

Data/R

Data Visualization

geom_hist and geom_density distribution of numerical columns
geom_bar number of occurrences in a categorical col
geom_boxplot shape & distribution of numerical vars
geom_scatter + geom_line* numerical vs. numerical
geom_bar bar plot for count of categorical vars
geom_hline(yintercept) horizontal line
geom_vline(xintercept) vertical line
geom_abline(slope, intercept) linear function, requires
geom_segment straight line between (x, y) and (xend, yend)
geom_smooth plots a line/curve of best fit
*geom_line only makes sense with an ordering (e.g. the x-axis is year and observations connect together)

Data Manipulation

arrange(asc(col)) arranges col by ascending order
arrange(desc(col)) arranges col by descending order
relocate(data, col, .before, .after) relocates a column relative to its neighbors*
arrange(desc(col)) arranges col by descending order
slice(data, pos) indexes rows
bind_rows(df1, df2, ...) dfs w/ same columns, concats rows
bind_cols(df1, df2, ...) dfs w/ same # rows, concats cols, renames repeated cols
semi_join(x, y, by) returns rows from x w/ matching val for by in y
anti_join(x, y, by) returns rows from x w/o a match in y
full_join(x, y, by) standard outer join
left_join(x, y, by) standard left join, x is the left df
right_join(x, y, by) standard right join, y is the right df
*specifying no neighbors moves col to leftmost col, specifying both is error
Suppose we have the following table fish_encounters

fish	station	seen
4842	Release	1
4842	IS0.1	1
4842	Lisbon	1
4842	Rstr	1
4842	Base.TD	1
4842	BCE	1
4842	BCW	1
4842	BCE2	1
4842	BCW2	1
4842	MAE	1
4845	BCE	0

pivot_wider(fish_encounters, names_from = station, values_from = seen, values_fill = 0)

Fish	Release	IS0.1	Lisbon	Rstr	Base.TD	BCE	BCW	BCE2	BCW2	MAE
1	4842	1	1	1	1	1	1	1	1	1
2	4843	1	1	1	1	1	1	1	1	1
3	4844	1	1	1	1	1	1	1	1	1
4	4845	1	1	1	1	0	0	0	0	0

Suppose we have the following table billboard

artist	track	date.entered	wk1	wk2	wk3	wk4	wk5	wk6	wk7
2 Pac	Baby...	2000-02-26	87	82	72	77	87	94	99
2Ge+her	The ...	2000-09-02	91	87	92	NA	NA	NA	NA
3 Doors D...	Kryp...	2000-04-08	81	70	68	67	66	57	54
3 Doors D...	Loser	2000-10-21	76	76	72	69	67	65	55
504 Boyz	Wobb...	2000-04-15	57	34	25	17	17	31	36

pivot_longer(billboard, cols = starts_with("wk"), names.to = "week", names_prefix = "wk", values.to = "rank", values_drop_na = TRUE)

artist	track	date.entered	week	rank
2 Pac	Baby Don't Cry (Keep...	2000-02-26	1	87
2 Pac	Baby Don't Cry (Keep...	2000-02-26	2	82
2 Pac	Baby Don't Cry (Keep...	2000-02-26	3	72
2 Pac	Baby Don't Cry (Keep...	2000-02-26	4	77
2 Pac	Baby Don't Cry (Keep...	2000-02-26	5	87
2 Pac	Baby Don't Cry (Keep...	2000-02-26	6	94
2 Pac	Baby Don't Cry (Keep...	2000-02-26	7	99
2Ge+her	The Hardest Part Of ...	2000-09-02	1	91
2Ge+her	The Hardest Part Of ...	2000-09-02	2	87
2Ge+her	The Hardest Part Of ...	2000-09-02	3	92

