Final cheat sheet data - Summary Data Science

Data Science (University of Sydney)

Module one

Cofounders

-to deal with cofounders into sub groups into subgroups

Observational vs-controlled studies

-controlled uses a treatment and control group and are allocated. Uses placebo(effect occurs when subject respond to the idea of the treatment) and bias. A observational study they two groups are not assigned, can establish association not causation.

Simpsons paradox

Sometimes there is a clear trend in individual groups of data that disappears when groups are pooled together

Histogram

Area of block =percentage of subjects

Height of block = % of block / length of class interval

Boxplot

-box is 50 percent of data (Q3-Q1= IQR)

Centre

Mean - good for symmetrical

Medium- robust therefore good for skewed data

For symmetrical data mean and medium are the same

For left skewed data mean is smaller than medium

For right skewed data mean is larger than medium

Spread

- -the mean gap must be 0 as the mean is the balancing point

Sd

- The standard deviation measures the **spread** of the data.

$$SD_{pop} = \text{RMS of (gaps from the mean)}$$

- Formally, $SD_{pop} = \sqrt{\text{Mean of (gaps from the mean)}^2} = \sqrt{\frac{\sum_{i=1}^{n}(x_i-\bar{x})^2}{n}}$

The area 1 SD from mean 0.68%

The area 2SD from mean is 0.95%

The area 3SD out from men is 0.997%

Population

RMS of gaps from the mean $\sigma = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(gaps)^2}$ `sd(data)*sqrt((n-1)/n))`

Sample

Adjusted RMS of gaps from the mean $s = \sqrt{\frac{1}{n-1}\sum_{i=1}^{n}(gaps)^2}$ `sd(data)`

Shortcut

$$SD = (\text{big} - \text{small})\sqrt{\text{proportion of big} \times \text{proportion of small}}$$

Standard zscore

Standard unit of data = how many sds it is below or below the mean

$$\text{Standard units} = \frac{\text{data point - mean}}{\text{standard deviation}}$$

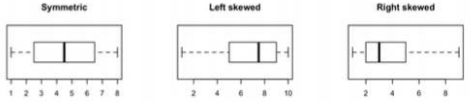
IQR

Range of middle 50 percent(Q3-Q1)

Q3= 75% Q1= 25%

Coefficient variant

$$CV = \frac{\text{mean}}{\text{standard deviation}}$$



Module 2

Normal curve

-use normal curve when histogram looked normal

Standard normal curve

-mean 0 and SD of 1

Special properties of curves

-satisfy the 68%,95% and 99.7%

-any general curve can be rescaled to standard curve

Measurement error

No matter how carefully any measurement is made, it could of turned out differently

Individual measurement = exact value + chance error

Chance error

The best way to estimate chance error is to replicate the measurement under the same conditions and calculate SD

Correlation coefficient

Measures clusters around a line

-1 <r< 1 the closer to -1 or 1 the more tightly points cluster

R =0 : points don't fit on a line

In R cor(x,y)

Properties

Symmetrical (changing variable wont effect) and scaling invariant (shifting variables wont effect)

R population = mean of the product of the variables in. S=

$$\frac{\text{data pt - mean(x)}}{\text{SD(x)}} \times \frac{\text{data pt - mean(y)}}{\text{SD(y)}}$$

Misleading conclusions

1)outliers overly influence

2)non-linear associations

3)rates of av tends to inflate the cor-coef

4)association is not causation

5)small sd makes the correlation look bigger

SD line

-on the point of av and plots line using SDs away from mean

Regression line

- **lm(y~x)**

SD Line	Regression Line
$(\bar{x}, \bar{y})$ to $(\bar{x}+SD_x, \bar{y}+SD_y)$	$(\bar{x}, \bar{y})$ to $(\bar{x}+SD_x, \bar{y}+rSD_y)$
$\frac{SD_y}{SD_x}$	$r\frac{SD_y}{SD_x}$

- **Predicting percentiles:** pnorm[qnorm(0.9)*cor(x,y)]
- **Predicting y value**: mean(y) + qnorm(0.9)*cor(x,y)*sd(y)

Graph of av

-plots the average y for each x

-the regression line is a smooth version

Predictions

1. Baseline p, given a certain value for x a basic prediction of y would be the av of y over all the x values
2. Prediction in a strip, given a certain value x, y would be the av of all the y values in the data corresponding to that x value
3. Regression line
4. Predicting percentile rates

Regression fallacy- test retest situations means changes in results is due to chance.

