Nasir Mahmood, PhD
Mississauga, ON
L5N 8B9 Canada

Phone: +1 (289) 327 - 2199
contact@nasirmaan.com
ca.linkedin.com/in/nmhamood/
www.nasirmaan.com

PROFILE:

- Certified data scientist from John Hopkins University
- > 7 years experience in statistical modeling and predictive analytics
- Experience in prediction methods using Bayesian statistics and classifications
- Experience in complex quantitative analysis & algorithm development
- Hands-on experience with R, SAS, C/C++, Python, Hadoop, Java and Perl
- During PhD and postdoctoral research, hands-on experience in statistical modeling, machine learning, and data analytics and visualizations
- Strong creative and analytical skills, problem solver, team player
- Strong verbal and communication skills in English, German, Urdu, Hindi

TECHNICAL EXPERTISE

- Statistical Programming: R, SAS, Microsoft Excel
- Languages: C/C++, C#, Java, Python, Perl, PHP, HTML/CSS, JQuery
- Libraries: Boost, OpenMPI, Win32, STL, MFC, GDI, .NET Framework
- Databases: DBMS, MySQL, SQL Server, MongoDB, NoSQL, Oracle 11g
- OS: Windows XP/Vista/7, Ubuntu, Debian, Rocks Cluster (SGE, OpenMPI)
- IDE: MS Visual Studio 2008/10, Eclipse, Emacs, RStudio, Dreamweaver
- Packages: Hadoop, PSI-BLAST, HHSearch, WURST, MODELLER, Tableau
- Version control: SVN, CVS, GIT

EMPLOYMENT:

Data Analyst and AI Developer
American Express, Markham ON, Canada **10/2012 – Present**

- Development of recommender systems using Bayesian statistics
- Data extraction from multiple sources, EDA and predictive modeling
- Problem & Change Management: data collection, statistical modeling, and generation and presentation of insightful advanced analytics
- CICS Regions and Mainframe: data collection, transformation and advanced analytics of CPU utilization and transactions.
- Project Management: project sizing, planning, task tracking, forecasting funds and resource allocation and risk management
- Problem and change management in E1, E2 and E3 environments
- Troubleshooting and application support
- Software and hardware consultations

Languages & Packages: Python, R, Hadoop, Microsoft Excel, Clarity, Tableau

Research Scientist – Statistical Prediction Methods 10/2011 – 06/2012
University of Hamburg, Hamburg, Germany
Prof. Andrew's group develops statistical models with application to biomolecules. His team consists of a team of computer scientists, statisticians, and computational chemists. The group is well known for its expertise in the development of low-resolution (statistical) force fields, computational prediction methods, advance analytics, and model systems on lattice.

Project detail:

- Upgrading prediction algorithm for pattern extraction of 3D building blocks of rigid (protein) structures on a large scale,
- Finding discriminatory analytics and features among building blocks,
- Unsupervised classification of building blocks using Bayesian statistics
- Extending statistical model and Monte Carlo simulations for blind predictions

Languages & Packages: R, SAS C/C++, Perl, Python, Bash scripting, Linux/Unix SGE, OpenMPI

Research Scientist – Predictive Modeling 08/2009 – 09/2011
Robotics and Biology Lab, Technical University Berlin, Berlin, Germany
Robotics and Biology Laboratory is known for its innovative work in robotics, and development of statistical models and efficient search methods. The scientific team is a nice mixture of roboticists, computer scientists, engineers, biologists and biophysicists.

MBS project:

- Extension and improvement of model based search prediction algorithm,
- Enhancing search method through proper balance of exploration and exploitation strategies for better predictions,
- Setting up prediction infrastructure for CASP biannual competition,
- Developing method for assessment of prediction models
- Implementing statistical modeling framework for teaching purposes, and
- Setting up and maintaining high performance computing cluster facility.

Building Blocks project:

- Proposed concept of building blocks for protein structure prediction
- Building block approach allows a system to dynamically adapt to an appropriate resolution of structural representation; hence making statistical modeling and conformational search space manageable
- Developed an algorithm to extract all possible building blocks from a given PDB database, by applying advance data mining and analytics
- Implemented model validation framework to see, whether 1) the anticipated building blocks exist at all, and 2) if they exist, could the representative set of building blocks be used to build models of protein structures
- Based on validation results, set up a PhD thesis project and two supporting master thesis projects, and supervised those projects.

