# **Workshop on Quantitative Methods in Linguistics (WoQuMeL)**

School of Languages and Linguistics | Jadavpur University | 22nd July - 24th July, 2024

# **Outline**

- Objectives
- To learn statistical methods for quantitative analyses of linguistic data
- Approach empirical questions in linguistics from a model-theoretic approach
- Models, similar to theories, make predictions, but not always.
- We tweak them till we arrive at a model whose unpredictable aspects are within acceptable bounds

#### **What we will be following**

- Quantitative methods in Linguistics (Johnson 2008)
- Code and datsets related to Johnson (2008)
	- **–** [Code and data](https://www.wiley.com/en-us/Quantitative+Methods+In+Linguistics-p-9781405144247)
- [Statistics for Linguistics: An Introduction Using R](https://appliedstatisticsforlinguists.org/bwinter_stats_proofs.pdf) (Winter 2020)

#### **Topics that we will cover**

- Descriptive statistics
	- **–** mean
- Distributions
- Models
- Data visualization
- Summary Stats
- Linear Models
- Correlations
- Multiple Regressions

#### **Working with R**

- Basic R functions and packages
- Designing and building the statistical components of experiments
- Writing code and debugging

#### **This document**

- We are writing R code and associated content in Quarto
- Markdown flavor syntax
- Weaving r code and text in the same document

#### **What statistic are and what they are not**

- Statistical analyses lend validity
- We perform tests that allow us to either accept or reject the null hypothesis
- They give us a means to uncover causal relationships
- They are, however, not magic wands
- Each test and set of analyses are specific to the conditions, variables, nature and distribution of the data; so we decide first before we conduct the experiment what tests to perform NOT after

#### **Statistical environment**

- R because it is:
	- 1. a powerful statistics package, good at reading data, wide range of statistical tests and techniques, good graphics, very flexible
	- 2. a usable package available for many platforms (PC, Mac, Unix, Linux…. ) programmable user community for support 3.it is noncommercial - distributed under the GNU "copyleft", maintained by a community of users, upgrades happen because the users need improvements, not because the company needs more money.
- Where: [R project page](http://www.r-project.org/)
- How:
	- 1. Go to the R project page,
	- 2. click the CRAN link to see the download servers on the Comprehensive R Archive Network,
	- 3. choose a download server near your location,
	- 4. choose your platform (Windows, Linux, Mac)

#### **Describing data**

• Let's say we ask 36 people to score a sentence on a grammaticality scale So that a score of 1 means that it sounds pretty ungrammatical, and 10 sounds perfectly OK. A simple way of generating data in R

 $x=round(rnorm(36,4.5,2))$ 

- *rnorm* needs some arguments: N, mean and the SD
- How many people gave the sentence a rating of "1"?
- How many rated it a "2"? When we answer these questions for all of the possible ratings we have the values that make up the *frequency distribution* of our sentence grammaticality ratings

#### **Getting the frequency distribution**

```
data = c(2,1,6,8,12,5,1,0,1)#c function to catenate individual values together
rating = c(1,2,3,4,5,6,7,8,9)plot(rating,data,type = "b", main="Sentence rating frequency distribution",
     xlab = "Rating", ylab = "Frequency")
```




- Here we defined two vectors, data and rating, data is the frequency data of ratings, and rating refers to a vector of the rating scale
- How many people gave a particular sentence the rating of 5? Or how frequently was the rating 5 given?

#### **What is a vector?**

- Container vector
	- **–** Ordered collection of numbers with no other structure
	- **–** The length of a vector is the number of elements in the container.
- Operations are applied componentwise.
	- **–** Given two vectors x and y of equal length, x\*y would be the vector whose nth component is the product of the nth components of x and y.
	- **–** log(x) would be the vector whose nth component is the logarithm of the nth component of x.

#### **How informative are frequency distributions?**

```
plot(rating,data,type = "b", main="Sentence rating frequency distribution",
     xlab = "Rating", ylab = "Frequency")
```


# **Sentence rating frequency distribution**

- Plotting rating and data gives us the frequency distribution
- Majority of subjects (12) rated the sentence to be 5 on the scale
- Few people rated the sentence to be absolutely ungrammatical rating of 1 (2) and absolutely grammatical rating of 9 (1)
- A lot many subjects rated the sentence to be 5 than 1 or 9
- This suggests that the frequency of ratings is crowded around the average rating of 4.5

#### **Changing the granularity of the rating scale**

- The rating scale we used forces the subject to rate in integers
- Imagine a situation were subjects are given the freedom to use decimals to rate
- If so, then: no two ratings are ever going to be the same; each subject will have a rating that is different from the other, and will have a frequency of 1

```
x=rnorm(36,4.5,2)
hist(x, breaks=300000, xlim=c(0,10))
```


• If we quantize this difference and put individual ratings in intervals, say between 0 and 1, 1 and 2, and 2 and 3, again we will get a distribution similar to the first one

#### **Frequency distribution in R**

- How did we generate these plots and distributions
- First we defined a vector using the function, rnorm

```
x = rnorm(36, 4.5, 2)#notice that this is different from round(rnorm(36,4.5,2)) where we had asked for rounded/in
```
- We defined a vector, x, with 36 values, a mean of 4.5 and standard deviation of 2.
- So decimal ratings would be ok
- Then we made two histograms
	- **–** First with:



#here we want to plot a histogram where the width of the cells/bins is very small

• Second with:

hist(x, xlim =  $c(0,10)$ )#here we want to plot a histogram where the width of the cells/bins is



**Histogram of x**



#### **Theoretical fequency distributions**

- Suppose we could draw from an infinite data set
- The larger our data set more detailed a representation of the frequency distribution
- If we keep collecting sentence grammaticality data for the same sentence, so that instead of ratings from 36 people we have ratings from 10,000 people
- With a histogram that has 1000 bars in it, we see that ratings near 4.5 are more common than those at the edges of the rating scale
- Adding observations up to infinity and reducing the size of the bars in the histogram of the frequency distribution
- Intervals between bars is vanishingly small i.e. we end up with a continuous curve, almost
- Plotting the normal distribution curve on the frequency distribution

```
x = rnorm(10000, 4.5, 2)hist(x,breaks=100,freq=FALSE, xlim = c(0,10))
plot(function(x)dnorm(x, mean=4.5, sd=2), 0,10, add=TRUE)
```


### **Adding the normal curve**

- Why the excellent fit between the "observed" and the theoretical distributions?
- The data is generated by random selection
	- **–** rnorm() observations from the theoretical normal distribution dnorm()
- The "normal distribution" is an very useful theoretical function because…
- 1. Let's assume that there is an underlying property that we are trying to measure like grammaticality, or
	- **–** typical duration, or
	- **–** amount of processing time
- 2. Assume that there is some source of random error that makes it difficult for us to get to this underlying property
- If so, then we can think that the "true" value of the underlying property we want to measure
	- **–** Must be at the center of the frequency distribution that we observe in our measurements
	- **–** And, the distribution (we observe) is caused by error with (the probability of) bigger errors being less likely than smaller errors

# **The Normal Distribution**

- The normal distribution is described by the normal curve, or the bell-shaped curve
- It is an exponential function of the mean value  $(\mu \text{ "new"} )$  and the variance  $(\sigma \text{ "sigma"} )$
- The sum of the area under the curve, fx is 1
- Derived from just two numbers, the mean value and a measure of how variable the data are
- The area under the curving equalling to 1, is also useful to go from frequency distributions to probability densities
- This is related to hypothesis testing

$$
-f(x) = \frac{1}{\sigma\sqrt{2\pi}}e^{-(x-\mu)^2/2\sigma^2}
$$

• *e* is Euler's constant

#### **Type of distributions**

- Uniform distribution: Every outcome is equally likely
	- **–** Six sides of a dice equal likelihood that either side will be rolled

