Ron O. Dror

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PROFESSIONAL EXPERIENCE

Associate Professor, Stanford University 2014–present

Faculty member in the Departments of Computer Science and, by courtesy, Molecular and Cellular Physiology and Structural Biology. Affiliated with the Institute for Computational and Mathematical Engineering, the Stanford Artificial Intelligence Lab, Bio-X, ChEM-H, and the Biophysics and Biomedical Informatics Programs. I lead a research group that applies high-performance computing, physics-based simulation, image analysis, and machine learning to structural biology in order to explain the workings of living systems and develop better medicines. I published 13 papers in *Science*, *Nature*, and *Cell* between 2015 and 2018, together with numerous experimental collaborators. In addition to teaching machine learning courses, I developed two new computational biology courses. Enrollment in each has grown eight-fold over the last three years.

Senior Research Scientist and Special Advisor to the Chairman, D. E. Shaw Research 2002–2014

Second in command of a 110-person research group focused on accelerating simulations of biomolecules, whose work was highlighted by *Science* as one of the top ten scientific breakthroughs of 2010. I helped build the group after starting as the first hire, and managed interdisciplinary projects together with founder and chief scientist David E. Shaw. I oversaw the group's operations; managed substantial parts of the design process for Anton, a special-purpose molecular dynamics supercomputer, and Desmond, a fast molecular dynamics software package for standard computer clusters; and played a leadership role in various projects involving application of molecular dynamics simulations to proteins and ligands of biological and pharmaceutical interest.

Lead Artificial Intelligence Engineer, Arch Healthcare 2001–2002

Developed image-processing software to detect signs of cancer in mammograms.

EDUCATION

Massachusetts Institute of Technology 2002
Ph.D. in Electrical Engineering and Computer Science
Advisors: Alan Willsky and Edward Adelson
Research area: Machine learning and statistical inference for computer vision and genomics

University of Cambridge 1998
M.Phil. in Biological Sciences (Churchill Scholar)
Advisor: Simon Laughlin
Research area: Computational and experimental neuroscience (visual motion detection)

Rice University 1997
B.S. in Electrical Engineering and B.A. in Mathematics
Summa cum laude (1st in class)

AWARDS

Gordon Bell Prize (Performance)	2014
Best Paper Award, International Parallel and Distributed Processing Symposium	2013
Best Paper Award, ACM/IEEE Conference on Supercomputing (SC11)	2011
Science Magazine Breakthrough of the Year runner-up (one of nine projects)	2010
Gordon Bell Prize (Special Achievement)	2009
Best Paper Award, ACM/IEEE Conference on Supercomputing (SC09)	2009
Profiled by MIT EECS Dept. in feature on "EECS Alums: Major Players and Thinkers"	2009
Best Paper Award, ACM/IEEE Conference on Supercomputing (SC06)	2006
Whitaker Foundation Fellowship in Biomedical Engineering	1999–2002
National Defense Science and Engineering Graduate Fellowship	1998–2001
Churchill Scholarship	1997–1998
National Science Foundation Graduate Fellowship	declined, 1998
Fulbright Scholarship	declined, 1997
MSTP Fellowship, Harvard-MIT M.D./Ph.D. Program	declined, 1997
Elected to Phi Beta Kappa, Sigma Xi, Tau Beta Pi, and Eta Kappa Nu	1996–2001
Graham Baker Studentship, highest scholastic standing in Rice University class	1996
William Marsh Rice Scholarship (full tuition)	1993–1997
Bronze Medalist, International Mathematical Olympiad (Istanbul, Turkey)	1993
National Merit Scholarship and National Science Scholarship	1992

PUBLICATION SUMMARY

I have published 98 papers, including 23 in *Nature*, *Science*, and *Cell*, generally considered the most selective scientific journals. 17 of these papers, including 12 in *Nature*, *Science*, and *Cell*, are based entirely on work done since arriving at Stanford in 2014. My papers have been cited over 17,000 times, and my h-index is 51.

In the publication list below:
† indicates papers based entirely on work done since arriving at Stanford
* indicates senior/corresponding authorship

PREPRINTS

1. R.J.L. Townshend, R. Bedi, and R.O. Dror*. Generalizable protein interface prediction with end-to-end learning. arXiv preprint arXiv:1807.01297 (2018).†

JOURNAL PAPERS

2. **N.R. Latorraca**, **J.K. Wang**, B. Bauer, **R.J.L. Townshend**, S.A. Hollingsworth, **J.E. Olivieri**, H.E. Xu, M.E. Sommer, and R.O. Dror*. Molecular mechanism of GPCR-mediated arrestin activation. **557**:452–456 (2018).†
3. K. Eichel, D. Julli**é**, B. Barsi-Rhyne, **N.R. Latorraca**, M. Masureel, J. Sibarita, R.O. Dror, and M. von Zastrow. Catalytic activation of β-arrestin by GPCRs. *Nature* **557**:381–386 (2018).†

4. A. Koehl, H. Hu, S. Maeda, Y. Zhang, Q. Qu, **J.M. Paggi**, **N.R. Latorraca**, D. Hilger, R. Dawson, H. Matile, G.F.X. Schertler, S. Granier, W.I. Weis, R.O. Dror, A. Manglik, G. Skiniotis, B.K. Kobilka. Structure of the μ opioid receptor-Gi protein complex. *Nature* **558**:547–552 (2018).†

5. N. van Eps, C. Altenbach, L.N. Caro, N.R. Latorraca, S.A. Hollingsworth, R.O. Dror, O.P. Ernst and W.L. Hubbell. Gi- and Gs-coupled GPCRs show different modes of G-protein binding. *Proceedings of the National Academy of Sciences of the United States of America* **115**:2383-2388 (2018).†

6. J.D. McCorvy, K.V. Butler, B. Kelly, K. Rechsteiner, J. Karpiak, R.M. Betz, B.L. Kormos, B.K. Shoichet, R.O. Dror*, J. Jin, B.L. Roth. Structure-inspired design of β-arrestin-biased ligands for aminergic GPCRs. *Nature Chemical Biology* **14**:126–134 (2018).†

7. S. Wang, D. Wacker, A. Levit, T. Che, R.M. Betz, J.D. McCorvy, A.J. Venkatakrishnan, X.-P. Huang, **R.O. Dror**, B.K. Shoichet, and B.L. Roth. D4 dopamine receptor high-resolution structures enable the discovery of selective agonists. *Science* **358**: 381–386 (2017).†

8. X. Liu, S. Ahn, A.W. Kahsai, K.C. Meng, N.R. Latorraca, B. Pani, A.J. Venkatakrishnan, A. Masoudi, W.I. Weis, **R.O. Dror**, X. Chen, R.J. Lefkowitz, and B.K. Kobilka. Mechanism of intracellular allosteric β_2AR antagonist revealed by X-ray crystal structure. *Nature* **548**: 480–484 (2017).†

