Lakens / ANOVApower

Simulation-Based Power Analysis for ANOVA Designs

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Lakens store lambda_2 — Latest commit `65340e5` on Sep 6

Meta	add vignette & update mu function	7 months ago
R	store lambda_2	2 months ago
README_files	update readme	6 months ago
jamovi	Added jamovi support	5 months ago
man	Updated functions to include adjustments for sphericity and include m…	2 months ago
mess	plot power for ANOVA	6 months ago
tests	Updated functions to include adjustments for sphericity and include m…	2 months ago
vignettes	reduce filesizes remove screenshots in vignette and readme	6 months ago
.Rbuildignore	Added jamovi support	5 months ago
.Rhistory	Updated functions to include adjustments for sphericity and include m…	2 months ago
.gitignore	Added jamovi support	5 months ago
.travis.yml	travis runs a lot faster if you cache the packages	5 months ago
ANOVApower.Rproj	minor updates	7 months ago
DESCRIPTION	Added jamovi support	5 months ago
LICENSE	initial commit	7 months ago
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NAMESPACE	Updated functions to include adjustments for sphericity and include m…	2 months ago
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README.md

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An Introduction to ANOVApower

The goal of ANOVApower is to easily simulate ANOVA designs and empirically calculate power using a simulation approach. This app is intended to be utilized for prospective (a priori) power analysis.

Installation

You can install the released version of ANOVApower from GitHub with:

```
devtools::install_github("Lakens/ANOVApower")
```

ANOVA_design function

Currently the ANOVA_design function can create designs up three factors, for both within, between, and mixed designs. It requires the following input: design, n, mu, sd, r, and optionally allows you to set labelnames.

1. design: string that specifies the design (see below).
2. n: the sample size for each between subject condition.
3. mu: a vector with the means for each condition.
4. sd: the population standard deviation. Assumes homogeneity of variances (only one standard deviation can be provided).
5. r: the correlation for within designs (or 0 for between designs).
6. labelnames: This is an optonal vector of words that indicates factor names and level names (see below).
7. A final optional setting is to specify if you want to output a plot or not (plot = TRUE or FALSE)

Specifying the design using 'design'

'design' is used to specify the design. Every factor is specified with a number, indicating the numner of levels of the factor, and a letter, b or w, to indicate whether the factor is manipulated between or within participants. For example, a `2b` design has two between-participant groups. A `12w` design has one factor with 12 levels, all manipulated within-participants. A "2b*3w" is a design with two factors (a 2b factor and a 3w factor), the first of which has 2 between participant levels (2b), and the second of which has 3 within participants levels (3w). **If there are multiple factors (the functions take up to three different factors) seperate factors with a * (asterisk)**. An example of a `2b*3w` design is a group of people in one condition who get a drug, and a group of people in another condition who get a placebo, and we measure their health before they take the pill, one day after they take the pill, and a week after they take the pill.

Specifying the means using 'mu'

Note that for each cell in the design, a mean must be provided. Thus, for a "2b*3w" design, 6 means need to be entered.

Means need to be entered in the correct order. ANOVA_design outputs a plot so you can check if you entered all means as you intended. Always carefully check if the plot that is generated matches your expectations.

The general principle is that the code generates factors, indicated by the factor names you entered in the labelnames variable, (i.e., *condition* and *time*). Levels are indicated by factor names and levels (e.g., control_time1, control_time2, control_time3, etc).

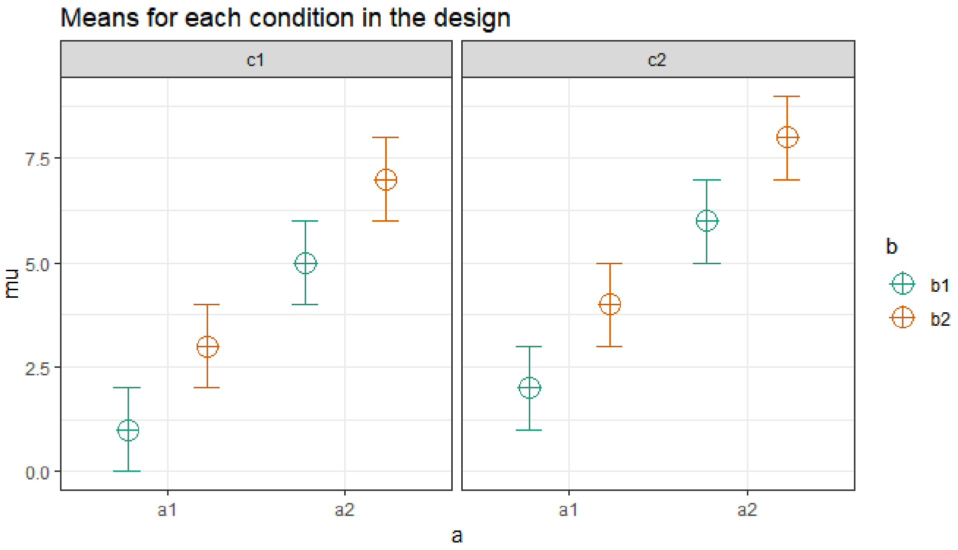
If your design has just one factor, just enter the means in the same order as the labelnames (see below). For more factors, note the general pattern in the example below. Means are entered in the following order for a 3 factors design (each with 2 levels):

1. a1 b1 c1

2. a1 b1 c2
3. a1 b2 c1
4. a1 b2 c2
5. a2 b1 c1
6. a2 b1 c2
7. a2 b2 c1
8. a2 b2 c2

So if you enter the means 1, 2, 3, 4, 5, 6, 7, 8 the first 4 means correspond to level 1 of factor 1, the second 4 means correspond to level 2 of factor 1. Within the first 4 means, the first 2 correspond to level 1 of factor 2, and within those 2 means, the first corresponds to level 1 of factor 3.

The plot below visualizes means from 1 to 8 being entered in a vector: mu = c(1, 2, 3, 4, 5, 6, 7, 8) so you can see how the basic ordering works.



Specifying label names

To make sure the plots and tables with simulation results are easy to interpret, it really helps to name all factors and levels. You can enter the labels in the ‘labelnames’ variable. You can also choose not to specify names. Then all factors are indicated by letters (a, b, c) and all levels by numbers (a1, a2, a3).

For the 2x3 design we have been using as an example, where there are 2 factors (condition and time of measurement), the first with 2 levels (placebo vs. medicine) and the second with three levels (time1, time2, and time3) we would enter the labels as follows:

c(“condition”, “placebo”, “medicine”, “time”, “time1”, “time2”, “time3”)

As you can see, you follow the order of the design (2b*3w), and first write the **FACTOR** label (condition) followed by the levels of that factor (placebo and medicine). Then you write the second factor name (time) followed by the three labels for each **LEVEL** (time1, time2, time3). **Do not use spaces in the names (so not “time 1” but “time1” or “time_1”).**

Some examples:

1. One within factor (time with 2 levels), 2w:

- `c("time", "morning", "evening")`

2. Two between factors (time and group, each with 2 levels), 2b*2b:

- `c("time", "morning", "evening", "group", "control", "experimental")`

3. Two between factors (time and group, first with 4 levels, second with 2 levels), 4b*2b:

- `c("time", "morning", "afternoon" ,"evening", "night", "group", "control", "experimental")`

Specifying the correlation

Depending on whether factors are manipulated within or between, variables are correlated, or not. You can set the correlation for within-participant factors. You can either assume all factors have the same correlation (e.g., r = 0.7), or enter the correlations for each pair of observations separately by specifying a correlation matrix.

Specifying the correlation matrix.

In a 2x2 within-participant design, with factors A and B, each with 2 levels, there are 6 possible comparisons that can be made.

1. A1 vs. A2
2. A1 vs. B1
3. A1 vs. B2
4. A2 vs. B1
5. A2 vs. B2
6. B1 vs. B2

The number of possible comparisons is the product of the levels of all factors squared minus the product of all factors, divided by two. For a 2x2 design where each factor has two levels, this is:

```
(((2*2)^2)-(2*2))/2
```

```
## [1] 6
```

The number of possible comparisons increases rapidly when adding factors and levels for each factor. For example, for a 2x2x4 design it is:

```
(((2*2*4)^2)-(2*2*4))/2
```

```
## [1] 120
```

Each of these comparisons can have their own correlation if the factor is manipulated within subjects (if the factor is manipulated between subjects the correlation is 0). These correlations determine the covariance matrix. Potvin and Schutz (2000) surveyed statistical tools for power analysis and conclude that most software packages are limited to one factor repeated measure designs and do not provide power calculations for within designs with multiple factor (which is still true for software such as G*Power). Furthermore, software solutions which were available at the time (DATASIM by Bradley, Russel, & Reeve, 1996) required researchers to assume correlations were of the same magnitude for all within factors, which is not always realistic. If you do not want to assume equal correlations for all paired comparisons, you can specify the correlation for each possible comparison.

The order in which the correlations are entered in the vector should match the covariance matrix. The order for a 2x2 design is given in the 6 item list above. The general pattern is that the matrix is filled from top to bottom, and left to right, illustrated by the increasing correlations in the table below.

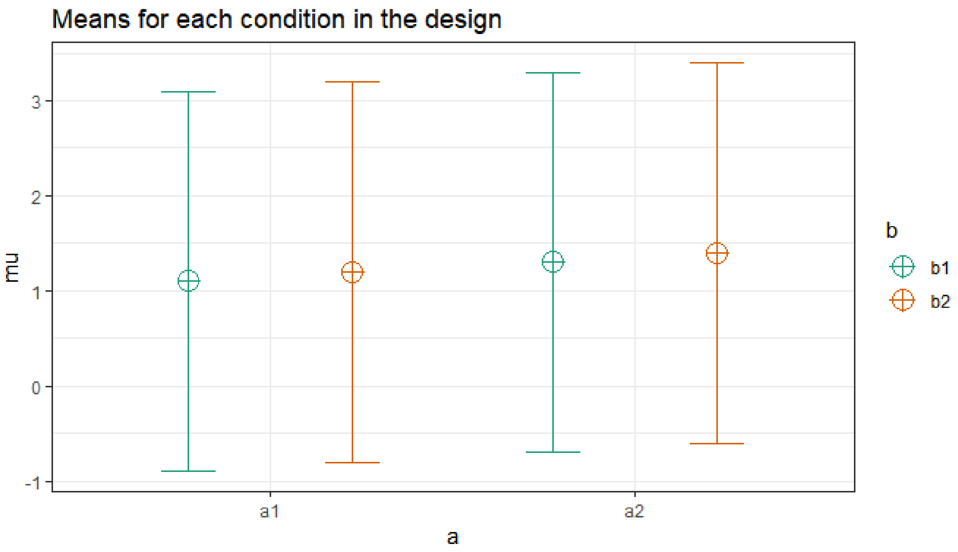
Factor	a1_b1	a1_b2	a2_b1	a2_b2
a1_b1	1.00	0.91	0.92	0.93
a1_b2	0.91	1.00	0.94	0.95

Factor	a1_b1	a1_b2	a2_b1	a2_b2
a2_b1	0.92	0.94	1.00	0.96
a2_b2	0.93	0.95	0.96	1.00

The diagonal is generated dynamically (and all conditions are perfectly correlated with themselves).

We would enter this correlation matrix as:

```
design_result <- ANOVA_design(design = "2w*2w",
                              n = 80,
                              mu = c(1.1, 1.2, 1.3, 1.4),
                              sd = 2,
                              r <- c(0.91, 0.92, 0.93, 0.94, 0.95, 0.96))
```



We can check the correlation matrix by asking for it from the design_result object to check if it was entered the way we wanted:

```
design_result$cor_mat
```

```
##       a1_b1 a1_b2 a2_b1 a2_b2
## a1_b1  1.00  0.91  0.92  0.93
## a1_b2  0.91  1.00  0.94  0.95
## a2_b1  0.92  0.94  1.00  0.96
## a2_b2  0.93  0.95  0.96  1.00
```

Note that we did not specify the labelnames, and thus they are automatically created.

Specifying the sample size

You can set the sample size **per condition** by setting a value for n. The assumption is that you will collect equal sample sizes in all conditions [expanding ANOVApower to allow different sample sizes in each group is a planned future option].

Specifying the standard deviation

You can set the standard deviation by setting a value of sd. Currently ANOVApower only allows you to perform calculations under the assumption of homogeneity of variances (the standard deviation is the same across conditions). Note that there is always some uncertainty in which values you can expect in the study you are planning. It is therefore useful to perform sensitivity analyses (e.g., running the simulation with the expected standard deviation, but also with more conservative or even worst-case-scenario values).

