

EDUCATION

- 2011 **Massachusetts Institute of Technology** **Cambridge, MA**
Ph.D., Computer Science (on non-resident status during 2007-2011)
- PhD Thesis: Algorithms for the Analysis of Protein Interaction Networks.
- 2002 **Stanford University** **Stanford, CA**
M.S., Computer Science (specializing in Artificial Intelligence and Computational Biology)
- MS Thesis: An efficient algorithm for identifying 3-D structural patterns in protein structures.
- 2000 **Indian Institute of Technology** **Kanpur, India**
B.Tech., Computer Science & Engineering

HONORS & AWARDS

- Test of Time Award at the RECOMB 2019 conference. The award was in recognition of the paper my co-authors and I presented at RECOMB 2007.
- George M. Sprowls Award for the Best Ph.D. Theses in Computer Science at MIT (2011).
- Christopher Stephenson Memorial Award for Best Masters Research in Computer Science at Stanford (2002).
- World Finalist, ACM Programming Contest (represented IIT Kanpur, the only Indian team) (2000).
- Ranked 17th nationwide (among approx. 150,000 applicants) in the IIT entrance examinations in India (1996).
- In 1996, I was the only student in India offered admission to the IITs as well as to AIIMS, India's premier medical school. Ranked 26th nationwide in the AIIMS entrance examination.
- National Talent Search Scholar, India (1994).

PUBLICATIONS

Below, "*" denotes shared first authorship. "\$" indicates that the paper has 50 or more citations while "\$\$" indicates the paper has 300 or more citations (as counted by Google Scholar in 2019).

- Park D*, Singh R*, Baym M, Liao CS, Berger B. *IsoBase: a database of functionally related proteins across PPI networks*. Nucleic Acids Res. 2011 Jan;39(Database issue):D295-300. \$
- Friedman AA, Tucker G, Singh R, et al. *Proteomic and functional genomic landscape of receptor tyrosine kinase and Ras to extracellular signal-regulated kinase signaling*. Science Signaling 2011; 4(196). \$
- Singh R*, Park D*, Xu J*, Hosur R, Berger B. *Struct2Net: a web service to predict protein-protein interactions using a structure-based approach*. Nucleic Acids Res. 2010 Jul;38(Web Server issue):W508-15. \$
- Liao CS, Lu K, Baym M, Singh R, Berger B. *IsoRankN: spectral methods for global alignment of multiple protein networks*. Bioinformatics. 2009 June 15; 25(12): i253-i258. \$\$
- Kaplow IM*, Singh R*, Friedman A, Bakal C, Perrimon N, Berger B. *RNAiCut: automated detection of significant genes from functional genomic screens*. Nature Methods. 2009 Jul;6(7):476-7.
- Singh R, Xu J, Berger B. *Global alignment of multiple protein interaction networks with application to functional orthology detection*. Proc Natl Acad Sci U S A. 2008 Sep 2;105(35):12763-8. \$\$
- Singh R, Xu J, Berger B. *Global alignment of multiple protein interaction networks*. Pac Symp Biocomput. (PSB) 2008:303-14. \$
- Singh R, Berger B. *Influence Flow: Integrating Pathway-specific RNAi data and Protein Interaction Data*. Int'l Symp of Intelligent Sys in Mol Bio (ISMB) 2007, PLoS Track.
- Singh R, Xu J, Berger B. *Pairwise Global Alignment of Protein Interaction Networks by Matching Neighborhood Topology*. Proc of Int'l Conf on Research in Comp Mol Bio (RECOMB) 2007. \$\$
 - We received the Test of Time Award for this paper at RECOMB 2019.
- Sontag D*, Singh R*, Berger B. *Probabilistic modeling of systematic errors in two-hybrid experiments*. Pac Symp Biocomput (PSB) 2007.