9. X.E. Zhou, Y. He, P.W. de Waal, X. Gao, Y. Kang, N. Van Eps, Y. Yin, K. Pal, D. Goswami, T.A. White, A. Barty, N.R. Latorraca, H.N. Chapman, W.L. Hubbell, **R.O. Dror**, R.C. Stevens, V. Cherezov, V.V. Gurevich, P.R. Griffin, O.P. Ernst, K. Melcher, and H.E. Xu. Identification of phosphorylation codes for arrestin recruitment by G protein-coupled receptors. *Cell* **170**: 457–469 (2017).†

10. N.R. Latorraca, N.M. Fastman, A.J. Venkatakrishnan, W.B. Frommer, **R.O. Dror***, and L. Feng. Mechanism of substrate translocation in an alternating access transporter. *Cell* **169**: 96-107 (2017).†

11. D. Wacker, S. Wang, J.D. McCorvy, R.M. Betz, A.J. Venkatakrishnan, A. Levit, K. Lansu, Z. Schools, T. Che, D.E. Nichols, B.K. Shoichet, **R.O. Dror***, and B.L. Roth. Crystal structure of an LSD-bound human serotonin receptor. *Cell* **168**: 377-389 (2017). **Cover story.**†

12. K.E. Komolov, Y. Du, N.M. Duc, R.M. Betz, J.P.G.L.M. Rodrigues, R.D. Leib, D. Patra, G. Skiniotis, C.M. Adams, **R.O. Dror**, K.Y. Chung, B.K. Kobilka, and J.L. Benovic. Structural and functional analysis of a β2-adrenergic receptor complex with GRK5. *Cell* **169**: 407-421 (2017).†

13. N.R. Latorraca, A.J. Venkatakrishnan, and **R.O. Dror*.** GPCR dynamics: structures in motion. *Chemical Reviews* **117:** 139–155 (2017).†

14. Crystal structure of a full-length human tetraspanin reveals a cholesterol-binding pocket. B. Zimmerman, B. Kelly, T. Seegar, B.J. McMillan, **R.O. Dror**, A.C. Kruse, and S. Blacklow. *Cell* **167**: 1041–1051 (2016).†

15. S. Hertig, N.R. Latorraca, and **R.O. Dror***. Revealing atomic-level mechanisms of protein allostery with molecular dynamics simulations. *PLOS Computational Biology*. **12**: e1004746 (2016).†

16. D. Guo, A.C. Pan, **R.O. Dror**, T. Mocking, R. Liu, L. Heitman, D.E. Shaw, and A.P. IJzerman. Molecular basis of ligand dissociation from the adenosine A_{2A} receptor. *Molecular Pharmacology* **89**: 485–491 (2016).

17. W. Huang, A. Manglik, A.J. Venkatakrishnan, T. Laeremans, E.N. Feinberg, A.L. Sanborn, H. Kato, K.E. Livingston, T.S. Thorsen, R. Kling, S. Granier, P. Gmeiner, S.M. Husbands, J.R. Traynor, W.I. Weis, J. Steyaert, **R.O. Dror**, and B.K. Kobilka. Structural insights into μ-opioid receptor activation. *Nature* **524**: 315–321 (2015).†

18. **R.O. Dror***, T.J. Mildorf, D. Hilger, A. Manglik, D.W. Borhani, D.H. Arlow, A. Philippsen, N. Villanueva, Z. Yang, M. Lerch, W.L. Hubbell, B.K. Kobilka, R.K. Sunahara, and D.E. Shaw. Structural basis for nucleotide exchange in heterotrimeric G proteins. *Science* **348**: 1361–1365 (2015).

19. J.S. Burg, J.R. Ingram, A.J. Venkatakrishnan, K.M. Jude, A. Dukkipati, E.N. Feinberg, A. Angelini, D. Waghray, **R.O. Dror**, H.L. Ploegh, and K.C. Garcia. Structural basis for chemokine recognition and activation of a viral G protein–coupled receptor. *Science* **347**: 1113–1117 (2015).†

20. Z. Fan, **R.O. Dror***, T.J. Mildorf, S. Piana, and D.E. Shaw. Identifying localized changes in large systems: change-point detection for biomolecular simulations. *Proceedings of the National Academy of Sciences of the United States of America* **112**: 7454–7459 (2015).

21. A. Ranganathan, **R.O. Dror**, J. Carlsson. Insights into the role of $Asp79^{2.50}$ in β_2 adrenergic receptor activation from molecular dynamics simulations. *Biochemistry* **53**: 7283–7296 (2014).†

22. **R.O. Dror***, H.F. Green, C. Valant, D.W. Borhani, J.R. Valcourt, A.C. Pan, D.H. Arlow, M. Canals, J.R. Lane, R. Rahmani, J.B. Baell, P.M. Sexton, A. Christopoulos, and D.E. Shaw. Structural basis for modulation of a GPCR by allosteric drugs. *Nature* **503**: 295–299 (2013).

23. R. Nygaard, Y. Zou, **R.O. Dror**, T.J. Mildorf, D.H. Arlow, A. Manglik, A.C. Pan, C.W. Liu, J.J. Fung, M.P. Bokoch, F.S. Thian, T.S. Kobilka, D.E. Shaw, L. Mueller, R.S. Prosser, and B.K. Kobilka. The dynamic process of β_2-adrenergic receptor activation. *Cell* **152**: 532–542 (2013).

24. A. Arkhipov, Y. Shan, E.T. Kim, **R.O. Dror**, and D.E. Shaw. Her2 activation mechanism reflects evolutionary preservation of asymmetric ectodomain dimers in the human EGFR family. *eLife* **2**: e00708 (2013).

25. A.C. Pan, D.W. Borhani, **R.O. Dror**, and D.E. Shaw. Molecular determinants of drug–receptor binding kinetics. *Drug Discovery Today* **18:** 667–673 (2013).

26. R.A. Lippert, C. Predescu, D.J. Ierardi, K.M. Mackenzie, M.P. Eastwood, **R.O. Dror**, and D.E. Shaw. Accurate and efficient integration for molecular dynamics simulations at constant temperature and pressure. *Journal of Chemical Physics* **139**: 164106 (2013).

27. T.H. Kim, K.Y. Chung, A. Manglik, A.L. Hansen, **R.O. Dror**, T.J. Mildorf, D.E. Shaw, B.K. Kobilka, and R.S. Prosser. The role of ligands on the equilibria between functional states of a G protein-coupled receptor. *Journal of the American Chemical Society* 135: 9465–9474 (2013).

28. **R.O. Dror***, R.M. Dirks, J.P. Grossman, H. Xu, and D.E. Shaw. Biomolecular simulation: A computational microscope for molecular biology. *Annual Review of Biophysics* **41**: 429–452 (2012).

29. C. Zhang, Y. Srinivasan, D.H. Arlow, J.J. Fung, D. Palmer, Y. Zheng, H.F. Green, A. Pandey, **R.O. Dror**, D.E. Shaw, W.I. Weis, S.R. Coughlin, and B.K. Kobilka. High-resolution crystal structure of human protease-activated receptor 1. *Nature* **492**: 387–392 (2012).

