

# Curriculum Vitae

## Raja Jothi

**Date of Birth:** May 26, 1977  
**Office address:** Biostatistics Branch, National Institute of Environmental Health Sciences (NIEHS)  
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### ACADEMIC & PROFESSIONAL POSITIONS

2009 -	<b>Investigator (tenure-track)</b>	<b>National Institutes of Health (NIH)</b> , National Institute of Environmental Health Sciences (NIEHS), Biostatistics Branch, Research Triangle Park, NC, USA
2007 - 2009	<b>Research Fellow</b>	<b>National Institutes of Health (NIH)</b> , National Heart Lung and Blood Institute (NHLBI), Laboratory of Molecular Immunology, Bethesda, MD, USA (Mentor: Keji Zhao)
2004 – 2007	<b>Research Fellow/Associate</b>	<b>National Institutes of Health (NIH)</b> , NCBI/NLM, Computational Biology Branch, Bethesda, MD, USA (Mentor: Teresa Przytycka)
2001 – 2004	<b>Research/Teaching Asst.</b>	<b>University of Texas at Dallas</b> , Department of Computer Science, Richardson, TX, USA
2000 – 2001	<b>Software Engineer</b>	<b>Westwave Communications</b> (acquired by Alcatel), Richardson, TX
1998 – 1999	<b>Database Engineer</b>	<b>P'Four Software and Marketing Services</b> , India

### HONORS AND AWARDS

<b>2009</b>	<b>Early Career “Rising Star” Award, NIEHS, National Institutes of Health</b>
2007 – 2009	Research Fellowship, National Institutes of Health, NHLBI
2007	Research Fellowship, National Institutes of Health, National Library of Medicine
2004 – 2007	Visiting Fellowship, National Institutes of Health, National Library of Medicine
2005	Travel Fellowship, International Society for Computational Biology (ISMB 2005)
2004	Travel Scholarship, European Association of Theoretical Computer Science (ICALP 2004)
2001 – 2004	Texas Public Educational Grant
2001 – 2004	University of Texas at Dallas Doctoral Scholarship
2003	Nominated for the Best Paper Award, PDCS
2003	IBM Student Travel Award (SODA 2003)
2003	DIMACS Travel Grant
2002	University of Texas at Dallas Engineering and Computer Science Special Fellowship

### EDUCATION

Ph.D.	Computer Science, University of Texas at Dallas, Richardson, Texas, USA, 08/2001 – 08/2004
M.S.	Computer Science, University of Texas at Dallas, Richardson, Texas, USA, 01/2000 – 12/2000
B.E.	Computer Science and Engineering, University of Madras, Chennai, India, 09/1994 – 04/1998

## PROFESSIONAL SERVICES

### Editorial Board Member

- PLoS ONE journal

### Conference/Symposium Organizing Committee

- **Workshop Co-chair** - IEEE International Conference on Computational Advances in Bio and medical Sciences, Orlando, FL, Feb 2011
- **Co-chair** - Symposium on "Epigenetics, Chromatin, and Gene Regulation", NIH Research Festival, Bethesda, MD, Oct 2010.
- **Chair** - Symposium on "Epigenetics, Chromatin, and Gene Regulation", NIH Research Festival, Bethesda, MD, Oct 2009.
- **Vice-chair** - The IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Philadelphia, CA, Nov 7-9, 2008.
- **Program Committee Member** - ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB), Niagara Falls, NY, Aug 2-4, 2010
- **Program Committee Member** - The 8th International Bioinformatics Workshop (IBW), Wuhan, China, June 4-6, 2010
- **Program Committee Member** - The IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Washington DC, Nov 1-4, 2009
- **Program Committee Member** - 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 6th European Conference on Computational Biology (ECCB), Vienna, Austria, Jul 21-25, 2007.
- **Program Committee Member** - The IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Silicon Valley, CA, Nov 2-4, 2007.
- **Conference Session Chair**, 7th INFORMS Telecommunications Conference, 2004.
- **Conference Session Chair**, 3rd IEEE International Conference on Networking, 2004.
- **Conference Session Chair**, 15th IASTED International Conference on Parallel and Distributed Computing and Systems, 2003.

