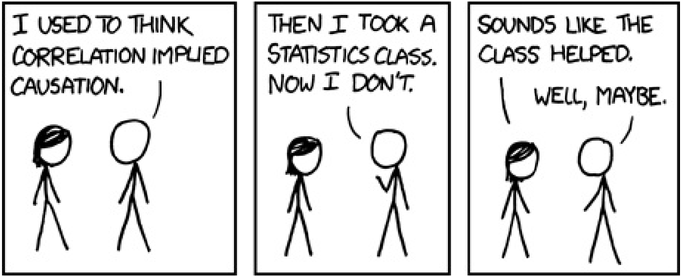
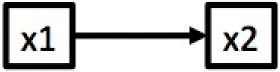
Correlation and Regression

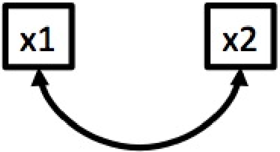

I USED TO THINK CORRELATION IMPLIED CAUSATION.
THEN I TOOK A STATISTICS CLASS. NOW I DON'T.
SOUNDS LIKE THE CLASS HELPED.
WELL, MAYBE.

http://xkcd.com/552/

How are X and Y Related

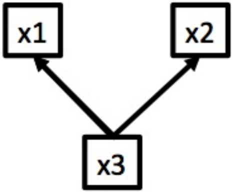


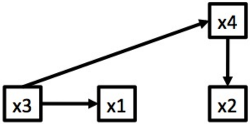
Causation (regression)
p(Y | X=x)

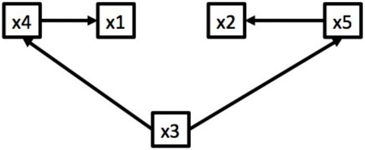


Correlation
p(Y=y, X=x)

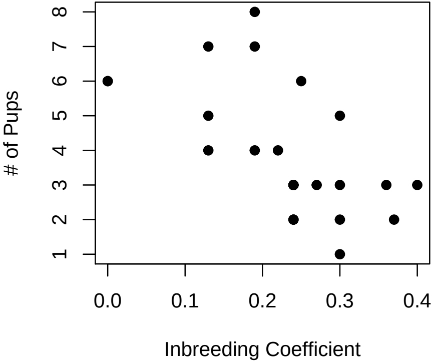
Correlation Can be Induced by Many Mechanisms



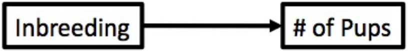




Example: Wolf Inbreeding and Litter Size

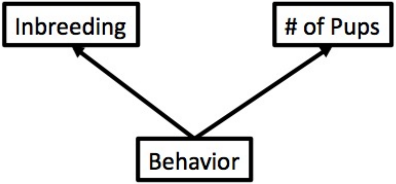


Example: Wolf Inbreeding and Litter Size



Inbreeding

# of Pups

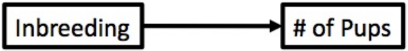


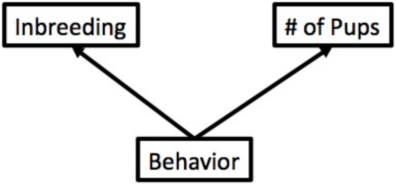
Inbreeding

# of Pups

Behavior

Example: Wolf Inbreeding and Litter Size





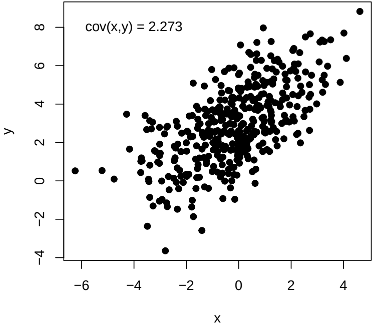
We don't know which is correct - or if another model is better. We can only examine *correlation*.

Covariance

Describes the relationship between two variables. Not scaled.

σ_{xy} = population level covariance, s_{xy} = covariance in your sample

$$\sigma_{XY} = \frac{\sum(X-\bar{X})(y-\bar{Y})}{n-1}$$

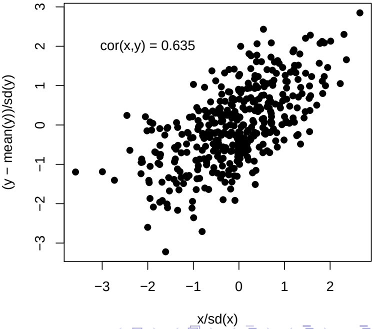


Pearson Correlation

Describes the relationship between two variables.
Scaled between -1 and 1.