 $uni=plot(function(x)$ dunif(x,min=-3,max=3), -3,3, main="Uniform distribution")



• Normal, bell-shaped distribution, measurements congregate around a typical value and values become less and less likely as they deviate from the central value

 $norm=plot(function(x)dnorm(x), -3,3, main="Normal distribution")$ 



# **Normal distribution**

- Skewed right: Skewed frequency distributions
	- **–** percentage data and reaction time data
	- **–** Mean is no longer 'central' to the distribution, or extreme values (from one end of the scale and less from the other) dominate the distribution





• The J-shaped distribution is a special kind of skewed distribution

- **–** Most observations come from the end of the measurement scale
- **–** Most speech errors counts per utterance will have a speech error count of 0

 $j=plot(function(x)df(x, 1, 10)/3, 0.2, 3, main="J-shaped distribution")$ 



# **J−shaped distribution**

x

• Bimodal distribution is a frequency distribution where clearly two modalities are involved. For instance

 $- f_0$  (or pitch) for men and women

```
bimodal=plot(function(x)dnorm(x, mean=3, sd=1)+dnorm(x, mean=-3, sd=1)/2,-6,6,
     main="Bimodal distribution")
```


the other

 $u=plot(function(x)-dnorm(x),-3,3,$ main="U-shaped distribution")

# **U−shaped distribution**



### **Measures of central tendency**

```
plot(function(x)df(x,5,100),0,4, main="Measures of central tendency")
lines(x=c(0.6,0.6),y=c(0,df(0.6,5,100)))
skew.data <- rf(10000,5,100)
lines(
  x=c(mean(skew.data), mean(skew.data)),
  y=c(0, df(mean(skew.data), 5, 100)))lines(
  x=c(median(skew.data),median(skew.data)),
  y=c(0,df(median(skew.data),5,100)))
text(1,0.75,labels="mode")
text(1.3, 0.67,labels="median")
text(1.35,0.6,labels="mean")
```
# **Measures of central tendency**



- Normal distribution the central 'values' (from our samples) have the highest probability of being part of the population
- What are these?
- The most frequently occurring value *mode* the tip of the frequency distribution. In the skewed distribution, the mode is 0.6
- The central value, that is in an ordered dataset of the values, the one in the middle is the *median*; aka, the center of gravity
- Arithmetic *mean*, or the sum of values divided by the total number of values, n
- *Least squares estimate of central tendency*
	- 1. take the difference between the mean and each value in our data set
	- 2. square these differences and
	- 3. add them up
- We will get a value that will be smaller than what we would get if we took the median or any other estimate of the "mid-point" of the data set

#### **Weighted means**

- Means represent the least squared estimate of the central tendency; say of ratings
- What if we also asked each subject to rate their ratings of grammaticality with a weight, wi
- This way those ratings with a higher weight will give a better estimate of the central tendency; confidence values
- The weights represent the confidence each rater has on her particular rating  $\boldsymbol{n}$

• Sample mean = 
$$
\bar{x} = \frac{\sum_{i=0}^{n} x_i}{n}
$$

• Weighted mean =  $\bar{x} = \frac{\sum_{i=0}^{n} w_i x_i}{\sum_{i=0}^{n} w_i}$  $\sum_{i=0}^{n} w_i$ 

- Population variance =  $\sigma^2 = \sum \frac{(x_i \mu)^2}{N}$
- Sample variance =  $s^2 = \sum \frac{(x_i \bar{x})^2}{n-1}$

#### **Measures of dispersion**

- The mean absolute deviation measures the absolute difference between the mean and each observation
- Absolute deviation could be one measure of difference, where absolute values of the difference for each  $x_i$  and sample mean,  $\bar{x}$  could be added
- We don't because the mean is the least squares estimator of central tendency
	- **–** so a measure of deviation that uses squared deviations is more comparable to the mean
	- **–** Sum of the squared deviations,  $d^2 = \sum_{i=0}^{n} (x_i \bar{x})^2$
- Variance
	- **–** We square the deviations before averaging them
	- **–** We have definitions for variance of a population and for a sample drawn from a larger population
	- **–** Notice that sample variance, 2 is calculated by dividing the sum of the squared deviations by n-1 and not n

#### **Why n-1**

- Generalize about the process but we only have access to the samples
- Relationship between scores, std. deviation and error
- Accurately talk about the population
	- **–** when we only have access to samples we divide by n-1
	- $-$  Taking (n-1) as the denominator in the definition of  $s^2$ , sample variance, because  $\bar{x}$  is not  $\mu$
	- **–** Sample mean  $\bar{x}$  is only an estimate of  $\mu$ , derived from the  $x_i$ , so in trying to measure variance we have to keep in mind that our estimate of the central tendency  $\bar{x}$  is probably wrong to a certain extent
- The mean of the underlying process (population) we don't know
- The mean of the n points we do, this however contains an error due to statistical noise
- Effect of the error is reduction in the calculated value of  $s^2$
- To make up for this, n is replaced by n-1
- *If n is large, the difference doesn't matter*
- *If n is small, this replacement provides a more accurate estimate of the standard deviation of the underlying process*

#### **Standard deviation**

- Variance is the average squared deviation the differences are squared
- To get to the original unit of deviation we take the square root of the variance; sample and population
- Aka, the RMS (root mean square) sample standard deviation
	- 1. first square the difference
	- 2. then take the mean and then
	- 3. square root of that
- Sample standard deviation

- 
$$
s = \sqrt{\sum \frac{(x_i - \bar{x})^2}{n-1}}
$$

- Area under the normal distribution is equal to 1
- Measures of the central tendency in terms of  $\bar{x}$  (sample mean) and also the sample standard deviation, s
- Normal distribution can be defined for any mean value  $\mu$ , and any standard deviation  $\sigma$
- This distribution is also used to calculate probabilities, where the total area under the curve is equal to 1
- That means that the area under any portion of the curve is equal to some proportion of 1
- This happens, when the mean of the bell-shaped distribution is 0 and the standard deviation is 1

$$
- f_x = \frac{1}{\sqrt{2\pi}} e^{-\frac{x^2}{2}}
$$

#### **Distributions**

- Throwing a six sided dice 20 times
- Let's note down all the 20 outcomes
- Drawing from a uniform distribution
- Sample distribution
- For every outcome count the number of times it appears

