

Lab meeting

Luke Hayden

14th November 2018

Did everybody get their bun?

Project

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

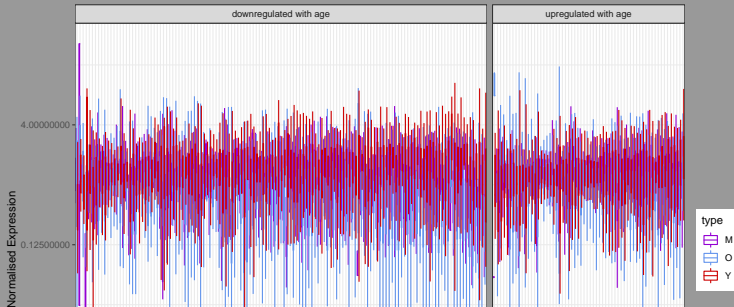
Designing codeset

- *Nanostring as method to quantify gene expression

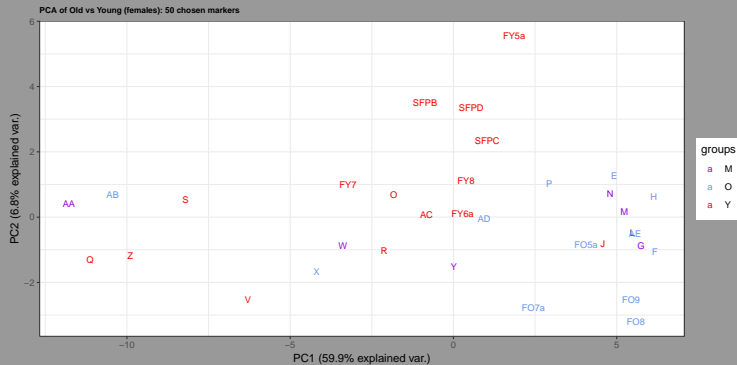
- *200 genes in codeset

- 195 genes chosen on the basis of differential expression analysis

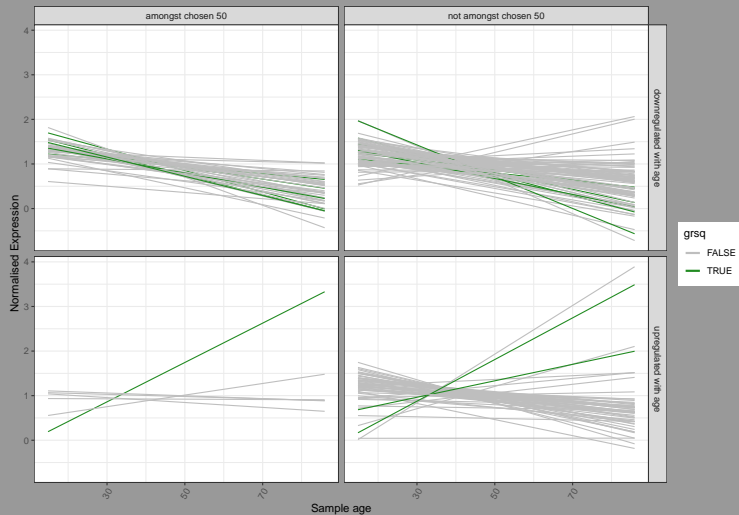
- 5 control genes: do not vary in expression between conditions



