

Chirag Parsania

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Research Interests

- Big data analytics, including the development of tools for the rigorous and reproducible analysis of genomics data.
- Statistical modeling, machine learning and deep learning.
- To understand the regulation of gene expression by integrative study of genomics and transcriptomics data such as TF-ChIP-Seq, PolII-ChIP, RNA-Seq and Epigenetic modifications.

Recent work

- Phylogenetic analysis of genes identified as potential horizontal gene transfer candidates in the species of kingdom fungi.
- Using R shiny and R markdown I developed a web-based platform for analyzing and visualizing data on fungal gene expression (FungiExpresZ).
- Approaching the fundamentals of statistical modeling, R tidymodels, TanserFlow and keras.

Education

PhD Candidate (Biomedical Sciences) University of Macau	2016 - 2020 (Expected) Macau (SAR)
Master of Science (Bioinformatics) University of Pune GPA: 4.85/6, GRADE: A, RANK: 5	2011 - 2013 Pune, India
Bachelor of Pharmacy Sardar Patel University GRADE: First Class	2007 - 2011 Vallabh Vidyanagar, India

Research Experience

PhD (Candidate)

Supervisor : [Chris, Koon Ho Wong](#)

Faculty of Health Sciences, University of Macau, Macau.

2016 - Current

1. **FungiExpresZ** [[GitHub](#)]: A web interface for fungal gene expression data analysis and visualizations.

Key features

- Contains more than 13,000 SRA fungal gene expression data processed through a streamline pipeline for easy comparison and/or integration with user uploaded data.
- Highly customizable, ggplot2 implemented data exploratory (12) and GO enrichment (6) visualizations.

- Standalone version (docker and R package) improves its scalability.

2. Identify horizontal gene transfer (HGT) events in the kingdom fungi: Using sequence similarity approach, we Identified potential inter kingdom HGT candidates in different fungal species.

Key features and findings

- We built Support Vector Machine (SVM) classifier to identify inter kingdom HGT candidates.
- Several pathogenic and non-pathogenic fungi have been screened through to identify potential HGT candidates.
- Further validation of HGT candidates by rigorous phylogenetic analysis, bias GC content, intron counts, genomic locations and histone modifications data.
- R-package ([phyloR \[GitHub\]](#)) and shiny-app (in preparation) for easy exploration of tool and data.

3. Genomics and transcriptomics data analysis: Functional characterization of transcription factor CgXbp1 of pathogenic fungi *Candida glabrata*.

Roles and responsibilities

- Bioinformatics analysis of time course *Candida glabrata* RNA Pol-II ChIP-seq, RNA-seq and CgXbp1 TF ChIP-seq data before and after macrophage infection.

Major findings

- Identification of a novel transcription factor, CgXbp1, which orchestrates a chronological transcriptional landscape in an opportunistic fungal pathogen *Candida glabrata* during interaction with macrophages and regulates antifungal drug resistance.

4. TidyWrappers [pkg site]: An R package to deal with an object tbl. It provides handy wrapper functions - `tbl_get_vars_*`, `tbl_count_vars_*`, `tbl_convert_*`, `tbl_keep_rows_*`, `tbl_remove_rows_*`, `tbl_remove_vars_*` and `tbl_replace_*` to handle data from tbl object.

5. phyloR [pkg site]: An R package to deal with NCBI-BLAST output. It helps to clean blast results for downstream phylogenetic analysis.

6. corplot [pkg site]: An R package to display correlation by heat box and scatter plots between complex datasets of gene expression. Specifically, useful when correlations between replicates for several samples need to be shown. It eliminates painstaking steps of data manipulation, data cleaning and data rearrangement.

7. Genome view [shinyApp]: An R shiny app to visualize gene set(s) on genome as a whole or chromosome wise.

PhD Exchange Student

Supervisor : [Dr. Joshua Wing Kei Ho](#)

**Victor Chang Cardiac Research Institute,
Sydney, Australia.**

2016 May. – 2016 Aug.

Roles and responsibilities

- Gained computational and statistics training under the guidance of Dr. Joshua Ho.
- Explored DNA bendability feature for gene regulatory elements to understand its influence on downstream gene expression changes.

Research Assistant

Supervisor : [Dr. Chris, Koon Ho Wong](#)

**Bioinformatics and Genomics Core,
Faculty of Health Sciences, University of Macau, Macau.**

2014 Nov. – 2015 Dec.

Roles and responsibilities

- Provided assistance in analyzing genomics data and gave briefing about bioinformatic tools to wet-lab researcher as a part of [Genomics and Bioinformatics Core](#).

- Actively involved in single cell RNA-seq and exome data analysis of breast cancer patients.
- Analyzed RNA-seq, small RNA-seq and whole genome data of different model organisms like human, mice and zebrafish.

Bioinformatics Analyst

Bionivid Technology [p] Ltd.

Bangalore, India.

2013 Aug. – 2014 Sep.

Roles and responsibilities

- RNA-seq and small RNA-seq data analysis of different plant species
- Designed and developed a Rice miRNA and mRNA interaction resource
 - Technology used: MySQL Workbench, MySQL, Core JAVA, Servlet, JSP, HTML, Apache Tomcat
- Trained wet lab researchers, undergrads and PhDs for whole genome and RNAseq data analysis.

