

Md Tamjidul HOQUE, Ph.D.

Phones: 1.504.280.2406 (*office*)

Email: thoque@uno.edu, tamjidul.hoque@gmail.com

Web : www.cs.uno.edu/~tamjid/

Current Position

Assistant Professor
Computer Science,
University of New Orleans (UNO),
Louisiana, USA.

Current Office Address

University of New Orleans, Lakefront
Department of Computer Science, Math 333
2000 Lakeshore Drive
New Orleans, LA 70148, USA.

Current Research area [see <http://cs.uno.edu/~tamjid/>]:

Bioinformatics: Disorder predictor, binding prediction, energy function development,
Protein structure prediction, Drug Design,

Computing: Machine learning, Algorithm development, Evolutionary computation, etc..

Education

Ph.D., Monash University, Australia — March, 2008

Information Technology (covering Bioinformatics and AI)

Thesis: Genetic Algorithm for *Ab initio* Protein Structure Prediction based on Low Resolution Models

MSc, Bangladesh University of Engineering and Technology (BUET) — August, 2002

Computer Science and Engineering

Thesis: Design and Development of a Bangla Spell Checker

BSc, Bangladesh University of Engineering & Technology (BUET), 1998

Computer Science and Engineering

Thesis: Internet System Architecture

Past Research Experiences

Post-doctoral Researcher (Feb, 2011 — July 2012)

Indiana Center for Computational Biology and Bioinformatics & School of Informatics,
Indiana University-Purdue University Indianapolis (IUPUI), Indiana, USA

Topic: Effective and efficient algorithm development for computational protein structure prediction, disordered protein prediction, and related.

Platforms: Unix/linux based clusters, Fortran 90/95, C, C++ and parallel design and executions based on MPI and OpenMP designs.

Research Fellow (Dec, 2008 — Jan, 2011)

Discovery Biology, Eskitis, Griffith University, Queensland, Australia.

Topics: High Throughput Screening (HTS) and High Content Analysis (HCA) in charge: the major focus was on algorithm development related to HTS and HCA, while continuing *ab initio* protein structure prediction. *More:* <http://www.discoverybiology.org/research/high-content-analysis>

Platform: Distributed and parallel computing, the Opera (Perkin Elmer) and INCell (GE) high content imaging systems: Acapella and InCell Developer, ImageJ (Java based), Java based JAMA, J LAPACK, JasperReports, MATLAB, NetBean, Visual Basic, CellProfiler, Imaris, R, Excel, Database (access) etc for 2D to 5D imaging and analysis, CUDA and JCUDA for GPU programming.

Research Fellow (Jan, 2007 — May, 2009)

Institute for Integrated and Intelligent Systems, Griffith University, Queensland, Australia.

Topic: Ab initio protein structure prediction applying Evolutionary Computation: ~ in a coarse grained parallel manner, enhancement of the Coarse-Grained Multicomputer (CGM) model, and so on.

Platform: Distributed and parallel computing (PBS), VB, Java, R, MATLAB, C, C++, Database (access) and so on.

Past Teaching Experiences

Teaching Assistance/Tutor (Casual), Griffith University, Australia (2007 – 2011):

Courses: Programming (Java, C, Web-programming), Digital Systems, Electronics, Microprocessor, Mathematics (Differential and Integral Calculus, Matrices, Vector, Economics).

Teaching Assistance/Tutor (Casual), Monash University, Australia (2004 – 2007):

Courses: Information and Network Security, Networks and Data Communications, Computer Organisation, Infrastructure for Electronic Commerce, Object Oriented Design.

Lecturer (Full Time), Computer Science and Engineering Dept., (1998 – 1999):

Ahsanullah University of Science & Technology (AUST), Dhaka, Bangladesh.

Courses: Assembly Language programming and Java (as main course teacher), Pascal, Computer Fundamentals, JavaScript, HTML, C, C++, Database Theory, FoxPro, Digital Pulse Technique, and so on.

Lecturer (Part Time, 1999-2000):

Center for Computer Studies (affiliation: Gold Smith College, London), Dhaka, Bangladesh.

Courses: Compiler design and graph theory.

Lecturer (Part Time) BRAC Information Technology Institute (BITI) Dhaka, Bangladesh, (1999)

Courses: Software Engineering, Pure Math, Programming Languages, Computer fundamentals, etc.

Industry Experiences

Bashundhara Group (www.bashundharagroup.com), Dhaka, Bangladesh

IT department-in-charge and Deputy General Manager (Full Time, 1999 – 2004).

Major focus: System Analysis, Technical Research and Programming.

Significant achievements: (a) Around 70+ (including variations) commercial software have been developed and maintained. (b) Establishment of massive heterogeneous computer and communication network, (c) massive automation designing for the Bashundhara city (<http://www.bashundharagroup.com/bc/>) (d) Several IT business development: Telecommunication and Mobile business, Internet Service Provider (ISP) etc.

