

Faruck Morcos, Ph.D.

Assistant Professor

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Department of Biological Sciences
University of Texas at Dallas

Education

- July 2010 - 2015 Postdoctoral Fellow
Center for Theoretical Biological Physics (CTBP)
Rice University / University of California San Diego
Advisors: Prof. José Onuchic and Prof. Terence Hwa
- 2005-2010 Ph.D. in Computer Science & Engineering
University of Notre Dame.
Advisor: Prof. Jesús Izaguirre
Thesis: Multiscale Protein Networks: Interactions, Two Component Systems
and Kinetics
- 2007-2010 M.S. in Applied Mathematics. Department of Mathematics.
University of Notre Dame
Advisor: Prof. Mark Alber
- 2002-2004 M.S. in Communications Engineering
Technische Universität München. Germany.
Advisor: Prof. Joachim Hagenauer and Prof. Zacher Dawy
- 1997-2001 B.S. Electronics and Communications Engineering
Instituto Tecnológico y de Estudios Superiores de Monterrey (ITESM).
Monterrey, Mexico.

Honors and Awards

- 2010 Research Excellence Award CSE Department, University of Notre Dame
- 2008 Kaneb Center Outstanding Graduate Student Teacher Award for Excellence in Teaching.
- 2008 Inducted to Upsilon Pi Epsilon (UPE) International Honor Society
for the Computing and Information Disciplines.
- 2005-2010 Kellogg Fellowship for Graduate Studies at ND given by the Kellogg Institute.
- 2002 Werner von Siemens Excellence Award. Scholar of Siemens AG (2002-2004)
- 2002 Fulbright-Garcia Robles Scholarship for graduate studies (declined)
- 2001 *Graduated with Honors* at ITESM (Electronics and Communications Engineering)

Research Experience

Research interests in statistical learning, information theory, network science, computational biophysics, bioinformatics and systems biology. Particularly, in the field of protein networks, including prediction of protein and domain interactions and protein structure.

Current projects

- Accurate prediction of dimeric complexes using direct couplings. We generalize our method to find evolutionary constraints for protein interactions and show how these constraints are enough to generate high resolution models of protein interaction complexes. Collaborators: Ricardo dos Santos and Prof. Adriano Andricic at University of Sao Paulo.
- Direct coupling and survival analysis in cancer tissue expression data. We analyze cancer specific gene expression and protein quantification data to uncover protein interactions important to cancer using our Direct Information framework.
- Connecting coevolutionary processes with physical models of protein folding. We show that genomic data, physical coarse-grained free energy functions, and family-specific information theoretic models can be combined to give consistent estimates of energy landscape characteristics of natural proteins. Collaborators: Dr. Nicholas Schafer, Dr. Ryan Cheng and Prof. Peter Wolynes at CTBP.
- Decoding recognition in two-component signaling using DCA. In this project we create a scoring function based on the joint probability function of amino acid occupancies in interacting protein families of sensor kinases and response regulators. This scoring function is used as a metric for phosphotransfer and recognition. Collaborators: Dr. Ryan Cheng, Prof. Herbert Levine at CTBP.
- Elucidating the interaction interface between Bcl-2 and NAF-1. Using sequence and structural information of proteins NAF-1 and Bcl-2, we study both experimentally and computationally the interaction interface between these two proteins involved in the regulation of autophagy and aging. Collaborators: Prof. Patricia Jennings, Prof. Rachel Nechushtai at UCSD and Hebrew University.

Past projects (selected)

