

# Sperm size figures

*jeremy*

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## Sperm size figures

This is the output of an R markdown script - a fancy way of embedding r in a page so we can rerun/tune it as needed and then have the commands

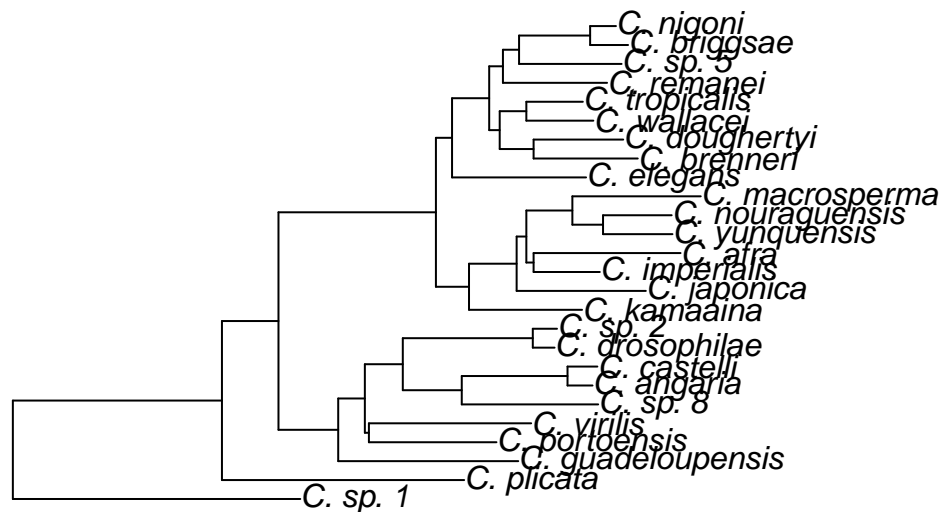
I'm embedding, but hiding a bunch of stuff for readability - the actual code is in the .Rmd file.

```
## Warning: package 'ggplot2' was built under R version 3.1.3
```

```
## Warning: package 'survival' was built under R version 3.1.3
```

```
## Warning: package 'psych' was built under R version 3.1.3
```

Here's the tree from Kiontke et al 2011, figure 3 initial values I recieved had angaria and sp12 flipped - I've corrected it here Here's the tree:



Now read in the compiled data - we have oocytesize, spermsize, primaryspermatocytesize, and oocytearea. The species names in the files are inconsistent - they are fixed now. For now, the oocyte area is using the

area formulation as made by the initial sperm size formula. All response variables are logged unless otherwise noted.

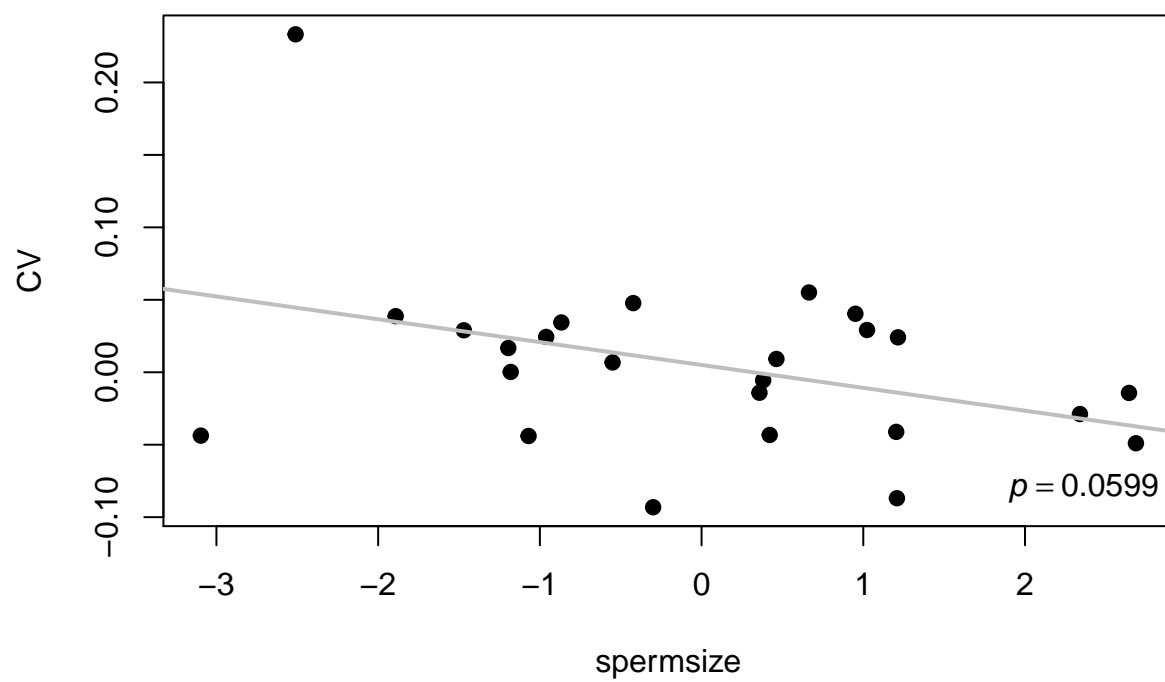
I have filtered out some of the data: Any oocytesize that is not stage -1, and any primaryspermatocyte data that is from hermaphrodites rather than males.

We now have clean data, clustered into species, strains or individuals. Variables ending in 1 are in species, 2 are strains and 3 are individuals. The non-clustered data is as is.

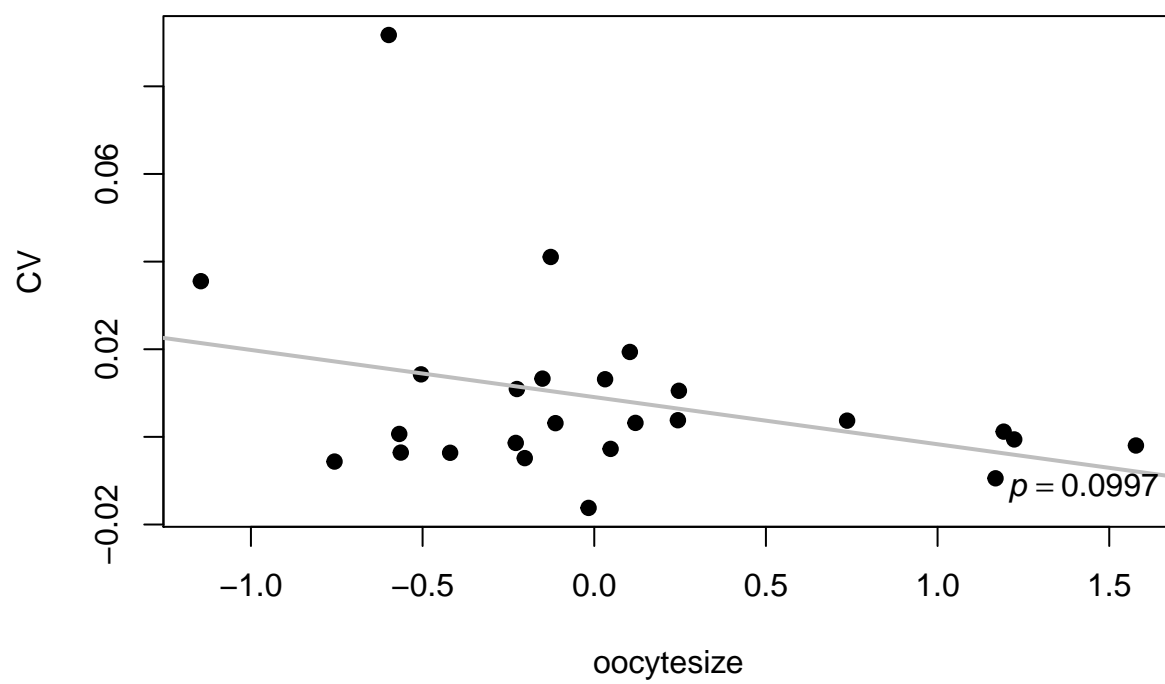
### **PIC plots - mean vs CV**

Plotting the phylogenetic independent contrasts (PIC) of means of traits vs CV of traits. All means and CVs are grouped at strain level.