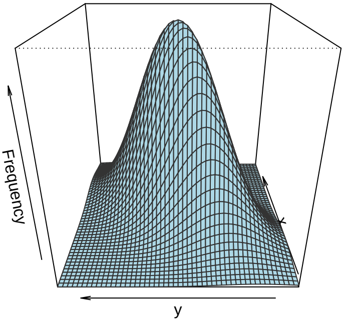
ρ_{xy} = population level correlation, r_{xy} = correlation in your sample

$$\rho_{xy} = \frac{\sigma_{xy}}{\sigma_x \sigma_y}$$



Assumptions of Pearson Correlation

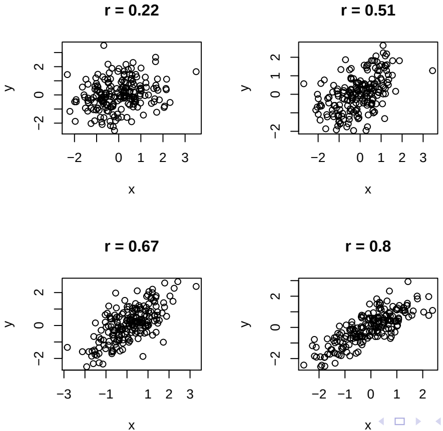
- Observations are from a **random sample**
- Each observation is **independent**
- X and Y are from a **Normal Distribution**



The meaning of r

Y is perfectly predicted by X if r = -1 or 1.

r^2 = the porportion of variation in y explained by x



Testing if r $\neq$ 0

Ho is r=0. Ha is r $\neq$ 0.

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Testing: $t = \frac{r}{SE_r}$ **with df=n-2**

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WHY n-2?

Testing if r $\neq$ 0

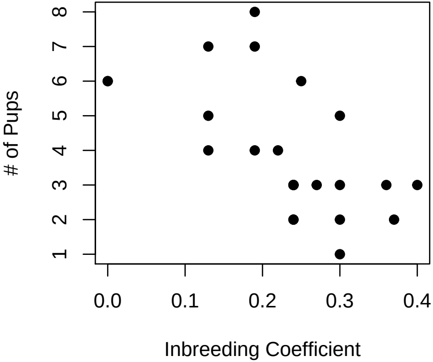
Ho is r=0. Ha is r $\neq$ 0.

Testing: $t = \frac{r}{SE_r}$ **with df=n-2**

WHY n-2?

$$SE_r = \sqrt{\frac{1-r^2}{n-2}}$$

Example: Wolf Inbreeding and Litter Size



Example: Wolf Inbreeding and Litter Size

```
cov(wolves)

##                       inbreeding.coefficient    pups
## inbreeding.coefficient              0.009922 -0.1136
## pups                               -0.113569  3.5199

cor(wolves)

##                       inbreeding.coefficient    pups
## inbreeding.coefficient                1.0000 -0.6077
## pups                                 -0.6077  1.0000
```

Example: Wolf Inbreeding and Litter Size

```
with(wolves, cor.test(pups, inbreeding.coefficient))

##
##  Pearson's product-moment correlation
##
## data:  pups and inbreeding.coefficient
## t = -3.589, df = 22, p-value = 0.001633
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.8120 -0.2707
## sample estimates:
##     cor
## -0.6077
```

Exercise: Pufferfish Mimics & Predator Approaches

- Load up the pufferfish mimic data from W&S
- Plot the data
- Assess the correlation and covariance
- Assess Ho.
- Challenge - Evaluate Ha1: the correlation is 1.

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Exercise: Pufferfish Mimics & Predator Approaches

```r
# get the correlation and se
puff_cor = cor(puffer)[1, 2]
se_puff_cor = sqrt((1 - puff_cor)/(nrow(puffer) - 2))

# t-test with difference from 1
t_puff <- (puff_cor - 1)/se_puff_cor
t_puff

## [1] -2.005



# 1 tailed, as > 1 is not possible
pt(t_puff, nrow(puffer) - 2)

## [1] 0.03013
```

Violating Assumptions?