Young vs old separation: PCA old vs young



Expression/length relationship



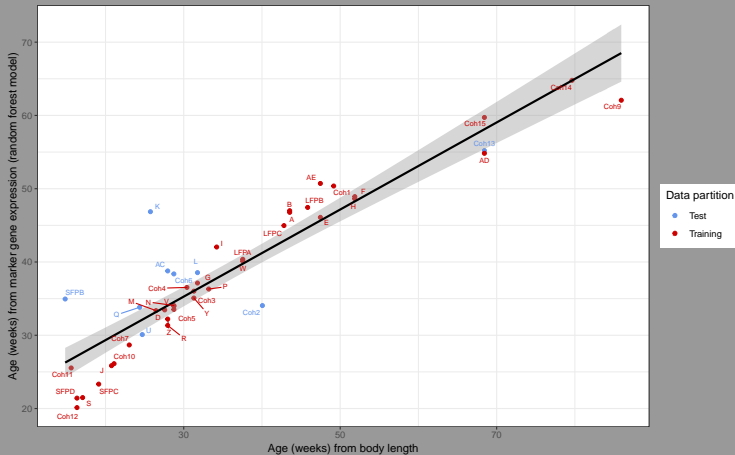
Old RF model

Using Marker gene expression to predict age

52 markers in model

RMSE in training data: 6.973

RMSE in test data: 12.631



Quality thresholds

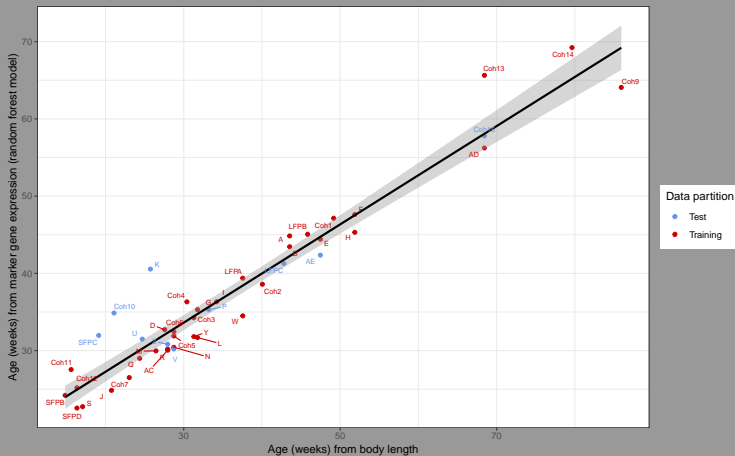
40-fold cross-validation

Using Marker gene expression to predict age

55 markers in model

RMSE in training data: 6.321

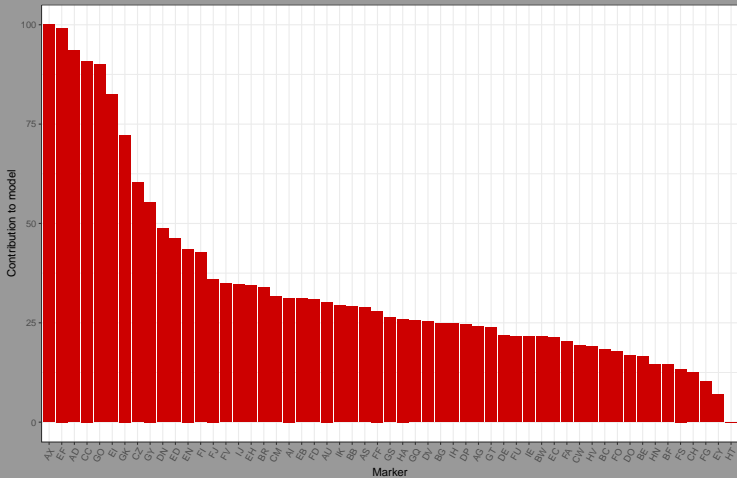
RMSE in test data: 8.812



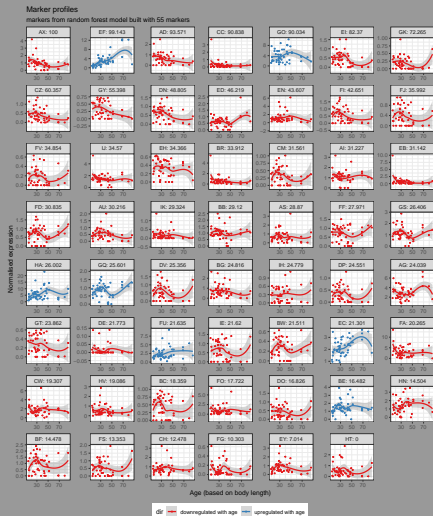
Contributions to model

Marker contributions

