Education

1984 Ph.D. Harvard University in applied mathematics

1980 M.Sc. Syracuse University (overlapped work at IBM Data Systems Division)

1977 B.Sc. Yale University

Academic Positions:

1995 – present Professor of Computer Science, Courant Institute of Mathematical Sciences New York University

1990-1995: Associate Professor of Computer Science Courant Institute of Mathematical Sciences New York University

1984-1990: Assistant Professor of Computer Science Courant Institute of Mathematical Sciences New York University

1991-1992, 1998-1999, 2006-2007: Invited Professor at INRIA, France

Journal Publications last Four Years:

1. “Parametric Bayesian Priors and Better Choice of Negative Examples Im- prove Protein Function Prediction” Noah Youngs, Duncan Penfold-Brown, Kevin Drew, Dennis Shasha, Richard Bonneau Bioinformatics 2013; doi: 10.1093/bioinformatics/btt110 http://bit.ly/11niyxr

2. “miR-EdiTar: A database of predicted A-to-I edited miRNA target sites” Alessandro Lagan, Alessio Paone, Dario Veneziano, Luciano Cascione, Pierluigi Gasparini, Stefania Carasi, Francesco Russo, Giovanni Nigita, Valentina Macca, Rosalba Giugno, Alfredo Pulvirenti, Dennis Shasha, Al- fredo Ferro and Carlo M. Croce Bioinformatics 2012

3. “Nitrogen economics of root foraging: Transitive closure of the nitrate- cytokinin relay and distinct systemic signaling for N supply vs. demand.” Sandrine Ruffel, Gabriel Krouk, Daniel Ristova, Dennis Shasha, Kenneth Birnbaum, and Gloria Coruzzi, Proc U.S. National Academy of Science November 8, 2011

4. “Rationaldesignoftemperature-sensitiveallelesusingcomputationalstruc- ture prediction.” Christopher S. Poultney, Glenn L. Butterfoss, Michelle R. Gutwein, Kevin Drew, David Gresham, Kristin C. Gunsalus, Dennis E. Shasha, Richard Bonneau. PLoS ONE 6(9): e23947. doi:10.1371/journal.pone.0023947

5. “The proteome folding project: proteome-scale prediction of structure and function” Kevin Drew, Patrick Winters, Glenn L. Butterfoss, Vik- torsBerstis, Keith Uplinger, Jonathan Armstrong, Michael Riffle, Eric Schweighofer, Bill Braverman, David R. Goodlett, Trisha N. Davis, Den- nis Shasha, Lars Malmstrom, and Richard Bonneau August 8, 2011, doi: 10.1101/gr.121475.111 Genome Res. 2011.

6. “Predictive network modeling of the high-resolution dynamic plant tran- scriptome in response to nitrate,” Gabriel Krouk, Piotr Mirowski, Yann LeCun, Dennis E Shasha and Gloria M Coruzzi Genome Biology 2010, 11:R123 doi:10.1186/gb-2010-11-12-r123 Published: 23 December 2010

7. “Estimation of genome-wide redundancy in Arabidopsis thaliana,” Huang- Wen Chen, Sunayan Bandyopadhyay, Dennis E. Shasha, and Kenneth D. Birnbaum accepted, BMC Evolutionary Biology 2010, 10:357; doi:10.1186/1471- 2148-10-357

8. “Fast Elastic Peak Detection for Mass Spectrometry Data Mining,” X. Zhang, D. Shasha, Y. Song and J. T. L. Wang, IEEE Transactions on Knowledge and Data Engineering, Issue 99. November 29, 2010, doi: 10.1109/TKDE.2010.238

9. ”SING: Subgraph search In Non-homogeneous Graphs” Raffaele Di Natale , Alfredo Ferro , Rosalba Giugno , Misael Mongiovi , Alfredo Pulvirenti and Dennis Shasha BMC Bioinformatics 2010, 11:96doi:10.1186/1471-2105- 11-96 http://www.biomedcentral.com/1471-2105/11/96

10. ”VirtualPlant: a software platform to support system biology research” Manpreet S. Katari, Steve D. Nowicki, Felipe F. Aceituno, Damion Nero, Jonathan Kelfer, Lee Parnell Thompson, Juan M. Cabello, Rebecca S. Davidson, Arthur P. Goldberg, Dennis E. Shasha, Gloria M. Coruzzi, and Rodrigo A. Gutierrez, Plant Physiology 152:500-515 (2010)

11. ”miRo: a miRNA knowledge base” A. Lagana, S. Forte, A. Giudice, M. R. Arena, P. L. Puglisi, R. Giugno,A. Pulvirenti,D. Shasha, A. Ferro Database: The Journal of Biological Databases and Curation,Oxford Uni- versity Press,2009 doi: 10.1093/database/bap008