30. M.Ø. Jensen, V. Jogini, D.W. Borhani, A.E. Lefler, **R.O. Dror**, and D.E. Shaw. Mechanism of voltage gating in K^+ channels. *Science* **336**: 229–233 (2012).

31. Y. Shan, M.P. Eastwood, X. Zhang, E.T. Kim, A. Arkhipov, **R.O. Dror**, J. Jumper, J. Kuriyan, and D.E. Shaw. Oncogenic mutations counteract intrinsic disorder in the EGFR kinase and promote receptor dimerization. *Cell* **149**: 860–870 (2012).

32. A.C. Kruse, J. Hu, A.C. Pan, D.H. Arlow, D.M. Rosenbaum, E. Rosemond, H.F. Green, T. Liu, P.S. Chae, **R.O. Dror**, D.E. Shaw, W.I. Weis, J. Wess, and B.K. Kobilka. Structure and dynamics of the M_3 muscarinic acetylcholine receptor. *Nature* **482**: 552–556 (2012).

33. A. Raval, S. Piana, M.P. Eastwood, **R.O. Dror**, and D.E. Shaw. Refinement of protein structure homology models via long, all-atom molecular dynamics simulations. *Proteins: Structure, Function, and Bioinformatics* **80**: 2071–2079 (2012).

34. C. Predescu, R.A. Lippert, M.P. Eastwood, D.J. Ierardi, H. Xu, M.Ø. Jensen, K.J. Bowers, J. Gullingsrud, C.A. Rendleman, **R.O. Dror**, and D.E. Shaw. Computationally efficient molecular dynamics integrators with improved sampling accuracy. *Molecular Physics* **110**: 967–983 (2012).

35. S. Piana, K. Lindorff-Larsen, R.M. Dirks, J.K. Salmon, **R.O. Dror**, and D.E. Shaw. Evaluating the effects of cutoffs and treatment of long-range electrostatics in protein folding simulations. *PLoS ONE* **7**: e39918 (2012).

36. Lindorff-Larsen, P. Maragakis, S. Piana, M.P. Eastwood, **R.O. Dror**, and D.E. Shaw. Systematic validation of protein force fields against experimental data. *PLoS ONE* **7**: e32131 (2012).

37. **R.O. Dror***, D.H. Arlow, P. Maragakis, T.J. Mildorf, A.C. Pan, H. Xu, D.W. Borhani, and D.E. Shaw. Activation mechanism of the β_2-adrenergic receptor. *Proceedings of the National Academy of Sciences of the United States of America*. **108**: 18684–18689 (2011).

38. K. Lindorff-Larsen, S. Piana, **R.O. Dror**, and D.E. Shaw. How fast-folding proteins fold. *Science*, **334**: 517–520 (2011).

39. **R.O. Dror***, A.C. Pan, D.H. Arlow, D.W. Borhani, P. Maragakis, Y. Shan, H. Xu, and D.E. Shaw. Pathway and mechanism of drug binding to G protein–coupled receptors. *Proceedings of the National Academy of Sciences of the United States of America*, **108**: 13118–13123 (2011).

40. Y. Shan, E.T. Kim, M.P. Eastwood, **R.O. Dror**, M.A. Seeliger, and D.E. Shaw. How does a drug molecule find its target binding site? *Journal of the American Chemical Society*, **133**: 9181–9183 (2011).

41. **R.O. Dror***, J.P. Grossman, K.M. Mackenzie, B. Towles, E. Chow, J.K. Salmon, C. Young, J.A. Bank, B. Batson, M.M. Deneroff, J.S. Kuskin, R.H. Larson, M.A. Moraes, and D.E. Shaw. Overcoming communication latency barriers in massively parallel scientific computation. *IEEE Micro*, **31**: 8–19 (2011).

42. D.M. Rosenbaum, C. Zhang, J.A. Lyons, R. Holl, D. Aragao, D.H. Arlow, S.G.F. Rasmussen, H.-J. Choi, B.T. DeVree, R.K. Sunahara, P.S. Chae, S.H. Gellman, **R.O. Dror**, D.E. Shaw, W.I. Weis, M. Caffrey, P. Gmeiner, and B.K. Kobilka. Structure and function of an irreversible agonist–β_2 adrenoceptor complex. *Nature* **469**: 236–240 (2011).

43. D.E. Shaw, P. Maragakis, K. Lindorff-Larsen, S. Piana, **R.O. Dror**, M.P. Eastwood, J.A. Bank, J.M. Jumper, J.K. Salmon, Y. Shan, and W. Wriggers. Atomic-level characterization of the structural dynamics of proteins. *Science*, **330**: 341–346 (2010).

44. **R.O. Dror**, M.Ø. Jensen, D.W. Borhani, and D.E. Shaw. Exploring atomic resolution physiology on a femtosecond to millisecond timescale using molecular dynamics simulations. *Journal of General Physiology*, **135**: 555–562 (2010).

45. M.P. Eastwood, K.A. Stafford, R.A. Lippert, M.Ø. Jensen, P. Maragakis, C. Predescu, **R.O. Dror**, and D.E. Shaw. Equipartition and the calculation of temperature in biomolecular simulations. *Journal of Chemical Theory and Computation*, **6**: 2045–2058 (2010).

46. M.Ø. Jensen, D.W. Borhani, K. Lindorff-Larsen, P. Maragakis, V. Jogini, M.P. Eastwood, **R.O. Dror**, and D.E. Shaw. Principles of conduction and hydrophobic gating in K+ channels. *Proceedings of the National Academy of Sciences of the United States of America*, **107**: 5833–5838 (2010).

47. K. Lindorff-Larsen, S. Piana, K. Palmo, P. Maragakis, J.L. Klepeis, **R.O. Dror**, and D.E. Shaw. Improved side-chain torsion potentials for the Amber ff99SB protein force field. *Proteins: Structure, Function, and Bioinformatics*, **78**: 1950–1958 (2010).

48. K.J. Bowers, R.A. Lippert, **R.O. Dror**, and D.E. Shaw. Improved twiddle access for fast Fourier transforms. *IEEE Transactions on Signal Processing*, **58**: 1122–1130 (2010).

49. D.K. Shenfeld, H. Xu, M.P. Eastwood, **R.O. Dror**, and D.E. Shaw. Minimizing thermodynamic length to select intermediate states for free-energy calculations and replica-exchange simulations. *Physical Review E*, **80**: 046705-1–046705-4 (2009).

50. W. Wriggers, K.A. Stafford, Y. Shan, S. Piana, P. Maragakis, K. Lindorff-Larsen, P.J. Miller, M.P. Eastwood, **R.O. Dror**, and D.E. Shaw. Automated event detection and activity monitoring in long molecular dynamics simulations. *Journal of Chemical Theory and Computation*, **5**: 2595–2605, (2009).

51. **R.O. Dror**, D.H. Arlow, D.W. Borhani, M.Ø. Jensen, S. Piana, and D.E. Shaw. Identification of two distinct inactive conformations of the β_2-adrenergic receptor reconciles structural and biochemical observations. *Proceedings of the National Academy of Sciences of the United States of America*, **106**: 4689–4694 (2009).

