# exploratory analysis

Did a bit of format cleaning, and ended up with a file called "brainclimatedata.txt"

First, I want a simple figure showing brain size over time

```r
library(ggplot2)
library(scales)

brains <- read.table("brainclimatedata.txt", header=TRUE, sep="\t")
brains$Species <- gsub(" ", "_", brains$Species) #remove spaces
zachos <- read.table("Zachos2001Climate.txt", header=TRUE, sep="\t")
zachos$filteredO18 <- filter(zachos$o18, filter = rep(1, 70), method = "convolution")


brainsOverTime_order <- ggplot(data=brains) +
  geom_point(aes(Actual.MYA, log(CC))) +
  facet_wrap(~Order) +
  geom_line(data=zachos,aes(x=age*-1, y=rescale(filteredO18*-1,c(-1,8))), color="red") +
  theme_bw(35) +
  labs(x="MYA", title="Brain Size by Order")
suppressWarnings(print(brainsOverTime_order))
```
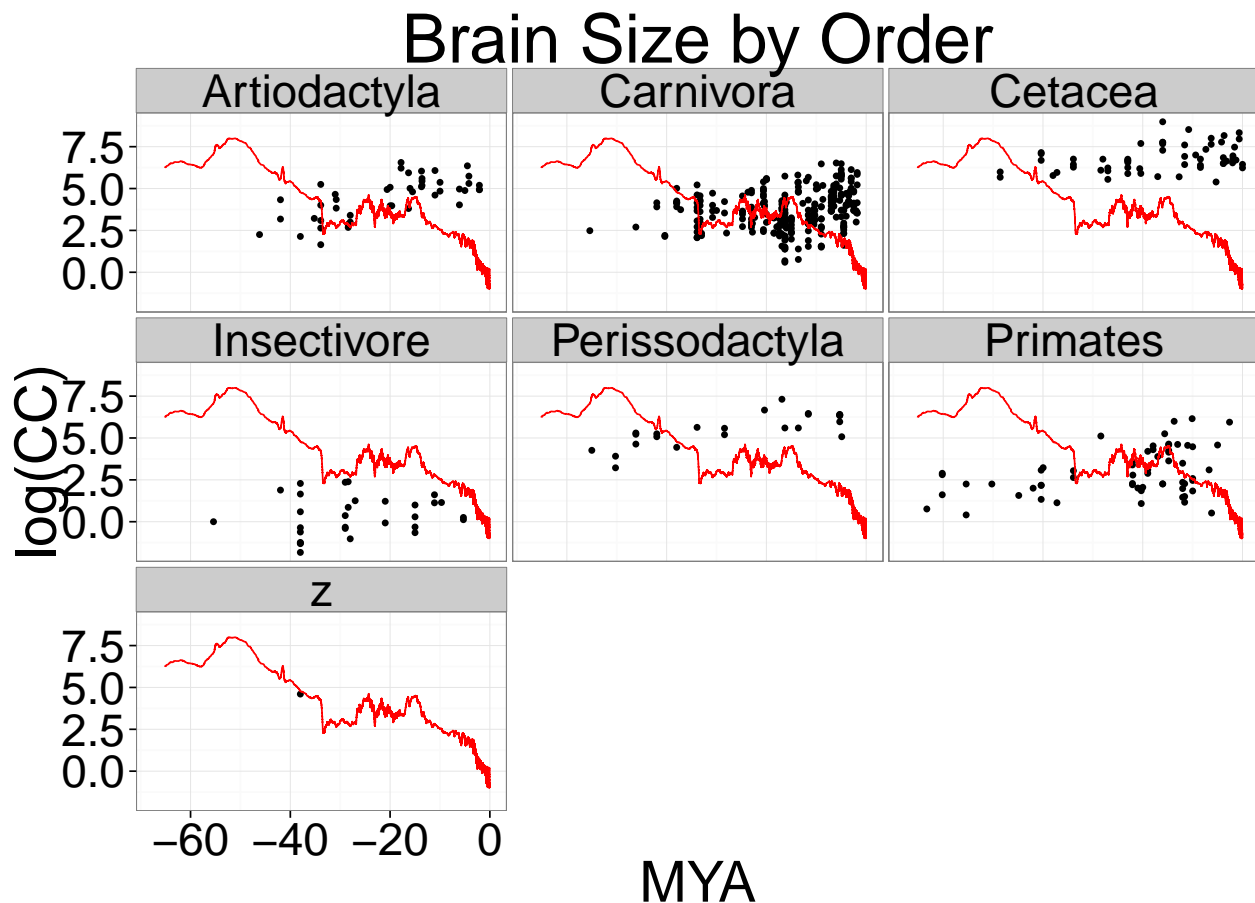


```r
suppressWarnings(ggsave("brainsOverTime_order.pdf", width=15, height=10, units="in"))
```

```
brainsOverTime_suborder <- ggplot(data=brains) +
  geom_point(aes(Actual.MYA, log(CC))) +
  facet_wrap(~Suborder) +
  geom_line(data=zachos,aes(x=age*-1, y=rescale(filteredO18*-1,c(-1,8))), color="red") +
  theme_bw(35) +
  labs(x="MYA", title="Brain Size by Suborder")
suppressWarnings(print(brainsOverTime_suborder))
```
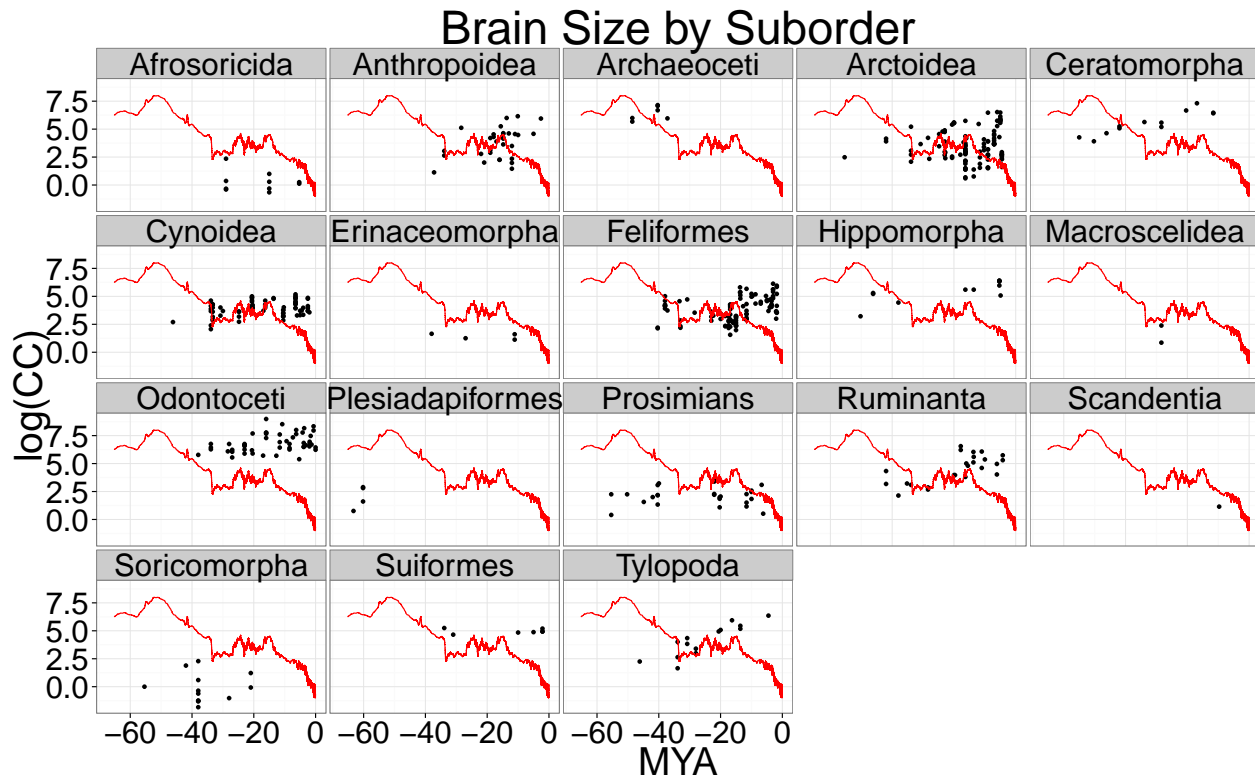


```
suppressWarnings(ggsave("brainsOverTime_suborder.pdf", width=15, height=10, units="in"))
```

