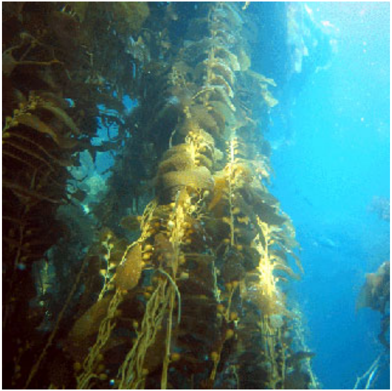
Handling Categorical Predictors: plyr, ANOVA, and more

Group Properties: Kelp

- Kelp sampled at multiple sites annually
- At each transect, holdfast diameter and # of fronds counted



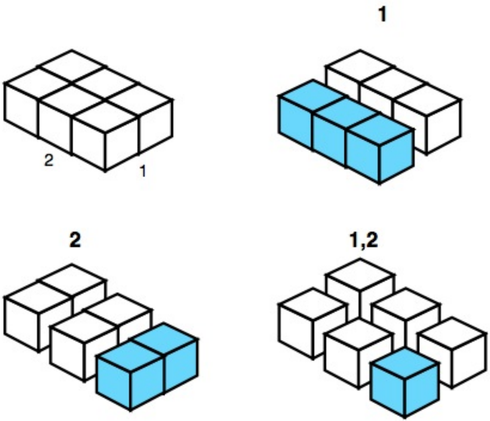
How can we get quick summaries by site?, year, or both?

```
#    YEAR MONTH       DATE SITE TRANSECT QUAD SIDE FRONDS
# 2  2000     9 2000-09-28 BULL        1   20            4
# 8  2000     9 2000-09-28 BULL        2   20           11
# 9  2000     9 2000-09-28 BULL        2   20           16
# 10 2000     9 2000-09-28 BULL        2   20           34
# 16 2000     9 2000-09-28 BULL        3   20           27
# 17 2000     9 2000-09-28 BULL        3   20           38
#    HLD_DIAM
# 2         7
# 8        65
# 9        55
# 10       55
# 16       65
# 17       60
```

For loops for Summarization by Site

```r
# number of groups
k <- length(levels(kelp$SITE))
#blank means vector
means <- rep(NA, k)
#the loop
for(i in 1:k) {
  #split the data first
  subdata <- subset(kelp, kelp$SITE == levels(kelp$SITE)[i])

  #apply the means function,
  #combine with previous means
  means[i] <- mean(subdata$FRONDS, na.rm=T)
}
```

The Split, Apply, Combine Strategy



Wickham 2011

ddply from Hadley Wickham's plyr library

```r
library(plyr)
#
kelpMeans <- ddply(kelp, .(SITE), summarize,
                   mean.FRONDS = mean(FRONDS, na.rm=T))
```

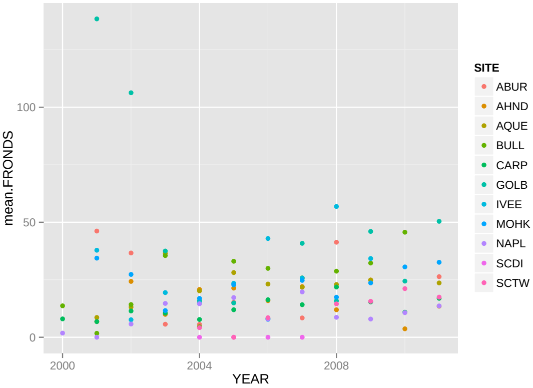
ddply from Hadley Wickham's plyr library

```
kelpMeans

#    SITE mean.FRONDS
# 1  ABUR       29.26
# 2  AHND       17.63
# 3  AQUE       21.04
# 4  BULL       27.30
# 5  CARP       13.11
# 6  GOLB       42.16
# 7  IVEE       25.81
# 8  MOHK       20.04
# 9  NAPL       13.16
# 10 SCDI        0.00
# 11 SCTW       14.73
```

Multiple Groups & ddply

```
kelpMeans2 <- ddply(kelp, .(YEAR, SITE), summarize,
                    mean.FRONDS = mean(FRONDS, na.rm=T))
```