Residual plot

a residual plot is the vertical distance gap of points above and below regression line

- error = actual value – predicted value

CLT

The **Central Limit Theorem** (CLT) that a large sample size from a population with a finite level of [illegible] from the same [illegible] ual to the mean

RMS error

The RMS error represents the gap between points and the regression line

- **RMS Error (population)**

RMS of (gaps from the line) = $\sqrt{\text{mean of (gaps)}^2}$

- **Baseline Prediction**

$$\text{RMS error}_{Pop} = SD_y$$

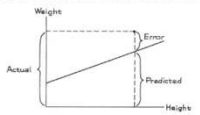
- **Normal Prediction**

$$\text{RMS error}_{Pop} = \sqrt{1-r^2}SD_y$$

Residual plot

Plots residuals vs x

If the linear fit is appropriate it should show no pattern



Vertical strips

equal spread in y direction data is homoscedastic and RMS can be used.

unequal spread the data is heteroscedastic and RMS cannot be used

Module 3 - chance

The prosecutor's fallacy

Assuming the prob of a random match is equal to the prob that the defendant is innocent

Basic properties of chance

1. Chances are between 0 – 100 %
2. The chance of something equals 100%- it's opposite

Conditional probability

Chance something occurs, given something else has occurred

$$P(\text{Event1}|\text{Event2})$$

Multiplication principal

The prob that two things occur is the chance of the 1st event multiples by the chance of the second

Addition rule

If the 2 things are mutually exclusive then the chance of at least 1 occurring is the sum of the individual chances

Mutually exclusive

2 things are mutually exclusive when the occurrence of the 1st event prevents the other

What	When	Formula	Condition
Addition Rule	P(At least 1 of 2 events occurs)	P(Event1) + P(Event2)	if mutually exclusive
Multiplication Rule	P(Both events occur)	P(Event1) x P(Event2)	if independent
		P(Event1) x P(Event2, given Event 1)	if dependent

Independence

P(2nd event|1st event) = p(2nd event), independent of the outcome of the 1st event

Drawing randomly with replacement is independent

2 things are independent if the product of their unconditional probabilities

Dependence

2 things are dependent if the chance of the second given the 1st is not the same as the 2nd, dependent of the outcome of the 1st event

Drawing without replacement ensures dependence.

Binomial model

$$\binom{n}{x}p^x(1-p)^{n-x}$$

binary trial is where 2 things can occur p = 1-p

binomial theorem is p at every trail is fixed and use equation

In R dbinom(x,n,p) where,

- X = number of heads
- N = total number of tosses
- P = probability of events

Chance variability/error

Observed = expected +chance error

As no. of tosses increase then the size of chance error increases and the absolute percentage size of chance decreases

Law of average

-States that the proportion of heads becomes more stable as the length of the simulation increases and approaches a -fixed number called the relative frequency

The chance error in the number of heads is likely to be large in absolute size, but small relative to no. of tosses

Box model

-mark1 on tickets you are counting

Replicate(N,sum(sample(box,n,rep=T) n=no.of draws N=replications

Parameter= fact about popEstimate = cal of sample values which predicts parameter

Sum of the Sample

Estimate:

$$EV_{sum} = \text{sample size} \times \text{mean}_{box}$$

Chance Error:

$$SE_{sum} = \sqrt{\text{sample size}} \times SD_{box}$$

Proportion in the Sample

Estimate:

$$EV_{proportion} = \text{population proportion} = \text{mean}_{box}$$

Chance Error:

$$SE_{proportion} = \frac{SD_{box}}{\sqrt{\text{sample size}}}$$

Correction Factor

$$SE_{withoutreplacement} = \text{correction factor} \times SE_{withreplacement}$$

where

$$\text{correction factor} = \sqrt{\frac{\text{number of tickets-number of draws}}{\text{number of tickets -1}}}$$

$$\text{correction factor} = \sqrt{\frac{\text{population size-sample size}}{\text{population size -1}}}$$

bootstrapping

is estimating properties of pop by using the properties of the sample

pop percentage ~ sample percentage

chance error

$$SE_{proportion} \approx \frac{SD_{box\ (with\ sample\ proportions)}}{\sqrt{\text{sample size}}}$$