Multiple regression

It strikes me that a single multiple regression is more appropriate than many individual correlation analyses. Of course, there are parametric assumptions that we need to address, and we should defnitely look into doing this in a phylogenetic context, as these data are likely phylogenetically autocorrelated.

5 Ma time bins

First I did a multiple regression of log(CC) by mean_oxy, sd_oxy, and slope_oxy, with all possible interaction terms. This is the 'fullMod_5MA'.

Second, I did a sparse model, with no interaction terms. This is the `sparseMod_5MA`

```
fullMod_5MA <- lm(log(CC) ~ X5Mya_M_oxy * X5Mya_slope_oxy * X5Mya_SD_oxy, data = brains)
summary(fullMod_5MA)
```

```
## 
## Call:
## lm(formula = log(CC) ~ X5Mya_M_oxy * X5Mya_slope_oxy * X5Mya_SD_oxy,
##     data = brains)
## 
## Residuals:
##    Min    1Q Median     3Q    Max
##  -5.35  -1.09  -0.07   1.10   5.64
## 
## Coefficients:
##                                         Estimate Std. Error t value
## (Intercept)                                0.554      2.055    0.27
## X5Mya_M_oxy                                1.756      0.947    1.85
## X5Mya_slope_oxy                           42.912     15.258    2.81
## X5Mya_SD_oxy                               7.412      6.980    1.06
## X5Mya_M_oxy:X5Mya_slope_oxy              -16.175      7.141   -2.26
## X5Mya_M_oxy:X5Mya_SD_oxy                  -4.294      3.257   -1.32
## X5Mya_slope_oxy:X5Mya_SD_oxy            -141.389     45.461   -3.11
## X5Mya_M_oxy:X5Mya_slope_oxy:X5Mya_SD_oxy  56.863     20.938    2.72
##                                         Pr(>|t|)
## (Intercept)                               0.7874
## X5Mya_M_oxy                               0.0643 .
## X5Mya_slope_oxy                           0.0051 **
## X5Mya_SD_oxy                              0.2888
## X5Mya_M_oxy:X5Mya_slope_oxy               0.0239 *
## X5Mya_M_oxy:X5Mya_SD_oxy                  0.1879
## X5Mya_slope_oxy:X5Mya_SD_oxy              0.0020 **
## X5Mya_M_oxy:X5Mya_slope_oxy:X5Mya_SD_oxy  0.0068 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.73 on 500 degrees of freedom
## Multiple R-squared:  0.0983, Adjusted R-squared:  0.0857
## F-statistic: 7.79 on 7 and 500 DF,  p-value: 5.81e-09
```

```
sparseMod_5MA <- lm(log(CC) ~ X5Mya_M_oxy + X5Mya_slope_oxy + X5Mya_SD_oxy, data = brains)
summary(sparseMod_5MA)
```

```
## 
## Call:
## lm(formula = log(CC) ~ X5Mya_M_oxy + X5Mya_slope_oxy + X5Mya_SD_oxy,
##     data = brains)
## 
## Residuals:
##     Min     1Q Median     3Q    Max
##  -5.269 -1.044 -0.068  1.175  5.319
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.384      0.426    5.59 3.7e-08 ***
## X5Mya_M_oxy        0.734      0.124    5.93 5.6e-09 ***
## X5Mya_slope_oxy    0.424      0.680    0.62    0.53
## X5Mya_SD_oxy      -0.153      1.011   -0.15    0.88
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.75 on 504 degrees of freedom
## Multiple R-squared:  0.0728, Adjusted R-squared:  0.0673
## F-statistic: 13.2 on 3 and 504 DF,  p-value: 2.64e-08
```

1 Ma time bins

```
fullMod_1MA <- lm(log(CC) ~ X1Mya_M_oxy * X1Mya_slope_oxy * X1Mya_SD_oxy, data = brains)
summary(fullMod_1MA)
```

```
##
## Call:
## lm(formula = log(CC) ~ X1Mya_M_oxy * X1Mya_slope_oxy * X1Mya_SD_oxy,
##     data = brains)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -5.498 -1.069 -0.047  1.101  5.289
##
## Coefficients:
##                                     Estimate Std. Error t value
## (Intercept)                          -0.0802     1.1445   -0.07
## X1Mya_M_oxy                           1.5066     0.5258    2.87
## X1Mya_slope_oxy                      11.5317     5.5200    2.09
## X1Mya_SD_oxy                          9.5055     4.4767    2.12
## X1Mya_M_oxy:X1Mya_slope_oxy          -4.5690     2.4437   -1.87
## X1Mya_M_oxy:X1Mya_SD_oxy             -3.0095     2.0415   -1.47
## X1Mya_slope_oxy:X1Mya_SD_oxy        -32.6204    19.1550   -1.70
## X1Mya_M_oxy:X1Mya_slope_oxy:X1Mya_SD_oxy 12.8164  8.6040    1.49
##                                     Pr(>|t|)
## (Intercept)                           0.9442
## X1Mya_M_oxy                           0.0043 **
## X1Mya_slope_oxy                       0.0372 *
## X1Mya_SD_oxy                          0.0342 *
## X1Mya_M_oxy:X1Mya_slope_oxy           0.0621 .
## X1Mya_M_oxy:X1Mya_SD_oxy              0.1411
## X1Mya_slope_oxy:X1Mya_SD_oxy          0.0892 .
## X1Mya_M_oxy:X1Mya_slope_oxy:X1Mya_SD_oxy  0.1370
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.74 on 500 degrees of freedom
## Multiple R-squared:  0.0964, Adjusted R-squared:  0.0837
## F-statistic: 7.62 on 7 and 500 DF,  p-value: 9.46e-09
```

```
sparseMod_1MA <- lm(log(CC) ~ X1Mya_M_oxy + X1Mya_slope_oxy + X1Mya_SD_oxy, data = brains)
summary(sparseMod_1MA)
```

```
##
## Call:
```

```
## lm(formula = log(CC) ~ X1Mya_M_oxy + X1Mya_slope_oxy + X1Mya_SD_oxy,
##     data = brains)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -5.432 -1.090 -0.053  1.109  5.467
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)        1.979      0.381    5.19  3.1e-07 ***
## X1Mya_M_oxy        0.705      0.113    6.26  8.1e-10 ***
## X1Mya_slope_oxy   -0.132      0.263   -0.50     0.62
## X1Mya_SD_oxy       1.524      1.222    1.25     0.21
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.75 on 504 degrees of freedom
## Multiple R-squared:  0.0795, Adjusted R-squared:  0.074
## F-statistic: 14.5 on 3 and 504 DF,  p-value: 4.49e-09
```