- Enhanced sampling of the functional conformational space for proteins. Using co-evolutionary signals in combination with molecular simulation of proteins we study how evolutionary constraints promote transition to functional states including hidden structural intermediate states. Collaborators: Dr. Biman Jana, Prof. Terence Hwa at CTBP.
- Designing Pooling Systems for Noisy High-Throughput Protein-Protein Interaction Experiments. We use the theory of compress sensing to propose an efficient way to design PPI experiments and decode experimental outcomes to reduce experimental error. Collaborator: Prof. Zaher Dawy at American University.
- Estimation of intra-domain and inter-domain protein contacts using statistical inference from protein sequences. We study hundreds of protein domain families and infer contacts that ultimately could lead to several applications like quaternary structure formation, protein structure prediction and protein-protein interaction estimation. Collaborators: Dr. Joanna Sulkowska, Prof. Terence Hwa (CTBP) and Prof. Martin Weigt (Université Pierre et Marie Curie).
- Research on algorithmic and computational approaches to estimate protein-protein interactions and domain-domain interactions in molecular networks. Inference of Protein and Domain interactions in the reversal switching system of myxobacterium *Myxococcus xanthus*. Under the supervision of Prof. Jesús Izaguirre, in collaboration with Prof. Mark Alber in Mathematics Department at Notre Dame and Prof. Dale Kaiser in Biochemistry Department at Stanford University.
- Investigation of slow functional dynamics in the Pin1-WW domain using molecular dynamics, data mining techniques and network science. Collaborator: Prof. Jeffrey W. Peng, Department of Chemistry and Biochemistry, University of Notre Dame.
- Estimation of domain-domain specificity in Two-Component Systems. Under the supervision of Prof. Jesús Izaguirre, in collaboration with Prof. Nitesh Chawla and Prof. Dale Kaiser in Biochemistry and Developmental Biology Departments at Stanford University.
- Prediction of Hinges in multi-domain proteins with three dimensional structure. Collaborator: with Dr. Samuel Flores at SimBios, Stanford University.

Publications

Journal Papers

1. Ricardo N. dos Santos*, **Faruck Morcos***, Biman Jana, Adriano D. Andricopulo and José N. Onuchic. *Dimeric interactions and complex formation using direct coevolutionary couplings*. Scientific Reports (* equivalent contribution) [accepted]
2. F.Bai*, **Faruck Morcos***, Y.S. Sohn, M. Darash-Yahana, C.O. Rezende, C.H. Lipper, M.L. Paddock, L. Song, Y. Luo, S.H. Holt, S. Tamir, E.A. Theodorakis, P.A. Jennings, J.N. Onuchic, R. Mittler and R. Nechushtai. *The Fe-S cluster-containing NEET proteins mitoNEET and NAF-1 as chemotherapeutic targets in breast cancer*. Proc Natl Acad Sci USA. 112(12) 3698-3703, 2015.
Highlighted in Mammalian Cell News
3. S. Tamir, M.L. Paddock, M. Darash-Yahana-Baram, S.H. Holt, Y.S. Sohn, L. Agranat, D. Michaeli, J.T. Stoffeth, C.H. Lipper, **Faruck Morcos**, I.Z. Cabantchik, J.N. Onuchic, P.A. Jennings, R. Mittler, R. Nechushtai. *Structure-function analysis of NEET proteins uncovers their role as key regulators of iron and ROS homeostasis in health and disease*. Biochim. Biophys. Acta, 1853(6) 1294-1315, 2015
4. **Faruck Morcos**, Nicholas P. Schafer, Ryan R. Cheng, José N. Onuchic and Peter G. Wolynes. *Coevolutionary Information, Protein Folding Landscapes and the Thermodynamics of Natural Selection*. Proc Natl Acad Sci USA 111(34): 12408-12413, 2014
Press Highlight in ScienceNewsline: From Eons to Seconds, Proteins Exploit the Same Forces
5. S. Tamir, S. Rotem, C. Katz, **Faruck Morcos**, K. Hailey, J. Zuris, C. Wang, A. Conlan, C. Lipper, M. Paddock, R. Mittler, J.N. Onuchic, P.A. Jennings, A. Frieddler, R. Nechushtai. *An Integrated Strategy Reveals the Protein Interface between the Cancer Targets Bcl-2 and NAF-1*. Proc Natl Acad Sci USA. 111(14) 5177-5182, 2014
6. Biman Jana, **Faruck Morcos** and José N. Onuchic. *From Structure to Function: the Convergence of Structure Based Models and Co-evolutionary Information*. Physical Chemistry Chemical Physics. Vol. 16, No. 14, Pages 6496-507, 2014
7. Ryan Cheng, **Faruck Morcos**, Herbert Levine and José N. Onuchic. *Towards rationally redesigning bacterial two-component signaling systems using coevolutionary information*. Proc Natl Acad Sci USA. 111(5): E563-71, 2014
Press Highlight in Phys.org: Researchers tune in to protein pairs: Team quantifies how mutations affect cell signaling in bacteria
8. **Faruck Morcos**, Biman Jana, Terence Hwa and José N. Onuchic. *Coevolutionary signals across protein lineages help capture multiple protein conformations*. Proc Natl Acad Sci USA. Vol 110, No. 51, p. 20533-20538. 2013
Press Highlight in ScienceDaily: Proteins' passing phases revealed
9. Ramy Mourad, Zaher Dawy and **Faruck Morcos**. *Designing Pooling Systems for Noisy High-Throughput Protein-Protein Interaction Experiments using Boolean Compressed Sensing*. IEEE/ACM Transactions on Computational Biology and Bioinformatics. 10(6): 1478-1490, 2013
10. Joanna Sulkowska*, **Faruck Morcos***, Martin Weigt, Terence Hwa, José N. Onuchic. *Genomics-Aided Structure Prediction*. Proc Natl Acad Sci USA. Vol 109, No. 26, p. 10340-10345. 2012 (* equivalent contribution)
Press Highlight in NSF.gov News: Protein Residues Kiss, Don't Tell
11. **Faruck Morcos**, A. Pagnini, B. Lunt, A. Bertolino, D. Marks, C. Sander, R. Zecchina, J. N. Onuchic, T. Hwa, M. Weigt. *Direct-coupling analysis of residue co-evolution captures native contacts across many protein families*. Proc Natl Acad Sci USA. Vol. 108, No. 49, E1293-E1301, 2011.
12. C. Harvey, **Faruck Morcos**, C. Sweet, D. Kaiser, S. Chatterjee, X. Liu, D. Chen and M. Alber. *Study of elastic collisions of Myxococcus xanthus in swarms*. Physical Biology. Vol. 8, No. 2, 2011.
13. **Faruck Morcos**, R. Lopez, S. Chatterjee, P. Brenner, C. McClendon, J. Zintsmaster, M. Ercsey-Ravasz, C.R. Sweet, M. Jacobson, J. Peng and J. Izaguirre. *Modeling conformational ensembles of slow functional motions in Pin1-WW*. PLoS Computational Biology. 6(12): e1001015. 2010.

