

Ashish Singh Tomar

Early Stage Researcher

Era7 Bioinformatics, Granada, Spain

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SKILLS

- **Programming Language:** Python, R, Scala and Perl.
- **Web Development:** CSS, HTML, Bootstrap, Angular, Javascript, flask and play framework.
- **Data Visualization:** D3.js, sigma.js and leaflet.js
- **Database:** MySQL and NoSQL (Mongodb, Neo4j and Titandb)
- **Bioinformatics:** Phylogenomics, metagenomics, data integration, biomedical ontologies and NGS data analysis (RNA-seq, CHIP-seq, Medip-seq and Bs-Seq).

EXPERIENCE

Era7 Bioinformatics, Granada, Spain - *Early Stage Researcher*

October 2015 - October 2018

- Visualization of phylogenomics, metagenomics and taxonomic data using D3. Created a complete and two prototype web application for metagenomics and metabarcoding data visualization. Also created a JavaScript libraries for [phylogenomics](#) and hierarchical data visualization using D3.js. The goal was to create a modular library for integrated visualization of phylogenetic tree with metadata. I worked on a [web app](#) using this library to demonstrate the power of modular code.
- Graph database storage of taxonomic and ontology data
Creating a graph-based storage for NCBI taxonomy tree and gene ontology. I used Neo4j, Titandb and Scala to create the graph storage.
- Web app for biodiversity and visualization of MCMC tree generation
 - **Visiting Researcher at NHM, Stockholm** September to November 2018
I am working on the visualization interface for taxonomy tree editing and taxonomy comparison web application. It is implemented using Javascript and D3.js. Another project I worked was to visualize the tree space generated during MCMC process, I implemented this as a density tree.
 - **Visiting Researcher at NHM, Copenhagen:**
March to Oct 2018
I have developed a web application using leaflet.js and D3.js, for [biodiversity map](#) to plot the occurrence of coordinate data on the map. I

have implemented a automation script to retrieve biodiversity coordinates from the address using google map api and pro4j for converting UTM to Lat Long coordinate system. Currently i am involved in developing biodiversity web app for visualization of [Danish beetle Atlas](#) occurrence data.

Scigenom Labs, Kochi, India - Bioinformatics Programmer

January 2015 - July 2015

- Automation pipeline development for variant annotation using perl
- R based pipeline for analysis, annotation and visualization of methylation data.
- Automated QC report generation from the stats files generated after fastqc and bam alignment, the automation script was implemented in python.

Dupont India, Hyderabad, India - Intern

July 2014 - December 2014

- Development of genome annotation pipeline using python (+numpy, panda and nltk). I used Numpy and panda to handle multidimensional data array and nltk was used to retrieve the names of organism from the unstructured blast output.
- Web service development using Flask web framework.
- Created a visualization for viewing the names of organism from blast output result, this was implemented using HTML, CSS, JavaScript and D3.js.

EDUCATION

Institute Of Bioinformatics And Applied Biotechnology, Bangalore - M.Sc.

Bioinformatics, August 2012 - June 2014

Thesis: “*Understanding correlation between hES and iPS using Chip-seq, Bis-seq and RNA seq*”.

Role : I was involved in designing and development of this project. A meta-analysis was done to capture a global profile of genes due to difference in coding and non-coding region. I used R for expression analysis and created custom script for methylation data visualization.

D.Y.Patil University, Pune - B.Tech. Bioinformatics,

August 2008 - June 2012

Thesis: “*An automated RNA-seq Pipeline development using R Bioconductor*”.

Role : I was involved in designing of an automation pipeline for RNA-seq data analysis. This automation pipeline was based on statistical models to predict differential expression mainly using R and Bioconductor libraries.

AWARDS

MARIE SKŁODOWSKA-CURIE Research Fellowship October 2015