### NIH Committee Service

- Bioinformatics Staff Scientist Search Committee, NIEHS, NIH, 2009-2010
- Next Generation Sequencing Projects Review Committee, NIEHS, NIH, 2009-
- Reviewer, applications for the NIH National Graduate Student Research Festival, NIH, 2010
- Reviewer, abstracts for NIH Research Festival, 2011
- Reviewer, abstracts for NIH Research Festival, 2010

### Peer-Reviewer

- Grants** Wellcome Trust, The Biotechnology and Biological Sciences Research Council (BBSRC) – UK
- Journals** Nature Methods, Genome Research, Genome Biology, Trends in Genetics, Nucleic Acids Research, Molecular Biology and Evolution, Proteins, Bioinformatics, PLoS Computational Biology, PLoS ONE, Molecular Biosystems, BMC Bioinformatics, BMC Genomics, BMC Systems Biology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE Transactions on NanoBioscience, Pattern Recognition Letters, Discrete and Computational Geometry, Networks, Journal of Graph Algorithms and Applications

### Membership

- International Society for Computational Biology (ISCB)

## INVITED TALKS (SELECTED)

- Apr 2011 **University of Texas at Dallas**, Richardson, TX – Embryonic stem cells and gene regulation.
- Mar 2011 **New York University**, New York, NY – Embryonic stem cells and gene regulation.
- Feb 2011 **University of Michigan**, Ann Arbor, MI - Embryonic stem cells and gene regulation.
- Oct 2010 **Duke University**, Institute for Genome Sciences & Policy, Durham, NC – Embryonic stem cells and gene regulation

- Oct 2010 **NIH Research Festival, Symposium on Epigenetics, Chromatin, and Gene Regulation**, Bethesda, MD - esBAF conditions the pluripotent genome for LIF/STAT3 signaling by opposing polycomb
- Mar 2010 **Keystone Meeting** on Biomolecular Interaction Networks: Function and Disease, Quebec, Canada – Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture.
- Feb 2010 **North Carolina State University**, Department of Environmental and Molecular Toxicology, Raleigh, NC – Systems biology and epigenetics of gene regulation
- Dec 2009 **RECOMB Conference on Regulatory Genomics, MIT**, Cambridge, MA – Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture.
- Nov 2009 **Laboratory of Signal Transduction (LST), National Institute of Environmental Health Sciences (NIEHS), National Institutes of Health (NIH)**, RTP, NC – Seeing the forest for the trees: stories on Brg1 and CTCF.
- Nov 2009 **NIEHS Science Awards Day, National Institute of Environmental Health Sciences (NIEHS), National Institutes of Health (NIH)**, RTP, NC – Seeing the forest for the trees: a systems level understanding of differential cell-fate outcome.
- Oct 2009 **Indian Institute of Technology**, Chennai, India – Systems biology and epigenetics of gene regulation.
- Oct 2009 **Center for Cellular and Molecular Biology (CCMB)**, Hyderabad, India – Systems biology and epigenetics of gene regulation.
- Oct 2009 **Center for DNA Finger Printing and Diagnostics (CDFD)**, Hyderabad, India – Systems biology and epigenetics of gene regulation.
- Oct 2009 **Indian Institute of Science**, Bangalore, India – Systems biology and epigenetics of gene regulation.
- Sep 2009 **Biostatistics Branch, National Institute of Environmental Health Sciences (NIEHS), National Institutes of Health (NIH)**, RTP, NC – Systems biology and epigenetics of gene regulation.
- Nov 2008 **RECOMB Conference on Regulatory Genomics, MIT**, Cambridge, MA – Genome-wide identification of in vivo protein-DNA binding sites from ChIP-Seq data.
- Jun 2008 **National Institute of Environmental Health Sciences (NIEHS), National Institutes of Health (NIH)**, RTP, NC – Chromatin modifications, gene expression, and regulatory networks.
- May 2008 **National Center for Biotechnology Information (NCBI), National Institutes of Health (NIH)**, Bethesda, MD – Chromatin modifications, gene expression, and regulatory networks.
- Jan 2008 **Rutgers University**, Camden, NJ - Regulatory proteins within a hierarchical framework have distinct dynamic properties.
- Aug 2007 **Department of Defense Biotechnology HPC Software Applications Institute (BHSAl)**, Fort Detrick, Frederick, MD - Inferring protein and domain interactions using sequence co-evolution and combinatorial optimization approaches.
- May 2007 **NCBI/NLM, National Institutes of Health (NIH)**, Bethesda, MD - Inferring molecular interactions using sequence co-evolution and co-inheritance: biases, strengths and weaknesses
- Apr 2007 **George Mason University**, Fairfax, VA – Co-evolution (correlated mutations) as an indicator of protein and domain interactions.
- Mar 2007 **Philips Research**, Briarcliff Manor, NY– Co-evolution as an indicator of protein and domain interactions.
- Feb 2007 **University of Connecticut**, Storrs, CT – Co-evolution as an indicator of protein and domain interactions.
- Dec 2006 **RECOMB Satellite Conferences on Systems Biology and Computational Proteomics**, San Diego, CA – Co-evolutionary analysis of domains in interacting proteins reveals insights into domain-domain interactions mediating protein-protein interactions.
- Oct 2006 **9th Annual Computational Genomics Conference**, Baltimore, MD – Co-evolutionary analysis of domains in interacting proteins reveals insights into domain-domain interactions mediating protein-protein interactions.
- Oct 2006 **NIH Research Festival**, Bethesda, MD – Co-evolutionary analysis of domains in interacting proteins reveals insights into domain-domain interactions mediating protein-protein interactions.
- Sep 2005 **NCBI/NLM, National Institutes of Health (NIH)**, Bethesda, MD - A new phylogenetic approach to delineate orthologous groups
- Jun 2005 **International Conference on Intelligent Systems for Molecular Biology (ISMB)**, Detroit, MI –Predicting protein-protein interaction by searching evolutionary tree automorphism space.