#### **Z-score and normalization**

- Two things to remember:
	- 1. Since the area under the normal distribution curve is 1, we can state the probability (area under the curve) of finding a value larger than any value of x, smaller than any value of  $x$ , or between any two values of x; relating individual scores to the normal distribution
- 2. Since, we can approximate our data with a normal distribution we can state these probabilities for our data given the mean and standard deviation; under the assumption that our data are normally distributed
- Relate the frequency distribution of our data to the normal distribution because we know the mean and standard deviation of both
- Key is to be able to express any value in a data set in terms of its distance in standard deviations from the mean
- z-score normalization,  $z_i = \frac{x_i \bar{x}}{s}$

```
#------- shade.tails -------------------
# draw probability density functions of t with critical regions shaded.
# by default the function draws the 95% confidence interval on the normal
# distribution.
#
# Input parameters
# crit - the critical value of t (always a positive number)
# df - degrees of freedom of the t distribution
# tail - "upper", "lower" or "both"
# xlim - the x axis range is -xlim to +xlim
shade.tails \le function(crit=1.96, df = 10000, tail = "both", xlim=3.5)
{
curve(dt(x,df),-xlim,xlim,ylab="Density",xlab="t")
ylow = dt(xlim, df)pcrit = pt(crit, df)caption = <math>past(\text{significant}(1-\text{pcrit},3))</math>if (tail == "both" | tail == "lower") {
    xx \leftarrow \text{seq}(-x \text{lim},-c \text{crit},0.05)yy \leftarrow dt(xx, df)polygon(c(xx,-crit,-xlim),c(yy,ylow,ylow),density=20,angle = -45)text(-crit-0.7,dt(crit,df)+0.02,caption)
}
if (tail == "both" | tail == "upper") {
    xx2 \leftarrow seq(crit, xlim, 0.05)yy2 \leftarrow dt(xx2, df)polygon(c(xx2,xlim,crit),c(yy2,ylow,ylow),density=20,angle = 45)
    text(crit+0.7,dt(crit,df)+0.02,caption)
}
}
```
## **Sampling from a uniform distribution**

- Storing outputs of functions in vectors
- Here, x, is a vector that stores the outout of the function *sample*

```
•
```

```
x \leftarrow sample(1:6,50,TRUE)hist(x)
```


```
Histogram of x
```
• Every time we run this code chunk the out of the sampling will change

 $x \leftarrow runif(10000, min = 1, max = 6)$  $hist(x)$ 

# **Histogram of x**



hist $(x, col = 'steelblue')$ abline( $v = mean(x)$ , lty = 1, lwd = 2)

**Histogram of x**



# **Uniform Distribution**

```
x_new <- rnorm(100)
hist(x_new, breaks=100000,col = 'steelblue')
abline(v = \text{mean}(x_new), lty = 2, lwd = 2)
```




# **Still Uniform Distribution**

```
x_new <- rnorm(1000)
hist(x_new, breaks=100000,col = 'steelblue')
abline(v = mean(x_new), lty = 2, lwd = 2)
```


## **Normal or Gaussian Distribution**

```
x_new <- rnorm(10000)
hist(x_new, breaks=100000,col = 'steelblue')
abline(v = mean(x_new), lty = 2, lwd = 2)
```
# **Histogram of x\_new**



**Increasing sampling in a normal or Gaussian Distribution**

```
x_new <- rnorm(100000)
hist(x_new, breaks=100000, col = 'steelblue')abline(v = mean(x_new), lty = 2, lwd = 2)
```




#### **Further increasing sampling in a normal or Gaussian Distribution**

```
x_new <- rnorm(1000000)
hist(x_new, breaks=100000,col = 'steelblue')
abline(v = mean(x_new), lty = 2, lwd = 2)
```


# **Increasing breaks now in a normal or Gaussian Distribution**

```
x_new <- rnorm(1000000)
hist(x_new, breaks=1000000,col = 'steelblue')
                                Histogram of x_new
      \frac{1}{2} 10 15
Frequency
      \overline{C}5
                                                              ШШ
                                                                    \mathbf{H}
```
Т

 $\circ$ 

 $\blacksquare$ 

ſ

 $\vert$ 



x\_new

−4 −2 0 2 4

Τ

Τ

**TININ II** I

**Getting some invariant parts of the sample: mean and standard deviation**

• Sum of x  $\sum x_i$ 

$$
- \sum x_i^2
$$

$$
- \sum x_i y_i
$$

- Mean of x  $\frac{1}{n} \sum_{i=i}^{n} x_i$
- StandardDeviation

$$
s = \sqrt{\frac{1}{n-1} \sum_{i=1}^{n} (x_i - \overline{x})^2}
$$

 $\sigma$  is the population parameter

• Variance =  $\sigma^2$ 

```
VOTk \le function(x) dnorm(x, mean = 100, sd = 10)
VOTp \leftarrow function(x) dnorm(x, mean = 120, sd = 25)
myYLim < -c(0, 0.04)myXlim < -c(0,140)plot(VOTk, from = 35, to = 160, ylim = myYLim, col="red",
     xlab="Voice Onset Time", myXlim)
plot(VOTp, from = 35, to = 200, add = TRUE, col="blue", ylim = myYLim, xlim=myXlim)
```


# **Plotting Vowels using PhonR**





# **Plotting Vowels using PhonR**

```
with(indo, plotVowels(f1, f2))
```


**Plotting Vowels using PhonR**





**Plotting Vowels using PhonR**

with(indo, plotVowels(f1, f2, var.sty.by = vowel, var.col.by = gender))



#### **Plotting Vowels using PhonR**

```
par(mfrow = c(1, 2))rounded <- ifelse(indo$vowel %in% c("o", "u"), "round", "unround")
with(indo, plotVowels(f1, f2, var.sty.by = gender, var.col.by = subj))
with(indo, plotVowels(f1, f2, var.sty.by = subj, var.col.by = rounded))
```


#### **Calculating vowel space areas**

```
poly.area <- with(indo, vowelMeansPolygonArea(f1, f2, vowel, poly.order = c("i",
    "e", "a", "o", "u"), group = subj))
hull.area <- with(indo, convexHullArea(f1, f2, group = subj))
rbind(poly.area, hull.area)
```
F02 F04 F08 F09 M01 M02 M03 poly.area 485051.4 337364.0 434816 302064.9 197746.1 229501.7 215713.3 hull.area 1254575.0 866109.5 1020835 751327.0 517212.5 666246.0 477518.5 M04 poly.area 177131.1 hull.area 568364.0

```
#par(mfrow = c(2, 2))with(indo, plotVowels(f1, f2, vowel, plot.tokens = TRUE, pch.tokens = vowel, cex.tokens = 1.3
   alpha.tokens = 0.2, plot.means = TRUE, pch.means = vowel, cex.means = 2, var.col.by = vow
   ellipse.line = TRUE, pretty = TRUE))
```


#### **Normalizing data**

- Speaker vocal tracts are variable different lengths and cross-sections
- Implies variable resonances
- $F_n = \frac{(2n-1)c}{4L}$ , for a tube that is open at one end and closed in the other

#### **Minimizing variation**

• In order to minimize the variation brought about by the variable vocal tract parameters, often we do a type of normalization that we call z-score normalization

### **Z-Score Normalization**

- This serves two purposes
	- 1. Allows us to reduce individual differences (between subjects)
	- 2. Makes data comparable
- Z-Score normalization

$$
\bullet\ z=\tfrac{x_i-\overline{x}}{\sigma}
$$

• Where  $\sigma = \sqrt{\frac{1}{n-1} \sum_{i=1}^{n} (x_i - \overline{x})^2}$ 

#### **Error in estimating population parameters**

- Two major sources of errors
	- 1. The underlying distribution
	- 2. The number of samples

• 
$$
SE = \frac{\sigma}{\sqrt{n}}
$$





# **Day 2**

#### **Normal distribution and standardization**

• With standardized values we can make probability statements

- In this figure, the area under the normal curve between -1.96 and 1.96 is 0.95.
- *95% of the values we draw from a normal distribution will be between 1.96 standard deviations below the mean and 1.96 standard deviations above the mean*



Figure 1: Z-score

#### **How normal**

- The normal distribution is a helpful way to describe data; Why? Because from this distribution, given a value, we can state the probability of its occurrence
- The normal distribution also provides a basis for making inferences about the accuracy of our statistical estimates.
- In data reduction, we use just the mean and standard deviation to describe the whole frequency distribution.
- It is important to find out whether or not the frequency distribution of our data is shaped like the normal distribution.
- First we will find out if our data are normally distributed, and then we'll look at a couple of transformations that we can use to MAKE data more normal

