USMAN W. ROSHAN

CONTACT INFORMATION

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EDUCATION

05/2004	Ph.D. Computer Sciences, The University of Texas at Austin Thesis title: "Algorithmic techniques for improving the speed and accuracy of phylogenetic methods" Advisor: Tandy Warnow

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RESEARCH EXPERIENCE

Bioinformatics: sequence alignment, evolutionary tree reconstruction, cancer and disease risk prediction from DNA with machine learning, GPU programs, DNA and protein sequence classification

Machine learning and AI: 0/1 loss optimization, random weights, representation learning

Current projects (12/25/18):

- Stroke lesion identification in brain MRI images with machine learning and AI
- Cancer and disease risk prediction from whole exome and whole genome sequence data
- Unsupervised feature learning for images with random convolutional neural networks
- Unsupervised feature learning random weights, feature learning
- Optimization and adversarial attacks on 0/1 loss
- Feature learning for DNA and protein sequence classification

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ACADEMIC EMPLOYMENT

08/2017-present	Director of Data Science, Department of Computer Science New Jersey Institute of Technology • Led the creation of NJIT's Master Data Science program • Created and teach core machine learning and deep learning courses
08/2010-present	Associate Professor, Department of Computer Science, New Jersey Institute of Technology
08/2007-present	Director of Bioinformatics, Department of Computer Science New Jersey Institute of Technology
08/2004-07/2010	Assistant Professor, Department of Computer Science, New Jersey Institute of Technology
07/2001-07/2004	Research Assistant, Department of Computer Science, The University of Texas at Austin

08/1998-05/2001 Teaching Assistant, Department of Computer Science,
The University of Texas at Austin

PROFESSIONAL CONSULTING

Services:

- Provide hands-on expertise for designing and implementing machine learning and artificial intelligence solutions to business problems
- Provide conceptual and hands-on training in machine learning methods

10/2018-11/2018 UPS, Parsippany, NJ, USA
Created and delivered a Python-based data science bootcamp to UPS employees. Curriculum included linear and non-linear classification, feature analysis, data visualization, time series, text classification and word embeddings, various software packages, convolutional neural nets for image classification and running them on cloud GPUs

10/2016-12/2017 Sollers College, Edison, NJ, USA
Developed and taught the machine learning module of Sollers Data Science certificate program. Hands-on delivery of self-designed curriculum with the Python scikit-learn machine learning library.

02/2017-10/2017 SWK Technologies, Livingston, NJ, USA
Created a machine learning program with the Python scikit-learn machine learning library to automatically and correctly classify a customer complaint ticket into problem category

10/2017 Allianz Global Investors, New York, NY, USA
Delivered hands-on machine lectures to the Research and Development group. Lectures cover basic and advanced machine learning methods demonstrated on finance problems with the Python scikit-learn machine learning library

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INDUSTRY EXPERIENCE

05/2000-08/2000 Kurion.com, Austin, TX, USA, *Software Intern*
Designed and implemented using Perl, HTML, JavaScript, and Java, an interactive web based program that allows one to create a customized web portal working on top of Kurion's existing architecture

05/1998-07/1998 National Instruments, Austin, TX, USA, *Software Intern*
Researched and implemented graph-drawing algorithms to design an automatic wire-routing algorithm to be used in National Instruments software product called Labview.

TEACHING

08/2004-present Created and taught new undergraduate and graduate courses at NJIT

Undergraduate:

- BNFO 135: Programming for bioinformatics
- BNFO 236: Introduction to bioinformatics algorithms

Graduate:

- BNFO 601: Foundations of bioinformatics I

- BNFO 602: Foundations of bioinformatics II
- BNFO 615: Machine learning for bioinformatics
- CS 675: Machine Learning
- CS 677: Deep Learning

08/1998-05/2001 Teaching assistant for *Calculus* and *Discrete Mathematics* courses

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GRANTS

1. NJIT internal faculty seed grant "GPU and machine learning solutions to problems in comparative genomics and data science" for $7,500, 2014-2015
2. Mini career grant award funded by UPS for $1,700, 2005
3. NJIT PI on National Science Foundation grant "Collaborative Research: Large-scale simultaneous alignment and phylogeny estimation" for $53,324, 2007-2012
4. Senior personnel of the Cyber Infrastructure for Phylogenetic Research grant (CIPRES). CIPRES was a collaboration of several institutions including NJIT and was funded by the NSF for $11.6 million. The goal of CIPRES was to develop the algorithms and software for building the evolutionary Tree of Life.