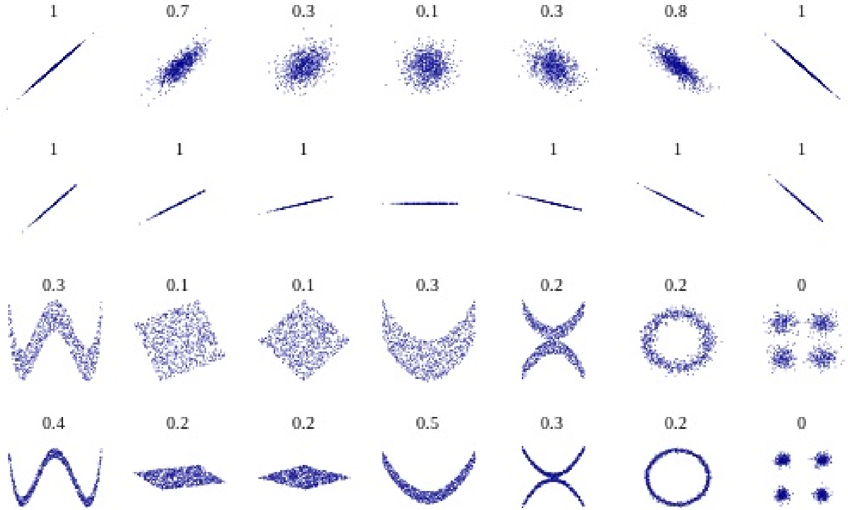
- Spearman's Correlation (rank based)
- Distance Based Correlation & Covariance (`dcor`)
- Maximum Information Coefficient (nonparametric)

All are lower in power for linear correlations

Spearman Correlation

1. Transform variables to ranks, i.e.,2,3... (`rank()`)
2. Compute correlation using ranks as data
3. If n $\leq$ 100, use Spearman Rank Correlation table
4. If n $>$ 100, use t-test as in Pearson correlation

Distance Based Correlation, MIC, etc.

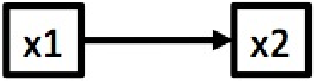


Least Squares Regression
$y = ax + b$

Then it's code in the data, give the keyboard a punch
Then cross-correlate and break for some lunch
Correlate, tabulate, process and screen
Program, printout, regress to the mean

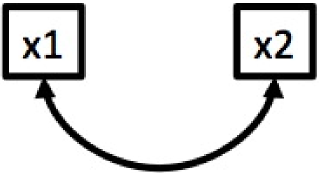
-White Coller Holler by Nigel Russell

How are X and Y Related



Causation (regression)

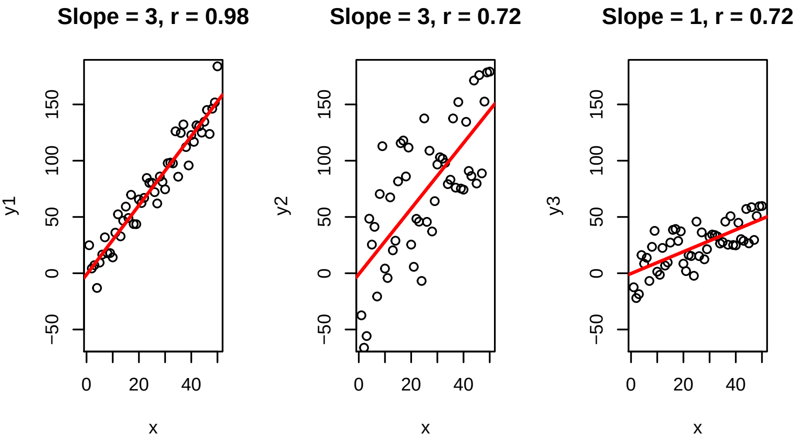
$p(Y \mid X=x)$



Correlation

$p(Y=y, X=x)$

Correlation v. Regression Coefficients

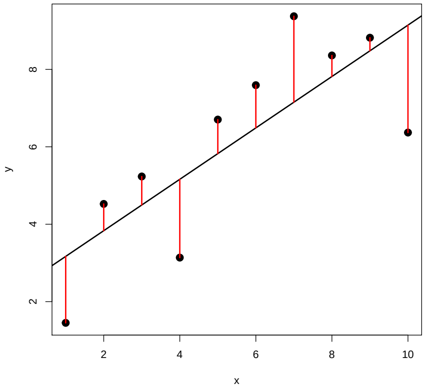


Basic Princples of Linear Regression

- Y is determined by X: p(Y | X=x)
- The relationship between X and Y is Linear
- The residuals of Y= a + bx are normall distributed (i.e., Y = a + bX + e where e   N(0,σ))

Basic Principles of Least Squares Regression

$\widehat{Y} = a + bX$ - a = intercept, b = slope



Minimize Residuals defined as $SS_{residuals} = \sum(Y_i - \widehat{Y})^2$

Solving for Slope

$$b = \frac{s_{xy}}{s_x^2}$$

Solving for Slope

$$b = \frac{s_{xy}}{s_x^2} = \frac{cov(x,y)}{var(x)}$$

Solving for Slope

$$b = \frac{s_{xy}}{s_x^2} = \frac{cov(x,y)}{var(x)}$$

$$= r_{xy}\frac{s_y}{s_x}$$

Solving for Intercept

Least squares regression line always goes through the mean of X and Y

$$\bar{Y} = a + b\bar{X}$$

Solving for Intercept

Least squares regression line always goes through the mean of X and Y

$$\bar{Y} = a + b\bar{X}$$

$$\text{a} = \bar{Y} - b\bar{X}$$

Fitting a Linear Model in R

```r
wolf_lm <- lm(pups ~ inbreeding.coefficient, data=wolves)
```