Simulation-based power calculations

There are two ways to calculate the statistical power of an ANOVA design based on simulations. The first is to repeatedly simulate data for each condition based on the means, sample size, standard deviation, and correlation, under specific statistical assumptions (i.e., normaly distributed data). The `ANOVA_power` function allows you to perform power analyses based on repeatedly simulating normaly distributed data. A second approach is to simulate a dataset that has *exactly* the desired properties - every cell of the design has n datapoints that have the desired mean and standard deviation, and correlation between groups (for a within design). By performing an ANOVA on this dataset, we can calculate the required statistics from the ANOVA result used to calculate the statistical power. The `ANOVA_exact` function allows you to calculate power based on this approach. The `ANOVA_power` function is a bit more flexible (e.g., we can use different ways to correct for multiple comparisons, or in future versions of the package allow you to simulate more realistic datasets that are not normally distributed), but the `ANOVA_exact` function is much faster (and takes seconds, instead of minutes or hours for a large number of simulations).

The ANOVA_power function

The ANOVA_power function takes the result from the ANOVA_design function, and simulates data nsims times using a specified alpha level. As output, it provides a table for the ANOVA results, and the results for all independent comparisons.

It requires the following input: ANOVA_design, alpha_level, p_adjust, nsims, seed, and verbose.

1. design_result: Output from the ANOVA_design function saved as an object
2. alpha_level: Alpha level used to determine statistical significance
3. p_adjust: Correction for multiple comparisons using the p.adjust function
4. nsims: number of simulations to perform
5. seed: Set seed for reproducible results
6. verbose: Set to FALSE to not print results (default = TRUE)

Simulations typically take some time. Larger numbers of simulations yield more accurate results, but also take a long time. We recommend testing the set up with 100 simulations, and run 1000 if the set-up is correct (or 10000 if you are getting a coffee, or 100.000 if you are about accuracy to digits behind the decimal).

The ANOVA_exact function

The ANOVA_exact function takes the result from the ANOVA_design function, and simulates one dataset that exactly matches the desired properties (using the `mvrnorm` function from the `MASS` package, using the setting `empirical = TRUE`). This dataset is used to perform a single ANOVA, and the results are used to compute power (thanks to Chris Aberson for inspiring this approach).

ANOVA_exact requires the following input: ANOVA_design, alpha_level, and verbose.

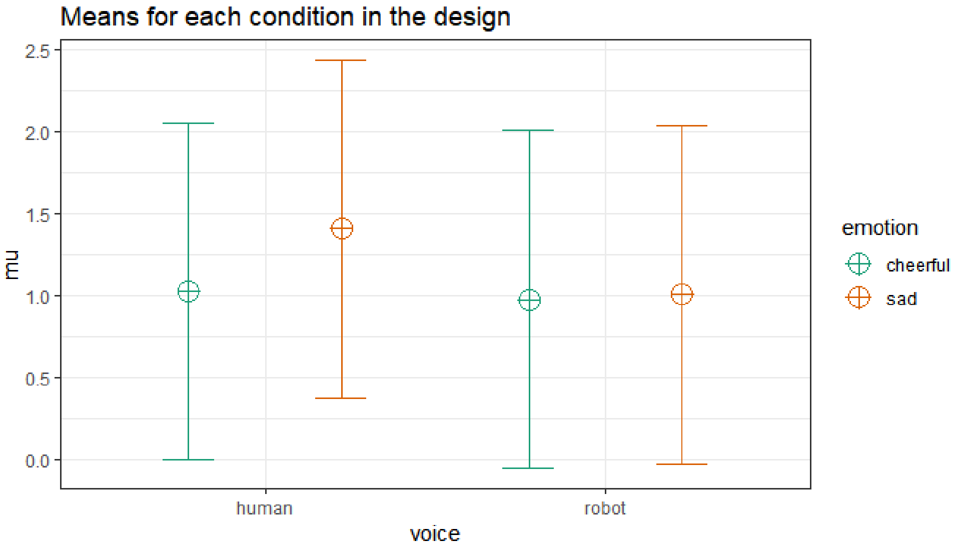
1. design_result: Output from the ANOVA_design function saved as an object
2. alpha_level: Alpha level used to determine statistical significance
3. verbose: Set to FALSE to not print results (default = TRUE)

Compared to the ANOVA_power function, the ANOVA_exact approach is much faster (it requires simulating only a single dataset). Currently the only difference is that ANOVA_exact does not allow you to examine the consequences of correcting for multiple comparisons (there is no `p_adjust` option), and that ANOVA_exact does not work for sample sizes smaller than 8 (because it is not possible to simulate a dataset with exactly the desired properties for very small sample sizes).

An Example

Imagine you plan to perform a study in which participants interact with an artificial voice assistant that sounds either like a human or like a robot, and who sounds either cheerful or sad. In the example below, 1000 simulations for a 2*2 mixed design (first factor, voice, is manipulated between participants, the second factor, emotion, is manipulated within participants) are performed. The sample size is 40 in each between subject condition (so 80 participants in total), the assumed population standard deviation is 1.03, the correlation for the within factors is 0.8, and the means are 1.03, 1.21, 0.98, 1.01. No correction for multiple comparisons is applied. The alpha level used as a significance threshold is set to 0.01 for this simulation.

```
design_result <- ANOVA_design(design = "2b*2w",
                              n = 40,
                              mu = c(1.03, 1.41, 0.98, 1.01),
                              sd = 1.03,
                              r=0.8,
                              labelnames = c("voice", "human", "robot", "emotion", "cheerful", "sad"))
```



```
# power_result_vig_1 <- ANOVA_power(design_result,
#                                   alpha = 0.05,
#                                   nsims = nsims,
#                                   seed = 1234)
# reduce file size for github - only save what is needed
# power_result_vig_1$sim_data <- NULL
# #power_result_vig_1$plot1 <- NULL
# power_result_vig_1$plot2 <- NULL
# saveRDS(power_result_vig_1, file = "vignettes/sim_data/power_result_vig_1_test.rds")
power_result_vig_1 <- readRDS(file = "vignettes/sim_data/power_result_vig_1.rds")
```

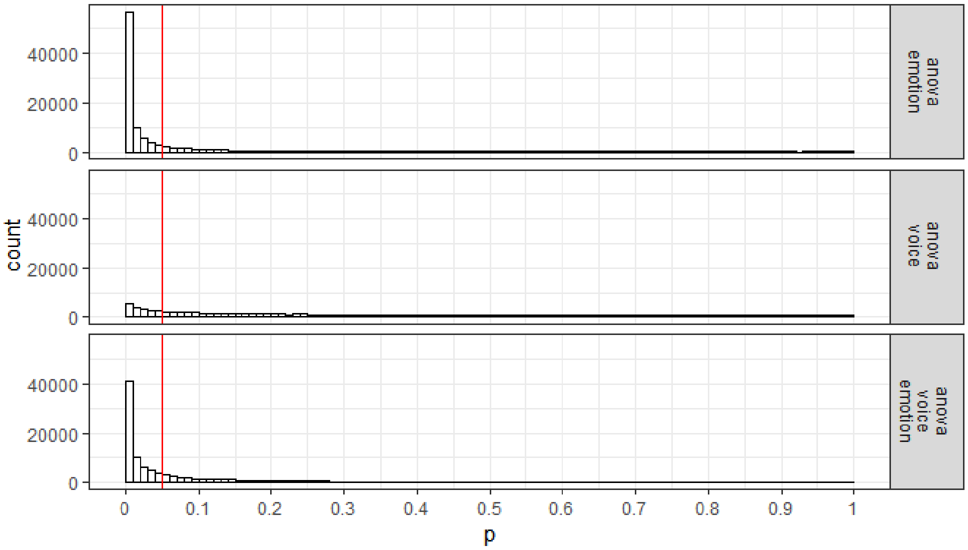
The result for the power simulation is printed, and has two sections (which can be surpressed by setting verbose = FALSE). The first table provides power (from 0 to 100%) and effect sizes (partial eta-squared) for the ANOVA result. We see the results for the main effects of factor voice, emotion, and the voice*emotion interaction.

The result for the power simulation reveal power is highest for the main effect of emotion. Remember that this is the within-subjects factor, and the means are highly correlated (0.8) - so we have high power for within comparisons. Power is lower for the interaction, and very low for the main effect of voice.

An ANOVA is typically followed up with contrasts. A statistical hypothesis often predicts not just an interaction, but also the shape of an interaction. For example, when looking at the plot of our design above, we might be specifically interested in comparing the independent effect for the cheerful vs sad human voice assistant, and the difference for sad voice when they are robotic or human. The second table provides the power for *t*-tests for all comparisons, and the effect sizes (Cohen's d for between-subject contrasts, and Cohen's d_z for within-subject contrasts, see Lakens, 2013).

Power is relatively high for the differences between within-participant conditions, and power is very low for the minor differences among the three similar means (1.03, 0.98, 1.01). In addition to the two tables, the ANOVA_power function returns the raw simulation data (all *p*-values and effect sizes for each simulation, see simulation_result$sim_data) and a plot showing the *p*-value distributions for all tests in the ANOVA.

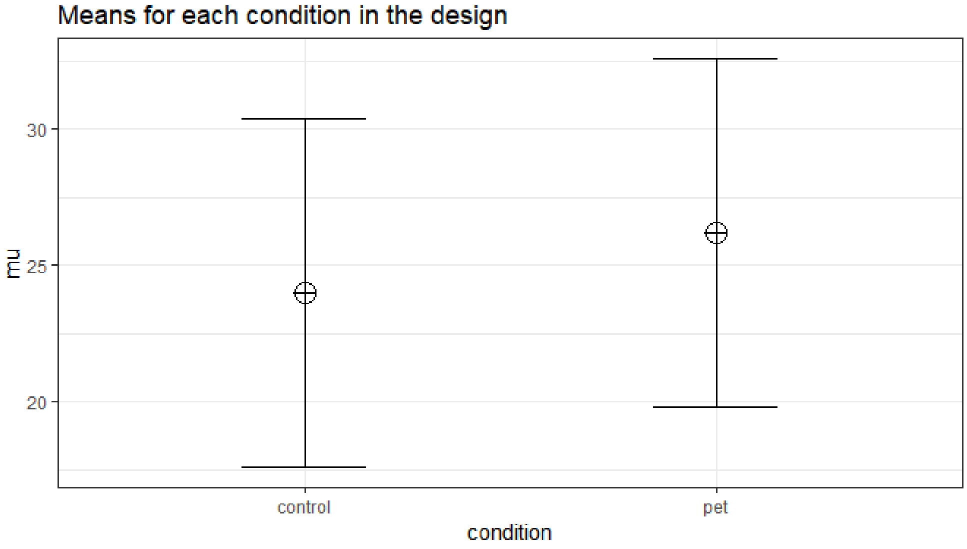
```
power_result_vig_1$plot1
```



Power in a Two Group One-Way ANOVA

Imagine we aim to design a study to test the hypothesis that giving people a pet to take care of will increase their life satisfaction. We have a control condition, and a condition where people get a pet, and randomly assign participants to either condition. We can simulate a One-Way ANOVA with a specified alpha, sample size, and effect size, on see which statistical power we would have for the ANOVA. We expect pets to increase life-satisfaction compared to the control condition. Based on work by Pavot and Diener (1993) we believe that we can expect responses on the life-satifaction scale to have a mean of approximately 24 in our population, with a standard deviation of 6.4. We expect having a pet increases life satisfaction with approximately 2.2 scale points for participants who get a pet. We plan to collect data from 200 participants in total, with 100 participants in each condition. We examine the statistical power our design would have to detect the differences we predict.

```
design <- "2b"
n <- 100
mu <- c(24, 26.2)
sd <- 6.4
labelnames <- c("condition", "control", "pet") #

design_result <- ANOVA_design(design = design,
                              n = n,
                              mu = mu,
                              sd = sd,
                              labelnames = labelnames)
```



```
# power_result_vig_2 <- ANOVA_power(design_result, nsims = nsims, seed = 1234)
#
# reduce file size for github - only save what is needed
# power_result_vig_2$sim_data <- NULL
# power_result_vig_2$plot1 <- NULL
# power_result_vig_2$plot2 <- NULL
# saveRDS(power_result_vig_2, file = "vignettes/sim_data/power_result_vig_2.rds")
power_result_vig_2 <- readRDS(file = "vignettes/sim_data/power_result_vig_2.rds")

#Note we do not specify any correlation in the ANOVA_design function (default r = 0), nor do we specify an alpha in
```

The result shows that we have exactly the same power for the ANOVA, as we have for the *t*-test. This is because when there are only two groups, these tests are mathematically identical. In a study with 100 participants per condition, we would have quite low power (around 67.7%). An ANOVA with 2 groups is identical to a *t*-test. For our example, Cohen's d (the standardized mean difference) is 2.2/6.4, or d = 0.34375 for the difference between the control condition and having pets, which we can use to easily compute the expected power for these simple comparisons using the pwr package.

```
library(pwr)
pwr.t.test(d = 2.2/6.4,
           n = 100,
           sig.level = 0.05,
           type="two.sample",
           alternative="two.sided")$power
```

```
## [1] 0.6768572
```