- May 2005 **DIMACS Workshop on Biomolecular Networks: Topological Properties and Evolution, Rutgers University**, New Brunswick, NJ – An Evolution-Based Clustering Method to Separate Orthologous Genes from Out-Paralogs.
- Dec 2004 **University of Maryland**, College Park, MD – The effects of evolutionary tree topology on predicting protein interaction specificity.
- Dec 2004 **Georgetown University**, Washington D.C – The effects of evolutionary tree topology on predicting protein interaction specificity.
- Nov 2004 **7th Annual Conference on Computational Genomics**, Reston, VA – Protein Folding in Hydrophobic-Hydrophilic Model: How Good is Theory in Practice?
- Apr 2004 **NCBI/NLM, National Institutes of Health (NIH)**, Bethesda, MD – Protein folding in the Hydrophobic-Hydrophilic Model.
- Mar 2004 **7th INFORMS Telecommunications Conference**, Boca Raton, FL – Survivable Network design: the capacitated minimum spanning network problem.
- Nov 2003 **International Conference on Parallel and Distributed Computing and Systems**, Marina del Rey, CA – Design of local access networks.
- May 2003 **DIMACS Workshop on Geometric Optimization, Rutgers University**, New Brunswick, NJ – Leave no stones unturned: improved approximation algorithms for degree-bounded minimum spanning trees.
- Apr 2003 **University of Maryland**, College Park, MD – Approximation algorithms for capacitated minimum spanning tree problem and its variants in network design.
- Jan 2003 **14th ACM-SIAM Symposium on Discrete Algorithms**, Baltimore, MD – A 5/4-approximation algorithm for minimum 2-edge-connectivity.

## PUBLICATIONS

Total – 40; First/Last author – 31/40; Corresponding author – 23/40; Total citations >600; H-index - 14

† indicates co-first author

\* indicates corresponding author (conceptualization of the research problem and methods to address it)

+Publications of particular importance

¶ Citation numbers obtained from *Thomson Scientific, Scopus, and/or Google Scholar*

### In preparation

- 40.<sup>+</sup> Yellaboina S, Freudenberg JM, Zheng X, Ghosh S, Zaykin DV, Wade PA, Hu G, Jothi R\*. Identification of novel regulators required for mouse embryonic stem cell maintenance.