14. **Faruck Morcos**, Marcin Sikora, Mark Alber, Dale Kaiser and Jesús A. Izaguirre. *Belief Propagation Estimation of Protein and Domain Interactions using the Sum-Product Algorithm*. IEEE Transactions on Information Theory. Vol. 56, No. 2, Pages 742-755, February, 2010.
15. Zaher Dawy, **Faruck Morcos**, Johanna Weindl and Jakob C. Mueller. *Translation initiation modeling and mutational analysis based on the 3-end of the Escherichia coli 16S rRNA sequence*. Elsevier BioSystems. 2009.
16. **Faruck Morcos**, Charles Lamanna, Marcin Sikora and Jesús Izaguirre. *Cytoprophet: a Cytoscape plug-in for the protein and domain interaction networks inference*. Bioinformatics, Vol. 24, Issue 19, Pages 2265-2266, July 2008.
17. S. Flores, K. Keating, J. Painter, **Faruck Morcos**, K. Nguyen, E. Merrit, L. Kuhn and M. Gerstein. *HingeMaster: normal mode hinge prediction approach and integration of complementary predictors*. Proteins: Structure, Function, and Bioinformatics. Vol. 73, Issue 2, Pages 299-319, Nov, 2008.
18. Zaher Dawy, Pavol Hanus, Johanna Weindl, Janis Dingel, **Faruck Morcos**. *On genomic coding theory*. European Transactions on Telecommunications, John Wiley & Sons, Ltd. Vol. 18, Issue 8, Pages 873-879, Dec. 2007.
19. Chengbang Huang, **Faruck Morcos**, Simon P. Kanaan, Stefan Wuchty, Danny Z. Chen, and Jesús A. Izaguirre. *Predicting Protein-Protein Interactions from Protein Domains Using a Set Cover Approach*. IEEE/ACM Transactions on Computational Biology and Bioinformatics, Vol. 4 pp. 78-87. Jan-March 2007.