UNIVERSITY SERVICE

- 2017 – 2018: Faculty search committee
- 2016 – 2017: Led creation of Masters in Data Science at NJIT
- 2016 – current: NJIT Faculty Senate representative from the Computer Science Department
- 2013 – 2013: NJIT Academic Plan committee for 2013-2015
- 2010 – current: Computer Science Department MS Committee
- 2007 – 2008: Chair of faculty search committee
- 2004 – 2006: Library representative

PROFESSIONAL SERVICE

- Program committee member of
    - 16th IEEE Conference on Machine Learning and Applications (2017)
    - 15th IEEE Conference on Machine Learning and Applications (2016)
    - 7th IEEE Bioinformatics and Bioengineering Conference (2007)
    - 35th IEEE Conference on Parallel Processing (2006)
- Referee for journals:
    - Bioinformatics
    - BMC Bioinformatics
    - BMC Evolutionary Biology
    - Nucleic Acids Research
    - Knowledge and Information Systems
    - Systematic Biology
    - Transactions on Parallel and Distributed Systems
    - Journal of Parallel and Distributed Computing
    - International Journal on Foundations of CS
    - Journal of Theoretical Biology
    - Pattern Recognition Letters
    - Transactions on Computational Biology and Bioinformatics

- International Journal of Bioinformatics Research and Applications

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PUBLICATIONS

In preparation

1. Yunzhe Xue, Fadi Farhat, William Graves, and Usman Roshan, A multi-path multi-modal 3D convolutional neural network system for predicting lesions in brain MRI images

2. Abdulrhman Aljouie and Usman Roshan, Predicting brain and kidney cancer survival times with somatic mutations from whole exome sequences and machine learning

3. Meiyan Xie and Usman Roshan, Stochastic coordinate descent for 0/1 loss and its sensitivity to adversarial attacks

4. Meiyan Xie and Usman Roshan, Unsupervised feature learning with random hyperplanes

Under revision

1. Yunzhe Xue and Usman Roshan, Unsupervised feature learning for image classification and image retrieval with random depthwise convolutional neural networks

Book Chapters

1. U. Roshan Multiple sequence alignment using Probcons and Probalign, in "Methods in Molecular Biology: Multiple Sequence Alignment Methods", ed. David J. Russell, Humana Press (Springer), 2013, 147-15
2. K. M. Kjer, U. Roshan, and J. J. Gillespie, Structural and evolutionary considerations for multiple sequence alignment of RNA, and the challenges for algorithms that ignore them, in “Perspectives on Biological Sequence Alignment: Where, How, and Why It Matters”, ed. Michael Rosenberg, University of California Press, USA, 2009, 105-151
3. D. Bader, U. Roshan, and A. Stamatakis, Computational grand challenges in assembling the Tree of Life: problems and solutions, in “Advances in Computers, Computational Biology and Bioinformatics”, ed. Marvin Zelkowitz and Chau-wen Tseng, Elsevier, 2006, 128-178
4. U. Roshan, B. M. E. Moret, T. L. Williams, T. Warnow, Performance of supertree methods on various dataset decompositions in “Phylogenetic Supertrees: Combining Information to Reveal the Tree of Life”, ed. O.R.P. Bininda Emonds, Springer, 2004, 301-329

Conferences (peer reviewed)

1. A. Aljouie, L. Zhong, and U. Roshan, High scoring segment selection for pairwise whole genome sequence alignment with the maximum scoring subsequence and GPUs, accepted to the *International Conference on Intelligent Biology and Medicine* (ICIBM), 2018

2. A. Aljouie, N. Patel, and U. Roshan, Cross-validation and cross-study validation of kidney cancer with machine learning and whole exome sequences from the National Cancer Institute, Proceedings of the *IEEE Computational Intelligence in Bioinformatics and Computational Biology* (CIBCB), 2018

3. P. Melman and U. Roshan, A k-means based feature learning method for protein sequence classification, Proceedings of the *10th International Conference on Bioinformatics and Computational Biology* (BICOB), 2018

4. N. Patel, A. Aljouie, B. Jadhav, and U. Roshan, Cross-validation and cross-study validation of chronic lymphocytic leukemia with exome sequences and machine learning, *Proceedings of IEEE International Conference on Bioinformatics and Biomedicine* (BIBM), 2015

5. A. Aljouie and U. Roshan, Prediction of continuous phenotypes in mouse, fly, and rice genome wide association studies with support vector regression SNPs and ridge regression classifier, *Proceedings of the 14th IEEE International Conference on Machine Learning and Applications* (ICMLA), 2015

