-5/15/10
46. **R. Bundschuh**, J. Altmüller, C. becker, P. Nürnberg, and J. Gott, *Complete characterization of mitochondrial insertional editing sites in Physarum polycephalum using deep sequencing of RNA*, contributed talk at the 2009 RustBelt RNA meeting, Mt. Sterling, OH, 10/16/09-10/17/09
45. **R. Forties** and R. Bundschuh, *Modeling the interplay of single-stranded binding proteins and nucleic acid secondary structure*, contributed poster at the 2009 RustBelt RNA meeting, Mt. Sterling, OH, 10/16/09-10/17/09
44. **R. Forties** and R. Bundschuh, *Modeling nucleic acid structure in the presence of single-stranded binding proteins*, contributed talk at the 2009 March meeting of the American Physical Society, Pittsburgh, PA, 3/16/09-3/20/09
43. **M. McCauley**, R. Forties, U. Gerland, and R. Bundschuh, *Anomalous scaling of nano-pore translocation times of structured biomolecules*, contributed talk at the 2009 March meeting of the American Physical Society, Pittsburgh, PA, 3/16/09-3/20/09
42. C. Beargie, T. Liu, M. Corriveau, W. Zhang, H.Y. Lee, M. Silliker, J. Gott, and **R. Bundschuh**, *Computational genome annotation in the presence of insertional RNA editing*, poster at Gordon conference on RNA editing, Galveston, TX, 1/11/09-1/16/09
41. **R. Forties**, R. Bundschuh, and M. Poirier, *Sequence and Temperature Dependence of DNA Bending Fluctuations*, contributed talk at the 2008 March meeting of the American Physical Society, New Orleans, LA, 3/10/08-3/14/08
40. **R. Forties**, R. Bundschuh, and M. Poirier, *A model for the flexibility of double-stranded DNA incorporating local melting*, contributed poster at the 2007 RustBelt RNA meeting, Mt. Sterling, OH, 10/19/07-10/20/07
39. **F. Habib**, A. Johnson, R. Bundschuh, and D. Janies, *Large scale genotype-phenotype correlation for continuous phenotypes*, contributed talk at the 2007 Ohio Collaborative Conference on Bioinformatics, Oxford, OH, 7/9/07-7/11/07

38. C. Ainsley, H. Lee, T. Liu, N. Parimi, J. Gott, and **R. Bundschuh**, *Computational prediction of RNA editing sites in Myxomycetes*, poster at the Gordon conference on RNA editing, Ventura, CA, 1/14/07-1/19/07
37. **F. Habib**, A. Johnson, R. Bundschuh, and D. Janies, *Genotype-Phenotype Correlations Using Phylogenetic Trees for Large Datasets*, contributed talk at the 2006 Ohio Collaborative Conference on Bioinformatics, Athens, OH, 6/28/06-6/30/06
36. **P. Messer**, R. Bundschuh, M. Vingron, and P. Arndt, *Alignment Statistics for Long-Range Correlated Genomic Sequences*, contributed talk at the Tenth Annual International Conference on Computational Molecular Biology (RECOMB2006), Venice, Italy, 4/2/06-4/5/06
35. **M. Lee**, R. Bundschuh, and M. Chan, *Distant Homology Detection Using a LEngth and STructure-based Sequence Alignment Tool (LESTAT)*, poster at the Tenth Annual International Conference on Computational Molecular Biology (RECOMB2006), Venice, Italy, 4/2/06-4/5/06
34. **Y. Li**, M. Lauria, and R. Bundschuh, *Suboptimal Alignments Improve the Detection of Weak Homologs in Sequence Database Searches*, contributed talk at BIBE05, Minneapolis, MN, 10/19/05-10/21/05
33. **R. Bundschuh** and T. Liu, *A model for codon position bias in RNA editing*, contributed talk at the March Meeting of the American Physical Society 2006, Baltimore, MD, 3/13/06-3/17/06
32. **V. Guttal** and R. Bundschuh, *A Model for Folding and Aggregation in RNA Secondary Structures*, contributed talk at the March Meeting of the American Physical Society 2006, Baltimore, MD, 3/13/06-3/17/06
31. **F. Habib**, D. Janies, and R. Bundschuh, *Phylogenetic methods for computationally correlating genotypes and phenotypes*, contributed talk at the 2005 Fall Meeting of the Ohio Section of the American Physical Society, Cleveland, OH, 10/14/05-10/15/05
30. **N. Chia** and R. Bundschuh, *A Practical Approach to Significance Assessment in Alignment with Gaps*, contributed talk at the Ninth Annual International Conference on Computational Molecular Biology (RECOMB2005), Cambridge, MA, 5/14/05-5/18/05
29. **F. Habib** and R. Bundschuh, *Modeling DNA unzipping in the presence of DNA binding proteins*, contributed talk at the 2005 Spring Meeting of the Ohio Section of the American Physical Society, Dayton, OH, 4/8/05-4/9/05
28. **N. Chia** and R. Bundschuh, *Universal scaling function in discrete time asymmetric exclusion processes*, contributed talk at the March Meeting of the American Physical Society 2005, Los Angeles, LA, 3/20/05-3/25/05
27. C. Ainsley, H. Lee, N. Parimi, J. Gott, and **R. Bundschuh**, *Computational identification of RNA editing sites in Physarum polycephalum*, poster at the Gordon conference on RNA editing, Ventura, CA, 1/23/05-1/28/05
26. **J. Gott**, N. Parimi, and R. Bundschuh, *Identification and characterization of new RNA editing substrates in Physarum mitochondria*, talk at the RustBelt RNA meeting, Mt. Sterling, OH, 11/19/04-11/20/04
25. **R. Bundschuh** and J. Gott, *Gene finding in the presence of RNA editing*, poster at the Eighth Annual International Conference on Computational Molecular Biology (RECOMB 2004), San Diego, CA, 3/27/04-3/31/04

