027 - Final Review

EPIB 607

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slides compiled on December 2, 2021

Exam Details

- **When:** December 9, 2021. The exam will be made available on Crowdmark as of 9am EST for 24 hours.

- This is a timed assessment. As soon as you download the exam, you will have 6 hours to complete and upload your solutions to Crowdmark.

- **There will be a 5% per hour lateness penalty.** Submissions by e-mail will not be accepted.

- This is an open book exam. Any material on myCourses (EPIB607/613) and personal notes are permitted.

- You are not permitted to use the internet and you must work alone. Using the internet or obtaining help from anyone else is considered Cheating as per Article 17 of the Code of Student Conduct and Disciplinary Procedures

- Provide units and state your assumptions when applicable. Label axes and write answers in complete sentences when appropriate.

- The format of the exam will follow the assignments and the midterm. That is, you will be required to complete a series of questions in an RMarkdown document and knit to pdf. Your solutions for each question must then be uploaded to Crowdmark. A template will be provided which will also include the questions.

Topics to be covered

Note that the exam is cumulative

1. Data visualization (histograms, boxplots, scatterplots, line plots), Tidy Data, Color Palettes, grammar of graphics

2. Descriptive statistics (mean, median, range, IQR, sd, correlation)

3. Normal Curve Calculations, Sampling Distributions, CLT, Bootstrap

4. Confidence intervals, Hypothesis Testing, p-values

5. One sample mean, one sample proportion, one sample rate

6. Power and Sample size calculations

7. Gaussian, Poisson, Binomial regression

8. Permutation testing

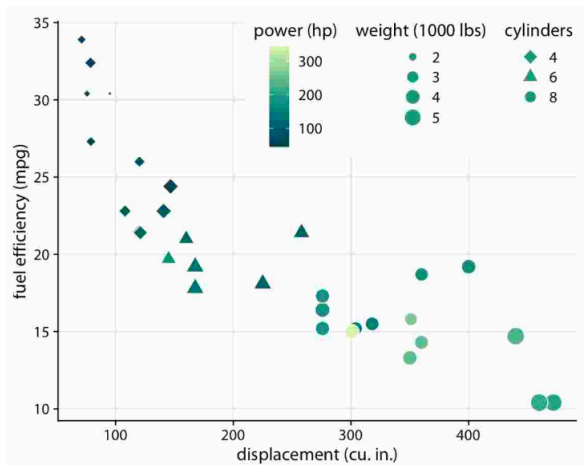9. χ^2 goodness of fit and ROC curves

Aesthetics

- Aesthetics
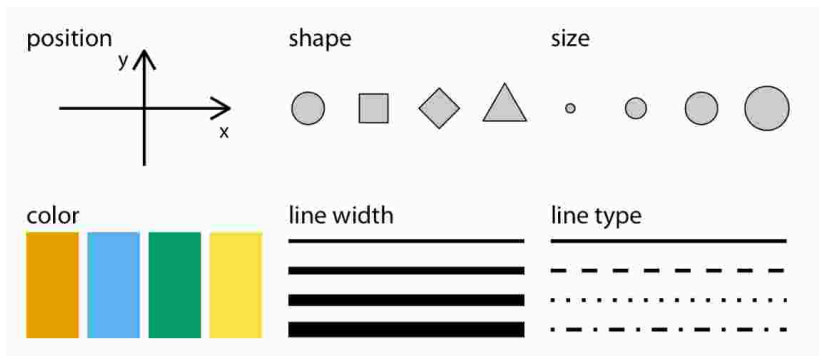
- Commonly used aesthetics in data visualization: position, shape, size, color, line width, line type. Some of these aesthetics can represent both continuous and discrete data (position, size, line width, color) while others can only represent discrete data (shape, line type)

Types of Graphs

- Review the types of graphs created in the assignments.
- You should be able to critique a graph and propose appropriate graphics for a given dataset. Be mindful of the research question. The graphic should try to answer the research question.
- `https://serialmentor.com/dataviz/directory-of-visualizations.html`
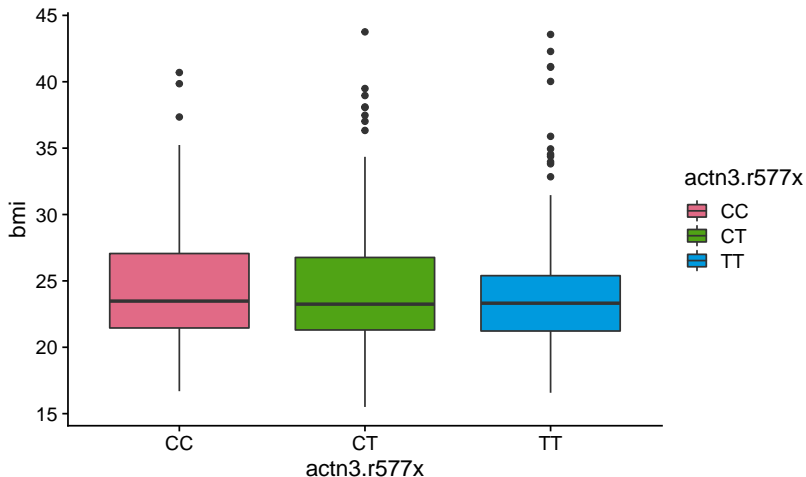- `https://www.data-to-viz.com/`

How many scales are being used?
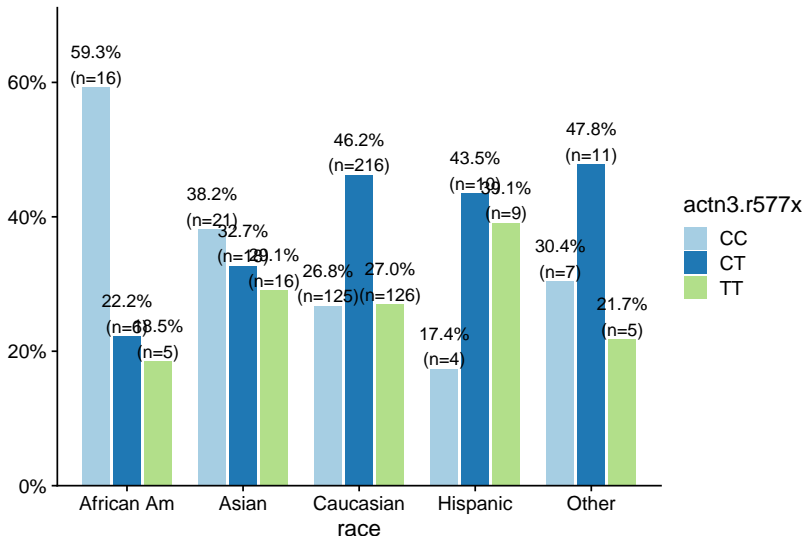
Boxplots with qualitative palette

```
library(oibiostat); data("famuss")
library(ggplot2)
library(colorspace)

ggplot(famuss, aes(x = actn3.r577x, y = bmi, fill = actn3.r577x)) +
geom_boxplot() +
colorspace::scale_fill_discrete_qualitative()
```
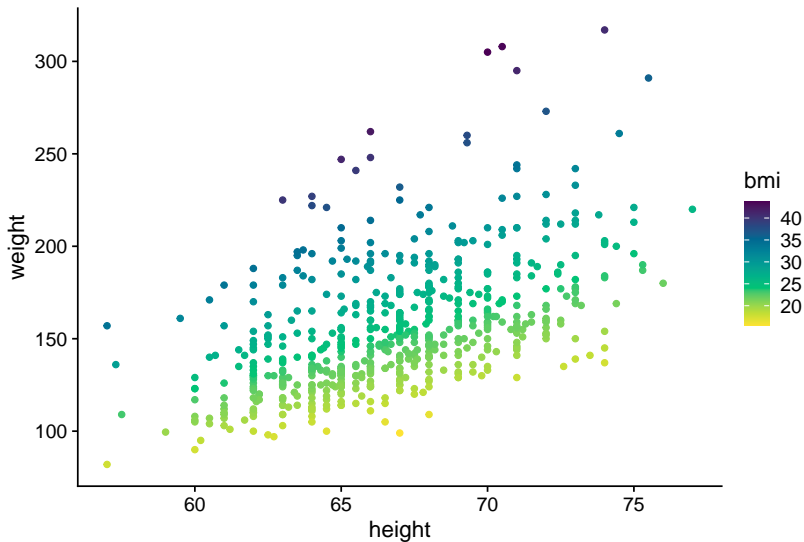
Conditional distribution of genotype *given* race

```
sjPlot::plot_xtab(famuss$race, famuss$actn3.r577x, margin = "row")
```

Scatter plots with sequential palette

```
ggplot(famuss, aes(x = height, y = weight, color = bmi)) +
geom_point() +
colorspace::scale_color_continuous_sequential(palette = "Viridis")
```

Variable Types

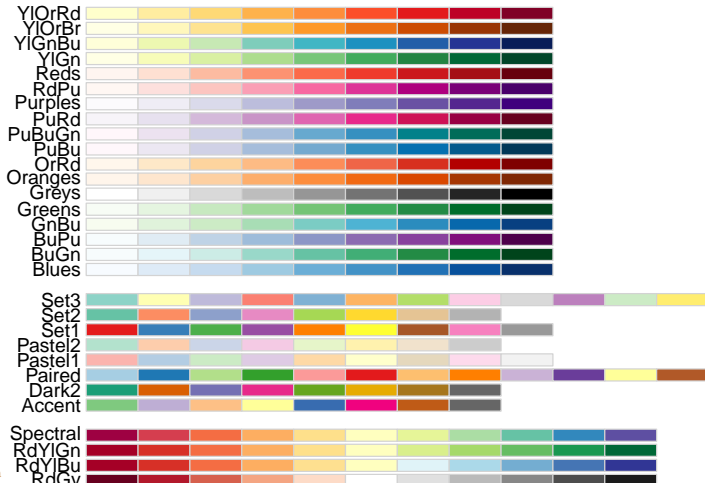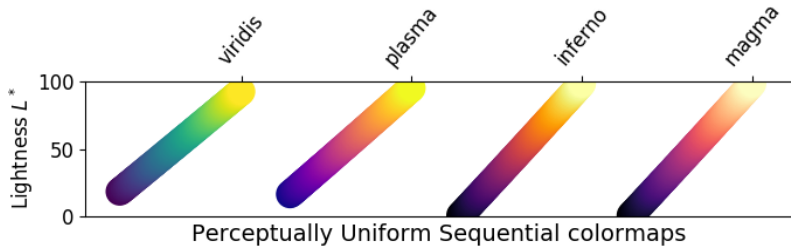- quantitative/numerical continuous (1.3, 5.7, 83, 1.5×10^{-2})

- quantitative/numerical discrete (1,2,3,4)

- qualitative/categorical unordered (dog, cat, fish)

- qualitative/categorical ordered (good, fair, poor)

Color Palettes: Cynthia Brewer

```
pacman::p_load(RColorBrewer)
RColorBrewer::display.brewer.all()
```

Color Palettes: viridis

Perceptually Uniform Sequential colormaps

Tidy data

- Each variable forms a column.
- Each observation forms a row.
- Each type of observational units forms a table
- Tidy data is ready for regression routines and plotting

variables   observations   values

Example: Does a full moon affect behaviour?