52. Y. Shan, M.A. Seeliger, M.P. Eastwood, F. Frank, H. Xu, M.Ø. Jensen, **R.O. Dror**, J. Kuriyan, and D.E. Shaw. A conserved protonation-dependent switch controls drug binding in the Abl kinase. *Proceedings of the National Academy of Sciences of the United States of America*, **106**: 139–144 (2009).

53. J.L. Klepeis, K. Lindorff-Larsen, **R.O. Dror**, and D.E. Shaw. Long-timescale molecular dynamics simulations of protein structure and function. *Current Opinion in Structural Biology*, **19**: 1–18 (2009).

54. M.Ø. Jensen, **R.O. Dror**, H. Xu, D.W. Borhani, I.T. Arkin, M.P. Eastwood, and D.E. Shaw. Dynamic control of slow water transport by aquaporin 0: implications for hydration and junction stability in the eye lens. *Proceedings of the National Academy of Sciences of the United States of America,* **105**: 14430–14435 (2008).

55. D.E. Shaw, M.M. Deneroff, **R.O. Dror**, J.S. Kuskin, R.H. Larson, J.K. Salmon, C. Young, B. Batson, K.J. Bowers, J.C. Chao, M.P. Eastwood, J. Gagliardo, J.P. Grossman, C.R. Ho, D.J. Ierardi, I. Kolossváry, J.L. Klepeis, T. Layman, C. McLeavey, M.A. Moraes, R. Mueller, E.C. Priest, Y. Shan, J. Spengler, M. Theobald, B. Towles, and S.C. Wang. Anton, a special-purpose machine for molecular dynamics simulation. *Communications of the ACM*, **51**: 91–97 (2008).

56. P. Maragakis, K. Lindorff-Larsen, M.P. Eastwood, **R.O. Dror**, J.L. Klepeis, I.T. Arkin, M.Ø. Jensen, H. Xu, N. Trbovic, R.A. Friesner, A.G. Palmer, and D.E. Shaw. Microsecond molecular dynamics simulation shows effect of slow loop dynamics on backbone amide order parameters of proteins. *Journal of Physical Chemistry B*, **112**: 6155–6158 (2008).

57. I.T. Arkin, H. Xu, M.Ø. Jensen, E. Arbely, E.R. Bennett, K.J. Bowers, E. Chow, **R.O. Dror**, M.P. Eastwood, R. Flitman-Tene, B.A. Gregersen, J.L. Klepeis, I. Kolossváry, Y. Shan, and D.E. Shaw. Mechanism of Na^+/H^+ antiporting. *Science* **317**: 799–803 (2007).

58. R.A. Lippert, K.J. Bowers, **R.O. Dror**, M.P. Eastwood, B.A. Gregersen, J.L. Klepeis, I. Kolossváry, and D.E. Shaw. A common, avoidable source of error in molecular dynamics integrators. *Journal of Chemical Physics* **126**: 046101 (2007).

59. K.J. Bowers, **R.O. Dror**, and D.E. Shaw. Zonal methods for the parallel execution of range-limited N-body simulations. *Journal of Computational Physics* **221**: 303–329 (2007).

60. K.J. Bowers, **R.O. Dror**, and D.E. Shaw. The midpoint method for parallelization of particle simulations. *Journal of Chemical Physics* **124**: 184109 (2006).

61. Y. Shan, J.L. Klepeis, M.P. Eastwood, **R.O. Dror**, and D.E. Shaw. Gaussian split Ewald: A fast Ewald mesh method for molecular simulation. *Journal of Chemical Physics* **122**: 054101 (2005).

62. **R.O. Dror***, A.S. Willsky, and E.H. Adelson. Statistical characterization of real-world illumination. *Journal of Vision* **4**: 821–837 (2004).

63. **R.O. Dror***, J.G. Murnick, N.J. Rinaldi, V.D. Marinescu, R.M. Rifkin, and R.A. Young. Bayesian estimation of transcript levels using a general model of array measurement noise. *Journal of Computational Biology* **10**: 433–452 (2003).

64. R.W. Fleming, **R.O. Dror**, and E.H. Adelson. Real-world illumination and the perception of surface reflectance properties. *Journal of Vision* **3**: 347–368 (2003).

65. **R.O. Dror**, D.C. O'Carroll, and S.B. Laughlin. Accuracy of velocity estimation by Reichardt correlators. *Journal of the Optical Society of America A* **18**: 241–252 (2001).

66. **R.O. Dror**, C.C. Canavier, R.J. Butera, J.W. Clark, and J.H. Byrne. A mathematical criterion based on phase response curves for stability in a ring of coupled oscillators. *Biological Cybernetics* **80**: 11–23 (1999).

67. C.C. Canavier, R.J. Butera, **R.O. Dror**, D.A. Baxter, J.W. Clark, and J.H. Byrne. Phase response characteristics of model neurons determine which patterns are expressed in a ring circuit model of gait generation. *Biological Cybernetics* **77**: 367–380 (1997).

68. **R.O. Dror**, S. Ganguli, and R.S. Strichartz. A search for best constants in the Hardy-Littlewood maximal theorem. *Journal of Fourier Analysis and Applications* **2**: 473–86 (1996).

REFEREED CONFERENCE PAPERS

69. D.E. Shaw, J.P. Grossman, J.A. Bank, B. Batson, J.A. Butts, J.C. Chao, M.M. Deneroff, R.O. Dror, A. Even, C.H. Fenton, A. Forte, J. Gagliardo, G. Gill, B. Greskamp, C.R. Ho, D.J. Ierardi, L. Iserovich, J.S. Kuskin, R.H. Larson, T. Layman, L.-S. Lee, A.K. Lerer, C. Li, D. Killebrew, K.M. Mackenzie, Shark Y.-H. Mok, M.A. Moraes, R. Mueller, L.J. Nociolo, J.L. Peticolas, T. Quan, D. Ramot, J.K. Salmon, D.P. Scarpazza, U.B. Schafer, N. Siddique, C.W. Snyder, J. Spengler, P.T.P. Tang, M. Theobald, H. Toma, B. Towles, B. Vitale, S.C. Wang, and C. Young. Anton 2: Raising the Bar for Performance and Programmability in a Special-Purpose Molecular Dynamics Supercomputer. *Proceedings of the International Conference for High Performance Computing, Networking, Storage and Analysis (SC14)*. Piscataway, NJ: IEEE. 41–53 (2014). **Gordon Bell Prize.**

70. D.P. Scarpazza, D.J. Ierardi, A.K. Lerer, K. M. Mackenzie, A.C. Pan, J.A. Bank, E. Chow, **R.O. Dror**, J.P. Grossman, D. Killebrew, M.A. Moraes, C. Predescu, J.K. Salmon, and D.E. Shaw. Extending the generality of molecular dynamics simulations on a special-purpose machine. *Proceedings of the 27th IEEE International Parallel and Distributed Processing Symposium (IPDPS)*. Boston, MA: IEEE Computer Society. 933–945 (2013). **Best Paper Award (Applications Track).**

71. J.P. Grossman, J.S. Kuskin, J.A. Bank, M. Theobald, **R.O. Dror**, D.J. Ierardi, R.H. Larson, U.B. Schafer, B. Towles, C. Young, and D.E. Shaw. Hardware support for fine-grained event-driven computation in Anton 2. *Proceedings of the Eighteenth International Conference on Architectural Support for Programming Languages and Operating Systems* (ASPLOS). New York, NY: ACM. 549–560 (2013).

