COGS2020: Final Exam Practice

Author: Matthew J. Crossley

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Lecture notes cheat sheet

single-sample t-test

$$t_{obs} = \frac{\bar{x} - \mu_{\bar{x}}}{s_{\bar{x}}}$$

$$\mu_{\bar{x}} = \mu_x$$

$$s_{\bar{x}} = \frac{s_x}{\sqrt{n}}$$

$$t_{obs} = \frac{\bar{x} - \mu_x}{\frac{s_x}{\sqrt{n}}}$$

$$t_{obs} \sim t(n-1)$$

two-sample t-tests

$$W = X - Y$$

$$\mu_W = \mu_X - \mu_Y$$

$$\sigma^2_W = \sigma^2_X + \sigma^2_Y$$

$$\bar{W} = \bar{X} - \bar{Y}$$

$$\mu_{\bar{W}} = \mu_{\bar{X}} - \mu_{\bar{Y}}$$

$$\sigma^2_{\bar{W}} = \sigma^2_{\bar{X}} + \sigma^2_{\bar{Y}}$$

equal sample size and equal variance

$$\begin{aligned} s_p^2 &= \frac{S_X^2 + S_Y^2}{2} \\ t_{obs} &= \frac{\overline{W} - \mu_{\overline{W}}}{s_{\overline{W}}} \\ &= \frac{\overline{X} - \overline{Y}}{\sqrt{\frac{S_X^2 + S_Y^2}{n}}} \\ &= \frac{\overline{X} - \overline{Y}}{s_p\sqrt{\frac{2}{n}}} \end{aligned}$$

$$t_{obs} \sim t(df)$$

$$\begin{aligned} df &= (n_X - 1) + (n_Y - 1) \\ &= 2n - 2 \end{aligned}$$

unequal sample sizes and equal variances

$$s_p^2 = \frac{(n_X - 1)s_X^2 + (n_Y - 1)s_Y^2}{n_X + n_Y - 2}$$

$$
\begin{aligned}
t_{obs} &= \frac{\overline{W} - \mu_{\overline{W}}}{s_{\overline{W}}} \\
&= \frac{\overline{X} - \overline{Y}}{s_p \sqrt{\frac{1}{n_X} + \frac{1}{n_Y}}}
\end{aligned}
$$

$$t_{obs} \sim t(df)$$

$$
\begin{aligned}
df &= (n_X - 1) + (n_Y - 1) \\
&= n_X + n_Y - 2
\end{aligned}
$$

unequal variance

$$t_{obs} = \frac{\overline{X} - \overline{Y}}{\sqrt{\frac{s_X^2}{n_X} + \frac{s_Y^2}{n_Y}}}$$

$$df = \frac{\left(\frac{s_X^2}{n_X} + \frac{s_Y^2}{n_Y}\right)^2}{\frac{\left(\frac{s_X^2}{n_X}\right)^2}{n_X - 1} + \frac{\left(\frac{s_Y^2}{n_Y}\right)^2}{n_Y - 1}}$$

one-way ANOVA

- k is the number of factor levels
- N is the total number of observations

$$G = \frac{\bar{x} + \bar{y} + \bar{z}}{3}$$

$$\text{ss}_{between} = l(\bar{x} - G)^2 + m(\bar{y} - G)^2 + n(\bar{z} - G)^2$$

$$\text{ss}_{within} = \sum_{i=1}^{l} (x_i - \bar{x})^2 + \sum_{i=1}^{m} (y_i - \bar{y})^2 + \sum_{i=1}^{n} (z_i - \bar{z})^2$$

$$
\begin{aligned}
&\text{df}_{between} = k - 1 \\
&\text{df}_{within} = N - k
\end{aligned}
$$

Effect	df	SS	MS	F
$Between$	k-1	see above	$\frac{SS_{between}}{df_{between}}$	$\frac{MS_{between}}{MS_{within}}$
$Within$	N-k	see above	$\frac{SS_{within}}{df_{within}}$	

repeated measures ANOVA

- k is the number of factor levels
- n is the number of subjects
- x_{ij} is observation from factor level i and subject j

$$SS_{between-levels} = n\sum_{i=1}^{k}(\bar{x_{i\bullet}} - \bar{x_{\bullet\bullet}})^2$$

$$SS_{within-levels} = \sum_{i=1}^{k}\sum_{j=1}^{n}(x_{ij} - \bar{x_{i\bullet}})^2$$

$$SS_{between-subject} = k\sum_{j=1}^{n}(\bar{x_{\bullet j}} - \bar{x_{\bullet\bullet}})^2$$

$$SS_{error} = SS_{within-levels} - SS_{between-subject}$$

Effect	Df	SS	MS	F
$Factor1$	k-1	see above	$\frac{SS_{between-levels}}{df_{between-levels}}$	$\frac{MS_{between-levels}}{MS_{error}}$
$Error$	(k-1)(n-1)	see above	$\frac{SS_{error}}{df_{error}}$	

two-way ANOVA

- SS_{total} is the total variability between all observations.
- $SS_{factor1}$ is the variability between different factor 1s.
- $SS_{factor2}$ is the variability between different factor 2s.
- $SS_{factor1\times factor2}$ is the variability between different factor 1s at different factor 2 levels.
- SS_{error} is the variability not accounted for by $SS_{factor1}$, $SS_{factor2}$, and $SS_{factor1\times factor2}$
- $n_{factor1}$ = number of unique factor 1 levels.
- $n_{factor2}$ = number of unique factor 2 levels.
- N = number of observations at level of factor 2 and factor 1, which in the following we assume is the same for all combinations of factor 1 and factor 2 (i.e., we assume a **balanced design**).

$$SS_{factor1} = n_{factor2}n_{total}\sum_{i}^{n_{factor1}}(\bar{y}_{i\bullet\bullet} - \bar{y}_{\bullet\bullet\bullet})^2$$

$$SS_{factor2} = n_{factor1}n_{total}\sum_{j}^{n_{factor2}}(\bar{y}_{\bullet j\bullet} - \bar{y}_{\bullet\bullet\bullet})^2$$

$$SS_{factor1\times factor2} = n_{total}\sum_{i}^{n_{factor1}}\sum_{j}^{n_{factor2}}(\bar{y}_{ij\bullet} - (\bar{y}_{i\bullet\bullet} + \bar{y}_{\bullet j\bullet} - \bar{y}_{\bullet\bullet\bullet}))^2$$

$$SS_{error} = \sum_{i}^{n_{factor1}}\sum_{j}^{n_{factor2}}\sum_{k}^{n_{total}}(\bar{y}_{ijk} - \bar{y}_{ij\bullet})^2$$

$$SS_{Total} = \sum_{i}^{n_{factor1}} \sum_{j}^{n_{factor2}} \sum_{k}^{n_{total}} (\bar{y}_{ijk} - \bar{y}_{\bullet\bullet\bullet})^2$$

$$SS_{total} = SS_{factor1} + SS_{factor2} + SS_{factor1 \times factor2} + SS_{error}$$

Effect	df	SS	MS	F
$Factor1$	$n_{Factor1} - 1$	see above	$\frac{SS_{Factor1}}{df_{Factor1}}$	$\frac{MS_{Factor1}}{MS_{error}}$
$Factor2$	$n_{Factor2} - 1$	see above	$\frac{SS_{Factor2}}{df_{Factor2}}$	$\frac{MS_{Factor2}}{MS_{error}}$
$Factor1 \times Factor2$	$(n_{Factor1} - 1)(n_{Factor2} - 1)$	see above	$\frac{SS_{Factor1 \times Factor2}}{df_{Factor1 \times Factor2}}$	$\frac{MS_{Factor1 \times Factor2}}{MS_{error}}$
$Error$	$N - n_{Factor1} n_{Factor2}$	see above	$\frac{SS_{error}}{df_{error}}$	

R help: `t.test`

Student's t-Test

Description

Performs one and two sample t-tests on vectors of data.

Usage

t.test(x, . . .)

Default S3 method:

t.test(x, y = NULL, alternative = c("two.sided", "less", "greater"), mu = 0, paired = FALSE, var.equal = FALSE, conf.level = 0.95, . . .)

S3 method for class 'formula'

t.test(formula, data, subset, na.action, . . .)