#### **Cherokee dataset**

#### **What is VOT**

- Voice Onset Time
- Duration of time it takes for regular voicing to get initiated following a stop into the vowel

#### **Cheroke VOT**

• VOT data Longitudinal data collected first in 1971 and then again 2001 Let's define two vectors that represent the two sets of data

vot01 = c(84, 82, 72,193, 129, 77, 72, 81, 45, 74, 102, 77, 187, 79, 86, 59, 74, 63, 75, 70, 106, 54, 49, 56, 58, 97) # And then vot71 =c(67, 127, 79, 150, 53, 65, 75, 109, 109, 126, 129, 119, 104, 153, 124, 107, 181, 166)

#The simplest way to means and standard deviations in R are to simply ask for them mean(vot01)#mean of the data set vot01, 84.65385

#### [1] 84.65385

mean(vot71)#mean of the data set vot71, 113.5

#### [1] 113.5

#### sd(vot01)

[1] 36.08761

sd(vot71)# We will get 36.08761 and 35.92844, respectively

#### [1] 35.92844

hist(vot01,freq=FALSE)#make a histogram by using probability densities and not the actual counts; #Getting help from R: type ?hist plot(function(x)dnorm(x, mean=84.654, sd=36.088), 40, 200, add=TRUE)#For 2001



# **Histogram of vot01**

vot01



**Histogram of vot71**



vot71

- We have two distributions; plot the frequency distribution as a histogram and then compare the observed distribution with the best-fitting normal curve
- Both the 2001 and the 1971 data sets are fairly similar to the normal curve
- The 2001 set has a pretty normal looking shape, but there are a couple of measurements at nearly 200 ms. that don't 'fit'.
- The 1971 set also looks like a normally distributed data set, though there are no observations between 80 and 100 ms in this data set. If these data came from a normal curve we would expect several observations in this range.
- Making things normal
- Let's see what happens if we remove the outliers from the 2001 dataset; does the fit get better? Let's assume that these outliers are caused due to speech errors for the moment
- Let's assume that the two VOT measurements in vot01 that are greater than 180 ms are outliers
- Calculate the mean and standard deviation for only those numbers in the vector that are less than 180

#### mean(vot01[vot01<180])

[1] 75.875

#### sd(vot01[vot01<180])

[1] 19.218

• **You must have good reasons for trimming data**

#### **q-q plots**

- Frequency distribution graphs give an indication of whether our data is distributed on a normal curve
- It would be nice to be able to measure just how "normally distributed" these data are
- Quantile means the fraction (or percent) of points/scores below the given value
- So the 0.3 (or 30%) quantile is the point at which 30% percent of the data fall below and 70% fall above that value.
- Quantiles are values that divide the distribution so that a given proportion of observations falls below the quantile. The median is a good example of a quantile.
- q-q plots: Measure the degree of fit between the data and the normal curve
- quantile/quantile plot are a correlation between
	- 1. the actual quantile scores and
	- 2. the quantile scores that are predicted by the normal curve
- The quantile-quantile (q-q) plot is a graphical technique for determining if two data sets come from populations with a shared distribution.
- Plot of the quantiles of the first data set against the quantiles of the second data set.
- The median is the central value of the distribution, such that half the points are less than or equal to it and half are greater than or equal to it.
- Quantiles are easily understood if you think about quartiles (3+ 1 Median);
- We use two tertiles to split data into three groups, four quintiles to split them into five groups, and so on.
- A 45-degree reference line is also plotted.
- If the two sets come from a population with the same distribution, the points should fall approximately along this reference line.
- Greater the departure from this reference line, the greater the evidence for the conclusion that the two data sets have come from populations with different distributions.
- Advantages of the q-q plot are:
	- 1. The sample sizes do not need to be equal.
	- 2. Many distributional aspects can be simultaneously tested
- Shifts in location, shifts in scale, changes in symmetry, and the presence of outliers can all be detected from this plot.
- If the two data sets come from populations whose distributions differ only by a shift in location, the points should lie along a straight line that is displaced either up or down from the 45-degree reference line.
- We expect our 71 data to be fairly normally distributed

 $vot71.qq = qqnorm(vot71)*x # make the quantile/quantile plot$ qqline(vot71) # put the line on the plot



**Normal Q−Q Plot**

Theoretical Quantiles

cor(vot71,vot71.qq) # compute the correlation

#### [1] 0.9868212

 $vot01.qq = qqnorm(vot01)*x # make the quantile/quantile plot$ qqline(vot01) # put the line on the plot



# **Normal Q−Q Plot**

cor(vot01,vot01.qq) # compute the correlation

#### [1] 0.8700187

- Departures from the straight line indicate departures from the specified distribution
- The 1971 data shows that there is a good fit between expected and actual quantiles; reflected in a correlation coefficient of 0.987 - almost a perfect 1
- Contrast this with the 2001 data
- Most of the data points in the 2001 data set are just where we would expect them to be in a normal distribution
- However, there are two or three large VOT values that are much larger than expected.
- Because of this the correlation between expected and observed quantiles for this data set ( $r =$ 0.87) is lower than what we found for the 1971 data.

### **Summary so far**

- We took two data sets and calculated their means and standard deviations
- We also learned how to manipulate data to see how we can remove outliers
- We compared the sample distributions to a theoretical distribution to see how well our data are correlated with the theoretical distribution
- We answered the question, "How normal are our data?"

# **Hypothesis testing**

- How to test hypotheses regarding means ...
	- 1. We can make probability statements about variables in normal distributions
	- 2. We can estimate the parameters of empirical distributions as the least squares estimates of  $\bar{x}$  and s
	- 3. Means of samples drawn from a population, fall in a normal distribution
	- 4. We can estimate the standard error (SE) of the normal distribution of  $\bar{x}$  values from a single sample.
- What this means is that we can make probability statements about means, and hence relate them to our hypotheses…let's start with Hypothesis 0, or the null hypothesis

### **H0:**  $\mu = 100$

- We want to make probability statements about observations using the normal distribution
- Remember, we converted our observation scores into z scores (the number of standard deviations different from the mean) using the z score formula.
- To test a hypothesis about the population mean  $(\mu)$  on the basis of our sample mean and the standard error of the mean we use a similar approach
- Big problem is !!! We don't know the population standard deviation.
- Instead, we estimate it with the sample standard deviation, and the uncertainty introduced by using s instead of σ means that we are off a bit and can't use the normal distribution to compare  $\bar{x}$  to  $\mu$ .
- To be a little more conservative, we use a distribution (or family of distributions), called the t-distribution
- Taking into account how certain we can be about our estimate of  $\sigma$ .
- Since, a larger sample size gives us a more stable estimate of the population mean, similarly we get a better estimate of the population standard deviation with larger sample sizes. So the larger the sample size, the closer the t distribution is to normal

#### **One-sample t-test**

- We use a slightly different distribution to talk about mean values, but the procedure is similar to using the normal distribution
- To make a probability statement about a z-score we refer to the normal distribution, and to make a probability statement about a t value we refer to the t distribution.
- It may seem odd to talk about comparing the sample mean to the population mean because we can easily calculate the sample mean but the population mean is not a value that we can know
- But, if we think of this as a way to test a hypothesis, then we have something.
- For example, with the Cherokee VOT data, we observed that  $\bar{x} = 84.7$  and  $s = 36.1$  for the stops produced in 2001
	- $\sim$  We can now ask whether the population mean  $\mu$  is different from 100. Plug the numbers into the formula.
- Here,  $s\bar{x}$  is the standard error