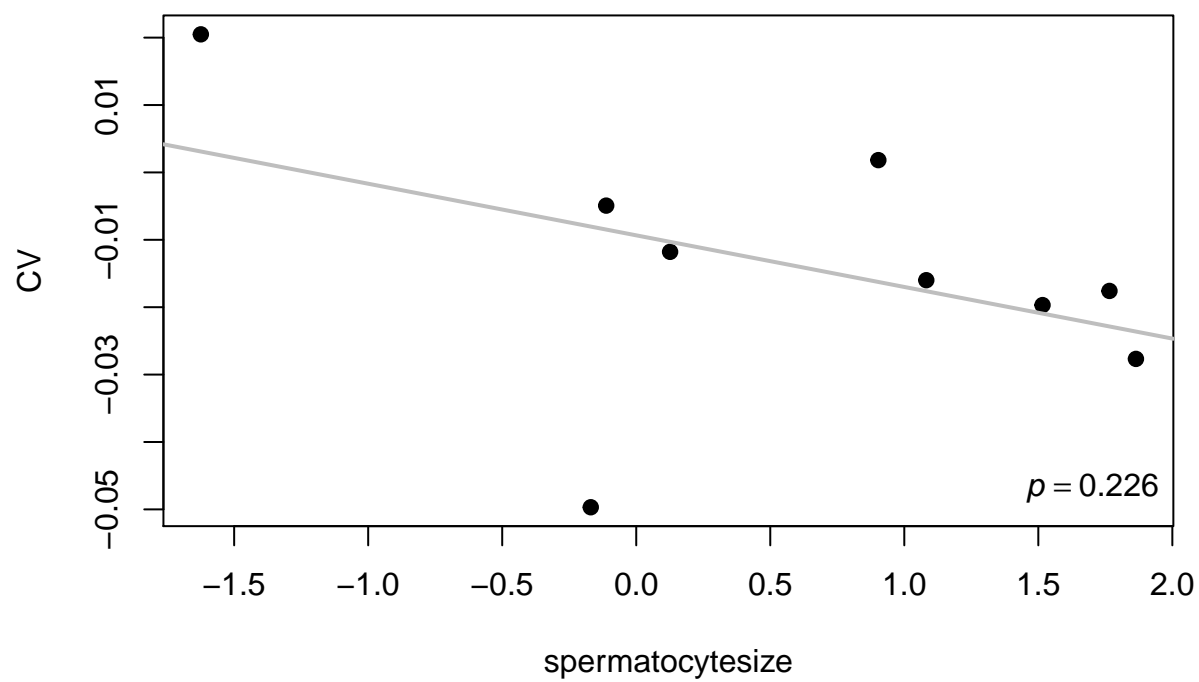
**PIC of spermsize means vs CV**



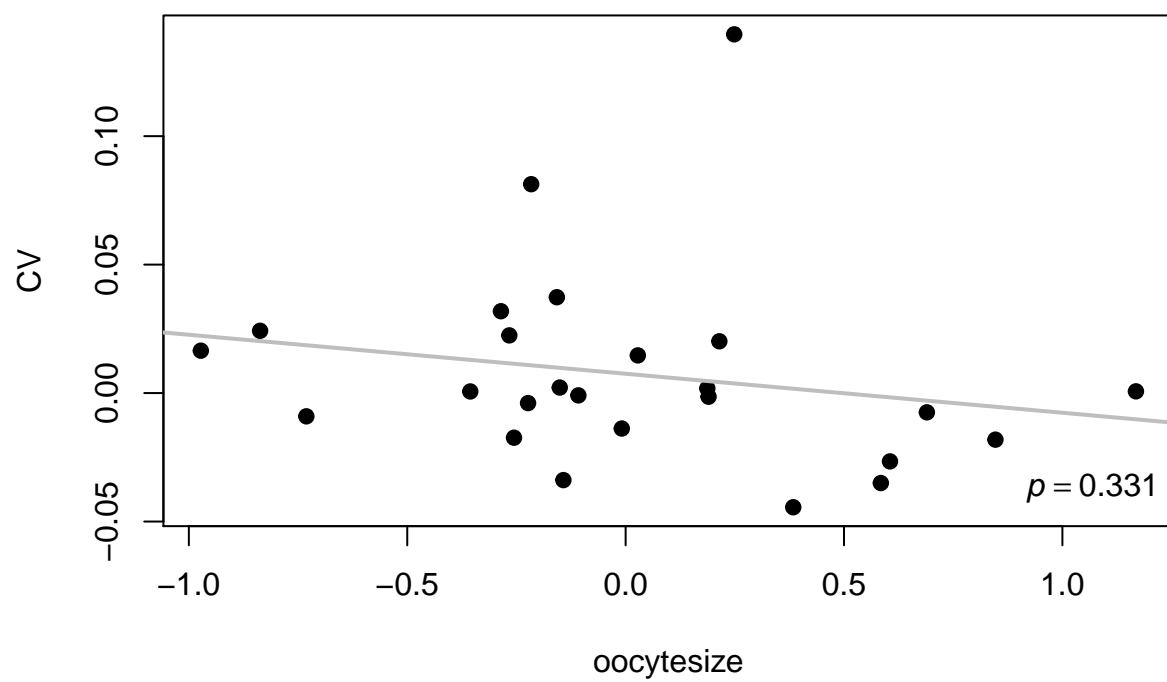
**PIC of oocytesize means vs CV**



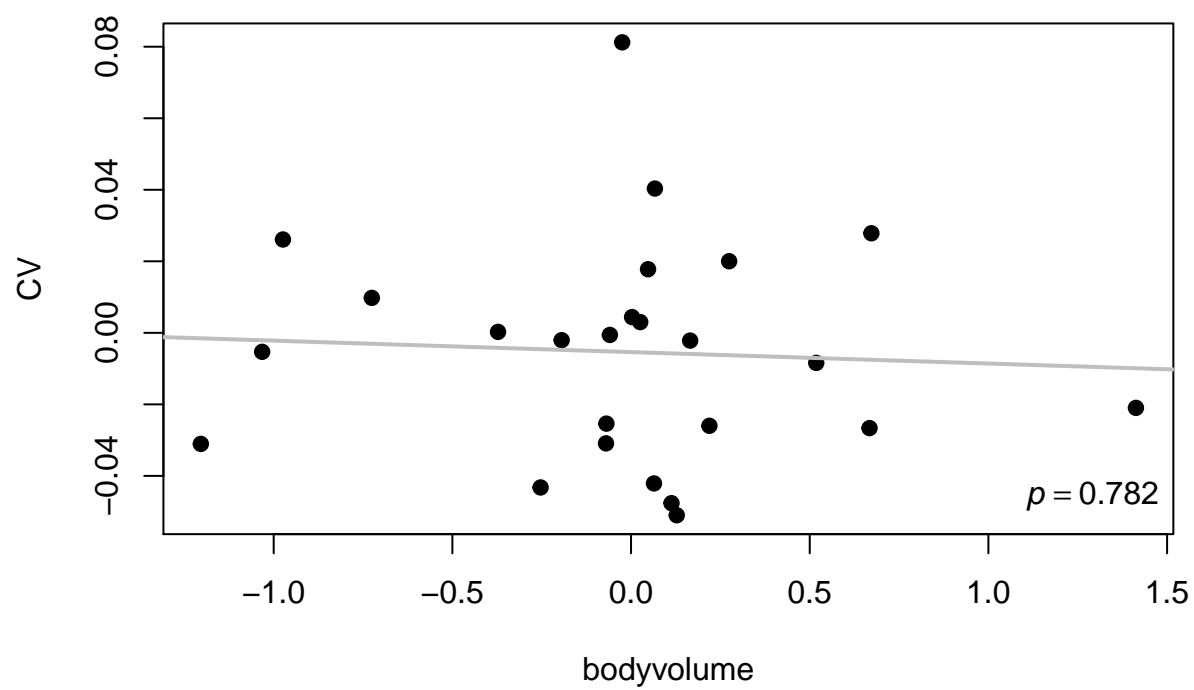
**PIC of spermatocytesize means vs CV**



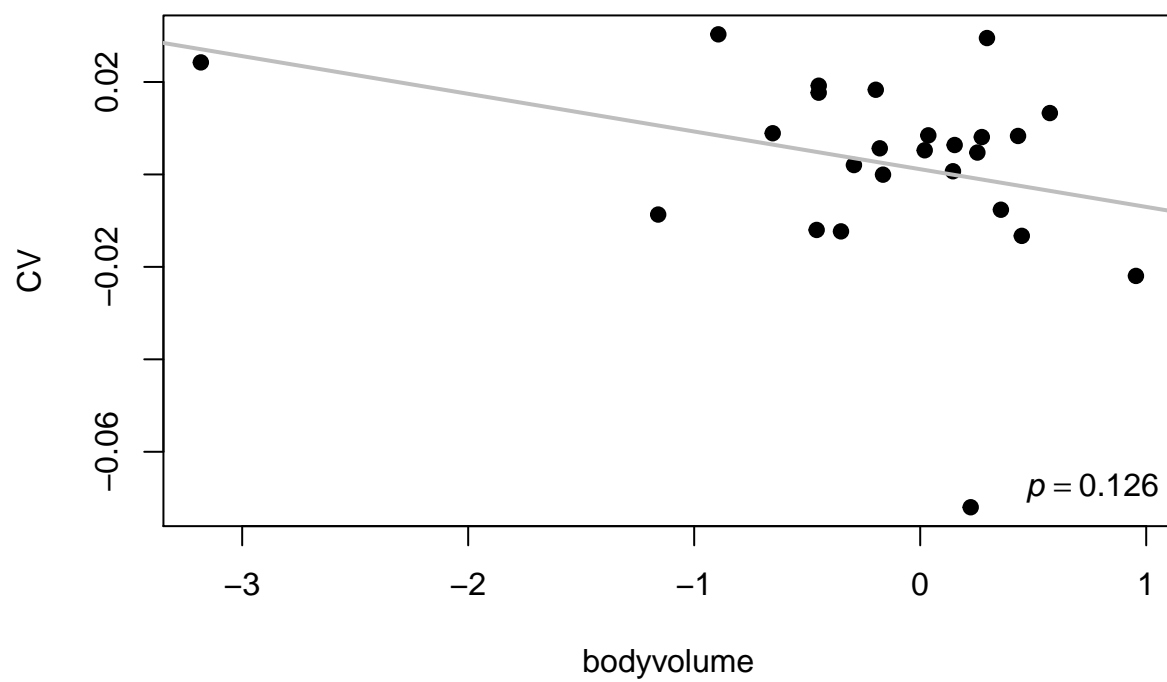
PIC of oocytesizearea means vs CV



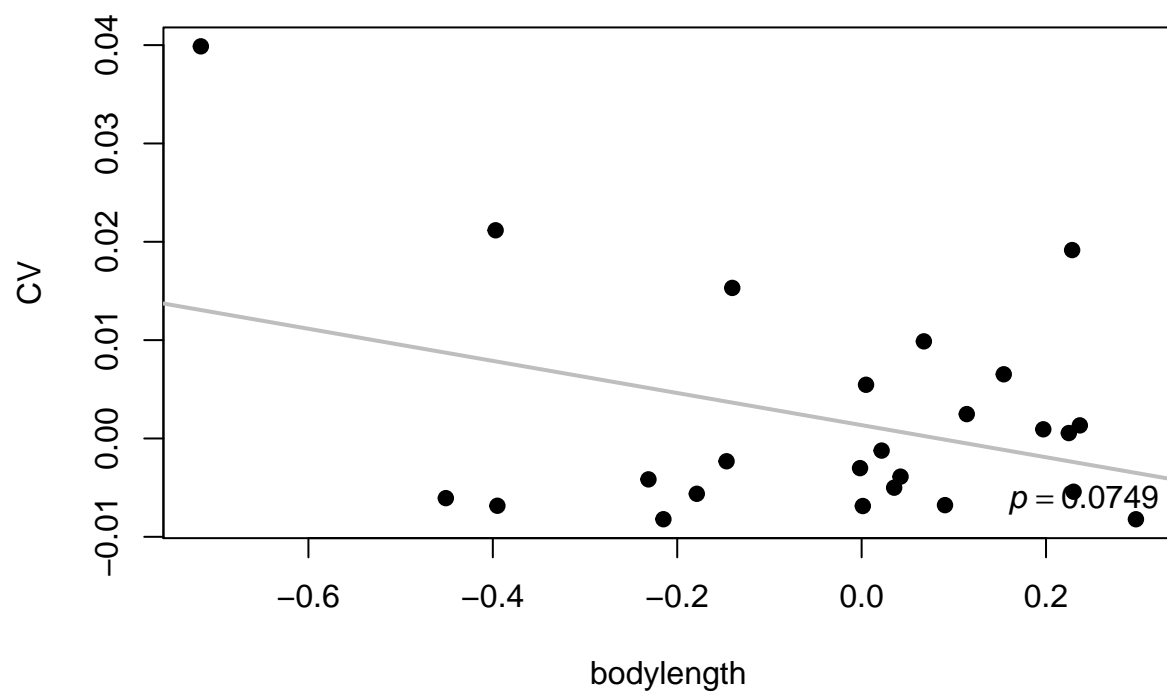
### PIC cv bodyvolume male



PIC cv bodyvolume female



### PIC cv bodylength male





## PIC cv bodylength female

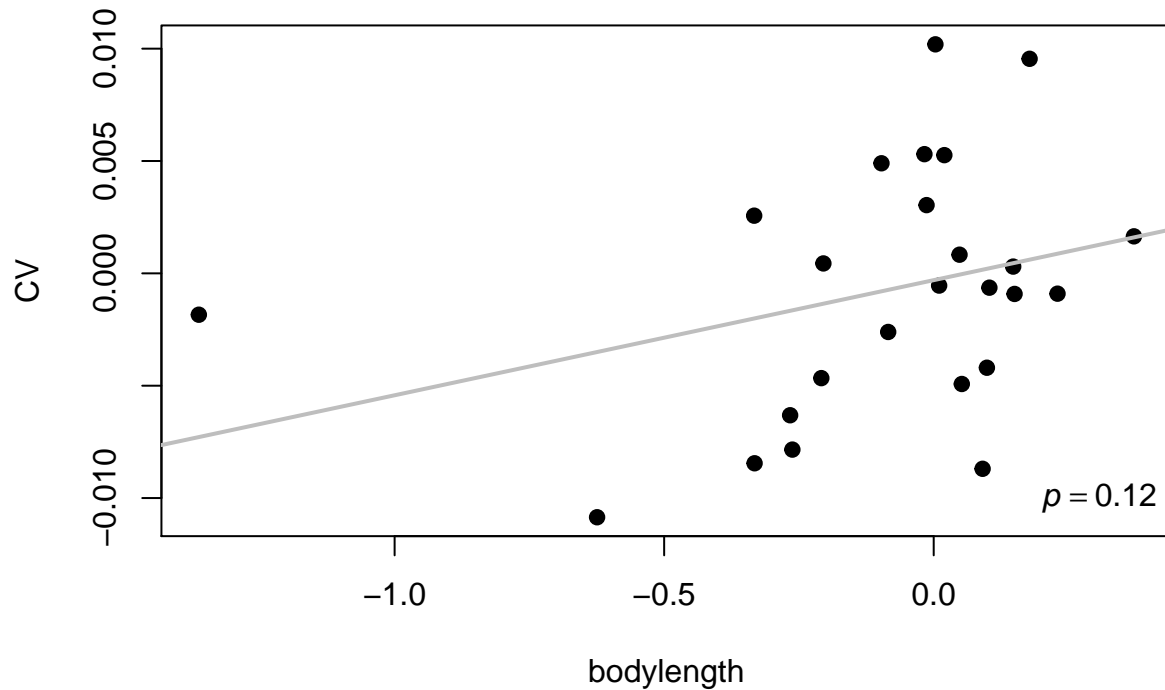


table of all pairwise PIC correlations and p-values

tables with all pairwise PIC correlations. For the p-value table, those above diagonal are holm corrected

```
## Call:corr.test(x = totaldata)
## Correlation matrix
##      spermsize oocytesizearea oocytesize malebodyarea
## spermsize      1.00         0.27      0.44         0.59
## oocytesizearea  0.27         1.00      0.96         0.58
## oocytesize      0.44         0.96      1.00         0.65
## malebodyarea    0.59         0.58      0.65         1.00
## femalebodyarea  0.36         0.39      0.51         0.81
## malebodylength  0.36         0.53      0.57         0.73
## femalebodylength 0.33         0.24      0.34         0.47
## malebodywidth   0.60         0.52      0.60         0.97
## femalebodywidth 0.27         0.35      0.44         0.73
## eggsize         -0.49         0.15     -0.01         0.21
## primaryspermatocyte 0.40         0.15      0.31         0.26
##      femalebodyarea malebodylength femalebodylength
## spermsize      0.36         0.36      0.33
## oocytesizearea  0.39         0.53      0.24
## oocytesize      0.51         0.57      0.34
## malebodyarea    0.81         0.73      0.47
## femalebodyarea  1.00         0.61      0.59
## malebodylength  0.61         1.00      0.84
```

```

## femalebodylength      0.59      0.84      1.00
## malebodywidth         0.77      0.53      0.27
## femalebodywidth       0.90      0.29      0.18
## eggsize               0.24      0.10     -0.06
## primaryspermatocyte   0.24     -0.03     -0.04
##      malebodywidth femalebodywidth eggsize
## spermsize             0.60      0.27     -0.49
## oocytesizearea        0.52      0.35      0.15
## oocytesize            0.60      0.44     -0.01
## malebodyarea          0.97      0.73      0.21
## femalebodyarea        0.77      0.90      0.24
## malebodylength        0.53      0.29      0.10
## femalebodylength      0.27      0.18     -0.06
## malebodywidth         1.00      0.80      0.19
## femalebodywidth       0.80      1.00      0.32
## eggsize               0.19      0.32      1.00
## primaryspermatocyte   0.28      0.22     -0.11
##      primaryspermatocyte
## spermsize             0.40
## oocytesizearea        0.15
## oocytesize            0.31
## malebodyarea          0.26
## femalebodyarea        0.24
## malebodylength       -0.03
## femalebodylength     -0.04
## malebodywidth         0.28
## femalebodywidth       0.22
## eggsize              -0.11
## primaryspermatocyte   1.00
## Sample Size
##      spermsize oocytesizearea oocytesize malebodyarea
## spermsize      25             25          25           25
## oocytesizearea  25             25          25           25
## oocytesize      25             25          25           25
## malebodyarea    25             25          25           25
## femalebodyarea  25             25          25           25
## malebodylength  25             25          25           25
## femalebodylength 25             25          25           25
## malebodywidth   25             25          25           25
## femalebodywidth 25             25          25           25
## eggsize         24             24          24           24
## primaryspermatocyte 9             9           9           9
##      femalebodyarea malebodylength femalebodylength
## spermsize          25             25           25
## oocytesizearea     25             25           25
## oocytesize         25             25           25
## malebodyarea       25             25           25
## femalebodyarea     25             25           25
## malebodylength     25             25           25
## femalebodylength   25             25           25
## malebodywidth      25             25           25
## femalebodywidth    25             25           25
## eggsize            24             24           24
## primaryspermatocyte 9             9           9

```

```

##          malebodywidth femalebodywidth eggsize
## spermsize          25          25      24
## oocytesizearea     25          25      24
## oocytesize         25          25      24
## malebodyarea       25          25      24
## femalebodyarea     25          25      24
## malebodylength     25          25      24
## femalebodylength   25          25      24
## malebodywidth      25          25      24
## femalebodywidth    25          25      24
## eggsize            24          24      24
## primaryspermatocyte 9          9       9
##          primaryspermatocyte
## spermsize          9
## oocytesizearea     9
## oocytesize         9
## malebodyarea       9
## femalebodyarea     9
## malebodylength     9
## femalebodylength   9
## malebodywidth      9
## femalebodywidth    9
## eggsize            9
## primaryspermatocyte 9
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##          spermsize oocytesizearea oocytesize malebodyarea
## spermsize          0.00          1.00      0.90      0.08
## oocytesizearea     0.20          0.00      0.00      0.09
## oocytesize         0.03          0.00      0.00      0.02
## malebodyarea       0.00          0.00      0.00      0.00
## femalebodyarea     0.07          0.05      0.01      0.00
## malebodylength     0.08          0.01      0.00      0.00
## femalebodylength   0.10          0.25      0.10      0.02
## malebodywidth      0.00          0.01      0.00      0.00
## femalebodywidth    0.20          0.09      0.03      0.00
## eggsize            0.02          0.49      0.98      0.33
## primaryspermatocyte 0.28          0.71      0.42      0.50
##          femalebodyarea malebodylength femalebodylength
## spermsize          1.00          1.00      1.00
## oocytesizearea     1.00          0.23      1.00
## oocytesize         0.34          0.12      1.00
## malebodyarea       0.00          0.00      0.57
## femalebodyarea     0.00          0.06      0.08
## malebodylength     0.00          0.00      0.00
## femalebodylength   0.00          0.00      0.00
## malebodywidth      0.00          0.01      0.20
## femalebodywidth    0.00          0.15      0.38
## eggsize            0.26          0.65      0.77
## primaryspermatocyte 0.54          0.94      0.93
##          malebodywidth femalebodywidth eggsize
## spermsize          0.07          1.00      0.52
## oocytesizearea     0.27          1.00      1.00
## oocytesize         0.07          0.90      1.00
## malebodyarea       0.00          0.00      1.00