Arguments

- x: a (non-empty) numeric vector of data values.
- y: an optional (non-empty) numeric vector of data values.
- alternative: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
- mu: a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
- paired: a logical indicating whether you want a paired t-test.
- var.equal: a logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.
- conf.level: confidence level of the interval.
- formula: a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs either 1 for a one-sample or paired test or a factor with two levels giving the corresponding groups. If lhs is of class "Pair" and rhs is 1, a paired test is done
- data: an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
- subset: an optional vector specifying a subset of observations to be used.
- na.action: a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
- . . . : further arguments to be passed to or from methods.

R help: `ezANOVA`

Compute ANOVA

Description

This function provides easy analysis of data from factorial experiments, including purely within-Ss designs (a.k.a. “repeated measures”), purely between-Ss designs, and mixed within-and-between-Ss designs, yielding ANOVA results, generalized effect sizes and assumption checks.

Usage

ezANOVA(data , dv , wid , within = NULL , within_full = NULL , within_covariates = NULL , between = NULL , between_covariates = NULL , observed = NULL , diff = NULL , reverse_diff = FALSE , type = 2 , white.adjust = FALSE , detailed = FALSE , return_aov = FALSE)

Arguments

- data: Data frame containing the data to be analyzed.
- dv: Name of the column in data that contains the dependent variable. Values in this column must be numeric.
- wid: Name of the column in data that contains the variable specifying the case/Ss identifier. This should be a unique value per case/Ss.
- within: Names of columns in data that contain predictor variables that are manipulated (or observed) within-Ss. If a single value, may be specified by name alone; if multiple values, must be specified as a .() list.
- within_full: Same as within, but intended to specify the full within-Ss design in cases where the data have not already been collapsed to means per condition specified by within and when within only specifies a subset of the full design.
- within_covariates: Names of columns in data that contain predictor variables that are manipulated (or observed) within-Ss and are to serve as covariates in the analysis. If a single value, may be specified by name alone; if multiple values, must be specified as a .() list.
- between: Names of columns in data that contain predictor variables that are manipulated (or observed) between-Ss. If a single value, may be specified by name alone; if multiple values, must be specified as a .() list.
- between_covariates: Names of columns in data that contain predictor variables that are manipulated (or observed) between-Ss and are to serve as covariates in the analysis. If a single value, may be specified by name alone; if multiple values, must be specified as a .() list.
- observed: Names of columns in data that are already specified in either within or between that contain predictor variables that are observed variables (i.e. not manipulated). If a single value, may be specified by name alone; if multiple values, must be specified as a .() list. The presence of observed variables affects the computation of the generalized eta-squared measure of effect size reported by ezANOVA.
- diff: Names of any variables to collapse to a difference score. If a single value, may be specified by name alone; if multiple values, must be specified as a .() list. All supplied variables must be factors, ideally with only two levels (especially if setting the reverse_diff argument to TRUE).
- reverse_diff: Logical. If TRUE, triggers reversal of the difference collapse requested by diff. Take care with variables with more than 2 levels.
- type: Numeric value (either 1, 2 or 3) specifying the Sums of Squares “type” to employ when data are unbalanced (eg. when group sizes differ). type = 2 is the default because this will yield identical ANOVA

results as type = 1 when data are balanced but type = 2 will additionally yield various assumption tests where appropriate. When data are unbalanced, users are warned that they should give special consideration to the value of type. type=3 will emulate the approach taken by popular commercial statistics packages like SAS and SPSS, but users are warned that this approach is not without criticism.

- white.adjust: Only affects behaviour if the design contains only between-Ss predictor variables. If not FALSE, the value is passed as the white.adjust argument to Anova, which provides heteroscedasticity correction. See Anova for details on possible values.
- detailed: Logical. If TRUE, returns extra information (sums of squares columns, intercept row, etc.) in the ANOVA table.
- return_aov: Logical. If TRUE, computes and returns an aov object corresponding to the requested ANOVA (useful for computing post-hoc contrasts).

Q: Stroop

Consider a Stroop experiment similar to that examined in Problem Set 10. Suppose that we are interested in assessing whether or not response times on incongruent trials are longer than on congruent trials. To do so we will perform an appropriate Null Hypothesis Significance Test (NHST) in which we assume that the random variable that generates response times on congruent trials has equal variance with the random variable that generates response times on incongruent trials. We perform an experiment and obtain the following data:

```
##     subject  trial_type response_time
##  1:       1   congruent     1.2446062
##  2:       1   congruent     0.8348303
##  3:       1 incongruent     1.0455885
##  4:       1 incongruent     1.2406372
##  5:       2   congruent     0.7408807
##  6:       2   congruent     1.0223179
##  7:       2 incongruent     0.9601173
##  8:       2 incongruent     0.9443862
##  9:       3   congruent     1.0757672
## 10:       3   congruent     0.9537816
## 11:       3 incongruent     0.9719098
## 12:       3 incongruent     1.0444594
## 13:       4   congruent     1.1326629
## 14:       4   congruent     1.0312416
## 15:       4 incongruent     1.1909621
## 16:       4 incongruent     1.0729594
```

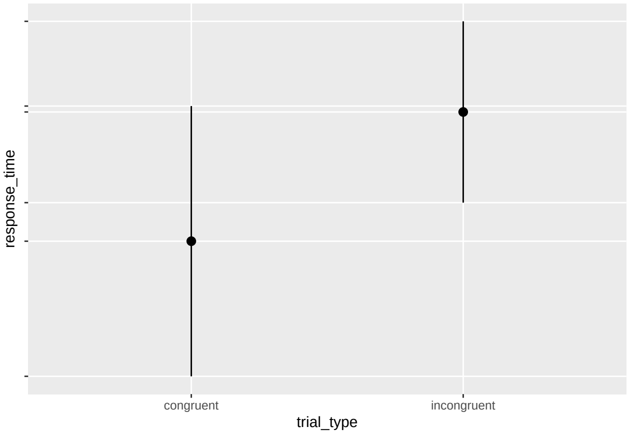
- Each row is an observation.
- The `subject` column indicates the subject from which each observation was obtained.
- The `trial_type` column indicates whether each observation was of a congruent or incongruent type.
- The `response_time` column contains response time observations.

We also calculate the following descriptive statistics:

```r
dd <- d[, .(mean(response_time),
            sd(response_time)/sqrt(.N)),
        .(trial_type)]
dd
```

```
##     trial_type       V1         V2
## 1:   congruent 1.004511 0.05685879
## 2: incongruent 1.058877 0.03814702
```

- The following figure shows the mean and SEM response time on congruent and incongruent trials. The error bars extend 1 SEM above and 1 SEM below the mean. Label all y-axis tick marks with numerical values.



- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q: Flanker

Consider a Flanker experiment similar to that examined in Problem Set 10. The classic finding from this experiment is that response time is longer on incongruent trials (i.e., trials for which the flanking stimuli point in the opposite direction as the central stimulus) than it is for congruent trials (i.e., trials for which the flanking stimuli point in the same direction as the central stimulus). To examine this effect, we perform an experiment and obtain the following data:

```
##     subject  trial_type stim_colour response_time
##  1:       1   congruent         red     1.0427818
##  2:       1   congruent         red     1.1947874
##  3:       1 incongruent         red     1.2659910
##  4:       1 incongruent         red     1.0921390
##  5:       2   congruent         red     0.7103685
##  6:       2   congruent         red     0.9479001
##  7:       2 incongruent         red     1.1058385
##  8:       2 incongruent         red     1.0749629
##  9:       3   congruent       green     0.9028686
## 10:       3   congruent       green     0.8166289
## 11:       3 incongruent       green     1.5563260
## 12:       3 incongruent       green     1.2632784
## 13:       4   congruent       green     1.1170429
## 14:       4   congruent       green     1.1037005
## 15:       4 incongruent       green     1.3455241
## 16:       4 incongruent       green     1.0005139
## 17:       5   congruent         red     0.9073030
## 18:       5   congruent         red     1.1190866
## 19:       5 incongruent         red     1.2291166
## 20:       5 incongruent         red     1.2204902
## 21:       6   congruent         red     0.6625113
## 22:       6   congruent         red     0.7668239
## 23:       6 incongruent         red     0.8675693
## 24:       6 incongruent         red     1.1743392
## 25:       7   congruent       green     1.1853180
## 26:       7   congruent       green     1.1848502
## 27:       7 incongruent       green     1.0420004
## 28:       7 incongruent       green     1.1084013
## 29:       8   congruent       green     1.0378365
## 30:       8   congruent       green     1.1009080
## 31:       8 incongruent       green     1.4946199
## 32:       8 incongruent       green     1.1014345
##     subject  trial_type stim_colour response_time
```

- Each row is an observation.
- The `subject` column indicates the subject from which each observation was obtained.
- The `trial_type` column indicates whether each observation was of a congruent or incongruent type.
- The `stim_colour` column indicates whether each observation was obtained from a red or green stimulus.
- The `response_time` column contains response time observations.