In both the sparse and full models, mean_oxy is highly significant.

PGLS

PGLS using the Bininda-Emonds tree, and the brain data for extant taxa that match the names in the tree.

```
library(caper)
```

```
## Loading required package: ape
## Loading required package: MASS
## Loading required package: mvtnorm
```

```
treez <- read.nexus("Bininda_Emonds_correctedDates_FULLPHYLOG.txt")
tree <- treez[[grep(pattern = "bestDates", names(treez))]] #get the best dates tree
rm(treez)

#remove a few rows that don't have real species names. Otherwise comparative.data() complains about dup
brains <- brains[brains$Species != "new_species", ]

#make comparative data object
braintree <- comparative.data(tree, brains, "Species")
```

Using the 228 taxa with exact matches in the Bininda Emonds tree

PGLS with 5 Mya Bins

```
PGLS_5Mya_sparse <- pgls(formula = log(CC) ~ X5Mya_M_oxy + X5Mya_slope_oxy + X5Mya_SD_oxy, data = brain
sumMod_sparse <- summary(PGLS_5Mya_sparse)
sumMod_sparse
```

```
## 
## Call:
## pgls(formula = log(CC) ~ X5Mya_M_oxy + X5Mya_slope_oxy + X5Mya_SD_oxy,
##     data = braintree, lambda = "ML")
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4841 -0.1239 -0.0197  0.0860  0.5910
## 
## Branch length transformations:
## 
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.995
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.56
##    95.0% CI   : (0.972, NA)
## delta  [Fix]  : 1.000
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2.2969     0.7275    3.16   0.0018 **
## X5Mya_M_oxy       0.2554     0.1477    1.73   0.0851 .
## X5Mya_slope_oxy   0.3392     0.6853    0.49   0.6211
## X5Mya_SD_oxy     -0.0689     1.0823   -0.06   0.9493
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.163 on 224 degrees of freedom
## Multiple R-squared: 0.0168,  Adjusted R-squared: 0.00364
## F-statistic: 1.28 on 3 and 224 DF,  p-value: 0.283
```

```r
PGLS_5Mya_full <- pgls(formula = log(CC) ~ X5Mya_M_oxy * X5Mya_slope_oxy * X5Mya_SD_oxy, data = braintre
sumMod_full <- summary(PGLS_5Mya_full)
sumMod_full
```

```
## 
## Call:
## pgls(formula = log(CC) ~ X5Mya_M_oxy * X5Mya_slope_oxy * X5Mya_SD_oxy,
##     data = braintree, lambda = "ML")
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4611 -0.0992 -0.0016  0.1158  0.6085
## 
## Branch length transformations:
## 
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.993
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.42
##    95.0% CI   : (0.969, NA)
## delta  [Fix]  : 1.000
## 
## Coefficients:
```

```
##                                      Estimate Std. Error t value
## (Intercept)                            -2.957      3.524   -0.84
## X5Mya_M_oxy                             2.587      1.636    1.58
## X5Mya_slope_oxy                        -0.989     14.253   -0.07
## X5Mya_SD_oxy                           20.978     14.306    1.47
## X5Mya_M_oxy:X5Mya_slope_oxy             1.633      6.302    0.26
## X5Mya_M_oxy:X5Mya_SD_oxy               -9.645      6.945   -1.39
## X5Mya_slope_oxy:X5Mya_SD_oxy          -27.502     50.144   -0.55
## X5Mya_M_oxy:X5Mya_slope_oxy:X5Mya_SD_oxy 11.253   23.441    0.48
##                                      Pr(>|t|)
## (Intercept)                              0.40
## X5Mya_M_oxy                              0.12
## X5Mya_slope_oxy                          0.94
## X5Mya_SD_oxy                             0.14
## X5Mya_M_oxy:X5Mya_slope_oxy              0.80
## X5Mya_M_oxy:X5Mya_SD_oxy                 0.17
## X5Mya_slope_oxy:X5Mya_SD_oxy             0.58
## X5Mya_M_oxy:X5Mya_slope_oxy:X5Mya_SD_oxy 0.63
##
## Residual standard error: 0.161 on 220 degrees of freedom
## Multiple R-squared: 0.0433,  Adjusted R-squared: 0.0129
## F-statistic: 1.42 on 7 and 220 DF,  p-value: 0.197
```

