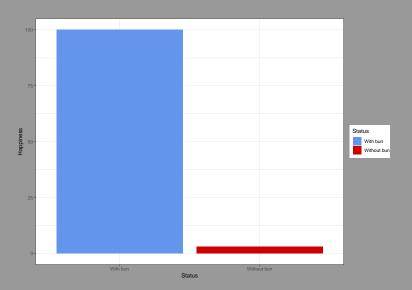
Lab meeting

Luke Hayden

14th November 2018

Did everybody get a bun?



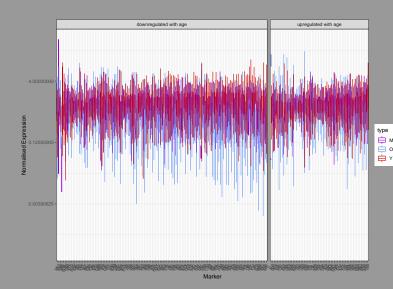
Project

Examine the effect of regeneration on the molecular age profile of *Parhyale* limbs

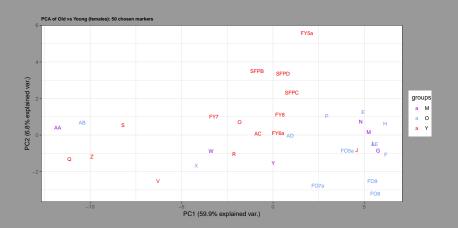
Designing codeset

- *Nanostring as method to quantify gene expression
- *200 genes in codeset
- -195 genes chosen on the basis of differential expression analysis
- -5 control genes: do not vary in expression between conditions

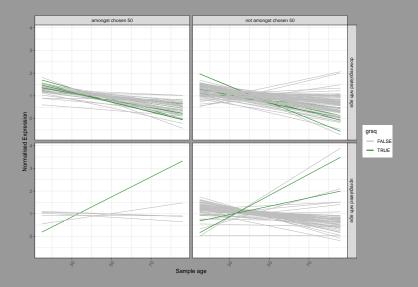
Old vs Young



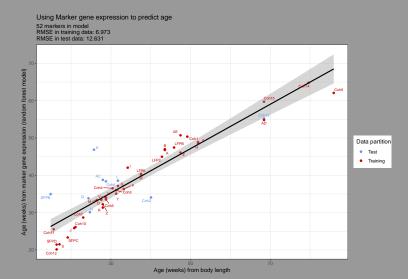
Young vs old separation: PCA old vs young



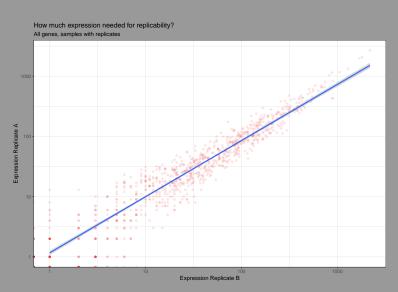
Expression/length relationship



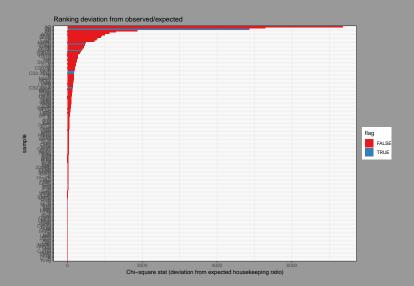
Old Random Forest model



Quality assurance 1: Read number



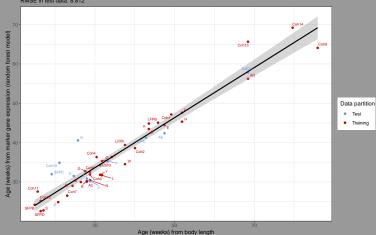
Quality assurance 2: Housekeeping gene ratio



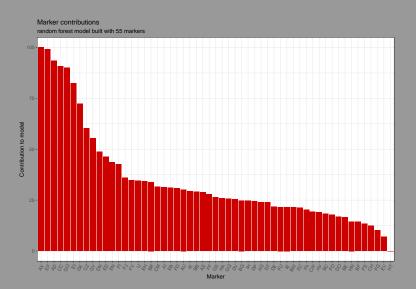
40-fold cross-validation

Using Marker gene expression to predict age

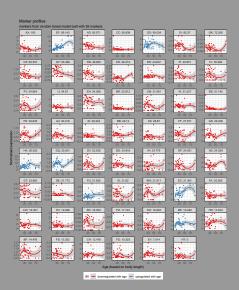
55 markers in model RMSE in training data: 6.321 RMSE in test data: 8.812



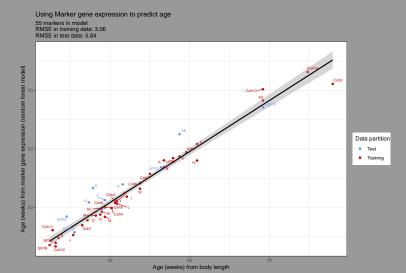
Contributions to model



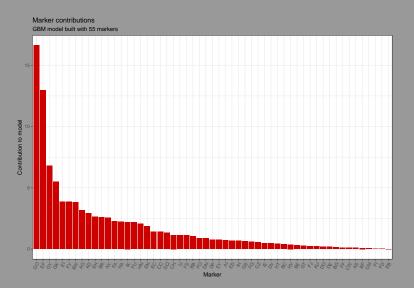
Marker profiles



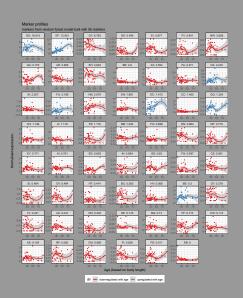
Gradient Boosting Machine



Marker contributions



Marker contributions and profiles



GBM vs Random Forest