The following analysis in `R` reveals that we observe the classic Flanker effect. That is, response time on congruent trials is significantly shorter than response time on incongruent trials:

```
dd <- d[, .(response_time = mean(response_time)), .(trial_type, subject)]
dd
```

```
##      trial_type subject response_time
##  1:   congruent       1     1.1187846
##  2: incongruent       1     1.1790650
##  3:   congruent       2     0.8291343
##  4: incongruent       2     1.0904007
##  5:   congruent       3     0.8597488
##  6: incongruent       3     1.4098022
##  7:   congruent       4     1.1103717
##  8: incongruent       4     1.1730190
##  9:   congruent       5     1.0131948
## 10: incongruent       5     1.2248034
## 11:   congruent       6     0.7146676
## 12: incongruent       6     1.0209543
## 13:   congruent       7     1.1850841
## 14: incongruent       7     1.0752009
## 15:   congruent       8     1.0693723
## 16: incongruent       8     1.2980272
```

```
x <- dd[trial_type=='congruent', response_time]
y <- dd[trial_type=='incongruent', response_time]
t.test(x,
       y,
       alternative='less',
       mu=0,
       paired=T,
       var.equal=T
       )
```

```
##
##  Paired t-test
##
## data:  x and y
## t = -2.8131, df = 7, p-value = 0.01301
## alternative hypothesis: true mean difference is less than 0
## 95 percent confidence interval:
##        -Inf -0.0641182
## sample estimates:
## mean difference
##      -0.1963643
```

Suppose that we are interested in assessing whether or not the colour of the stimuli influences the magnitude of the classic Flanker effect. We need a bit more data wrangling to set our data up for this question.

```
dd <- d[, .(mean(response_time)),  .(subject, trial_type, stim_colour)]
dd
```

```
##     subject  trial_type stim_colour        V1
##  1:       1   congruent         red 1.1187846
##  2:       1 incongruent         red 1.1790650
##  3:       2   congruent         red 0.8291343
##  4:       2 incongruent         red 1.0904007
##  5:       3   congruent       green 0.8597488
##  6:       3 incongruent       green 1.4098022
##  7:       4   congruent       green 1.1103717
##  8:       4 incongruent       green 1.1730190
##  9:       5   congruent         red 1.0131948
## 10:       5 incongruent         red 1.2248034
## 11:       6   congruent         red 0.7146676
## 12:       6 incongruent         red 1.0209543
## 13:       7   congruent       green 1.1850841
## 14:       7 incongruent       green 1.0752009
## 15:       8   congruent       green 1.0693723
## 16:       8 incongruent       green 1.2980272
```

```
ddd <- dd[, .(response_time_difference = diff(V1)), .(subject, stim_colour)]
ddd
```

```
##    subject stim_colour response_time_difference
## 1:       1         red               0.06028041
## 2:       2         red               0.26126640
## 3:       3       green               0.55005343
## 4:       4       green               0.06264726
## 5:       5         red               0.21160860
## 6:       6         red               0.30628666
## 7:       7       green              -0.10988324
## 8:       8       green               0.22865493
```

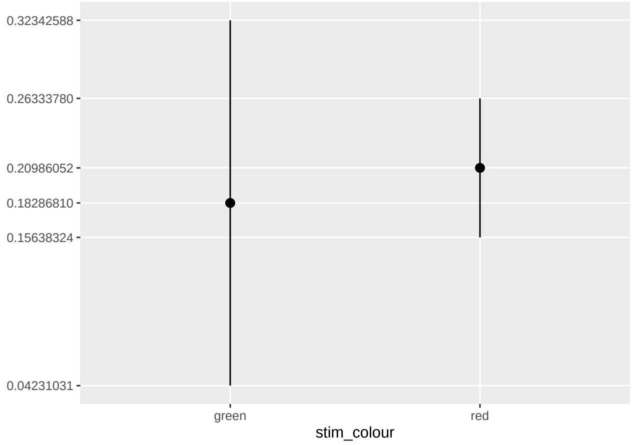
- The `subject` indicates the same as above.
- The `stim_colour` indicates the same as above.
- The `response_time_difference` column contains the difference in mean response time on congruent versus incongruent trials.

From this position, we proceed to perform an appropriate NHST to assess whether or not stimulus colour influences the magnitude of the Flanker effect. For the purposes of the following questions, use `ddd` as the raw data.

- Given the following `data.table` and `ggplot` code, what is the mean response time difference on green, and red trials? What is the SEM response time difference on green and red trials?

```r
dddd <- ddd[, .(mean(response_time_difference),
                sd(response_time_difference)/sqrt(.N)),
            .(stim_colour)]

ggplot(dddd, aes(x=stim_colour, y=V1)) +
  geom_pointrange(aes(ymin=V1-V2, ymax=V1+V2)) +
  ylab('') +
  scale_y_continuous(breaks=c(dddd[, V1], dddd[, V1-V2], dddd[, V1+V2]),
                     minor_breaks=NULL)
```



- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q: Visual Search

Consider a visual search experiment similar to that examined in Problem Set 10. Suppose that we are interested in assessing whether or not the colour of the stimuli, the set size, or their interaction influences the visual search time. To do so we will perform an appropriate Null Hypothesis Significance Test(NHST). We perform an experiment and obtain the following data:

```
##     subject set_size stim_colour search_time
##  1:       1        5         red   1.0508429
##  2:       2        5       green   0.8193217
##  3:       3       10         red   1.2823403
##  4:       4       10       green   1.3206497
##  5:       5       15         red   1.6982711
##  6:       6       15       green   1.7249772
##  7:       7        5         red   1.1436059
##  8:       8        5       green   1.1154922
##  9:       9       10         red   0.9778468
## 10:      10       10       green   1.5143405
## 11:      11       15         red   1.7943233
## 12:      12       15       green   1.5372585
## 13:      13        5         red   0.8721752
## 14:      14        5       green   0.8668113
## 15:      15       10         red   1.7835308
## 16:      16       10       green   1.1449562
## 17:      17       15         red   1.9347964
## 18:      18       15       green   1.6777965
## 19:      19        5         red   0.9160544
## 20:      20        5       green   1.0880297
## 21:      21       10         red   1.1407313
## 22:      22       10       green   1.2643417
## 23:      23       15         red   1.9669412
## 24:      24       15       green   1.7436173
##     subject set_size stim_colour search_time
```

- Each row is an observation.
- The `subject` column indicates the subject from which each observation was obtained.
- The `set_size` column indicates the number of stimuli on the screen.
- The `stim_colour` column indicates whether each observation was obtained from red or green stimuli.
- The `search_time` column contains search time observations.

Preliminary analyses reveal the following:

```
d[, .(mean(search_time),
      sd(search_time) / sqrt(.N)),
  .(set_size)]
```

```
##    set_size        V1         V2
## 1:        5 0.9840417 0.04551842
## 2:       10 1.3035922 0.08811905
## 3:       15 1.7597477 0.04932267
```

```
d[, .(mean(search_time),
      sd(search_time) / sqrt(.N)),
  .(stim_colour)]
```

```
##    stim_colour       V1         V2
## 1:         red 1.380122 0.12166672
## 2:       green 1.318133 0.09300681
```

```
d[, .(mean(search_time),
      sd(search_time) / sqrt(.N)),
  .(set_size, stim_colour)]
```

```
##    set_size stim_colour        V1         V2
## 1:        5         red 0.9956696 0.06226200
## 2:        5       green 0.9724137 0.07551354
## 3:       10         red 1.2961123 0.17397380
## 4:       10       green 1.3110720 0.07702163
## 5:       15         red 1.8485830 0.06256942
## 6:       15       green 1.6709124 0.04665455
```

Finally, we also know the following sums of squared variabilities:

- $SS_{\text{set\_size}} = 2.43$
- $SS_{\text{stim\_colour}} = 0.02$
- $SS_{\text{set\_size} \times \text{stim\_colour}} = 0.041607$
- $SS_{\text{error}} = 0.62$

- Draw 3 point range plots showing (1) the main effect of set size, (2) the main effect of stim colour, (3) the interaction of set size and stim colour. The error bars on each should extend 1 SEM above and below the mean.