- Many people believe that the moon influences the actions of some individuals.

- A study of dementia patients in nursing homes recorded various types of disruptive behaviors every day for 12 weeks.

- Days were classified as moon days if they were in a 3-day period centered at the day of the full moon.

- For each patient, the average number of disruptive behaviors was computed for moon days and for all otherdays.

patient	moon_days	other_days
1	3.33	0.27
2	3.67	0.59
3	2.67	0.32
4	3.33	0.19
5	3.33	1.26
6	3.67	0.11
7	4.67	0.30

Not tidy vs. tidy data

patient	moon_days	other_days
1	3.33	0.27
2	3.67	0.59
3	2.67	0.32
4	3.33	0.19
5	3.33	1.26

patient	day_type	mean_behavior
1	moon_days	3.33
1	other_days	0.27
2	moon_days	3.67
2	other_days	0.59
3	moon_days	2.67
3	other_days	0.32
4	moon_days	3.33
4	other_days	0.19
5	moon_days	3.33
5	other_days	1.26

Not tidy vs. tidy data

patient	moon_days	other_days
1	3.33	0.27
2	3.67	0.59
3	2.67	0.32
4	3.33	0.19
5	3.33	1.26

Not tidy

tidy

patient	day_type	mean_behavior
1	moon_days	3.33
1	other_days	0.27
2	moon_days	3.67
2	other_days	0.59
3	moon_days	2.67
3	other_days	0.32
4	moon_days	3.33
4	other_days	0.19
5	moon_days	3.33
5	other_days	1.26

tidyr::pivot_longer()

patient	moon_days	other_days
1	3.33	0.27
2	3.67	0.59
3	2.67	0.32
4	3.33	0.19
5	3.33	1.26

key   value

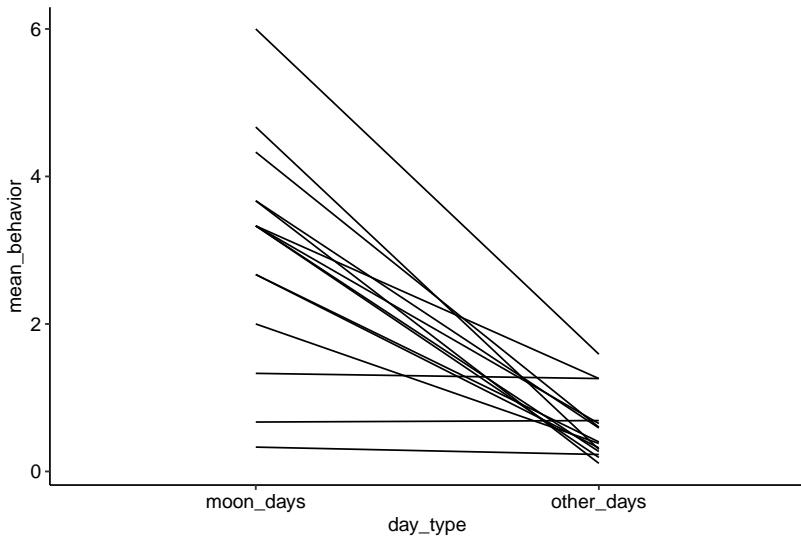| patient	day_type	mean_behavior
1	moon_days	3.33
1	other_days	0.27
2	moon_days	3.67
2	other_days	0.59
3	moon_days	2.67
3	other_days	0.32
4	moon_days	3.33
4	other_days	0.19
5	moon_days	3.33
5	other_days	1.26
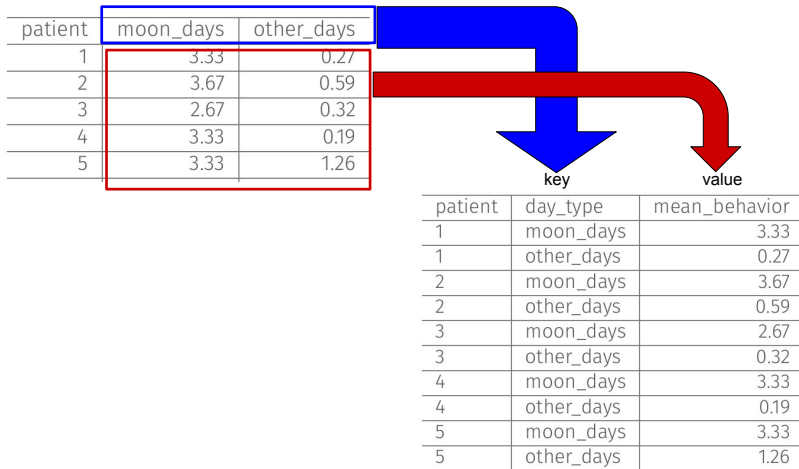
```
tidyr::pivot_longer(data = df, cols = -patient, names_to = "day_type", values_to = "mean_behavior")
```

Plotting with tidy data

```
ggplot(data = df_tidy, mapping = aes(x = day_type, y = mean_behavior, group = patient)) + geom_line()
```

Regression with tidy data

```
fit <- lme4::lmer(mean_behavior ~ day_type + (1|patient), data = df_tidy)
summary(fit)

## Linear mixed model fit by REML ['lmerMod']
## Formula: mean_behavior ~ day_type + (1 | patient)
##    Data: df_tidy
##
## REML criterion at convergence: 90.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2728 -0.3014 -0.0408  0.4860  2.4482
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  patient  (Intercept) 0.1559   0.3948
##  Residual             1.0663   1.0326
## Number of obs: 30, groups:  patient, 15
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           3.0220     0.2854  10.587
## day_typeother_days   -2.4327     0.3771  -6.452
##
## Correlation of Fixed Effects:
##             (Intr)
## dy_typthr_d -0.660
```

Example: Is it tidy?

Mode of Delivery	Covariate			No. of Mother–Child Pairs	No. of HIV-1–Infected Children
	No. of Periods of Antiretroviral Therapy	Advanced Maternal Disease	Low Birth Weight of Infant (<2500 g)		
Elective cesarean	0	No	No	372	30
Other	0	No	No	3850	652
Elective cesarean	0	Yes	No	28	5
Other	0	Yes	No	303	74
Elective cesarean	0	No	Yes	110	17
Other	0	No	Yes	767	196
Elective cesarean	0	Yes	Yes	27	4
Other	0	Yes	Yes	114	40
Elective cesarean	1 or 2	No	No	41	0
Other	1 or 2	No	No	441	49
Elective cesarean	1 or 2	Yes	No	23	3
Other	1 or 2	Yes	No	186	33
Elective cesarean	1 or 2	No	Yes	7	0
Other	1 or 2	No	Yes	83	22
Elective cesarean	1 or 2	Yes	Yes	10	3
Other	1 or 2	Yes	Yes	54	19
Elective cesarean	3	No	No	124	2
Other	3	No	No	878	49
Elective cesarean	3	Yes	No	34	1
Other	3	Yes	No	208	24
Elective cesarean	3	No	Yes	25	0
Other	3	No	Yes	109	11
Elective cesarean	3	Yes	Yes	8	1
Other	3	Yes	Yes	38	6

Descriptive statistics

- Boxplots, histograms, density plot

- IQR, median, mode, mean, min, max, range

- Q1, Q3

- Skewness (long left/right tail)

- Correlation

Descriptive stats by group

```r
library(oibiostat); data("famuss")
library(dplyr)

famuss %>%
dplyr::group_by(actn3.r577x) %>%
dplyr::summarise(mean_bmi = mean(bmi),
sd_bmi = sd(bmi))

## # A tibble: 3 x 3
##   actn3.r577x mean_bmi sd_bmi
##   <fct>          <dbl>  <dbl>
## 1 CC              24.5   4.41
## 2 CT              24.5   4.55
## 3 TT              24.2   4.81
```

Subsetting data

```r
library(oibiostat); data("famuss")
library(dplyr)

f.male <- famuss %>%
dplyr::filter(sex == "Male")


f.male.cauc <- famuss %>%
dplyr::filter(sex == "Male" & race == "Caucasian")

f.bmi.low <- famuss %>%
dplyr::filter(bmi <= 23)
```

Standard error (SE) of a sample statistic

- Recall: When we are talking about the variability of a **statistic**, we use the term **standard error** (not standard deviation). The standard error of the sample mean is $\sigma/\sqrt{n}$.

> **Remark 1 (SE vs. SD).**
>
> *In quantifying the instability of the sample mean ($\bar{y}$) statistic, we talk of SE of the mean (SEM)*
>
> *$SE(\bar{y})$ describes how far $\bar{y}$ could (typically) deviate from μ;*
>
> *$SD(y)$ describes how far an individual y (typically) deviates from μ (or from $\bar{y}$).*

ggplot2 to make plots

- ggplot provides you with a set of tools to map data
  1. to visual elements on your plot
  2. to specify the kind of plot you want, and
  3. then subsquently to control the fine details of how it will be displayed.

Aesthetic mappings

1. Tidy Data

```
p ← ggplot(data = gapminder, ...
```

gdp	lifexp	pop	continent
340	65	31	Euro
227	51	200	Amer
909	81	80	Euro
126	40	20	Asia

2. Mapping

```
p ← ggplot(data = gapminder,
           mapping = aes(x = gdp,
           y = lifexp, size = pop,
           color = continent))
```

- The code you write specifies the connections between the variables in your data, and the colors, points, and shapes you see on the screen.
- In ggplot, these logical connections between your data and the plot elements are called *aesthetic mappings* or just *aesthetics*.
- You begin every plot by telling the `ggplot()` function what your data is, and then how the variables in this data logically map onto the plot's aesthetics.

Geometry


```
        2. Mapping
p ← ggplot(data = gapminder,
           mapping = aes(x = gdp,
           y = lifexp, size = pop,
           color = continent))
        3. Geom




p + geom_point()
```

- Then you take the result and say what general sort of plot you want, such as a scatterplot, a boxplot, or a bar chart. In ggplot, the overall type of plot is called a geom.

- Each geom has a function that creates it. For example, geom_point() makes scatterplots, geom_bar() makes barplots, geom_boxplot() makes boxplots, and so on.

- You combine these two pieces, the ggplot() object and the geom, by literally adding them together in an expression, using the "+" symbol.

Customization

4. Co-Ordinates & Scales

```
p + coord_cartesian() +
    scale_x_log10()
```
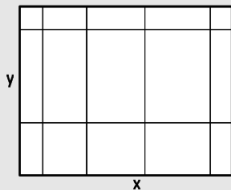
- At this point, ggplot will have enough information to be able to draw a plot for you. ggplot will use a set of defaults that try to be sensible about what gets drawn.

- But more often, you will want to specify exactly what you want, including information about the scales, the labels of legends and axes, and other guides that help people to read the plot.

- Each component has it own function, you provide arguments to it specifying what to do, and you literally add it to the sequence of instructions.

- In this way you systematically build your plot piece by piece.