random forest model built with 55 markers



Marker profiles



It looks like some optimisation on the basis of these profiles may

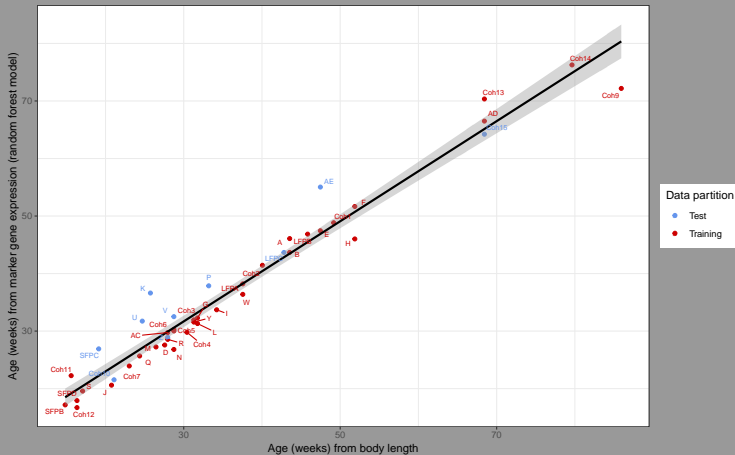
GBM

Using Marker gene expression to predict age

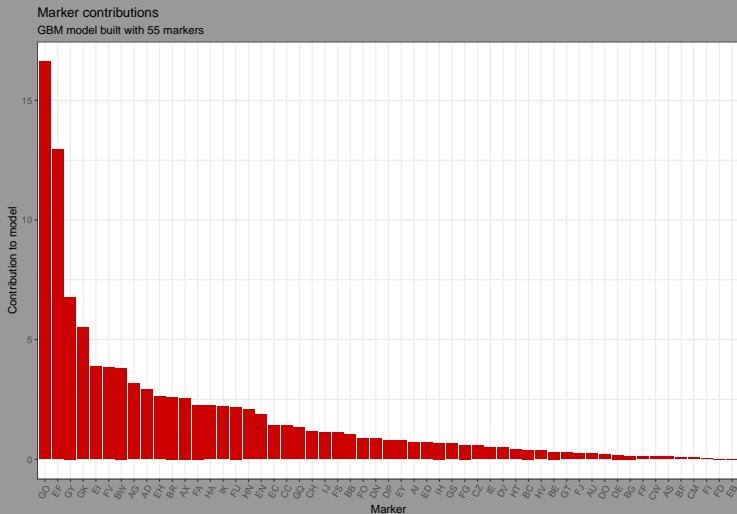
55 markers in model

RMSE in training data: 3.06

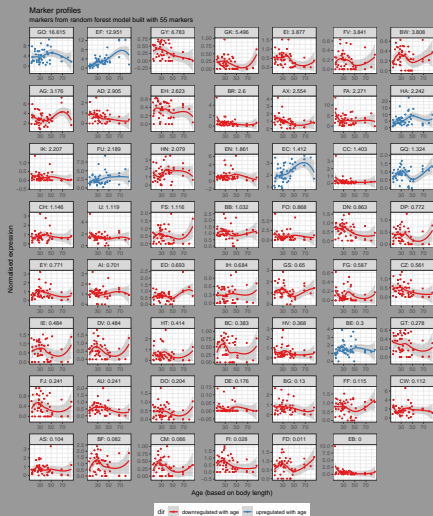
RMSE in test data: 5.84



Marker contributions



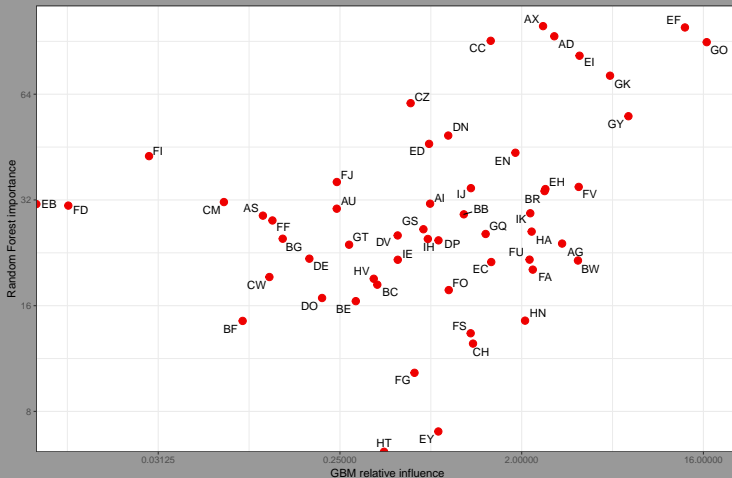
Marker contributions and profiles



GBM vs Random Forest

Marker importance: GBM vs Random Forest

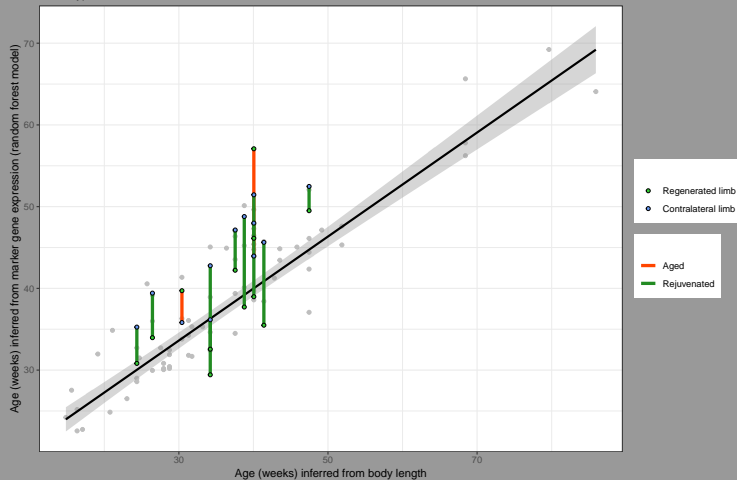
Same 55 markers



Does regeneration rejuvenate?