Monash Regional Centre for ICT (MRCICT), Monash University, Australia (2005 – 2006).

Software Developer (part time): Commercial software development for local industries.

Publication [* indicates corresponding author, Full list: <http://cs.uno.edu/~tamjid/publications.html>]

2017

- **Md Tamjidul Hoque***, Sumaiya Iqbal, “Genetic Algorithm based Improved Sampling for Protein Structure Prediction,” *International Journal of Bio-Inspired Computation*, International Journal of Bio-Inspired Computation, Volume 9, Issue 3, 2017 pp. 129 – 141, [Published: <http://www.inderscienceonline.com/doi/abs/10.1504/IJBIC.2017.083702>], [PDF: <http://cs.uno.edu/~tamjid/pub/2017/IJBIC.pdf>].

- Sumaiya Iqbal, **Md Tamjidul Hoque***, “hGRGA: A Scalable Genetic Algorithm using Homologous Gene Schema Replacement”, in Journal: *Swarm and Evolutionary Computation, Elsevier*, Volume 34, June 2017, Pages 33-49, [published: <http://www.sciencedirect.com/science/article/pii/S2210650216304862>], [PDF: <http://cs.uno.edu/~tamjid/pub/2017/hGRGA.pdf>].
- Avdesh Mishra, **Md Tamjidul Hoque***, “Three-Dimensional Ideal Gas Reference State based Energy Function”, *Current Bioinformatics, Bentham Journal*, Volume 12, 6 Issues, pp. 171 – 180, 2017, [Published: <http://www.eurekaselect.com/147209/article>], [PDF: <http://cs.uno.edu/~tamjid/pub/2017/3DIGARS.pdf>].
- Kenneth R. Walsh, **Md Tamjidul Hoque**, Kim H. Williams, “Human Machine Learning Symbiosis”, *Journal of Learning in Higher Education*, vol. 13, 1, p55-62, 2017, [Published: <https://eric.ed.gov/?id=EJ1139707>], [PDF: <http://cs.uno.edu/~tamjid/pub/2017/JLHE.pdf>].
- Sumaiya Iqbal, **Md Tamjidul Hoque***, “Prediction of Peptide-Binding Residues of Receptor Proteins in a Complex”, *The 5th Annual Conference on Computational Biology and Bioinformatics*, Louisiana, USA, 2017, [Presentation: http://cs.uno.edu/~tamjid/Papers/2017_Presentation_CCBB_SI.pptx]
- Avdesh Mishra, **Md Tamjidul Hoque***, “Improved Protein Structure Prediction using Advanced Scoring Function and Effective Sampling”, *The 5th Annual Conference on Computational Biology and Bioinformatics*, Louisiana, USA, 2017, [Presentation: http://cs.uno.edu/~tamjid/Papers/2017_Presentation_CCBB_AM.pptx].
- Avdesh Mishra, **Md Tamjidul Hoque***, “Next Generation Evolutionary Sampling and Energy Function Guided Ab Initio Protein Structure Prediction”, *61st Annual Meeting of the Biophysical Society*, New Orleans, USA, 2017, [Poster: http://cs.uno.edu/~tamjid/Papers/2017_Ab-Initio-PSP-BPS.pptx], [Abstract: [http://www.cell.com/biophysj/fulltext/S0006-3495\(16\)31365-0](http://www.cell.com/biophysj/fulltext/S0006-3495(16)31365-0)].
- Sumaiya Iqbal, **Md Tamjidul Hoque***, “A Study of Disorder-to-Order Transition by Characterizing the Binding Partners using a Statistical Potential”, *61st Annual Meeting of the Biophysical Society*, New Orleans, USA, 2017, [Poster: http://cs.uno.edu/~tamjid/Papers/2017_BPS_P1.pdf], [Abstract: [http://www.cell.com/biophysj/fulltext/S0006-3495\(16\)32183-X](http://www.cell.com/biophysj/fulltext/S0006-3495(16)32183-X)]

2016

- **Md Tamjidul Hoque***, Yuedong Yang, Avdesh Mishra, Yaoqi Zhou, “sDFIRE: Sequence-specific statistical energy function for protein structure prediction by decoy selections”, *Journal of Computational Chemistry, Wiley*, Volume 37, Issue 12, Pages 1119–1124, 2016, [published: <http://onlinelibrary.wiley.com/doi/10.1002/jcc.24298/abstract>], [PDF: <http://cs.uno.edu/~tamjid/pub/2016/sDFIRE.pdf>].
- Mahmood A. Rashid, Firas Khatib, **Md Tamjidul Hoque**, Abdul Sattar, “An Enhanced Genetic Algorithm for *Ab initio* Protein Structure Prediction”, *IEEE Transactions on Evolutionary*

Computation, Volume: 20, Issue: 4, pp. 627-644, Aug. 2016, [Published: <http://ieeexplore.ieee.org/document/7346476/>], [PDF: http://cs.uno.edu/~tamjid/pub/2016/EGA_TEVC.pdf].