- Sterner B, Singh R, Berger B. *Predicting and annotating catalytic residues: an information theoretic approach*. J Comput Biol. 2007 Oct;14(8):1058-7.
- Singh R*, Xu J*, Berger B. *Struct2net: integrating structure into protein-protein interaction prediction*. Pac Symp Biocomput (PSB) 2006. §
- Hosur R, Singh R, Berger B. *Sparse estimation for structural variability*. Algorithms Mol Biol. 2011; 6: 12.
- Singh R, Berger B. *Chaintweak: sampling from the neighbourhood of a protein conformation*. Pac Symp Biocomput (PSB) 2005:52-63.
- Singh R, Palmer N, Gifford D, Berger B, Bar-Joseph Z. *Active Learning for Sampling in Time-Series Experiments With Application to Gene Expression Analysis*. Proc. of the 22nd International Conference on Machine Learning (ICML), 2005.
- Singh R, Saha M. *Identifying structural motifs in proteins*. Pac Symp Biocomput (PSB) 2003:228-39.
- Deshpande H, Nam U, Singh R. *Classification of Music Signals in the Visual Domain*. Proc of Digital Audio Effects Conf, 2001. §

EMPLOYMENT

- 2012-2019 **Tech Square Trading** **Boston, MA**
Co-founder, Chief Executive Officer & Portfolio Manager
 Tech Square Trading (TST) was a quantitative market-neutral equities fund. The firm traded large and mid-cap equities in US, Europe and Japan.
- Led a high-caliber, collegial team of 4 quantitative and 2 finance/marketing professionals.
 - Oversaw all research and trading efforts within the firm, covering ideas from market-microstructure, portfolio construction, machine learning and use of alternative data etc.
 - As the CEO of this fund, became intimately familiar with all aspects of the business management: prime-brokerage relationships, data acquisition and licensing, and technology providers. Established and nurtured a high-impact internship program. About 30 students, primarily from MIT and Harvard, have interned with the firm. Along with my team-members, I guided the interns' work towards expanding TST's alpha-library. This alpha-library, in turn, enabled a machine learning based systematic capital-allocation framework.
- 2008-2011 **SAC Capital Advisors, Multiquant Division (now Cubist Systematic)** **New York, NY**
Research Analyst
- Designed, implemented and operated statistical arbitrage strategies.
 - Performed computational and statistical analysis of large datasets to generate trading signals.
- 2007-2008 **Merrill Lynch** **New York, NY**
Associate, Global Strategic Risk Group (GSRG is a proprietary trading group within ML)
- As part of a small team, I maintained, monitored and enhanced a family of high-frequency and statistical-arbitrage strategies that traded in U.S., Europe, and Canada.
- 2003-2007 **Prof. Bonnie Berger's Research Group, MIT** **Cambridge, MA**
Research Assistant
- My research was on modeling proteins and their interactions.
- 2002-2003 **Accelrys Inc.** **San Diego, CA**
Software Engineer (Bioinformatics Applications Group, Life Sciences R&D Divn.)
- I co-led the initial design work for a new version of DS GCG, a bioinformatics application with a multi-million dollar revenue-stream.

PATENT

Berger B. and Singh R., *Method for Identifying Network Similarity by Neighborhood Matching*, USPTO # 8000262.

SOFTWARE AND COMMUNITY RESOURCES

- *IsoRank and IsoRank-N*: executables for the IsoRank/IsoRankN programs, along with test data (<http://isorank.csail.mit.edu>).

- *IsoBase*: a web-database of functional ortholog predictions, using IsoRank/IsoRankN (<http://isobase.csail.mit.edu>).
- *Struct2Net*: a web-service for predicting interaction between two proteins, given just sequence data (<http://struct2net.csail.mit.edu>).
- *ChainTweak*: a program for sampling the neighborhood of a given protein's backbone structure (<http://theory.csail.mit.edu/chaintweak/>).
- *RNAiCut*: a web-service for choosing the right cut-offs in the results from RNAi gene-perturbation assays (<http://rnaicut.csail.mit.edu>).

TEACHING & COMMUNITY SERVICE

- Have reviewed manuscripts for various journals and conferences: Bioinformatics, J of Comp Bio (JCB), ACM Trans on Comp Bio and Bioinformatics (TCBB), Int'l Conf of Machine Learning (ICML), RECOMB etc.
- Teaching Assistant for 6.867, MIT's main graduate-level course on Machine Learning (2005).
- Designed and taught a 12-week, 3-hours-per-week class on Classical Mechanics for local high school students, as part of MIT's Educational Studies (Outreach) Program (2003).