5 Mya summary

- full Model

  - overall P value = 0.1971
  - ML value for lambda = 0.9931
  - adjusted R^2 = 0.0129

- sparse Model

  - overall P value for sparse model = 0.2832
  - ML value for lambda sparse model = 0.9953
  - adjusted R^2 = 0.0036

PGLS with 1 Mya Bins

```
PGLS_1Mya_sparse <- pgls(formula = log(CC) ~ X1Mya_M_oxy + X1Mya_slope_oxy + X1Mya_SD_oxy, data = brain
sumMod_sparse <- summary(PGLS_1Mya_sparse)
sumMod_sparse
```

```
##
## Call:
## pgls(formula = log(CC) ~ X1Mya_M_oxy + X1Mya_slope_oxy + X1Mya_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##    Min      1Q Median     3Q    Max
## -0.594 -0.110 -0.009  0.109  0.397
##
```

```
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.996
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.59
##    95.0% CI   : (0.973, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2.5251     0.6902    3.66  0.00032 ***
## X1Mya_M_oxy       0.2301     0.1540    1.49  0.13640
## X1Mya_slope_oxy   0.0703     0.2774    0.25  0.80015
## X1Mya_SD_oxy     -0.8666     1.1975   -0.72  0.47005
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.164 on 224 degrees of freedom
## Multiple R-squared: 0.0164,  Adjusted R-squared: 0.00319
## F-statistic: 1.24 on 3 and 224 DF,  p-value: 0.295
```

```r
PGLS_1Mya_full <- pgls(formula = log(CC) ~ X1Mya_M_oxy * X1Mya_slope_oxy * X1Mya_SD_oxy, data = braintr
sumMod_full <- summary(PGLS_1Mya_full)
sumMod_full
```

```
##
## Call:
## pgls(formula = log(CC) ~ X1Mya_M_oxy * X1Mya_slope_oxy * X1Mya_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5877 -0.1029 -0.0192  0.0704  0.5635
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.994
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.48
##    95.0% CI   : (0.970, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##                                      Estimate Std. Error t value
## (Intercept)                             0.424      1.815    0.23
## X1Mya_M_oxy                             0.932      0.665    1.40
## X1Mya_slope_oxy                        -1.634      8.221   -0.20
## X1Mya_SD_oxy                            6.863      6.702    1.02
## X1Mya_M_oxy:X1Mya_slope_oxy             0.878      3.317    0.26
## X1Mya_M_oxy:X1Mya_SD_oxy               -2.421      2.499   -0.97
## X1Mya_slope_oxy:X1Mya_SD_oxy            8.420     29.333    0.29
## X1Mya_M_oxy:X1Mya_slope_oxy:X1Mya_SD_oxy -3.961    11.892   -0.33
```

```
##                                                    Pr(>|t|)
## (Intercept)                                            0.82
## X1Mya_M_oxy                                            0.16
## X1Mya_slope_oxy                                        0.84
## X1Mya_SD_oxy                                           0.31
## X1Mya_M_oxy:X1Mya_slope_oxy                            0.79
## X1Mya_M_oxy:X1Mya_SD_oxy                               0.33
## X1Mya_slope_oxy:X1Mya_SD_oxy                           0.77
## X1Mya_M_oxy:X1Mya_slope_oxy:X1Mya_SD_oxy              0.74
##
## Residual standard error: 0.163 on 220 degrees of freedom
## Multiple R-squared: 0.0291,  Adjusted R-squared: -0.00176
## F-statistic: 0.943 on 7 and 220 DF,  p-value: 0.474
```

