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

Building an age-length model

Model performance

Young vs old separation

Using age classes: old vs young (plus middle)

Multiple Regression approach

Model overfitting

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, not because we