72. J.K. Salmon, M.A. Moraes, **R.O. Dror**, and D.E. Shaw. Parallel random numbers: as easy as 1, 2, 3. *Proceedings of the Conference for High Performance Computing, Networking, Storage and Analysis (SC11)*. New York, NY: IEEE (2011). **Best Paper Award**.

73. J.A. Butts, P.T.P. Tang, **R.O. Dror**, and D.E. Shaw. Radix-8 digit-by-rounding: achieving high-performance reciprocals, square roots, and reciprocal square roots. *Proceedings of the 20th IEEE Symposium on Computer Arithmetic (ARITH20)*. Washington, DC: IEEE Computer Society (2011).

74. P.T.P. Tang, J.A. Butts, **R.O. Dror**, and D.E. Shaw. Tight certification techniques for digit-by-rounding algorithms with application to a new $1/\sqrt{x}$ design. *Proceedings of the 20th IEEE Symposium on Computer Arithmetic (ARITH20).* Washington, DC: IEEE Computer Society (2011).

75. **R.O. Dror**, J.P. Grossman, K.M. Mackenzie, B. Towles, E. Chow, J.K. Salmon, C. Young, J.A. Bank, B. Batson, M.M. Deneroff, J.S. Kuskin, R.H. Larson, M.A. Moraes, and D.E. Shaw. Exploiting 162-nanosecond end-to-end communication latency on Anton. *Proceedings of the Conference for High Performance Computing, Networking, Storage and Analysis (SC10)*. New York, NY: IEEE (2010). **Best Paper Award Finalist.**

76. T. Tu, C.A. Rendleman, P. Miller, F. Sacerdoti, **R.O. Dror**, and D.E. Shaw. Accelerating parallel analysis of scientific simulation data via Zazen. *Proceedings of the USENIX Conference on File and Storage Technologies (FAST)*. Berkeley, CA: USENIX Association (2010).

77. D.E. Shaw, **R.O. Dror**, J.K. Salmon, J.P. Grossman, K.M. Mackenzie, J.A. Bank, C. Young, M.M. Deneroff, B. Batson, K.J. Bowers, E. Chow, M.P. Eastwood, D.J. Ierardi, J.L. Klepeis, J.S. Kuskin, R.H. Larson, K. Lindorff-Larsen, P. Maragakis, M.A. Moraes, S. Piana, Y. Shan, and B. Towles. Millisecond-scale molecular dynamics simulation on Anton. *Proceedings of the Conference for High Performance Computing, Networking, Storage and Analysis (SC09)*. New York, NY: ACM (2009). **Gordon Bell Prize; Best Paper Award.**

78. C. Young, J.A. Bank, **R.O. Dror**, J.P. Grossman, J.K. Salmon, and D. E. Shaw. A $32\times32\times32$, spatially distributed 3D FFT in five microseconds on Anton. *Proceedings of the Conference for High Performance Computing, Networking, Storage and Analysis (SC09)*. New York, NY: ACM (2009).

79. **R.O. Dror**, M.Ø. Jensen, and D.E. Shaw. Elucidating membrane protein function through long-timescale molecular dynamics simulation. *Proceedings of the IEEE Engineering in Medicine and Biology Society (EMBC)*. New York, NY: IEEE (2009).

80. C.R. Ho, M. Theobald, B. Batson, J.P. Grossman, S.C. Wang, J. Gagliardo, M.M. Deneroff, **R.O. Dror**, and D.E. Shaw. Post-silicon debug using formal verification waypoints. *Proceedings of the Design and Verification Conference and Exhibition (DVCon),* San Jose (2009).

81. T. Tu, C.A. Rendleman, D.W. Borhani, **R.O. Dror**, J. Gullingsrud, M.Ø. Jensen, J.L. Klepeis, P. Maragakis, P. Miller, K.A. Stafford, and D.E. Shaw. A scalable parallel framework for analyzing terascale molecular dynamics trajectories. *Proceedings of the ACM/IEEE Conference on Supercomputing (SC08).* New York, NY: IEEE (2008). **Best Paper Award Finalist.**

82. J.P. Grossman, C. Young, J.A. Bank, K. Mackenzie, D.J. Ierardi, J.K. Salmon, **R.O. Dror**, and D.E. Shaw. Simulation and embedded software development for Anton, a parallel machine with heterogenous multicore ASICs. *Proceedings of the 6th IEEE/ACM/IFIP International Conference on Hardware/Software Codesign and System Synthesis (CODES/ISSS)*. New York, NY: ACM (2008).

83. J.P. Grossman, J.K. Salmon, C.R. Ho, D.J. Ierardi, B. Towles, B. Batson, J. Spengler, S.C. Wang, R. Mueller, M. Theobald, C. Young, J. Gagliardo, M.M. Deneroff, **R.O. Dror**, and D.E. Shaw. Hierarchical simulation-based verification of Anton, a special-purpose parallel machine. *Proceedings of the 26th IEEE International Conference on Computer Design (ICCD)*. New York, NY: IEEE (2008).

84. C.R. Ho, M. Theobald, M.M. Deneroff, **R.O. Dror**, J. Gagliardo, and D.E. Shaw. Early formal verification of conditional coverage points to identify intrinisically hard-to-verify logic. *Proceedings of the 45th Design Automation Conference (DAC)*, Anaheim (2008).

85. R.H. Larson, J.K. Salmon, **R.O. Dror**, M.M. Deneroff, R.C. Young, J.P. Grossman, Y. Shan, J.L. Klepeis, and D.E. Shaw. High-throughput pairwise point interactions in Anton, a specialized machine for molecular dynamics simulation. *Proceedings of the 14th International Symposium on High-Performance Computer Architecture (HPCA)*. New York, NY: IEEE (2008).

86. J.S. Kuskin, R.C. Young, J.P. Grossman, B. Batson, M.M. Deneroff, **R.O. Dror**, and D.E. Shaw. Incorporating flexibility in Anton, a specialized machine for molecular dynamics simulation. *Proceedings of the 14th International Symposium on High-Performance Computer Architecture (HPCA)*. New York, NY: IEEE (2008).

87. D.E. Shaw, M.M. Deneroff, **R.O. Dror**, J.S. Kuskin, R.H. Larson, J.K. Salmon, C. Young, B. Batson, K.J. Bowers, J.C. Chao, M.P. Eastwood, J. Gagliardo, J.P. Grossman, C.R. Ho, D.J. Ierardi, I. Kolossváry, J.L. Klepeis, T. Layman, C. McLeavey, M.A. Moraes, R. Mueller, E.C. Priest, Y. Shan, J. Spengler, M. Theobald, B. Towles, and S.C. Wang. Anton: A special-purpose machine for molecular dynamics simulation. *Proceedings of the 34rd Annual International Symposium on Computer Architecture (ISCA).* New York, NY: ACM (2007).