1 Mya summary

- full Model

    - overall P value = 0.4741
    - ML value for lambda = 0.9942
    - adjusted R^2 = -0.0018

- sparse Model

    - overall P value for sparse model = 0.2951
    - ML value for lambda sparse model = 0.9957
    - adjusted R^2 = 0.0032

PGLS with 400 Ka Bins

```
PGLS_400k_sparse <- pgls(formula = log(CC) ~ X400k_M_oxy + X400k_slope_oxy + X400k_SD_oxy, data = brain
sumMod_sparse <- summary(PGLS_400k_sparse)
sumMod_sparse
```

```
##
## Call:
## pgls(formula = log(CC) ~ X400k_M_oxy + X400k_slope_oxy + X400k_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4077 -0.1064 -0.0096  0.0966  0.5907
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.996
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.59
##    95.0% CI    : (0.973, NA)
## delta  [Fix]  : 1.000
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.556      0.634    4.03  7.6e-05 ***
## X400k_M_oxy       0.176      0.127    1.38     0.17
## X400k_slope_oxy   0.137      0.139    0.98     0.33
## X400k_SD_oxy     -0.464      1.065   -0.44     0.66
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.163 on 224 degrees of freedom
## Multiple R-squared: 0.0189,  Adjusted R-squared: 0.00575
## F-statistic: 1.44 on 3 and 224 DF,  p-value: 0.233
```

```
PGLS_400k_full <- pgls(formula = log(CC) ~ X400k_M_oxy * X400k_slope_oxy * X400k_SD_oxy, data = braintre
sumMod_full <- summary(PGLS_400k_full)
sumMod_full
```

```
##
## Call:
## pgls(formula = log(CC) ~ X400k_M_oxy * X400k_slope_oxy * X400k_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min       1Q  Median      3Q     Max
## -0.4798 -0.1070 -0.0290  0.0625  0.6185
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.995
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.51
##    95.0% CI   : (0.972, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##                                       Estimate Std. Error t value
## (Intercept)                              1.426      1.355    1.05
## X400k_M_oxy                              0.607      0.472    1.29
## X400k_slope_oxy                          2.558      2.720    0.94
## X400k_SD_oxy                             4.240      5.109    0.83
## X400k_M_oxy:X400k_slope_oxy             -1.211      1.095   -1.11
## X400k_M_oxy:X400k_SD_oxy                -1.737      1.861   -0.93
## X400k_slope_oxy:X400k_SD_oxy            -7.245     10.499   -0.69
## X400k_M_oxy:X400k_slope_oxy:X400k_SD_oxy  3.808      4.169    0.91
##                                       Pr(>|t|)
## (Intercept)                              0.29
## X400k_M_oxy                              0.20
## X400k_slope_oxy                          0.35
## X400k_SD_oxy                             0.41
## X400k_M_oxy:X400k_slope_oxy             0.27
## X400k_M_oxy:X400k_SD_oxy                0.35
## X400k_slope_oxy:X400k_SD_oxy           0.49
## X400k_M_oxy:X400k_slope_oxy:X400k_SD_oxy  0.36
```

```
##
## Residual standard error: 0.163 on 220 degrees of freedom
## Multiple R-squared: 0.032,   Adjusted R-squared: 0.0012
## F-statistic: 1.04 on 7 and 220 DF,  p-value: 0.405
```

400Ka summary

- full Model

    - overall P value = 0.4048
    - ML value for lambda = 0.9946
    - adjusted R^2 = 0.0012

- sparse Model

    - overall P value for sparse model = 0.2325
    - ML value for lambda sparse model = 0.9957
    - adjusted R^2 = 0.0058