Dates & Strings

ymd(), dmy(), ... converts string to datetime according to order of y-m-d
vdate(date) gets the day of the week for a given date
str_c(str1, str2, ...) concatenates strings/vectors of strings
str_detect(str, pattern) TRUE if ∃ a substring of str that matches pattern
str_extract(str, pat, group) finds 1st match in str for pat, group takes matched pattern, returns text matching group
str_extract_all(string, pattern) returns all matches to pattern
str_sub(string, start, end) indexes into string
str_count(string, pattern) count # of matches to pattern in string
str_replace(string, pattern, replacement), str_replace_all(string, pattern, replacement) - these exist
putting color, fill, alpha, etc. outside of aes(), i.e. typically inside of geom_x() functions will set it as a constant for the whole graph
putting color, fill, alpha, etc. inside of aes() typically implies you have a column in your df (like year) that sets the groups appropriately
every geom_x() function inherits the aes() from ggplot, unless they have their own aes() which overrides the ggplot
R always prints dates as YYYY-MM-DD

Regex

\d digits
\s whitespace
\w alphabetic and numeral
^ matches the start of each line
\$ matches the end of each line
? 0 or 1
+ 1 or more
* 0 or more
{n} exactly n
{n, } n or more
{n, m} between n and m
Capitalizing any of the above is the complement

You can also create your own character classes using []:

[abc] matches a, b, or c
[a-z] matches every character between a and z
[^abc] matches anything except a, b, or c
[\\^\\-] matches ^ or -

Parenthesis make groups which can be backreferenced
pattern <- "(.\\.\\.\\1)" #(.\\.\\. is some pair of anything, and 1 takes that same pair
fruit %>% str_subset(pattern)
"banana" "coconut" "cucumber" "jujube" "papaya" "salal berry"

Basic Probability

Probability Theory

For some random variable X , $E(X) = \sum_{x=0}^n x * P(X = x)$.
The expected value is just the sum of each outcome multiplied by its probability.
 $Var(X) = E((X - \mu)^2)$, $\mu = E(X)$
Again, this is just multiplying the squared difference of the mean from each observation with each observation's respective probability,
 $sum((x - mu)^2 * p)$.

Suppose that the distribution of X is proportional with the function $g(x) = 6 - |x - 5|$.
Say that we have outcomes 1, 2, . . . , 10, this means $P(X = x) = a(6 - |x - 5|)$.
We know that the total number of outcomes and number of current outcomes must be proportional to the function.
The way to make the number of outcomes proportional is to find $\sum_{i=1}^{10} 6 - |i - 5|$.

To keep the possible values proportional, each probability is $\frac{j}{\sum_{i=1}^{10} 6 - |i - 5|}$,

$j \in g(1), g(2), \dots, g(10)$.

Binomial Distributions

Properties of Binomials

b binary outcomes
i independence*
n fixed sample size
s same probability

Sampling w/o replacement violates this (when drawing from a set of outcomes you remove outcomes sampled).

Binomial Formulas

$\mu = np$ $\sigma^2 = np(1 - p)$
binom prob $P(X = k) = \binom{n}{k} p^k (1 - p)^{n-k}$

R Binomial Functions

rbinom(n, size, prob) random binomial samples
dbinom(x, size, prob) density fcn at x
qbinom(p, size, prob) get the smallest value in the qth quantile
pbinom(q, size, prob) $P(X \leq q)$
pbinom(q, size, prob, lower.tail = T) $1 - P(X \leq q) = P(X > q)$

Note that $\binom{n}{k} = \frac{n!}{k!(n-k)!}$

Normal Distributions

R Normal Functions*
pnorm(q, size, prob) $P(X < q)$
At any given x , $X \sim N(\mu, \sigma)$, $P(X = x) = 0$.
The standard normal is $X \sim N(0, 1)$.
Any normal has its z-scores as equivalent observations in the standard normal. In other words, $X \sim N(\mu, \sigma) \implies Z = \frac{X - \mu}{\sigma} \sim N(0, 1)$.