- Sumaiya Iqbal, **Md Tamjidul Hoque***, “Estimation of Position Specific Energy as a Feature of Protein Residues from Sequence alone for Structural Classification”, *PLoS One Journal* [Published: <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0161452>].
- Mahmood A. Rashid, Sumaiya Iqbal, Firas Khatib, **Md Tamjidul Hoque**, Abdul Sattar, “Guided macro-mutation in a graded energy based genetic algorithm for protein structure prediction”, *Computational Biology and Chemistry Journal, Elsevier*, Volume 61, April 2016, Pages 162-177 (published: <http://www.sciencedirect.com/science/article/pii/S1476927116300469>], [PDF: <http://cs.uno.edu/~tamjid/pub/2016/Gmacro.pdf>].
- Avdesh Mishra, Sumaiya Iqbal and **Md Tamjidul Hoque***, “Discriminate Protein Decoys from Native by using a Scoring Function based on Ubiquitous Phi and Psi Angles Computed for All Atom”, *Journal of Theoretical Biology*, Volume 398, pp.112-121, 2016, [Published: <http://www.sciencedirect.com/science/article/pii/S0022519316001764>, PDF: <http://cs.uno.edu/~tamjid/pub/2016/UbPPA.pdf>].
- Nasrul Islam, Sumaiya Iqbal, Aatur R Katebi, **Md Tamjidul Hoque***, “A Balanced Secondary Structure Predictor”, *Journal of Theoretical Biology*, Volume 389, 21 January 2016, Pages 60-71, [Published: <http://www.sciencedirect.com/science/article/pii/S0022519315005147>], [PDF: <http://cs.uno.edu/~tamjid/pub/2016/MetsSSPred.pdf>].
- Kenneth R. Walsh, **Md Tamjidul Hoque**, Kim H. Williams, “Human Machine Learning Symbiosis”, International Conference on Learning and Administration in Higher Education, TN, USA, 2016 [PDF: <http://cs.uno.edu/~tamjid/pub/2016/JLHECon.pdf>].
- Sumaiya Iqbal, **Md Tamjidul Hoque***, “A Homologous Gene Replacement based Genetic Algorithm”, *GECCO*, 2016, [Paper: http://cs.uno.edu/~tamjid/Papers/2016_GECCO_hGR_paper.pdf], [Poster: http://cs.uno.edu/~tamjid/Papers/2016_GECCO_P4.pdf]
- Sumaiya Iqbal, Denson Smith, **Md Tamjidul Hoque***, “Accurate Identification of disordered protein residues using deep neural network”, 4th Annual LA *Conference on Computational Biology and Bioinformatics*, 2016 [Oral: http://cs.uno.edu/~tamjid/Papers/2016_LA_O1.pptx], [Poster: http://cs.uno.edu/~tamjid/Papers/2016_LA_P1.pdf].
- Avdesh Mishra, Sumaiya Iqbal, **Md Tamjidul Hoque***, “An Eclectic Energy Function to Discriminate Native from Decoys”, 4th Annual LA *Conference on Computational Biology and Bioinformatics*, 2016, [Oral: http://cs.uno.edu/~tamjid/Papers/2016_LA_O2.pptx], [Poster: http://cs.uno.edu/~tamjid/Papers/2016_LA_P2.pptx].

- Denson Smith, Sumaiya Iqbal, **Md Tamjidul Hoque***, “A Hybrid Evolutionary Feature Selection Method for Microarray Data”, 4th Annual LA *Conference on Computational Biology and Bioinformatics*, 2016, [Oral: http://cs.uno.edu/~tamjid/Papers/2016_LA_O3.pdf], [Poster: http://cs.uno.edu/~tamjid/Papers/2016_LA_P3.pdf]
- Sumaiya Iqbal and **Md Tamjidul Hoque***, “Estimation of Free Energy Contribution of Protein Residues as Feature for Structure Prediction from Sequence”, *CCBC/GLBIO* 2016.

2015

- Sumaiya Iqbal, **Md Tamjidul Hoque***, “DisPredict: A Predictor of Disordered Protein using Optimized RBF Kernel”, *PLOS One Journal* [Published: <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0141551>].
- Sumaiya Iqbal, Avdesh Mishra, **Md Tamjidul Hoque***, “Improved Prediction of Accessible Surface Area Results in Efficient Energy Function Application”, *Journal of Theoretical Biology*, Volume 380, 7 September 2015, Pages 380-391, [published: <http://www.sciencedirect.com/science/article/pii/S002251931500291X>], [PDF: http://cs.uno.edu/~tamjid/pub/2015/ASA_JTB.pdf].