Customization
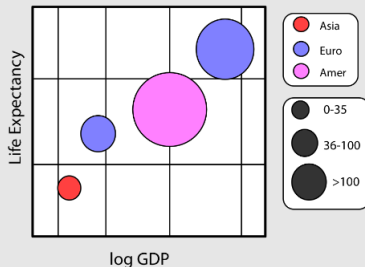
Probability function

- The probability function of a random variable is defined for any value that the random variable may obtain and produces the **distribution** of the random variable. The probability function may emerge as a relative frequency as in the given example or it may be a result of theoretical modeling.

- Consider the following probability distribution:

Value	Probability	Cum.Prob
0	0.50	0.50
1	0.25	0.75
2	0.15	0.90
3	0.10	1.00

- What is $P(Y = 0)$, the probability that Y is equal to 0?:

- What is the probability of Y falling in the interval $[0.5, 2.3]$?

Expectation

- The average of the data can be computed as the weighted average of the values that are present in the data, with weights given by the relative frequency. Specifically, for the data

$$1, \ 1, \ 1, \ 2, \ 2, \ 3, \ 4, \ 4, \ 4, \ 4, \ 4,$$

the mean can be calculated via

$$\bar{y} = \frac{1 + 1 + 1 + 2 + 2 + 3 + 4 + 4 + 4 + 4 + 4}{11}$$
$$= 1 \times \frac{3}{11} + 2 \times \frac{2}{11} + 3 \times \frac{1}{11} + 4 \times \frac{5}{11}$$

producing the value of $\bar{y} = 2.727$ in both representations.

- Using a formula, the equality between the two ways of computing the mean is given in terms of the equation:

$$\bar{y} = \frac{\sum_{i=1}^{n} y_i}{n} = \sum_{y} \left(y \times (f_y/n) \right) ,$$

where f_y represents the frequency of y in the data.

Expectation

- Using a formula, the equality between the two ways of computing the mean is given in terms of the equation:

$$\bar{y} = \frac{\sum_{i=1}^{n} y_i}{n} = \sum_y \left(y \times (f_y / n) \right) ,$$

  where f_y represents the frequency of y in the data.

- The expectation of a random variable is computed in the spirit of the second formulation, and is define via the equation:

$$E(Y) = \sum_y \left(y \times P(y) \right) .$$

Variance

- The sample variance (s^2) is obtained as the sum of the squared deviations from the average, divided by the sample size (n) minus 1:

$$s^2 = \frac{\sum_{i=1}^{n}(y_i - \bar{y})^2}{n-1} \ .$$

- A second formulation for the computation of the same quantity is via the use of relative frequencies. The formula for the sample variance takes the form

$$s^2 = \frac{n}{n-1} \sum_y \left((y - \bar{y})^2 \times (f_y/n)\right) \ .$$

- In a similar way, the variance of a random variable may be defined via the deviation from the expectation. This deviation is then squared and multiplied by the probability of the value. The multiplications are summed up in order to produce the variance:

$$\mathrm{Var}(Y) = \sum_y \left((y - \mathrm{E}(Y))^2 \times \mathrm{P}(y)\right) \ .$$

Expected value for a discrete RV

Definition 1.

Let Y be a discrete random variable with set of possible values $D = \{y_1, y_2, \ldots, y_k\}$ and corresponding probabilities for each value, e.g., y_1 with probability $P(y_1)$, y_2 with probability $P(y_2)$, y_3 with probability $P(y_3)$, ..., y_k with probability $P(y_k)$. Furthermore, let $g(Y)$ be some real-valued function of Y. Then the expected value of $g(Y)$ is:

$$E(g(Y)) = \sum_{y \in D} g(y) \times P(y) \ .$$

i.e. it is a weighted mean of the $g(y)$'s, with $P(y)$'s as weights.

A sum of n random variables

- Up to now, to keep things general, we used n non-identical – but independent – random variables. If we consider the Variance and the sum of n **identical** – and independent – random variables, so the n Variances (each abbreviated to Var) are all equal, the laws simplify:

- First, since the variances add, we have that

$$\text{Var}(RV_1 + RV_2 + \cdots + RV_n) = \text{Var}_1 + \text{Var}_2 + \cdots + \text{Var}_n = n \times \textit{each} \text{ Var}.$$

- Taking square roots,

$$SD(\, RV_1 + RV_2 + \cdots + RV_n \,) = \sqrt{n \times \text{ each Var}} = \sqrt{n} \times \text{ each } SD$$

-
$$SD\left(\frac{RV_1 + RV_2 + \cdots + RV_n}{n}\right) = \frac{\sqrt{n} \times \text{ each } SD}{n} = \frac{\text{common } SD}{\sqrt{n}}$$

-
$$\text{Var}\left(\frac{RV_1 + RV_2 + \cdots + RV_n}{n}\right) = \frac{\text{common Var}}{n}$$

Difference of 2 Random Variables via Simulation

```r
set.seed(12)
B <- 999; N <- 200
var_diff <- replicate(B, {
RV1 <- rnorm(N, mean = 2, sd = 3)
RV2 <- rnorm(N, mean = 4, sd = 4)
var(RV1 - RV2)
})

hist(var_diff, col = "lightblue", xlab = "Var(RV1 - RV2)",
main = sprintf("Median of Var(RV1-RV2) over 999 replications is %0.2f",median(var_diff)))
abline(v = median(var_diff), col = "red", lty = 2, lwd = 3)
```

Median of Var(RV1−RV2) over 999 replications is 25.11
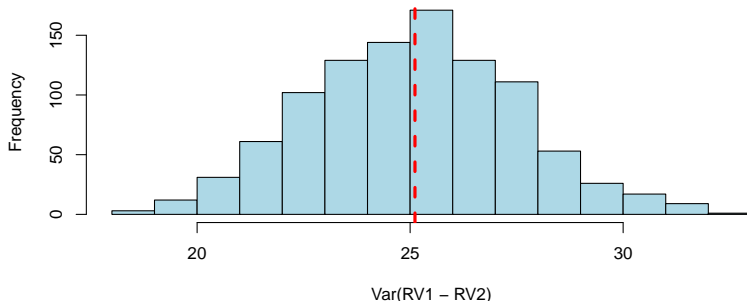
Parameters, Samples, and Statistics

- **Paramter**: An unknown numerical constant pertaining to a population/universe, or in a statistical model.
  - ▶ μ: population mean π: population proportion
- **Statistic**: A numerical quantity calculated from a sample. The empirical counterpart of the parameter, used to *estimate* it.
  - ▶ $\bar{y}$: sample mean p: sample proportion
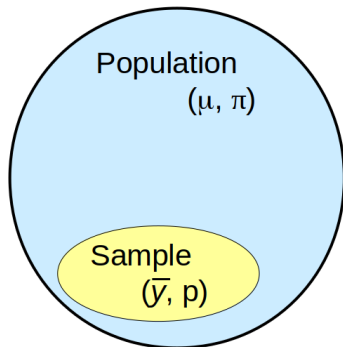
Samples must be random

- The validity of inference will depend on the way that the sample was collected. If a sample was collected badly, no amount of statistical sophistication can rescue the study.

- Samples should be **random**. That is, there should be no systematic set of characteristics that is related to the scientific question of interest that causes some people to be more likely to be sampled than others. The simplest type of randomization selects members from the population with equal probability (a uniform distribution).

- **Do not cheat by**
  - Taking 5 people from the <u>same</u> household to estimate
    - proportion of Québécois who don't have a family doctor
    - who saw a medical doctor last year
    - average rent
  - Sampling the depth of the ocean <u>only around Montreal</u> to estimate
    - proportion of Earth's surface covered by water

Sampling Distributions

Definition 2 (Sampling Distribution).

- The sampling distribution of a statistic is the distribution of values taken by the statistic in **all possible samples of the same size** from the same population.

- The standard deviation of a sampling distribution is called a **standard error**

Sampling Distributions
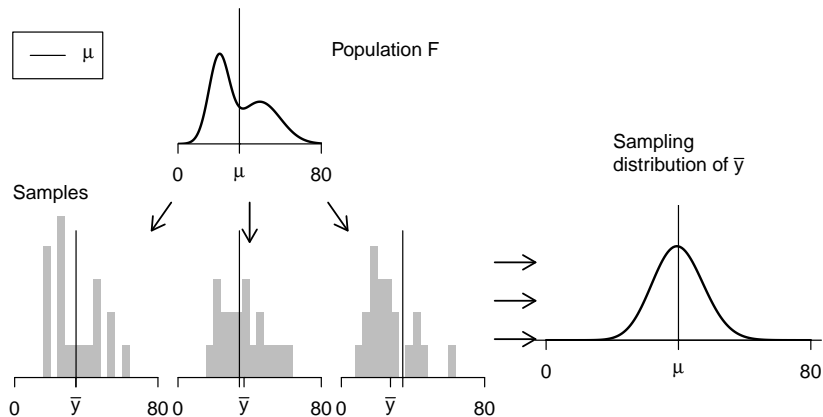
Figure: Ideal world. Sampling distributions are obtained by drawing repeated samples from the population, computing the statistic of interest for each, and collecting (an infinite number of) those statistics as the sampling distribution

Why are sampling distributions important?

- They tell us how far from the target (true value of the parameter) our statistical <u>shot</u> at it (i.e. the statistic calculated form a sample) is likely to be, or, to have been.

- Thus, they are used in confidence intervals for parameters. Specific sampling distributions (based on a null value for the parameter) are also used in statistical tests of hypotheses.

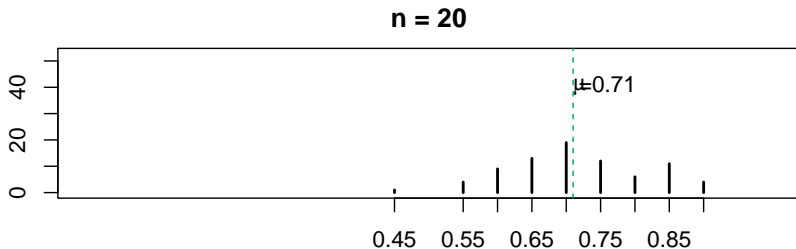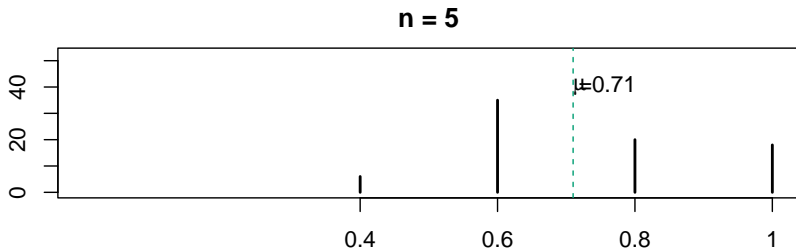# Sampling distribution: mean depth of the ocean
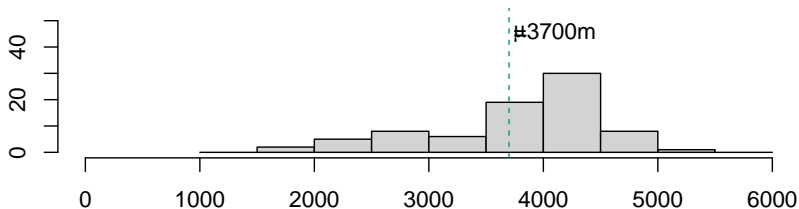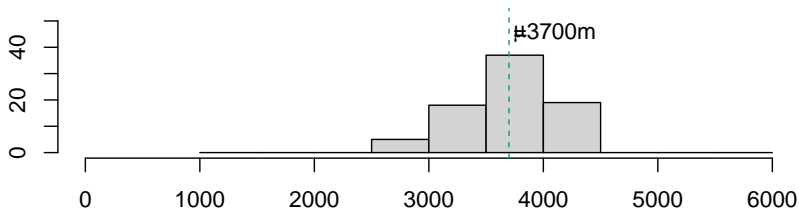
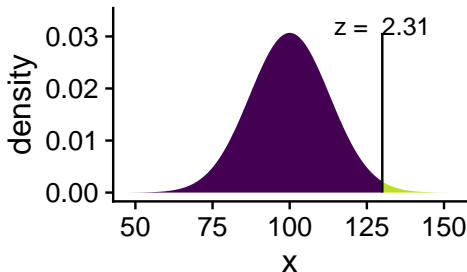# Sampling distribution: proportion covered by water