We can also directly compute Cohen's f from Cohen's d for two groups, as Cohen (1988) describes, because f = $\frac{1}{2}d$. So f = 0.5*0.34375 = 0.171875. And indeed, power analysis using the pwr package yields the same result using the pwr.anova.test as the power.t.test.

```
pwr.anova.test(n = 100,
               k = 2,
               f = 0.171875,
               sig.level = 0.05)$power
```

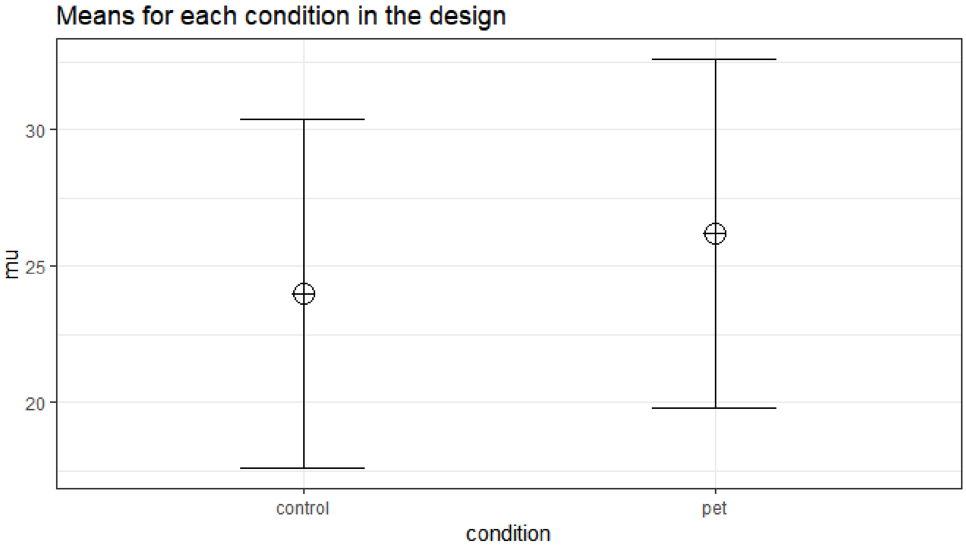
```
## [1] 0.6768572
```

This analysis tells us that running the study with 100 participants in each condition is quite likely to *not* yield a significant test result, even if our expected pattern of differences is true. This is clearly not optimal. If we perform a study, we would like to get informative results, which means we should be likely to detect effect we expect or care about, if these effects exist, and not find effects, if they are absent.

How many participants do we need for sufficient power? Given the expected difference and standard deviation, d = 0.34375, and f = 0.171875, we can increase the number of participants and run the simulation until we are content. The desired power depends on the cost of a Type 2 error. Cohen recommended to aim for 80% power, or a Type 2 error rate of 20%. I personally find a 20% Type 2 error rate too high, and not balanced enough compared to a much stricter Type 1 error rate (often by default 5%, although you should justify your alpha, for example by reducing it as a function of the sample size, or by balancing error rates). Let’s say we want to aim for 90% power.

Especially when you are increasing the sample size in your design to figure out how many participants you would need, it is much more efficient to use the `ANOVA_exact` function. You can see in the code below that we slowly increase the sample size and find that 180 participants give a bit more than 90% power.

```
design_result <- ANOVA_design(design = "2b",
                   n = 100,
                   mu = c(24, 26.2),
                   sd = 6.4,
                   labelnames = c("condition", "control", "pet"))
```



```
ANOVA_exact(design_result)$main_results$power
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition 67.69               0.029  0.1727         5.9082
##
## Power and Effect sizes for contrasts
##                                power effect_size
## p_condition_control_condition_pet 67.69      0.3437

## [1] 67.69
```

```
# power of 67.7 is a bit low. Let's increase it a bit to n = 150 to see if we are closer to our goal of 90% power.

design_result <- ANOVA_design(design = "2b",
                   n = 150,
                   mu = c(24, 26.2),
                   sd = 6.4,
                   labelnames = c("condition", "control", "pet"),
                   plot = FALSE)

ANOVA_exact(design_result)$main_results$power
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition 84.31              0.0289  0.1725         8.8623
##
## Power and Effect sizes for contrasts
##                                   power effect_size
## p_condition_control_condition_pet 84.31      0.3437

## [1] 84.31
```

```
# Close, but not there yet. Let's try n = 175

design_result <- ANOVA_design(design = "2b",
                   n = 175,
                   mu = c(24, 26.2),
                   sd = 6.4,
                   labelnames = c("condition", "control", "pet"),
                   plot = FALSE)

ANOVA_exact(design_result)$main_results$power
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition 89.37              0.0289  0.1724        10.3394
##
## Power and Effect sizes for contrasts
##                                   power effect_size
## p_condition_control_condition_pet 89.37      0.3437

## [1] 89.37
```

```
#Very close. Let's add a few more and try n = 180

design_result <- ANOVA_design(design = "2b",
                   n = 180,
                   mu = c(24, 26.2),
                   sd = 6.4,
                   labelnames = c("condition", "control", "pet"),
                   plot = FALSE)

ANOVA_exact(design_result)$main_results$power
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition 90.19              0.0288  0.1724        10.6348
##
## Power and Effect sizes for contrasts
##                                   power effect_size
## p_condition_control_condition_pet 90.19      0.3437

## [1] 90.19
```

The plot_power function

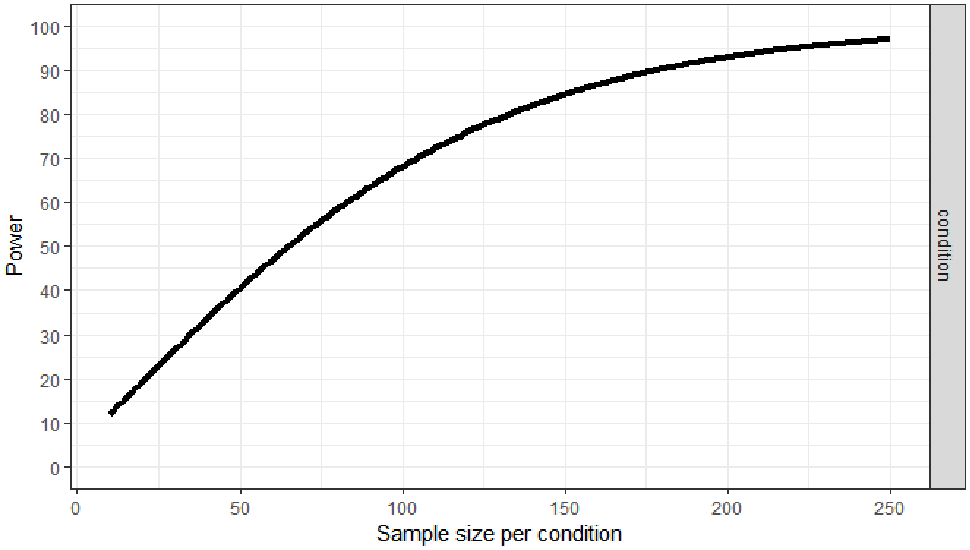
Simulation based power analyses require you to increase to sample size until power is high enough to reach your desired Type 2 error rate. To facilitate this trial and error process you can use the `plot_power` function to plot the power across a range of sample sizes to produce a power curve.

plot_power requires the following input: ANOVA_design, max_n, and plot.

1. design_result: Output from the ANOVA_design function saved as an object
2. min_n: The minimum sample size you want to plot in the power curve
3. max_n: The maximum sample size you want to plot in the power curve
4. plot: Set to FALSE to not print the plot (default = TRUE)

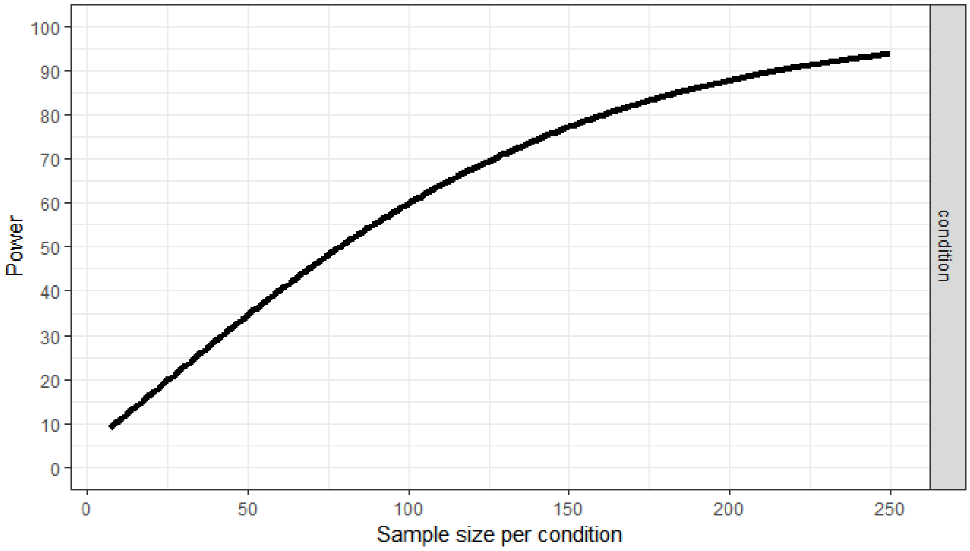
The `plot_power` functions simulates power up to a sample size of `max_n` using the `ANOVA_exact` function. ALthough it is relatively fast, with large sample size to can take some time to produce. In the figure below we can easily see that, assuming the true pattern of means and standard deviations represents our expected pattern of means and standard deviations, we have 80% power around 135 participants per condition, 90% power around 180 participants per condition, and 95% power around 225 participants per condition.

```
plot_power(design_result, min_n = 10, max_n = 250)
```



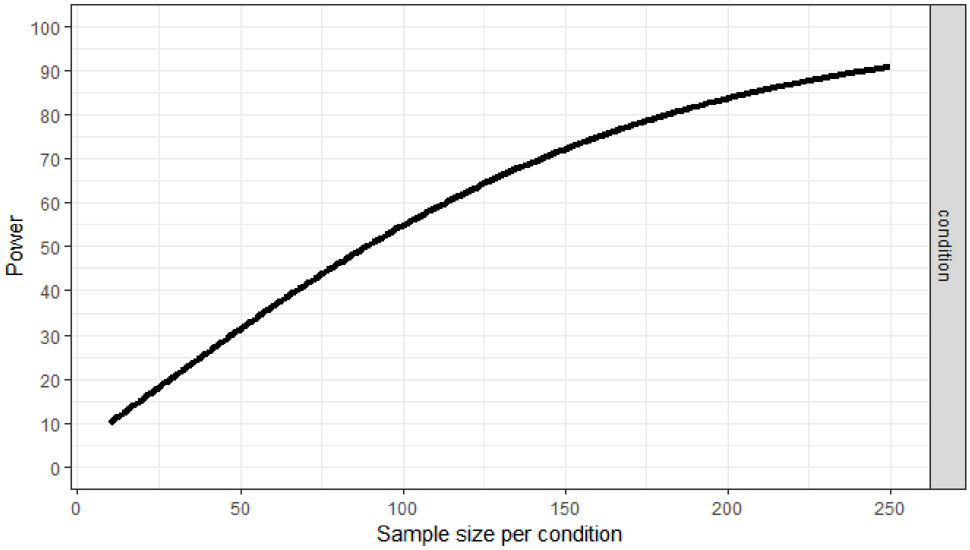
Because the true pattern of means is always unknown, it is sensible to examine the power across a range of scenarios. For example, is the difference in means is somewhat smaller,because the means are 24 and 26 instead of 24 and 26.2, we can compare the power curve above with the power curve for a slightly less optimistic scenario (where the true effect size is slightly smaller).

```
design_result <- ANOVA_design(design = "2b",
                   n = 180,
                   mu = c(24, 26),
                   sd = 6.4,
                   labelnames = c("condition", "control", "pet"),
                   plot = FALSE)

plot_power(design_result, max_n = 250)
```



It could be that in ddition to a slightly smaller effect size, the standard deviation is slighty larger than we expected as well. This will reduce the power even further, and is thus an even less optimistic scenario. Let’s assume the true standard deviation is 6.8 instead of 6.4.

```
design_result <- ANOVA_design(design = "2b",
                   n = 180,
                   mu = c(24, 26),
                   sd = 6.8,
                   labelnames = c("condition", "control", "pet"),
                   plot = FALSE)

plot_power(design_result, min_n = 10, max_n = 250)
```

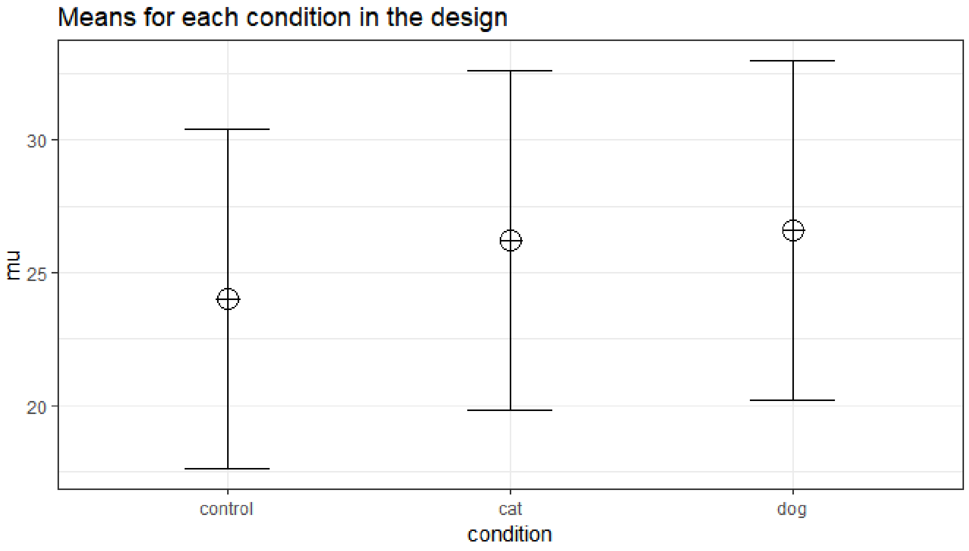


As these different plots make clear, your study never realy has a known statistical power. Because the true effect size (i.e., the pattern of means and standard deviations) is unknown, the true power of your study is unknown. A study has 90% power *assuming a specific effect size*, but if the effect size is different than what you expected, the true power can be either higher or lower. We should therefore always talk about the ‘expected’ power when we do an a-priori power analysis, and provide a good justification for our expectations (i.e., for the pattern of means, standard deviations, and correlations for within designs).