- 
$$
SE = s\bar{x} = \frac{\sigma}{\sqrt{N}}
$$
; population  
\n-  $SE = s\bar{x} = \frac{s_x}{\sqrt{n}}$   
\n-  $t = \frac{\bar{x} - \mu}{s\bar{x}} = \frac{84.7 - 100}{36.1/\sqrt{26}} = \frac{-15.3}{7.08} = -2.168$ 

#### **Interpreting t values**

- t value in this test is -2.168.
- But what does that mean?
- We were testing the hypothesis that the average VOT value of 84.7 ms is not different from 100 ms.
- This can be written as H0:  $\mu = 100$ .
- Meaning that the null hypothesis (the "no difference" hypothesis H0) is that the population mean is 100.
- Now we know that, observations that are more than 1.96 standard deviations away from the mean in a normal distribution are pretty unlikely - only 5% of the area under the normal curve.
- So this t value of -2.168 (-15.3 is a little more than 2 standard errors than the hypothesized mean) will be a pretty unlikely one to find if the population mean is actually 100 ms.
- The more likely conclusion that we could draw is that the population mean is less than 100.

## **Type of errors**

- We want to test the hypothesis (null) that the true Cherokee VOT in 2001 ( $\mu$ ) is 100ms by taking a sample from a larger population of possible measurements.
- If the sample mean  $\bar{x}$  is different enough from 100ms then we reject this hypothesis otherwise we accept it.
- How different is different enough?
- We can quantify the difference between the sample mean and the hypothesized population mean in terms of a probability.
- If the population mean is 100 ms, then only 2 times in 100 could we get a sample mean of 84.7 or less.
- Suppose we decide then that this is a big enough difference
- The probability of a sample of 84.7 mean coming from a population that has a mean of 100 ms is preedeetty low - so we reject the hypothesis that  $\mu = 100$  (let's call it H0)
- Instead, we accept the alternative hypothesis that  $\mu$  < 100 (call this H1; this is only one of several possible alternatives)
- H0:  $\mu = 100$  (Reject); H1:  $\mu$  < 100 (Accept)

### **Type of errors - Type I**

- But wait… 2 times out of 100 we will be **wrong** to reject the null hypothesis
- This error probability (0.02) is called the probability of making a type I error.
- A type I error is that we incorrectly reject the null hypothesis
- We claim that the population mean is less than 100, when actually we just got unlucky and happened to draw one of the 2 out of 100 samples for which the sample mean was equal to or less than 84.7.
- No matter what the sample mean is, we can't reject the null hypothesis with certainty because the normal distribution extends from negative infinity to positive infinity
- In practice, going with our best guess means choosing a type I error probability that we are willing to tolerate.
- Most often we are willing to accept a 1 in 20 chance (5 in 100, if you will) that we just got an unlucky sample that led us to make a type I error.
- This means that if the probability of the t value that we calculate to test the hypothesis is less than 0.05, we are willing to reject H0 ( $\mu$  = 100)
- And conclude that the sample mean comes from a population that has a mean that is less than  $100 \ (\mu < 100)$ .
- This criterion probability value ( $p<0.05$ ) is called the "alpha" α level of the test.
- The  $\alpha$  level is the acceptable type I error rate for our hypothesis test

#### **Type of errors - Type II**

- Where there is a type I error, there is a type II error as well
- A type II error occurs when we incorrectly accept the null hypothesis.
- Suppose we test the hypothesis that the average VOT for Cherokee (or at least this speaker) is 100 ms, but the actual true mean VOT is 95 ms.
- If our sample mean is 95 ms and the standard deviation is again about 35 ms we are surely going to conclude that the null hypothesis (H0:  $\mu = 100$ ) is probably true.
- At least our data is not inconsistent with the hypothesis because  $24\%$  of the time (p=0.24) we can get a t value that is equal to or less than -0.706.
- By accepting the null hypothesis we made a type II error. Just as we can choose a criterion  $\alpha$  level for the acceptable type I error rate, we can also require that our statistics avoid type II errors.
- The probability of making a type II error is called  $\beta$ , and the value we are usually interested in is 1-β, called the power of our statistical test

$$
- t = \frac{\bar{x} - \mu}{s\bar{x}} = \frac{95 - 100}{36.1/\sqrt{26}} = \frac{-5}{7.08} = -0.706
$$

• Preregistration of studies in linguistics and setting the power

## **t-tests in R**

```
t.test(vot01,mu=100, alternative="less")
```

```
One Sample t-test
```

```
data: vot01
t = -2.1683, df = 25, p-value = 0.01993
alternative hypothesis: true mean is less than 100
95 percent confidence interval:
     -Inf 96.74298
sample estimates:
mean of x
 84.65385
```
• In this t.test(), we entered the name of the vector that contains our data, the hypothesized population mean for these data, and that we want to know how likely it is to have a lower t value

# **Correlations**

- So far we have been looking at the statistical background assumptions that make it possible to test hypotheses about the population mean.
- The aim is to explain some of the key concepts that underlie studies of relationships among variables.
- One way to explore the relationship between two variables is by looking at counts in a contingency table.
- We have a data set of two measurements of the first formant (F1).
- We have F1 values for men and women for the vowels  $\pi i / \sqrt{e}$ ,  $\pi i / \sqrt{e}$ ,  $\pi i / \sqrt{e}$ , and  $\pi i / \sqrt{u}$  in four different languages
- Women tend to have shorter vocal tracts than men and thus have higher resonance frequencies. The average F1 of the women is 534.6 Hz and the average F1 for men is 440.9.
- We can construct a contingency table by counting how many of the observations in this data set fall above or below the mean on each of the two variables being compared.
- For example, we have the five vowels in Sele measured on two variables male F1and female F1 - and we are interested in studying the relationship or correlation between male and female F1 frequency.

```
F1_data <- read.csv("F1_data.csv", header = TRUE, sep=",")
attach(F1_data)
plot(female,male)
lines(x=c(mean(female),mean(female)), y=c(200,900),lty=2)lines(x=c(200,1100),y=c(mean(male),mean(male)),lty=2)
abline(lm(male~female))
```




- The grid lines mark the average female (vertical line) and male (horizontal line) F1 values. The diagonal line is the best fitting straight line (the linear regression) that relates female F1 to male F1
- If the male F1 falls below the average male F1, then the female F1 for that vowel will probably also fall below the average F1 for female speakers. In only one case does this relationship not hold.
- Contingency tables are a useful way to see the relationship, or lack of one, between two variables
- From this plot/table all we know is that if the male F1 is above average so is the female F1
- But we don't know whether they tend to be the **same amount above average** or if sometimes the amount above average for males is much more than it is for females. It would be much better to explore the relationship of these two variables without throwing out this information

		female F1	
		below	above
male F1	above		
	below	12	
		$\Box$	

Figure 2: Contingency table

- Here, we can see the four cells of the contingency table
- There are 6 data points in the upper right quadrant of the graph
- 12 data points in the lower left
- And 1 that just barely ended up in the lower right quadrant.
- These quadrants were marked in the graph by drawing a dashed line at the mean values for the male (441 Hz) and female (535 Hz) talkers.
- We can see, that the relationship between male and female F1 values goes beyond simply being in one quadrant of the graph or not.
- In fact, if we can divide the lower left and the upper right quadrants into quadrants again
- We would still have the relationship, higher male F1 is associated with higher female F1.
- **We need a measure of association that will give us a consistent indication of how closely related two variables are**
- Developing a measure of association between two variables is to measure deviation from the mean  $(x_i - \bar{x})$
- The association of male F1 and female F1 can be captured by seeing that when female F1 (let's call this variable x) was higher than the female mean, male  $F1(y)$  was also higher than the male mean.
- That means that if  $(x_i \bar{x})$  is positive
	- then  $(y_i \bar{y})$  is also positive
- The association is strongest when the **magnitudes of these deviations are matched**
- when  $x_i$  is quite a bit larger than the  $\bar{x}$  and  $y_i$  is also quite a bit larger than the  $\bar{y}$