2014

- Mahmood A. Rashid, **Md Tamjidul Hoque**, M.A.Hakim Newton, Abdul Sattar and Swakkhar Shatabda, “A parallel framework for multi-point spiral search in *ab initio* protein structure prediction,” *Advances in Bioinformatics Journal*, [Published: <http://downloads.hindawi.com/journals/abi/aip/985968.pdf>]
- Sumaiya Iqbal, Md Nasrul Islam, **Md Tamjidul Hoque***, “Improved Protein Disorder Predictor by Smoothing Output”, 17th International Conference on Computer and Information Technology (ICIT), 2014, [Published: <http://ieeexplore.ieee.org/document/7073113/>], [PDF: <http://cs.uno.edu/~tamjid/pub/2014/sDis.pdf>].
- Mahmood A. Rashid, Md. Masbaul Alam, M.A.Hakim Newton, **Md Tamjidul Hoque**, Abdul Sattar “Amino Acids Pattern-Biased Spiral Search for Protein Structure Prediction”, PRICAI-2014, [PDF: http://cs.uno.edu/~tamjid/pub/2014/AAP_PSP.pdf].

2013

- **Md Tamjidul Hoque**, Louisa Windus, Carrie Lovitt, Vicky M Avery, “PCaAnalyser: A 2D-Image Analysis Based Module for Effective Determination of Prostate Cancer Progression in 3D Culture”, *PLOS One Journal* [published: <http://dx.plos.org/10.1371/journal.pone.0079865>].
- **Md Tamjidul Hoque***, “Genetic Algorithm for *Ab Initio* Protein Structure Prediction”, ISBN-10: 3659419427, ISBN-13: 978-3659419423, July 2013 [Book: <https://www.amazon.com/Genetic-Algorithm-Protein-Structure-Prediction/dp/3659419427>].
- Mahmood Abdur Rashid, M.A.Hakim Newton, **Md Tamjidul Hoque** and Abdul Sattar, “Mixing energy models in genetic algorithms for on-lattice protein structure prediction”, *Journal of BioMed Research International* [Published: <http://www.hindawi.com/journals/bmri/2013/924137/>]

- Mahmood Abdur Rashid, M.A.Hakim Newton, **Md Tamjidul Hoque** and Abdul Sattar, “Collaborative Parallel Local Search for Simplified Protein Structure Prediction”, 2013 12th *IEEE International Conference on Trust, Security and Privacy in Computing and Communications*.
- Mahmood Abdur Rashid, M.A.Hakim Newton, **Md Tamjidul Hoque** and Abdul Sattar, “A Local Search Embedded Genetic Algorithm for Simplified Protein Structure Prediction”, *IEEE CEC* 2013.
- Mahmood Abdur Rashid, M.A.Hakim Newton, **Md Tamjidul Hoque**, Swakkhar Shatabda, Duc Nghia Pham and Abdul Sattar, “Spiral search: a Hydrophobic-Core Directed Local Search for Simplified PSP on 3D FCC Lattice”, *BMC Bioinformatics*, 2013 [Published: <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/1471-2105-14-S2-S16>].

2012

- Mahmood A Rashid, **Md Tamjidul Hoque**, M.A.Hakim Newton, Duc Nghia Pham and Abdul Sattar, “A New Genetic Algorithm for Simplified Protein Structure Prediction”, AI, 2012
- Mahmood A Rashid, Swakkhar Shatabda, M.A.Hakim Newton, **Md Tamjidul Hoque**, Duc Nghia Pham and Abdul Sattar, “Random-Walk: A Stagnation Recovery Technique for Simplified Protein Structure Prediction”, ACM-BCB, 2012
- Trent Higgs, Bela Stantic, **Md Tamjidul Hoque** and Abdul Sattar, “Refining Genetic Algorithm Twin Removal for High-Resolution Protein Structure Prediction”, IEEE CEC 2012.
- Trent Higgs, Bela Stantic, **Md Tamjidul Hoque** and Abdul Sattar, “Applying Feature-Based Resampling to Protein Structure Prediction”, BiCoB, 2012 [PDF: http://cs.uno.edu/~tamjid/Papers/2012_FBR_PSP.pdf].
- Trent Higgs, Bela Stantic, **Md Tamjidul Hoque** and Abdul Sattar, "Benefits of Genetic Algorithm Feature-Based Resampling for Protein Structure Prediction", Bioinformatics, 2012.