Master's Dissertation

National Chemical Laboratory

Supervisor : [Dr. Manali Joshi](#)

Pune, India.

Co- Supervisor : [Dr. Durba Sengupta](#)

Roles and responsibilities

- Performed molecular dynamics and simulations of human β -2 Adrenergic Receptor (β 2AR).
- Identified key differences between pharmacogenetically important N-terminal polymorphism of β 2AR at the 16th position Arg16Gly.

Publications

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- Ang Li, **Chirag Parsania**, Richard B. Todd, Koon Ho Wong. Fungal co-option of an insect protease gene for extracellular nutrient degradation and transcriptional control. (**Manuscript under revision in nature communication biology**)
 - P Sethiya, MN Rai, R Rai, **C Parsania**, K Tan, KH Wong. "Transcriptomic analysis reveals global and temporal transcription changes during Candida glabrata adaptation to an oxidative environment", **Fungal Biology** Dec-2019, (Available as a journal preprint).
 - Wong QW, Sun MA, Lau SW, **Parsania C**, Zhou S2, Zhong S2, Ge W1. "Identification and characterization of a specific 13-miRNA expression signature during follicle activation in the zebrafish ovary", **Biol Reprod.** 2018 Jan 1;98(1):42-53.
 - Szot PS, Yang A, Wang X, **Parsania C**, Röhm U, Wong KH, Ho JWK. "PBrowse: A web-based platform for real-time collaborative exploration of genomic data" **Nucleic Acids Res.** 2017 May 19;45(9): e67.
 - Shahane G**, **Parsania C****, Sengupta D, Joshi M, "Molecular insights into the dynamics of pharmacogenetically important N-terminal variants of the human β 2-adrenergic receptor", **PLoS Comput Biol.** 2014 Dec 11;10(12): e1004006. **equal contribution
 - Sharma R, Mishra M, Gupta B, **Parsania C**, Singla-Pareek SL, Pareek A. "De novo assembly and characterization of stress transcriptome in a salinity-tolerant variety CS52 of Brassica juncea", **PLoS One.** 2015 May 13;10(5): e0126783

Skills

- **Programming**
 - **Current:** R, Shiny, Rmarkdown
 - Mostly follow tidydata philosophy and tidyverse in day to day programming.
 - **Frequently used shiny dev packages:**
 - Shiny, ShinyBS, shinyWidgets
 - Experience of working with **golem** framework for building production-grade shiny applications
 - **Frequently used core R packages:**
 - Data wrangling and visualizations: dplyr, purrr, tidyr, readr, tibble, stringr, rlang, ggplot2
 - Reproducible workflow: packrat, renv
 - Package development: devtools, roxygen2
 - **Frequently used Bioconductor R packages:**
 - Biostrings, ComplexHeatmap, EnrichedHeatmap, GenomicRanges, AnnotationHub, GO.db
 - **Docker:** Have proven experience of app containerization through docker and distribution of image via dockerHub.
 - **Past:** Core JAVA, JSP-Servlet, MySQL
- **Version Control:** GitHub, GitKraken
- **Operating System Exposure:** Mac OS, Linux, HPC, Windows
- **NGS Data Exposure:** RNA-seq, TF ChIP-seq, PolII-ChIP seq, Single Cell RNA-seq, Whole genome variant analysis, Small RNA-seq
- **NGS Tools Exposure:** BWA, TopHat, Bowtie, Cufflink, Velvet, Trinity, DESeq, HTSeq, IGV, Samtools, Bedtools, GATK, Varscan, deeptools, MACS
- **Phylogenetic Tools Exposure:** Mafft, TrimAL, IQtree, MrBayes, iTOL, phyloT. Tree visualization – ggtree, ape, tree.io, tidytree
- **Structural Bioinformatics Exposure:** GROMACS, VMD, Discovery Studio

Conferences & Presentations

- Participated and presented poster in 26th Conference “Intelligent System on Molecular Biology (ISMB) 2018”, Chicago, IL, USA.
- Participated and presented poster in 5th and 6th “Macau Symposium on Biomedical Sciences” in 2016 and 2017 respectively, organized by University of Macau at Macau (SAR).

Online Certifications

University of California San Diego Bioinformatics Algorithm -1 Grade: 71%	Coursera 2014-Feb
Johns Hopkins University Computing for Data Analysis Grade - 89%	Coursera 2013-Dec
University of Toronto Bioinformatics Methods-1 Grade: 100%	Coursera 2014-Mar
Building Web Applications in R with Shiny	Datacamp 2018-Mar
Intermediate Functional Programming with purrr	Datacamp 2019-Sep
Working with the RStudio IDE (Part 1)	Datacamp 2018-Mar

Other Interests

- Photography [[Instagram](#)], Hiking and Running.

References

1. Dr. Chris, Koon Ho Wong
Assistant Professor,
Faculty of Health Sciences,
University of Macau.
Email: koonhowong@umac.mo
2. Dr. HO. Joshua Wing Kei
Associate Professor,
School of Biomedical Sciences,
The University of Hong Kong.
Email: jwkho@hku.hk