Book Chapters

1. **Faruck Morcos**, Terence Hwa, Martin Weigt and José N. Onuchic. *Direct Coupling Analysis for protein contact prediction*. Methods in Molecular Biology, Protein Structure Prediction 3rd Edition. Vol. 1137, pp 55-70, 2014

Peer-reviewed Conference Papers

1. **Faruck Morcos**, Marcin Sikora, Dale Kaiser, Mark Alber and Jesús Izaguirre. *Estimation of protein and domain interactions in the switching motility system of Myxococcus xanthus*. Pacific Symposium of Biocomputing (PSB). 157-65, January, 2010.
2. **Faruck Morcos**, Charles Lamanna, Nitesh V. Chawla and Jesús Izaguirre. *Determination of Specificity Residues in Two Component Systems using Graphlets*. International Conference on Bioinformatics and Computational Biology (BIOCOMP). July, 2009
3. Marcin Sikora, **Faruck Morcos**, Daniel J. Costello, Jr., and Jesús A. Izaguirre. *Bayesian Inference of Protein and Domain Interactions Using The Sum-Product Algorithm*. Information Theory and Applications Workshop. UCSD, San Diego, January 2007.
4. **Faruck Morcos**, Mike Boxem, Niels Klitgord, Marc Vidal, and Jesús A. Izaguirre. *Prediction of domain interactions in C. elegans*. Proc. Workshop Computational Biophysics to Systems Biology CBSB06, Forschungszentrum Jülich, Germany, June 2006.
5. **Faruck Morcos**, Thidapat Chantem, Philip Little, Tiago Gasiba, and Douglas Thain. *iDIBS: An Improved Distributed Backup System*. IEEE Conference on Parallel and Distributed Systems (ICPADS), Minneapolis MN, July 2006.
6. Zaher Dawy, **Faruck Morcos González**, Joachim Hagenauer and Jakob C. Müller. *Modeling and Analysis of Gene Expression Mechanisms: A Communication Theory Approach*. IEEE International Conference on Communications. Seoul, Korea, 16-20 May, 2005.
7. Pedro Tejera, Mario Castaneda, **Faruck Morcos** and Wolfgang Utschick. *Degradation and Performance Issues of MIMO/OFDM in the Presence of Motion*. Proceedings of IEEE Vehicular Technology Conference. Milan, Italy, May 17-19, 2004.

Presentations & Conferences

- Direct Coupling Analysis Tutorial. Protein Folding Consortium Workshop. University of California at Berkeley, May 2015

- Coevolutionary information: structural diversity, complex formation and protein recognition in signaling networks. Department of Biomedical Engineering. University of Iowa, Feb. 2015 (invited talk)

- Using coevolutionary information to unveil protein structural diversity, complex formation and protein recognition in signaling networks. Department of Molecular Biosciences. University of Texas at Austin, Jan. 2015 (invited talk)

- The role of coevolutionary information in the study of protein structure and association. Significance of Knotted Structures for Functions in Proteins and Nucleic Acids, Poland, Sept. 2014 (talk)

- A relationship between coevolutionary information, folding landscapes and the thermodynamics of natural sequence selection. Zing Conference on Protein Folding, Dominican Republic, July, 2014 (invited talk)

- Uncovering protein structural diversity and protein recognition in signaling pathways using coevolutionary information. ICM Seminar, Uppsala University, Sweden. April, 2014 (invited talk)

- Uncovering protein structural diversity and protein recognition in signaling pathways using coevolutionary information. University of Warsaw, Poland. April, 2014 (invited talk)

Uncovering protein structural diversity and protein recognition in signaling pathways using coevolutionary information. FAS Center for Systems Biology, Harvard University, Jan. 2014 (invited talk)

- Exploring co-evolutionary information to uncover amino acid interactions, protein structure, complex formation and conformational plasticity. 5th Meeting on Molecular Simulations: from simple fluids to chemical reactions. Mexico City, Mexico. December 2013 (invited talk).

- Conformational changes leave an evolutionary footprint across protein lineages. Zing Protein/RNA Structure Prediction Conference. Riviera Maya, Mexico. Dec., 2013 (talk).

- Conformational changes leave an evolutionary footprint across protein lineages. GRC Proteins Conference, Holderness, NH. June, 2013 (poster).

