Lab Meeting

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Background

Project

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

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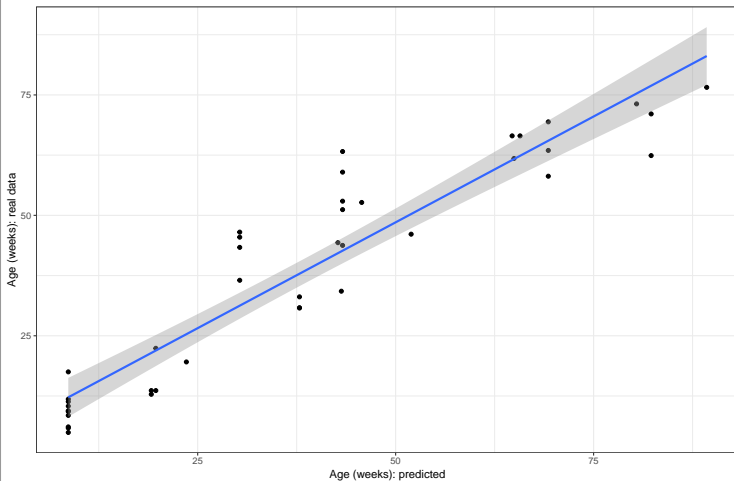
*Nanostring as method to quantify gene expression
*200 genes in codeset
-195 genes chosen on the basis of differential expression analysis
-5 control genes: do not vary in expression between conditions
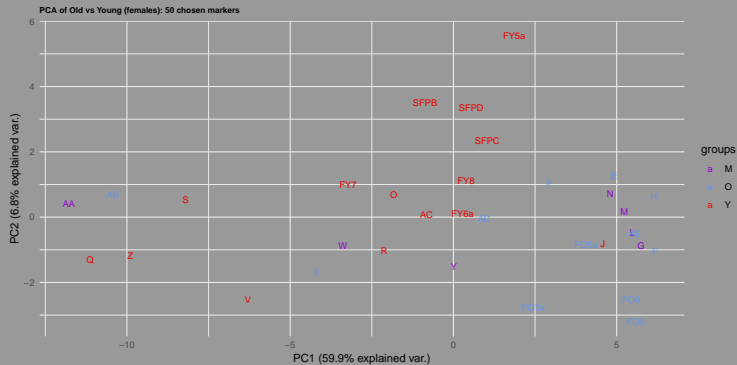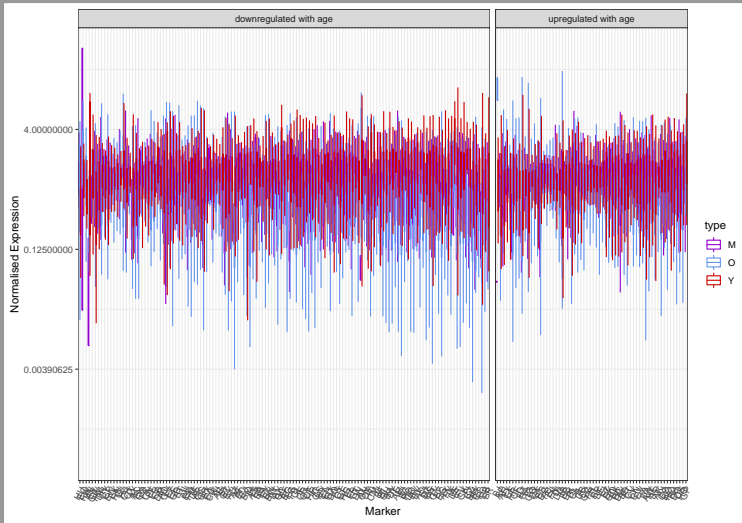
Age-length relationship

Age–length relationship in female Parhyale
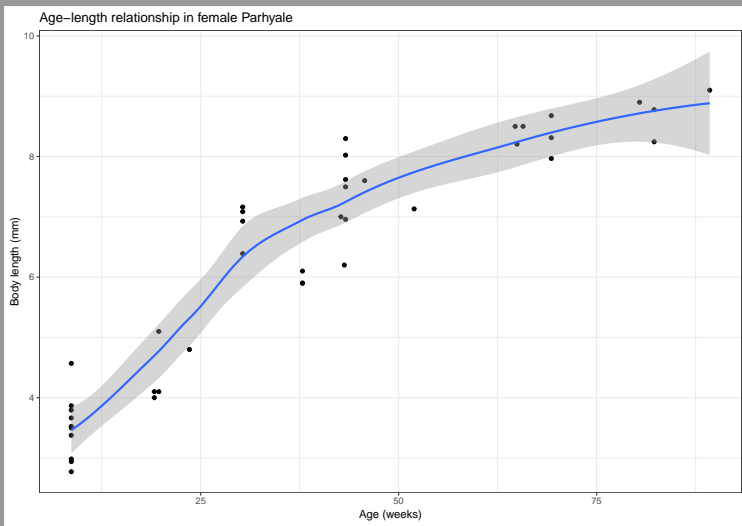
Building an age-length model