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q

Consider the following data from some experiment:

```
##              x
##   1: 62.07908
##   2: 37.68677
##   3: 59.83896
##   4: 52.19925
##   5: 35.32750
##  ---
## 196: 38.32338
## 197: 49.91691
## 198: 51.28855
## 199: 48.54124
## 200: 48.36089
```

- The `x` column contains dependent variable observations from an experiment condition named `x`.
- Suppose that we know that each observation was acquired from a different participant. Next, consider the following NHST result:

```
## 
##  One Sample t-test
## 
## data:  x
## t = -2.6105, df = 199, p-value = 0.009728
## alternative hypothesis: true mean is not equal to 52
## 95 percent confidence interval:
##  48.77070 51.54999
## sample estimates:
## mean of x 
##  50.16034
```

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q

Consider the following data from some experiment:

```
##             x        y
##   1: 67.63552 40.35079
##   2: 57.62587 38.23481
##   3: 61.11431 53.67680
##   4: 40.76793 67.84629
##   5: 51.64342 68.77889
##  ---
## 196: 58.48420 51.37279
## 197: 59.86770 42.19098
## 198: 55.75620 62.87150
## 199: 70.24842 53.39327
## 200: 30.37647 48.13728
```

- The `x` column contains dependent variable observations from an experiment condition named `x`.
- The `y` column contains dependent variable observations from an experiment condition named `y`.
- Suppose that we know that every observation from `x` or `y` was acquired from a different participant. Next, consider the following NHST result:

```
##
##  Two Sample t-test
##
## data:  x and y
## t = -1.0395, df = 398, p-value = 0.1496
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##       -Inf 0.6605075
## sample estimates:
## mean of x mean of y
##  49.82999  50.95692
```

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q

Consider the following data from some experiment:

```
##              x        y
##   1: 61.23585 52.64627
##   2: 42.40154 56.63659
##   3: 61.48959 52.74778
##   4: 41.57524 47.13164
##   5: 53.91413 59.48911
##  ---
## 196: 20.03051 61.88092
## 197: 40.38948 64.46123
## 198: 53.80188 48.70133
## 199: 55.05068 60.44345
## 200: 70.27056 42.18924
```

- The `x` column contains dependent variable observations from an experiment condition named `x`.
- The `y` column contains dependent variable observations from an experiment condition named `y`.
- Suppose that we know that every observation from `x` or `y` was acquired from a different participant. Next, consider the following NHST result:

```
##
##  Welch Two Sample t-test
##
## data:  x and y
## t = -1.0575, df = 392.72, p-value = 0.1455
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##       -Inf 0.6136781
## sample estimates:
## mean of x mean of y
##  50.03877  51.13640
```

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q

Consider the following data from some experiment:

```
##              x        y
##   1: 48.60779 50.42018
##   2: 71.85438 45.18490
##   3: 49.87172 39.79899
##   4: 46.94691 44.91087
##   5: 44.15787 44.51320
##  ---
## 196: 60.56070 42.93311
## 197: 52.43502 46.70650
## 198: 61.14363 65.43577
## 199: 49.23447 56.69434
## 200: 59.32925 49.46895
```

- The `x` column contains dependent variable observations from an experiment condition named `x`.
- The `y` column contains dependent variable observations from an experiment condition named `y`.
- Suppose that we know that observations from `x` and `y` were acquired from the same group of participants, and that measurements in each column are in the same order. Next, consider the following NHST result:

```
## 
##  Paired t-test
## 
## data:  x and y
## t = -1.7969, df = 199, p-value = 0.07386
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -4.0245200  0.1868993
## sample estimates:
## mean difference 
##        -1.91881
```

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q

Consider the following data from some experiment:

```
##              y factor_1 factor_2 subject
##  1: 11.8455186        A        1       1
##  2:  3.2664640        A        1       2
##  3: 15.8596771        A        1       3
##  4:  0.4563183        A        1       4
##  5: 24.9780459        A        2       5
##  6: 33.3834376        A        2       6
##  7: 35.7616087        A        2       7
##  8: 15.6609650        A        2       8
##  9: 43.0065443        B        1       9
## 10: 41.7082516        B        1      10
## 11: 39.8235950        B        1      11
## 12: 36.8691749        B        1      12
## 13: 15.7201440        B        2      13
## 14: 20.7588892        B        2      14
## 15: 26.0318635        B        2      15
## 16: 12.5571106        B        2      16
## 17: 34.7481294        C        1      17
## 18: 48.1893706        C        1      18
## 19: 33.9633291        C        1      19
## 20: 26.8692246        C        1      20
## 21: 20.0873163        C        2      21
## 22: 21.7209701        C        2      22
## 23: 20.0635992        C        2      23
## 24: 15.6327493        C        2      24
##              y factor_1 factor_2 subject
```

- The `y` column contains dependent variable observations.
- The `factor_1` column indicates levels of an independent variable named `factor_1`.
- The `factor_2` column indicates levels of an independent variable named `factor_2`.
- The `subject` column indicates the subject from which each observation (row) was obtained.

Next, consider the following NHST result:

```
## Coefficient covariances computed by hccm()
```

```
##              Effect DFn DFd       SSn      SSd         F            p p<.05
## 1          factor_1   2  18  654.8432 789.2052  7.467752 4.349844e-03     *
## 2          factor_2   1  18  229.7041 789.2052  5.239036 3.439194e-02     *
## 3 factor_1:factor_2   2  18 2018.4584 789.2052 23.018254 1.095478e-05     *
##         ges
## 1 0.4534773
## 2 0.2254412
## 3 0.7189103
```

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q

Consider the following data from some experiment:

```
##             y factor_1 factor_2 subject
##  1: 11.714001        A        1       1
##  2:  9.113061        A        1       2
##  3: 14.607166        A        1       3
##  4: 11.504722        A        1       4
##  5: 33.466934        A        2       5
##  6: 31.627360        A        2       6
##  7: 32.040255        A        2       7
##  8: 33.799211        A        2       8
##  9: 28.564232        B        1       1
## 10: 42.589191        B        1       2
## 11: 33.263819        B        1       3
## 12: 41.815799        B        1       4
## 13: 26.573763        B        2       5
## 14: 17.758470        B        2       6
## 15: 15.959178        B        2       7
## 16: 19.568658        B        2       8
## 17: 47.927121        C        1       1
## 18: 40.505287        C        1       2
## 19: 40.743811        C        1       3
## 20: 37.267827        C        1       4
## 21: 17.361622        C        2       5
## 22: 19.300642        C        2       6
## 23: 12.052943        C        2       7
## 24: 26.170521        C        2       8
##             y factor_1 factor_2 subject
```

- The `y` column contains dependent variable observations.
- The `factor_1` column indicates levels of an independent variable named `factor_1`.
- The `factor_2` column indicates levels of an independent variable named `factor_2`.
- The `subject` column indicates the subject from which each observation (row) was obtained.