PGLS with 200 Ka Bins

```
PGLS_200k_sparse <- pgls(formula = log(CC) ~ X200k_M_oxy + X200k_slope_oxy + X200k_SD_oxy, data = brain
sumMod_sparse <- summary(PGLS_200k_sparse)
sumMod_sparse
```

```
##
## Call:
## pgls(formula = log(CC) ~ X200k_M_oxy + X200k_slope_oxy + X200k_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4549 -0.1151 -0.0087  0.1004  0.5766
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.995
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.57
##    95.0% CI   : (0.973, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.7548     0.6207    4.44  1.4e-05 ***
## X200k_M_oxy    0.1285     0.1234    1.04    0.299
## X200k_slope_oxy 0.1546    0.0704    2.20    0.029 *
## X200k_SD_oxy   -0.5548     0.6161   -0.90    0.369
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.162 on 224 degrees of freedom
## Multiple R-squared: 0.0388,  Adjusted R-squared: 0.026
## F-statistic: 3.02 on 3 and 224 DF,  p-value: 0.0307
```

```
PGLS_200k_full <- pgls(formula = log(CC) ~ X200k_M_oxy * X200k_slope_oxy * X200k_SD_oxy, data = braintre
sumMod_full <- summary(PGLS_200k_full)
sumMod_full
```

```
##
## Call:
## pgls(formula = log(CC) ~ X200k_M_oxy * X200k_slope_oxy * X200k_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5664 -0.1066 -0.0143  0.0934  0.4415
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.993
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.39
##    95.0% CI   : (0.970, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##                                      Estimate Std. Error t value
## (Intercept)                           1.30899    1.26926    1.03
## X200k_M_oxy                           0.73779    0.44322    1.66
## X200k_slope_oxy                      -0.07114    0.75770   -0.09
## X200k_SD_oxy                          5.08864    4.84320    1.05
## X200k_M_oxy:X200k_slope_oxy          -0.00537    0.22605   -0.02
## X200k_M_oxy:X200k_SD_oxy             -2.34662    1.73828   -1.35
## X200k_slope_oxy:X200k_SD_oxy         -0.19718    2.55672   -0.08
## X200k_M_oxy:X200k_slope_oxy:X200k_SD_oxy  0.49015  0.73657   0.67
##                                      Pr(>|t|)
## (Intercept)                             0.304
## X200k_M_oxy                             0.097 .
## X200k_slope_oxy                         0.925
## X200k_SD_oxy                            0.295
## X200k_M_oxy:X200k_slope_oxy             0.981
## X200k_M_oxy:X200k_SD_oxy                0.178
## X200k_slope_oxy:X200k_SD_oxy            0.939
## X200k_M_oxy:X200k_slope_oxy:X200k_SD_oxy  0.506
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.16 on 220 degrees of freedom
## Multiple R-squared: 0.0512,  Adjusted R-squared: 0.021
## F-statistic:  1.7 on 7 and 220 DF,  p-value: 0.111
```

200Ka summary

- full Model
    - overall P value = 0.1109
    - ML value for lambda = 0.9931
    - adjusted R^2 = 0.021
- sparse Model
    - overall P value for sparse model = 0.0307
    - ML value for lambda sparse model = 0.9955
    - adjusted R^2 = 0.026

PGLS with 100 Ka Bins

```
PGLS_100k_sparse <- pgls(formula = log(CC) ~ X100k_M_oxy + X100k_slope_oxy + X100k_SD_oxy, data = brain
sumMod_sparse <- summary(PGLS_100k_sparse)
sumMod_sparse
```

```
##
## Call:
## pgls(formula = log(CC) ~ X100k_M_oxy + X100k_slope_oxy + X100k_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4023 -0.0994 -0.0021  0.0989  0.5890
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.995
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.56
##    95.0% CI   : (0.972, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2.6094     0.6149    4.24  3.2e-05 ***
## X100k_M_oxy       0.1820     0.1094    1.66    0.097 .
## X100k_slope_oxy   0.0315     0.0188    1.67    0.095 .
## X100k_SD_oxy     -0.6700     0.6605   -1.01    0.312
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.162 on 224 degrees of freedom
## Multiple R-squared: 0.0301,  Adjusted R-squared: 0.0171
## F-statistic: 2.32 on 3 and 224 DF,  p-value: 0.0762
```

```
PGLS_100k_full <- pgls(formula = log(CC) ~ X100k_M_oxy * X100k_slope_oxy * X100k_SD_oxy, data = braintr
sumMod_full <- summary(PGLS_100k_full)
sumMod_full
```

```
##
## Call:
## pgls(formula = log(CC) ~ X100k_M_oxy * X100k_slope_oxy * X100k_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.3979 -0.0959  0.0191  0.1056  0.5773
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.995
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.58
##    95.0% CI   : (0.972, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##                                        Estimate Std. Error t value
## (Intercept)                             2.61606    0.96440    2.71
## X100k_M_oxy                             0.19745    0.30752    0.64
## X100k_slope_oxy                        -0.17391    0.43303   -0.40
## X100k_SD_oxy                           -0.79354    2.68392   -0.30
## X100k_M_oxy:X100k_slope_oxy             0.11951    0.16610    0.72
## X100k_M_oxy:X100k_SD_oxy                0.00419    0.95873    0.00
## X100k_slope_oxy:X100k_SD_oxy            0.48051    1.38692    0.35
## X100k_M_oxy:X100k_slope_oxy:X100k_SD_oxy -0.32485   0.53719   -0.60
##                                        Pr(>|t|)
## (Intercept)                              0.0072 **
## X100k_M_oxy                              0.5215
## X100k_slope_oxy                          0.6884
## X100k_SD_oxy                             0.7678
## X100k_M_oxy:X100k_slope_oxy              0.4726
## X100k_M_oxy:X100k_SD_oxy                 0.9965
## X100k_slope_oxy:X100k_SD_oxy             0.7293
## X100k_M_oxy:X100k_slope_oxy:X100k_SD_oxy 0.5460
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.163 on 220 degrees of freedom
## Multiple R-squared: 0.0416,  Adjusted R-squared: 0.0111
## F-statistic: 1.36 on 7 and 220 DF,  p-value: 0.222
```