### 2011

- 39.<sup>+</sup> Ho L†, Miller EL, Ronan JL, Ho W, Jothi R†\*, Crabtree GR\*. esBAF facilitates pluripotency by conditioning the genome for LIF/STAT3 signaling and by regulating Polycomb function. ***Nature Cell Biology*** (In press) (\***Co-corresponding authors**; †**Co-first authors**)
38. Wei G†, Abraham B†, Yagi R†, Jothi R†, Cui K, Sharma S, Narlikar N, Northrup DL, Tang Q, Paul WE, Zhu J, Zhao K. Genome-wide analyses of GATA3-mediated gene regulation in distinct T cell types. ***Immunity*** (In press) (†**Co-first authors**)
- 37.<sup>+</sup> Li L, Jothi R, Cui K, Lee JY, Cohen T, Gorivodsky M, Tzhori I, Zhao Y, Hayes SM, Zhao K, Westphal H, Love PE. Nuclear adaptor Ldb1 regulates a transcriptional program essential for the maintenance of hematopoietic stem cells. ***Nature Immunology***, 12(20):129-136, 2011.
- Highlighted in *Nature Immunology News and Views* commentary, "Ldb1, a new guardian of hematopoietic stem cell maintenance" (Welinder & Murre, *Nature Immunology* 12:113-114, 2011).
36. Yellaboina S, Tasneem A, Zaykin DV, Raghavachari B, Jothi R\*. DOMINE: a comprehensive collection of known and predicted domain-domain interactions. ***Nucleic Acids Research***, 39(Database issue): D730-735, 2011
35. Narlikar L and Jothi R\*. Analyzing ChIP-Seq data to identify protein-DNA binding sites. ***Methods in Molecular Biology***, 2010 (In press).
- 34.<sup>+</sup> Yu S†, Cui K†, Jothi R†, Zhao DM, Jing X, Zhao K, Xue HH. GABP is required for survival of HSCs and constitutes a core component of HSC-specific gene regulatory circuitry. ***Blood*** (In press). (†**Co-first authors**)

## 2010

33. Yu S, Zhao DM, [Jothi R](#), and Xue HH, Critical requirement of GABP $\alpha$  for normal T Cell Development. *Journal of Biological Chemistry*, 285(14): 10179-88, 2010.

## 2009

- 32.<sup>+</sup> [Jothi R](#)<sup>\*</sup>†, Balaji S<sup>1</sup>, Wuster A, Grochow JA, Gsponer J, Przytycka TM, Aravind L, and Madan Babu M, Genomic analysis reveals a tight link between transcription factor dynamics and regulatory network architecture. *Molecular Systems Biology (Nature Press)*, 5:294, 2009. (†Co-first author; >20 citations<sup>¶</sup>)
- Work highlighted in Nature Reviews Genetics, October 2009
  - 2nd, 2nd, and 5th most downloaded article for the months of Aug, Sept, and Oct 2009, respectively.
- 31.<sup>+</sup> Barski A†, [Jothi R](#)†, Cuddapah S†, Cui K, Roh TY, Schones DE, and Zhao K, Chromatin poises miRNA- and protein-coding genes for activation. *Genome Research*, 19: 1742-51, 2009. (†Co-first author; >15 citations<sup>¶</sup>)
- Featured on the cover page
30. Liu M, Chen XW, and [Jothi R](#), Knowledge-guided inference of domain-domain interactions from incomplete protein-protein interaction networks, *Bioinformatics*, 25(19):2492-99, 2009. (5 citations<sup>¶</sup>)
29. Kallin E, Cao R, [Jothi R](#), Xia K, Cui K, Zhao K, and Zhang Y. Genome wide uH2A localization analysis highlights Bmi1-dependent deposition of the mark at repressed genes. *PLoS Genetics*, Jun;5(6):e1000506, 2009. (>10 citations<sup>¶</sup>)
- 28.<sup>+</sup> Ho L†, [Jothi R](#)†, Ronan JL, Cui K, Zhao K, and Crabtree GR, An embryonic stem cell chromatin remodeling complex, esBAF, is an essential component of the core pluripotency transcriptional network. *Proc National Academy of Sciences (PNAS)*, 106(13):5187-91, 2009. (†Co-first author; >45 citations<sup>¶</sup>)
- 27.<sup>+</sup> Cuddapah S†, [Jothi R](#)†, Schones DE, Roh TY, Cui K, and Zhao K, Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. *Genome Research*, 19(1):24-32, 2009. (†Co-first author; >90 citations<sup>¶</sup>)
- Recommended by Faculty of 1000 Biology
26. [Jothi R](#)<sup>\*</sup> and Raghavachari B, Improved approximation algorithms for single-sink buy-at-bulk network design problem. *Journal of Discrete Algorithms*, 7(2):249-55, 2009. (12 citations<sup>¶</sup>)
25. [Jothi R](#)<sup>\*</sup> and Raghavachari B, Degree-bounded minimum spanning trees, *Discrete Applied Mathematics*, 157(5):960-70, 2009. (15 citations<sup>¶</sup>)