Normal Distribution: For probabilities we use *pnorm*

```
stats::pnorm(q = 130, mean = 100, sd = 13)
```

```
## [1] 0.9894919
```

```
mosaic::xpnorm(q = 130, mean = 100, sd = 13)
```



```
## [1] 0.9894919
```

- pnorm returns the integral from $-\infty$ to q for a $\mathcal{N}(\mu, \sigma)$
- pnorm goes from *quantiles* (think Z scores) to probabilities

Normal Distribution: For quantiles we use *qnorm*

```
stats::qnorm(p = 0.0104, mean = 100, sd = 13)

## [1] 69.94926
```

```
mosaic::xqnorm(p = 0.0104, mean = 100, sd = 13)
```
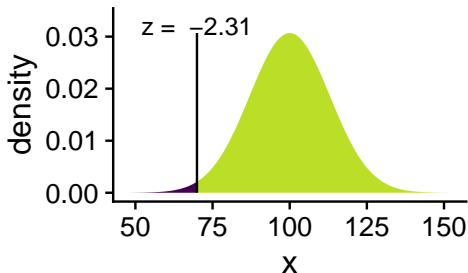


```
## [1] 69.94926
```

- `qnorm` answers the question: What is the Z-score of the *p*th percentile of the normal distribution?
- `qnorm` goes from *probabilities* to quantiles

Empirical Rule or 68-95-99.7% Rule
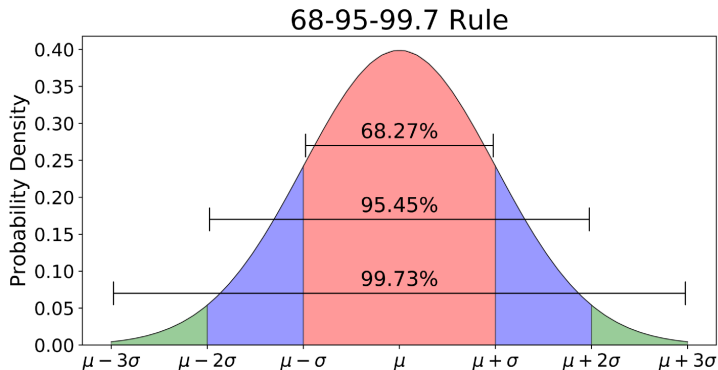
Quadruple the work, half the benefit
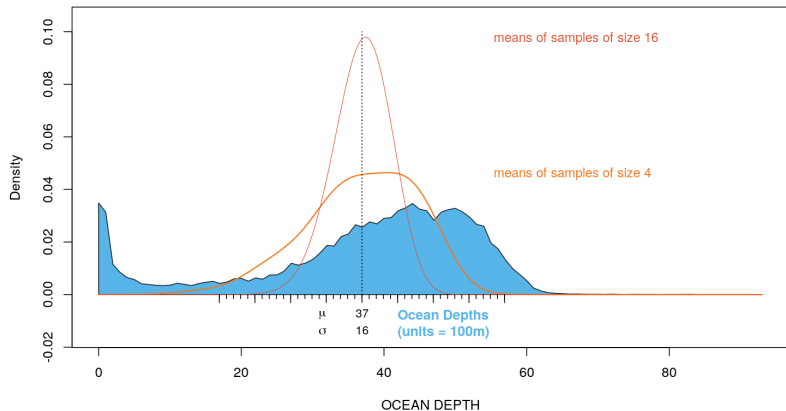
Figure: When the sample size increases from 4 to 16, the spread of the sampling distribution for the mean is reduced by a half, i.e., the range is cut in half. This is known as the curse of the $\sqrt{n}$

The Central Limit Theorem (CLT)

- The sampling distribution of $\bar{y}$ is, for a large enough n, close to Gaussian in shape no matter what the shape of the distribution of individual Y values.
- This phenomenon is referred to as the CENTRAL LIMIT THEOREM
- The CLT applied also to a sample proportion, slope, correlation, or any other statistic created by aggregation of individual observations

Theorem 3 (Central Limit Theorem).

$$if\ Y \sim ???(\mu_Y, \sigma_Y),\ then$$

$$\bar{y} \sim \mathcal{N}(\mu_Y, \sigma_Y/\sqrt{n})$$
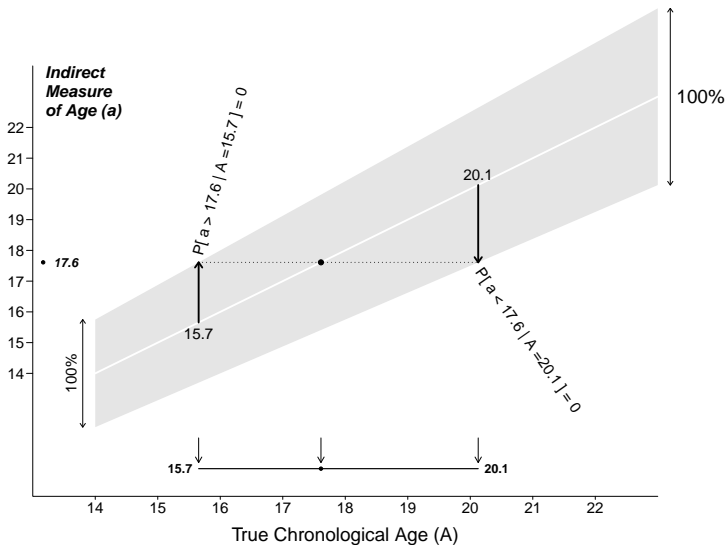
Figure: 100% Confidence Intervals for a person's chronological age when error distributions (that in this example are wider at the older ages) are 100% confined within the shaded ranges.

Confidence Interval

> **Definition 4 (Confidence Interval).**
>
> A level C confidence interval for a parameter has two parts:
>
> 1. An interval calculated from the data, <u>usually</u> of the form
>
> $$\text{estimate} \pm \text{margin of error}$$
>
>   where the estimate is a sample statistic and the margin of error represents the accuracy of our guess for the parameter.
> 2. A confidence level C, which gives the probability that the interval will capture the true parameter value in *different possible samples.* That is, the confidence level is the success rate for the method

Confidence Interval: A simulation study
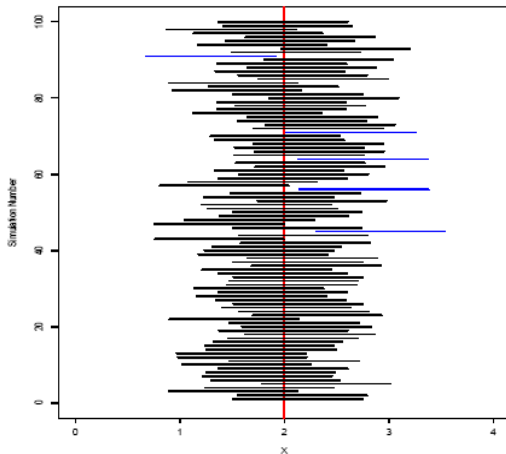
Figure: True parameter value is 2 (red line). Each horizontal black line represents a 95% CI from a sample and contains the true parameter value. The blue CIs do not contain the true parameter value. 95% of all samples give an interval that contains the population parameter.

Interpreting a frequentist confidence interval

- The confidence level is the success rate of the method that produces the interval.

- We don't know whether the 95% confidence interval from a <u>particular sample</u> is one of the 95% that capture θ (the unknown population parameter), or one of the unlucky 5% that miss.

- To say that we are <u>95% confident</u> that the unknown value of θ lies between U and L is shorthand for "We got these numbers using a method that gives correct results 95% of the time."

68% Confidence interval using qnorm
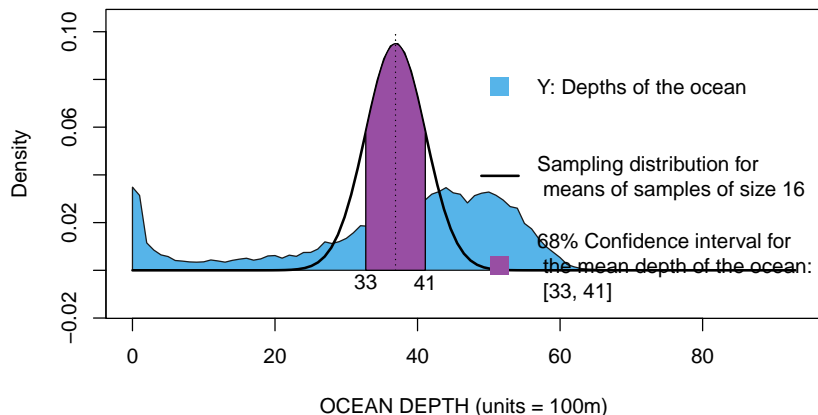
Figure: 68% Confidence interval calculated using
`qnorm(p = c(0.16,0.84), mean = 37, sd = 4.2)`

95% Confidence interval using qnorm
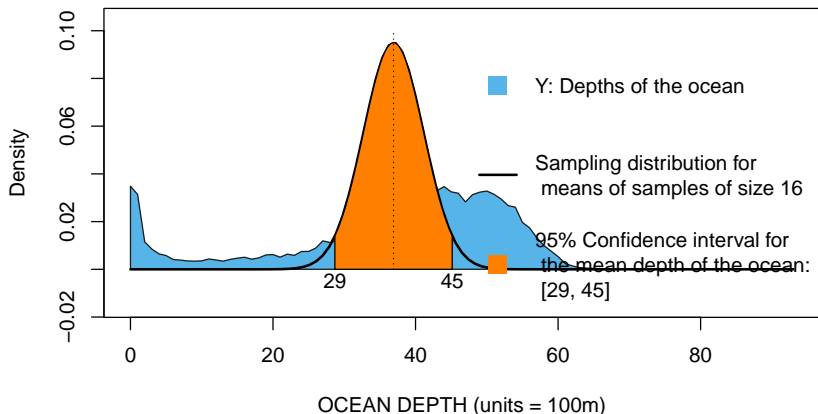
Figure: 95% Confidence interval calculated using
qnorm(p = c(0.025,0.975), mean = 37, sd = 4.2)

Example: Inference for a single population mean

So what does the CI allow us to learn about μ??

