

# Abhilash Dhal

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EDUCATION	<p><b>University of California, Davis, CA, USA</b> MS, Biophysics <i>Sep' 17 - Sep' 19 (Expected)</i></p> <p><b>Indian Institute of technology(IIT), Varanasi, India</b> Integrated Dual Degree (B.Tech and M.Tech), Biochemical Engineering, <i>Jul' 11 - Jul' 16</i></p> <p><b>Relevant Coursework</b> Algorithm Design, AI and Deep-learning, Advanced Statistics and Probability, Biophysics Techniques, Big Data and High Performance Statistical Computing</p>
INTERESTS	Data science, Algorithm Design, Machine learning and AI, Multivariate analysis and Statistical Modelling, Bayesian Modelling, Integrative Genomics, Bioinformatics
RESEARCH PROJECTS	<p><b>Single step GWAS and QTL analysis method using bayesian modelling and bayesian multiple testing(Research Paper In Progress)</b> <i>Advisor: Dr. Hao Cheng</i></p> <ul style="list-style-type: none"><li>- Using a bayesian regression model for application in genome wide association studies(GWAS)</li><li>- Devised a novel bayesian inference testing for controlling false positives in GWAS</li></ul> <p><b>Tactical decision making agents in starcraft II</b> <i>Advisor: Dr. Joshua Mccoy</i> <i>January'19 - March'19</i></p> <ul style="list-style-type: none"><li>- Built 2 reward agents based on CNN architecture and Q-learning algorithms</li><li>- CNN performance was evaluated by F-1, precision and recall</li><li>- Q-learning performance evaluated over 1000 games for convergence</li><li>- Testing against medium and hard scripted AI's for starcraft II</li></ul> <p><b>Genomic prediction of commercial chicken traits using JWAS</b> <i>Advisor: Dr. Hao Cheng</i> <i>August'18 - January '19</i></p> <ul style="list-style-type: none"><li>- Developed a julia module(XSimPreProcess) for automating Data Simulation and Bayesian Analysis <a href="https://github.com/adhal007/SSBR-JWAS-Implementation">https://github.com/adhal007/SSBR-JWAS-Implementation</a></li><li>- Feature visualization using R with my own smoothing function for a custom visualization plot <a href="https://github.com/adhal007/PhenoCorr">https://github.com/adhal007/PhenoCorr</a></li><li>- JWAS : Bayesian modelling for single trait analysis of estimated breeding values(EBV's) <a href="https://github.com/reworkhow/JWAS.jl">https://github.com/reworkhow/JWAS.jl</a></li><li>- <b>Prediction accuracy</b> for all pairwise traits by pearson's correlation.</li></ul> <p><b>Behaviour Recognition of animal activity using Deep learning methods</b> <i>Advisor: Dr. Ilias Tagopolous</i> <i>September'18 - Dec '18</i></p> <ul style="list-style-type: none"><li>- Built 5 different neural network classifiers(CNN, CNN-LSTM, RNN, CNN-MLP and MLP) for classifying GPS and remote sensing data</li><li>- Grid Search hyper parameter optimization with best F-1 Score of 0.75</li><li>- Statistical significance of F-1 scores using Paired t-tests</li></ul> <p><b>API for ROSIE Homology modelling enzyme family suite</b> <i>Advisor: Dr. Justin Siegel</i> <i>Jan'18 - March '18</i></p> <ul style="list-style-type: none"><li>- Built Controller functions to handle data formats from PostgreSQL server for front end hosting</li><li>- Added new protein folding features in the Validator module for user functionality</li><li>- Prototyped new application on VM to analyze new protein folding functionality</li></ul>
COMPUTER SKILLS	<p><b>Languages:</b> C, C++, Python, Bash, Julia, L<sup>A</sup>T<sub>E</sub>X, R, HTML, java</p> <ul style="list-style-type: none"><li>• Machine Learning: Tensorflow, Pandas, PyTorch, SciPy, Keras, Numpy</li><li>• Statistical Modelling: JWAS, LinearAlgebra, Distributions</li><li>• Web Development and Frameworks: PostgreSQL, SQLite, MongoDB, UCSC Genome Browser, GTE<sub>x</sub>, 1000 Bulls genome database, Google Cloud Platform(GCP), Turbogears</li></ul>