## 2008

- 24.<sup>+</sup> [Jothi R](#), Cuddapah S, Barski A, Cui K, and Zhao K, Genome-wide identification of in vivo protein-DNA binding sites from ChIP-Seq data. *Nucleic Acids Research*, 36(16):5221-31, 2008. (>150 citations<sup>¶</sup>)
- Featured on the cover page
23. Przytycka TM, [Jothi R](#), Aravind L, and Lipman DJ, Comprehensive analysis of uniformity of selective pressure in orthologous proteins. *BMC Evolutionary Biology*, 8:208, 2008. (1 citation<sup>¶</sup>)
- 22.<sup>+</sup> Raghavachari R, Tasneem A, Przytycka TM, and [Jothi R](#)<sup>\*</sup>, DOMINE: a database of protein domain interactions, *Nucleic Acids Research*, 36:D656-D661, 2008. (>50 citations<sup>¶</sup>)
21. [Jothi R](#)<sup>\*</sup> and Przytycka TM\*, Computational approaches to predict protein-protein and domain-domain interactions, *Bioinformatics Algorithms: Techniques and Applications*, (Eds: Alexander Zelikovsky and Ion Mandoiu), Wiley, John & Sons, Feb 2008. (3 citations<sup>¶</sup>)

## 2007

20. [Jothi R](#)<sup>\*</sup>, Przytycka TM\*, and Aravind L, Discovering functional linkages and uncharacterized cellular pathways using phylogenetic profile comparisons: a comprehensive assessment, *BMC Bioinformatics*, 8:173, 2007. (>25 citations<sup>¶</sup>)
- Biomed Central "Highly Accessed" distinction
19. Kann MG, [Jothi R](#), Cherukuri PF, and Przytycka TM, Predicting protein domain interactions from co-evolution of conserved regions, *Proteins*, 67(4):811-20, 2007. (20 citations<sup>¶</sup>)
18. [Jothi R](#)<sup>\*</sup> and Raghavachari B, Approximating the k-traveling repairmen problem with repair times, *Journal of Discrete Algorithms*, 5(2): 293-303, 2007. (8 citations<sup>¶</sup>)