Model 4

Hypothesis testing

The null hypothesis h0 assumes that the difference between OV and EV is due to chance alone

1 sided, specifies the change in expected by the treatment h1 p>0.5

2 sided does not specify the change expected by the treatment H1 cannot equal 0.5

Test statistic OV – EV / SE

P- value

Small <0.05 statistically different

The p value is a way of weighing up whether the sample is consistent with H0

Proportion test

HO any participants in the treatment group reporting an improvement is due to chance alone(Ho = 0,5)H1 improvement is due to treatment

Assumptions

Participants are independent of each other and chance of becoming desensitised is the same for all participants P test - >4.3

Accuracy of means

Ev mean = ev sum divided by number of draws

SE mean = Se sum divided by number of draws or sdbox divided by square root number of box

-CLT popbox is normally distributed

-The more skewed the bigger the sample size needs to be

Gauss model a measurement of error, different, tomake it unbiased we set the meanerrorbox = 0

Z test

Hypothesis

- **2 sided** → 2*pnorm(x)

H: H_0 : population mean $= c$ vs H_1 : population mean $\neq c$

- **One sided:**

H: H_0 : population mean $= c$ vs H_1 : population mean $< c$ (or $>$)

Assumptions: Sample is random. Know the population SD or the sample SD can estimate the population SD.
ONLY APPROPRIATE FOR LARGE SAMPLE SIZES FOR the CLT.

Test Statistic: uses normal curve

$$\text{T: Test statistic} = \frac{\text{observed mean - population mean}}{\frac{\text{population SD}}{\sqrt{n}}}$$

T-test

Hypothesis

H: H_0 : population mean $= c$ vs H_1 : population mean $\neq c$

Test statistic

P: Use t_{n-1} curve to find tail area for observed test statistic.

$$\text{T: Test statistic} = \frac{\text{observed mean - population mean}}{\frac{\text{sample SD}}{\sqrt{n}}}$$

2 Sample T-test

CODE: var.equal = T

Hypothesis:

Let μ_1 = mean heart rate of our control (no Red Bull)

Let μ_2 = mean heart rate of our treatment (Red Bull)

H_0 : There is no difference: $\mu_1 = \mu_2$

H_1 : There is a difference: $\mu_1 \neq \mu_2$

Assumptions:

- Two samples are **independent** (eg. treatments not on same person)
- **Normality:**
  - **Boxplot** → symmetry (if not, then diff spread)
  - **QQ Plot for Normality** → line formed by points should be straight
  - **Shapiro-Wilk Test for Normality** → p > 0.05 is normality
- **Same variation/spread**
  - **Levene's Test (F-test)** for equal spread → p > 0.05 is equal variance
    - H_0 : There is no difference: $\sigma_1^2 = \sigma_2^2$
    - H_1 : There is a difference: $\sigma_1^2 \neq \sigma_2^2$

T-statistic

$$\text{test statistic} = \frac{\mu_1 - \mu_2 - 0}{\text{standard error of the difference}}$$

Paired T-test

CODE: paired = T

- Non-Independence between two groups
- **Assumptions** for paired t-test: data of difference is normal (check using QQ plot)

Hypothesis

H_0 : The difference in means is zero : $\mu_d = 0$

H_1 : The difference in means is not zero : $\mu_d \neq 0$

Welch Sample T-test

CODE: var.equal = FALSE

- **Assumptions**: Unequal variance → Check variance by conducting Levene's Test (F-test)
  - p < 0.05 is unequal variance

Chi-squared Tests

Hypothesis

H_0: Model fits data vs H_1: Model doesn't fit data.

Test Statistic

$$\chi^2 = \text{Sum of}\left[\frac{(\text{Observed frequency - Expected frequency})^2}{\text{Expected frequency}}\right]$$

Types

1) **Goodness of Fit:** distribution of qualitative variable in a population

CODE: pchisq(x2, degrees of freedom, lower.tail = F)
Deg of freedom = no. of catergories – 1

2) **Homogeneity:** distribution of qualitative variable in several populations
3) **Independence:** test a hypothesis about the relationship between 2 qualitative variables in a population

CODE: chisq.test(data)
Deg of freedom = (m-1)*(n-1) (m = row, n = columns)