```

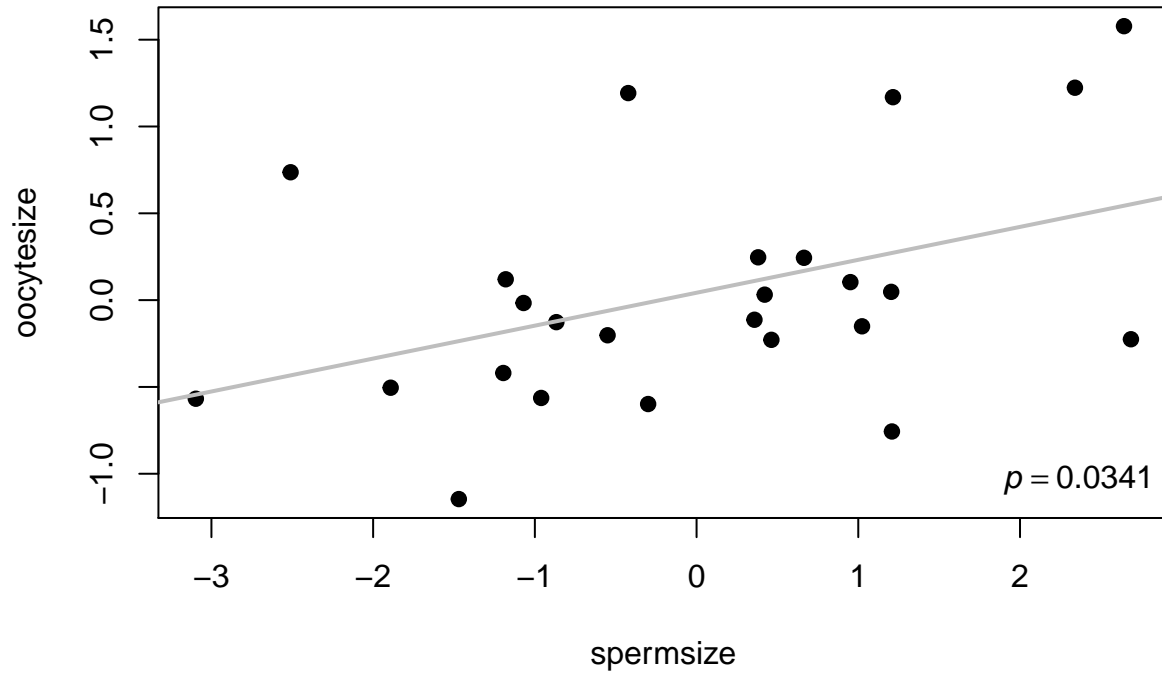
```

## femalebodyarea          0.00          0.00      1.00
## malebodylength          0.26          1.00      1.00
## femalebodylength        1.00          1.00      1.00
## malebodywidth           0.00          0.00      1.00
## femalebodywidth         0.00          0.00      1.00
## eggsize                 0.37          0.12      0.00
## primaryspermatocyte     0.47          0.57      0.77
##           primaryspermatocyte
## spermsize                1
## oocytesizearea           1
## oocytesize               1
## malebodyarea             1
## femalebodyarea           1
## malebodylength           1
## femalebodylength         1
## malebodywidth            1
## femalebodywidth          1
## eggsize                  1
## primaryspermatocyte      0
##
## To see confidence intervals of the correlations, print with the short=FALSE option

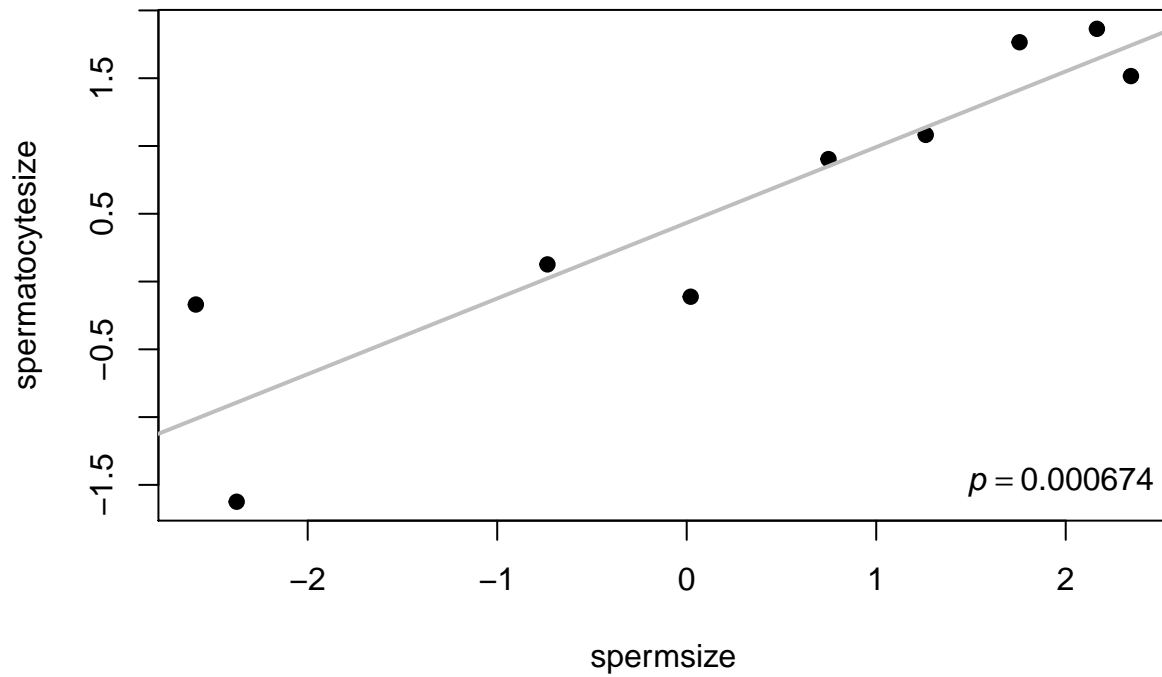
```

PIC plots - traits vs traits

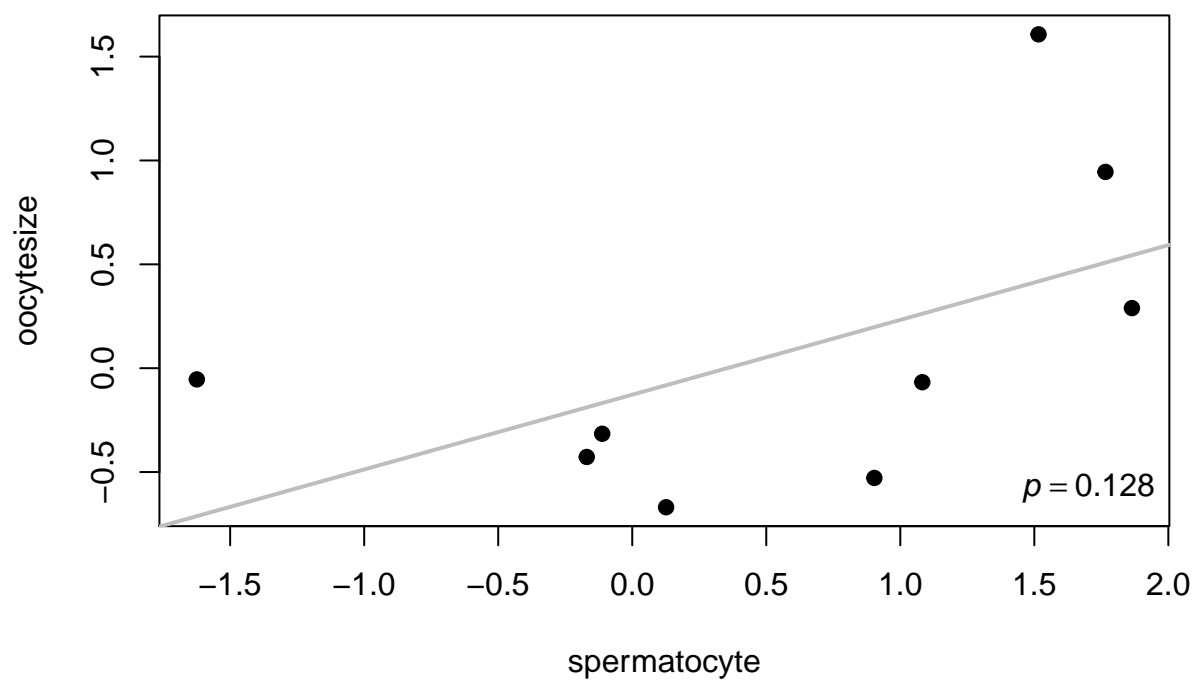
**PIC of spermsize vs oocytesize**



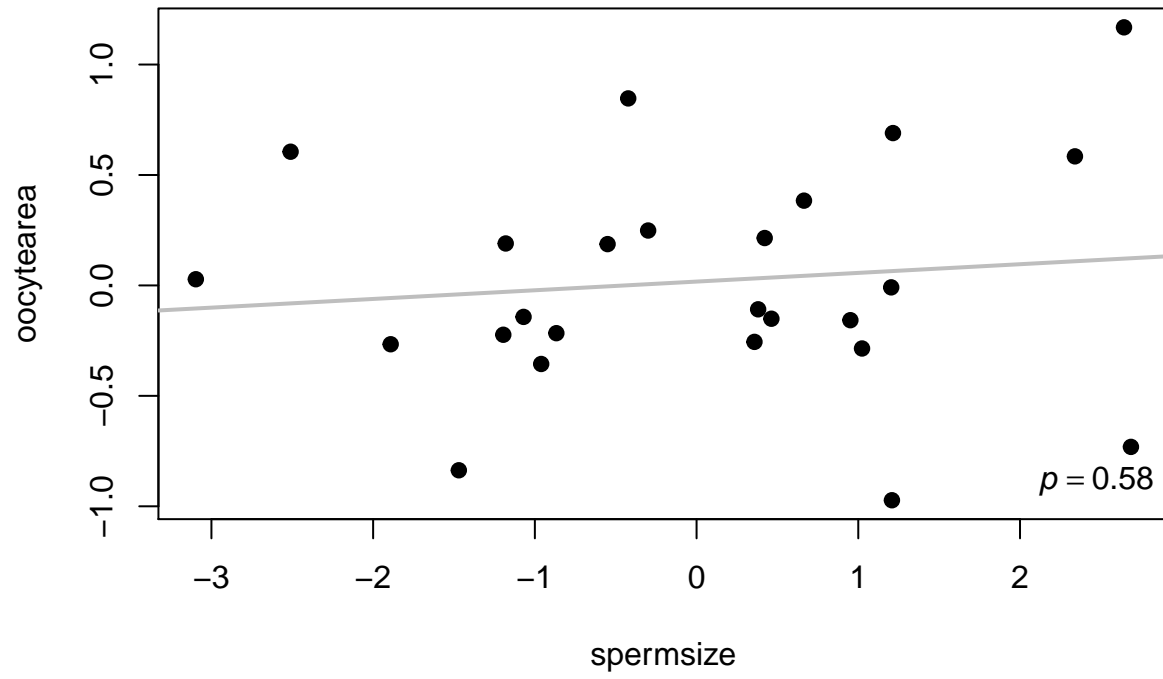
**PIC of spermsize vs spermatocytesize**



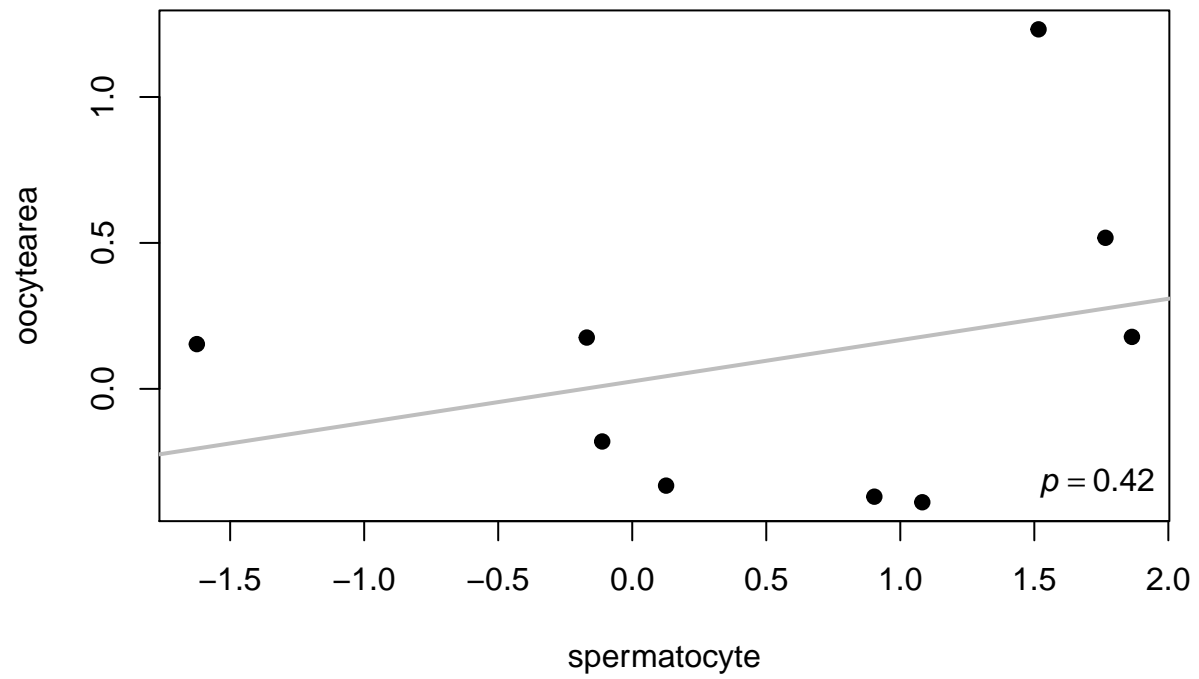
**PIC of spermatocytesize vs oocytesize**