*includes rnorm(), qnorm() which have same functionality as the binom fcns
Suppose that $\exists X \sim Binom(n, p)$, with $np(1 - p) \geq 10$
Note the conditions this tests, p can't be too close to 0 or 1 (causes skew), and n must be sufficiently large (reduces variance).
We can approximate that binomial with $X \sim N(np, \sqrt{np(1 - p)})$.
Recall that this approximation isn't perfect, the normal has an effect of "cutting off" the binomial distribution.
Correct for this with $P(X \leq x + .5)$ wheing finding $P(X \leq x)$, $P(X \geq x - .5)$ when finding $P(X \geq x)$

As a general rule,
65% of data 1 SD from the mean
95% of data 2 SD from the mean
99% of data 3 SD from the mean

Inference

Inference on Proportions

Formulas (\hat{P} * is a random estimator for point estimate \hat{p}):

$Var(\hat{P})$ $Var(\frac{X}{n}) = \frac{Var(X)}{n}$
 $Var(X)$ $\frac{p(1-p)}{n}$
 $SE(\hat{p})$ $\sqrt{Var(\hat{P})}$
CI $\hat{p} \pm z * SE$
 z $qnorm(1 - \frac{\alpha}{2})^*$

* $\hat{P} \sim N(p, \sqrt{\frac{p(1-p)}{n}})$, this is still random

*where p is the desired conf interval
Agresti-Coull Method (use \tilde{p} in place of \hat{p})

\tilde{p} $\frac{\tilde{x} + 2}{n + 4}$
 $SE(\tilde{p})$ $\sqrt{\frac{\tilde{p}(1-\tilde{p})}{n + 4}}$
CI $\tilde{p} \pm z * SE$
 z $qnorm(1 - \frac{\alpha}{2})^*$

*where p is the desired conf interval
In theory this is a better estimate, still when SE is too small the CI can be too narrow.

Using \tilde{p} moves the estimate closer to .5.
When \tilde{p} is closer to 0 or 1 than p , SE tends to be underestimated, and vice versa for \tilde{p} closer to .5 than p .
Hypothesis testing - determine if a result we found was due to random chance

1. Have a binomial model
2. State H_0 and H_A
3. Choose test statistic
4. Find p-value and see if it's under some α^*

*Conventionally, we call $p < .05$ statistically significant and $p < .01$ highly statistically significant.
Assume H_0 is true. Now find probability we observed a certain outcome.
Suppose $H_0 | X \sim Binom(n, k)$ and $H_0 : k = .5$, $H_A : k \neq .5$. We observe j successes and n observations in total. Then p is $2 * pbinom(j, n, .5)$, since the probability distribution is symmetric and \neq necessitates a 2-sided test.
 H_0 also assumes a binomial distribution w/ chance of success being .5.
Findings are summarized in the following way: There is strong evidence ($p=0.0021$) , two-sided binomial test) that the chimpanzee in this experiment will make the pro-social choice more than half the time in the long run under similar experimental conditions.

Difference in Proportions

\tilde{p} $\frac{\tilde{x}_1 + \tilde{x}_2}{n_1 + n_2}$
 $SE(\tilde{p}_1 - \tilde{p}_2)$ $\sqrt{\frac{\tilde{p}(1-\tilde{p})}{n_1} + \frac{\tilde{p}(1-\tilde{p})}{n_2}}$
CI $\tilde{p} \pm z * SE$
 z $qnorm(1 - \frac{\alpha}{2})^*$

*where p is the desired conf interval
Agresti-Coffe Method (use \tilde{p} in place of \hat{p})

\tilde{p} $\frac{\tilde{x} + 1}{n + 2}$
 $SE(\tilde{p}_1 - \tilde{p}_2)$ $\sqrt{Var(\tilde{p}_1) + Var(\tilde{p}_2)}$
 $Var(\tilde{p}_i)$ $\frac{\tilde{p}_i * (1 - \tilde{p}_i)}{(n_i + 2)}$
CI $\tilde{p} \pm z * SE$
 z $qnorm(1 - \frac{\alpha}{2})^*$

Hypothesis Testing Difference in Proportions - determine if result was due to random chance

1. Have 2 binomial models
2. State H_0 and H_A
3. Choose test statistic
4. Find p-value and see if it's under some α

Say that $H_0 : p_1 - p_2 = 0$, $H_A : p_1 \neq p_2$. Say that the number of success is i_1 and i_2 respectively.

