KONIKA CHAWLA
Senior Engineer (May, 2013 - present)
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Research work experience

I have been worked on developing RNA/smallRNA sequencing and microarray data analysis pipelines analysis of different datasets such as:

- Liver cancer RNA, sRNA and microarray data.
- Breast milk RNA sequencing data.
- Reverse phase protein array data.
- Bacterial whole genome sequencing data etc.

Also created a pipeline for analysis of correlation of microRNAs and their candidate target gene expression profiles.

Education

Trondheim,
Norway
2009 – 2017

Doctor of philosophy, Department of Biology,
Norwegian University of Science and Technology (NTNU)
Supervisor: Prof. Martin Kuiper, *Ph.D.* (Semantic Systems Biology group, Dept. of Biology, NTNU)
PhD Title: *"Discovering, analysing and taking care of knowledge."*

Research Expertise:

- Microarray, SmallRNA Deep Sequencing Data Analysis
- Data integration and Database development
- Network construction and modularization
- R web application development

Projects:

- A Systems biology study of Arabidopsis defence response mechanism, which includes analysis and integration of Microarray, sRNA deep sequencing and integration with mass spectrometry data. Part of this study included identification of miRNA and their target genes in Arabidopsis now available at ftp://ftp.arabidopsis.org/home/tair/Genes/

- Creation of an R based web application for GO Attribute matrix construction. http://norstore-trd-bio0.hpc.ntnu.no:8080/Genes2GO/

- Development of Transcription Factor Checkpoint (http://www.tfcheckpoint.org/), a manually curated TF database, in collaboration with Gastrin Functional Genomics group at Faculty of Medicine, NTNU, Trondheim.

- Creating a modular view and finding novel signalling module in a gastrin and cholecystokinin mediated molecular signalling pathway, in collaboration with Gastrin Functional Genomics group at Faculty of Medicine, NTNU, Trondheim.

Teaching Experience:

- Fall 2009-2013: Computational tools in Systems Biology, NTNU.
- Fall 2011: Lecture and practical course on Microarray data analysis, NTNU.
- Fall 2011-2012: Lecture and practical course on Introduction to Bioinformatics, NTNU.

Courses:

• Statistical analysis of gene expression data with R and Bioconductor, DTU, 2009. • Microarray Technology and Data Analysis - with Laboratory Training, NTNU • System Biology and Biological Networks, NTNU • Metabolomics- Methods and Applications, NTNU • Systems Biology: Examples from Current Literature, NTNU	
Masters of science in Bioinformatics Department of Computer Science, Jamia Millia Islamia Subjects: • Microarray data analysis • Bioinformatics with focus on sequence alignment • Structural and Functional Genomics • Database management systems • Advanced Programming (Implemented solutions for biological problems using languages such as C, C++, PERL and SHELL Scripts) **Grades:** 80 % marks	New Delhi, India 2006 – 2008
Bachelor of Science (H) Biotechnology Amity University Subjects: Cell Molecular Biology, Botany and Chemistry **Grades:** CGPA 8.69 /10	Noida, UP, India 2003-2006

FELLOWSHIPS

• Summer Research fellowship, sponsored jointly by IASc (Bangalore), INSA (New Delhi) and NASI (Allahabad).	2007
• Studentship by Department of Biotechnology, Govt. of India for six months to work at NIPGR Delhi, 2008	2008
• Project trainee fellowship by Department of Biotechnology, Govt. of India for six months to work at IIT Delhi, 2008-09	2008-2009

TECHNICAL SKILLS

- Programming Languages: R (Bioconductor) (Intermediate Expert), Python (Intermediate), PHP (Intermediate), PERL (Intermediate), MATLAB (Intermediate).
- Markup languages: HTML, XML
- Operating Systems: Linux, Windows, Mac
- Database: MySQL
- Development platforms: Apache, Tomcat
- Network modeling and analyses Tools: Cytoscape, CellDesigner
- Others: Bowtie, SAMtools, Integrative Genomics Viewer, GSEA, HTseq, Makefiles.

REFERENCES

Prof. Martin Kuiper - martin.kuiper@ntnu.no

Prof. Astrid Lægreid - astrid.lagreid@ntnu.no

Prof. Pål Sætrom - pal.satrom@ntnu.no

LIST OF PUBLICATIONS

Book Chapter

Systems Biology: a Promising Tool to Study Abiotic Stress Responses. Konika Chawla*, Pankaj Barah*, Martin Kuiper and Atle M. Bones. *"Omics and Plant Abiotic Stress Tolerance", N. Tuteja and S.S.Gill and R. Tuteja, Editors. 2011, Bentham Science Publishers Ltd, USA (***eISBN:** 978-1-60805-058-1*).*

Papers

1. **Comprehensive transcriptomic analyses of tissue, serum, and serum exosomes from hepatocellular carcinoma patients.** Mjelle R, Dima SO, Bacalbasa N, **Chawla K**, Sorop A, Cucu D, Herlea V, Sætrom P, Popescu I. *BMC Cancer*. 2019 Oct 28;19(1):1007
2. **Nephronectin mediates p38 MAPK-induced cell viability via its integrin-binding enhancer motif.** Toraskar J, Magnussen SN, Chawla K, Svineng G, Steigedal TS. *FEBS Open Bio. 2018 Nov*
3. **Genes2GO: An R based web application for fetching gene annotations**. Konika Chawla and Martin Kuiper. *Bioinformation 2016* **12**: 231-232
4. **Gene regulation knowledge commons: community action takes care of DNA binding transcription factors.** Tripathi S, Vercruysse S, Chawla K, Christie KR, Blake JA, Huntley RP, Orchard S, Hermjakob H, Thommesen L, Lægreid A, Kuiper M. *Database (Oxford). 2016*
5. **The gastrin and cholecystokinin receptors mediated signaling network: a scaffold for data analysis and new hypotheses on regulatory mechanisms.** Sushil Tripathi*, Åsmund Flobak*, Konika Chawla, Anaïs Baudot, Torunn Bruland, Liv Thommesen, Martin Kuiper and Astrid Lægreid. *BMC Systems Biology 2015* **9**:40
6. **Experimental Verification of the Quality of Clusterings Produced by Hard Clustering Algorithms after the Removal of Unstable Data Elements.** Wim De Mulder*, Zahra Zavareh*, Konika Chawla and Martin Kuiper. *BIOTECHNO conference 2014*
7. **EssOilDB: a database of essential oils reflecting terpene composition and variability in the plant kingdom.** Kumari S, Pundhir S, Priya P, Jeena G, Punetha A, Chawla K, Firdos Jafaree Z, Mondal S, Yadav G. Database (Oxford). 2014
8. **TFcheckpoint: a curated compendium of specific DNA-binding RNA polymerase II transcription factors.** Sushil Tripathi*, Konika Chawla*, Astrid Laegrid and Martin Kuiper. *Bioinformatics 2013* **29**(19): 2519-2520
9. **ZifBASE: a database of zinc finger proteins and associated resources.** Mannu Jayakanthan, Jayaraman Muthukumaran, Sanniyasi Chandrasekar, Konika Chawla, Ankita Punetha, and Durai Sundar. *BMC genomics, September 2009*

*These authors have contributed equally