Model predicted vs real values

Young vs old separation: PCA old vs young

PCA of Old vs Young (females): 50 chosen markers

Young vs old separation: Old vs young by marker

Expression/length relationship
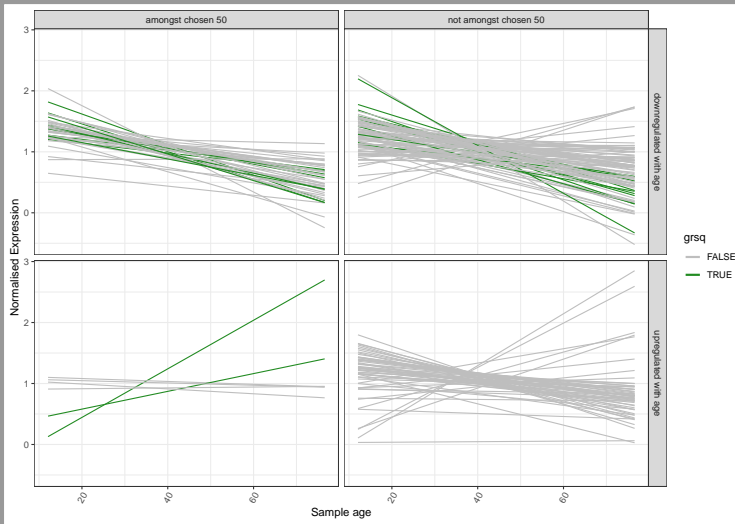
Multiple Regression approach

Simple linear regression:

Age = X(marker1) + c

We try to find values for x & c that come as close as possible to solving the equation for each set of values for *Age* and *marker1* we have.
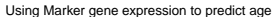
Two predictors:

Age = X(marker1) + Y(marker2) + c

Many predictors

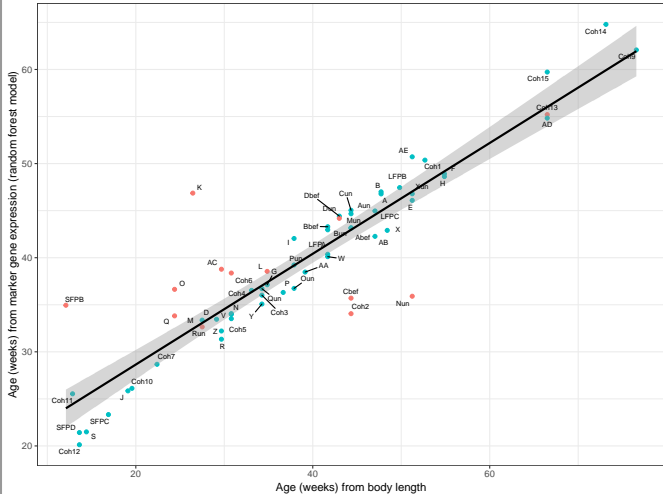**Age = X(marker1) + Y(marker2) + Z(marker3) + W(marker4) + ... + c**

Where we have many different markers, we can find values of x,y,z,w, etc that solve this equation very well but don't provide predictive power
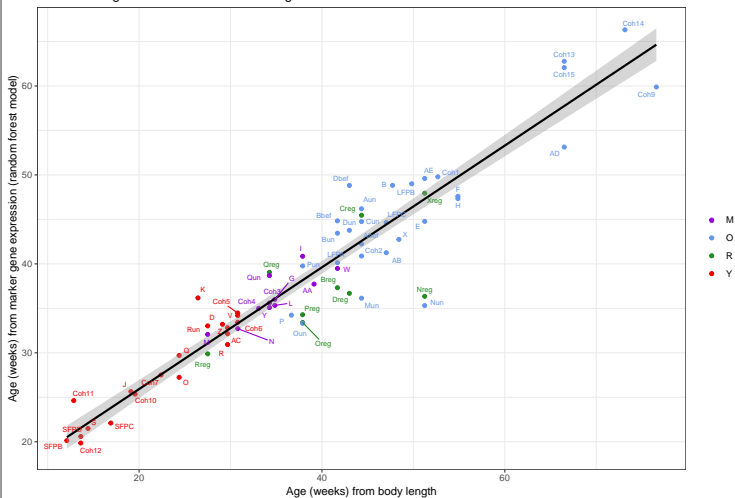
Random Forest approach

Examining this model

Out-of-sample errors

Using Marker gene expression to predict age

Effect of regeneration

How does regeneration affect molecular age?

Testing this effect

```
##
##  One Sample t-test
##
## data:  md$lmresid[md$reg == "R"]
## t = -1.4697, df = 8, p-value = 0.08992
## alternative hypothesis: true mean is less than 0
## 95 percent confidence interval:
##       -Inf 0.5763361
## sample estimates:
## mean of x
## -2.172771
```