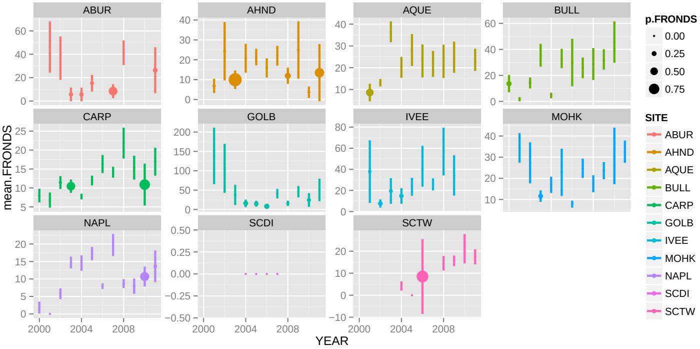
Multiple Groups & ddply



Complex Functions & ddply

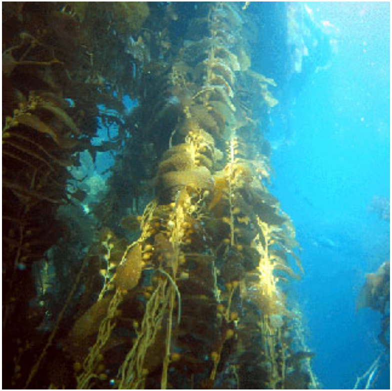
```
kelpMeans3 <- ddply(kelp, .(YEAR, SITE), function(aFrame){
  #calculate metrics for a 1-sample T test comparison against
  #grand mean of 10 fronds/m^2
  m <- mean(aFrame$FRONDS, na.rm=T)
  n<-length(na.omit(aFrame$FRONDS))
  se <- sd(aFrame$FRONDS, na.rm=T)/sqrt(n)
  t <- (m-10)/se
  p <- 2*pt(abs(t), df=n-1, lower.tail=F)

  # return everything
  return(c(mean.FRONDS=m, n.FRONDS=n,
           se.FRONDS=se, t.FRONDS=t,
           p.FRONDS = p))
})
```

Complex Functions & ddply



Exercise: Correlation!

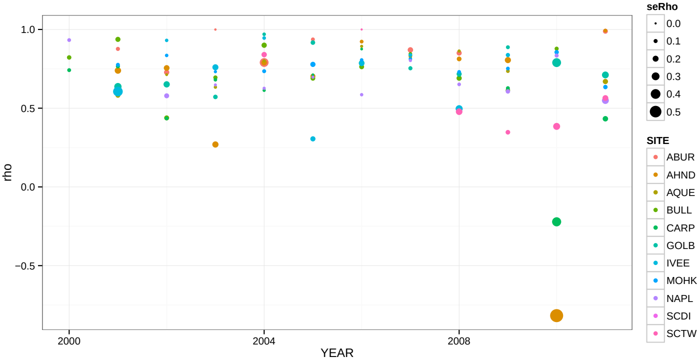
- Evaluate the correlation between fronds and holdfasts by site and year
- Plot it
- Extra: include the SE of the correlation visually



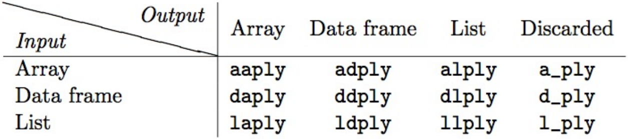
Exercise: Correlation!

```r
kelpCor <- ddply(kelp, .(YEAR, SITE), function(adf){
  #first get the correlation
  cors <- cor(adf$FROND, adf$HLD_DIAM)

  #use this to calculate it's SE
  seCor <- sqrt((1-cors^2) / (nrow(adf)-2))

  #return both
  return(c(rho = cors, seRho = seCor))

})
```

Exercise: Correlation!



Many plyr Functions

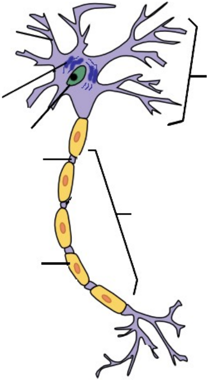


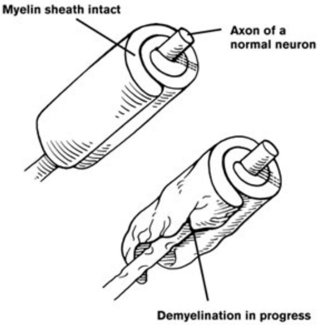
Output *Input*	Array	Data frame	List	Discarded
Array	`aaply`	`adply`	`alply`	`a_ply`
Data frame	`daply`	`ddply`	`dlply`	`d_ply`
List	`laply`	`ldply`	`llply`	`l_ply`

Also r*ply to replicate an action and return an object. Great for simulation.

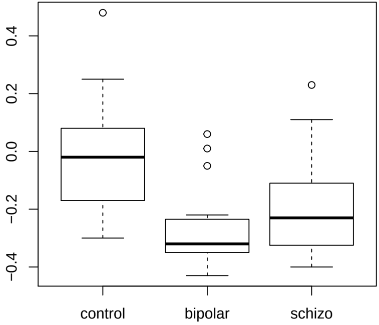
See also `colwise` and `each` for everyday use!