88. K.J. Bowers, E. Chow, H. Xu, **R.O. Dror**, M.P. Eastwood, B.A. Gregersen, J.L. Klepeis, I. Kolossváry, M.A. Moraes, F.D. Sacerdoti, J.K. Salmon, Y. Shan, and D.E. Shaw. Scalable algorithms for molecular dynamics simulations on commodity clusters. *Proceedings of the ACM/IEEE Conference on Supercomputing (SC06*). New York, NY: IEEE (2006). **Best Paper Award.**

89. K.J. Bowers, **R.O. Dror**, and D.E. Shaw. Overview of neutral territory methods for the parallel evaluation of pairwise particle interactions. *Proceedings of the Scientific Discovery through Advanced Computing (SciDAC)*, San Francisco, June 2005. *Journal of Physics: Conference Series* 16:300–304 (2005).

90. **R.O. Dror**[*], J.G. Murnick, N.J. Rinaldi, V.D. Marinescu, R.M. Rifkin, and R.A. Young. A Bayesian approach to transcript estimation from gene array data: The BEAM technique. *Proceedings of the Sixth Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Washington, DC (2002).

91. **R.O. Dror**, T.K. Leung, E.H. Adelson, and A.S. Willsky. Statistics of real-world illumination. *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*, Hawaii (2001).

92. **R.O. Dror**, E.H. Adelson, and A.S. Willsky. Recognition of surface reflectance properties from a single image under unknown real-world illumination. *Proceedings of the Workshop on Identifying Objects Across Variations in Lighting at the IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*, Hawaii (2001).

93. R.W. Fleming, **R.O. Dror**, and E.H. Adelson. How do humans determine reflectance properties under unknown illumination? *Proceedings of the Workshop on Identifying Objects Across Variations in Lighting at the IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*, Hawaii (2001).

94. **R.O. Dror**, E.H. Adelson, and A.S. Willsky. Surface reflectance estimation and natural illumination statistics. *Proceedings of the Second International Workshop on Statistical and Computational Theories of Vision at the IEEE International Conference on Computer Vision (ICCV)*, Vancouver (2001).

95. **R.O. Dror**, E.H. Adelson, and A.S. Willsky. Estimating surface reflectance properties from images under unknown illumination. *Proceedings of SPIE 4299: Human Vision and Electronic Imaging VI (HVEI)*, San Jose (2001).

96. **R.O. Dror**, D.C. O'Carroll, and S.B. Laughlin. The role of natural image statistics in biological motion estimation. *IEEE International Workshop on Biologically Motivated Computer Vision (BMCV)*, Seoul (2000). *Lecture Notes in Computer Science* **1811**: 492–501 (2000).

BOOK CHAPTERS

97. E. Chow, J.L. Klepeis, C.A. Rendleman, **R.O. Dror**, and D.E. Shaw. New technologies for molecular dynamics simulations. In *Comprehensive Biophysics*, E.H. Egelman, ed., Amsterdam: Elsevier. **9**:86–104 (2012).

98. **R.O. Dror***, C. Young, and D.E. Shaw. Anton: A special-purpose molecular simulation machine. In *Encyclopedia of Parallel Computing*, D. Padua, ed., New York, NY: Springer (2011).

99. **R.O. Dror***, A.C. Pan, D.H. Arlow, and D.E. Shaw. Probing the conformational dynamics of GPCRs with molecular dynamics simulation. In *G Protein–Coupled Receptors: From Structure to Function*. J. Giraldo and J.-P. Pin, eds., London: Royal Society of Chemistry, 384–400 (2011).

THESES

100. **R.O. Dror**. Surface reflectance recognition and real-world illumination statistics. Ph.D. thesis, Massachusetts Institute of Technology (2002).

101. **R.O. Dror**. Accuracy of visual velocity estimation by Reichardt correlators. M.Phil. thesis, University of Cambridge (1998).

RECENT INVITED TALKS

Les Houches Protein Dynamics Workshop, Les Houches, France, May 2018.

Annual Meeting of the American Society for Pharmacology and Experimental Therapeutics, San Diego, CA, April 2018.

Arizona State University Biological Physics Seminar, Tempe, AZ, April 2018.

American Chemical Society National Meeting, Symposium on Large-Scale Molecular Modeling, New Orleans, LA, March 2018.

American Chemical Society National Meeting, Symposium on Structure-Based Drug Design for GPCRs, New Orleans, LA, March 2018.

Keystone Symposium on GPCR Structure and Function: Taking GPCR Drug Development and Discovery to the Next Level, Santa Fe, NM, February 2018.

Biophysical Society Annual Meeting, Atoms to Cells: Modeling Biological Complexity. San Francisco, CA, February 2018.

Azrielli Institute for Systems Biology seminar, Weizmann Institute of Science, Israel, December, 2017.

Frontiers in Systems Biology seminar, Weizmann Institute of Science, Israel, December, 2017.

Binding Kinetics: Time is of the Essence (International Meeting), Berlin, Germany, October 2017.

Biophysics Seminar, Charité Universitätsmedizin, Berlin, Germany, October 2017.

Hertz Foundation West Coast Retreat, San Francisco, CA, October 2017.

International Symposium on GPCRs and G-Proteins, Bonn, Germany, September 2017.

American Chemical Society National Meeting, Symposium on Membrane Proteins, Washington, DC, August 2017.

American Chemical Society National Meeting, Symposium on Computational Studies of Membranes and Membrane-Bound Systems, Washington, DC, August 2017.

Pfizer Global Research and Development Seminar, Cambridge, MA, June 2017.

Presidential Symposium, Annual Meeting of the American Society for Pharmacology and Experimental Therapeutics, Chicago, IL, April 2017.

Biomedical Computation at Stanford Symposium, Stanford, CA, April 2017.

Peter Kollman Lecture, University of California, San Francisco, April 2017.

Stanford Biostatistics Workshop, Stanford, CA, March 2017.

Discovery Chemistry Seminar, Genentech, South San Francisco, CA, February 2017.

External Seminar Series, The Scripps Research Institute, Jupiter, FL, December 2016.

Chemistry and Biochemistry Department Seminar, University of California, San Diego, November 2016.

Molecular Architecture of Life Meeting, Shanghai, China, November 2016.

Statistical Mechanics Seminar, University of California, Berkeley, September 2016.

GPCR-Based Drug Discovery Symposium, Discovery on Target Meeting, Boston, MA, September 2016.

HP Labs Seminar, Hewlett Packard Enterprise, Palo Alto, CA, August 2016.

Bioengineering Department Seminar, University of California, Riverside, June 2016.

Los Alamos Conference on Energy Landscapes: From Protein Folding to Molecular Assembly, Santa Fe, NM, May 2016.