#### **Correlations and covariance**

- The strength of the association can be gauged by multiplying the deviations
- If indeed is  $x_i$  quite a bit larger than  $\bar{x}$  and  $y_i$  is also much larger than  $\bar{y}$ 
	- then the product will be greater than if  $y_i$  is only a little larger than the  $\bar{y}$
- Also if  $x_i$  is quite a bit less than  $\bar{x}$  and  $y_i$  is also quite a bit less than  $\bar{y}$  the product will again be a large positive value
- Product of the deviations will be larger as we have a larger and larger data set,
- So we normalize this value to the size of the data set by taking the average of the paired deviations.
- This average product of the deviations is called the covariance of X and Y
- Sum of the product of the deviations,  $\sum_{i=0}^{n} (x_i \bar{x})(y_i \bar{y})$
- Covariance of x and y,  $\frac{\sum_{i=0}^{n}(x_i-\bar{x})(y_i-\bar{y})}{n}$
- The size of a deviation from the mean can be standardized so that we can compare deviations from different data sets on the same measurement scale.
- Deviation can be expressed in units of standard deviation with the z-score normalization.
- This is also done when we measure association as well.
- The correlation coefficient rxy is simply a scaled version of the sum of the product of the deviations using the idea that this value will be highest when x and y deviate from their means in comparable magnitude.
- **Correlation is identical to covariance, except that correlation is scaled by the standard deviations**
- While covariance can have any value, correlation ranges from 1 to -1 (perfect positive correlation is 1 and perfect negative correlation is -1)
- Correlation of x and y,  $\frac{\sum_{i=0}^{n} \frac{(x_i \bar{x})}{s_x} \frac{(y_i \bar{y})}{s_y}}{n} = \frac{\sum_{i=0}^{n} (z_x)(z_y)}{n} = r_{xy}$

# **Day 3**

# **The LM function**

summary(lm(male~female))

```
Call:
lm(formula = male ~ female)Residuals:
   Min 1Q Median 3Q Max
-70.619 -18.170 3.767 26.053 51.707
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) 47.59615 23.85501 1.995 0.0623 .
female 0.73564 0.04162 17.676 2.23e-12 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 37.49 on 17 degrees of freedom
Multiple R-squared: 0.9484, Adjusted R-squared: 0.9454
F-statistic: 312.4 on 1 and 17 DF, p-value: 2.23e-12
cor(male,female)
```
[1] 0.9738566

#### **Finding the best fitting line**

- Assuming we have a perfect correlation between x and y we can say that:
- $\cdot \frac{y_i \bar{y}}{s}$  $\frac{i-\bar{y}}{s_y} = \frac{\breve{x}_i-\bar{x}}{s_x}$  $\frac{i^{-x}}{s_x}$  Assuming deviations are equivalent, i.e.,  $r_{xy} = 1$
- Now we can predict the  $\hat{y}_i$ , estimating  $y_i$  from  $x_i$  when  $r_{xy} = 1$
- $\hat{y}_i = \frac{s_y}{s_x}$  $\frac{s_y}{s_x}(x_i - \bar{x}) + \bar{y}$
- Even if the correlation is not perfect (not equal to 1) we would like to get the predicted  $\hat{y}_i$
- The best prediction of  $z_x$  is  $r_{xy}$  times  $z_x$ , making our prediction of  $\hat{y}_i$
- $\hat{y}_i = r_{xy} \frac{s_y}{s_x}$  $\frac{s_y}{s_x}(x_i - \bar{x}) + \bar{y}$
- Now we can fit this into a line equation of the form:
	- **–** "slope-intercept", y = Bx +A
	- **–** Here, "B" is the slope and "A" gives the y-intercept
	- **–** Or where the line crosses the y-axis

# **T-test for two-samples**

#### **Comparing Cherokee VOTs from 1971 and 2001**

- Previously, we saw that we can test the hypothesis that a sample mean value x is the same as or different from a particular hypothesized population mean μ
- **The key question of interest** could be about comparison of two sample means; such as in the Cherokee 1971/2001 data
- **Is the mean VOT in 1971 different from the mean VOT in 2001, as the boxplot suggests**
- We want to test whether the average VOT in 1971 was equal to the average VOT in 2001
- We think that for this speaker there may have been a slow drift in the aspiration of voiceless stops as a result of language contact
- This question provides us with the null hypothesis that there was no reliable difference in the true, population, means for these two years - that is: H0:  $\mu$ 1971 =  $\mu$ 2001

vot <- read.delim("cherokeeVOT.txt") vot





# attach(vot) summary(vot)



```
# We need to treat year as a nominal variable and not a continuous variable
vot$year <- factor(vot$year)
summary(vot)
```

```
VOT year Consonant
Min. : 45.00 1971:18 Length:44
1st Qu.: 71.50 2001:26 Class :character
Median : 81.50 Mode : character
Mean : 96.45
3rd Qu.:120.25
Max. : 193.00
```

```
boxplot(VOT~year, data = vot, col="lightgrey", ylab = "Voice Onset Time (ms)")
```


year

```
library(ggplot2)
vot_bp<-ggplot(vot, aes(x=year, y=VOT)) + geom_boxplot(aes(fill = factor(year))) +
  ylab("VOTs from Cherokee") +
  theme(axis.text.x = element_text(size=20, face="bold"), axis.text.y = element_text(face="bold"),
        axis.title.x=element_blank(), axis.title.y = element_text(size=16, face="bold"))
vot_bp= vot_bp + theme(panel.background = element_rect(fill = "gray",colour = NA), legend.pos
vot_bp
```


#### **Testing our two-samples**

- We can test this hypothesis with a t- test similar to the "one sample" t-test that we discussed earlier
- There, we tested the null hypothesis: H0:  $\mu$ 1971 =  $\mu$ hyp
- We supplied the hypothesized population mean.
- The idea with the t-test is that we expect the difference between means to be zero
- The null hypothesis is that there is no difference
	- **–** and we measure the magnitude of the observed difference relative to the magnitude of random or chance variation we expect in mean values (the standard error of the mean)
- If the difference between means is large, more than about 2 standard errors (a t value of 2 or -2)
- We are likely to conclude that the sample mean comes from a population that has a different mean than the hypothesized population mean
- In testing whether the mean VOT in 1971 is different from the mean VOT in 2001 for this talker we are combining two null hypotheses:
	- **–** H0: μ1971 = μ
	- **–** H0: μ2001 = μ
	- **–** H0: μ1971 = μ2001
- In other words, the expected mean value of the 1971 sample is the same as the expected value of the 2001 sample
- Same as with a one-sample t-test the expected value of the difference is 0.
- Therefore we can compute a t statistic from the difference between the means of our two samples.
- **But, when we compare the two means in this computation of t. We have two samples of data; one from 1971 and one from 2001**
- We have *two estimates* of the standard error of the mean (SE). In calculating the t statistic we need to take information from both the 1971 data set and the 2001 data set when we compute the SE for this test.
- $t = \frac{\bar{x}_{1971} \bar{x}_{2001}}{SE}$ ; the two-sample *t* value
- We need to compute the SE for this test, and we have two SEs, one for 1971 and one for 2001
- **What is our estimate of the standard error of the mean?**
- With only one sample we used the standard deviation or the variance of the sample to estimate the standard error
- With two samples, there are two estimates of variance,  $s_{1971}^2$  and  $s_{2001}^2$
- If we can assume that these two represent essentially the same value then we can pool them by taking the weighted average as our best estimate of SE
- Before pooling the variances from our 1971 and 2001 samples we need to test the hypothesis that they do not differ
- This hypothesis can be tested using the F distribution
	- **–** a theoretical probability distribution that gives probabilities for ratios of variances
- If we want to know whether the two estimates of variance are equal to each other
- We can simply take their ratio and test the probability of this ratio, given the degrees of freedom that went into each variance estimate
- We are testing the hypothesis that  $H0=s_{1971}^2=s_{201}^2$
- $SE = \frac{s}{\sqrt{n}} = \sqrt{\frac{s^2}{n}}$  $\overline{n}$

