AshisSaha

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Research Interest

Computational Biology
Machine Learning
Gene Regulation

Education

2014 − Now	**Ph.D. in Computer Science** Johns Hopkins University, Baltimore, USA. Adviser: Dr. Alexis Battle.
2013	**M.Sc. in Computer Engineering** Korea University, Seoul, South Korea. Adviser: Dr. Jaewoo Kang.
2007	**B.Sc. in Computer Science and Engineering** Bangladesh University of Engineering and Technology (BUET), Dhaka, Bangladesh.

Research Experience

2014−Now **Research Assistant** Department of Computer Science, Johns Hopkins University, USA
Adviser: Dr. Alexis Battle.
At the Battle Lab, I work to develop and use computational methods to understand, analyze and interpret gene regulation in humans. Here, my responsibilities include:
- Improving accuracy and interpretability of co-expression networks [ongoing],
- Studying regulation of transcription and splicing using bulk [4,arxiv-3] and single-cell RNA-seq [ongoing],
- Establishing best practices for co-expression and trans-eQTL analysis [5],
- Uncovering genetic effects on gene expression across diverse human tissues as part of two big consortia (GTEx and eQTLGen) and other collaborations [3,6,7,8,arxiv-1,arxiv-2,arxiv-4],
- Mentoring junior lab members.

2019−2020 **Qualifying Project Development** Department of Computer Science, Johns Hopkins University, USA
Supervisor: Dr. Ben Langmead.
With Dr. Langmead, I studied the application of sketch data structures in computational genomics. We showed that the conservative count-min sketch consistently provides more accurate estimates than the regular count-min sketch. We also developed two sketch algorithms − offline count-min sketch and offline conservative count-min sketch − that visit the k-mers multiple times to improve estimates. A manuscript is under preparation.

2011−2014 **Research Assistant** Department of Computer Science, Korea University, South Korea
Adviser: Dr. Jaewoo Kang.
As a member of the Bioinformatics group in the Data Mining and Information Systems Lab, my responsibility was to:
- Develop methods to find disease-causing pathways or co-expressed genes using microarray data [1], and
- Create tools to visualize and interpret gene interactions [2].

Industry Experience

2009−2011 **Software Engineer, Vizrt Bangladesh** Dhaka, Bangladesh
Vizrt (`www.vizrt.com`) creates leading-edge content production tools for the digital media industry. As a Scrum Master of the Media Asset Management (MAM) application team, I designed and developed `a media logger tool` to annotate scenes in a video. As a developer of the `Escenic Widget Framework` team, I developed templates for displaying contents on a publication page.

2007−2009 **Software Engineer, Structured Data Systems Limited** Dhaka, Bangladesh
Structured Data Systems Limited is an offshore branch of AfriGIS (`www.afrigis.co.za`) - a geographic information based company in South Africa. I designed and developed the `javascript API` framework for their map services.

Publications

Google scholar profile: `https://scholar.google.com/citations?user=e6Ku7IIAAAAJ`

Peer-reviewed

8   Vosa U, Claringbould A, Westra HJ, Bonder MJ, Deelen P, Zeng B, Kirsten H, **Saha A**, Kreuzhuber R, Kasela S, et al. (2020). Unraveling the polygenic architecture of complex traits using blood eQTL meta-analysis. Nature Genetics (accepted).

7   **The GTEx Consortium (one of the analysts)** (2020). The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 369(6509), 1318–1330.

6   Wheeler HE, Ploch S, Barbeira AN, Bonazzola R, Andaleon, A, Fotuhi SA, **Saha A**, Battle A, Roy S, Im HK (2019). Imputed gene associations identify replicable trans-acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 43(6), 596–608.

5   **Saha A,** Battle A (2018). False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. F1000Research 7: 1860.

4   **Saha A,** Kim Y, Gewirtz ADH, Jo B, Gao C, McDowell IC, The GTEx Consortium, Engelhardt BE, Battle A (2017). Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research 27: 1843-1858.

3   **The GTEx Consortium (member of the eQTL manuscript group)** (2017). Genetic effects on gene expression across human tissues. Nature 550: pages 204–213.

2   **Saha A,** Jeon M, Tan AC, Kang J (2015). iCOSSY: An Online Tool for Context-Specific Subnetwork Discovery from Gene Expression Data. PLoS One 10: e0131656.

1   **Saha A,** Tan AC, Kang J (2014). Automatic context-specific subnetwork discovery from large interaction networks. PLoS One 9: e84227.