Three between subject conditions

Imagine we aim to design a study to test the hypothesis that giving people a pet to take care of will increase their life satisfaction. We have a control condition, a 'cat' pet condition, and a 'dog' pet condition. We can simulate a One-Way ANOVA with a specified alpha, sample size, and effect size, and see the statistical power we would have for the ANOVA and the follow-up comparisons. We expect all pets to increase life-satisfaction compared to the control condition. Obviously, we also expect the people who are in the 'dog' pet condition to have even greater life-satisfaction than people in the 'cat' pet condition. Based on work by Pavot and Diener (1993) we again assume that we can expect responses on the life-satisfaction scale to have a mean of approximately 24 in our population, with a standard deviation of 6.4. We expect having a pet increases life satisfaction with approximately 2.2 scale points for participants who get a cat, and 2.6 scale points for participants who get a dog. We initially consider collecting data from 150 participants in total, with 50 participants in each condition. But before we proceed with the data collection, we examine the statistical power our design would have to detect the differences we predict.

```
design <- "3b"
n <- 50
mu <- c(24, 26.2, 26.6)
sd <- 6.4
labelnames <- c("condition", "control", "cat", "dog") #

design_result <- ANOVA_design(design = design,
                   n = n,
                   mu = mu,
                   sd = sd,
                   labelnames = labelnames)
```



```
ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition 47.69              0.0315  0.1804         4.7852
##
## Power and Effect sizes for contrasts
##                                 power effect_size
## p_condition_control_condition_cat 39.83      0.3437
## p_condition_control_condition_dog 52.05      0.4063
## p_condition_cat_condition_dog      6.10      0.0625
```

The result shows that you would have quite low power with 50 participants, both for the overall ANOVA (just below 50% power), as for the follow up comparisons (approximately 40% power for the control vs cat condition, just above 50% for the control vs dogs condition, and a really low power (around 6%, just above the Type 1 error rate of 5%) for the expected difference between cats and dogs. We can easily confirm the expected power for these simple comparisons using the pwr package. For our example, Cohen's d (the standardized mean difference) is 2.2/6.4, or d = 0.34375 for the difference between the control condition and cats, 2.6/6.4 of d = 0.40625 for the difference between the control condition and dogs, and 0.4/6.4 or d = 0.0625 for the difference between cats and dogs as pets.

```
pwr.t.test(d = 2.2/6.4,
           n = 50,
           sig.level = 0.05,
           type="two.sample",
           alternative="two.sided")$power
```

```
## [1] 0.3983064
```

```
pwr.t.test(d = 2.6/6.4,
           n = 50,
           sig.level = 0.05,
           type="two.sample",
           alternative="two.sided")$power
```

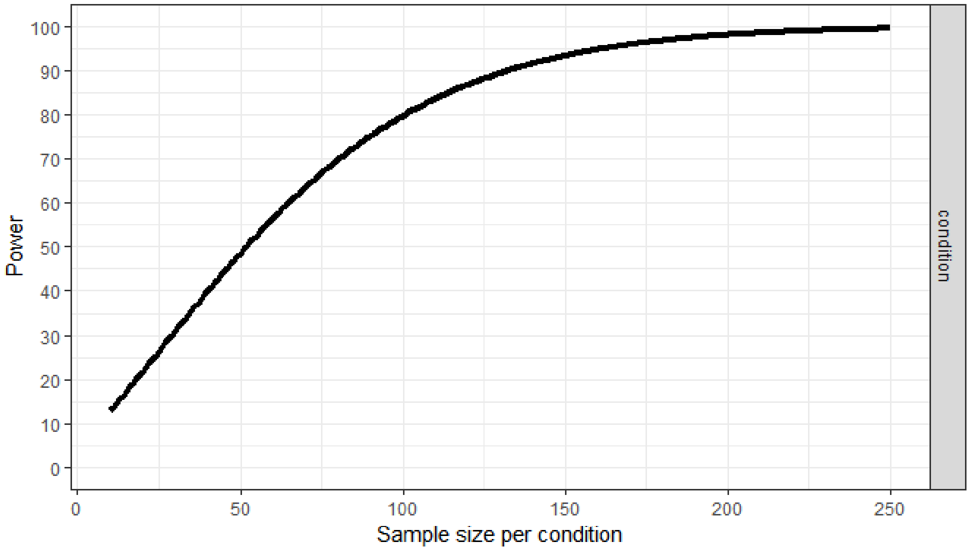
```
## [1] 0.5205162
```

```
pwr.t.test(d = 0.4/6.4,
           n = 50,
           sig.level = 0.05,
           type="two.sample",
           alternative="two.sided")$power
```

```
## [1] 0.06104044
```

It is clear we would need to collect more participants in each group to increase our power. Let's plot a power curve across a range of sample sizes to see how much we need to increase the sample size.

```
plot_power(design_result, min_n = 10, max_n = 250)
```



We see 134 participants give us aroud 90% power for the ANOVA. But we should also check the power for the comparison of the control condition and the cat condition.

```
design <- "3b"
n <- 134
mu <- c(24, 26.2, 26.6)
sd <- 6.4
labelnames <- c("condition", "control", "cat", "dog") #

design_result <- ANOVA_design(design = design,
                   n = n,
                   mu = mu,
                   sd = sd,
                   labelnames = labelnames,
                   plot = FALSE) #do not print the plot (same as above)

ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition 90.18              0.0311  0.1793        12.8242
##
## Power and Effect sizes for contrasts
##                                 power effect_size
## p_condition_control_condition_cat 80.05      0.3437
## p_condition_control_condition_dog 91.20      0.4063
## p_condition_cat_condition_dog      8.03      0.0625
```

```
n <- 180
design_result <- ANOVA_design(design = design,
                   n = n,
                   mu = mu,
                   sd = sd,
                   labelnames = labelnames,
                   plot = FALSE) #do not print the plot (same as above)

ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition 96.78              0.0311  0.1791        17.2266
##
## Power and Effect sizes for contrasts
##                                 power effect_size
## p_condition_control_condition_cat 90.19      0.3437
## p_condition_control_condition_dog 97.02      0.4063
## p_condition_cat_condition_dog      9.09      0.0625
```

```
n <- 5380
design_result <- ANOVA_design(design = design,
                   n = n,
                   mu = mu,
                   sd = sd,
                   labelnames = labelnames,
                   plot = FALSE) #do not print the plot (same as above)

ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##           power partial_eta_squared cohen_f non_centrality
## condition   100              0.0309  0.1786       514.8828
```

```
##
## Power and Effect sizes for contrasts
##                                    power effect_size
## p_condition_control_condition_cat   100      0.3437
## p_condition_control_condition_dog   100      0.4063
## p_condition_cat_condition_dog        90      0.0625
```

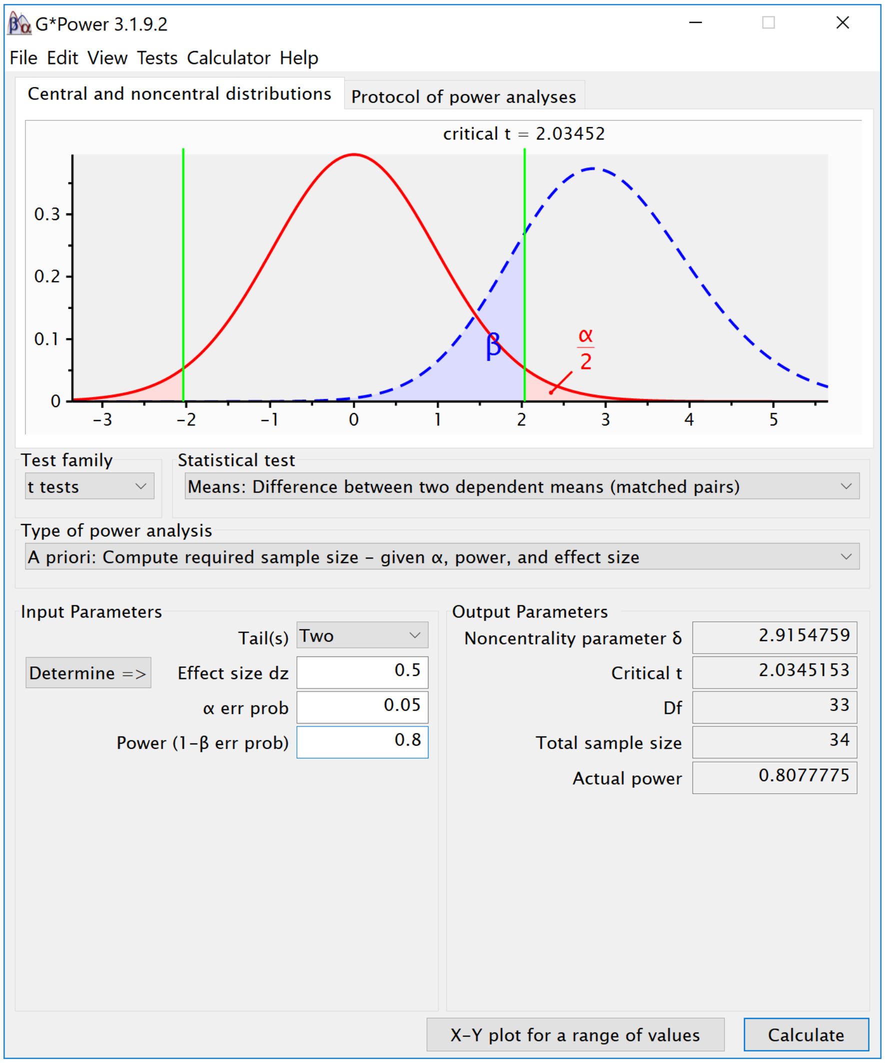
With 134 participants per condition, power for this simple comparison is only 80%. If we want to aim for 90% power for follow up tests, we need more participants. 180 participants provides good power for the follow-up comparison between control and cats. But power for the difference between cats and dogs is incredibly low. We would need 5380 participants to have 90% power for that comparison. This is possible if you can easily collect data, but might make this specific question impossible to reliably answer if data collection is costly. Realizing you can not reliably study a question is an important aspect of a-priori power analysis.

Power in Repeated Measures ANOVA

In a repeated measures design multiple observations are collected from the same participants. In the simplest case, where there are two repeated observations, a repeated measures ANOVA equals a dependent or paired *t*-test. Let’s explore the impact of this correlation on the power of a repeated measures ANOVA.

Two within conditions

To illustrate the effect of correlated observations, we start by simulating data for a medium effect size for a dependent (or paired, or within-subject) *t*-test. Let’s first look at G*power. If we want to perform an a-priori power analysis, we are asked to fill in the effect size d_z. As Cohen (1988) writes, “The Z subscript is used to emphasize the fact that our raw score unit is no longer X or Y, but Z”, where Z are the difference scores of X-Y.