6. T. Turki, M. A. Ihsan, N. Turki, J. Zhang, U. Roshan, and Z. Wei, Top-k parameterized boost, *Proceedings of the Second International Conference on Mining Intelligence and Knowledge Exploration,* University College Cork, Ireland, 2014, Lecture Notes in Computer Science, Springer, Rajendra Prasath, Philip O'Reilly, and T. Kathirvalavakumar eds

7. T. Turki and U. Roshan , Weighted maximum variance dimensionality reduction, *Proceedings of the 6th Mexican Conference on Pattern Recognition,* Cancun, Mexico, 2014, Lecture Notes in Computer Science, Springer, JF. Martínez-Trinidad, JA. Carrasco-Ochoa, JA. Olvera-Lopez, J. Salas-Rodríguez, Y. C. Suen

8. U. Roshan, D. R. Livesay, and S. Chikkagoudar, Improving progressive alignment for phylogeny reconstruction using parsimonious guide-trees, Proceedings of The IEEE 6th Symposium on Bioinformatics and Bioengineering (BIBE06) Washington D.C., USA, 2006
9. U. Roshan, D. R. Livesay, D. La, Improved phylogenetic motif detection using parsimony, Proceedings of The IEEE 5th Symposium on Bioinformatics and Bioengineering (BIBE05) Minneapolis, Minnesota, USA, 2005
10. Z. Du, A. Stamatakis, F. Lin, U. Roshan, L. Nakhleh, Parallel divide-and-conquer phylogeny reconstruction by maximum likelihood, Proceedings of The 2005 International Conference on High Performance Computing and Communications (HPCC05) 2005, Naples, Italy, 2005
11. C. Coarfa, Y. Dotsenko, J. Mellor-Crummey, L. Nakhleh, and U. Roshan, PRec-I-DCM3: A Parallel Framework for Fast and Accurate Large Scale Phylogeny Reconstruction, Proceedings of The First IEEE Workshop on High Performance Computing in Medicine and Biology (HiPCoMB 2005), Fukuoka, Japan, 2005
12. U. Roshan, B. M. E. Moret, T. L. Williams, T. Warnow, Rec-I-DCM3: A Fast Algorithmic Technique for Reconstructing Large Phylogenetic Trees, Proceedings of the IEEE Computational Systems Bioinformatics (CSB04) Stanford (CA), USA, 2004
13. B. M. E. Moret, U. Roshan, T. Warnow, "Sequence length requirements for phylogenetic methods", Proc. 2nd Int'l Workshop on Algorithms in Bioinformatics (WABI02) Rome, Italy, 2002 Lecture Notes in Computer Science 2452, 343-356, Springer Verlag, Roderic Guido and Dan Gusfield, eds
14. L. Nakhleh, U. Roshan, L. Vawter, and T. Warnow, "Estimating the deviation from a molecular clock", Proc. 2nd Int'l Workshop on Algorithms in Bioinformatics (WABI02) Rome, Italy, 2002 Lecture Notes in Computer Science 2452, 287-299, Springer Verlag, R. Guido and D. Gusfield, eds
15. L. Nakhleh, B. M. E. Moret, U. Roshan, K. St. John, J. Sun, T. Warnow, "The accuracy of fast phylogenetic methods for large datasets", Proc. 7th Pacific Symposium on BioComputing (PSB02) Kauai, USA, 2002, World Scientific Pub, 211-222
16. L. Nakhleh, U. Roshan, K. St. John, J. Sun, T. Warnow, "The performance of phylogenetic methods on trees of bounded diameter", Proc. 1st Workshop on Algorithms in Bioinformatics (WABI01) Aarhus, Denmark, 2001, Lecture Notes in Computer Science 2149, 189-203, Springer Verlag, Olivier Gascuel and B. M. E. Moret, eds
17. L. Nakhleh, U. Roshan (*corresponding author*), K. St. John, J. Sun, T. Warnow, Designing fast converging phylogenetic methods", Proceedings of The 9th Int'l Conference on Intelligent Systems on Molecular Biology (ISMB01) Copenhagen, Denmark, 2001

Journals (peer reviewed)