2011

- **Md Tamjidul Hoque***, M. Chetty, Andrew Lewis, Abdul Sattar, “Twin Removal in Genetic Algorithms for Protein Structure Prediction using Low Resolution Model.” *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, Jan-Mar: 2011, Vol 8, no. 1, pp.234-245 [Published: <http://ieeexplore.ieee.org/stamp/stamp.jsp?arnumber=4803828>]

2010

- **Md Tamjidul Hoque***, M. Chetty, Andrew Lewis, and Abdul Sattar, Vicky M Avery, DFS Generated Pathways in GA Crossover for Protein Structure Prediction, *NeuroComputing, Elsevier*, 73:2308-2316, 2010.
- **Md Tamjidul Hoque*** and Vicky Avery, Novel Strategies to Speed-up Query Response. Research Journal of Information Technology (RJIT), Vol 2, Issue 1, Pp. 11-20, 2010.

- Trent Higgs, Bela Stantic, **Md Tamjidul Hoque** and Abdul Sattar, Genetic Algorithm Feature-Based Resampling for Protein Structure Prediction,” in WCCI/IEEE CEC, 2010.
- M A Rashid, **Md Tamjidul Hoque** and Abdul Sattar, “Association Rules Mining Based Diseases Correlation Prediction”, in Medinfo2010.
- Trent Higgs, Bela Stantic and **Md Tamjidul Hoque**, Mutation operator and its Effects on protein Structure Prediction in Genetic Algorithms,” in Medinfo2010.

2009

- **Md Tamjidul Hoque***, M. Chetty, Abdul Sattar, Extended HP Model for Protein Structure Prediction.” Journal of Computational Biology (JCB), Vol. 16, Number 1, Pp. 85-103, 2009.
- **Md Tamjidul Hoque***, M. Chetty, Abdul Sattar, Genetic Algorithm in *Ab Initio* Protein Structure Prediction using Low Resolution Model: A Review,” *Biomedical Data and Applications, pringer-Verlag, series in Studies in Computational Intelligence (SCI) series*, 2009.
- Gregory A. Fechner, Anthony R. Carroll, **Md Tamjidul Hoque**, Vicky M. Avery, The use of high content analysis to determine the chemotherapeutic potential of marine and plant natural products, Society for Biomolecular Sciences (SBS) conference, 2009.

2008

- **Md Tamjidul Hoque***, M. Chetty, A Lewis, A Sattar “DFS based partial pathways in GA for protein structure prediction”, PRIB 2008.
- Trent Higgs, Bela Stantic and **Md Tamjidul Hoque**, Hydrophobic-Hydrophilic Forces and their Effects on Protein Structural Similarity, LNBI/PRIB 2008.
- T. Higgs, B. Stantic, **Tamjidul Hoque**, Hydrophobic-hydrophilic patterns and their effects on the protein folding prediction process, International Conference on Genome Informatics’, Gold Coast, Australia, 2008.
- Trent Higgs, Bela Stantic, **Md Tamjidul Hoque**, Optimal Length of Fragments for use in Protein Structure Prediction. Advances in Computer Science and Technology (ACST), Langkawi, Malaysia, 2008.

2007

- **Md Tamjidul Hoque***, M. Chetty, Abdul Sattar, Protein Folding Prediction in 3D FCC HP Lattice Model Using Genetic Algorithm.” Bioinformatics special session, IEEE Congress on Evolutionary Computation (CEC), Singapore, 2007.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, Significance of Hybrid Evolutionary Computation for *Ab Initio* Protein Folding Prediction, Hybrid Evolutionary Algorithms (Volume 75), *Springer-Verlag, Berlin, series in the SCI*, pages 241-268, 2007.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, “Generalized schemata theorem incorporating twin removal for protein structure predictions”, PRIB 2007.

2006

- **Md Tamjidul Hoque*** and Muhammad Towhidul Hoque, New Strategies to Speed-Up Query Response Significantly, *9th International Conference on Computer and Information Technology (ICCIT)*, 2006.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, Non-Isomorphic Coding in Lattice Model and its Impact for Protein Folding Prediction Using Genetic Algorithm, *IEEE Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*, 2006.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, A Guided Genetic Algorithm for Protein Folding Prediction Using 3D Hydrophobic-Hydrophilic Model, special session, in WCCI / IEEE Congress on Evolutionary Computation, 2006.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, A Hybrid Genetic Algorithm for 2D FCC Hydrophobic-Hydrophilic Lattice Model to Predict Protein Folding, AI 2006 (19th ACS Australian Joint Conference on Artificial Intelligence), 2006, LNAI.

2005

- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, Fast computation of the fitness function for protein folding prediction in a 2D hydrophilic-hydrophobic model, Journal published in the special issue of the *International Journal of Simulation Systems, Science and Technology*, 2005.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, Efficient Computation of Fitness Function by Pruning in Hydrophobic-Hydrophilic Model, *in the 6th International Symposium on Biological and Medical Data Analysis (ISBMDA) LNBI*, 2005.
- **Md Tamjidul Hoque*** and Muhammad Towhidul Hoque, Development of Software Tool for Safety Checking by Generating Coverability Tree Using Petri Nets, *8th International Conference on Computer and Information Technology (ICCIT)*, 2005.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, A New Guided Genetic Algorithm for 2D Hydrophobic-Hydrophilic Model to Predict Protein Folding, IEEE Congress on Evolutionary Computation (CEC), pp. 259-266, ISBN 0-7803-9364-3, Edinburgh, 2005.