PIC of spermsize vs oocytearea

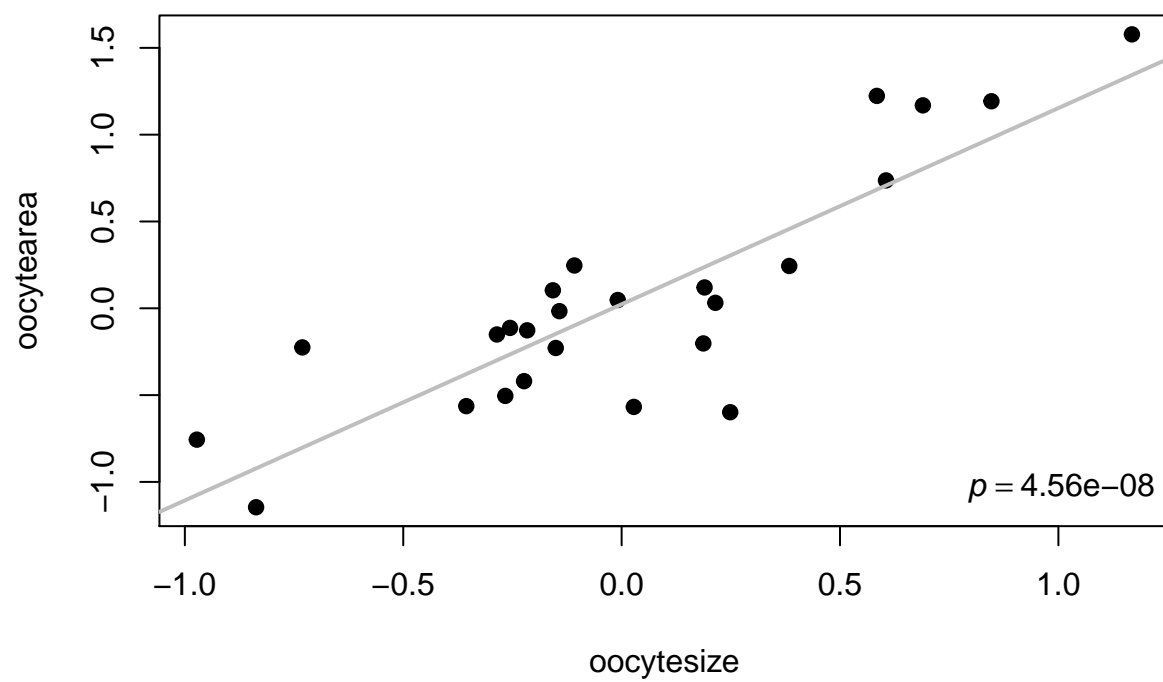


**PIC of spermatocytesize vs oocytearea**

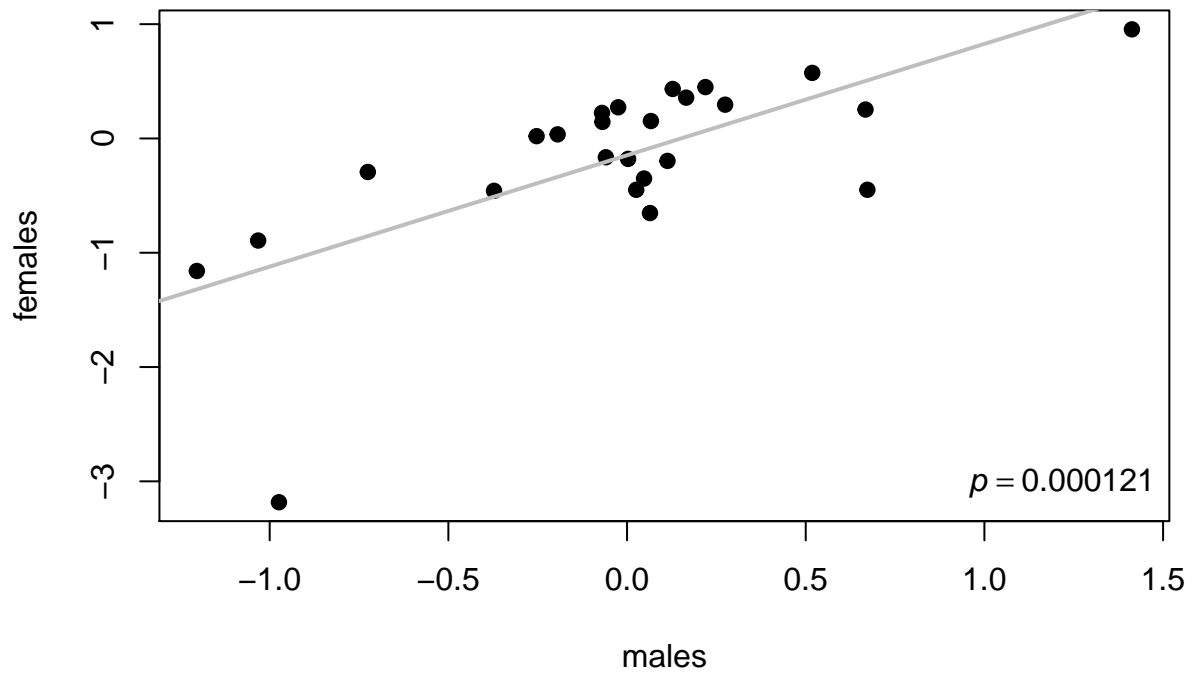




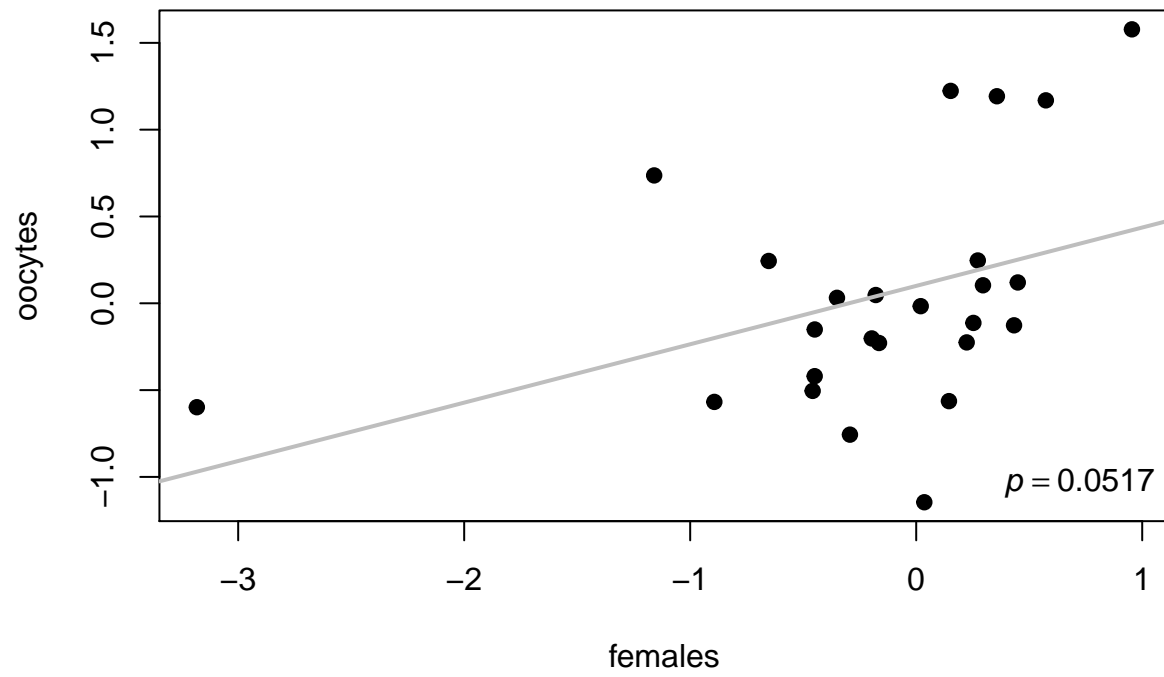
PIC of oocytesize vs oocytearea



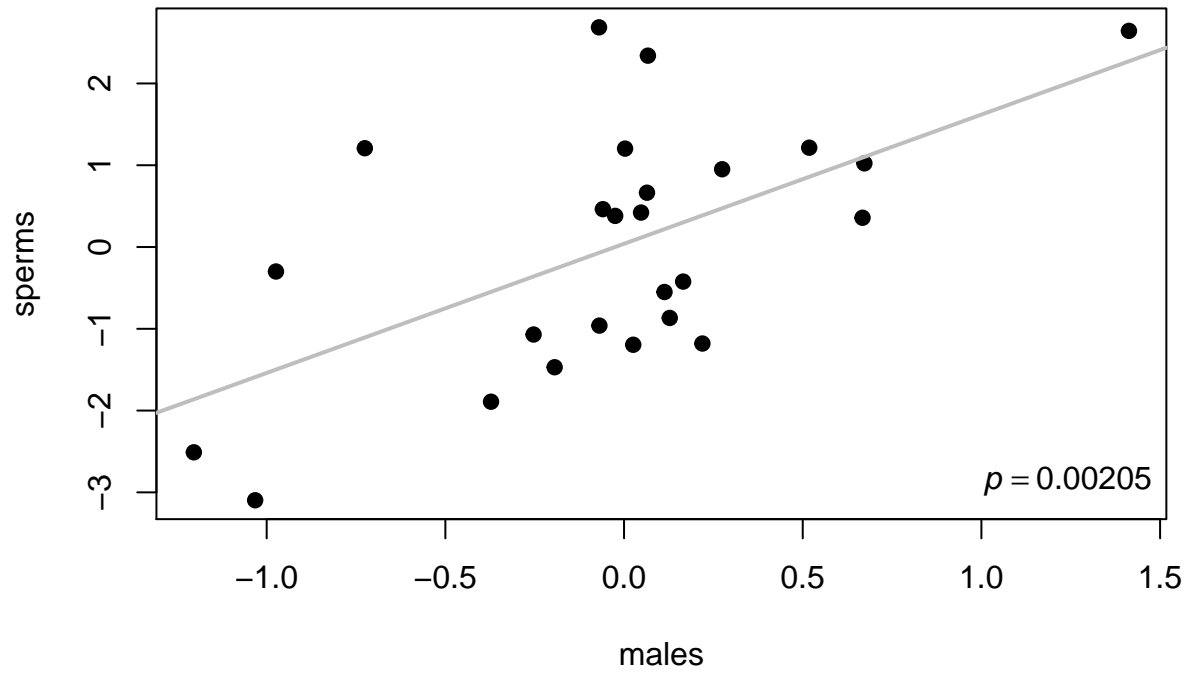
Body area male vs female



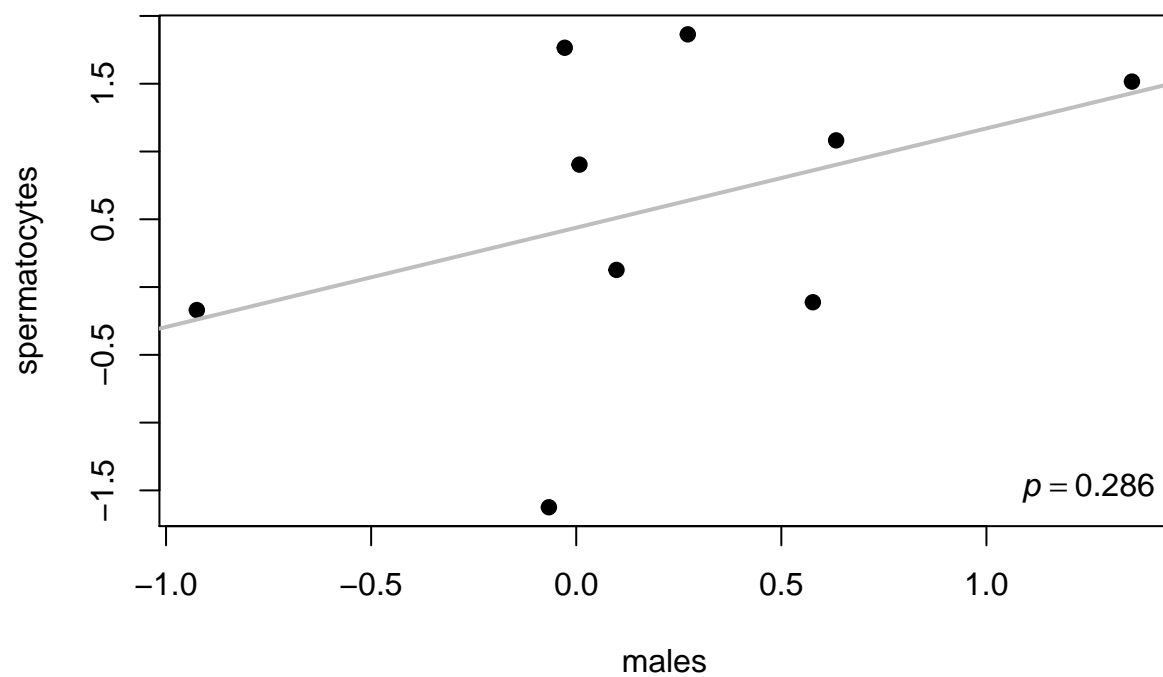
### Body area female vs oocytesize



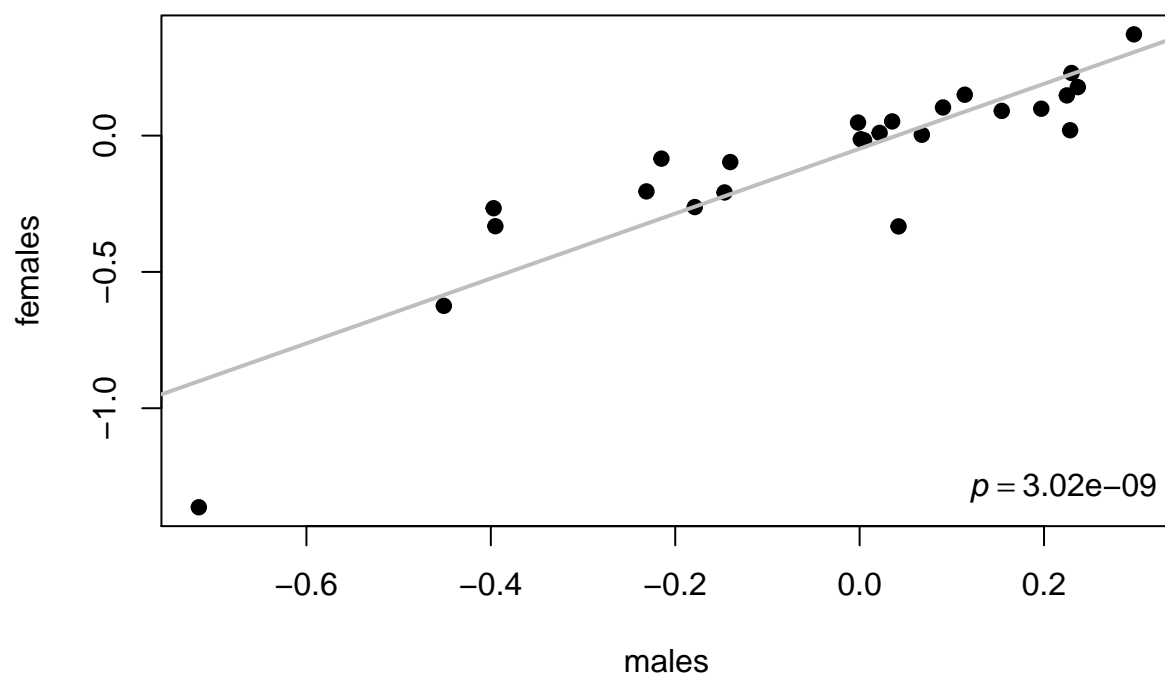
Body area male vs spermsize



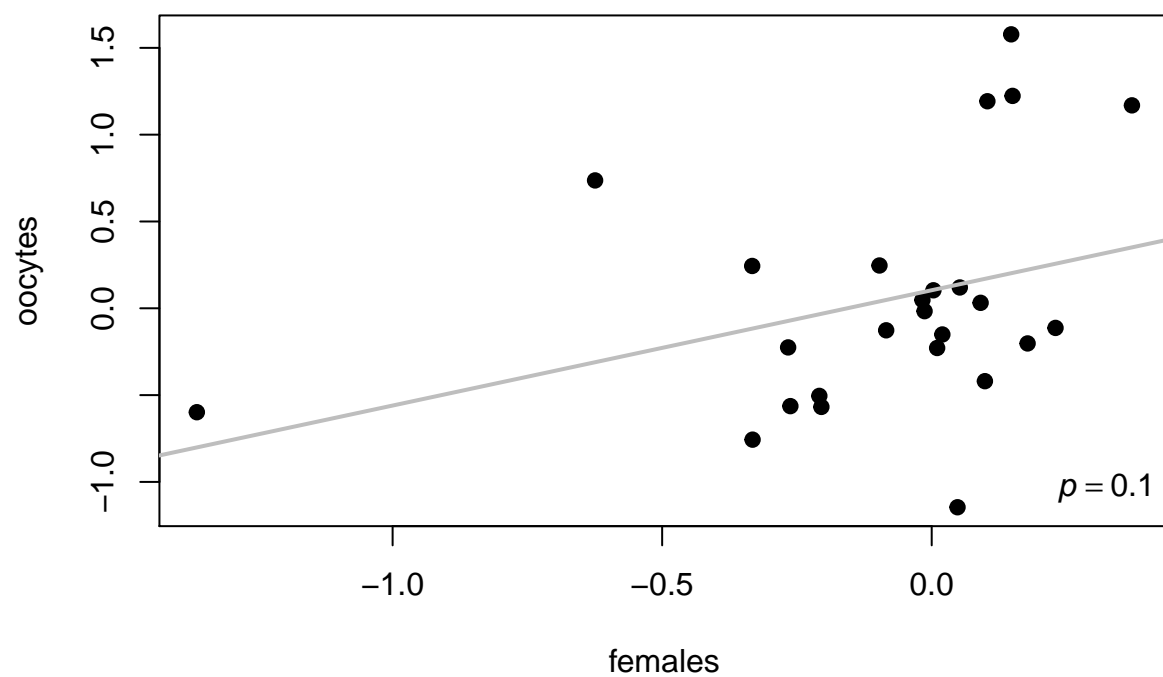
**Body area male vs spermatocytesize**



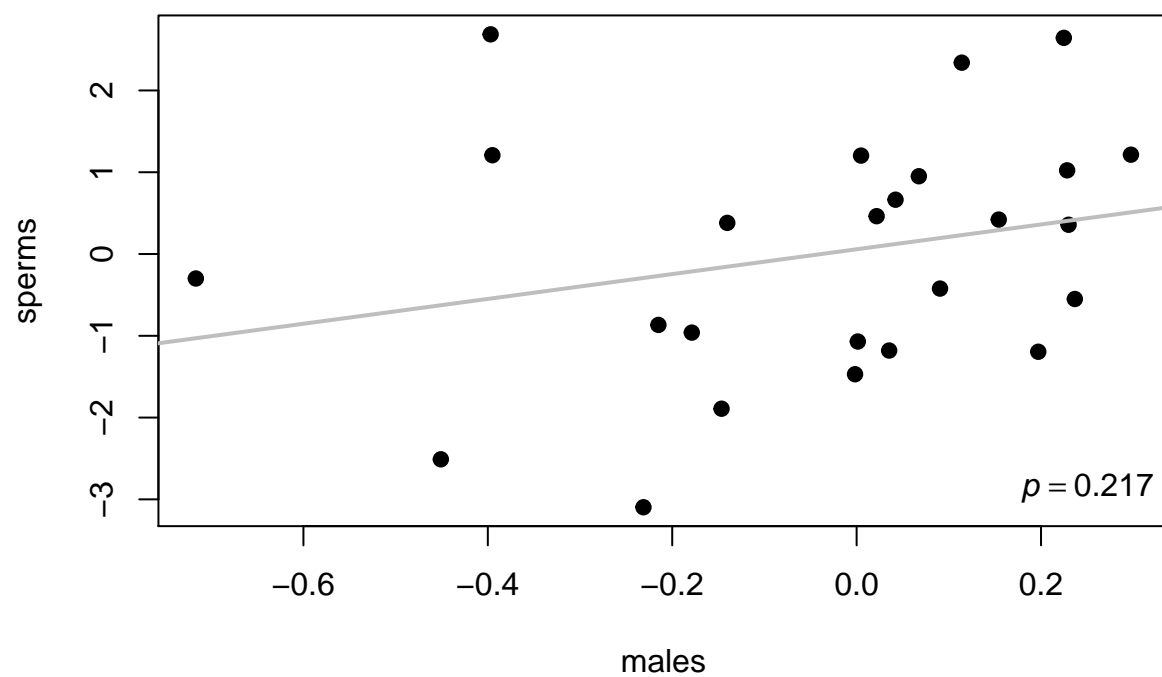
Body length male vs female



Body length female vs oocytesize

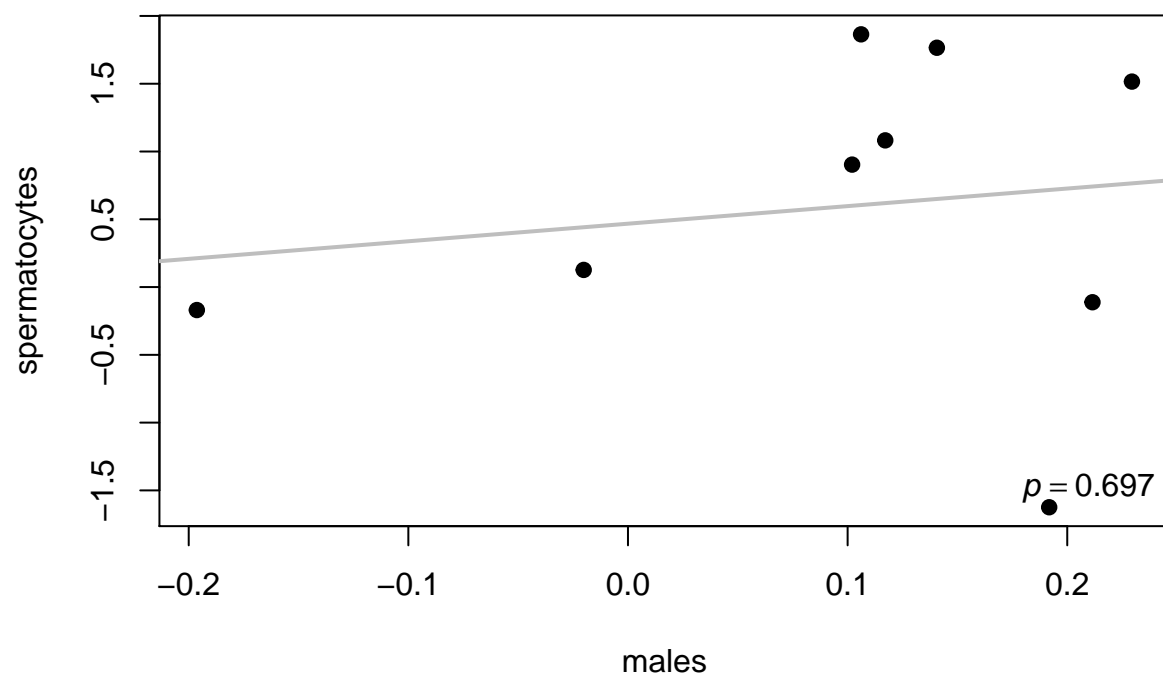


Body length male vs spermsize

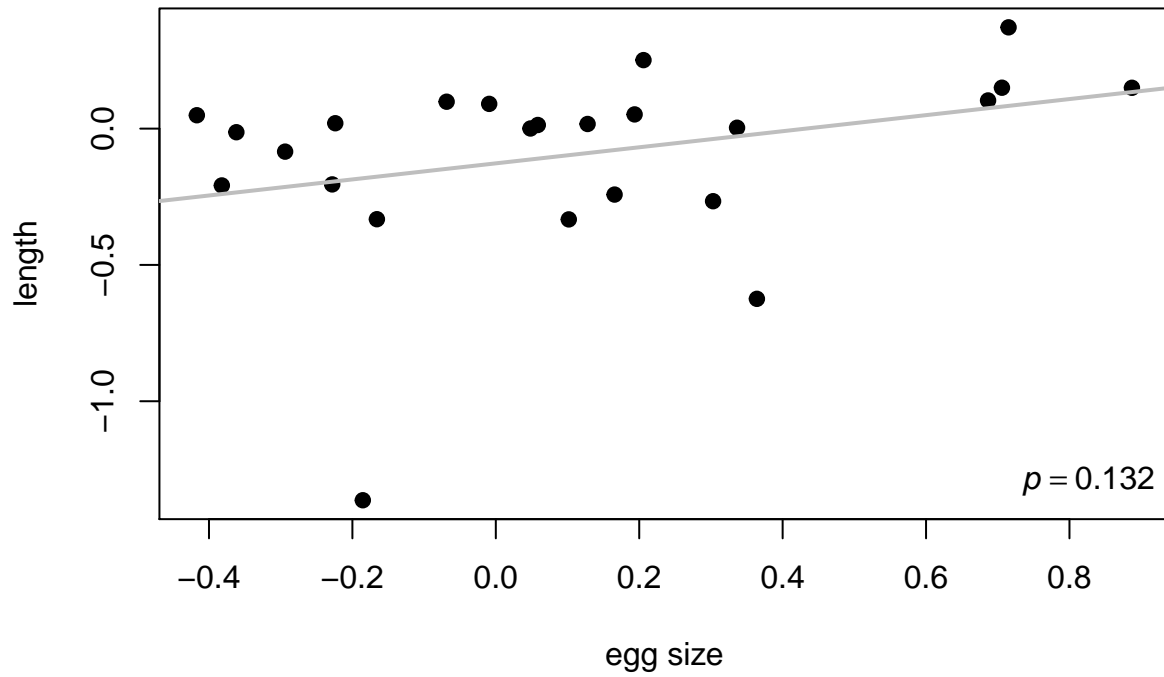




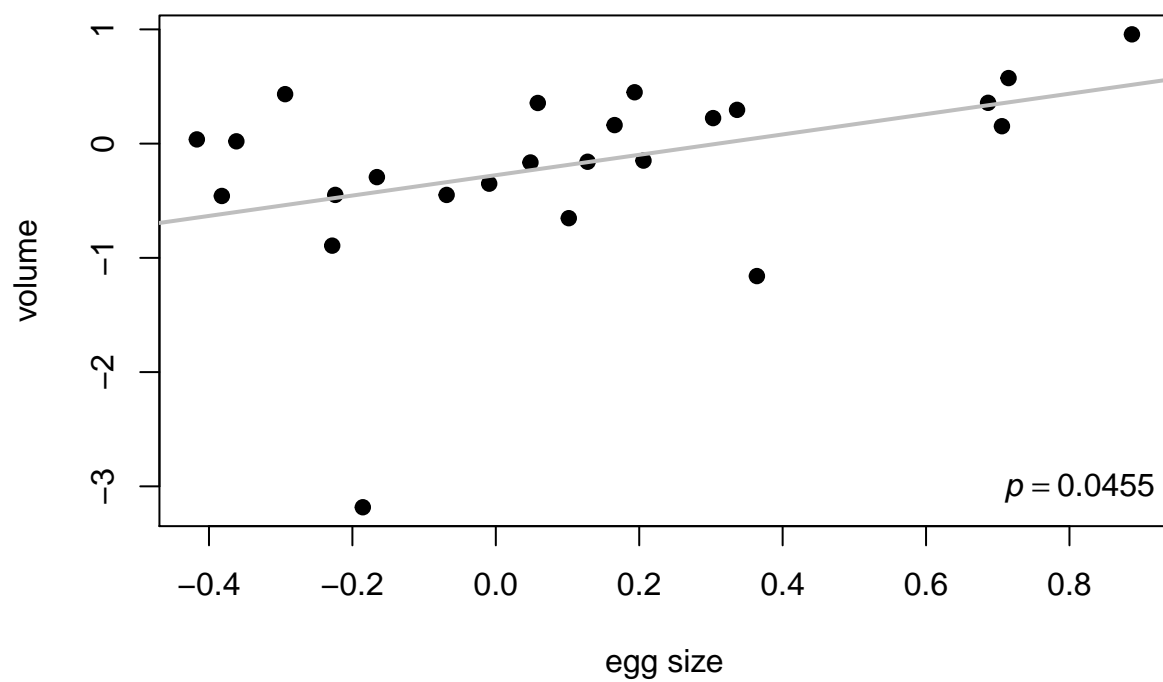
### Body length male vs spermatocytesize

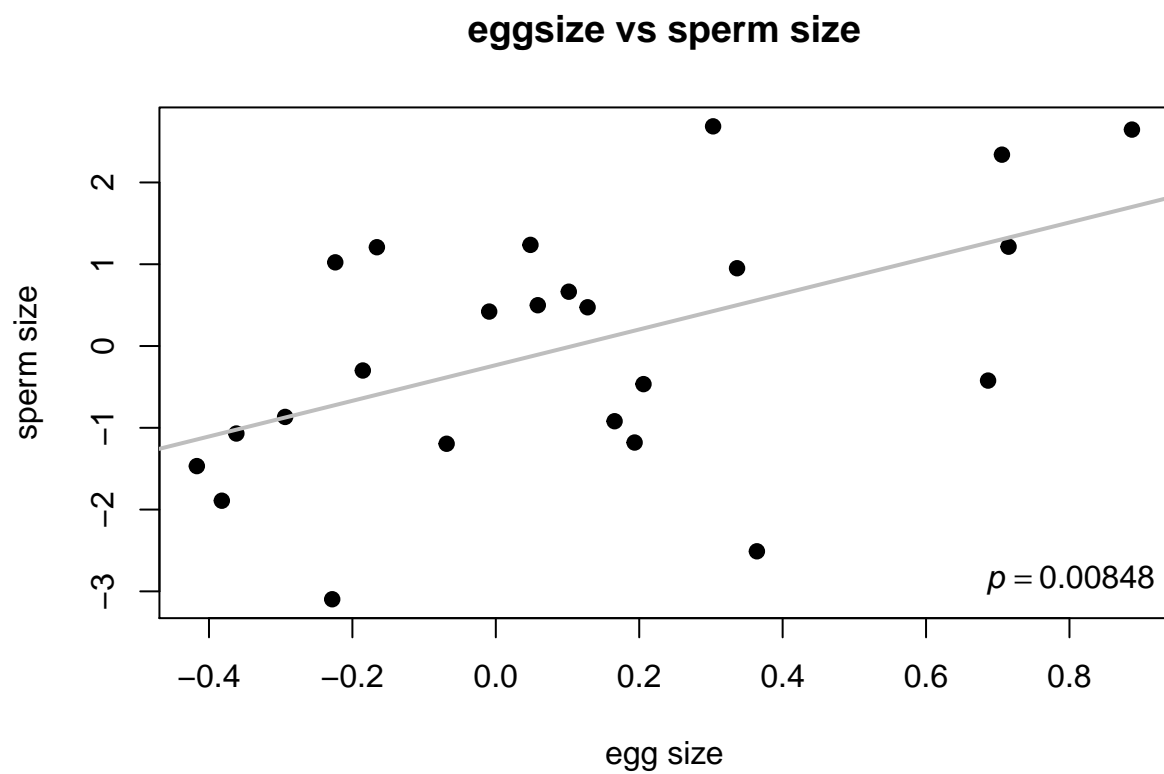


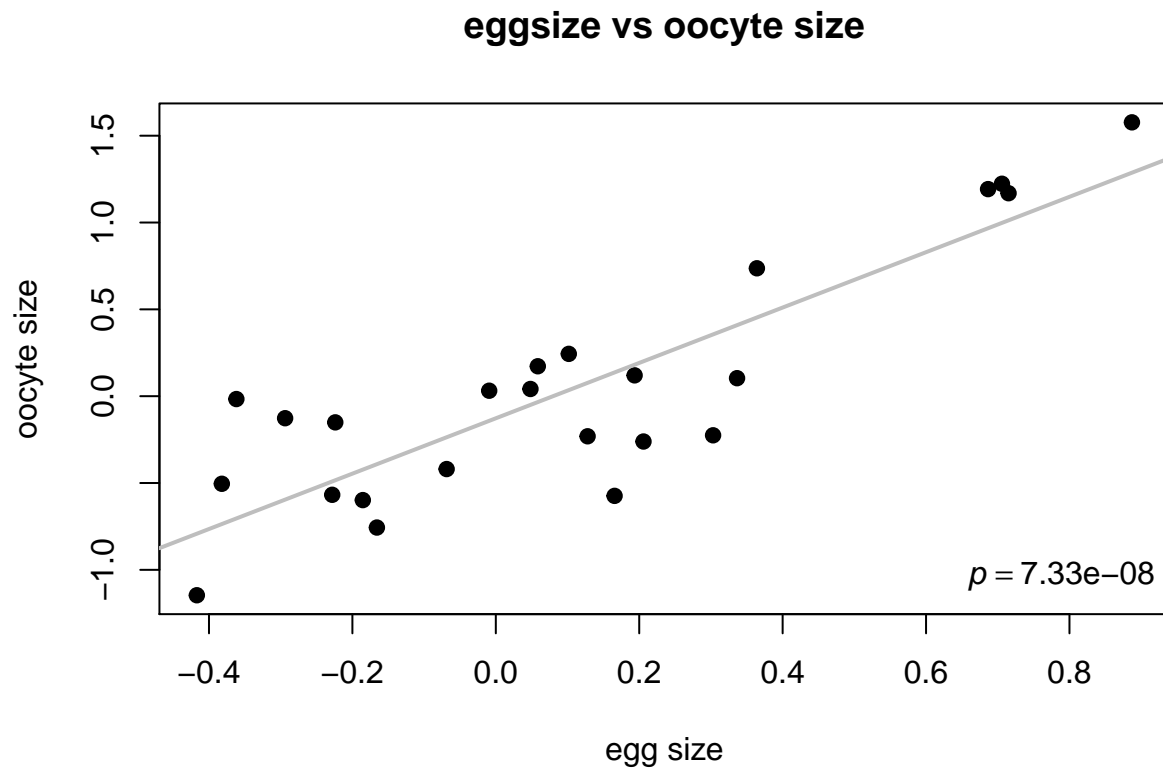
eggsize vs female length



eggsize vs female volume







#### PGLS - testing for correlation with evolutionary models

Output are summary tables from fits. The OU model won't fit the spermatocyte fits due to overparameterisation.

```
##
## Call:
## pglS(formula = meansperm ~ meanooarea, data = comp sperm, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.9643 -0.5988  0.4323  0.6861  1.8263
##
## Branch length transformations:
##
## kappa  [Fix]   : 1.000
## lambda [ ML]   : 0.000
##   lower bound : 0.000, p = 1
##   upper bound : 1.000, p = 0.11287
##   95.0% CI    : (NA, NA)
## delta  [Fix]   : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -6.09037    6.57159  -0.9268  0.3812
```