Next, consider the following NHST result:

```
##              Effect DFn DFd        SSn      SSd           F            p p<.05
## 1       (Intercept)   1   6 17350.2669  82.9045 1255.680891 3.366908e-08     *
## 2          factor_2   1   6   227.7751  82.9045   16.484640 6.649540e-03     *
## 3          factor_1   2  12   274.3401 302.0440    5.449672 2.070853e-02     *
## 4 factor_2:factor_1   2  12  2252.6530 302.0440   44.748182 2.731395e-06     *
##         ges
## 1 0.9782947
## 2 0.3717421
## 3 0.4161153
## 4 0.8540536
```

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

Q

Consider the following data from some experiment:

```
##                 y factor_1 factor_2 subject
##  1:  8.322725758        A        1       1
##  2: -0.005012534        A        1       2
##  3:  9.912707986        A        1       3
##  4:  8.795165521        A        1       4
##  5: 21.040053005        A        2       1
##  6: 40.248457556        A        2       2
##  7: 24.413911942        A        2       3
##  8: 23.232252276        A        2       4
##  9: 42.256511555        B        1       1
## 10: 45.166137124        B        1       2
## 11: 39.020571524        B        1       3
## 12: 41.136551934        B        1       4
## 13: 14.489001250        B        2       1
## 14: 24.776386843        B        2       2
## 15: 21.564152230        B        2       3
## 16: 20.505028566        B        2       4
## 17: 43.740577071        C        1       1
## 18: 42.574038550        C        1       2
## 19: 36.337423455        C        1       3
## 20: 42.404476201        C        1       4
## 21: 15.052748459        C        2       1
## 22: 31.147795242        C        2       2
## 23: 22.283682998        C        2       3
## 24: 19.820922782        C        2       4
##                 y factor_1 factor_2 subject
```

- The `y` column contains dependent variable observations.
- The `factor_1` column indicates levels of an independent variable named `factor_1`.
- The `factor_2` column indicates levels of an independent variable named `factor_2`.
- The `subject` column indicates the subject from which each observation (row) was obtained.

Next, consider the following NHST result:

```
##              Effect DFn DFd        SSn       SSd          F            p p<.05
## 1       (Intercept)   1   3 16972.7305 142.90861 356.298966 3.246222e-04     *
## 2          factor_1   2   6  1106.7288  11.62268 285.664382 1.122494e-06     *
## 3          factor_2   1   3   273.9658 242.98118   3.382556 1.631722e-01
## 4 factor_1:factor_2   2   6  2230.7974 141.76787  47.206692 2.133433e-04     *
##         ges
## 1 0.9692051
## 2 0.6723710
## 3 0.3368793
## 4 0.8053194
```

- State how each random variable that generates raw data in this experiment is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- Draw each distribution from the previous bullet. Wherever possible, include labels that indicate population means.

- State all Null and Alternative hypotheses for this test.

- Write equations that state exactly how you will estimate the parameters used in all Null hypotheses stated in the previous bullet.

- For each null hypothesis included in this test, state how the random variable that generates the observed test statistic is defined under the assumption that H_0 is true.

- For each null hypothesis included in this test, what is the observed value of the test statistic? Plug the relevant numbers into the equations from the previous bullet. You do not have to evaluate the resulting expression exactly, but write down what you think it evaluates to approximately (this is so you can add it to a drawing in a later bullet).

- For each null hypothesis included in this test, state how the random variable that generates the test statistic is distributed under the assumption that H_0 is true. Include numerical values for population parameters wherever possible.

- For each null hypothesis included in this test, draw the distribution from the previous bullet. Add labels to this drawing that indicate upper and lower bounds, its population mean, and the observed value of the test statistic.

- For each null hypothesis included in this test, illustrate the p-value of the test by redrawing the appropriate distribution from previous bullets and shading the region that it corresponds to. Here, you do not need to calculate an exact numerical value.

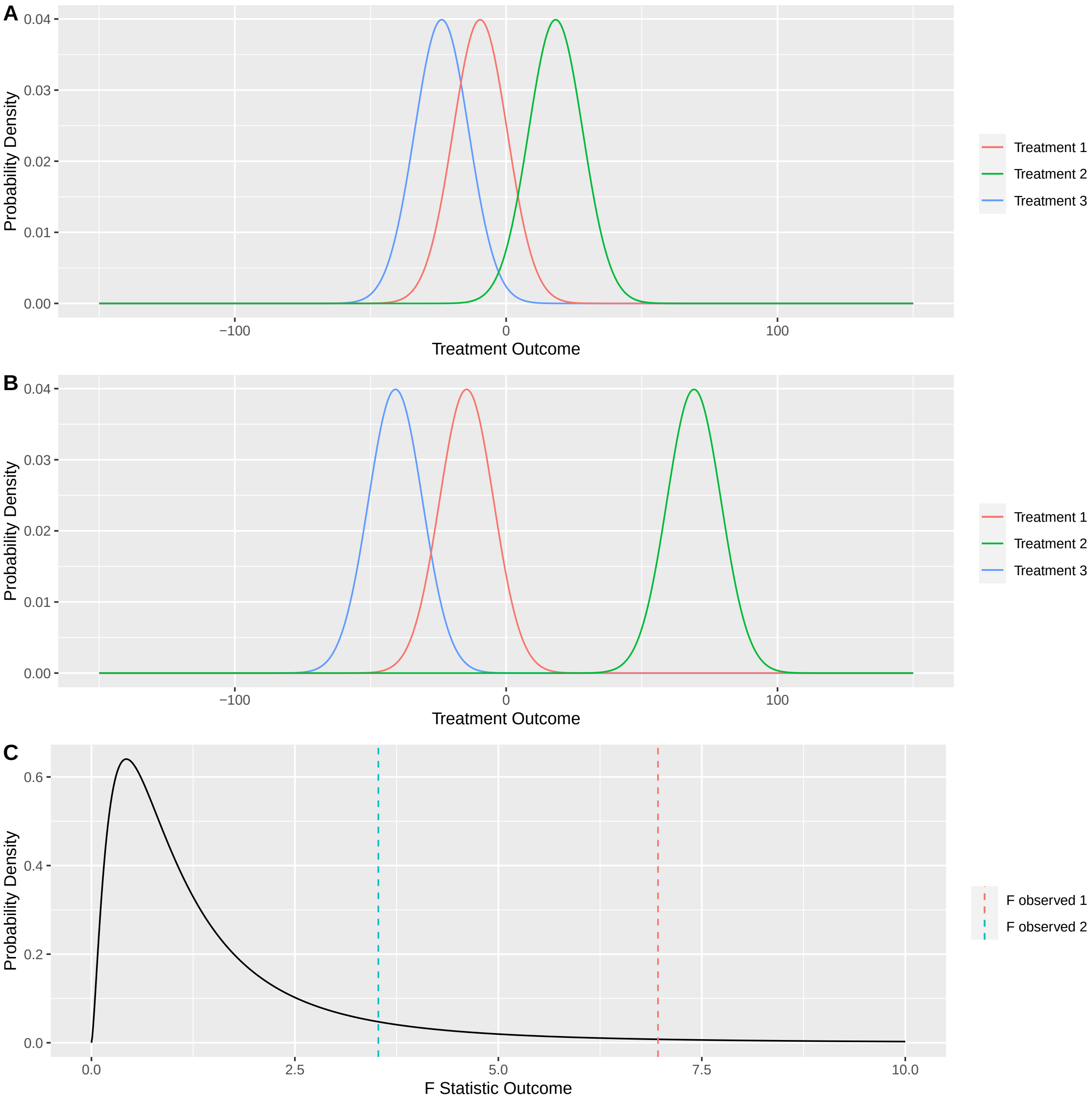
- For each null hypothesis included in this test, illustrate the critical value(s) of this test by redrawing the appropriate distribution from previous bullets and marking the relevant location on the x-axis of the plot. Here, you do not need to calculate an exact numerical value.

- For each null hypothesis included in this test, if it is two-tailed, illustrate its 95% confidence interval by redrawing the appropriate distribution from previous bullets and adding annotations. Otherwise, simply write *N/A* in the space below.

- Write `R` code (using your pen or pencil) that would perform this NHST using either `t.test()` or `ezANOVA()`.

1.

Consider an experiment in which three different treatments are given to people and the overall effect on sleep quality is measured for each person. Panel A in the figure below shows one possible arrangement of treatment effect population distributions, and panel B shows another. Panel C shows the sampling distribution of an F test statistic and two observed F statistic values. One of these F observed values corresponds to the arrangement of treatment effects in panel A, and the other corresponds to the arrangement of treatment effects in panel B.



- Assuming that this is a repeated measures design, which of the two F observed statistics illustrated in panel C most likely corresponds to the arrangement of population means in panel A, and which corresponds to the arrangement in panel B?
- Assuming that this is a factorial design, which of the two F observed statistics illustrated in panel C most likely corresponds to the arrangement of population means in panel A, and which corresponds to

the arrangement in panel B?