2004

- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, An Efficient Algorithm for Computing the Fitness Function of a Hydrophobic-Hydrophilic Model, *4th International Conference on Hybrid Intelligent Systems (HIS 2004)*, pp. 285-290, Japan, 2004.
- **Md Tamjidul Hoque***, M. Chetty, L. S. Dooley, Partially Computed Fitness Function Based Genetic Algorithm for Hydrophobic-Hydrophilic Model, *4th International Conference on Hybrid Intelligent Systems (HIS 2004)*, pp. 285-290, Japan, 2004.

2003

- **Md Tamjidul Hoque*** and M. Kaykobad, Quantitative Approaches for Bangla Spell Checker, *6th International Conference on Computer and Information Technology (ICCIT)*, 2003.

2002

- **Md Tamjidul Hoque*** and M. Kaykobad, Coding System for Bangla Spell Checker, 5th *International Conference on Computer and Information Technology (ICCIT)*, 2002.
- **Md Tamjidul Hoque*** and M. Kaykobad, Use of Phonetic Similarity Property for Bangla Spell Checker, 5th *International Conference on Computer and Information Technology (ICCIT)*, 2002.

2000

- **Md Tamjidul Hoque*** and Ahmed Tareq, Development of Software Tool for Generating Coverability Tree in Petri Nets, IASTD, 2000.

1997

- **Md Tamjidul Hoque*** and Muhammad Masroor Ali, Noise Removal Algorithm from Images by using Breadth First Search Strategy, National Conference on Computer and Information Sys., (NCCIS), 1997.

Currently Submitted Article

- Sumaiya Iqbal and **Md Tamjidul Hoque***, “Modeling Sequence Pattern of Peptide-Binding Domain Residue using Stacking”, **Journal Submission** [PDF: <http://cs.uno.edu/~tamjid/sub/PBRp.pdf>].
- Sumaiya Iqbal and **Md Tamjidul Hoque***, “PBRpredict-Suite: A Suite to Predict Residues of Peptide-Binding Domain from Sequence using Stacked Generalization”, **Journal Submission** [PDF: <http://cs.uno.edu/~tamjid/sub/PBRs.pdf>].
- Sumaiya Iqbal and **Md Tamjidul Hoque***, “AMLGA: A Genetic Algorithm with Adaptive and Memory-Assisted Local Operators”, **Journal Submission** [PDF: <http://cs.uno.edu/~tamjid/sub/AMLGA.pdf>].
- Sumit Tarafder, Md. Toukir Ahmed, Sumaiya Iqbal, **Md Tamjidul Hoque** and M Sohel Rahman, “RBSURFpred : Modeling Protein Accessible Surface Area in Real and Binary Space using Regularized and Optimized Regression”, **Journal Submission** [PDF: <http://cs.uno.edu/~tamjid/sub/RBSURF.pdf>].
- Avdesh Mishra and **Md Tamjidul Hoque***, “3DIGARS-PSP: A Novel Statistical Energy Function and Effective Conformational Search Strategy based ab initio Protein Structure Prediction” **Journal Submission** [PDF: <http://cs.uno.edu/~tamjid/sub/3DPSP.pdf>].
- Devin Joseph Frey, **Md Tamjidul Hoque***, Mahdi Abdelguerfi and Thomas M. Soniat, “A Machine Learning Approach to Determine Oyster Vessel Behavior”, **Journal Submission** [PDF: <http://cs.uno.edu/~tamjid/sub/VMS.pdf>].
- Chaitanya Anne, Avdesh Mishra, **Md Tamjidul Hoque*** and Shengru Tu, “Multiclass Patent Document Classification”, **Journal Submission** [PDF: <http://cs.uno.edu/~tamjid/sub/MNLP.pdf>].

Developed Research Tools/Software:

My research team and I have developed about 15 different useful research tools [see <http://cs.uno.edu/~tamjid/Software.html>]

Research Supervision [see http://cs.uno.edu/~tamjid/Lab_Members.html]

Current Graduate Research Students

- Avdesh Mishra (PhD)
- Denson Smith (PhD)
- Md Kauser Ahmmed (PhD)
- Corey Charles Maryan (MS)
- Sylvia Charchut (MS)
- Michael Anthony Flot Jr (MS)

Current Undergraduate Research Students

- Pujan Pokhrel
- Joel Andrepont

Past Research Supervision:

- 3 PhD students
- 12 MS students
- 46 undergraduate students

Teaching Courses @UNO [see <http://cs.uno.edu/~tamjid/Courses.html>]:

2017

- Machine Learning I – CSCI 6990 (Graduate level), Spring 2017.
- Assembly Language Programming – CSCI 2450 (Undergraduate level), Spring 2017.
- Computer Graphics – CSCI 4631 (Undergraduate level), Fall 2017.
- Computer Graphics – CSCI 5631 (Graduate level), Fall 2017.
- Computer Organization – CSCI 3301 (Undergraduate level), Fall 2017.