Department of Molecular Physiology and Biological Physics Seminar, University of Virginia, Charlottesville, VA, April 2016.

British Pharmacological Society Cell Signaling Meeting, Leicester, UK, April 2016.

Pharmacology Department Seminar, University of North Carolina at Chapel Hill, March 2016.

Keystone Symposium on G Protein-Coupled Receptors: Structure, Signaling and Drug Discovery, Keystone, CO, February 2016.

Nervana Systems, Palo Alto, CA, January 2016.

Jerusalem School in the Life Sciences, Jerusalem, Israel, January 2016.

Pacifichem Symposium on Challenges and Opportunities for Exascale Computational Chemistry, Honolulu, HI, December 2015.

Pacifichem Symposium on Conformational Dynamics of Biomolecules and the Biomolecule-Solvent Interface, Honolulu, HI, December 2015.

Mathematical Biosciences Institute Workshop on Mathematical Challenges in Drug and Protein Design, Columbus, OH, December 2015.

PACT 2015 Workshop on Software Tools and Techniques for HPC, Clouds, and Server-Class SoCs, San Francisco, CA, October 2015.

UCB Pharma, Braine l'Alleud, Belgium, September 2015.

Frontiers in Medicinal Chemistry, Antwerp, Belgium, September 2015.

Zing Computational Chemical Biology Conference, Cairns, Australia, August 2015. **Plenary speaker**.

Pfizer Gene Family Forum, Rye Brook, NY, June 2015.

Schrödinger User Meeting, South San Francisco, CA, May 2015. **Keynote speaker**.

Delaware Membrane Protein Symposium, Newark, DE, May 2015.

Stanford SystemX Headlights Workshop, Stanford, CA, April 2015.

New York Academy of Sciences Symposium on Positive Allosteric Modulators for Challenging GPCRs: Identification and Optimization, New York, NY, March 2015.

Novartis Institutes for BioMedical Research Symposium, Cambridge, MA, December 2014.

Bioengineering Department Colloquium, Stanford, CA, November 2014.

GPCR-Based Drug Discovery Symposium, Discovery on Target Meeting, Boston, MA, October 2014. **Featured speaker**.

Amgen Colloquium, South San Francisco, CA, October 2014.

American Chemical Society National Meeting, San Francisco, CA, August 2014.

Structural Biology Seminar, Weizmann Institute, Rehovot, Israel, July 2014.

Gordon Research Conference on Phosphorylation & G-Protein Mediated Signaling Networks, Biddeford, ME, June 2014.

Biomolecular Structure, Dynamics, and Function: Membrane Proteins, Nashville, TN, May 2014.

Stanford Computer Forum Annual Meeting, Stanford, CA, April 2014.

Keystone Symposium on G Protein-Coupled Receptors, Snowbird, UT, April 2014.

Gordon Research Conference on Ligand Recognition & Molecular Gating, Ventura, CA, March 2014.

Telluride Workshop on Protein Dynamics, Telluride, CO, August 2013.

CHI Structure-Based Drug Design Conference, Cambridge, MA, June 2013.

Gordon Research Conference on Proteins, Holderness, NH, June 2013.

International Symposium on Structural Neurobiology, Toronto, Canada, June 2013.

Schrodinger User Meeting, Princeton, NJ, June 2013

Biophysical Society Meeting on Membrane Protein Folding, Seoul, Korea, May 2013.

Gordon Research Conference on Molecular Pharmacology, Barga, Italy, April 2013.

American Physical Society March Meeting, Baltimore, MD, March 2013.

Student Conference of the MIT Laboratory for Information and Decision Systems, Cambridge, MA, January 2013.

7th International meeting on the Molecular Pharmacology of G Protein-Coupled Receptors, Melbourne, Australia, December 2012.

New England Structural Biology Association Meeting on Protein-Ligand Thermodynamics and Kinetics: Building Bridges between In Silico and Biophysical Realms, Waltham, MA, November 2012.

MIT Computational and Systems Biology Graduate Program Retreat, Kennebunkport, ME, September 2012.

RIKEN Quantitative Biology Center Inaugural Symposium, Kobe, Japan, November 2012.

Biophysics Seminar, University of Texas Southwestern Medical Center at Dallas, October 2012.

GPCR-Based Drug Discovery Symposium, Discovery on Target Meeting, Boston, MA, October 2012.

Tenth International Catecholamine Symposium, Asilomar, CA, September 2012.

High Performance Computing Workshop, Cetraro, Italy, June 2012.

PrP Canada Annual Meeting and Protein Folding and Disease Conference, Toronto, Canada, June 2012.

Institute for Computational and Mathematical Engineering Seminar, Stanford University, Stanford, CA, May 2012.

Thirtieth Noordwijkerhout-Camerino-Cyprus 2012 Symposium, Amsterdam, Netherlands, May 2012.

Computational Biology Seminar, Memorial Sloan Kettering Cancer Center, April 2012.

Department of Applied Mathematics and Applied Physics Seminar, Columbia University, New York, NY, April 2012.

Electrical and Computer Engineering Department Seminar, University of Texas at Austin, April 2012.

Computer Science Department Seminar, Stanford University, April 2012.

Systems Biology Department Seminar, Harvard Medical School, March 2012.

Lane Center for Computational Biology Seminar, Carnegie Mellon University, Pittsburgh, PA, March 2012.

Computer Science and Engineering Seminar, University of Michigan, Ann Arbor, MI, March 2012.

Department of Applied Mathematics Seminar, Brown University, March 2012.

Biological Signal Transduction Seminar, Department of Molecular and Cellular Physiology, Stanford University, Stanford, CA, February 2012.

Biophysics Seminar, Johns Hopkins University, Baltimore, MD, January 2012.

UCLA Molecular Biology Institute Seminar, Los Angeles, CA, January 2012.

PAPER REVIEWS

Reviewer for Nature, Science, Cell, PNAS, eLife, Nature Methods, Nature Communications, Science Translational Medicine, Neuron, Journal of the American Chemical Society, Structure, PLoS Computational Biology, Drug Discovery Today, Journal of Molecular Biology, Biophysical Journal, Molecular Pharmacology, Journal of Physical Chemistry, Journal of Chemical Theory and Computation, Journal of Computational Physics, Journal of Computational Chemistry, Protein Science, Journal of Computer-Aided Molecular Design, Accounts of Chemical Research, Advanced Drug Delivery Reviews, Biopolymers, Future Medicinal Chemistry, BBA Biomembranes, Scientific Reports, RECOMB, SIGGRAPH, IEEE Conference on Computer Vision and Pattern Recognition, IEEE International Conference on Computer Vision, ACM Transactions on Applied Perception, IEEE Transactions on Pattern Analysis and Machine Intelligence, International Journal of Computer Vision, IEEE Transactions on Image Processing, IEEE Transactions on Parallel and Distributed Systems, Journal of Machine Learning Research.