- Co-evolutionary information helps uncover amino acid interactions, protein structure, complex formation and conformational plasticity. Department of Computer Science and Engineering Seminar, University of Notre Dame, November, 2012 (invited talk).

- Large Scale Direct Coupling Analysis of Residue-Residue Co-evolution Reveals Native Contacts in Many Domain Families. Dept. of Chemistry & Biochemistry Seminar Series at California State University Long Beach. February, 2012 (invited talk).

- Estimation of residue-residue coevolution using DCA identifies many native contacts across a large number of domain families. 56th Biophysical Society Meeting. San Diego, February, 2012 (poster).

- Folding with incomplete information. Gordon Research Conference on Protein Folding Dynamics. Ventura, California. Jan., 2012 (poster).

- Large Scale Direct Coupling Analysis of Residue-Residue Co-evolution Reveals Native Contacts in Many Domain Families. Protein/RNA Structure Prediction Conference. Riviera Maya, Mexico. Dec. 2011 (talk).

- Fast Identification of directly co-evolving residues in large protein families. San Diego Microbiology Group Annual Meeting. San Diego, May, 2011 (talk).

- Determination of Specificity Residues in Two Component Systems using Graphlets. International Conference on Bioinformatics and Computational Biology (BIOCOMP). Las Vegas, July, 2009 (talk).

- Protein and domain interaction inference in the switching motility system of *Myxococcus xanthus* using Cytoprop-het. International Conference on Systems Biology. Gothenburg, Sweden. August, 2008 (poster).

- Simulating reversals in swarming and fruiting body formation in *Myxococcus Xanthus* and implications for genetic modification. Indy Bioinformatics Conference. UIPU, Indianapolis, IN. June, 2007 (poster).

Service and peer review

I have participated as a scientific reviewer for the following journals and organizations:

- Bioinformatics, eLife, FEBS Letters, Molecular Biology and Evolution, Proceedings of the National Academy of Sciences, PROTEINS: Structure, Function and Bioinformatics, CONACYT (Mexico's National Council for Science and Technology).

Software

Project: DCA software/Server. An implementation of the DCA algorithm and a public web service of to compute direct coupling in sequence data is available at <http://dca.rice.edu>. The code and service is used by scientists of more than 30 countries and has more than 300 active users.

Project: *Cytoprophet*. Developed a *Cytoscape* plug-in to infer molecular interactions based on experimental data available in biological online databases. Version 1.0 available at <http://cytoprophet.cse.nd.edu>

Project: *3D Network Viewer*. A java interactive tool for visualization of networks in 3D space. Used to represent Fibrin networks observed in experiments and any other biological or social networks in 3D space. Output can be used in 3D Hardware with appropriate 3D glasses.

Teaching Experience

- *Mentor*. Member of the Frontiers In Science (FIS) program that invites undergraduate students from under-represented groups to participate in research projects at CTBP.
- *Advisor* of graduate students for several research projects. CTBP at Rice University. 2013
- *Instructor*. Teaching computer science department class CSE 20232: C/C++ Programming. University of Notre Dame. Fall 2009.
- *Advisor* of undergraduate research projects. Laboratory for Computational Life Sciences at the University of Notre Dame. 2007-2009
- *Teaching Assistant*. Ethics and Professional Issues in Computing. Spring 2009.
- *Teaching Assistant*. Graduate Networks. University of Notre Dame. Spring 2007.
- *Laboratory Tutor*. Master of Science course: *Image and Video Compression Lab*. TUM. Summer Semester 2004/ Winter Semester 2005.

Languages

Spanish (native)
English (fluent)
German (advanced)

Professional Memberships

Upsilon Pi Epsilon (UPE)
Institute of Electrical and Electronics Engineers (IEEE)
IEEE Signal Processing Society, Computer Society & Information Theory Society
Biophysical Society (BPS)

References

Prof. José N. Onuchic	Center for Theoretical Biological Physics Physics Department, Rice University	email: jonuchic@rice.edu
Prof. Terence Hwa	Center for Theoretical Biological Physics Physics Department, UCSD	email: hwa@ucsd.edu
Prof. Jesús A. Izaguirre	Computer Science and Engineering University of Notre Dame	email: izaguirr@nd.edu