

LINKS

Github:// [adhal007](#)

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Website:// [abhilashdhal.com](#)

EDUCATION

UC DAVIS, USA

MS IN BIOPHYSICS | GRAD. DEC' 2019

IIT-VARANASI, INDIA

B.TECH/M.TECH IN BIOCHEMICAL
ENGG | GRAD. AUG' 2016

RELEVANT COURSEWORK GRADUATE

Quant. and Population Genetics
Macromolecule structure and
interactions

Intro to Mathematical Statistics
Probability theory
Artificial Intelligence

UNDERGRADUATE

Intro to Bioinformatics
Mol. Bio and Genetic Engg.
Biochemistry
Protein Engineering
Bioprocess Calculations
Numerical Analysis

OTHER PROJECTS

- **OmixHub**: Streamlined data accession, differential gene expression, and gene set enrichment analysis for bulk RNA-Seq data.
- **Deep Learning**: Multi-label classification of chest X-rays using DenseNet, Intracranial hemorrhage detection with CNNs

SKILLS

PROGRAMMING

OVER 5000 LINES:

Python • R • MySQL

OVER 1000 LINES:

Shell • Julia • GO

FAMILIAR:

• C • C++ • Perl

METHODS

GWAS, Biomarker Discovery,
Hypothesis Testing, Deep Learning,
NLP, Bayesian and Frequentist
Modeling, Algorithm Design

SELECTED PUBLICATIONS

- Profiling antibody epitopes induced by mRNA-1273 vaccines and boosters, *Frontiers* (2024).
- Distinguishing features of long COVID identified through immune profiling, *Nature* (2023).
- Utilizing the autoantibody immune response for kidney cancer early detection, *JCO* (2022).
- High-resolution epitope mapping in COVID-19 patients, *Commun Biol* (2021).

EXPERIENCE

UNIVERSITY OF TRIESTE | RESEARCH FELLOW (SEP' 2024 - PRESENT)

- Developed **topological scoring dashboard** for microbiome analysis aiding clinicians and bioinformaticians. ([TOPOSCORE](#))

GOOGLE SUMMER OF CODE | CONTRIBUTOR (MAY 2024 - SEP' 2024)

- Developed automated tools for cancer **clinical metadata harmonization** across 375+ studies, improving accuracy by 80%.
- Built an **ontology mapping framework** using GPT-3.5, reducing manual curation efforts by 85%. ([METAHARMONIZER](#))

SERIMMUNE INC, CA | ASSOCIATE DATA SCIENTIST (FEB'2020 - NOV'2023)

- Collaboratively worked to drive **revenue projects for healthcare business partnerships** (Moderna, Genentech, Verily, Cedar-Sinai, LabCorp, Yale and Stanford)
- Designed **statistical methods** for identifying population-level disease signatures in infectious disease and oncology.
- Deployed **feature selection tools** for motif selection achieving high specificity (99.5%) for SARS-CoV-2 IgG panels. ([PCT/US2021/038960](#))
- Developed **proteome-wide epitope discovery tools** for vaccine evaluation, anti-drug antibody profiling and disease differentiation.
- Engineered **Kmer-based networks** leveraging Hamming distance to enhance linear protein signal in sequencing data by 75%, marking the highest performance improvement among production models.
- Implemented advanced **batch correction algorithms** to normalize technical variations and correct signal abnormalities, significantly improving cancer subtype and autoimmune disease classification accuracy.

UC DAVIS | GRADUATE RESEARCH (AUG' 2018 - FEB' 2020)

- **Thesis Project**: Evaluated single step and classical bayesian regression models for genomic prediction and GWAS, achieving 90% accuracy for trait prediction in cattle. ([SSBR-JWAS](#))

MENTORING

- Mentored a data analyst in statistical method development and software best practices. [Serimmune \(2020-2023\)](#)
- Mentored 50+ students in developing GWAS software and 100+ students in a computational drug design course. ([UC Davis, 2018](#))

ACCOMPLISHMENTS

2024	1st/100	Research Grant Winner (PNRR Project, UNITS, Italy)
2017	4th/50	Grad. Research Fellow (UC Davis, USA)
2016	1st/25	Junior Research Fellow (IISC, India)
2015	8th/100,000	Graduate aptitude examination (GATE, India),
2011	5443/500,000	Indian Inst. of Tech. Joint Entrance Exam(IIT-JEE, India)