Categorical Predictors: Gene Expression and Mental Disorders





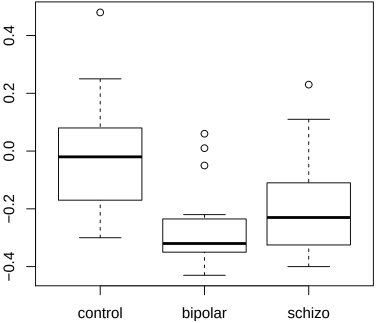
Categorical Predictors



How do we determine the importance of categorical predictors?

Aside: Reordering Factors

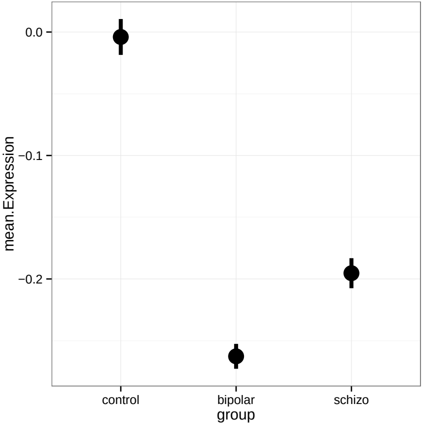
```r
brainGene$group <- factor(brainGene$group,
                          levels=c("control", "bipolar", "schizo"))
```



Categorical Predictors Ubiquitous

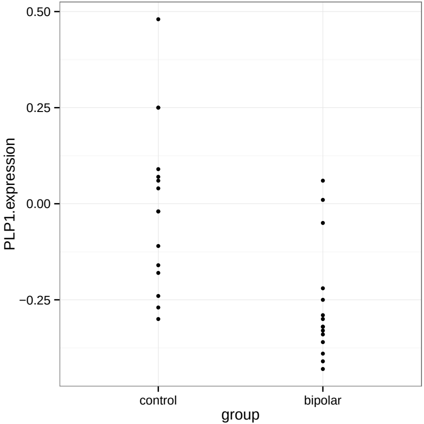
- Treatments in an Experiment
- Spatial groups - plots, Sites, States, etc.
- Individual sampling units
- Temporal groups - years, seasons, months

Traditional Way to Think About Categories



What is the variance between groups v. within groups?

But How is the Model Fit?



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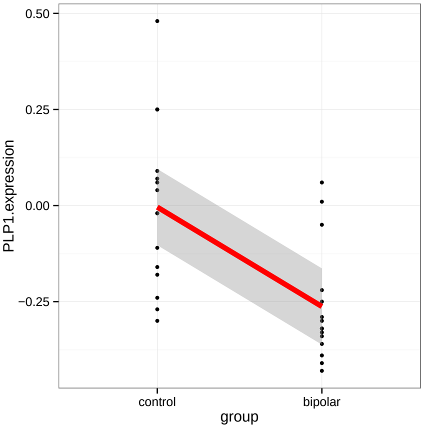

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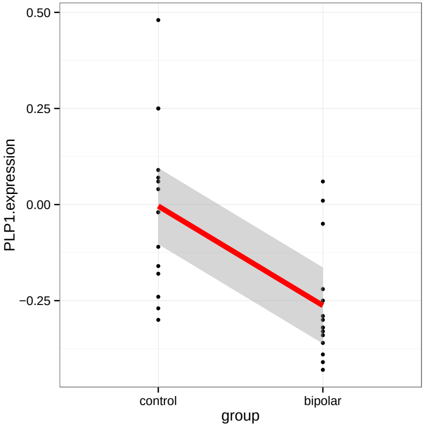

Underlying linear model with control = intercept, dummy variable for bipolar

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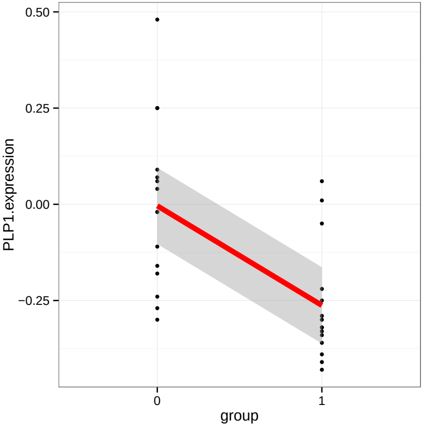