- It tells us that if we repeated this procedure again and again (collecting a sample mean, and constructing a 95% CI), 95% of the time, the CI would *cover* μ.

- That is, with 95% probability, the *procedure* will include the true value of μ. Note that we are making a probability statement about the CI, not about the parameter.

- Unfortunately, we do not know whether the true value of μ is contained in the CI in the particular experiment that we have performed.

Motivation for the Bootstrap

- The $\pm$ and `qnorm`/`qt` methods to calculate a CI both require the CLT

Q: What happens if the CLT hasn't 'kicked in'? Or you don't believe the CLT?

Q: What happens if there is no formula available to calculate a CI?

A: Bootstrap

Ideal world: known sampling distribution
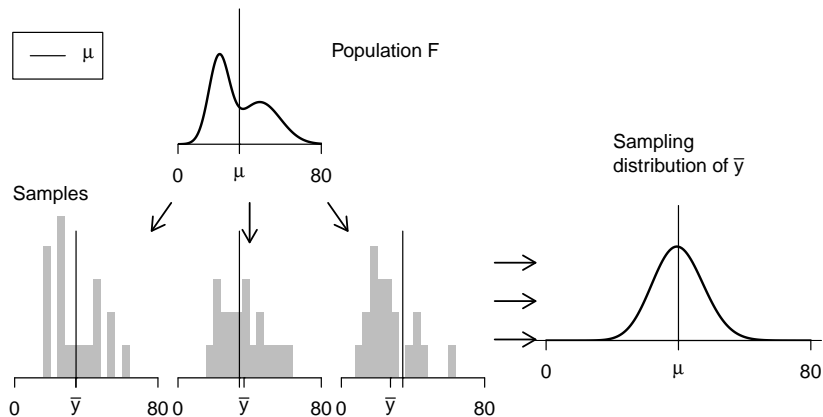
Figure: Ideal world. Sampling distributions are obtained by drawing repeated samples from the population, computing the statistic of interest for each, and collecting (an infinite number of) those statistics as the sampling distribution

Reality: use the bootstrap distribution instead
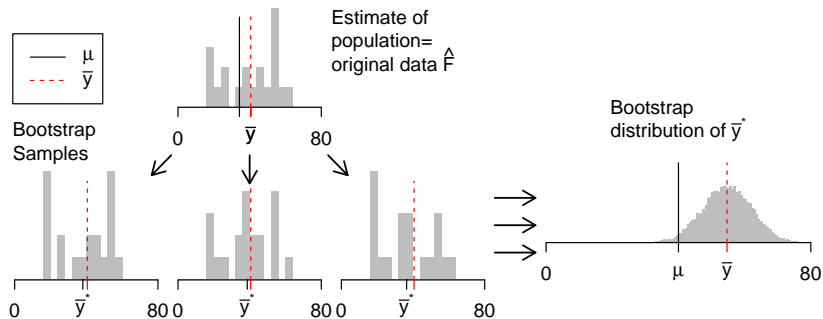
Figure: Bootstrap world. The bootstrap distribution is obtained by drawing repeated samples from an estimate of the population, computing the statistic of interest for each, and collecting those statistics. The distribution is centered at the observed statistic ($\bar{y}$), not the parameter (μ).

Main idea: simulate your own sampling distribution

```r
R <- replicate(B, {
dplyr::sample_n(depths.n.20, size = N, replace = TRUE) %>%
dplyr::summarize(r = mean(alt)) %>%
dplyr::pull(r)
})
CI_95 <- quantile(R, probs = c(0.025, 0.975))
```
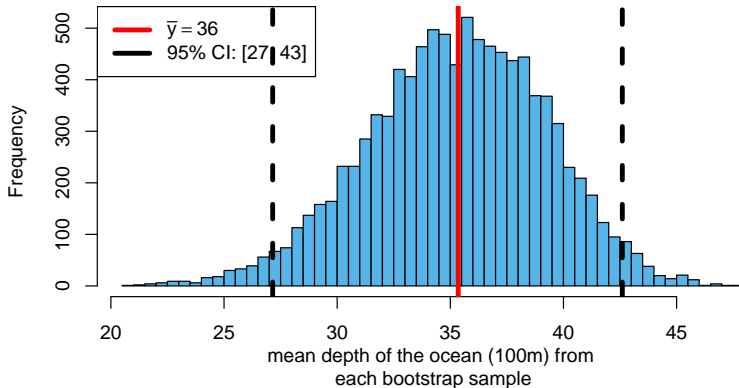
Bootstrap can be used for other statistics (e.g. R^2)
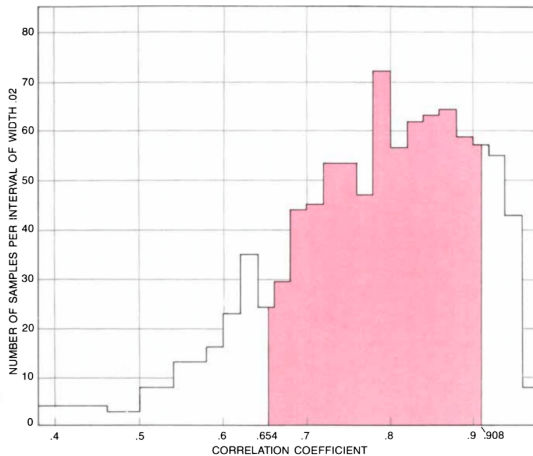
source: Bootstrap article in Scientific American

σ known vs. unknown

σ	known	unknown
Data	$\{y_1, y_2, ..., y_n\}$	$\{y_1, y_2, ..., y_n\}$
Pop'n param	μ	μ
Estimator	$\overline{y} = \frac{1}{n}\sum_{i=1}^{n} y_i$	$\overline{y} = \frac{1}{n}\sum_{i=1}^{n} y_i$
SD	σ	$s = \sqrt{\frac{\sum_{i=1}^{n}(y_i - \overline{y})^2}{n-1}}$
SEM	$\sigma/\sqrt{n}$	$s/\sqrt{n}$
$(1-\alpha)100\%$ CI	$\overline{y} \pm z^{\star}_{1-\alpha/2}(\text{SEM})$	$\overline{y} \pm t^{\star}_{1-\alpha/2,(n-1)}(\text{SEM})$
test statistic	$\frac{\overline{y}-\mu_0}{\text{SEM}} \sim \mathcal{N}(0,1)$	$\frac{\overline{y}-\mu_0}{\text{SEM}} \sim t_{(n-1)}$

Assumptions

	z	t	Bootstrap
SRS	✓	✓	✓
Normal population	✓*	✓*	✗
needs CLT	✓*	✓*	✗
σ known	✓	✗	✗
Sampling dist. center at	μ	μ	$\bar{y}$
SD	σ	s	s
SEM	$\sigma/\sqrt{n}$	$s/\sqrt{n}$	SD(bootstrap statistics)

[a]*If population is Normal then CLT is not needed. If population is not Normal then CLT is needed.

Application: How fast is your reaction time?

```
reaction.times <- c(325,327,357,299,378)/1000
summary(reaction.times)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.2990  0.3250  0.3270  0.3372  0.3570  0.3780

round(sd(reaction.times),3)

## [1] 0.031

length(reaction.times)

## [1] 5
```

5 ways of calculating a confidence interval

We are interested in calculating a 95% confidence interval for the mean reaction time based on the sample of 5 reaction times.

Five ways of doing this:

1. By hand (using the $\pm$ formula and R as a calculator)

2. Using the quantile function for the t distribution `stats::qt`

3. Fitting an intercept-only regression model ($y = \beta_0 + \varepsilon$)

4. Using a canned function (`mosaic::t.test`, `stats::t.test`)

5. Bootstrap

1. By hand using the $\pm$ formula

```r
n <- length(reaction.times)
SEM <- sd(reaction.times)/sqrt(n)

## [1] 0.01372734

ybar <- mean(reaction.times)

## [1] 0.3372

multiple.for.95pct <- stats::qt(p = c(0.025, 0.975), df = n-1)

## [1] -2.776445  2.776445

by_hand_CI <- ybar + multiple.for.95pct * SEM

## [1] 0.29909 0.37531
```

2. Using `stats::qt`

Note: R only provides the standard t distribution. In order to get a scaled version we must define our own function.

```r
n <- length(reaction.times)
SEM <- sd(reaction.times)/sqrt(n)
ybar <- mean(reaction.times)

# scaled version of the standard t distribution
qt_ls <- function(p, df, mean, sd) qt(p = p, df = df) * sd + mean

qt_ls(p = c(0.025, 0.975), df = n - 1, mean = ybar, sd = SEM)

## [1] 0.2990868 0.3753132
```

3. Fitting an intercept-only regression model

```
fit <- stats::lm(reaction.times ~ 1)
summary(fit)

## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.33720    0.01373   24.56 1.63e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0307 on 4 degrees of freedom

stats::confint(fit)

##                 2.5 %    97.5 %
## (Intercept) 0.2990868 0.3753132
```

3. Fitting an intercept-only regression model

In the regression output:

- `Estimate`: the mean reaction time (an estimate of the intercept β_0)

- `t value`: the test statistic

- `Std. Error`: the standard error of the mean (SEM)

- `Pr(>|t|)`: is the p-value

3. Fitting an intercept-only regression model

These are based on the (useless) null hypothesis $H_0 : \mu_0 = 0$

- `t value` $= \frac{\bar{y} - \mu_0}{s/\sqrt{n}} = \frac{0.33720 - 0}{0.01373} = 24.56$
- `Pr(>|t|)`

  $= P(\text{t value} > t_{(n-1)}) + P(-\text{t value} < t_{(n-1)})$

  $= $ `pt(q = 24.56, df = n-1, lower.tail = FALSE)` $+$ `pt(q = -24.56, df = n-1)`

  $= 8.155 \times 10^{-6} + 8.155 \times 10^{-6} = 1.631 \times 10^{-5}$

4. Canned function

```
stats::t.test(reaction.times)

## One Sample t-test with reaction.times
## t = 24.6, df = 4, p-value = 1.63e-05
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.299 0.375
## sample estimates:
## mean of x
##    0.337
```

5. Bootstrap

```
df_react <- data.frame(reaction.times) # need data.frame to bootstrap
B <- 10000 ; N <- nrow(df_react)
R <- replicate(B, {
dplyr::sample_n(df_react, size = N, replace = TRUE) %>%
dplyr::summarize(r = mean(reaction.times)) %>%
dplyr::pull(r)
})

## 2.5% 97.5%
## 0.315 0.363
```


mean reaction time (s) from each bootstrap sample
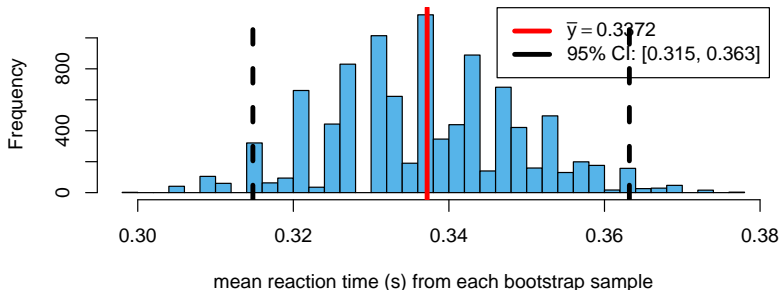
p-values and statistical tests

> **Definition 5 (*p*-value).**
>
> A **probability concerning the observed data**, calculated under a **Null Hypothesis** assumption, i.e., assuming that the only factor operating is sampling or measurement variation.