## 2006

17. Guimaraes K, Jothi R, Zotenko E, and Przytycka TM, Predicting Domain-Domain Interactions Using a Parsimony Approach, **Genome Biology**, 7: R104, 2006. (>50 citations<sup>¶</sup>)
  - Biomed Central "Highly Accessed" distinction
- 16.<sup>+</sup> Jothi R\*, Cherukuri PF, Tasneem A, and Przytycka TM\*, Relative co-evolution of domains in interacting proteins reveals insights into domain-domain interactions mediating protein-protein interactions, **Journal of Molecular Biology**, 362(4):861-75, 2006. (>70 citations<sup>¶</sup>)
  - Recommended by Faculty of 1000 Biology
  - Ranked 12th on the ScienceDirect "Top25 Hottest Articles" for the period Jul-Sep 2006.
15. Zotenko E, Guimaraes K, Jothi R, and Przytycka TM, Decomposition of overlapping protein complexes: a graph theoretical method for analyzing static and dynamic protein associations, **Algorithms for Molecular Biology**, 1: 7, 2006. (22 citations<sup>¶</sup>)
  - Biomed Central "Highly Accessed" distinction
14. Jothi R\*, Zotenko E, Tasneem A, and Przytycka TM\*, COCO-CL: hierarchical clustering of homology relations based on evolutionary correlations, **Bioinformatics**, 22(7), 779-88, 2006. (>25 citations<sup>¶</sup>)
13. Gong C, Sarac K, Daescu O, Raghavachari B, and Jothi R, Load balanced agent activation for value added network services, **Computer Communications**, 29(11), 1905-16, 2006.

## 2005

12. Jothi R, Kann MG, and Przytycka TM, Predicting protein-protein interaction by searching evolutionary tree automorphism space, **Bioinformatics**, 21 Suppl 1, i240-i250, 2005. (>30 citations<sup>¶</sup>)
- 11.<sup>+</sup> Jothi R\* and Raghavachari B, Approximation algorithms for the capacitated minimum spanning tree problem and its variants in network design, **ACM Transactions on Algorithms**, 1(2), 265-82, 2005. (>25 citations<sup>¶</sup>)
10. Vokkarane V, Wang J, Jothi R, Qi X, Raghavachari B, and Jue J, Dual-homing protection in IP-over-WDM networks, **IEEE/OSA Journal of Lightwave Technology**, Vol. 23 (10), 3111-24, 2005. (6 citations<sup>¶</sup>)

## 2004

09. Jothi R\* and Raghavachari B\*, Survivable network design: the capacitated minimum spanning network problem, **Information Processing Letters**, 91(4), 183-90, 2004. (6 citations<sup>¶</sup>)
  - Ranked 5th on the ScienceDirect "Top25 Hottest Articles" for the period Jul-Sep 2004.
08. Daescu O\*, Jothi R\*, Raghavachari B\*, and Sarac K\*, Optimal placement of NAK-suppressing agents for reliable multicast: a partial deployment case, **Proc 19th ACM Symposium on Applied Computing**, 334-38, 2004. (5 citations<sup>¶</sup>)
07. Jothi R\* and Vokkarane V, Threshold-based differentiated intermediate-node initiated (TDINI) signaling for optical burst-switched networks, **Proc 7th INFORMS Telecommunications Conference**, 190-91, 2004.
06. Jothi R\*, A note on Altinkemer-Gavish's algorithm for the design of tree networks, **Proc 7th INFORMS Telecommunications Conference**, 78-80, 2004.
05. Jothi R\* and Raghavachari B\*, Revisiting Esau-Williams' algorithm: on the design of local access networks, **Proc 7th INFORMS Telecommunications Conference**, 104-107, 2004. (3 citations<sup>¶</sup>)
04. Jothi R\* and Raghavachari B\*, Dynamic capacitated minimum spanning trees, **Proc 3rd IEEE International Conference on Networking**, ISBN 0-86341-326-9, 2004.
03. Jothi R\* and Raghavachari B\*, Placement of proxy servers to support server-based reliable multicast, **Proc 3rd IEEE International Conference on Networking**, ISBN 0-86341-326-9, 2004.
02. Jothi R\* and Raghavachari B\*, Design of local access networks, **Proc 15th IASTED International Conference on Parallel and Distributed Computing and Systems**, 883-888, 2004. (4 citations<sup>¶</sup>)

## 2003

- 01.<sup>+</sup> Jothi R\*, Varadarajan S\*, and Raghavachari B\*, A 5/4-approximation algorithm for minimum 2-edge-connectivity, **Proc 14th Annual ACM/SIAM Symposium on Discrete Algorithms**, 725-34, 2003. (>30 citations<sup>¶</sup>)