Since we test $p_1 - p_2$ the differences will be normally distributed.

Estimate the combined probability as $\bar{p} = \frac{i_1 + i_2}{n_1 + n_2}$.

Again, assuming H_0 is true calculate z . $z = \frac{(\tilde{p}_1 - \tilde{p}_2) - (p_1 - p_2)}{SE}$. THIS $p_1 - p_2$ IS THE $p_1 - p_2$ DEFINED BY H_0 .
 p is the area area under the standard normal, or $2 * P(X > z)$ in this case.

Inference on Means

Formulas:
CI $z * SE$
 z $qt(p, n - 1)$
 $SE(\bar{x})$ $\frac{s}{\sqrt{n}}$
 T $\frac{\bar{X} - \mu_0}{s / \sqrt{n}}$
 s $\sqrt{\frac{\sum_{i=1}^n (x_i - \bar{x})^2}{n - 1}}$

* μ_0 is the value assumed to be μ under H_0 . Interpret this as the # of SE above/below the mean of the null distribution.
The p value is the area under the t distribution WRT the T statistic, with $n - 1$ degrees of freedom.

WHEN FINDING THE CI OF ANY NORMAL/T DISTRIBUTIONS THE CRITICAL VALUE IS SOME QNORM/QT ACCORDING TO THE DESIRED CONFIDENCE LEVEL.

Inference on Multiple Means

Data can be paired or unpaired. Paired data is observations that are similar, and we are interested in differences between them.

For paired data:

Consider a new distribution of the differences in each pair of observations. Hypothesis testing, confidence intervals, etc. are exactly the same as inference on a single mean, just on the difference between means this time.

For unpaired data:

If the variance of the 2 distributions is similar, use the 2-sample:

$SE(\bar{X} - \bar{Y})$	$SE = \sqrt{\frac{\sum(x_i - \bar{x})^2 + \sum(y_i - \bar{y})^2}{n_x + n_y - 2}} \cdot \sqrt{\frac{1}{n_x} + \frac{1}{n_y}}$
Statistic	$t_{obs} = \frac{(\bar{X} - \bar{Y}) - (\mu_{X0} - \mu_{Y0})}{SE(\bar{X} - \bar{Y})}$
Degrees of freedom	$DF = n_x + n_y - 2$
Interval	$(\bar{X} - \bar{Y}) \pm t_{crit} * SE$

Welch when variance different:

$SE(\bar{X} - \bar{Y})$	$SE = \sqrt{\frac{s_x^2}{n_x} + \frac{s_y^2}{n_y}}$
Statistic	$t_{obs} = \frac{(\bar{X} - \bar{Y}) - (\mu_{X0} - \mu_{Y0})}{SE(\bar{X} - \bar{Y})}$
Degrees of freedom	$DF = \frac{(s_x^2/n_x + s_y^2/n_y)^2}{(s_x^2/n_x)^2/(n_x - 1) + (s_y^2/n_y)^2/(n_y - 1)}$
Interval	$(\bar{X} - \bar{Y}) \pm t_{crit} * SE$

Where $\mu_{X0} - \mu_{Y0}$ is the difference in means assumed under H_0 . p process is same as before, find area under t distribution according to H_a WRT the T statistic.

T Distributions

Recall the T statistic for inference on means.