G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical t = 2.03452
0.3
0.2
0.1
0
-3
-2
-1
0
1
2
3
4
5
β
α/2
Determine =>
X-Y plot for a range of values
Calculate

Test family: t tests

Statistical test: Means: Difference between two dependent means (matched pairs)

Type of power analysis: A priori: Compute required sample size – given α, power, and effect size

Input Parameters

Tail(s)	Two
Effect size dz	0.5
α err prob	0.05
Power (1-β err prob)	0.8

Output Parameters

Noncentrality parameter δ	2.9154759
Critical t	2.0345153
Df	33
Total sample size	34
Actual power	0.8077775

Within designs can have greater power to detect differences than between designs because the values are correlated, and a within design requires less participants because each participant provides multiple observations. One difference between an independent *t*-test and a dependent *t*-test is that an independent *t*-test has 2(n-1) degrees of freedom, while a dependent *t*-test has (n-1) degrees of freedom. The sample size needed in a two-group within-design (NW) relative to the sample needed in two-group between-designs (NB), assuming normal distributions, and ignoring the difference in degrees of freedom between the two types of tests, is (from Maxwell & Delaney, 2004, p. 561, formula 45):

$$N_W = \frac{N_B(1-\rho)}{2}$$

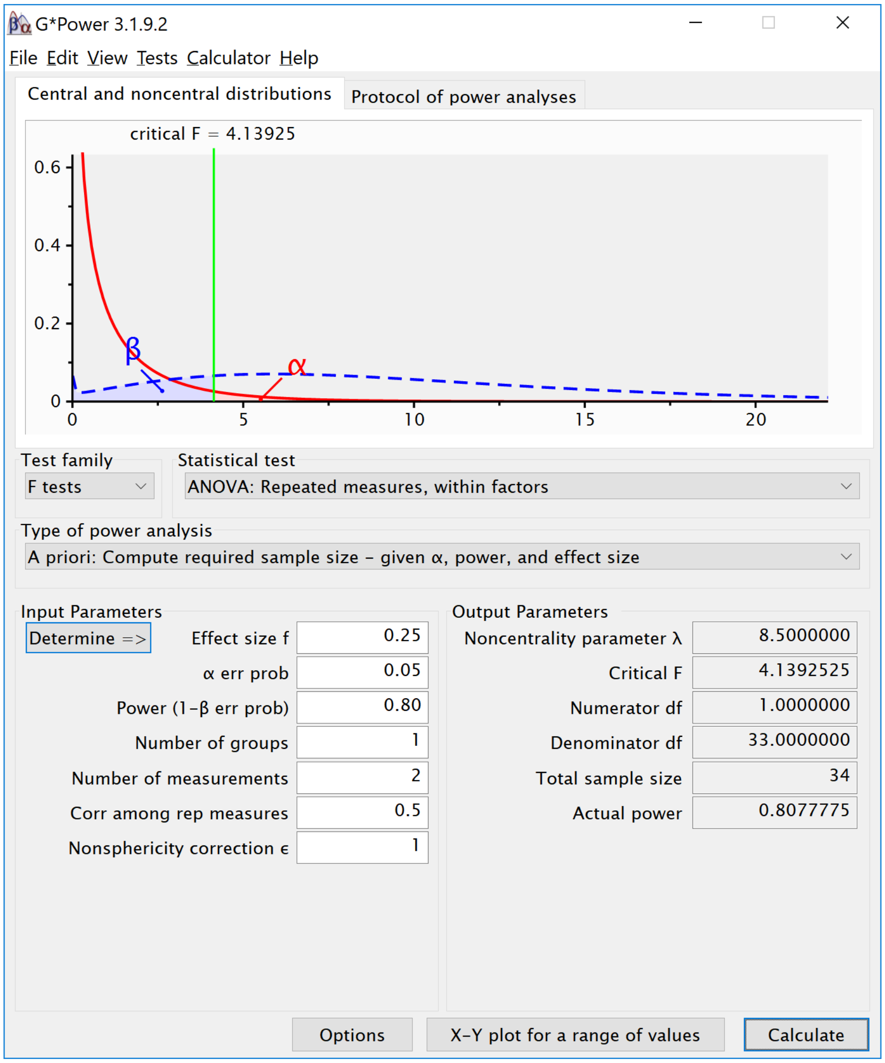
The division by 2 in the equation is due to the fact that in a two-condition within design every participant provides two data-points. The extent to which this reduces the sample size compared to a between-subject design depends on the correlation (*r*) between the two dependent variables, as indicated by the 1-r part of the equation. If the correlation is 0, a within-subject design needs half as many participants as a between-subject design (e.g., 64 instead 128 participants), simply because every participants provides 2 datapoints. The higher the correlation, the larger the relative benefit of within designs, and whenever the correlation is negative (up to -1) the relative benefit disappears.

Whereas in an independent *t*-test the two observations are uncorrelated, in a within design the observations are correlated. This has an effect on the standard deviation of the difference scores. In turn, because the standardized effect size is the mean difference divided by the standard deviation of the difference scores, the correlation has an effect on the standardized mean difference in a within design, Cohen's d_z. The relation, as Cohen (1988, formula 2.3.7) explains, is:

$$\sigma_z = \sigma\sqrt{2(1-\rho)}$$

Therefore, the relation between dz and d is $\sqrt{2(1-\rho)}$. As Cohen (1988) writes: "In other words, a given difference between population means for matched (dependent) samples is standardized by a value which is $\sqrt{2(1-\rho)}$ as large as would be the case were they independent. If we enter a correlation of 0.5 in the formula, we get $\sqrt{2(0.5)} = 1$. When the correlation is 0.5, d = d_z. When there is a strong correlation between dependent variables, for example r = 0.9, we get $d = d_z\sqrt{2(1-0.9)}$, and a d_z of 1 would be a d = 0.45. Reversely, $d_z = \frac{d}{\sqrt{2(1-r)}}$, so with a r = 0.9, a d of 1 would be a d_z = 2.24. Some consider this increase in d_z compared to d when observations are strongly correlated an 'inflation' when estimating effect sizes, but since the reduction in the standard deviation of the difference scores due to the correlation makes it easier to distinguish signal from noise in a hypothesis test, it leads to a clear power benefit.

There is no equivalent f_z for Cohen's f for a within subject ANOVA. For two groups, we can directly compute Cohen's f from Cohen's d, as Cohen (1988) describes, because f = $\frac{1}{2}d$. For a d = 0.5, f = 0.25. In G*power we can run a 2 group within-subject power analysis for ANOVA. We plan for 80% power, and reproduce the anaysis above for the dependent *t*-test. This works because the correlation is set to 0.5, when d = d_z, and thus the transformation of f=$\frac{1}{2}d$ works.


G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical F = 4.13925
0.6
0.4
0.2
0
0
5
10
15
20
β
α
Determine =>
Options
X-Y plot for a range of values
Calculate

Test family: F tests

Statistical test: ANOVA: Repeated measures, within factors

Type of power analysis: A priori: Compute required sample size – given α, power, and effect size

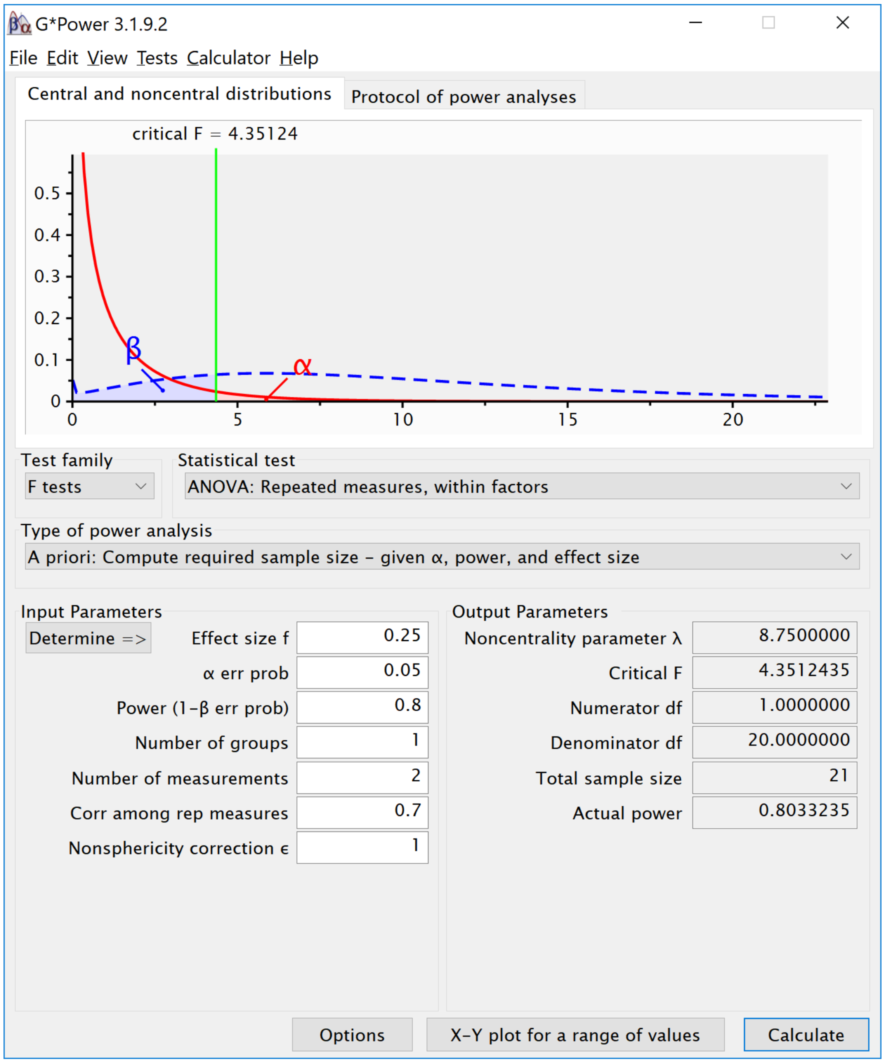
Input Parameters

Effect size f: 0.25
α err prob: 0.05
Power (1−β err prob): 0.80
Number of groups: 1
Number of measurements: 2
Corr among rep measures: 0.5
Nonsphericity correction ε: 1

Output Parameters

Noncentrality parameter λ: 8.5000000
Critical F: 4.1392525
Numerator df: 1.0000000
Denominator df: 33.0000000
Total sample size: 34
Actual power: 0.8077775

If we change the correlation to 0.7 and keep all other settings the same, the repeated measure a-priori power analysis yields a sample of 21. The correlation increases the power for the test.


G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical F = 4.35124
0.5
0.4
0.3
0.2
0.1
0
0
5
10
15
20
β
α
Determine =>
Options
X-Y plot for a range of values
Calculate

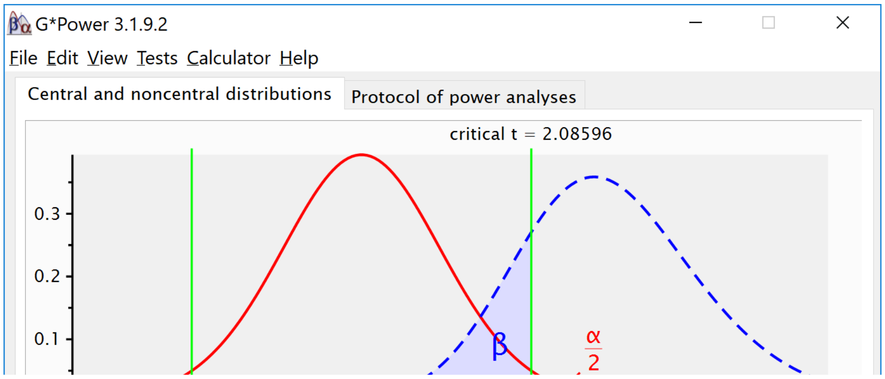
Test family: F tests

Statistical test: ANOVA: Repeated measures, within factors

Type of power analysis: A priori: Compute required sample size – given α, power, and effect size

Input Parameters		Output Parameters	
Effect size f	0.25	Noncentrality parameter λ	8.7500000
α err prob	0.05	Critical F	4.3512435
Power (1–β err prob)	0.8	Numerator df	1.0000000
Number of groups	1	Denominator df	20.0000000
Number of measurements	2	Total sample size	21
Corr among rep measures	0.7	Actual power	0.8033235
Nonsphericity correction ϵ	1		

To reproduce this analysis in G*power with a dependent *t*-test we need to change d_z following the formula above, $d_z = \frac{0.5}{\sqrt{2(1-0.7)}}$, which yields d_z = 0.6454972. If we enter this value in G*power for an a-priori power analysis, we get the exact same results (as we should, since an repeated measures ANOVA with 2 groups equals a dependent *t*-test). This example illustrates that the correlation between dependent variables always factors into a power analysis, both for a dependent *t*-test, and for a repeated measures ANOVA. Because a dependent *t*-test uses d_z the correlation might be less visible, but given the relation between d and d_z, the correlation is always taken into account and can greatly improve power for within designs compared to between designs.