```

## meanooarea    1.46171    0.94975    1.5390    0.1624
##
## Residual standard error: 1.057 on 8 degrees of freedom
## Multiple R-squared: 0.2284, Adjusted R-squared: 0.132
## F-statistic: 2.369 on 1 and 8 DF, p-value: 0.1624

##
## Call:
## pgls(formula = meansperm ~ meanoo, data = compsperm, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4586 -1.1960  0.6374  1.0989  1.4686
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.895
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.79696
## 95.0% CI : (NA, NA)
## delta [Fix] : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -11.31303     6.94067  -1.6300  0.14176
## meanoo       1.50685     0.65983   2.2837  0.05177 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.315 on 8 degrees of freedom
## Multiple R-squared: 0.3946, Adjusted R-squared: 0.319
## F-statistic: 5.215 on 1 and 8 DF, p-value: 0.05177

##
## Call:
## pgls(formula = meansperm ~ meanprimsp, data = compsperm, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.8244 -0.3185 -0.1789  0.1091  0.5614
##
## Branch length transformations:
##
## kappa [Fix] : 1.000
## lambda [ ML] : 0.000
## lower bound : 0.000, p = 1
## upper bound : 1.000, p = 0.0066141
## 95.0% CI : (NA, 0.708)
## delta [Fix] : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -2.63590     0.94589  -2.7867  0.0236793 *