$T = \frac{\bar{X} - \mu_0}{s/\sqrt{n}}$, notice that we use s , a point estimate for σ . This introduces randomness, so T is not quite normally distributed, so we use t distribution. The standard deviation is $\frac{d}{d-2}$, $d > 2$ where d is degrees of freedom. If $d \in \mathbb{Z}$, round it down. In practice, the t distribution converges to the normal as d increases. Still, it resembles a stretched normal.

Regression

Linear Regression

$y = \beta_0 + \beta_1 x_i + \epsilon_i$ ST the line minimizes the sum squared error.

Formulas:

$r = Corr(x, y) = \frac{1}{n-1} \sum_{i=1}^n \frac{x_i - \bar{x}}{s_x} \frac{y_i - \bar{y}}{s_y}$

$\hat{\beta}_1 = \frac{s_y}{s_x} r$

$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x}$

$\sigma(lm)$ extract SD of errors

$*r$ assumes x & y linearly related, measures strength of assumed relationship. The regression line always goes thru (\bar{x}, \bar{y}) .

If the residual graph is curved, $\bar{\epsilon} \neq 0$. If there's fanning out/narrowing in residual plot, $SE(\epsilon)$ is not constant.

Confidence intervals for $E(y | x^*)$

This is a confidence interval for the mean y given some x^* . For example, if there were infinite observations of x^* we would be $p\%$ confident they fall into a given range (you can also think of this as a confidence interval for points regression line passes thru).

$s_{\hat{y}} = \sqrt{\left((n-2)^{-1} \sum_{i=1}^n (y_i - \hat{y}_i)^2 \right) \left(n^{-1} + \frac{(x^* - \bar{x})^2}{\sum_{i=1}^n (x_i - \bar{x})^2} \right)}$

Prediction intervals for $E(y^* | x^*)$

This is a confidence interval for some random y^* . So not only do we account for uncertainty in β_0 and β_1 , we also have randomness in ϵ . Since, by nature observations have randomness baked in which is encoded by ϵ . As such, this interval is wider than the confidence interval.

Prediction interval is an interval that 95% of observations in the dataset will be in

$s_{\hat{y}^*} = \sqrt{\left((n-2)^{-1} \sum_{i=1}^n (y_i - \hat{y}_i)^2 \right) \left(1 + n^{-1} + \frac{(x^* - \bar{x})^2}{\sum_{i=1}^n (x_i - \bar{x})^2} \right)}$

Power Law

Sometimes a relationship can only be expressed as $y = C * x^\theta$, this is the power law.

In this case apply a log transform to the data, that way it is normal. Any models fit on this data will predict $log_l(y)$, however.

The regression line is trying to predict the mean for each observation. That is, each observation will have a bit of randomness, the regression line wants to capture the mean of all the hypothetical observations. So we say

$y_i \sim N(log_l(C) + \theta x_i, \sigma)$

To hypothesis test whether the power law is appropriate we carry out the following hypothesis test (assuming $\epsilon \sim N(0, \sigma)$):

$H_0 : \theta = 1, H_a : \theta \neq 1$. This is called a t-test for regression slope.

Hypothesis testing:

$T = \frac{\hat{\theta} - \theta_0}{\frac{s_{\hat{\theta}}}{\sqrt{\frac{\sum_{i=1}^n \epsilon_i^2 / (n-2)}{\sum_{i=1}^n (x_i - \bar{x})^2}}}}$

Use $n - 2$ degrees of freedom when doing inference on regression. This has the same process as inference on a single mean.

Specifics

Inference

For any type of inference dealing w/ difference, if

$H_a : u_1 \neq u_2 \equiv u_1 - u_2 < 0 \vee u_1 - u_2 > 0$.

If you find u_1 and u_2 are not the same you can say something about which is greater. If there are any transformations done to θ in the power law. For

example, $y = C * x^{-\theta}$, then the confidence intervals, etc. must reflect this. In practice, this involves multiplying the given x from the linear model by -1 .