#### **Establishing equal variance(s)**

- We do this with the F distribution because this distribution lets us specify degrees of freedom for the numerator and the denominator of the ratio
- The variances are not very different from each other (36.1 ms versus 35.9 ms)
- Also, the variances are very similar in magnitude
- Thus the F ratio is close to one
- $F = \frac{s_{2001}^2}{s_{1971}^2} = \frac{36.0876^2}{35.9284^2} = \frac{1302.32}{1290.85} = 1.0089$ , F-test of equality of variance
- We look up the probability of getting an F of 1.0089 or higher using the R pf() function
- In this function, we specify the F value, the degrees of freedom the numerator (n2001  $1 = 25$ ) and of the denominator  $(n1971 - 1 = 17)$
- We also specify that we are looking at the upper tail of the F distribution because, we put the larger of the two variances as the numerator.
- The probability of getting an F value of 1.0089 or higher when the variances are in fact equal is quite high p=0.5 so we have no reason to believe that the variance of the 1971 data is any different

from the variance of the 2001 data

pf(1.0089,25,17,lower.tail=F)

[1] 0.5034847

#### **Pooling variance**

- We can estimate SE for our test of whether VOT was different in 2001 than it was in 1971 by pooling the two sample variances
- This is done using the weighted average of the variances where each variance is weighted by its degrees of freedom.
- Let's calculate the weighted average of the pooled variances?

```
attach(vot)
```

```
The following objects are masked from vot pos = 4:
```
Consonant, VOT, year

```
pooled_variance=(var(VOT[year=="1971"])*17 + var(VOT[year=="2001"])*25) / (17+25)
pooled_variance
```
[1] 1297.676

- The pooled variance for our Cherokee VOT data is 1297.7 and hence the pooled standard deviation is  $s = 36.02$
- The t statistic that we use to compare two means uses the pooled variance from the two samples to estimate SE - the standard error of the mean(s), and t is a ratio of
	- 1. The difference between the two means  $\bar{x}_a \bar{x}_b$
	- 2. SE calculated from the pooled variance

$$
\bullet\ t=\tfrac{\bar{x}_a-\bar{x}_b}{\sqrt{\tfrac{s_p^2}{(n_a+n_b)}}}
$$

t.test(VOT[year=="1971"],VOT[year=="2001"], var.equal=TRUE, alternative="greater")

```
Two Sample t-test
```

```
data: VOT[year == "1971"] and VOT[year == "2001"]
t = 2.6116, df = 42, p-value = 0.006223
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
 10.2681 Inf
sample estimates:
mean of x mean of y
113.50000 84.65385
```
#### **Paired t-test**

- Naturally occurring pairs of observations
- F1 data for men and women for each language and vowel in the data set
- The male F1 of /a/ in Sele  $\sim$  the female F1 of /a/ in Sele
- The male F1 of /i/ in Sele  $\sim$  the female F1 of /i/ in Sele
- Men and women tend to have different vowel F1 frequency
- However, the difference between vowels can be bigger than the overall male/female difference
- To test the male/female difference we have to have a control for the vowel differences
- Pairing the male/female differences by vowel gives us this control
- Define a derived variable
- The difference between the paired observations,  $d_i = x_{ai} x_{bi}$
- Calculate the mean and variance of this difference such as for any other variable
- Test the null hypothesis there is no difference between the paired observations,  $H_0: d = 0$

attach(F1\_data)

The following objects are masked from  $F1$ <sup>data (pos = 6):</sup>

female, language, male, vowel

t.test(female, male, alternative="greater", var.equal = TRUE) # Two Sample t-test

Two Sample t-test

data: female and male  $t = 1.5356$ , df = 36, p-value = 0.06669

```
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
-9.323753 Inf
sample estimates:
mean of x mean of y
534.6316 440.8947
```
t.test(female, male, paired="TRUE", alternative="greater") # Paired t-test

Paired t-test

```
data: female and male
t = 6.1061, df = 18, p-value = 4.538e-06
alternative hypothesis: true mean difference is greater than 0
95 percent confidence interval:
 67.11652 Inf
sample estimates:
mean difference
       93.73684
```
#### **Paired test in comparison to two-samples**

- Paired t-tests help us remove systematic differences due to vowel or language influence
- This is because the F1 difference is immune to any vowel or language influences
- F1 variation due to language or vowel category is automatically controlled by taking paired F1 measurements from the same vowels spoken by speakers of the same language
- The paired t-test, due to the underlying controls, tends to be more sensitive compared to the two sample t test
- Comparing between the independent samples t-test and the paired t-test, the paired t-test gives us more reliable results
- True difference in means between males and females; controlled by vowel quality and language

# **Multiple regressions**

• X-ray Microbeam uses a narrow high-energy x-ray beam to track gold pellets attached to articulators while synchronously acquiring the physiological data. Not very portable: 15 tons. Gold pellets are secured by wires

- EMA (Electromagnetic Articulograph) consists of a helmet with three transmitters, microscopic sensor coils (which are attached to a subject's articulators such as the tongue, the jaw, and the lips), and a control computer
- These articulatory tracking systems tell us about speech production directly
- Tongue modeling; but without the root of the tongue
- Interpolation: Let us assume that we can use the data from the location of points on the top surface of the tongue to make predictions about the location of a point on the root of the tongue
- We have seen that we can define a regression line  $y = a + bx$
- This simple equation allows us to express a linear relationship that might exist between two variables
- We also have the ability to measure the strength of this linear association with the Pearson's correlation coefficient r
- Assume that each pellet that is placed on the tongue can take two variable positions, x and y; x representing the front-back axis and y representing the high-low axis
- So there are 30 variables in all. Why?
- Some highly correlated pellets can be seen
- A regression formula predicts 99.7% of the variance of pellet 14's y location if we know the y location of pellet 15
- Aside from predicting y-y relationships, we could also predict the xy location of one of the back pellets from one of the front pellets.
- The correlation between the y locations of pellet 1 and pellet 14 is  $r = 0.817$
- Highest correlation between the x location of pellet 14 and any of the front pellets is with the y location of pellet 6 ( $r = 0.61$ )
- We could keep looking into individual correlations (435 in all) and find out more about the predictions, but…that would become tedious



Figure 3: Tongue shape recorded in the x and y locations of the pellets for the corner vowels [i], [a], and [u]