24. Y. Li, M. Lauria, and **R. Bundschuh**, *Can Hybrid Alignment Enhance PSI-BLAST*, Poster-Blitz presentation at the BISTI workshop Digital Biology: The Emerging Paradigm, Bethesda, MD, 11/6/03-11/7/03
23. **T. Liu** and R. Bundschuh, *Analytical description of finite size effects for RNA secondary structures*, contributed talk at the March Meeting of the American Physical Society 2003, Austin, TX, 3/03/03-3/07/03
22. **R. Bundschuh**, *Computational prediction of RNA editing sites*, talk at the RustBelt RNA meeting, Mt. Sterling, OH, 11/1/02-11/2/02
21. **R. Bundschuh** and T. Hwa, *Two possible phases for the secondary structure of random RNA sequences*, talk at the March Meeting of the American Physical Society 2002, Indianapolis, IN, 3/18/02-3/22/02
20. **R. Bundschuh**, U. Gerland, and T. Hwa, *Force-induced denaturation of RNA*, talk at the RustBelt RNA meeting, Mt. Sterling, OH, 11/2/01-11/3/01
19. **R. Bundschuh**, *Rapid Significance Estimation in Local Sequence Alignment with Gaps*, talk at Fifth Annual International Conference on Computational Molecular Biology (RECOMB 2001), Montreal, 4/23/01-4/25/01
18. **U. Gerland**, R. Bundschuh, and T. Hwa, *Force-induced denaturation of RNA*, talk at the 221st ACS National Meeting, San Diego, 4/01/01-4/05/01
17. **U. Gerland**, R. Bundschuh, and T. Hwa, *Force-induced denaturation of RNA*, talk at the March Meeting of the American Physical Society 2001, Seattle, WA, 3/12/01-3/16/01
16. **R. Bundschuh**, *A New Method in Rapid Significance Assessment of Smith-Waterman Alignments*, poster at the Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB 2000), San Diego, CA, 8/19/00-8/23/00
15. **U. Gerland**, R. Bundschuh, and T. Hwa, *Force-induced denaturation of RNA*, poster at the Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB 2000), San Diego, CA, 8/19/00-8/23/00
14. **Y.-K. Yu**, T. Hwa, and R. Bundschuh, *Statistical Significance of Probabilistic Hybrid Alignment*, poster at the Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB 2000), San Diego, CA, 8/19/00-8/23/00
13. **R. Bundschuh**, *An Analytic Approach to Significance Assessment in Local Sequence Alignment with Gaps*, talk at Fourth Annual International Conference on Computational Molecular Biology (RECOMB 2000), Tokyo, 4/8/00-4/11/00
12. U. Gerland, **R. Bundschuh**, and T. Hwa, *Weak Glassiness in the Secondary Structure of Random RNA Sequences*, talk at the March Meeting of the American Physical Society 2000, Minneapolis, 3/20/00-3/24/00
11. **R. Bundschuh**, *The Asymmetric Exclusion Process and Computational Biology*, talk at the March Meeting of the American Physical Society 2000, Minneapolis, 3/20/00-3/24/00
10. T. Hwa, **R. Bundschuh**, and Y.-K. Yu, *Generating Rare Events in Systems with Quenched Disorder*, talk at the March Meeting of the American Physical Society 2000, Minneapolis, 3/20/00-3/24/00