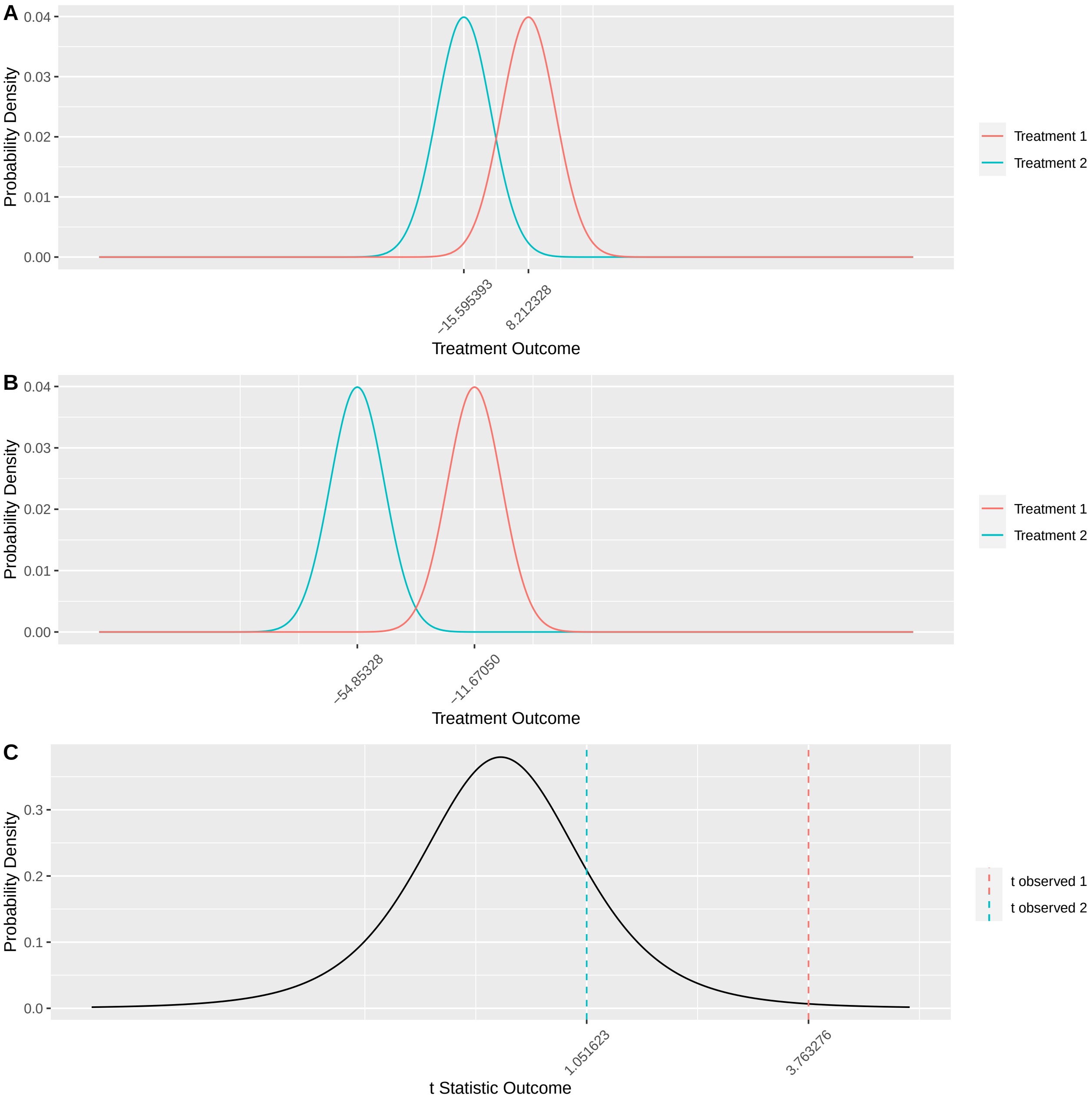
In reasoning though this question, please assume that every participant provides exactly that same amount of variability as every other participant. In addition to responding as instructed above, please explain your rationale in comments.

2.

Consider an experiment in which two different treatments are given to two different groups of people and the overall effect on sleep quality is measured for each person. Panel A in the figure below shows one possible arrangement of treatment effect population means, and panel B shows another.

- What observed t-statistic value is most likely to arise if panel A is the true state of the universe?
- What observed t-statistic value is most likely to arise if panel B is the true state of the universe?

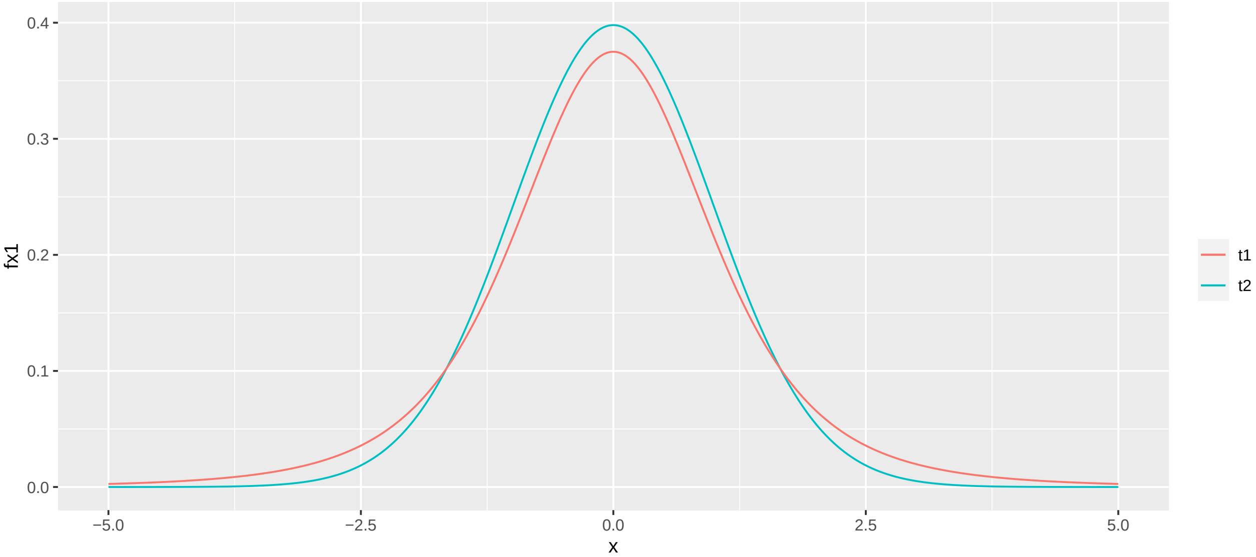
In reasoning though this question, please assume that every participant provides exactly the same amount of variability as every other participant. In particular, please assume that the standard deviation of the population distributions illustrated in panels A and B have the numerical value $\sigma = 10$.



3.

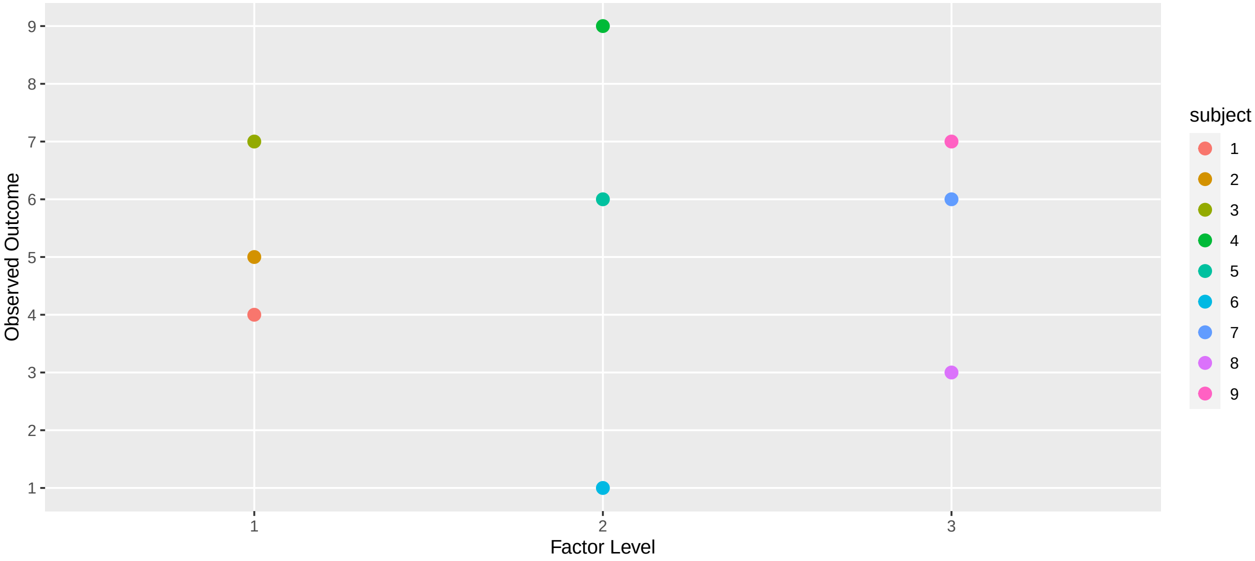
Consider the t-distributions illustrated below.