Fitting a Linear Model in R

```r
wolf_lm <- lm(pups ~ inbreeding.coefficient, data=wolves)
```

```r
wolf_lm

##
## Call:
## lm(formula = pups ~ inbreeding.coefficient, data = wolves)
##
## Coefficients:
##            (Intercept)  inbreeding.coefficient
##                   6.57                  -11.45
```

Extracting Coefficients from a LM

```
coef(wolf_lm)

##            (Intercept) inbreeding.coefficient
##                  6.567                -11.447


coef(wolf_lm)[1]

## (Intercept)
##       6.567
```

Extracting Fitted Values from a LM

```
fitted(wolf_lm)
```

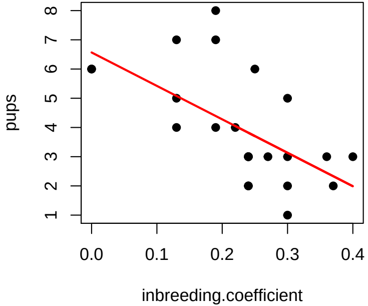
```
##     1     2     3     4     5     6     7     8     9    10 
## 6.567 6.567 5.079 5.079 5.079 4.392 4.392 4.392 3.706 3.820 
##    11    12    13    14    15    16    17    18    19    20 
## 3.820 3.820 3.820 3.820 3.820 3.477 3.133 3.133 3.133 3.133 
##    21    22    23    24 
## 2.446 1.989 2.332 4.049
```

```
coef(wolf_lm)[1] + coef(wolf_lm)[2]*0.25
```

```
## (Intercept) 
##       3.706
```

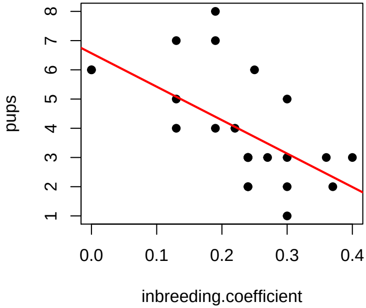
Plotting Fitted LMs

```
plot(pups ~ inbreeding.coefficient, data=wolves, pch=19)

matplot(wolves$inbreeding.coefficient, fitted(wolf_lm),
        add=T, lwd=2, col="red", type="l")
```



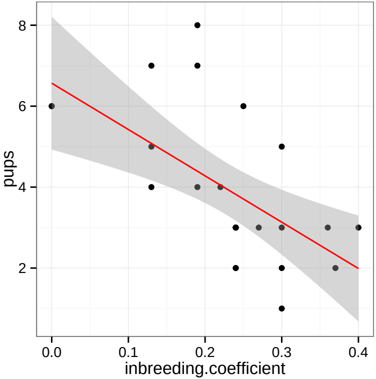
Plotting Fitted LMs

```
plot(pups ~ inbreeding.coefficient, data=wolves, pch=19)

abline(wolf_lm, col="red", lwd=2)
```



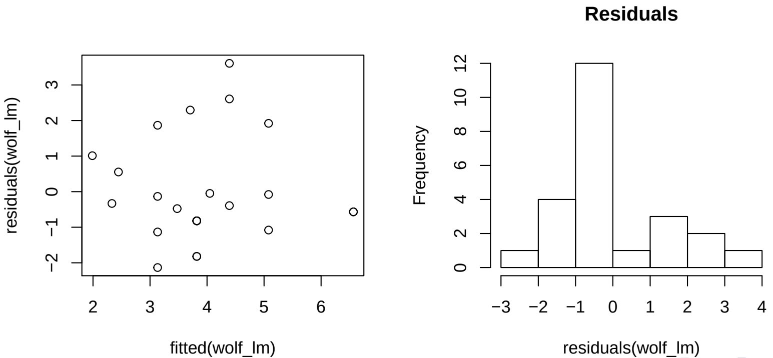
Ggplot2 and LMs

```
ggplot(data=wolves, aes(y=pups, x=inbreeding.coefficient)) +
  geom_point() +
  theme_bw() +
  stat_smooth(method="lm", color="red")
```



Checking Residuals

```
par(mfrow=c(1,2))
plot(fitted(wolf_lm), residuals(wolf_lm))
#
hist(residuals(wolf_lm), main="Residuals")
```



Exercise: Pufferfish Mimics & Predator Approaches

- Fit the pufferfish data
- Visualize the linear fit
- Examine whether there is any relationship between fitted values, residual values, and treatment

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