Languages & Packages: R, C/C++, Boost, Perl, Python, Ruby, Bash scripting, PSI-BLAST, HHSearch, ROSETTA, Ubuntu, Chimera, Rasmol, SGE/Rocks, OpenMPI

Research Scientist – Protein Predictive Modeling **04/2006 – 07/2009**
University of Hamburg, Hamburg, Germany

I worked on highly complex scientific problem, protein structure prediction problem; prediction of 3D protein structure from its 1D amino acid sequences. Statistical model I developed mainly relied on descriptive statistics, classical finite mixture model and Bayesian (unsupervised) classification. I used traditional Monte Carlo simulated annealing (MCSA) as search method.

Project details:

- Developed computational simulations using Bayesian classification models, statistical score function and Monte Carlo Simulated Annealing (MCSA)
- Implemented interplay between Cartesian coordinates and dihedral angles
- Extracted water-molecule interactions from PDB database and performed unsupervised Bayesian re-classification of existing statistical models
- Incorporated water effect into existing classification models
- Implemented routines to calculated hydrogen bonding energies in proteins

Languages & Packages: R, SAS, C/C++, Perl, PSI-BLAST, WURST, ROSETTA, Chimera, Gnuplot, Linux/Unix

Research Scientist **04/2005 – 03/2006**
University of Cologne, Cologne, Germany

The group of Prof. Dietmar Schmoburg consisted of an interdisciplinary team of computer scientists, engineers, chemists and biologists. The key objective of the group was to apply state of the art computational methods to solve complex biological problems.

Project details:

- Worked on an algorithm for structural alignment, an NP-hard problem
- Alignment accuracy was quite low compared to other alignment methods
- Modified core algorithm with 2nd round of optimization on found global solutions
- New modifications led to significant increase in overall algorithmic performance
- Benchmarked the new algorithm against other existing methods
- Transformed the implementation from C to C++
- Implemented a web interface

Languages & Packages: C/C++, Perl, CCP4, HTML, Suse Linux

EDUCATION/PROFESSIONAL DEVELOPMENT:

Ph.D. Informatics, Computational Biology **02/2010**
UNIVERSITY OF HAMBURG, Hamburg, Germany

M.Sc. Computational Visualistics **11/2007**
OTTO-VON-GUERICKE UNIVERSITY, Magdeburg, Germany

PG Dipl. in Applied Bioinformatics **03/2006**
UNIVERSITY OF COLOGNE, Cologne, Germany

MS Computer Science **03/2003**
UNIVERSITY OF CENTRAL PUNJAB, Lahore, Pakistan

B.Sc. (Hons) Agri. Entomology **10/2000**
BAHAUDDIN ZAKARIA UNIVERSITY, Multan, Pakistan

CERTIFICATES:

- Data Science Specialization - Johns Hopkins University 05/2015
- Statistics in Medicine - Stanford University 09/2014
- Analytics Edge – Massachusetts Institute of Technology (MIT) 05/2015
- Matrix Algebra and Linear Models
- Statistics and R for the Life Sciences

PRESENTATIONS:

- Software Development in Biological Domain, Thermo Fischer Scientific, 11/05/12
- Structural Biology and Statistical Bioinformatics, AMS Goettingen, 04/04/12
- Molecular Modeling and Bayesian Statistics, FMP Berlin, 14/01/12
- Protein Building Blocks & Structure Prediction, Max Planck for Biophysics, 03/01/12
- Molecular Modeling and Bayesian Statistics, FMP Berlin, 14/01/12
- Ab Initio Modeling and Coarse Graining, Leibniz Institute for Biochemistry, 03/12/11

POSTERS:

1. Nasir Mahmood, TJ Brunette, Oliver Brock Combining Comparative Modeling and Ab Initio Structure Prediction at 9th Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction 2010, California, USA.
2. Nasir Mahmood and Andrew Torda Monte Carlo Simulation with Herrn Boltzmann at 8th Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction 2008, Cagliari, Italy.
3. Nasir Mahmood and Andrew Torda Protein Structure Prediction using Coarse Grain Force Fields at From Computational Biophysics to Systems Biology 2008, Juelich, Germany.

4. Nasir Mahmood and Andrew Torda Protein Structure Prediction: Probabilistic Force Fields at Computer Simulation and Theory of Macromolecules 2008, Huenfeld, Germany.
5. Nasir Mahmood, Gundolf Schenk and Andrew Torda Monte Carlo Simulations with Unusual Probability Sampling at Methods of Molecular Simulation 2007, Heidelberg, Germany.
6. Nasir Mahmood and Andrew Torda Protein Structure Prediction using Coarse Grain Force Fields at German Conference on Bioinformatics 2007, Potsdam, Germany.
7. Nasir Mahmood, Tina Stehr, Steve Hoffmann, Thomas Margraf, Martin Mosisch, Gundolf Schenk, Paul Reuter, Thomas Huber, Andrew Torda CASP7 Predictions using the Wurst Server at 7th Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction 2006, USA.