Preprints

arxiv-4   Dutta D, He Y, **Saha A**, Arvanitis M, Battle A, Chatterjee N (2020). Novel Aggregative trans-eQTL Association Analysis of Known Genetic Variants Detect Trait-specific Target Gene-sets. medRxiv.

arxiv-3   Hartl CL, Ramaswami G, Pembroke W, **Saha A**, Parsana P, Muller S, Pintacuda G, Lage K, Battle A, Geschwind DH (2020). The architecture of brain co-expression reveals the brain-wide basis of disease susceptibility. bioRxiv.

arxiv-2   Hawe JS, **Saha A,** Waldenberger B, Kunze S, Wahl S, Mueller-Nurasyid M, Prokisch H, Grallert H, Herder C, Peters A, Strauch K, Theis FJ, Gieger C, Chambers J, Battle A, Heinig M (2020). Network reconstruction for trans acting genetic loci using multi-omics data and prior information. bioRxiv.

arxiv-1   Gill D, Arvanitis A, Carter P, Cordero AIH, Jo B, Karhunen V, Larsson SC, Li X, Lockhart SM, Mason AM, Pashos E, **Saha A,** Tan V, Zuber V, Bosse Y, Fahle S, Hao K, Jiang T, Joubert P, Lunt AC, Ouwehand WH, Roberts DJ, Timens W, Berge MVD, Watkins NA, Battle A, Butterworth AS, Danesh J, Engelhard BE, Peters JE, Sin D, Burgess S (2020). ACE inhibition and cardiometabolic risk factors, lung ACE2 and TMPRSS2 gene expression, and plasma ACE2 levels: a Mendelian randomization study. medRxiv.

Teaching and Mentoring Experience

2018–Now	**Mentor** Matthew Figdore, an undergraduate student in the Dept. of Computer Science, JHU.
Spring 2019	**Guest Lecturer,** Computational Genomics: Data Analysis, CS 601.448/648, JHU. Topic: Single-cell genomics.
Spring 2019	**Mentor** Zeinab Mousavi, PhD student in the Dept. of Biomedical Engineering, JHU.

Spring 2016	**Teaching Assistant,** Computational Genomics: Data Analysis, CS 601.438/638, JHU. Instructor: Dr. Alexis Battle. An upper-level course with about 40 senior undergraduate and graduate students. I prepared assignment problems & solutions, graded, and evaluated projects.
Fall 2015	**Mentor** Amy He, an undergraduate student in the Dept. of Computer Science, JHU.
Fall 2014	**Teaching Assistant,** Databases, CS 601.315/415, JHU. Instructor: Dr. David Yarowsky. An undergraduate-level course with about 70 students. My responsibilities included teaching, preparing solution manual, grading, and coordination of co-TAs.

Conferences and Workshops

2020	**RECOMB,** Attendee.	Virtual
2020	**Biology of Genomes Conference,** Attendee.	Virtual
2018	**Poster at the Biological Data Science Conference** Alignment errors in RNA-sequencing produce false positives in association analyses.	Cold Spring Harbor Lab, New York, USA
2018	**Human Cell Atlas Jamboree,** Selected attendee.	Broad Institute, Cambridge, USA
2018	**NCBI Genomics Hackathon,** Selected attendee.	National Library of Medicine, Bethesda, USA
2018	**ISCB Bioinformatics, Genomcis, and Computational Biology Workshop**	UMD, College Park, USA
2016	**Poster at the Biological Data Science Conference** Transcriptome-wide networks reveal candidate splicing regulatory relationships.	Cold Spring Harbor Lab, New York, USA
2015	**Talk at the American Society of Human Genetics Conference** Tissue-specific transcriptome-wide networks reflect joint regulation of alternative splicing and gene expression.	Baltimore, USA
2012	**Talk at the Translational Bioinformatics Conference** Gene Interaction-Level Cancer Classification using Gene Expression Profiles.	Jeju, South Korea

Professional Services

Organizer	Monthly Bioinformatics seminar for current students, faculties and alumni of the Department of Computer Science, BUET (2020-now). Youtube: `https://www.youtube.com/channel/UCvmcrTlnUncxNA78x49jQNQ`
Junior Reviewer	MLCB Conference (2019), RECOMB Conference (2016), Plos ONE Journal (2013), Computers in Biology and Medicine Journal (2013), IEEE BIBM Conference (2013), WWW Conference (2013), DTMBio Conference (2012), LBM Conference (2011).
Seminar Czar	Johns Hopkins University, 2016−2017.
Volunteer	HopHacks, JHU, 2016.

Extracurricular Activities

Volunteer	**Badhan, a voluntary blood donors' organization** `https://badhan.org/` • 2009-now: Adviser, Central Committee. • 2006-2009: Adviser, Buet Zone. • 2005: President, Buet Zone. • 2004: President, Ahsan Ullah Hall Unit, Buet. • 2003: Member, Ahsan Ullah Hall Unit, Buet. **Badhan Foundation** `http://badhanfoundation.org` Life member.
Hobby	Photography: `https://500px.com/p/alorchhota` Reading books: `https://www.goodreads.com/user/show/745264-ashis-saha` Travelling, Camping, Hiking.