Use
: To assess the evidence provided by the sample data in relation to a pre-specified claim or 'hypothesis' concerning some parameter(s) or data-generating process.

Basis
: As with a confidence interval, it makes use of the concept of a *distribution*.

Caution
: A *p*-value is NOT the probability that the null 'hypothesis' is true

More about the *p*-value

- The *p*-value is a **probability concerning data**, **conditional on the Null Hypothesis being true**.

- **It is not the probability that Null Hypothesis is true**, *conditional on the data.*

$$p_{value} = P(\text{this or more extreme data}|H_0)$$
$$\neq P(H_0|\text{this or more extreme data}).$$

- Statistical tests are often coded as statistically significant or not according to whether results are extreme or not with respect to a reference (null) distribution. But a test result is just one piece of data, and needs to be considered *along with rest of evidence* before coming to a 'conclusion.'

- **Likewise with statistical 'tests': the *p*-value is just one more piece of *evidence*, hardly enough to 'conclude' anything**.

The prosecutor's fallacy [1]

- Restating this both more succinctly, and in terms better suited to a statistically literate readership, the prosecutor's fallacy is to calculate P(evidence | innocence) and interpret it as P(innocence | evidence).

- It may be true that if the accused were innocent, there is only one chance in 3 million of a DNA match. But the DNA match does not necessarily imply that there is only one chance in 3 million of the accused being innocent.

- Stated more generally, the prosecutor's fallacy is

$$P(A|B) = P(B|A)$$

- We know, from Bayes' rule, that

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

---

[1] The Bayesian flip Correcting the prosecutor's fallacy. Significance. August 2015.

The Bayesian Flip

- In many investigations we may be presented with P(data | theory), but what we would really like to know is P(theory | data): the probability that our theory is correct, given what we have observed

- To move from P(data | theory) to P(theory | data), we need to do the Bayesian flip.

- Every year in the United States 38 million women are tested for breast cancer with mammograms. Of these, 140 000 have cancer. Mammograms have been determined to be 90% accurate for women with breast cancer.

- This figure was calculated by tallying all of the women who were eventually determined to have breast cancer and looking back to see if their initial mammograms were positive, thus:

$$P(+mammogram|cancer) = 0.90$$

and, using a similar empirical investigation,

$$P(+mammogram|nocancer) = 0.10$$

The Bayesian Flip

- It is important to know that a test is both powerful and has a relatively low rate of false positives. But when one is faced with a positive mammogram result, these are hardly useful. We administer a mammogram because we do not know whether or not someone has cancer.

- What we want to know is

$$P(cancer\,|\,+\,mammogram)$$

- This probability is a fraction that has as its numerator the number of women annually diagnosed with breast cancer via mammograms, or 140 000, and as its denominator the number of positive mammograms (including both true cancer cases and false positives):

$$
\begin{aligned}
P(cancer\,|\,+\,mammogram) &= \frac{True\ positives}{(True\ positives + False\ positives)} \\
&= 140000/(140000 + 0.1{\times}38\ million) \\
&= 140000/(140000 + 3800000) \\
&= 140000/3940000 = 0.036 = 3.6\%
\end{aligned}
$$

Close relationship between *p*-value and CI
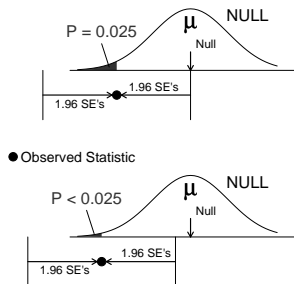
- (Upper graph) If upper limit of 95% CI *just touches* null value, then the 2 sided *p*-value is 0.05 (or 1 sided *p*-value is 0.025).

- (Lower graph) If upper limit *excludes* null value, then the 2 sided *p*-value is less than 0.05 (or 1 sided *p*-value is less than 0.025).

- (Graph not shown) If CI *includes* null value, then the 2-sided *p*-value is greater than (the conventional) 0.05, and thus observed statistic is "not statistically significantly different" from hypothesized null value.

Power = $1 - \beta$

Definition 6 (Power = $1 - \beta$).

The probability that a fixed level α significance test will reject H_0 when a particular alternative value of the parameter is true is called the **power** of the test to detect the alternative.

Distribution of $\overline{y}$ under the null hypothesis:

Distribution of $\overline{y}$ under an alternative hypothesis:

1-β

Reject H_0

Reject H_0

β

α/2

α/2

μ_0

μ_A

Δ
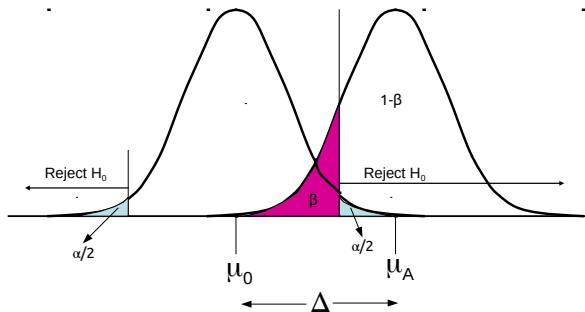
Power and Sample Size: 3 questions

1. How much water a supplier could add to the milk before they have a 10% , 50%, 80% chance of getting caught, i.e., of the buyer detecting the cheating ?

2. Assume a 99:1 mix of milk and water. What are the chances of detecting cheating if the buyer uses samples n=10, 15 or 20 rather than just 5 measurements?

3. At what n does the chance of detecting cheating reach 80%? (*a commonly used, but arbitrary, criterion used in sample-size planning by investigators seeking funding for their proposed research*)

If the supplier added 1% water to the milk

$\alpha = 0.050$
$\beta = 0.554$
$1 - \beta = 0.446$

$\mu_{H_A} = -0.5346$

$\mu_{H_0} = -0.5400$

cutoff $= -0.5341$
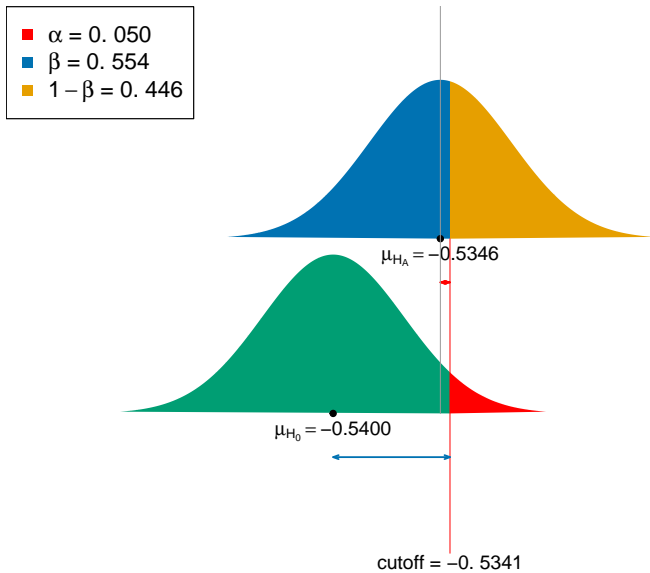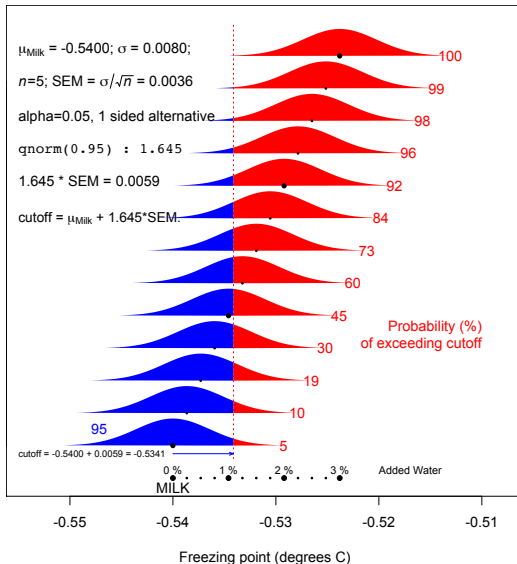
The probabilities in red were calculated using the formula: `stats::pnorm(cutoff, mean = mu.mixture, sd = SEM, lower.tail=FALSE)`

The balancing formula
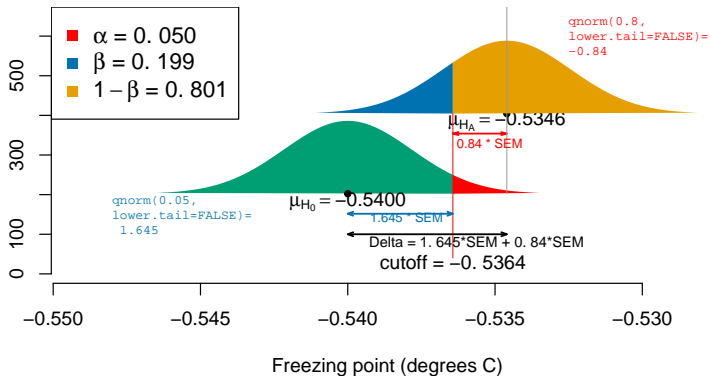
What sample size needed?

- The 'balancing formula', in SEM terms, is simply the n where

$$1.645 \times SEM + 0.84 \times SEM = \Delta.$$

Replacing each of the SEMs (assumed equal, because we assumed the variability is approx. the same under both scenarios) by $\sigma/\sqrt{n}$, i.e.,

$$1.645 \times \sigma/\sqrt{n} + 0.84 \times \sigma/\sqrt{n} = \Delta.$$

and solving for n, one gets

$$n = (1.645 + 0.84)^2 \times \left\{ \frac{\sigma}{\Delta} \right\}^2 = (1.645 + 0.84)^2 \times \left\{ \frac{Noise}{Signal} \right\}^2.$$

The Poisson Distribution

- The (infinite number of) probabilities $P_0, P_1, ..., P_y, ...$, of observing $Y = 0, 1, 2, \ldots, y, \ldots$ events in a given amount of "experience."

- These probabilities, $P(Y = k) \to$ dpois(), are governed by a single parameter, the mean $E[Y] = \mu$ which represents the expected **number** of events in the amount of experience actually studied.