- Which distribution has the greater degrees of freedom?
- Assuming that these are sampling distributions of a test statistic obtained by performing an experiment on n participants, which distribution arose from the experiment with the greater number of participants?
- Assuming t1 is the sampling distribution of a test statistic arising from experiment 1, and Assuming t2 is the sampling distribution of a test statistic arising from experiment 2, which experiment requires more extreme outcomes in order to reject the null?
- Assuming that one of these distributions corresponds to an independent samples t-test, and the other to a repeated-measures t-test, and assuming equal n per condition, which is which?



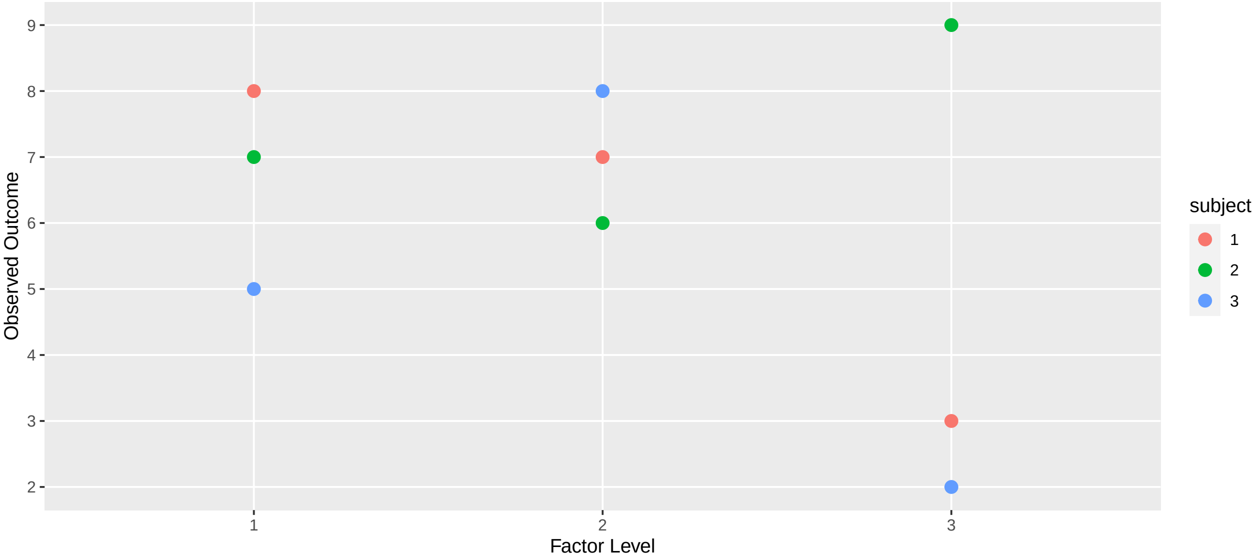
4.

Consider the data shown in the plot below, which come from some experiment in which the effects of three levels of some factor were explored. Test the hypothesis that the mean effect of the factor under investigation if different depending on the level of that factor.



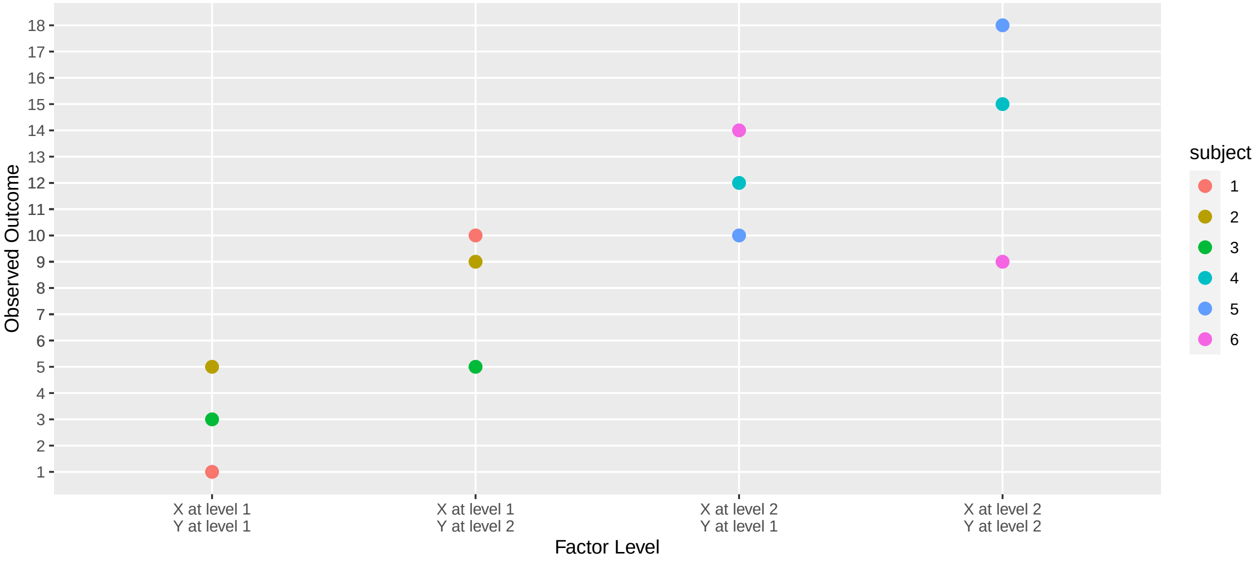
5.

Consider the data shown in the plot below, which come from some experiment in which the effects of three levels of some factor were explored. Test the hypothesis that the mean effect of the factor under investigation is different depending on the level of that factor.



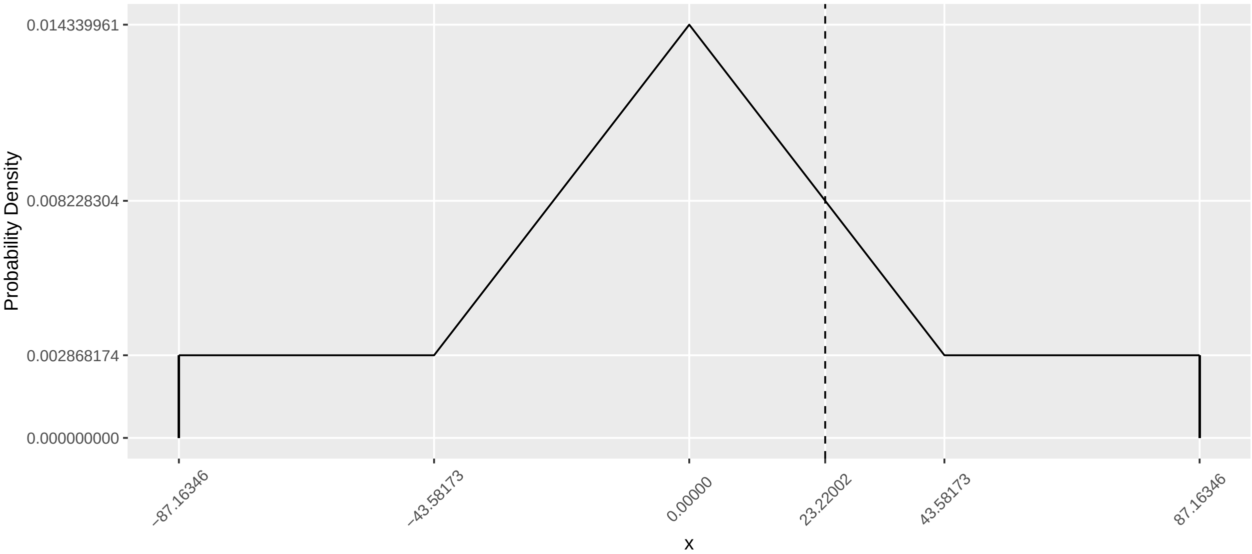
6.