Change in molecular age due to regeneration

Model type: RANGER, 55 markers used



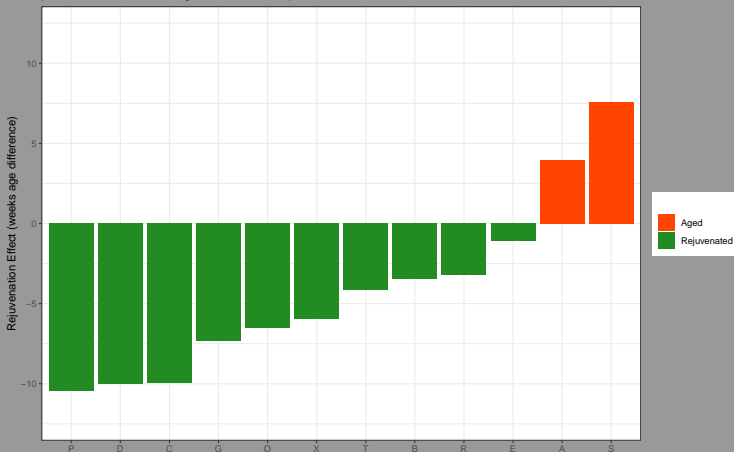
Does regeneration rejuvenate?

[1] 0.114

Rejuvenation Effect

Model type: RANGER, 55 markers used

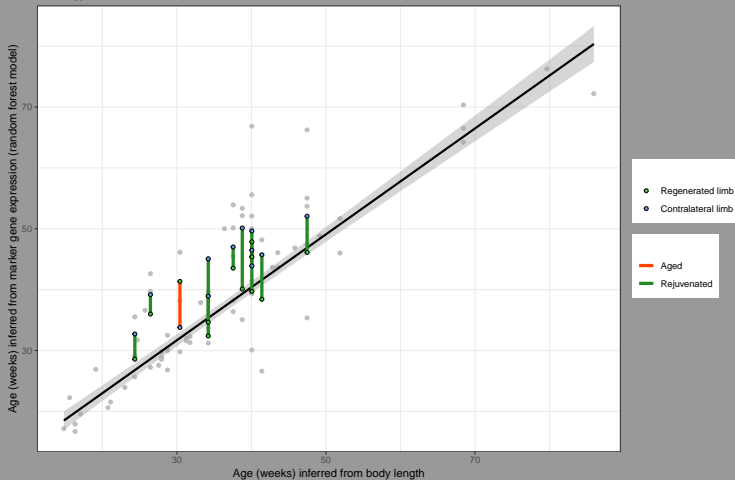
p-value of t-test between regenerated and unamputated: 0.103



Does regeneration rejuvenate?

Change in molecular age due to regeneration

Model type: GBM, 55 markers used



Does regeneration rejuvenate?

[1] 0.319

Rejuvenation Effect

Model type: GBM, 55 markers used

p-value of t-test between regenerated and unamputated: 0.32