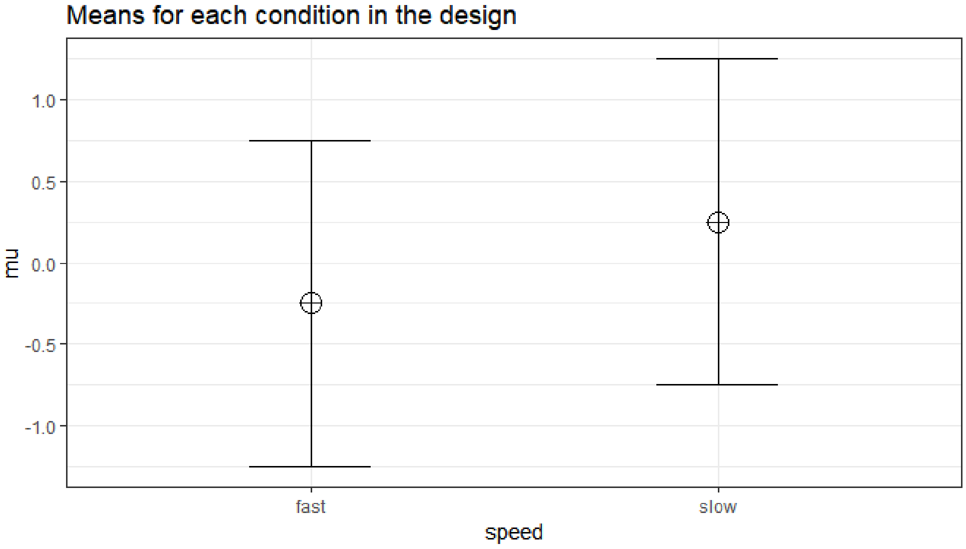

G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical t = 2.08596
0.3
0.2
0.1
β
α
2

We can perform both these power analyses using simulations as well. We set groups to 2 for the simulation, n = 34 (which should give 80.777 power, according to g*power), a correlation among repeated measures of 0.5, and an alpha of 0.05. In this case, we simulate data with means -0.25 and 0.25, and set the sd to 1. This means we have a mean difference of 0.5, and a Cohen's d of 0.5/1 = 0.5. In the first example, we set the correlation to 0.5, and the result should be 80.777% power, and an effect size estimate of 0.5 for the simple effect. We also calculate partial eta-squared for the ANOVA, which equals $\frac{f^2}{f^2+1}$, or 0.05882353.

```
K <- 2
n <- 34
sd <- 1
r <- 0.5
alpha = 0.05
f <- 0.25
f2 <- f^2
ES <- f2/(f2+1)
ES
```

```
## [1] 0.05882353
```

```
mu <- mu_from_ES(K = K, ES = ES)
design = paste(K,"w",sep="")
labelnames <- c("speed", "fast", "slow")

design_result <- ANOVA_design(design = design,
                              n = n,
                              mu = mu,
                              sd = sd,
                              r = r,
                              labelnames = labelnames)
```



```
ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##       power partial_eta_squared cohen_f non_centrality
## speed 80.78              0.2048  0.5075            8.5
##
## Power and Effect sizes for contrasts
##                         power effect_size
## p_speed_fast_speed_slow 80.78         0.5
```

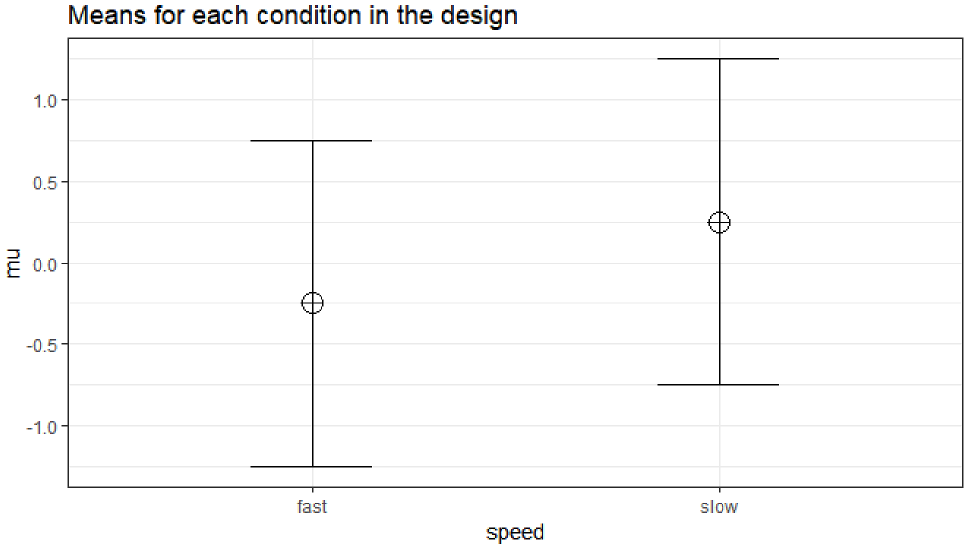
The results of the exact simulation approach are indeed to 80.777%. Note that the simulation calculates Cohen's d_z effect sizes for paired comparisons - which here given the correlation of 0.5 is also 0.5 for a medium effect size.

We should see a larger d_z if we increase the correlation, keeping the sample size the same, following the example in Gpower above. We repeat the simulation, and the only difference is a correlation between dependent variables of 0.7. This should yield an effect size d_z = 0.6454972.

```
K <- 2
n <- 34
sd <- 1
r <- 0.7
alpha = 0.05
f <- 0.25
f2 <- f^2
ES <- f2/(f2+1)
ES
```

```
## [1] 0.05882353
```

```
mu <- mu_from_ES(K = K, ES = ES)
design = paste(K,"w",sep="")
labelnames <- c("speed", "fast", "slow")

design_result <- ANOVA_design(design = design,
                              n = n,
                              mu = mu,
                              sd = sd,
                              r = r,
                              labelnames = labelnames)
```



```
ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##       power partial_eta_squared cohen_f non_centrality
## speed 95.47              0.3004  0.6552        14.1667
##
## Power and Effect sizes for contrasts
##                            power effect_size
## p_speed_fast_speed_slow 95.47      0.6455
```

Power in Repeated Measures ANOVA with More than 2 Groups

We will examine a repeated measures experiment with 3 within-participant conditions, to illustrate how a repeated measures ANOVA extends a dependent *t*-test. In the example for a two-group within design we provided a specific formula for the sample size benefit for two groups. The sample size needed in within-designs (NW) with more than 2 conditions, relative to the sample needed in between-designs (NB), assuming normal distributions and compound symmetry, and ignoring the difference in degrees of freedom between the two types of tests, is (from Maxwell & Delaney, 2004, p. 562, formula 47):

$$N_W = \frac{N_B(1-\rho)}{a}$$

Where a is the number of within-subject levels.

The relation between Cohen's f and Cohen's d

Whereas in the case of a repeated measures ANOVA with 2 groups we could explain the principles of a power analysis by comparing our test against a *t*-test and Cohen's d, this becomes more difficult when we have more than 2 groups. It is more useful to explain how to directly calculate Cohen's f, the effect size used in power analyses for ANOVA. Cohen's f is calculated following Cohen, 1988, formula 8.2.1 and 8.2.2:

$$f = \sqrt{\frac{\frac{\sum(\mu-\overline{\mu})^2)}{N}}{\sigma}}$$

Imagine we have a within-subject experiment with 3 conditions. We ask people what they mood is when their alarm clock wakes them up, when they wake up naturally on a week day, and when they wake up naturally on a weekend day. Based on pilot data, we expect the means (on a 7 point validated mood scale) are 3.8, 4.2, and 4.3. The standard deviation is 0.9, and the correlation between the dependent measurements is 0.7. We can calculate Cohen’s f for the ANOVA, and Cohen’s dz for the contrasts:

```
mu <- c(3.8, 4.2, 4.3)
sd <- 0.9
f <- sqrt(sum((mu-mean(mu))^2)/length(mu))/sd #Cohen, 1988, formula 8.2.1 and 8.2.2
f
```

```
## [1] 0.2400274
```

```
r <- 0.7
(4.2-3.8)/0.9/sqrt(2*(1-r))
```

```
## [1] 0.5737753
```

```
(4.3-3.8)/0.9/sqrt(2*(1-r))
```

```
## [1] 0.7172191
```

```
(4.3-4.2)/0.9/sqrt(2*(1-r))
```

```
## [1] 0.1434438
```

The relation between Cohen’s d or dz and Cohen’s f becomes more difficult when there are multiple groups, because the relationship depends on the pattern of the means. Cohen (1988) presents calculations for three patterns, minimal variability (for example, for 5 means: -0.25, 0, 0, 0, 0.25), medium variability (for example, for 5 means: -0.25, -0.25, 0.25, 0.25, 0.25 or -0.25, -0.25, -0.25, 0.25, 0.25). For these three patterns, formula’s are available that compute Cohen’s f from Cohen’s d, where d is the effect size calculated for the difference between the largest and smallest mean (if the largest mean is 0.25 and the smallest mean is -0.25, 0.25 - -0.25 = 0.5, so d is 0.5 divided by the standard deviation of 0.9). In our example, d would be (4.3-3.8)/0.9 = 0.5555556. If we divide this value by sqrt(2*(1-r)) we have dz = 0.5555556/0.7745967 = 0.7172191. If the means and standard deviation is known, it is best to calculate Cohen’s f directly from these values.

We can perform power analyses for within designs using simulations. We set groups to 3 for the simulation, n = 20, and the correlation between dependent variables to 0.8. If the true effect size is f = 0.25, and the alpha level is 0.05, the power is 96.9%.

In this case, we simulate data with means -0.3061862, 0.0000000, and 0.3061862, and set the sd to 1.

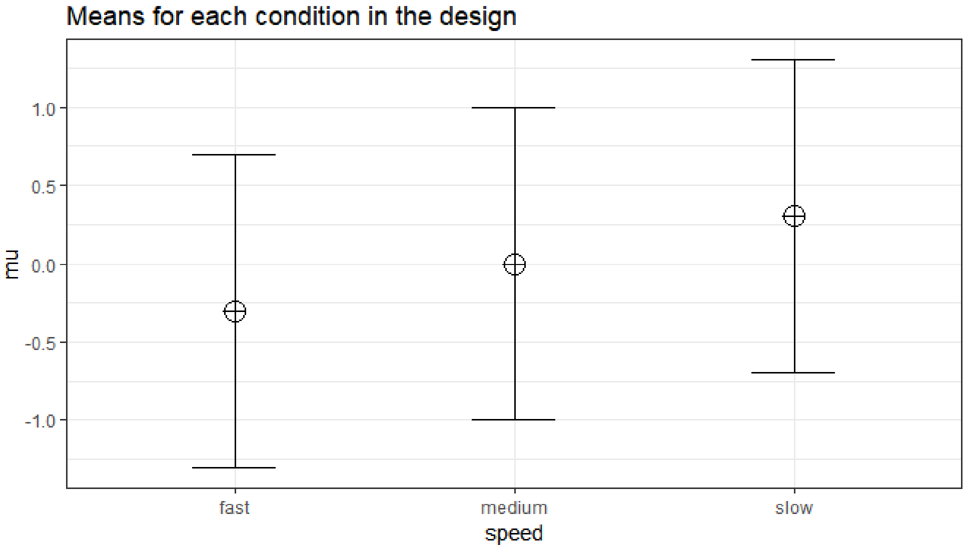
```
K <- 3
n <- 20
sd <- 1
r <- 0.8
alpha = 0.05
f <- 0.25
f2 <- f^2
ES <- f2/(f2+1)
ES
```

```
## [1] 0.05882353
```

```
mu <- mu_from_ES(K = K, ES = ES)
sqrt(sum((mu-mean(mu))^2)/length(mu))/sd #Cohen, 1988, formula 8.2.1 and 8.2.2
```