```

```

## meanprimsp    1.21417    0.17131    7.0873 0.0001033 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.446 on 8 degrees of freedom
## Multiple R-squared:  0.8626, Adjusted R-squared:  0.8454
## F-statistic: 50.23 on 1 and 8 DF,  p-value: 0.0001033

## Generalized least squares fit by REML
##   Model: meansperm ~ meanooarea
##   Data: fullpglsframe
##       AIC      BIC    logLik
##  54.95884 59.67106 -23.47942
##
## Correlation Structure: corMartins
## Formula: ~1
## Parameter estimate(s):
##   alpha
## 6.841132
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept) -3.044212  3.398811 -0.8956698  0.3793
## meanooarea   1.005070  0.498035  2.0180725  0.0549
##
## Correlation:
##      (Intr)
## meanooarea -0.999
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.7775727 -0.6837636 -0.2886598  0.4237510  2.2862305
##
## Residual standard error: 0.6334179
## Degrees of freedom: 26 total; 24 residual

## Generalized least squares fit by REML
##   Model: meansperm ~ meanoo
##   Data: fullpglsframe
##       AIC      BIC    logLik
##  50.30285 55.01506 -21.15142
##
## Correlation Structure: corMartins
## Formula: ~1
## Parameter estimate(s):
##   alpha
## 5.469326
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept) -7.068653  3.346328 -2.112361  0.0452
## meanoo       1.074887  0.329803  3.259179  0.0033
##
## Correlation:

```

```
##      (Intr)
## meanoo -0.999
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.9084685 -0.7013875 -0.3474741  0.5038124  2.4034645
##
## Residual standard error: 0.5843052
## Degrees of freedom: 26 total; 24 residual
```

Some phylogenetic signal methods - lambda

```
## Loading required package: parallel
```

```
##      Length Class      Mode
## lik   1      bm      function
## bnd   2    data.frame list
## res 400    -none-    numeric
## opt   8    -none-    list
```

```
##      Length Class      Mode
## lik   1      bm      function
## bnd   2    data.frame list
## res 400    -none-    numeric
## opt   8    -none-    list
```

```
##      Length Class      Mode
## lik   1      bm      function
## bnd   2    data.frame list
## res 400    -none-    numeric
## opt   8    -none-    list
```

```
##      Length Class      Mode
## lik   1      bm      function
## bnd   2    data.frame list
## res 400    -none-    numeric
## opt   8    -none-    list
```

Blombergs K

```
##      K PIC.variance.obs PIC.variance.rnd.mean PIC.variance.P
## 1 0.3738911      2.289904      3.925537      0.037
##      PIC.variance.Z
## 1      -1.364685
```

```
##      K PIC.variance.obs PIC.variance.rnd.mean PIC.variance.P
## 1 0.670685      0.4572932      1.207694      0.001
##      PIC.variance.Z
## 1      -1.875729
```



```
## [1] "Dropping tips from the tree because they are not present in the data:"
## [1] "C. sp. 1"      "C. portoensis"  "C. virilis"
## [4] "C. sp. 8"      "C. angaria"     "C. castelli"
## [7] "C. sp. 2"      "C. kamaaina"    "C. imperialis"
## [10] "C. afra"       "C. nouraguensis" "C. doughertyi"
## [13] "C. wallacei"   "C. tropicalis"  "C. sp. 5"
## [16] "C. nigoni"
```

```
##          K PIC.variance.obs PIC.variance.rnd.mean PIC.variance.P
## 1 1.218587      1.696502      2.590635      0.035
## PIC.variance.Z
## 1      -1.916097
```

```
##          K PIC.variance.obs PIC.variance.rnd.mean PIC.variance.P
## 1 0.5877787      0.2622437      0.6041613      0.003
## PIC.variance.Z
## 1      -1.719288
```

Morans I

```
## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs Std.Obs Alter Pvalue
## 1 x -0.09396389 -1.485136 greater 0.95
##
## other elements: adj.method call
```

```
## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs Std.Obs Alter Pvalue
## 1 x -0.01730539 0.6015673 greater 0.219
##
## other elements: adj.method call
```

```
## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
```

```

##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs Std.Obs  Alter Pvalue
## 1      x -0.1482137 -0.98979 greater 0.835
##
## other elements: adj.method call

## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs Std.Obs  Alter Pvalue
## 1      x -0.03082416 0.2503773 greater 0.34
##
## other elements: adj.method call

abouheifs cmean

## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs Std.Obs  Alter Pvalue
## 1      x -0.09396389 -1.487591 greater 0.953
##
## other elements: adj.method call

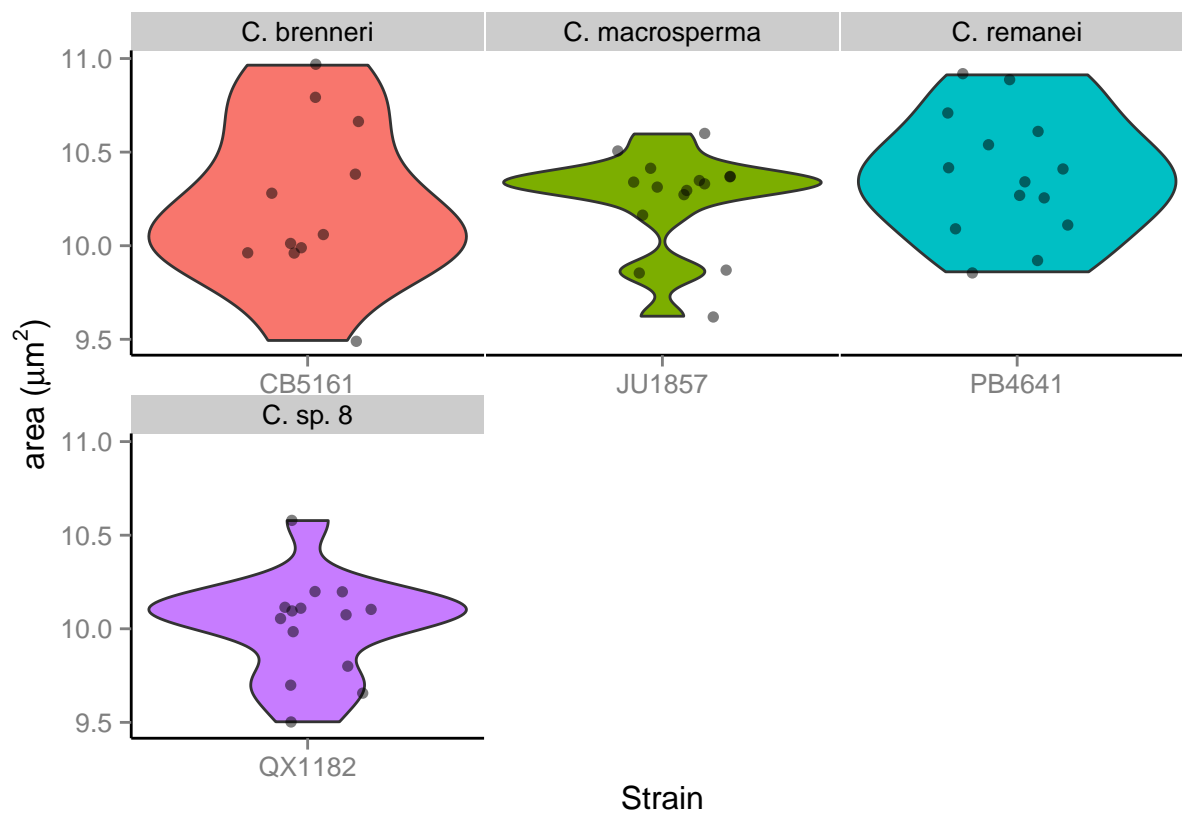
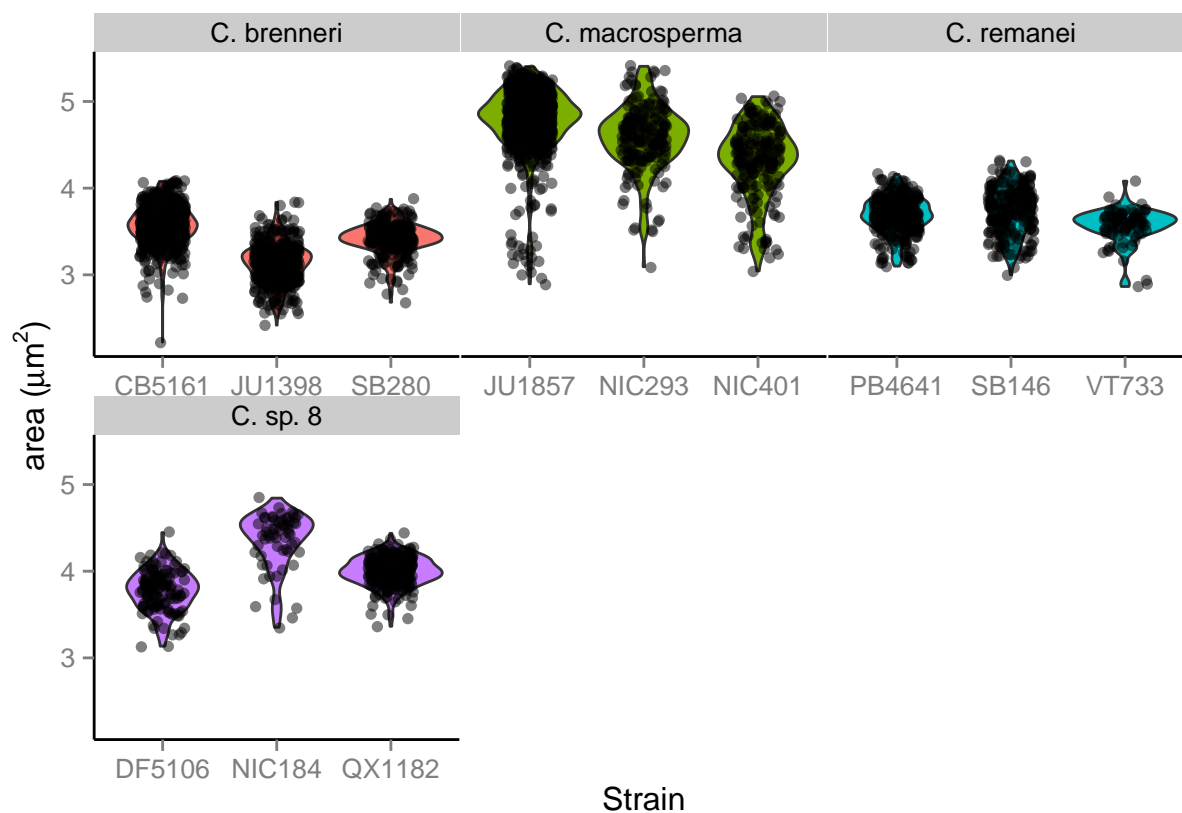
## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs Std.Obs  Alter Pvalue
## 1      x -0.01730539 0.6018441 greater 0.217
##
## other elements: adj.method call

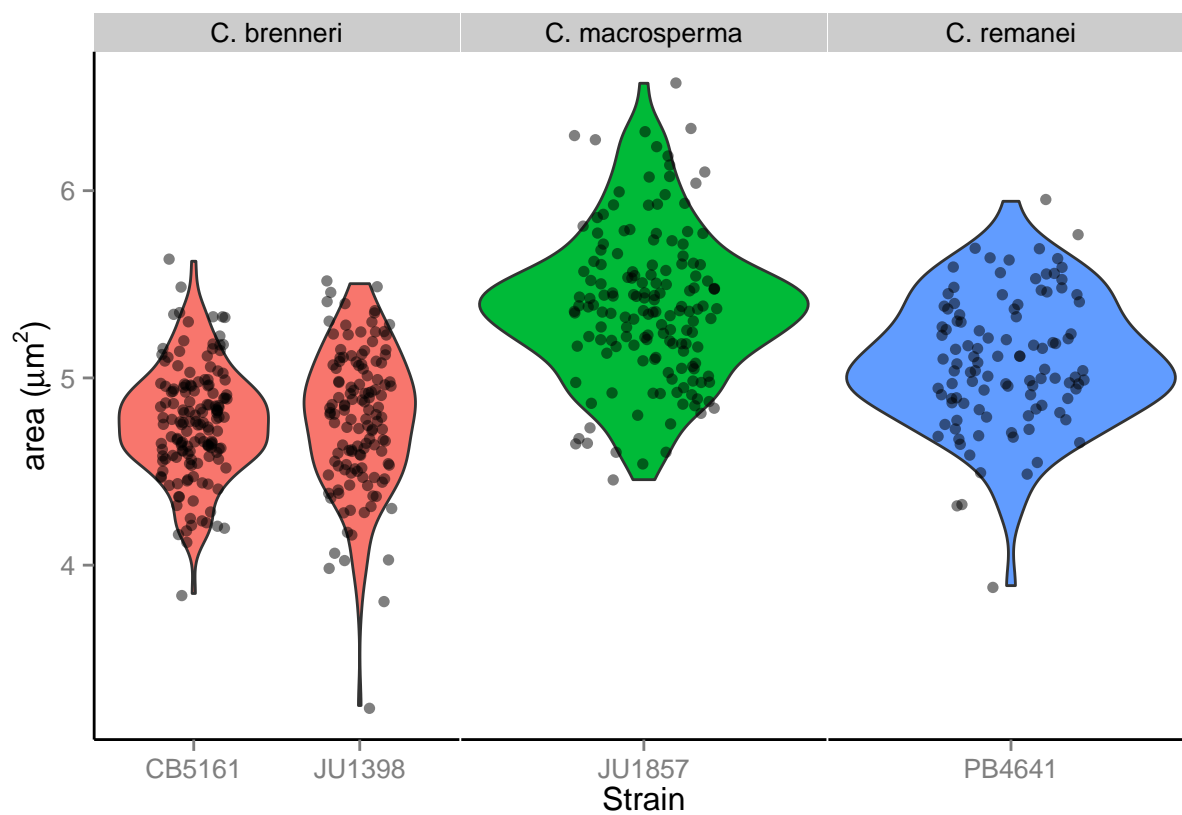
```

```
## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs      Std.Obs  Alter Pvalue
## 1      x -0.1482137 -0.9865783 greater 0.828
##
## other elements: adj.method call

## class: krandtest
## Monte-Carlo tests
## Call: as.krandtest(sim = matrix(res$result, ncol = nvar, byrow = TRUE),
##      obs = res$obs, alter = alter, names = test.names)
##
## Number of tests: 1
##
## Adjustment method for multiple comparisons: none
## Permutation number: 999
## Test      Obs      Std.Obs  Alter Pvalue
## 1      x -0.03082416 0.2602781 greater 0.341
##
## other elements: adj.method call
```