- We say that a random variable $Y \sim \text{Poisson}(\mu)$ distribution if

$$P(Y = k) = \frac{\mu^k}{k!} e^{-\mu}, \quad k = 0, 1, 2, \ldots$$

- Note: in dpois() μ is referred to as lambda

- Note the distinction between μ and λ
  - ▶ μ: expected **number** of events
  - ▶ λ: **rate** parameter

Confidence interval for μ

- If the CLT hasn't kicked in, then the usual CI might not be appropriate:

$$\text{point-estimate} \pm z^\star \times \text{standard error}$$

- qpois function doesn't work either:

```
# middle area is not 95%
mosaic::xqpois(c(0.025, 0.975), lambda = 6)
```
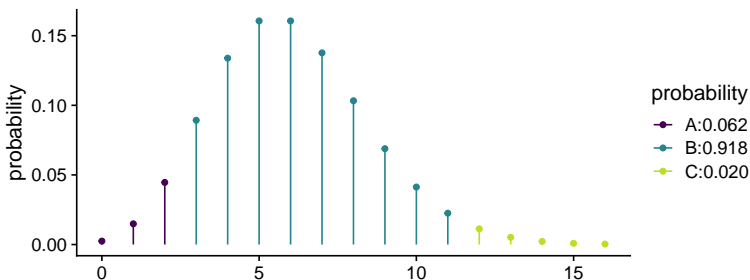


```
## [1]  2 11
```

Confidence interval for μ

- Similar to the binomial (Clopper-Pearson CI), we consider a *first-principles* $100(1 - \alpha)\%$ CI $[\mu_{LOWER}, \mu_{UPPER}]$ such that

$$P(Y \geq y \,|\, \mu_{LOWER}) = \alpha/2 \quad \text{and} \quad P(Y \leq y \,|\, \mu_{UPPER}) = \alpha/2.$$

- For example, the 95% CI for μ, based on $y = 6$, is $[\underline{2.20}, \underline{13.06}]$.

- **Exercise:** can we use `glm` to get a CI for μ ?

LOWER
$\mu = 2.2$

y prob(y|2.2)

y	prob
4	0.0182
5	0.0476
6	0.0174
7	0.0055
8	0.0015
9	0.0004
10	0.0001
..	..

Prob (y >= 6)

= 0.0250

if mean = 2.2

count (y)

0 1 2 3 4 5 (6) 7 8 9 10 11 12 13 14 15 16 17...
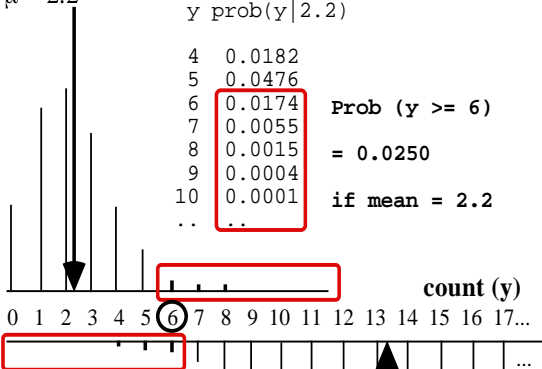
y prob(y|13.06)

y	prob
0	0.0000
1	0.0000
2	0.0002
3	0.0008
4	0.0026
5	0.0067
6	0.0147
7	0.0274
..	..

Prob (y <= 6)

= 0.0250

if mean = 13.06

UPPER
$\mu = 13.06$

(6) **observed count**

μ

Mean Ocean depth (Km)

$$\mu_1 = \mu_0 + \Delta$$
$$\mu = \mu_0 + \Delta \times South$$

$$\theta = \frac{\mu_1}{\mu_0} \; ; \; \mu_1 = \mu_0 \times \theta$$

$$\log(\mu) = \log(\mu_0) + \log(\theta) \times South$$

Log of Mean Depth (base 2) — Log of Mean Depth (base e)

NORTH (South=0) — SOUTH (South=1)

'Δx' = 1

fn. of $\mu_x = \beta_0$ (i.e., this fn. at South = 0) + an additional 'β' if South = 1

π

Proportion Water

$$\pi_1 = \pi_0 + \Delta$$
$$\pi = \pi_0 + \Delta \times South$$

$$\theta = \frac{\pi_1}{\pi_0} \; ; \; \pi_1 = \pi_0 \times \theta$$

$$\log(\pi) = \log(\pi_0) + \log(\theta) \times South$$

$$\omega = \frac{W}{L} = \frac{1-\pi}{\pi} \; ; \; \theta = \frac{\omega_1}{\omega_0}$$

$$\log(\omega) = \log(\omega_0) + \log(\theta) \times South$$

log of W:L — Water(W) : Land(L)

NORTH (South=0) — SOUTH (South=1)

'Δx' = 1

fn. of $\pi_x = \beta_0$ (i.e., this fn. at South = 0) + an additional 'β' if South = 1

λ
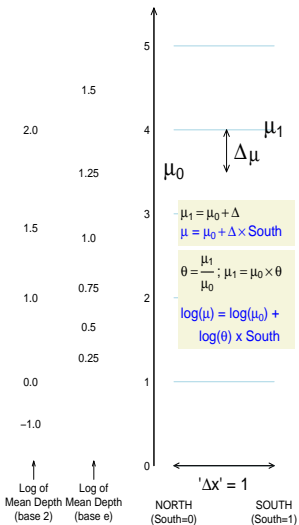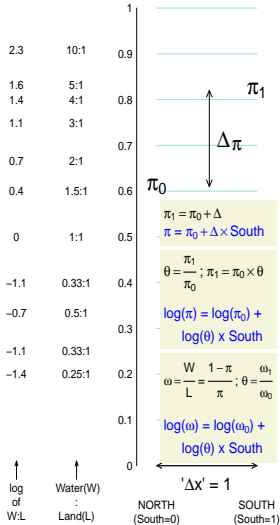
Magnitude 6 or higher Earthquakes/Month
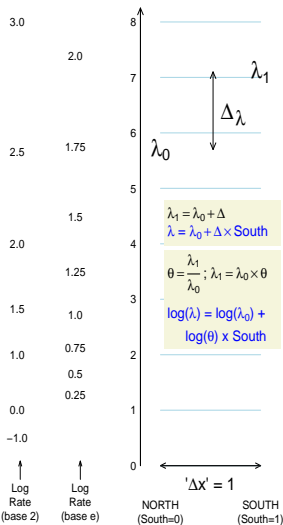
$$\lambda_1 = \lambda_0 + \Delta$$
$$\lambda = \lambda_0 + \Delta \times South$$

$$\theta = \frac{\lambda_1}{\lambda_0} \; ; \; \lambda_1 = \lambda_0 \times \theta$$

$$\log(\lambda) = \log(\lambda_0) + \log(\theta) \times South$$

Log Rate (base 2) — Log Rate (base e)

NORTH (South=0) — SOUTH (South=1)

'Δx' = 1

fn. of $\lambda_x = \beta_0$ (i.e., this fn. at South = 0) + an additional 'β' if South = 1

Deterministic and stochastic model components

- The regression equation specifies the deterministic part of the model.
- This is defined in terms of parameters, conditional on the values of X.
- To complete the model specification, we need to specify the stochastic component of the model, a statistical distribution for the outcome Y_X.
- The appropriate distribution is

$$Y_X \sim \text{Gaussian}\left(\mu_X, \sigma^2\right)$$

- Here the mean μ_X is given by the regression equation as

$$\mu_X = \mu_0 + \Delta_\mu \cdot X$$

```
depths <- readr::read_csv("depths.csv")
fit <- lm(alt ~ 1, data = depths); print(summary(fit), signif.stars = F)

## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3628.5       86.5      42   <2e-16
##
## Residual standard error: 1730 on 399 degrees of freedom


fit <- lm(alt ~ South, data = depths); print(summary(fit), signif.stars = F)

## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)     3523     122      28.82   <2e-16
## South            211     173       1.22     0.22
##
## Residual standard error: 1730 on 398 degrees of freedom
## Multiple R-squared: 0.00372,^^IAdjusted R-squared: 0.00122
## F-statistic: 1.49 on 1 and 398 DF,  p-value: 0.223


fit <- glm(alt ~ South, data = depths, family = gaussian(link=log)); print(summary(fit), signif.stars = F)


##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   8.1671     0.0347  235.41   <2e-16
## South         0.0581     0.0477    1.22     0.22
##
## (Dispersion parameter for gaussian family taken to be 2988040)
##
##     Null deviance: 1193681102  on 399  degrees of freedom
## Residual deviance: 1189239546  on 398  degrees of freedom
## AIC: 7103
##
## Number of Fisher Scoring iterations: 5
```

```
coef(fit)
```

```
## (Intercept)       South
##      8.1671      0.0581
```

```
vcov(fit)
```

```
##             (Intercept)    South
## (Intercept)      0.0012 -0.00120
## South           -0.0012  0.00228
```

```
confint(fit)
```

```
##                2.5 % 97.5 %
## (Intercept)  8.0967  8.233
## South       -0.0353  0.152
```

2.2 Bootstrap CI for mean difference using canned function

```
pacman::p_load(car)
betahat.boot <- car::Boot(fit, R=999)
head(betahat.boot$t)

##      (Intercept)  South
## [1,]        8.17 0.0713
## [2,]        8.14 0.0923
## [3,]        8.20 0.1109
## [4,]        8.18 0.0398
## [5,]        8.21 0.0135
## [6,]        8.13 0.1086


dim(betahat.boot$t)

## [1] 999   2


deltamuhat.boot <- betahat.boot$t[,2]
median(deltamuhat.boot)

## [1] 0.057


quantile(deltamuhat.boot, probs = c(0.025, 0.975))

##    2.5%   97.5%
## -0.0373  0.1551
```
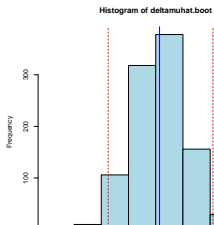

Histogram of deltamuhat.boot

2.2 Bootstrap CI for mean difference using canned function (continued)
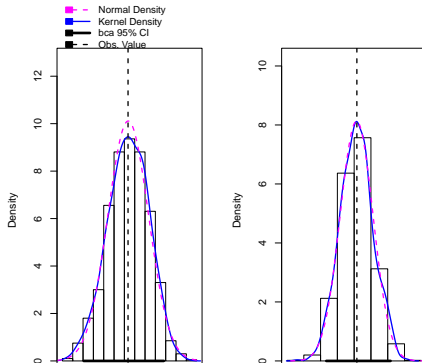
```
summary(betahat.boot)
```

```
##
## Number of bootstrap replications R = 999
##             original  bootBias bootSE bootMed
## (Intercept)  8.1671  0.000348 0.0395   8.169
## South        0.0581 -0.000736 0.0490   0.057
```

```
confint(betahat.boot)
```

```
## Bootstrap bca confidence intervals
##
##             2.5 % 97.5 %
## (Intercept) 8.081  8.236
## South      -0.033  0.158
```

```
hist(betahat.boot)
```

## 2.3 Bootstrap CI for mean difference using `boot` package

```r
plot(results)
```


Histogram of t

```r
library(boot)
# function to obtain deltamu hat
deltamu <- function(data, indices) {
# allows boot to select sample
d <- data[indices,]
fit <- lm(alt ~ South, data=d)
coef(fit)["South"]
}

results <- boot::boot(data = depths,
statistic = deltamu, R=999)

results
```