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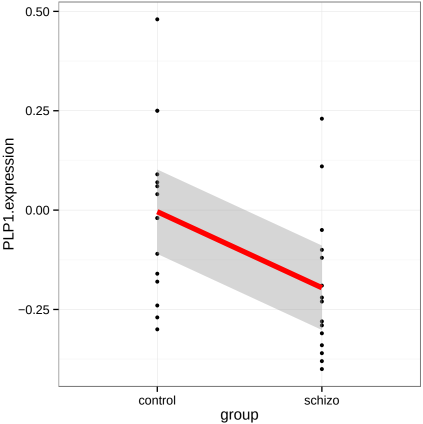

Underlying linear model with control = intercept, dummy variable for schizo

Different Ways to Write a Categorical Model

$$y_{ij} = \bar{y} + (\bar{y}_i - \bar{y}) + (y_{ij} - \bar{y}_i)$$

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Traditional ANOVA special case where all x_i are orthogonal

Often one category set to β_0 for ease of fitting

This is a Linear Model

```
bg.sub.lm <- lm(PLP1.expression ~ group, data=brainGene)
```

Hypothesis Testing with a Categorical Model: ANOVA

$$H_0 = \mu_1 = \mu 2 = \mu 3 = ...$$

Hypothesis Testing with a Categorical Model: ANOVA

$$H_0 = \mu_1 = \mu 2 = \mu 3 = ...$$

OR

$$\beta_0 = \mu, \qquad \beta_i = 0$$

Assumptions of Ordinary Least Squares Regression

- Independence of data points
- Normality within groups
- Homoscedasticity (homogeneity of variance)

F-Test to Compare

$$SS_{Total} = SS_{Between} + SS_{Within}$$

$SS_{Between} = \sum_i \sum_j (\bar{Y_i} - \bar{Y})^2$, df=k-1

$SS_{Within} = \sum_i \sum_j (Y_{ij} - \bar{Y_i})^2$, df=n-k

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$$SS_{Total} = SS_{Between} + SS_{Within}$$

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$$SS_{Within} = \sum_i \sum_j (Y_{ij} - \bar{Y_i})^2, \text{ df=n-k}$$

To compare them, we need to correct for different DF. This is the Mean Square.

MS = SS/DF, e.g, $MS_W = \frac{SS_W}{n-k}$

F-Test to Compare

$F = \frac{MS_B}{MS_W}$ with DF=k-1,n-k

F-Test to Compare

$F = \frac{MS_B}{MS_W}$ with DF=k-1,n-k

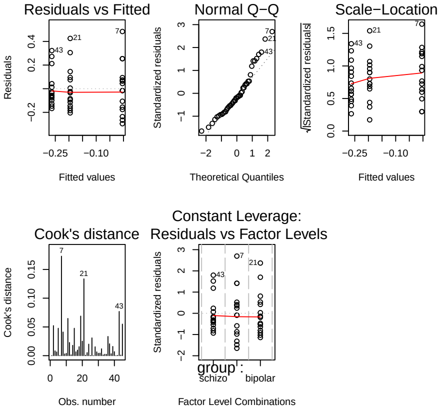
(note similarities to SS_R and SS_E notation of regression)

ANOVA

```
anova(bg.sub.lm)

# Analysis of Variance Table
#
# Response: PLP1.expression
#           Df Sum Sq Mean Sq F value Pr(>F)
# group      2   0.54  0.2701    7.82 0.0013
# Residuals 42   1.45  0.0345
```

Inspecting Assumptions

```r
par(mfrow=c(2,3))
plot(bg.sub.lm, which=1:5 )
```



Levene's Test of Homogeneity of Variance

```
library(car)

# Loading required package:  MASS
# Loading required package:  nnet

leveneTest(PLP1.expression ~ group, data=brainGene)

# Levene's Test for Homogeneity of Variance (center = median)
#       Df F value Pr(>F)
# group  2    1.01   0.37
#       42
```

Levene's test robust to departures from normality

What do I do if I Violate Assumptions?

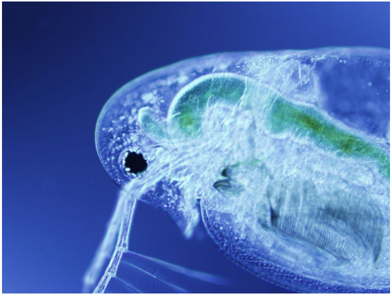
- Nonparametric Kruskal-Wallace (uses ranks)
- Transform?
- GLM with ANODEV