1. A. Aljouie, L. Zhong, and U. Roshan, High scoring segment selection for pairwise whole genome sequence alignment with the maximum scoring subsequence and GPUs, to be published in the *International Journal of Computational Biology and Drug Design,* 2018
2. A. Aljouie, N. Patel, B. Jadhav, and U. Roshan (*corresponding author*), Cross-validation and cross-study validation of chronic lymphocytic leukemia with exome sequences and machine learning, *International Journal of Data Mining and Bioinformatics,* Vol 16, No. 1, 2016
3. A. Aljouie, M. Esfandiari, S. Ramakrishnan, and U. Roshan (*corresponding author*), Chi8: a GPU program for detecting significant interacting SNPs with the chi-square 8-df test, *BMC Research Notes*, 8:436, 2015
4. T. Turki and U. Roshan (*corresponding author*), MaxSSmap: A GPU program for mapping divergent short reads to genomes with the maximum scoring subsequence*, BMC Genomics*, 15:969, 2014
5. U. Roshan (*corresponding author*), S. Chikkagoudar, Z. Wei, K. Wang, and H. Hakonarson, Ranking causal SNPs and disease associated regions in genome wide association studies by the support vector machine and random forest, *Nucleic Acids Research*, 39(9): e62-e62, 2011
6. S. Chikkagoudar , D. R. Livesay, and U. Roshan (*corresponding author*), PLAST-ncRNA: Partition function Local Alignment Search Tool for non-coding RNA sequences, *Nucleic Acids Research*, 38, no. suppl 2: W59-W63, 2010
7. U. Roshan (*corresponding author*), S. Chikkagoudar, and D. R. Livesay, Searching for RNA homologs within large genomic sequences using partition function posterior probabilities, BMC Bioinformatics, 9:61, 2008
8. D. R. Livesay, P. D. Kidd, S. Eskandari, and U. Roshan, Assessing the ability of sequence-based methods to provide functional insight within membrane integral proteins: a case study analyzing the neurotransmitter/Na+ symporter family BMC Bioinformatics, 8:397, 2007
9. S. Chikkagoudar, U. Roshan (*corresponding author*) and D. R. Livesay, eProbalign: generation and manipulation of multiple sequence alignments using partition function posterior probabilities, Nucleic Acids Research, Vol 35, 2007, W675-W677
10. U. Roshan (*corresponding author*) and D. R. Livesay, Probalign: multiple sequence alignment using partition function posterior probabilities, Bioinformatics, 22(22), 2006, 2715-21
11. C. Coarfa, Y. Dotsenko, J. Mellor-Crummey, L. Nakhleh, and U. Roshan, PRec-I-DCM3: A Parallel Framework for Fast and Accurate Large Scale Phylogeny Reconstruction, International Journal on Bioinformatics Research and Applications, 2(4), 2006, 407-419
12. Z. Du, F. Lin, and U. Roshan, Reconstruction of large phylogenetic trees: a parallel approach, Computational Biology and Chemistry, 29(4), 2005, 273-280
13. I. S. Dhillon, E. M. Marcotte, U. Roshan (*corresponding author*), Diametrical Clustering for identifying anti- correlated gene clusters, Bioinformatics, 19, 2003, 1612-1619
14. L. Nakhleh, U. Roshan (*corresponding author*), K. St. John, J. Sun, T. Warnow, Designing fast converging phylogenetic methods", Bioinformatics, 17, 2001, S190-S198

Tutorials (peer reviewed)

1. D. Bader, A. Stamatakis, and U. Roshan, Computational challenges in assembling the Tree of Life, Supercomputing 2005 (SC05), Seattle, WA, USA

Unpublished

1. Usman Roshan, An iterated coordinate descent algorithm for regularized 0/1 loss minimization, 2017
2. Pranitha Surya Andalam and Usman Roshan, Semi-supervised weighted maximum variance dimensionality reduction, 2016
3. Paras Garg and Usman Roshan, A study of multiple kernel learning for predicting type 1 diabetes from WTCCC genome wide association studies, 2010
4. Usman Roshan, Fast and accurate population structure identification with a greedy support vector machine clustering algorithm, 2008
5. Usman Roshan, Semi-supervised feature extraction for population structure identification using the Laplacian linear discriminant, 2008