2016

- Computer Networks and Telecom – CSCI 4311 (Undergraduate level), Spring 2016.
- Computer Networks and Telecom – CSCI 5311 (Graduate level), Spring 2016.
- Computer Organization – CSCI 3301 (Undergraduate level), Spring 2016.
- Pattern Recognition – CSCI 6635 (Graduate level), Fall 2016.

2015

- Pattern Recognition – CSCI 6635 (Graduate level), Spring 2015.
- Computer Organization – CSCI 3301 (Undergraduate level), Spring 2015.
- Pattern Recognition – CSCI 6635 (Graduate level), Fall 2015.
- Operating System I – CSCI 4401 (Undergraduate level), Fall 2015.
- Operating System I – CSCI 5401 (Graduate level), Fall 2015.

2014

- Computer Organization – CSCI 3301 (Undergraduate level), Spring 2014.
- Operating System I – CSCI 4401 (Undergraduate level), Spring 2014.
- Operating System I – CSCI 5401 (Graduate level), Spring 2014.
- Theory of Computation – CSCI 3102 (Undergraduate level), Fall 2014.
- Computer Organization – CSCI 3301 ((Undergraduate level), Fall 2014.
- Pattern Recognition – CSCI 6635 (Graduate level), Fall 2014.

2013

- Pattern Recognition – CSCI 6635 (Graduate level), Spring 2013.
- Introduction to the Theory of Computation – CSCI 3102 (Undergrad. level), Fall 2013.
- Operating System I – CSCI 4401 (Undergraduate level), Fall 2013.
- Operating System I – CSCI 4401G (Graduate level), Fall 2013.

2012

- Operating System I – CSCI 4401 (Undergraduate level), Fall 2012.
- Operating System I – CSCI 4401G (Graduate level), Fall 2012.

Honors and Awards

- AI (19th ACS Australian Joint Conference on Artificial Intelligence) 2006, Student travel grant, Hobart/Tasmania, Australia.
- IEEE CIS Student travel grant for CEC 2005, Edinburgh (**1 of 1 from Australia**).
- International Research Scholarship - Faculty of IT, Monash University (for PhD), 2004 to 2007.
- Faculty of Information Technology Partial Tuition Scholarship - Faculty of IT, Monash University (for PhD), 2004 to 2007.
- Merit Scholarship in most of the academic years (given to the topmost 10% undergraduate students of the University, BUET).
- Merit Scholarship based on *admission test result* in BUET (given to the topmost 50 students. Note that selected 3500 students having very good results were appeared in the admission test and 500 students were selected for admission). I secured 26th position in this test.
- Technical Scholarship during the four years study period at BUET.
- Board Scholarship based on HSC result (not taken as moved from Sir Salimullah Medical to BUET).
- Board Scholarship based on SSC results.

Successful Grant Summary

| Grant | Role | Sponsor | Award Date | Total Fund | Description |
|--|-----------------|---|------------|------------|---|
| Startup | PI (Sole) | University of New Orleans, LA, USA | 07/01/2012 | \$148,409 | Startup |
| Accurate prediction of drug-potent proteins in critical diseases | PI (Sole) | Research Competitiveness Subprogram grant, Louisiana Board of Regents (BoR) | 08/01/2013 | \$183,527 | The proposal has been ranked #1 |
| Combining disparate ontologies using machine learning to resolve polysemy | PI (Sole) | Contract | 05/18/2015 | \$9,700 | QUERTLE.com LLC |
| Multidimensional Anomaly Detection in DNA-Profile Based Personalized Medication Administration | PI (Sole) | Institutional | 05/16/2015 | \$12,000 | UNO |
| Optimized Metabolic Network based Biofuel Production Modeling in Algae | PI (+ 2 Co-PIs) | Institutional | 10/26/2015 | \$20,000 | UNO |
| Data Analysis and Decision Support Using Advanced Text Analytics and Machine Learning | PI (+1 Co-PI) | Federal | 05/06/2016 | \$60,073 | NASA |

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|--|------------------|---------------|------------|-----------------------------------|-------------------------------------|
| Gene Regulatory Network Based Biofuel Production Modeling in Algae | PI (Sole) | BoR (ITRS) | 06/01/2016 | \$141,453 (+tuition fee \$36,728) | Industry Tie Grant / BoR, ranked #8 |
| Travel Grant | PI (Sole) | Institutional | 09/30/2016 | \$1,500 | UNO |
| Travel Grant | PI (Sole) | Institutional | 07/10/2017 | \$1,500 | UNO |
| CC* Network Design: ARCHES (Advanced Research Computing in the Humanities Engineering and Sciences) Network at the University of New Orleans | SI (+PI & CoPIs) | NSF | 07/01/2017 | \$330,000 | NSF |

Professional Activities/ External Activities

Guest Editor

Special issue on Computational Intelligence in Proteomics, Journal of Advanced Computational Intelligence & Intelligent Informatics (JACIII), 2013-2014.