Kruskal Wallace Test

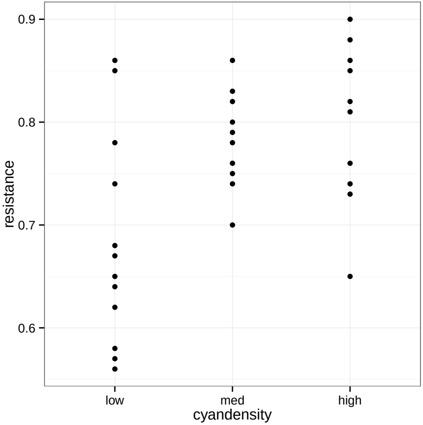
```
kruskal.test(PLP1.expression ~ group, data=brainGene)

#
#  Kruskal-Wallis rank sum test
#
# data:  PLP1.expression by group
# Kruskal-Wallis chi-squared = 13.2, df = 2, p-value =
# 0.001361
```

Exercise: Daphnia Resistance

- Plot the mean and SE of the data by group
- Evaluate whether the data is appropriate for ANOVA
- Fit an ANOVA and check diagnostics
- Evaluate results & compare to Kruskal-Wallace and a glm with a Gamma distribution



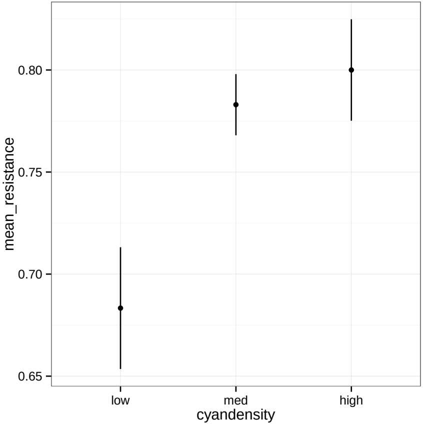
Daphnia Data



Daphnia Means

```r
#first use plyr to get means and SE
dsummary <- ddply(daphnia, .(cyandensity), summarize,
                  mean_resistance = mean(resistance),
                  se = sd(resistance) / sqrt(length(resistance)))
#
ggplot(dsummary, aes(x=cyandensity, y=mean_resistance,
                     ymin=mean_resistance-se,
                     ymax=mean_resistance+se)) +
  geom_pointrange() + theme_bw()
```

Daphnia Means



How about HOV?

```
leveneTest(resistance ~ cyandensity, data=daphnia)

# Levene's Test for Homogeneity of Variance (center = median)
#       Df F value Pr(>F)
# group  2       2   0.15
#       29
```

ANOVA shows an Effect

```
daphniaLM <- lm(resistance ~ cyandensity, data=daphnia)
anova(daphniaLM)

# Analysis of Variance Table
#
# Response: resistance
#             Df Sum Sq Mean Sq F value Pr(>F)
# cyandensity  2 0.0892  0.0446    6.69 0.0041
# Residuals   29 0.1933  0.0067
```

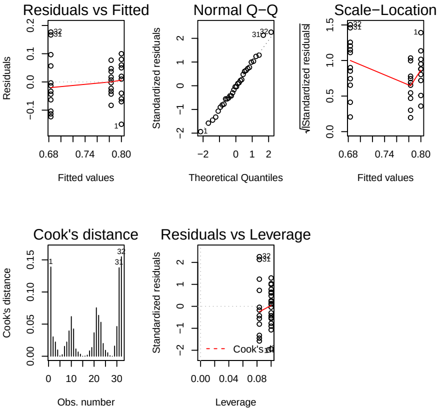
KW shows an Effect

```
#
#  Kruskal-Wallis rank sum test
#
# data:  resistance by cyandensity
# Kruskal-Wallis chi-squared = 8.2, df = 2, p-value =
# 0.01658
```

Bad GLM Does Not

```
# Analysis of Deviance Table
#
# Model: Gamma, link: identity
#
# Response: resistance
#
# Terms added sequentially (first to last)
#
#
#             Df Deviance Resid. Df Resid. Dev
# NULL                           31      0.529
# cyandensity  2    0.162        29      0.367
```

Diagnostics Also Good


Residuals vs Fitted
Residuals
Fitted values
0.68
0.74
0.80
−0.1
0.0
0.1
0.2
32
31
1
Normal Q−Q
Standardized residuals
Theoretical Quantiles
−2
0
1
2
−2
−1
0
1
2
31
32
1
Scale−Location
√|Standardized residuals|
Fitted values
0.68
0.74
0.80
0.0
0.5
1.0
1.5
32
31
1
Cook's distance
Cook's distance
Obs. number
0
10
20
30
0.00
0.05
0.10
0.15
1
32
31
Residuals vs Leverage
Standardized residuals
Leverage
0.00
0.04
0.08
−2
−1
0
1
2
32
31
1
Cook's d