

More than 9-year experience of working as Research Engineer in OMICS data analysis which include analysis of data from: Bacterial genome, Metagenomics, Transcriptomics, Metatranscriptomics, Amplicon sequencing, Single Cell Analysis, Pacbio-hifi and nanopore, and worked as web developer of research group webpages and HPC Clusters and Galaxy Administrator. Major objectives are to analyze, develop and implement bioinformatics tools, databases and methods for analysis of genomic data.



Work History



**2023-09 -
Current**

PhD Researcher

Bordeaux University

- ➔ Research focus on deciphering Sézary syndrome heterogeneity using bioinformatics approaches
- Analysis of whole exome sequencing (WES) data, single-cell RNA sequencing data, and BioNano optical mapping data
- Advanced single-cell transcriptomics and tumor heterogeneity characterization



**2022-06 -
2023-08**

Research engineer

IRBI Insect Biology Research Institute

- ➔ HPC clusters management, Data Analysis (RnaSeq, Pacbio, Nanopore)
- Performed analysis of pacbio-hifi data originated from ovaries of 20 females cotesia congregata wasps



**2020-05 -
2021-04**

Research engineer

INRAE, National Institute of Agriculture

- ➔ Small RNA-seq data analysis for brachypodium, Maize and wheat including both siRNA and miRNA
- Performed benchmarking of different bioinformatics tools for siRNA and miRNA to make these plants better suited to environment stress by studying different aspects of genome regulation



**2019-03 -
2020-05**

Research engineer

INRAE, National Institute of Agriculture



Nasir Mahmood Abbasi

Bioinformatician

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Digital Skills

Programming Languages:

R PROGRAMMING | UNIX
Programming |
Programming languages
(Python, Php, Perl, SQL) |
C, C++ C# | JavaScript

Markup Languages:

Good knowledge of CSS
and HTML markup
languages

→ Galaxy administration, Transcriptomics data analysis, Amplicon and Metatranscriptomics analysis data analysis
→ Analysis to check the affect of drugs on animals by Metatranscriptomics data analysis

◆ 2017-01 -
2018-04

Research assistant

Hong Kong University of Science and Technology (HKUST)

→ Cancer genomics data analysis, Web maintenance for their personal webpage and Data management using synology
→ Management of personal webpage and data management using synology for research group
→ Performed benchmarking of different tools for exome+whole genome sequencing analysis for variant identification in patient data from cancer

◆ 2017-01 -
2017-07

Instructor of Bioinformatics

Virtual University of Pakistan, VU

→ Taught courses in Bioinformatics
→ Helped with lab experiments (Molecular biology, Microbiology, cell biology)
→ Helped with bioinformatics data analysis on Unix

◆ 2015-05 -
2016-05

Research engineer

University Miguel Hernandez de Elche

→ Web development, Data management and Analysis of marine prokaryotic genomes
→ Studied difference between bacteroides from two different environments

◆ 2013-07 -
2014-01

Research assistant

Evolutionary Biology Centre

→ Genetic and epigenetic consequences of personality and social rank
→ Matlab analysis of data

◆ 2013-01 -
2013-07

Research engineer

Karolinska Hospital

→ Bioinformatics analysis of bacterial genomes (capnocytophaga)
→ Studied newly characterized capnocytophaga species and discovered

Databases:

Databases Administration (MYSQL Oracle MS) | Microsoft Access

Operating Systems:

Advanced knowledge of Unix Ubuntu and Mac OS - Client | HPC Cluster(Slurm) Administration | Galaxy Administration

Single-Cell Analysis :

Core Workflow:

Seurat | Scanpy | SingleCellExperiment | DoubletFinder | Scrublet | SCTransform | Harmony |

Quality Control &

Normalization:

Ambient RNA removal | SCTransform | Log normalization | Batch correction (Harmony, Seurat methods)

Dimensionality Reduction & Clustering:

PCA | UMAP | t-SNE | Louvain clustering | Leiden clustering

Differential Expression Analysis:

LIBRA (pseudobulk framework) | DESeq2 (with LRT) | edgeR | MAST | Wilcoxon rank-sum test

Cell Type Annotation methods:

Azimuth | scAtomic | SingleR | CytetypeR (top marker-based) | scType

Trajectory Analysis: PAGA (Partition-based graph abstraction) | Slingshot | Monocle3 | Velocity |

capnocytophaga stomatis

2009-10 -
2010-07

Research assistant

COMSATS University

→ Wet lab experiments and Bioinformatics analysis (exome sequencing data analysis)

scVelo (RNA velocity) |
Pseudotime inference

Cell-Cell Communication:

LIANA (meta-framework with consensus ranking) |
CellChat | CellPhoneDB |
NicheNet | NATMI |
Connectome |
SingleCellSignalR | SCpubr wrapper

Copy Number Variation (CNV) Detection:

inferCNV | SCEVAN |

Transcription Factor & Gene Regulatory Network Analysis:

SCENIC | GENIE3 |
DoRothEA | RcisTarget

Visualization:

ggplot2 |
ComplexHeatmap |
SCpubr | Nebulosa |
dittoSeq | ggblend |
DimPlot | FeaturePlot | SCP
| ScPlotter

Related Skills:

Whole genome sequencing (WGS) | Whole exome sequencing (WES) | Transcriptomics | Metatranscriptomics | Amplicon Sequencing | Metagenomics | small RNAseq | Biological Databases knowledge | Rough sets (Machine learning) | Whole exome sequencing (WES) | Pacbio-hifi and nanopore data analysis | Phylogenetics analysis

Education

2023-09 -
Present

PhD in Cancer Biology

France

2010-08 -
2012-10

Master of Science: Bioinformatics

Sweden

Conferences & Seminars

- **The Mathematics of Deep learning**, Honkkong
- **The Hong Kong epigenomics project**, Hongkong
- **gdec-bioinfo-workshop# 2 - tidyverse / r-markdown for genomics**, France
- Flash Talk and Poster Presentation - **SBM Day**, France (September 2024 & 2025)
- Poster Presentation - **Doctoral School Day 2025**, France

Publications

1. Zajitschek, S., James E. Herbert-Read, Abbasi N, Immler. Paternal personality and social status influence offspring personality in offsprings. BMC Evolutionary Biology (2017) 17:157
2. Zangenah S, Abbasi N, Anders F A, Bergman P. Whole Genome Sequencing Reveals Novel Species of genus Capnocytophaga isolated from dog and cat bite wounds in humans . Scientific Reports (2016)
3. Ajmal M, Khan M, Neveling K, Tayyab A, Jaffar S, Sadeque A, Ayub H, Abbasi N, Riaz M, Micheal S, Gilissen C, Ali S, Azam M, Collin R, Cremers F, Qamar R. Exome sequencing identifies a novel and a recurrent BBS1 mutation in Pakistani families with Bardet-Biedl syndrome. Molecular vision (2013)



Final Thesis & Research Projects

- **Current PhD Project:** Working on deciphering Sézary syndrome heterogeneity using bioinformatics approaches including WES data, single-cell RNA data, and BioNano optical mapping data
- Research based project on Adaptive evolution in birds
- Machine learning project on Rough Set-based model of HIV-1 using Dmlab for Montecarlo feature selection and Rosetta
- Model validation using Swiss-pdb viewer
- Web development Project (Drug assistant) in laboratory information management system using PHP and Mysql
- Base Composition analyses in the Spironucleus salmonicidi genome using Linux, Perl, R, GC tools
- Analysis of regulatory regions of genes expressed in eye with Dr Mehmood Ahmed kayani and Dr Ansar



References

References will be provided on request

Other important skills:

Package management system (Conda) | Workflow management system (Snakemake) | Cloud computing | Github and version control system (Git) | Singularity containers and Docker