9. **R. Olsen**, R. Bundschuh, and T. Hwa, *Rapid Assessment of Extremal Statistics for Gapped Local Alignment*, talk at the Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB 99), Heidelberg, 8/20/99-8/23/99.
8. **R. Bundschuh** and T. Hwa, *An Analytic Study of the Phase Transition Line in Local Sequence Alignment with Gaps*, talk at the Third Annual International Conference on Computational Molecular Biology (RECOMB99), Lyon, 4/11/99-4/14/99
7. **R. Bundschuh**, K. Hamacher, and T. Hwa, *Statistical Mechanics of RNA folding*, talk at the march meeting of the American Physical Society 1999, Atlanta, 3/21/99-3/26/99
6. **R. Bundschuh** and T. Hwa, *Detectability of Sequence Homology by DNA Hybridization*, poster at the Program for Mathematics and Molecular Biology Meeting, Mathematics and Molecular Biology VI, Understanding Structure, Santa Fe, 1/9/99-1/14/99
5. **R. Bundschuh** and T. Hwa, *Detectability of Sequence Homology by DNA Hybridization*, talk at the German Conference on Bioinformatics 98, Bensberg, 10/7/98-10/10/98
4. **R. Bundschuh** and T. Hwa, *Secondary Structure Formation in Model RNA*, poster at STATPHYS 20, Paris, 7/20/98-7/24/98
3. **R. Bundschuh**, M. Lässig, and R. Lipowsky, *Unbinding Transitions of Semi-flexible Polymers*, poster at "Applications of Field Theory to Statistical Physics" workshop, Bonn, 7/15/98-7/18/98
2. **R. Bundschuh** and T. Hwa, *Detectability of Sequence Homology by DNA Hybridization*, poster at the Second Annual International Conference on Computational Molecular Biology (RECOMB98), New York, 3/22/98-3/25/98
1. **R. Bundschuh** and T. Hwa, *Structure Formation in Model Heteropolymers*, talk at the march meeting of the American Physical Society 1998, Los Angeles, 3/16/99-3/20/99

Funding:

Current:

- NSF DMR-1719316, Quantitative modeling of nucleic acid-protein interactions, $335,787, 9/1/2017-8/31/2020
- NIH T32 GM118291-01A1 (MPI Bundschuh, Kuret, Magliery), Molecular Biophysics predoctoral training at The Ohio State University, $859,771, 7/1/2017-6/30/2022
- NIH NIGMS R01GM120209-01A1 (PI Singh), Regulation of RNA surveillance by the dynamic exon junction complex, $1,848,329 (17% for Bundschuh lab), 1/9/2017-8/31/2022
- NIH NIGMS R01GM084277-05A1 (PI Schoenberg), Relationship of cytoplasmic capping to post-transcriptional gene regulation, $256,000 (amount is fraction for Bundschuh lab), 7/1/2015-6/30/2020
- NSF MCB-1614990 (PI Fredrick), Studies of translation initiation in bacteria, $645,000 (11% for Bundschuh lab), 9/1/2016-8/31/2019
- NIH NAID R21AI122981 (PI Yoder), $19,250 (amount is fraction for Bundschuh lab), 9/1/2016-6/30/2021

- NIH NHLBI R01HL134544 (PI Funderburg), Cellular mediators of vascular inflammation in treated HIV infection, $43,318 (amount is fraction for Bundschuh lab), 9/1/2016-6/30/2021
- NIH NCI R01CA188269 (PI Garzon) Developing CRM1 inhibitors in AML, $19,988 (amount is fraction for Bundschuh lab), 7/16/2014-5/31/2019

Completed:

- NSF DMR-1410172, Cooperativity in nucleic-acid protein interactions, $252,603, 9/1/2014-8/31/2017
- NIH NCI R01CA102031 (PI Marcucci, Guzman), Pharmacological modulation of epigenetic changes in AML, $19,773 (amount is fraction for Bundschuh lab), 7/1/2013-3/31/2018
- NSF MCB-1243997 (PI Fredrick), Studies of translation initiation in bacteria, $709,396 (12% for Bundschuh lab), 9/1/2013-8/31/2016
- NIH NCI P50CA140158 subaward (PI Byrd), Genome wide methylation as a prognostic tool in leukemia, $245,000, 11/1/2011-7/31/2015
- NSF DMR-1105458, Biophysics of protein nucleic acids interactions, $259,000, 9/15/2011-8/31/2015
- Statistical Physics approaches to RNA editing, $240,000, NSF, 9/1/2007–8/31/2012
- RustBelt RNA meeting 2007, $5,000, NSF, 9/1/2007–8/31/2010
- Translocation of structured polymers through nanopores, $35,000, ACS–PRF, 9/1/2005–8/31/2009
- Statistical physics of biological sequence analysis, $167,000, NSF, 9/1/2004–8/31/2009
- Iterative hybrid alignment: improving the sensitivity of biological database searches, $350,141, NSF, 9/1/2003–8/31/2006

Graduate students:

- Kyle Crocker, current
- Elan Shatoff, current
- Robert Patton, current
- Blythe Moreland, current
- Dengke Zhao, current
- Bill Baez, current
- Kenji Oman, 2015, Bioinformatics Specialist, Fred Hutchinson Cancer Center
- Yi-Hsuan Lin, 2015, Postdoctoral Researcher, University of Toronto
- Cai Chen, 2014, Postdoctoral Researcher, University of North Carolina at Chapel Hill

- Robert Forties, 2011, Software Engineer, Advion Biosciences
- Marianne Lee, 2009, Assistant Professor, The Chinese University of Hong Kong
- Wei Zhang, 2008, Operation Manager, Independent clinical laboratory group
- Farhat Habib, 2007, Researcher, Indian Institute of Science Education and Research
- Tsunglin Liu, 2006, Assistant Professor, National Cheng-Kung University Taiwan
- Nicholas Chia, 2006, Associate Professor, Mayo Clinic
- Yuheng Li, 2006, Bioinformatics Consultant, BLC Consulting