STUDENTS AND POSTDOCS SUPERVISED

PhD students

1. Naomi Latorraca, Biophysics (2014–present). National Science Foundation Fellowship
2. Robin Betz, Biophysics (2015–present). National Science Foundation Fellowship and Nvidia Fellowship
3. Raphael Townshend, Computer Science (2015–present). National Science Foundation Fellowship
4. Joseph Paggi, Computer Science (2016–present). Stanford Graduate Fellowship; Honorary Bio-X Fellow
5. Alex Powers, Chemical Biology/Chemistry (2018–present). National Science Foundation Fellowship.
6. Alex Tseng, Computer Science (2018–present).
7. Stephan Eismann, Applied Physics (2018–present).
8. Adrian Sanborn, Computer Science (2014–present). National Defense Science and Engineering Graduate Fellowship. I am Adrian's official Stanford advisor, but his primary research supervisor is Erez Lieberman Aiden (Rice University and Baylor College of Medicine, Houston)

I also supervised rotations for over 25 PhD students: William Allen (Neuroscience), Robin Jia (Computer Science), Evan Feinberg (Computational and Mathematical Engineering), Chris Probert (Genetics), Kalli Kappel (Biophysics), Tudor Achim (Computer Science), Johannes Birgmeier (Computer Science); Shenglan Qiao (Physics); Jimmy Yu (Biophysics); Anjan Dwaraknath (Computational and Mathematical Engineering); Raj Setaluri (Computer Science); Ethan Richman (Neuroscience); Evan Antoniuk (Chemistry); Abhimanyu Banerjee (Physics), Reid Pryzant (Computer Science), Caleb Geniesse (Biophysics), Nimit Sohoni (Computational and Mathematical Engineering), Julia Olivieri (Computational and Mathematical Engineering), Kevin Goncalves (Biophysics), Y.J. Tan (Immunology); Julia Belk (Computer Science); Ramya Rangan (Biophysics); Ben Park (Computer Science); Alex Chu (Biophysics); Lydia Hamburg (Biophysics); Shaked Regev (Computational and Mathematical Engineering)

Postdocs

1. A.J. Venkatakrishnan (2014–present; joint with Prof. Brian Kobilka). ChEM-H Seed Grant Award Recipient
2. Samuel Hertig (2015)
3. Brendan Kelly (2015–2017)
4. Joao Rodrigues (2016–present; joint with Prof. Michael Levitt). Stanford School of Medicine Dean's Fellowship
5. Scott Hollingsworth (2016–present). National Library of Medicine Fellowship
6. Siri van Keulen (2017–present). Swiss National Science Foundation Fellowship
7. Carl-Mikael Suomivuori (2018–present). Sigrid Jusélius Foundation Fellowship and Human Frontiers Science Program Fellowship.

MS students

1. Anthony Ma (2015–2017)
2. Rishi Bedi (2016–2018)

Undergraduate students

Chaitanya Asawa (Computer Science), Esha Maiti (Math and Computational Science), Richard Mu (Computer Science and Electrical Engineering), Jason Wang (Math and Computational Science),

Jessica Zhao (Computer Science), Connor Brinton (Computer Science), Michael Hashe (Computer Science), Niranjan Balachander (Computer Science), Jonathan Tynan (Mathematics), Ramin Ahmari (Computer Science), Augustine Chemparathy (Bioengineering), Milind Jagota (Electrical Engineering)

TEACHING

Summary

I created two completely new computational biology courses, CS 279 and CS 371, after arriving at Stanford in 2014. The former has grown from 17 to 142 students between 2014 and 2017, and the latter has grown from 5 to 39 students. A majority (58%) of the 142 students enrolled in CS 279 in 2017 were undergraduates. This fall I will be teaching (with Andrew Ng) Stanford's main machine learning course, CS 229, projected to have approximately 1000 students. I also coordinated two for-credit seminar series in computational biomedicine, the most recent of which had 287 students. Comments on recent student evaluations include:

> "Best class I've taken at Stanford so far. Ron is an incredible lecturer that makes the most complex topics seem simple."
>
> "One of the best teachers I've had at Stanford in all four years as an undergrad … one of the best courses I've taken at Stanford."

Computer Science (CS) 279: Computational Biology: Structure and Organization of Biomolecules and Cells

Cross-listed in Computational and Mathematical Engineering, Bioengineering, Biophysics, and Biomedical Informatics
Stanford, 2014, 2015, 2016, 2017
http://cs279.stanford.edu
Computational techniques for investigating and designing the three-dimensional structure and dynamics of biomolecules and cells. These computational methods play an increasingly important role in drug discovery, medicine, bioengineering, and molecular biology. Course topics include protein structure prediction, protein design, drug screening, molecular simulation, cellular-level simulation, image analysis for microscopy, and methods for solving structures from crystallography and electron microscopy data.

Computer Science (CS) 371: Computational Biology in Four Dimensions

Cross-listed in Computational and Mathematical Engineering, Biophysics, and Biomedical Informatics
Stanford, 2014, 2016, 2017, 2018
http://cs371.stanford.edu
Cutting-edge research on computational techniques for investigating and designing the three-dimensional structure and dynamics of biomolecules, cells, and everything in between. These techniques, which draw on approaches ranging from physics-based simulation to machine learning, play an increasingly important role in drug discovery, medicine, bioengineering, and molecular biology. Course is devoted primarily to reading, presentation, discussion, and critique of papers describing important recent research developments.

Computer Science (CS) 229: Machine Learning

Stanford, 2018
http://cs229.stanford.edu
Topics: statistical pattern recognition, linear and non-linear regression, non-parametric methods, exponential family, GLMs, support vector machines, kernel methods, model/feature selection, learning theory, VC dimension, clustering, density estimation, EM, dimensionality reduction, ICA, PCA, reinforcement learning and adaptive control, Markov decision processes, approximate dynamic programming, and policy search. Prerequisites: linear algebra, and basic probability and statistics.

Computer Science (CS) 109: Introduction to Probability for Computer Scientists
Stanford, 2015
Topics include: counting and combinatorics, random variables, conditional probability, independence, distributions, expectation, point estimation, and limit theorems. Applications of probability in computer science including machine learning and the use of probability in the analysis of algorithms.

Computational and Mathematical Engineering (CME) 500: Seminar on Computation and Mathematics in Biology
Stanford, 2014
This course serves as the main seminar series of the Institute for Computational and Mathematical Engineering. My version featured experts on a variety of topics in computational and mathematical biology.

Computer Science (CS) 522: Seminar in Artificial Intelligence in Healthcare
Stanford, 2017
Artificial intelligence is poised to make radical changes in healthcare, transforming areas such as diagnosis, genomics, surgical robotics, and drug discovery. In the coming years, artificial intelligence has the potential to lower healthcare costs, identify more effective treatments, and facilitate prevention and early detection of diseases. This class is a seminar series featuring prominent researchers, physicians, entrepreneurs, and venture capitalists, all sharing their thoughts on the future of healthcare. I am the faculty sponsor for this course, which is largely student-organized.

LANGUAGES

Fluent in English, French, Hebrew, and Norwegian. Basic German.