PROFESSIONAL PRESENTATIONS

1. U. Roshan, K-means based feature learning for protein sequence classification, International Conference on Bioinformatics and Computational Biology (BICOB), March 2018 (refereed)
2. U. Roshan, Introduction to machine learning with Python scikit learn, 4th Annual New Jersey Big Data Alliance Symposium, NJIT, Newark, March 2017 (invited)
3. U. Roshan, Large-scale genomics and machine learning on Kong, Symposium on "Research and Teaching using IST-ARCS managed high performance computing, big data, and database resources", NJIT, Newark, New Jersey, January 2016 (invited)
4. U. Roshan, BSP: an iterated local search heuristic for the hyperplane with the minimum number of classifications, 12th Annual conference on Frontiers in Applied and Computational Mathematics, NJIT, Newark, New Jersey, Fall 2015 (invited)
5. U. Roshan, GPU and machine learning solutions for comparative genomics, Phylolab reunion, The University of Texas at Austin, June 2014 (invited)
6. U. Roshan, Bioinformatics at NJIT, Symposium on "Careers in Bioinformatics: From the Lab to the Clinic and Beyond", Science, New York Academy of Sciences and NYU-Poly Graduate Center-Bioinformatics, May 2011 (invited)
7. U. Roshan, Discriminative learning methods for analyzing genome-wide association studies, Center of Applied Genomics, Children's Hospital of Philadelphia, Fall 2009 (invited)
8. U. Roshan, Population structure prediction using support vector machines, Seminar series in the Program for Integrative Information, Computer and Application Sciences (PICASso), Princeton University, Spring 2008 (invited)
9. U. Roshan, Sequence Alignment Using Partition Function Posterior Probabilities, Bioinformatics Seminar, University of North Carolina at Charlotte, Fall 2007 (invited)
10. U. Roshan, Improved progressive alignment for phylogeny reconstruction using parsimony and likelihood guide-trees, Society for Molecular Biology and Evolution, Tempe, Arizona, Spring 2006 (refereed)
11. U. Roshan, Towards optimal tree alignments: heuristics and applications to phylogeny reconstruction and phylogenomics, Department of Chemical Engineering Seminar Series, NJIT, 2006 (invited)

12. U. Roshan, Towards optimal tree alignments: heuristics and applications to phylogeny reconstruction and phylogenomics, Mathematical Biology Seminar, Department of Mathematical Sciences, NJIT, 2006 (invited)
13. U. Roshan, Coevolution of DCMs and base methods, Workshop on The problems of phylogenetic analysis of large datasets, Mathematical Biosciences Institute, Ohio State University, Fall 2005 (invited)
14. D. Bader, U. Roshan, and A. Stamatakis, Computational challenges in assembling the Tree of Life, Supercomputing 2005 conference, Seattle, Washington, USA, Fall 2005 (refereed)
15. U. Roshan, Improved phylogenetic motif detection using parsimony, IEEE Bioinformatics and Bioengineering 2005 conference, Minneapolis, Minnesota, USA, Fall 2005 (refereed)
16. U. Roshan, Multiple sequence alignment using parsimony: techniques and performance study, Ward Wheeler's Lab, American Museum of Natural History, NY, USA, Spring 2005
17. U. Roshan, Fast algorithmic techniques for reconstructing large evolutionary trees, Emerging Information Technology Conference 2004, Princeton University, USA, Fall 2004
18. U. Roshan, Rec-I-DCM3: A fast algorithmic technique for reconstructing large phylogenetic trees, IEEE Computational Systems Bioinformatics Conference 2004, Stanford, CA, USA, Summer 2004 (refereed)
19. U. Roshan, Rec-I-DCM3: A fast algorithmic technique for reconstructing large phylogenetic trees, Department of Computer Science, University of Western Ontario, London, Ontario, Canada, Spring 2004 (invited)
20. U. Roshan, Rec-I-DCM3: A fast algorithmic technique for reconstructing large phylogenetic trees, Department of Computer Science, The University of Texas at Dallas, Dallas, TX, USA, Spring 2004 (invited)
21. U. Roshan, Rec-I-DCM3: A fast algorithmic technique for reconstructing large phylogenetic trees, Department of Computer Science, Florida International University, Miami, FL USA, Spring 2004 (invited)
22. U. Roshan, Sequence length requirements for phylogenetic methods, Workshop on Algorithms in Bioinformatics Conference 2002, Rome, Italy, Fall 2002 (refereed)
23. U. Roshan, Designing fast converging phylogenetic methods, International Conference on Intelligent Systems and Molecular Biology, Copenhagen, Denmark, Summer 2001 (refereed)