- $y = a + b_1 x_1 + b_2 x_2 + \ldots + b_n x_n$
- We are working with the assumption that there are 15 points on the tongue that model the dynamic nature of the tongue
- Are these 15 adjacent points independent of each other; both statistically and physically?
- The question we are trying to answer: how many independent parameters of tongue movement are there?
- If we are able to identify the actually independent parameters/factors that influence the movement of the tongue, then we have successfully modeled the dynamic nature of the tongue
- There are many patterns that suggest some inter-relationships between the different x and y points and some of these could be causal
- Now we need to employ techniques that will help us unearth the nature of these relationships
- Let's take a close look at  $y = a + b_1x_1 + b_2x_2 + ... + b_nx_n$
- The above linear equation can be thought of expressing a complex relationship between y and parameters  $x_1...x_n$
- $x_{15} = -51.69 0.97y_5 + 1.05x_2 4.04x_6 + 4.66x_4 + 0.61y_2 3.69x_3 + 2.66x_5 + 1.48y_4$
- So a linear combination of some of the tongue pellet xy variables, produces an estimate of  $x_{15}$ that accounts for 98% of the variance of the x location of pellet 15
- Estimating  $\hat{y} = A + Bx$ , where A is the intercept and B is the slope
- Multiple regression is an extension of linear regression where the y position is estimated based on both  $x_i$  and  $y_i$  values and their corresponding coefficients

```
chain<-read.delim("chaindata.txt")
PL1<-subset(chain, talker=="PL1",x1:y15)
cor(PL1)
```








cov(PL1)









summary( $lm(y15 - y2 + y6 + y5 + x6 + x5$ , data = PL1))

Call:  $lm(formula = y15 - y2 + y6 + y5 + x6 + x5, data = PL1)$ 

Residuals:

23 24 25 26 27 28 29 30 31 32 -0.7107 -1.0186 0.6163 1.4168 0.3217 0.5271 -0.5677 -1.2789 1.2641 -0.7737 33 0.2036

```
Coefficients:
          Estimate Std. Error t value Pr(>|t|)
(Intercept) -16.8100 6.8275 -2.462 0.05708 .
y2 1.2785 0.1937 6.599 0.00120 **
y6 3.8458 0.6110 6.294 0.00149 **
y5 -4.1140 0.6104 -6.740 0.00109 **
x6 1.4703 0.8134 1.808 0.13048
x5 -1.1467 0.8165 -1.404 0.21919
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 1.304 on 5 degrees of freedom
Multiple R-squared: 0.9826, Adjusted R-squared: 0.9652
F-statistic: 56.46 on 5 and 5 DF, p-value: 0.000213
```
#### **Multiple regressions: Step by step**

# **Model selection**

- Regression coefficients can be found by using the lm() function
- That is the  $b_i$  values in the regression equation  $y = a + b_1x_1 + b_2x_2 + ... + b_nx_n$
- But how should we go about selecting a model that predicts the y
- Principle followed so far: predicting the root of the tongue from the top of the tongue
- This involves models that use some combination of the x and y locations of pellets 2, 3, 4, 5 and 6
- Using five pellets to predict the root of the tongue gives us 10 variables That is a whopping  $2^{10}$ regression models
- Why?
- The balance hangs between 1. high within-dataset accuracy on the one hand, and 2. high predictive accuracy for new data on the other
- More the number of parameters, more our ability to account for all the variation that is present in a set of data; that being said
- "Over-fitted" models or ones with too many predictors/parameters suffer from the problem of breaking down when new data are presented
- We want to find a model with few parameters and get as good a fit as possible with a minimum of predictive variables.
- For this, the step() function in R is used, which in turn uses the Akaike Information Criterion.
- This is a log-likelihood measure of model fitness that adds a penalty for each new parameter.
- Adding parameters incurs penalties, and so the predictions have to improve not by tiny increments but by large values for a new model with added parameters to be acceptable.
- Log-likelihood is similar to least-squares in terms of selecting a model that is the best fit.
- Recall, that the arithmetic average, i.e., the least-squares estimate of central tendency minimizes the squared deviations.
- A log likelihood estimate maximizes the likelihood of the model; is similar to least squares in that regard

#### **Likelihood of a Model**

- L(M) the likelihood of model M, has two terms
	- 1. Model fitness and the
	- 2. Model size, where nm is the number of coefficients in the regression equation
- $AIC = -2logL(M) + 2nm$
- step() is used to select a model to predict the y location of pellet 15 in the PL1chain data
- Let's say, step 1, the initial model has only one parameter the intercept value
- This is specified with  $y15~1$ .
- The second argument, is the largest model we would like to consider; i.e., has the xy locations for pellets 2,3,4,5,and 6.

summary(y.step <- step(lm(y15 ~ 1,data=PL1),y15~ x2+y2 + x3+y3+ x4+y4 + x5+y5+ x6+y6))

```
Start: AIC=43.74
v15 - 1
```


+ x5 1 105.75 383.08 43.054 + x3 1 93.55 395.28 43.399 <none> 488.82 43.735 + x6 1 56.78 432.05 44.377 Step: AIC=26.97 y15 ~ y2 Df Sum of Sq RSS AIC + y3 1 20.84 67.95 26.030 + y4 1 15.87 72.92 26.806 <none> 88.79 26.972  $+ y5 1 10.68 78.11 27.562$ + x2 1 2.83 85.96 28.616 + y6 1 2.10 86.69 28.709 + x4 1 1.78 87.01 28.750<br>+ x3 1 0.93 87.86 28.857 + x3 1 0.93 87.86 28.857 + x6 1 0.61 88.18 28.896 + x5 1 0.50 88.29 28.910 - y2 1 400.03 488.82 43.735

Step: AIC=26.03 y15 ~ y2 + y3



Step: AIC=20.9  $y15 - y2 + y3 + y6$ 





Step: AIC=17.83 y15 ~ y2 + y3 + y6 + y5



Step: AIC=11.98 y15 ~ y2 + y3 + y6 + y5 + x6



Step: AIC=10.83

y15 ~ y2 + y6 + y5 + x6



Step: AIC=9.17 y15 ~ y2 + y6 + y5 + x6 + x5



Call:

 $lm(formula = y15 - y2 + y6 + y5 + x6 + x5, data = PL1)$ 

Residuals: 23 24 25 26 27 28 29 30 31 32 -0.7107 -1.0186 0.6163 1.4168 0.3217 0.5271 -0.5677 -1.2789 1.2641 -0.7737 33 0.2036

Coefficients:

Estimate Std. Error t value Pr(>|t|) (Intercept) -16.8100 6.8275 -2.462 0.05708 . y2 1.2785 0.1937 6.599 0.00120 \*\* y6 3.8458 0.6110 6.294 0.00149 \*\* y5 -4.1140 0.6104 -6.740 0.00109 \*\* x6 1.4703 0.8134 1.808 0.13048 x5 -1.1467 0.8165 -1.404 0.21919  $---$ Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1 Residual standard error: 1.304 on 5 degrees of freedom Multiple R-squared: 0.9826, Adjusted R-squared: 0.9652 F-statistic: 56.46 on 5 and 5 DF, p-value: 0.000213

### **References**

Johnson, K. 2008. *Quantitative Methods in Linguistics*. Wiley. [https://books.google.co.in/books?id=](https://books.google.co.in/books?id=kJJpAAAAMAAJ) [kJJpAAAAMAAJ](https://books.google.co.in/books?id=kJJpAAAAMAAJ).

Winter, B. 2020. *Statistics for Linguists: An Introduction Using r*. Routledge. [https://books.google.co.](https://books.google.co.in/books?id=IXhpxQEACAAJ) [in/books?id=IXhpxQEACAAJ](https://books.google.co.in/books?id=IXhpxQEACAAJ).