figure 3A with violin plots





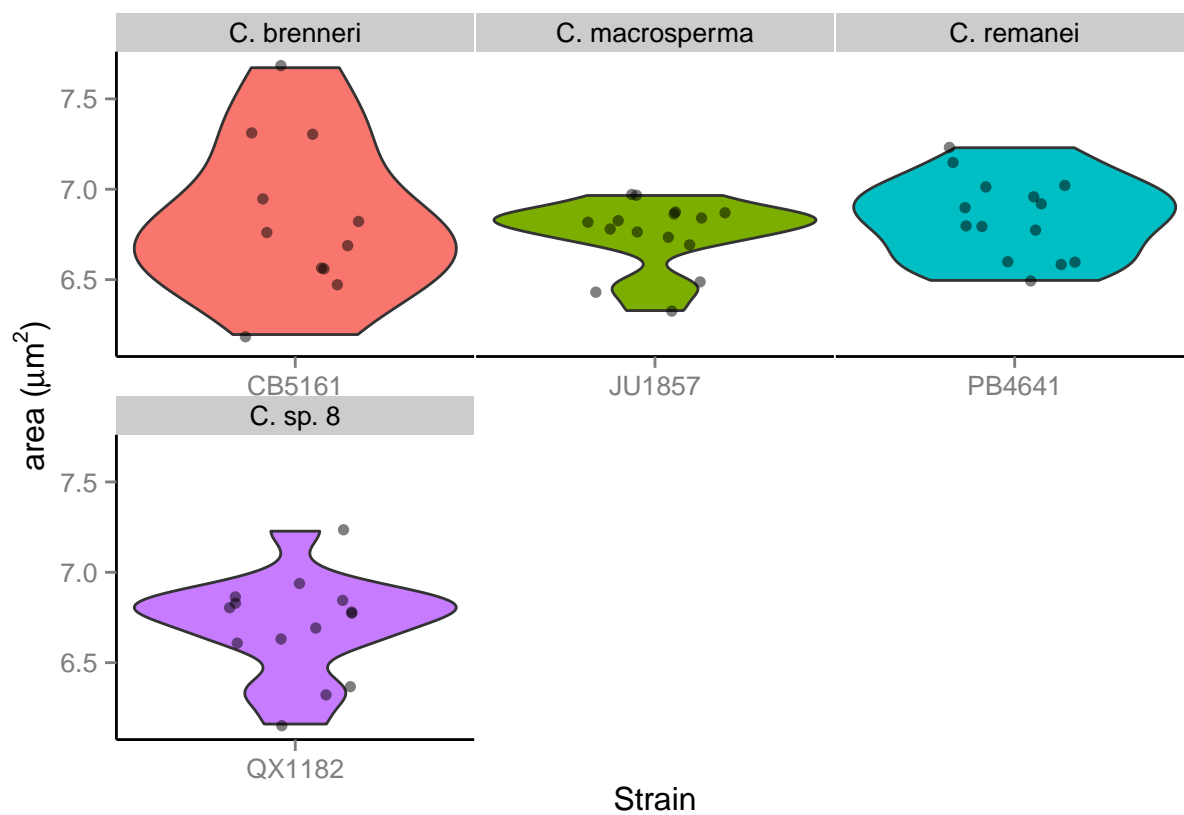
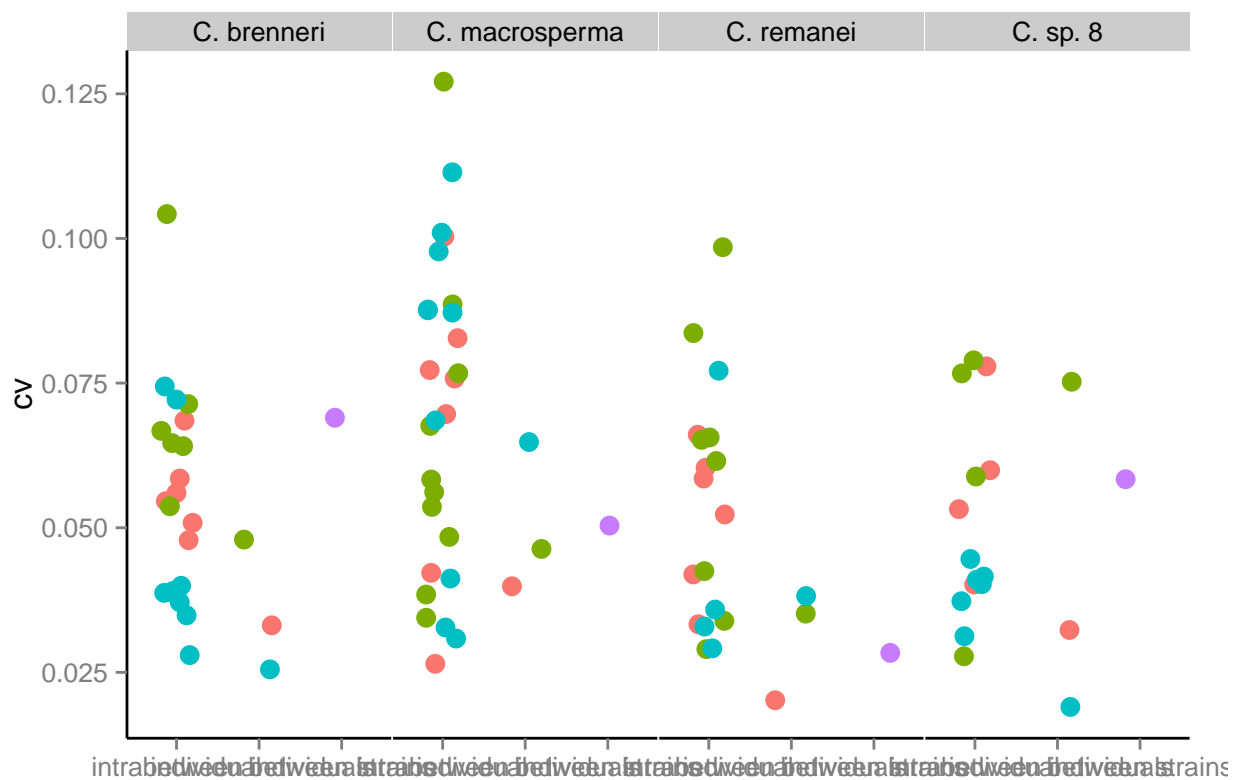
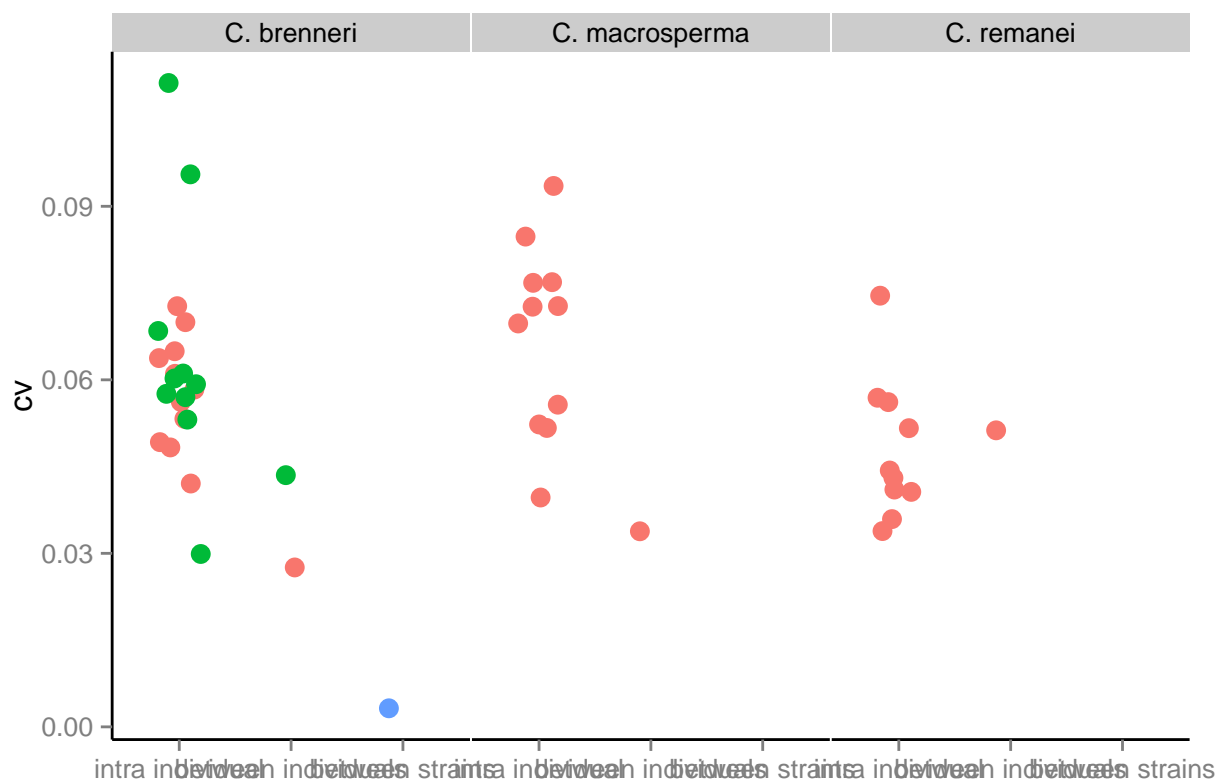
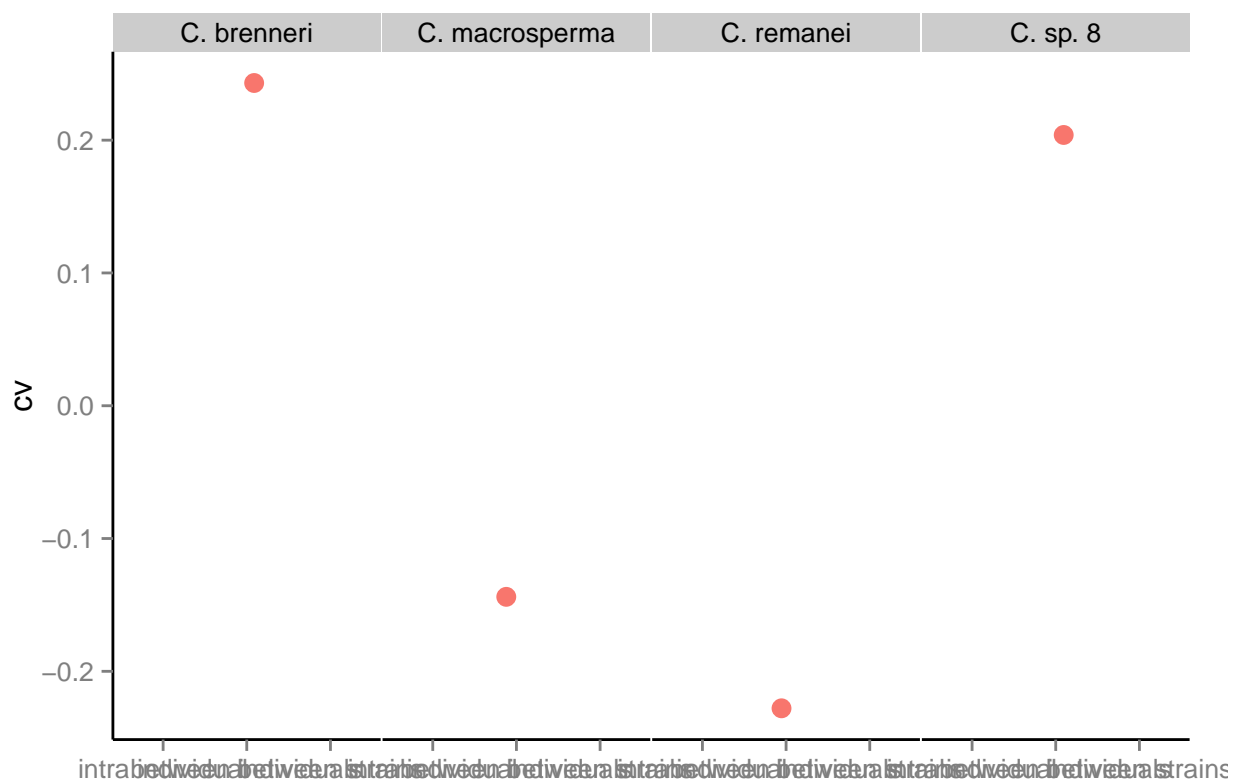


figure 3B







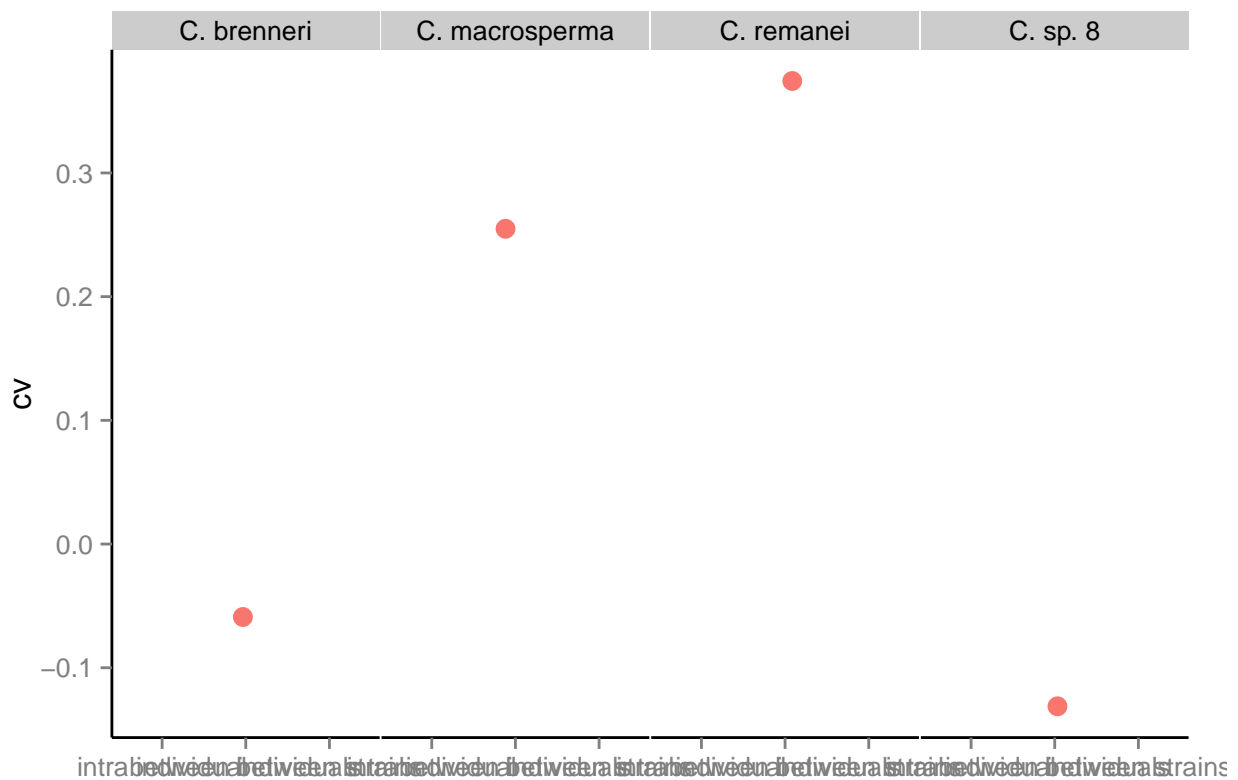


figure mockup a we are starting agin here, as I've modified some of the variables etc above Easier to start with a clean slate Clean and read in data:

mean and sd

```
groupedmeans=ff %>% group_by(Species,sex) %>% summarise(mean=mean(area,na.rm=T),n=n(),sd=sd(area,na.rm=T))
limits <- aes(ymax = mean + 1.96*sd/sqrt(n), ymin=mean - 1.96*sd/sqrt(n))
dodge <- position_dodge(width=0.9)
ggplot(data=groupedmeans, aes(x=Species, y=mean, fill=sex)) + geom_bar(stat="identity", position=position_dodge()) +
  scale_fill_manual(values=c("gray","white"))+ylab( expression(paste("area (", mu, m^{2},")")))+xlab(
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
    panel.background = element_blank(),axis.line = element_line(colour = "black"),legend.position = "n
```