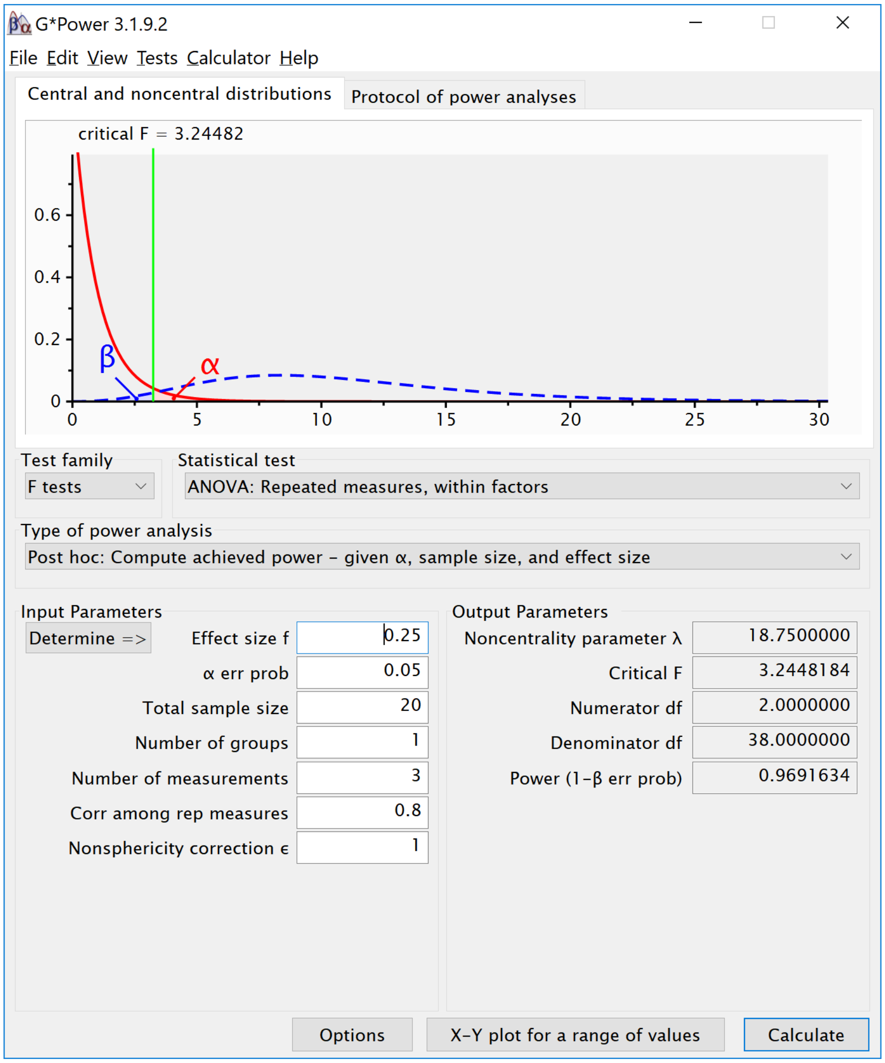
```
## [1] 0.25
```

```
design = paste(K,"w",sep="")
labelnames <- c("speed", "fast", "medium", "slow")

design_result <- ANOVA_design(design = design,
                              n = n,
                              mu = mu,
                              sd = sd,
                              r = r,
                              labelnames = labelnames)
```



```
# power_result_vig_3 <- ANOVA_power(design_result, nsims = nsims)
# reduce file size for github - only save what is needed
# power_result_vig_3$sim_data <- NULL
# power_result_vig_3$plot1 <- NULL
# power_result_vig_3$plot2 <- NULL
# saveRDS(power_result_vig_3, file = "vignettes/sim_data/power_result_vig_3.rds")
power_result_vig_3 <- readRDS(file = "vignettes/sim_data/power_result_vig_3.rds")
```

The results of the simulation are indeed very close to 96.9%. We can see this is in line with the power estimate from Gpower:


G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical F = 3.24482
0.6
0.4
0.2
0
β
α
0
5
10
15
20
25
30
Determine =>
Options
X-Y plot for a range of values
Calculate

Test family: F tests

Statistical test: ANOVA: Repeated measures, within factors

Type of power analysis: Post hoc: Compute achieved power – given α, sample size, and effect size

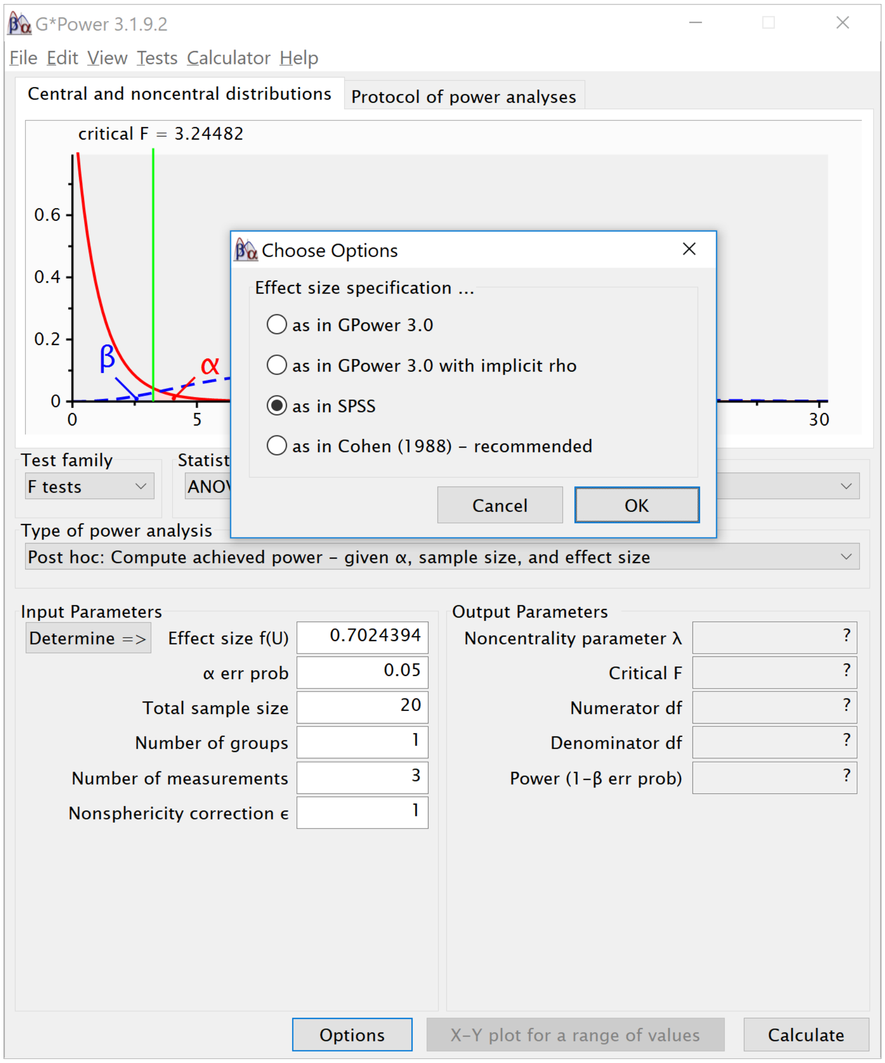
Input Parameters

Effect size f	0.25
α err prob	0.05
Total sample size	20
Number of groups	1
Number of measurements	3
Corr among rep measures	0.8
Nonsphericity correction ϵ	1

Output Parameters

Noncentrality parameter λ	18.7500000
Critical F	3.2448184
Numerator df	2.0000000
Denominator df	38.0000000
Power (1–β err prob)	0.9691634

We can even check the calculation of Cohen's f SPSS style in GPower. We take the GPower settings as illustrated above. We click the 'Options' button, and check the radio button next to 'As in SPSS'. Click ok, and you will notice that the 'Corr among rep measures' field has disappeared. The correlation does not need to be entered separately, but is incorporated in Cohen's f. The value of Cohen's f, which was 0.25, has changed into 0.7024394. This is the SPSS equivalent. The value is much larger. This value, and it's corresponding partial eta-squared, incorporate the correlation between observations.


G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical F = 3.24482
0.6
0.4
0.2
0
0
5
30
β
α
Choose Options
Cancel
OK
Determine =>
Options
X-Y plot for a range of values
Calculate

Effect size specification ...

○ as in GPower 3.0

○ as in GPower 3.0 with implicit rho

● as in SPSS

○ as in Cohen (1988) – recommended

Test family: F tests

Statist… ANOV…

Type of power analysis: Post hoc: Compute achieved power – given α, sample size, and effect size

Input Parameters

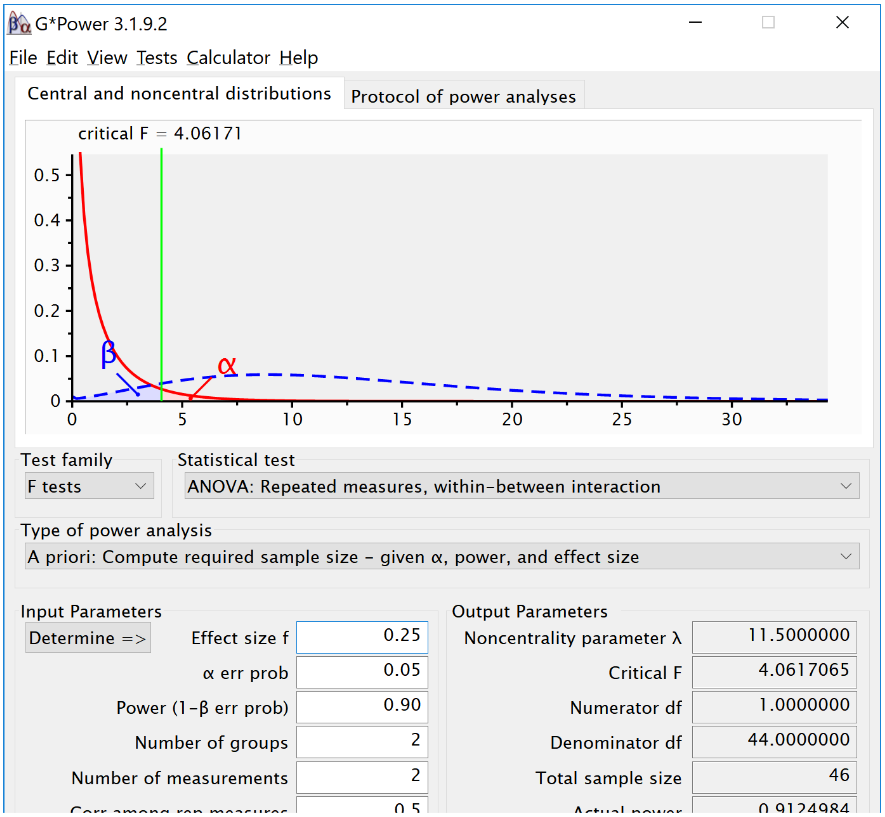
Effect size f(U)	0.7024394
α err prob	0.05
Total sample size	20
Number of groups	1
Number of measurements	3
Nonsphericity correction ϵ	1

Output Parameters

Noncentrality parameter λ	?
Critical F	?
Numerator df	?
Denominator df	?
Power (1–β err prob)	?

2x2 ANOVA, within-between design

We can simulate a two-way ANOVA with a specific alpha, sample size and effect size, to achieve a specified statistical power. We will try to reproduce the power analysis in G*power for an *F*-test, ANOVA: Repeated measures, within-between interaction.


G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical F = 4.06171
0.5
0.4
0.3
0.2
0.1
0
β
α
0
5
10
15
20
25
30
Determine =>

Test family: F tests

Statistical test: ANOVA: Repeated measures, within-between interaction

Type of power analysis: A priori: Compute required sample size – given α, power, and effect size

Input Parameters

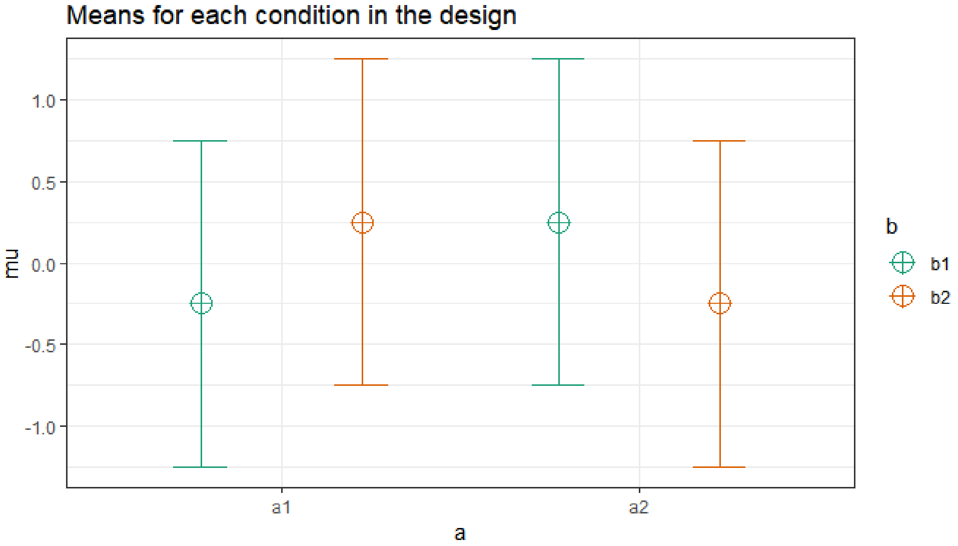
Effect size f	0.25
α err prob	0.05
Power (1–β err prob)	0.90
Number of groups	2
Number of measurements	2
Corr among rep measures	0.5

Output Parameters

Noncentrality parameter λ	11.5000000
Critical F	4.0617065
Numerator df	1.0000000
Denominator df	44.0000000
Total sample size	46
Actual power	0.9124984

For the 2-way interaction, the result should be a power of 91.25% if we have a total sample size of 46. Since we have 2 levels for the between-participants factor, that means the number of groups 2 (and both these groups collect 2 repeated measures).