100ka summary

- full Model

    - overall P value = 0.2217
```

- ML value for lambda = 0.9955
- adjusted R^2 = 0.0111

- sparse Model
  - overall P value for sparse model = 0.0762
  - ML value for lambda sparse model = 0.9953
  - adjusted R^2 = 0.0171

## PGLS with 40 Ka Bins

```
PGLS_40k_sparse <- pgls(formula = log(CC) ~ X40k_M_oxy + X40k_slope_oxy + X40k_SD_oxy, data = braintree
sumMod_sparse <- summary(PGLS_40k_sparse)
sumMod_sparse
```

```
##
## Call:
## pgls(formula = log(CC) ~ X40k_M_oxy + X40k_slope_oxy + X40k_SD_oxy,
##     data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4939 -0.1207 -0.0246  0.0772  0.5918
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.995
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.53
##    95.0% CI   : (0.972, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.39753    0.59599    4.02  7.9e-05 ***
## X40k_M_oxy     0.23948    0.11276    2.12    0.035 *
## X40k_slope_oxy -0.00158    0.00488   -0.32    0.746
## X40k_SD_oxy   -0.39129    0.60688   -0.64    0.520
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.162 on 224 degrees of freedom
## Multiple R-squared: 0.0238,  Adjusted R-squared: 0.0107
## F-statistic: 1.82 on 3 and 224 DF,  p-value: 0.145
```

```
PGLS_40k_full <- pgls(formula = log(CC) ~ X40k_M_oxy * X40k_slope_oxy * X40k_SD_oxy, data = braintree,la
sumMod_full <- summary(PGLS_40k_full)
sumMod_full
```

```
##
## Call:
```

```
## pgls(formula = log(CC) ~ X40k_M_oxy * X40k_slope_oxy * X40k_SD_oxy,
##      data = braintree, lambda = "ML")
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5974 -0.1091 -0.0239  0.0590  0.6155
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.994
##    lower bound : 0.000, p = <2e-16
##    upper bound : 1.000, p = 0.45
##    95.0% CI   : (0.970, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##                                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)                               2.2300     0.8230    2.71   0.0073
## X40k_M_oxy                                0.2871     0.2616    1.10   0.2737
## X40k_slope_oxy                           -0.0629     0.0424   -1.48   0.1398
## X40k_SD_oxy                              -0.1017     2.9128   -0.03   0.9722
## X40k_M_oxy:X40k_slope_oxy                 0.0263     0.0178    1.47   0.1423
## X40k_M_oxy:X40k_SD_oxy                   -0.0798     1.0759   -0.07   0.9409
## X40k_slope_oxy:X40k_SD_oxy                0.0733     0.1032    0.71   0.4778
## X40k_M_oxy:X40k_slope_oxy:X40k_SD_oxy    -0.0307     0.0364   -0.85   0.3989
##
## (Intercept)                              **
## X40k_M_oxy
## X40k_slope_oxy
## X40k_SD_oxy
## X40k_M_oxy:X40k_slope_oxy
## X40k_M_oxy:X40k_SD_oxy
## X40k_slope_oxy:X40k_SD_oxy
## X40k_M_oxy:X40k_slope_oxy:X40k_SD_oxy
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.162 on 220 degrees of freedom
## Multiple R-squared: 0.0341,  Adjusted R-squared: 0.00336
## F-statistic: 1.11 on 7 and 220 DF,  p-value: 0.358
```

40ka summary

- full Model

  - overall P value = 0.3581
  - ML value for lambda = 0.9939
  - adjusted R^2 = 0.0034

- sparse Model

  - overall P value for sparse model = 0.1448
  - ML value for lambda sparse model = 0.9949
  - adjusted R^2 = 0.0107