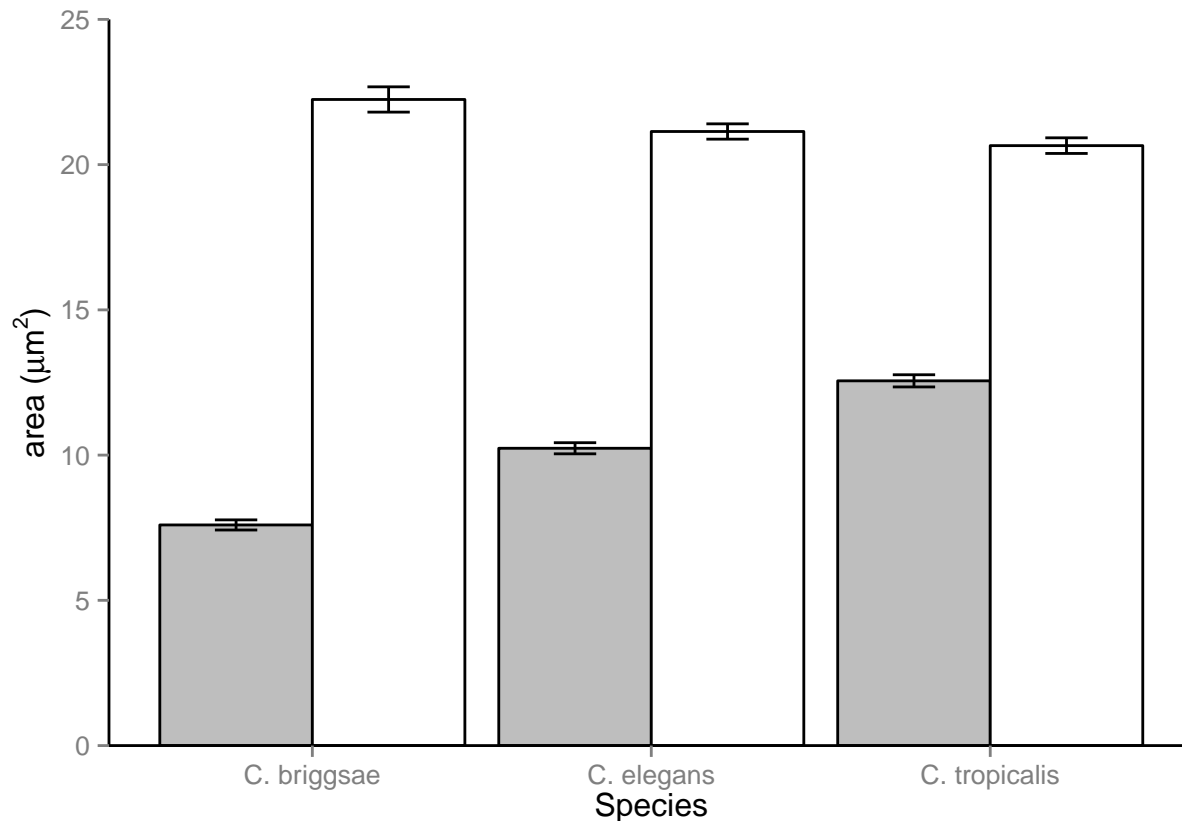


Figure mockup b group to get the data I want it's ugly, but it works

```
groupedstrains=ff %>% group_by(Species,Strain) %>%
  do(data.frame(meanM=mean(. [which(. $sex=="M"),]$area,na.rm=T),meanH=mean(. [which(. $sex=="H"),]$area,
    sdM=sd(. [which(. $sex=="M"),]$area,na.rm=T),sdH=sd(. [which(. $sex=="H"),]$area,na.rm=T))
groupedstrains$sem=1.96*groupedstrains$sdM/sqrt(groupedstrains$nM)
groupedstrains$seh=1.96*groupedstrains$sdH/sqrt(groupedstrains$nH)
p=ggplot(data=groupedstrains, aes(x=meanM, y=meanH, colour=Species, ymin = meanH - seh,ymax=meanH + seh))
p+geom_point(size=5)+coord_cartesian(ylim=c(0,15),xlim=c(0,33))+theme(panel.grid.major = element_blank(),
  panel.background = element_blank(),axis.line = element_line(colour = "black"),legend.position = "none")
p+ylab(expression(paste("Hermaphrodite Sperm area (", mu, "m^{2},")")))+xlab(expression(paste("Male Sperm area (", mu, "m^{2},")")))
p+geom_smooth(aes(group=Species), method="lm",size=1.5,colour="black")
```

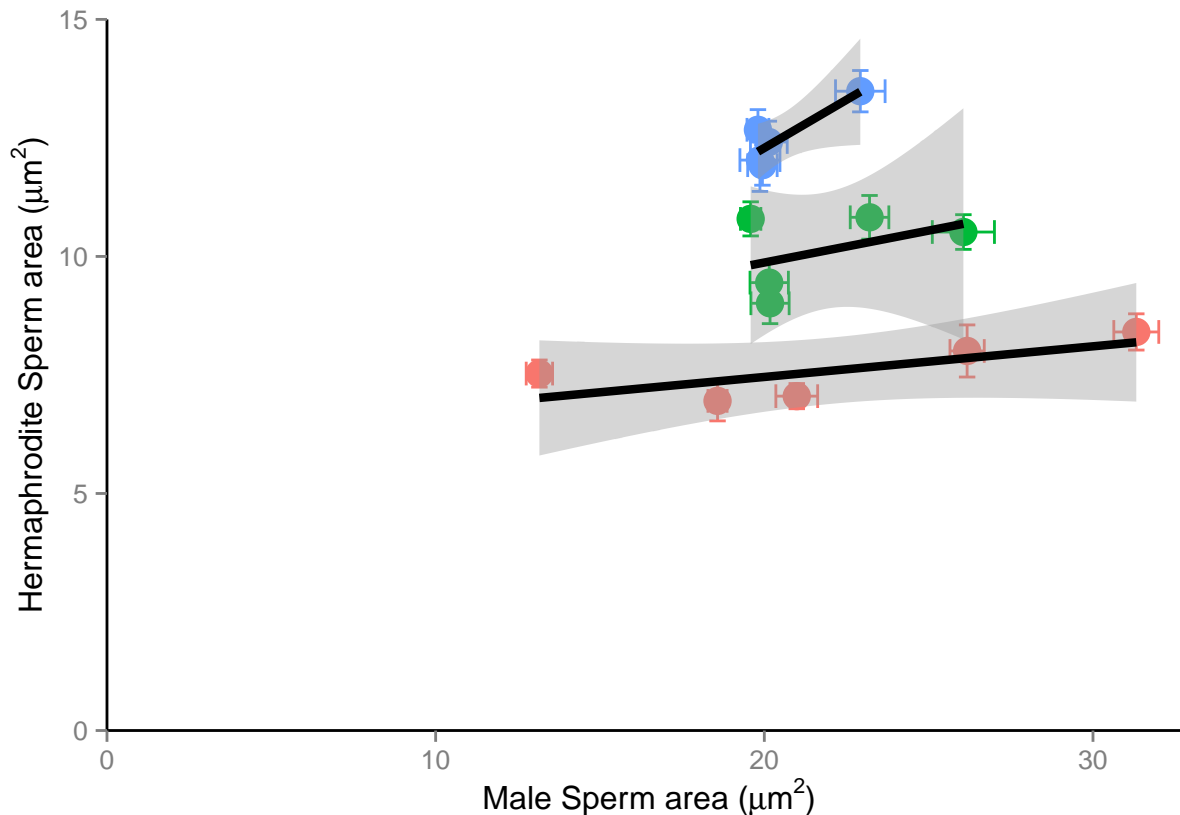


figure1a - bars need to rerun the above

```
ff<-spermsizes<-read.table("C:/Users/jeremy/Desktop/geiger/compileddata.csv",header=T,sep=",")
ff<-renameworms(ff)
spermsize2<-ff %>% group_by(Species,Strain) %>% summarise(means=mean(area,na.rm=T),cv=sd(area,na.rm=T)/
countspec=function(dataframe){
  holding=c()
  for(i in 1:nrow(dataframe)){
    holding=c(holding,sum(dataframe$Species==dataframe[i,]$Species))
  }
  return(holding)
}
spermsize2$Species<-ordered(spermsize2$Species,levels=c(tr$tip.label))
spermsize2<-spermsize2[order(spermsize2$Species),]
spermsize2$Strain<-factor(spermsize2$Strain, levels = spermsize2$Strain)
spermsize2$specnum=countspec(spermsize2)
spermsize2$cols=cut(spermsize2$means,3)
findchange<-function(df){
  holding=c()
  for(i in 1:length(df$Species)){
    if(i==1){
      holding=c(holding,0)
    } else if(df$Species[i]==df$Species[i-1]){
      holding=c(holding,0)
    } else {
      holding=c(holding,1)
    }
  }
}
```

```

    }
  }
  return(holding)
}

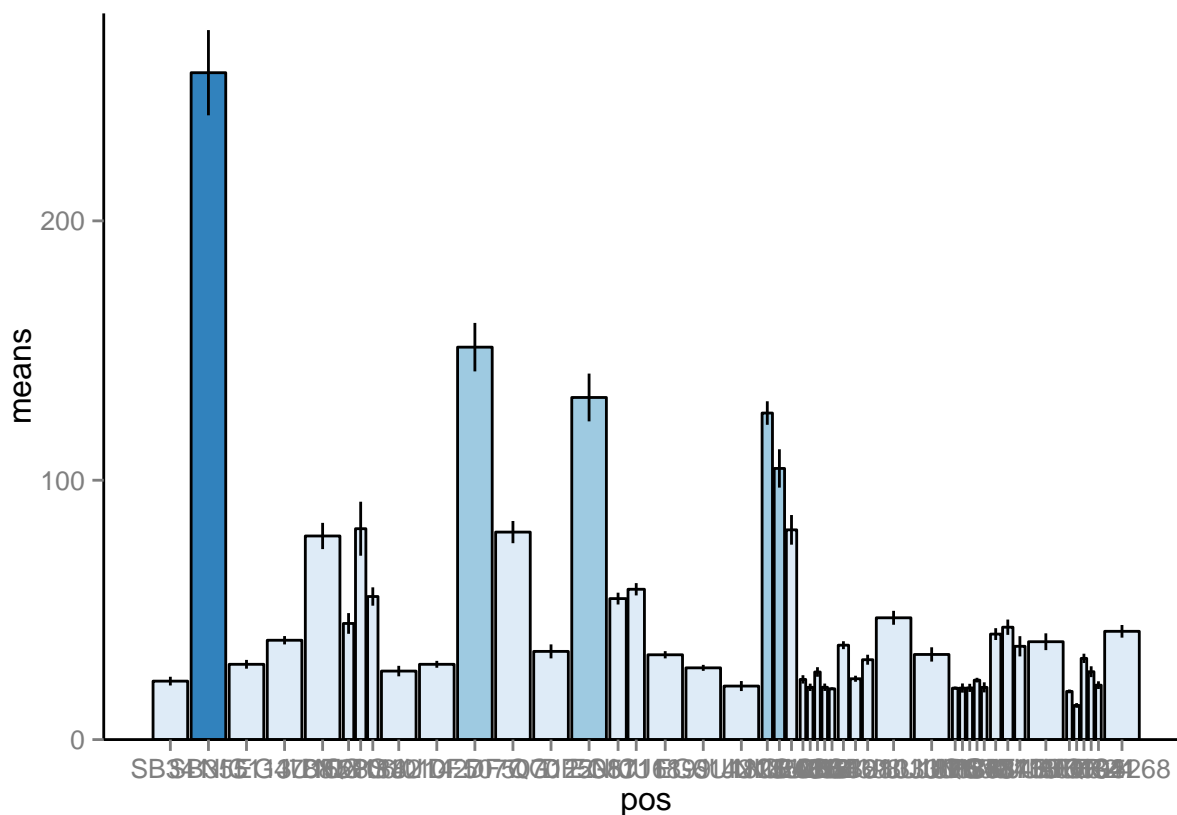
spermsize2$change<-findchange(spermsize2)
w<-(1-(spermsize2$specnum-1)*0.05)/spermsize2$specnum
pos <- 0.5 * (cumsum(w) + cumsum(c(0, w[-length(w)])))

gapsizes<-function(df,pos){
  pos1<-pos
  for(i in 1:length(df$specnum)){
    if(df$specnum[i]==1){
      pos1[i:length(pos1)]<-pos1[i:length(pos1)]+0.1
    } else if(df$change[i]==1){
      pos1[i:length(pos1)]<-pos1[i:length(pos1)]+0.1
    } else {
      pos1[i:length(pos1)]<-pos1[i:length(pos1)]+0.05
    }
  }
  return(pos1)
}

pos<-gapsizes(spermsize2,pos)
ggplot(data=spermsize2,aes(x = pos, width = w, y = means, fill=cols,ymin=means-sem,ymax=means+sem)) +
  geom_bar(stat = "identity",colour="black") + scale_x_continuous(labels = spermsize2$Strain, breaks =
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
    panel.background = element_blank(),axis.line = element_line(colour = "black"),legend.position = "n

```

## Warning: position\_stack requires constant width: output may be incorrect



large tree first group all the data

```
spermsize1<-ff %>% group_by(Species) %>% summarise(means=mean(area,na.rm=T))
spermsize2<-ff %>% group_by(Species,Strain) %>% summarise(means=mean(area,na.rm=T))
spermsize3<-ff %>% group_by(Species,Strain,individual) %>% summarise(means=mean(area,na.rm=T))
```

function to fix the format of spermsizes, and fit tree

```
fitace <- function(spermsizes,tree){
  holding<-spermsizes$means
  names(holding)<-spermsizes$Species
  return(fastAnc(tree,holding,CI=T))
}
```

function to choose a subset - works on any level, just chooses one from each species

```
subsetter<-function(spermsizes){
  x=lapply(split(spermsizes, spermsizes$Species),function(subdf) subdf[sample(1:nrow(subdf), 1),])
  do.call("rbind",x)
}
```

example usage fitace(subsetter(spermsizes2),tr) now need to loop and keep the values

```

looper<-function(spermsizes, reps, tree){
  outputdata=data.frame()
  outputCI=data.frame()
  for(i in 1:reps){
    outputdata=rbind(outputdata, fitace(subsetter(spermsizes), tree)$ace)
    outputCI=rbind(outputCI, fitace(subsetter(spermsizes), tree)$CI95)
  }
  names(outputdata)=seq(from=27, to=51)
  return(c(outputdata, outputCI))
}

```

ok we can call eg x=looper(spermsize3,10,tr) then mean and sd, etc. etc.

```

x<-fitace(spermsize1, tr)
AncSperm=x$ace
#or AncSperm=apply(x,2,mean) if it's bootstrapped
spermsize1$Species <- factor(spermsize1$Species, levels = c("C. sp. 1", "C. plicata", "C. guadeloupensis"))
spermsize=spermsize1[order(spermsize1$Species),]$means
names(spermsize)<-spermsize1[order(spermsize1$Species),]$Species
plotfancytree<-function(tree, nodesizes, terminalsizes){
  nodesizes<-nodesizes
  terminalsizes<-terminalsizes
  print(ggtree(tree)+geom_text(subset=.(isTip), aes(label=label), hjust=-0.19, fontface="italic")+
    geom_point(subset=.(!isTip), color="#1b9e77", size=sqrt(exp(nodesizes)/pi))+
    geom_point(subset=.(isTip), color="#7570b3", size=sqrt(exp(terminalsizes)/pi))+
    geom_text(subset=.(isTip), aes(label=round(exp(terminalsizes),1)), hjust=1, vjust=-0.4, size=3)+
    geom_text(subset=.(!isTip), aes(label=round(exp(nodesizes),1)), hjust=1.5, vjust=-0.4, size=3)+
    scale_x_continuous(expand = c(0.1, 0.1)))
  rm(list=c("terminalsizes", "nodesizes"), pos=".GlobalEnv")
}
plotfancytree(tr, AncSperm, spermsize)

```

1348572408035977728  
 690724111109299  
 13427454562368902 2079712575.3  
 23992000240045324 24386207906126452  
 609141254201283840  
 25657786565051804 1077663948.5  
 57248395634417.6 180069895032390  
 6130888406214095 24681318755965e+20  
 4874719646870305792 23030260435401284 27802653936284.7  
 941033988.3  
 920266548.8  
 7.06488257093739129 1343313561609547520 1024658623536.8  
 8.47748757153576e+24  
 1.7032178760181e+26 5.57932450921274e+49  
 158764331848256  
 3.51152481082395e+25  
 2.029981376762329 2.56268586586717e+24  
 1.77987164262507e+22 1.94181928438648e+57  
 586810626013128  
 1.80188471017626e+35 4035887643501.3  
 24369416664398.1  
 1.78252188464029e+24 295258667201.3  
 2.03103556598583e+30 1.75806028926582e+24  
 5.54205138243576e+34  
 2.185956933270534e+46 2.29760027485194e+49  
 5.15744982739556e+65  
 1.02391788683257e+28 1.23494693312621e+34  
 43070079433854488  
 4047755611626.8  
 4.6889934488133e+111  
 6170217959.9

+30