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot::boot(data = depths, statistic = deltamu, R = 999)
##
##
## Bootstrap Statistics :
##     original  bias    std. error
## t1*     211   -7.25       172
```
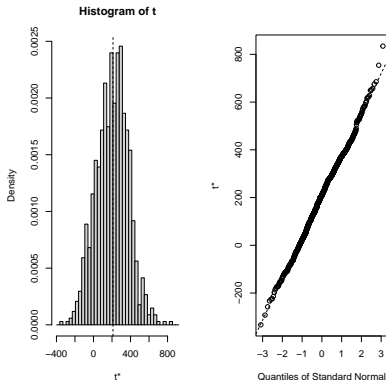
```r
boot.ci(results)
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 999 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = results)
##
## Intervals :
## Level      Normal              Basic
## 95%   (-119,  555 )   (-125,  552 )
##
```

Permutation Testing

- In testing a null hypothesis we need a test statistic that will have different values under the null hypothesis and the alternatives we care about

- We then need to compute the sampling distribution of the test statistic when the null hypothesis is true. For some test statistics and some null hypotheses this can be done analytically.

- The pvalue is the probability that the test statistic would be at least as extreme as we observed, if the null hypothesis is true.

- A permutation test gives a simple way to compute the sampling distribution for any test statistic, under the null hypothesis that there is no effect (i.e. South is not a determinant of the mean depth of the ocean)

- https://www.jwilber.me/permutationtest/

Permutation Testing

- To estimate the sampling distribution of the test statistic we need many samples generated under the strong null hypothesis.

- If the null hypothesis is true, changing the exposure would have no effect on the outcome. By randomly shuffling the determinants we can make up as many data sets as we like.

- If the null hypothesis is true, the shuffled data sets should look like the real data, otherwise they should look different from the real data.

- The ranking of the real test statistic among the shuffled test statistics gives a p-value

Permutation Testing

```
one.test <- function(x,y) {
xstar <- sample(x)
mean(y[xstar==1]) - mean(y[xstar==0])
}

null.dist <- replicate(1000, one.test(x = depths$South, y = depths$alt))
hist(null.dist)
abline(v=coef(fit)["South"], lwd=2, col="blue")
```


Histogram of null.dist
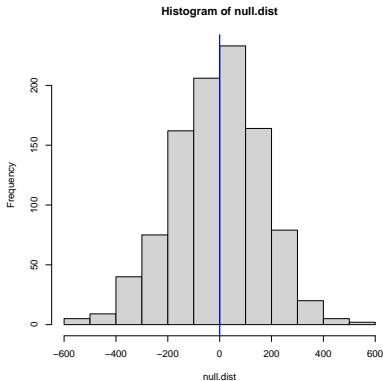
```
mean(abs(null.dist) > abs(coef(fit)["South"]))
```

```
## [1] 1
```

Deterministic and stochastic model components

- The regression equation specifies the deterministic part of the model.
- This is defined in terms of parameters, conditional on the values of X.
- To complete the model specification, we need to specify the stochastic component of the model, a statistical distribution for the outcome Y_X (counts).
- The appropriate distribution is

$$Y_X \sim \text{Poisson}\left(\mu_X\right)$$

- Here the mean μ_X is given by the regression equation as

$$\mu_X = \lambda \cdot \text{PT}$$

See the 2018 Lancet article *Efficacy of Olyset Duo, a bednet containing pyriproxyfen and permethrin, versus a permethrin-only net against clinical malaria in an area with highly pyrethroid-resistant vectors in rural Burkina Faso: a cluster-randomised controlled trial* by Tiono et. al. Reproduce the Rate ratio (95% CI) in Table 2. Calculate the rate difference and 95% CI comparing PPF-treated to Standard long-lasting insecticidal nets. Check the goodness of fit.

```
## Call:
## glm(formula = cases ~ exposure + offset(log(years)), family = poisson(link = log),
##     data = df)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.6831     0.0243   28.09  < 2e-16
## exposure     -0.2669     0.0329   -8.12  4.6e-16
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 1381.2  on 23  degrees of freedom
## Residual deviance: 1316.0  on 22  degrees of freedom
## AIC: 1477
##
## Number of Fisher Scoring iterations: 5
```

Deterministic and stochastic model components

- The regression equation specifies the deterministic part of the model.
- This is defined in terms of parameters, conditional on the values of Z and X.
- To complete the model specification, we need to specify the stochastic component of the model, a statistical distribution for the outcome D_{ZX}.
- It is already obvious that the appropriate distribution is

$$D_{ZX} \sim \text{Binomial}\,(N_{ZX}, \pi_{ZX})$$

- Here the risk π_{ZX} is given by the regression equation as (verify)

$$\pi_{ZX} = \frac{e^{\alpha + \beta Z + \gamma X}}{1 + e^{\alpha + \beta Z + \gamma X}} = \frac{1}{1 + e^{-(\alpha + \beta Z + \gamma X)}}$$

- This inverse transformation is the so-called *expit* function:

$$\pi_{ZX} = \text{logit}^{-1}(\alpha + \beta Z + \gamma X) = \text{expit}(\alpha + \beta Z + \gamma X)$$

Regression equation with logit link

- Reparametrizing the log-odds is referred to as logistic regression.
- In the ongoing example we may take

$$\log \left(\frac{\pi_{ZX}}{1 - \pi_{ZX}} \right) = \alpha + \beta Z + \gamma X$$

- The original four parameters are now expressed in terms of three new parameters: an intercept term α and regression coefficients β and γ.
- The function $\log \frac{\pi}{1-\pi}$ is referred to as the logit transformation of the risk parameter π.
- Thus, the same model can be specified as a reparametrization of the risk parameter together with the *logit link* function:

$$\text{logit} \left(\pi_{ZX} \right) = \alpha + \beta Z + \gamma X$$

Log-linear model for risk

- Is there some particular reason why we *have* to use the logit link when modeling risk?

- Why could we not just parametrize the log-risk as
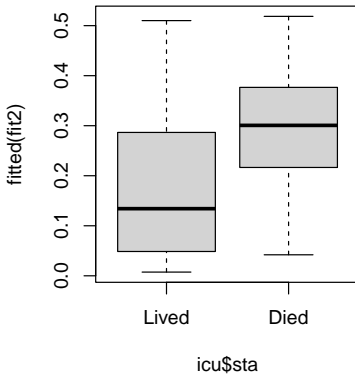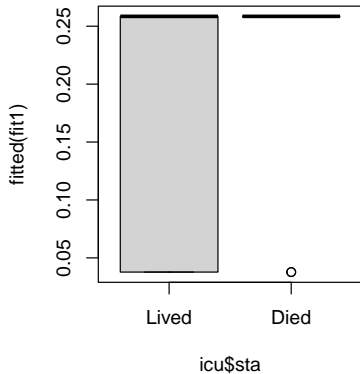
$$\log(\pi_{ZX}) = \alpha + \beta Z + \gamma X?$$

- We can; in this case the regression coefficient β would be interpreted as a log-risk ratio:

$$\frac{\pi_{1X}}{\pi_{0X}} = \frac{e^{\alpha + \beta + \gamma X}}{e^{\alpha + \gamma X}}$$

$$= \frac{e^{\alpha} e^{\beta} e^{\gamma X}}{e^{\alpha} e^{\gamma X}}$$

$$= e^{\beta}$$

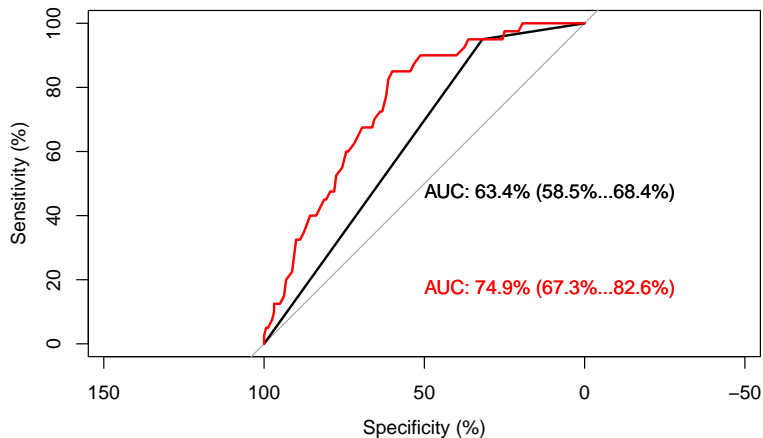$$\Leftrightarrow \log\left(\frac{\pi_{1X}}{\pi_{0X}}\right) = \beta$$

ROC Curves

```
fit1 <- glm(sta ~ type, family=binomial(link=logit), data=icu)
fit2 <- glm(sta ~ type + age, family=binomial(link=logit), data=icu)
```

ROC Curves

Session Info

```
R version 4.1.1 (2021-08-10)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Pop!_OS 21.04

Matrix products: default
BLAS:   /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblasp-r0.3.13.so

attached base packages:
[1] tools     stats     graphics  grDevices utils     datasets  methods
[8] base

other attached packages:
 [1] pROC_1.16.2          boot_1.3-27          car_3.0-9            carData_3.0-4
 [5] latex2exp_0.4.0      RColorBrewer_1.1-2   colorspace_2.0-2     oibiostat_0.2.0
 [9] DT_0.16              mosaic_1.7.0         Matrix_1.3-2         mosaicData_0.20.1
[13] ggformula_0.9.4      ggstance_0.3.4       lattice_0.20-41      kableExtra_1.2.1
[17] socviz_1.2           gapminder_0.3.0      here_0.1             NCStats_0.4.7
[21] FSA_0.8.30           forcats_0.5.1        stringr_1.4.0        dplyr_1.0.7
[25] purrr_0.3.4          readr_1.4.0          tidyr_1.1.4          tibble_3.1.5
[29] ggplot2_3.3.5.9000   tidyverse_1.3.0      knitr_1.36

loaded via a namespace (and not attached):
 [1] readxl_1.3.1         backports_1.2.1      plyr_1.8.6
 [4] splines_4.1.1        crosstalk_1.1.1      leaflet_2.0.3
 [7] TH.data_1.0-10       digest_0.6.28        htmltools_0.5.2
[10] fansi_0.5.0          magrittr_2.0.1       mosaicCore_0.8.0
[13] openxlsx_4.1.5       modeltr_0.1.8        sandwich_2.5-1
[16] blob_1.2.1           rvest_1.0.0          ggrepel_0.9.1.9999
[19] haven_2.3.1          xfun_0.26            crayon_1.4.1
[22] jsonlite_1.7.2       lme4_1.1-23          survival_3.2-13
[25] zoo_1.8-8            glue_1.4.2           polyclip_1.10-0
[28] gtable_0.3.0         emmeans_1.5.1        webshot_0.5.2
[31] sjstats_0.18.0       sjmisc_2.8.5         abind_1.4-5
[34] scales_1.1.1         mvtnorm_1.1-1        DBI_1.1.1
[37] rstatix_0.6.0        ggeffects_0.16.0     Rcpp_1.0.7
[40] viridisLite_0.4.0    xtable_1.8-4         performance_0.8.0
[43] foreign_0.8-81       datawizard_0.2.1     htmlwidgets_1.5.3
[46] httr_1.4.2           ellipsis_0.3.2       pkgconfig_2.0.3
[49] farver_2.1.0         dbplyr_1.4.4         utf8_1.2.2
[52] tidyselect_1.1.1     labeling_0.4.2       rlang_0.4.12
```