International Conference Program Committee and Reviewer

- Computational Intelligence in Bioinformatics and Computational Biology - CIBCB, 2012
- 10th International Workshop on Data Mining in Bioinformatics (BIOKDD '11),
- The 2011 IEEE Congress on Evolutionary Computation (CEC 2009 to 2011),
- International Conference on Computer and Information Technology (ICCIT, 2005 to Current),
- IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 08, 14).

Publicity Chair

- Third IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2008), <http://www.infotech.monash.edu.au/about/news/conferences/prib08/>

Reviewer (Journal)

- Nature (Since 2015 to present)
- IEEE Transaction of Evolutionary Computation (IEEE TEC since 2009 to present).
- Oxford Bioinformatics (Since 2017 to present)
- Journal of Mathematical Biology (JMB), Springer (since 2010 to present).
- Journal of Biophysics and Structural Biology, since 2009 to present.
- Neurocomputing, Elsevier, since 2009 to present.
- International Journal of Computational Intelligence Research (IJCIR), since 2005 to present.

Member:

- Protein-Society (<http://www.proteinsociety.org/>), since June/2014 to present.
- International Society for Computational Biology (ISMB), iscb.org, since June/2014 to present.

PhD Thesis Examiner

- Central Queensland University, Australia

Thesis/Dissertation Committee Service @UNO

Chair

- (PhD) Sumaiya Iqbal, Machine Learning based Protein Sequence to (un)Structure Mapping and Interaction Prediction, 2017-07-19 Fall 2013 – Summer 2017.

- (PhD) Avdesh Mishra, Effective Statistical Energy Function Based Improved Protein Un/Structure Prediction, Fall 2013 – Ongoing.
- (PhD) Denson Smith, Effective Feature Selection, Summer 2013 – Ongoing.
- (MS) Chaitanya Anne, Advanced Text Analytics and Machine Learning Approach for Document Classification, 2017-04-05 Fall 2016 - Spring 2017.
- (MS) Avdesh Mishra, Three-Dimensional Ideal Gas Reference State based Energy Function, 2015-03-30 Fall 2013 - Spring 2015.
- (MS) Md Nasrul Islam, A Balanced Secondary Structure Predictor, 2015-03-30 Fall 2013 - Spring 2015
- (MS) Corey Charles Maryan, Effective Rip-Current Detection, Spring 2017 – Ongoing.

Member

- (MS) Rachelyn Farrell, Predicting User Choices in Interactive Narratives using Indexer’s Pairwise Event Salience Hypothesis, 2017-03-28 Spring 2017.
- (MS) Dharmesh Rajendra Desai, Measuring Presence in a Police Use of Force Simulation, 2017-03-28 Spring 2017.
- (MS) Matt Avery Toups, A study of three paradigms for storing geospatial data: distributed-cloud model, relational database, and indexed flat file, 2016-04-06 Spring 2016.
- (MS) Devin Frey, A Machine Learning Approach to Determine Oyster Vessel Behavior, 2016-10-26 Fall 2015 - Fall 2016.
- (MS) Abe Handler, An empirical study of semantic similarity in WordNet and Word2Vec, 2014-11-05 Fall 2014.
- (MS) Alexander,Julie Gloria, Hydrographic Surface Modeling Through A Raster Based Spline Creation Method, 2014-04-11 Spring 2014.
- (MS) Barre,Brent A, Techniques for the Visualization of Positional Geospatial Uncertainty, 2013-11-14 Fall 2013.

Programming Skills

Applied and familiar with the following programming language and tools:

C/C++, Visual C/C++, Visual Basic, VB.Net, Java, JavaScript Assembly Language, Machine Language, SQL Server 6.5/2000, MySQL, MATLAB, several Bioinformatics tools (e.g. VMD, Rasmol, NAMD2 etc), Foxpro, Access, Oracle, HTML, XML, PHP, Latex, Telnet, FTP, SSh, PBS (for cluster computing), Crystal Report Writer, PASCAL, PROLOG, LISP, SimJava, Simulink, FORTRAN 95 and gFortran compiler , DBase, MS-Office product MS Visio, various Linux/Unix based editors and various C compliers, various Shell (Bourne Shell, CShell, etc), Acapella (in High content image analysis), INCell Analyzer, Imaris, MPI, OpenMP, OpenCV, OpenGL, WebGL, so on.

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