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# ABHISHEK BISWAS

#### Current Status

- Postdoc Researcher at UT Battelle, LLC (Oak Ridge National Laboratory, Tennessee, USA), 4<sup>th</sup> Jan 2016 – present
  - ⇒ I work in the Computer Science and Mathematics Division under the Computing and Computational Sciences Directorate. I develop and implement high performance computing algorithms for problems in genomics and proteomics. I am currently working on scaling the Disco metagenomics assembler for ORNL, NERSC and DoD clusters.

## Academic Qualifications

- Ph.D. at Old Dominion University advised by Desh Ranjan and Mohammad Zubair, graduation on 11<sup>th</sup> December, 2015. GPA: 3.96
- Bachelor of Engineering in Computer Science from Visvesvaraya Technological University, Belgaum, India; August 2007; Graduation Percentage Score: 78%

## **Research & Teaching Experience**

- Instructor for CS350: Introduction to Software Engineering at Old Dominion University for Fall 2014. I was awarded the Outstanding Graduate Teaching Assistant award for year, 2015.
- Graduate Research Assistant working on High Performance Computing at Old Dominion University supervised by Desh Ranjan and Mohammad Zubair, August 2009-December 2015. I was awarded the Outstanding Graduate Research Assistant award for year 2012.

#### **Industry Work Experience**

- Research Associate for SAP Research Lab funded project on Healthcare Data Mining at People's <u>E</u>ducation <u>Society Institute of Technology</u> (PESIT), Bangalore, India. (January-July, 2009)
- Assistant System Engineer at Tata Consultancy Services Ltd., India. (September, 2007-December, 2008)

## Volunteer Experience

Ι of the founding members of the Sarada Research Labs • am one (http://www.saradaresearchlabs.org/) a non-government organization that develops free software for charity hospitals in India. We have developed a patient management and accounting system called PSAS (Patient Services and Accounting System) using Oracle Application Express. This has been used by Ramakrishna Trust hospitals in Kankhal, Vrindaban and Delhi. We also developed a system for management of Revised Tuberculosis Control Program and we received 500,000 INR for pilot testing of the tool from World Health Organization.

## Important Technical Skills (Computer Science)

- End-to-End software development experience in C++, Java & .NET.
  - $\Rightarrow$  C++ Technology Stack: (auto)configure, (auto/c)make, gcc, doxygen, gdb, Valgrind, Qt
  - ⇒ Java Technology Stack: Java/J2EE, Glassfish 2.1.1, Tomcat, Spring 2.5, JavaFX 2.0.3, Eclipse, NetBeans, Maven, Ant, Ivy, Jenkins, Hudson, Javadoc
  - ⇒ .NET Technology Stack: Framework 3.5 4.5, C#, VB.NET, ASP.NET
  - $\Rightarrow$  Expertise in Perl, Python and Go.
- Database Management Systems
  - $\Rightarrow$  Proficient with SQL, PL/SQL and Oracle NoSQL
  - $\Rightarrow$  Experience with Apache Accumulo and MongoDB.
- Web Development Technologies
  - $\Rightarrow$  Client side: HTML5, JavaScript, JQuery.
  - $\Rightarrow$  Server side: PHP, CGI, ASP.NET, Ruby, Oracle APEX.

- Parallel development experience in OpenMP, MPI, Hadoop, Intel Parallel Studio, TBB and CUDA.
  - ⇒ Capable of developing programs and scripts for job scheduling on various Cray and IBM clusters. I am quite familiar with tools like BCM and RRDtool.
  - ⇒ Expert in parallel program (MPI, OpenMP) debugging using gdb and valgrind. I also have extensive experience with debugging and profiling with Allinea DDT/MAP.
  - $\Rightarrow$  Extensively used the Zoltan Library for parallel load balancing, partitioning and approximation algorithm solving.
- Expert in Linux administration and with shell scripting.
- Experienced in using MATLAB and R for statistical computation. I have used them for implementation Gaussian models, PCA and visualization.

# Important Technical Skills (Bioinformatics)

- Metagenome, whole genome and transcriptomic assembly experience of microbial organisms from complex soil communities.
  - ⇒ Assembly of various plant metagenomes and strains of M. Marinum, M. Shotsii and M. pseudoshottsii.
  - ⇒ Assembly tools: Omega3, SPADes, MegaHit, Celera WGS, Trinity, Cufflinks
  - ⇒ Assembly visualization: Geneious, CLC Workbench and Hawkeye
- Experience with **Next Generation Sequencing** data.
  - $\Rightarrow$  Illimuna, RNA-Seq and PacBio reads and error profiles.
  - $\Rightarrow$  Handling paired-end and mate-pair data and appropriate usage is assembly.
- Alignment tools: STAR, BWA, TopHat, Bowtie and BLAST
- Annotation and Gene Finding tools: Manatee, JCVI Prokaryotic Annotation Pipeline, kSNP, GenMark (variants), Glimmer, Prodigal, Sipros
- Genomic Databases: Ensembl, IS Finder, UCSC Genome Database, JGI Denome JGI Denome DB, NCBI, Uniprot, dbSNP, Medline, GTEx and 1000 Genomes
- Capable of working with Geneious and CLC Workbench.

# Selected Publications

- A. Biswas, J. J. Chai-Crosskey, A. Clum, X. Guo, B. Bushnell, Q Yao, S. G. Tringe, W J. Hervey, IV, and C. Pan, "Disco: a distributed high-performance assembler for large metagenomes.", Under review Nature Communication, 2017
- A. Biswas, D. Gauthier, D. Ranjan, and M. Zubair, "ISQuest: Finding Insertion Sequences in Prokaryote Sequence Fragment Data", Bioinformatics, June 2015
- A. Biswas, D. Ranjan, M. Zubair, J. He, "A dynamic programming algorithm for finding the optimal placement of a secondary structure topology in cryo-EM data", Journal of Computational Biology, (9): 837-43, 2015.
- Other publications: http://www.informatik.uni-trier.de/~ley/pers/hd/b/Biswas:Abhishek.html

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#### REFERENCES