Consider an experiment in which the effects of two factors (X and Y) were explored across two levels each. The results of this experiment are shown in the figure below. Test the hypothesis that there was a significant main effect of X, a significant main effect of Y, or a significant interaction between X and Y.



7.

Consider a random variable named X that is distributed as illustrated below.



It is clear that X is the sum of a triangular distribution and a uniform distribution. From this, we know that the variance of of X is the following:

$$Var\{X\} = \frac{a^2 + b^2 + c^2 - ab - ac - bc}{18} + \tfrac{1}{12}(d - e)^2$$

Here, $a = -43.5817301$, $b = 43.5817301$, $c = 0$, $d = 87.1634601$, and $e = -87.1634601$. Plugging these numbers into the equation above gives:

$$Var\{X\} = 331.0884427$$

Suppose that an experiment is performed and the following sample is obtained from X (sample mean = 23.22002 and sample standard deviation = 12.70787):

```
##  [1] 35.759359 34.068605  1.810036 19.539943  5.667715
##  [6] 35.283252 32.506321 21.127648 16.308652 13.205427
## [11] 27.214788 11.469669  6.545744  3.354562 32.495561
## [16] 28.738390  6.714626 38.136393  9.010533 26.411576
## [21]  3.558347 33.194009 20.144628 36.513377 43.215785
## [26] 34.135504 31.921658 41.142946 25.321534 22.084068
```

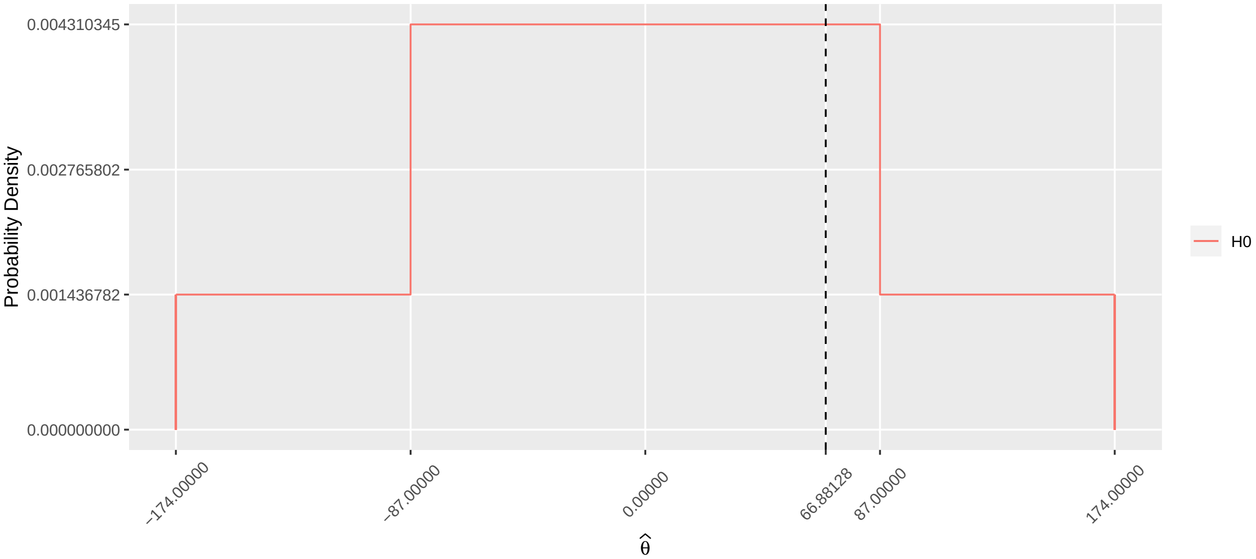
Please test the hypothesis that μ_X is non-zero. Ensure that the type I error rate of this test is 0.05. Note that the dashed line in the plot indicates the observed sample mean. Please show your work and explain your rationale in comments.

- What is the test statistic?
- What is the distribution of the random variable that generates test statistics?
- What is the observed value of the test statistic?
- What is the observed p-value of this test?

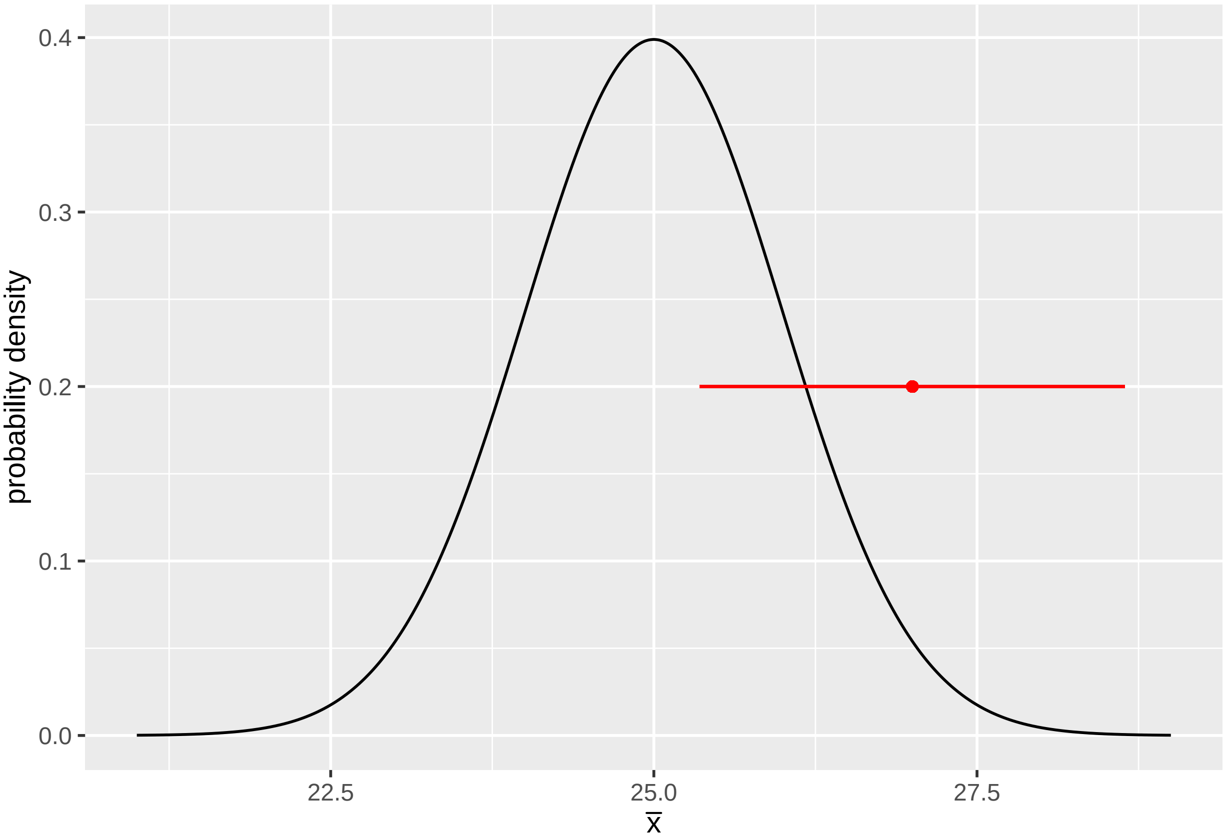
8.

Consider a random variable X defined by a single parameter named θ. Further consider a null hypothesis significance test designed to determine if θ is non-zero with confidence 0.95. The sampling distribution of $\widehat{\theta}$ in this test is illustrated below. The dashed line in the plot indicates the observed value of the test statistic. When compared against an alternative hypothesis that $\theta = 10$, compute the following quantities:

- Calculate the probability of making a type I error.
- Calculate the probability of making a type II error.
- Calculate the power of this hypothesis test.
- Calculate the confidence of this hypothesis test.



9.



The above figure shows the distribution of the random variable that generates sample means $\bar{X}$ for a particular NHST (black line) and the 95% confidence interval estimate of $\mu_{\bar{X}}$.

- What is null hypothesis of this test? Be specific and give numerical values if possible.
- Is the p-value of this test greater than or less than 0.05?