SOFTWARE AND BENCHMARKS

1. *RDCNN*: Python/Tensorflow programs for generating features for unsupervised feature learning for image recognition from random depthwise convolutional neural networks; Python programs available at https://web.njit.edu/~usman/rdcnn/
2. *MSGA*: Whole genome sequence alignment with the maximum scoring sequence on GPUs available at https://web.njit.edu/~usman/MSGA
3. K-means based feature learning for protein sequence classification; Python programs available at https://web.njit.edu/~usman/kmeans_fl_protein/
4. *ICD*: Iterated coordinate descent algorithm for regularized 0/1 loss; C programs available at https://web.njit.edu/~usman/icd/
5. *MaxSSmap*: GPU program for mapping short DNA sequence fragments to a large DNA genome sequence; available at https://web.njit.edu/~usman/MaxSSmap/

6. *WMV:* C program for weighted dimensionality reduction available at https://web.njit.edu/~usman/wmv/
7. *Chi8*: GPU program for determining the chi-square 8-df test between pairs of SNPs in a genome wide association dataset; available at https://web.njit.edu/~usman/Chi8/
8. *SVMSNPs*: program for selecting SNPs that best separate case from control subjects in genome-wide association studies; available at https://web.njit.edu/~usman/SVMSNPs/.
9. *PLAST-ncRNA*: webserver for a local alignment implementation of Probalign with parameters optimized for RNA homology search in long genomic sequences; server at http://probalign.njit.edu/local
10. *eProbalign*: webserver for Probalign that features the Probalign Alignment Viewer applet for viewing and manipulating alignments by partition function posterior probabilities; server at http://probalign.njit.edu; also available in the CIPRES portal at http://www.phylo.org
11. *Recursive-Iterative-DCM3 (Rec-I-DCM3):* divide-and-conquer approach for reconstructing very large phylogenetic trees with high speed and high accuracy; available from https://web.njit.edu/~usman/RecIDCM3.html and also in the CIPRES portal at http://www.phylo.org
12. Diametrical clustering for gene expression data; available at https://web.njit.edu/~usman/diametrical/

STUDENTS

Current students

- Meiyan Xie, PhD thesis advisor (expected 2021)
- Yunzhe Xue, PhD thesis advisor (expected 2020)
- Abdulrhman Aljouie, PhD thesis advisor (expected 2019)
- Wei Chun Chen, PhD thesis advisor (expected 2021)
- Fadi Farhat, MS thesis advisor (expected 2019)

Previous students

- Paul Melman, MS thesis advisor, 2017
- Ling Zhong, PhD thesis advisor, 2017
- Pranitha Andalam, MS thesis advisor, 2016 (first position at Xilinx, Colorado)
- Nandini Ghosh, MS thesis advisor, 2015
- Nihir Patel, MS thesis advisor, 2014 (first position at Mt. Sinai Hospital)
- Wei Wang, PhD committee member 2014, (first position as data scientist in industry)
- Bharati Jhadav, MS thesis advisor, 2014, (first position at Mt. Sinai Hospital)
- Harishitha Damerla, MS project advisor, 2013
- Amiel Meiseles, MS project advisor, 2013
- Srividya Ramakrishnan, MS thesis advisor, 2013 (first position at Cold Spring Harbor Lab)
- Shuo Chen, PhD committee member, 2012
- Andrew Roberts, MS thesis advisor, 2012 (Merck)
- Meera Prasad, MS thesis advisor, 2011 (first position at NYU Langone Medical Center)
- Seif Shahidain, MS thesis advisor, 2011 (first position at NIH)
- Satish Chikkagoudar, PhD thesis advisor, 2010 (first position as postdoc at UPenn, second position as scientist at Pacific Northwest National Lab)
- Tao Wu, PhD committee member, 2010 (first position at Microsoft)
- Suresh Solaimuthu, PhD committee member, 2010 (first position at UBS)
- Paras Garg, MS thesis, 2010 (first position as bioinformatics researcher at Mount Sinai Hospital)

Selected students from the bioinformatics program

- Xiao Ling, MS Bioinformatics 2013 (first position as bioinformatician at Yale University School of Medicine)
- Jharna Miya, MS Bioinformatics 2013 (first position as bioinformatics analyst at Comprehensive Cancer Center, Ohio State University)
- Hajira Naqvi, MS Bioinformatics 2013 (Memorial Sloan Kettering)
- Sagar Changawalla, BS Bioinformatics 2011 (first position at Cornell)
- Aparna Agrawal, MS Bioinformatics 2009 (first position at Roche)
- Wasay Hussain, BS and MS Bioinformatics 2009 (first position as bioinformatics researcher at Cornell)
- Monika Bihan, MS Bioinformatics 2008 (first position as bioinformatics engineer at J. Craig Venture Institute)

REFERENCES

Available upon request