

Abhilash Dhal

EDUCATION	University of California, Davis, CA, USA PhD, Biophysics,	<i>Sep' 17 - Sep' 22 (Expected)</i>
	Indian Institute of technology(IIT), Varanasi, India Integrated Dual Degree (B.Tech and M.Tech), Biochemical Engineering,	<i>Jul' 11 - Jul' 16</i>
	Relevant Coursework: Algorithm Design, AI and Deep-learning Advanced Statistics and Probability, Biophysics Techniques, Big Data and High Performance Statistical Computing	
INTERESTS	Data science, Algorithm Design, Machine learning and AI, Multivariate analysis and Statistical Modelling, Bayesian Modelling, Integrative Genomics, Bioinformatics	

RESEARCH PROJECTS	Single step GWAS and QTL analysis method using bayesian modelling and bayesian multiple testing(Research Paper In Progress) <i>Advisor: Dr. Hao Cheng</i>	
	<ul style="list-style-type: none">- Using a bayesian regression model for application in genome wide association studies(GWAS)- Devising a novel bayesian inference testing for controlling false positives in GWAS	
	Genomic prediction of five commercial chicken traits using JWAS <i>Advisor: Dr. Hao Cheng</i>	
	<i>August '18 - January '19</i>	
	<ul style="list-style-type: none">- Developed a julia module for automating pre-processing of pedigree, phenotype and genotype file https://github.com/adhal007/SSBR-JWAS-Implementation for simulated data from XSim https://github.com/reworkhow/XSim.jl- Performed preliminary exploratory data analysis and visualization feature correlation in R - Statistical modelling with BayesC and BayesCπ, bayesian regression with julia. - Preliminary analysis involved calculation of trait distribution/density and correlation value R^2 for pairs of traits and was visualized using R with my own functionshttps://github.com/adhal007/PhenoCorr for making a grid plot with density and correlations in a 5 x 5 grid. JWAS https://github.com/reworkhow/JWAS.jl was used for bayesian modelling with single trait bayesian analysis of estimated trait values and correlation between true and estimated trait values as well as estimated marker effects and variances.- Highest correlation obtained among all the traits was for body weight and equal to 0.63. While other traits showed a correlation in the range of 0.45 to 0.6	
	Behaviour Recognition using Deep learning methods <i>Advisor: Dr. Ilias Tagopolous</i>	
	<i>Sept '18 - Dec '18</i>	
	<ul style="list-style-type: none">- Implemented 5 different neural network architectures of CNN, CNN-LSTM, RNN, CNN-MLP and MLP on animal activity data from remote sensing and GPS devices. F-1 scores, Accuracy, recall and precision scores were calculated for each model with 5 replicate runs after hyper parameter optimization using grid search.- Grid Search for hyper parameter optimization provided best hyper-parameter weights for a F-1 Score of 0.75-Statistically evaluated the significance of prediction accuracy scores using Paired t-tests for the mean of prediction accuracy scores for all model pairs.- Found that a CNN that predicts a label for every five seconds of activity performs better than all other models, achieving an F1 score of 74.7 ± 0.01 and an accuracy of 76.0 ± 0.02 on a class balanced dataset.	

COMPUTER SKILLS	Languages: C, C++, Python, Bash, Julia, L ^A T _E X, R, HTML Platforms and Databases: <ul style="list-style-type: none">• Machine Learning: Tensorflow, Pandas, PyTorch, SciPy, Keras• Statistical Modelling: JWAS, LinearAlgebra, Distributions• Databases: SQL, MongoDB, UCSC Genome Browser, GTEX, 1000 Bulls genome database	
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