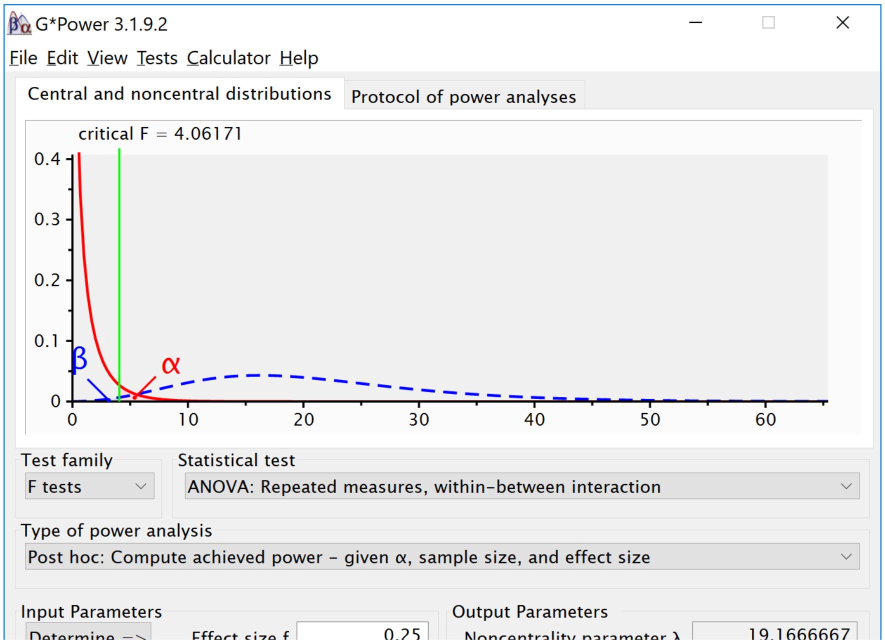
```
mu <- c(-0.25, 0.25, 0.25, -0.25)
n <- 23
sd <- 1
r <- 0.5
design = "2w*2b"
design_result <- ANOVA_design(design = design,
                              n = n,
                              mu = mu,
                              sd = sd,
                              r = r)
```



```
ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##     power partial_eta_squared cohen_f non_centrality
## b    5.00              0.0000  0.0000            0.0
## a    5.00              0.0000  0.0000            0.0
## b:a 91.25              0.2072  0.5112           11.5
##
## Power and Effect sizes for contrasts
##                        power effect_size
## p_a_a1_b_b1_a_a1_b_b2 38.17         0.5
## p_a_a1_b_b1_a_a2_b_b1 63.02         0.5
## p_a_a1_b_b1_a_a2_b_b2  5.00         0.0
## p_a_a1_b_b2_a_a2_b_b1  5.00         0.0
## p_a_a1_b_b2_a_a2_b_b2 63.02        -0.5
## p_a_a2_b_b1_a_a2_b_b2 38.17        -0.5
```

We can simulate the same Two-Way ANOVA increasing the correlation to 0.7. Power should be 98.98% for the two-way interaction.


G*Power 3.1.9.2
File Edit View Tests Calculator Help
Central and noncentral distributions
Protocol of power analyses
critical F = 4.06171
0.4
0.3
0.2
0.1
0
β
α
0
10
20
30
40
50
60
Determine =>

Test family: F tests

Statistical test: ANOVA: Repeated measures, within-between interaction

Type of power analysis: Post hoc: Compute achieved power – given α, sample size, and effect size

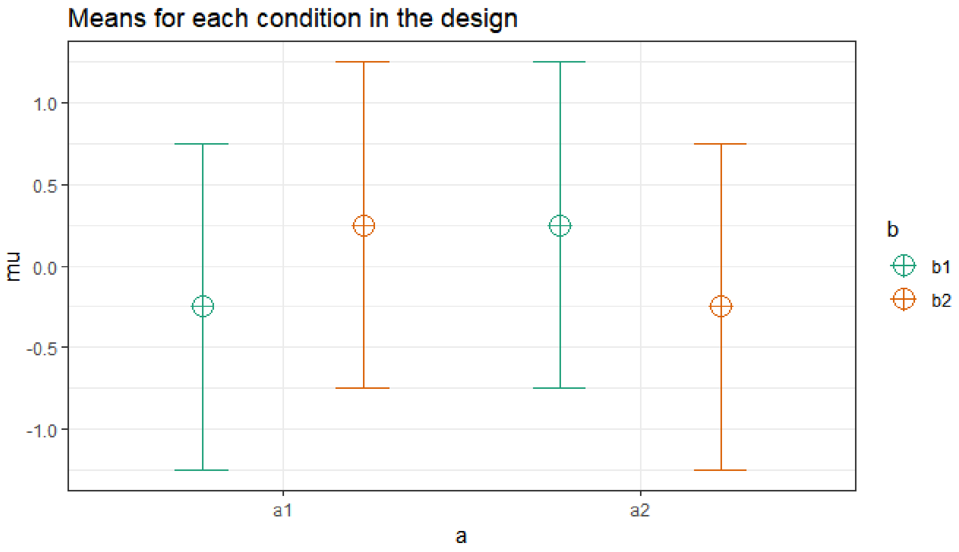
Input Parameters

Effect size f 0.25

Output Parameters

Noncentrality parameter λ 19.1666667

```
mu <- c(-0.25, 0.25, 0.25, -0.25)
n <- 23
sd <- 1
r <- 0.7
design = "2w*2b"
design_result <- ANOVA_design(design = design,
                              n = n,
                              mu = mu,
                              sd = sd,
                              r = r)
```

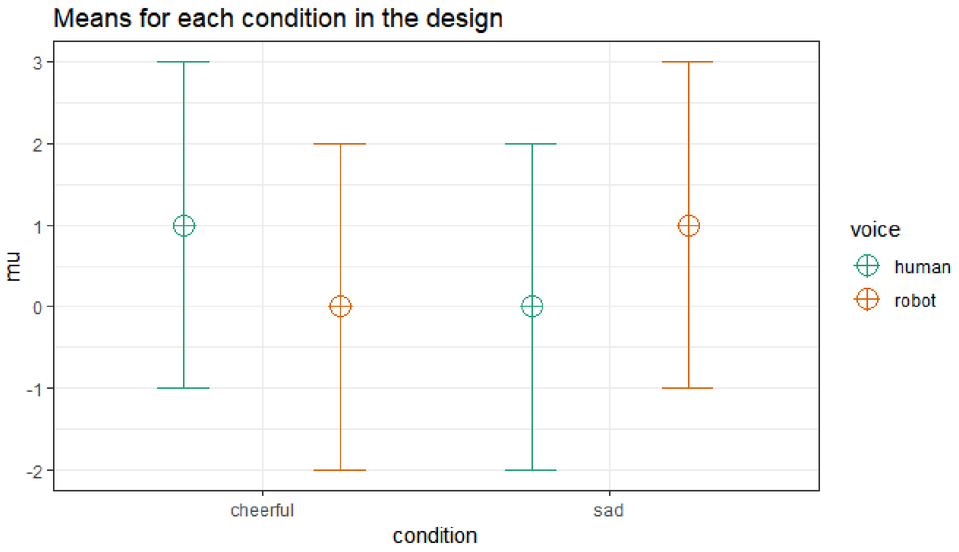


```
ANOVA_exact(design_result)
```

```
## Power and Effect sizes for ANOVA tests
##     power partial_eta_squared cohen_f non_centrality
## b    5.00              0.0000    0.00         0.0000
## a    5.00              0.0000    0.00         0.0000
## b:a 98.98              0.3034    0.66        19.1667
##
## Power and Effect sizes for contrasts
##                          power effect_size
## p_a_a1_b_b1_a_a1_b_b2 38.17      0.5000
## p_a_a1_b_b1_a_a2_b_b1 84.09      0.6455
## p_a_a1_b_b1_a_a2_b_b2  5.00      0.0000
## p_a_a1_b_b2_a_a2_b_b1  5.00      0.0000
## p_a_a1_b_b2_a_a2_b_b2 84.09     -0.6455
## p_a_a2_b_b1_a_a2_b_b2 38.17     -0.5000
```

Two-way ANOVA, between participants Design

The effect size for interactions in ANOVA designs depends on the pattern of means. Let’s assume the researcher plans to perform an experiment where the voice of an artificial assistant sounds cheerful or sad, and as a second factor the voice sound more robotic or more human-like. Different patterns of results could be expected. Either the cheerful voices are appreciated more than sad voices for both human and robotic-sounding voice assistants. Or cheerful human voices are preferred above sad human voices, but no difference is expected for robotic voices, or the opposite effect is observed for robotic voices (a ‘Marvin-the-Depressed-Robot Effect’). In the first case, we will only observe a main effect of voice, but in the other two scenarios there is an interaction effect between human-likeness of the voice and the emotional tone of the voice. We can start by simulating the power for a cross-over interaction for a 2x2 between-participant design with 80 participants in each group (see the figure below for the expected pattern of means).



Mathematically the interaction effect is computed as the cell mean minus the sum of the grand mean, the marginal mean in each row minus the grand mean, and the marginal mean in each column minus grand mean. For example, for the cheerful human-like voice condition this is 1 - (0.5 + (0.5) + (0.5)) = -0.5. Completing this for all four cells gives the values -0.5, 0.5, 0.5, -0.5. Cohen's f is then $f = \frac{\sqrt{\frac{-0.5^2 + 0.5^2 + 0.5 + -0.5^2}{4}}}{2} = 0.25$. Simulations show we have 99.379% power when we collected 80 participants per condition. A cross-over (also called disordinal) interaction with two levels per factor has exactly the same power as the initial two-group design. if we halve the sample size per group for the cross-over interaction from 80 to 40. Power with 40 participants per condition is 88.315%. Main effects in an ANOVA are based on the means for one factor averaged over the other factors (e.g., the main effect of human-like versus robot-like voice, irrespective of whether it is cheerful or sad). The interaction effect, which can be contrast coded as 1, -1, -1, 1, is similarly a test of whether the effects are non-additive based on the scores in each cell, where the null-hypothesis of no additive effect can be rejected if the deviation expected when effects in each cell would be purely additive can be rejected. The key insight here is that not the sample size per condition, but the total sample size over all other factor determines the power for the main effects and the interaction.

We can also examine the statistical power for a pattern of results that indicated that there was no difference in interacting with a cheerful of sad conversational agent with a robot voice. In this case, we expect an 'ordinal' interaction (the means for the human-like voice are never lower than the means for the robot-like voice, and thus there is no cross-over effect). The pattern of means is now 1, 0, 0, 0, with only a single mean that differs from the rest. These designs require larger samples sizes to have the same power to detect the interaction, compared to the two-group comparison. The reason for this is that the effect size is only half as large, with Cohen's f = 0.125 (compared to 0.25 in the cross-over interaction). By steadily increasing the sample size in the simulation, we see that to achieve the same power as for the two-group comparison, a total sample size of 635 is required, almost four times as large as the sample size for the two-group comparison (160).

The power in the 2x2 ordinal interaction where only one cell mean differs from the other three cell means is identical to the power we would have if the single mean was twice as far from the remaining means (for a pattern of means of 2, 0, 0, 0). Similarly, if we would examine a 2x2x2 interaction where only one cell differs from the other means, Cohen's f would be 0.25 when the pattern of means is 4, 0, 0, 0, 0, 0, 0, 0 across the eight cells. The take-home message is that a 'medium' effect size translates into a much more extreme pattern of means in an ordinal interaction than in a disordinal (crossover) interaction, or in a 2x2x2 interaction compared to a 2x2 interaction. It might therefore be more intuitive to perform a power analysis based on the expected pattern of means, and compute Cohen's f based on this pattern, than to specify an effect size directly. The same effect size can represent very different patterns of means depending on the type of interaction and the number of factors.

3x3 Between Subject ANOVA

If we extend the design with an extra level for each factor, we have a 3x3 design (two factors, three levels each).

```
design <- "3b*3b"
n <- 20
```

```
mu <- c(20, 20, 20, 20, 20, 20, 20, 20, 25) #All means are equal - so there is no real difference.
# Enter means in the order that matches the labels below.
sd <- 5
labelnames <- c("Factor_A", "a1", "a2", "a3", "Factor_B", "b1", "b2", "b3") #
# the label names should be in the order of the means specified above.

design_result <- ANOVA_design(design = design,
                   n = n,
                   mu = mu,
                   sd = sd,
                   labelnames = labelnames)
```

```
ANOVA_exact(design_result, alpha_level = 0.05)
```

```
## Power and Effect sizes for ANOVA tests
##                   power partial_eta_squared cohen_f non_centrality
## Factor_A          44.86              0.0253  0.1612         4.4444
## Factor_B          44.86              0.0253  0.1612         4.4444
## Factor_A:Factor_B 64.34              0.0494  0.2280         8.8889
##
## Power and Effect sizes for contrasts
##                                                  power effect_size
## p_Factor_A_a1_Factor_B_b1_Factor_A_a1_Factor_B_b2   5.0           0
## p_Factor_A_a1_Factor_B_b1_Factor_A_a1_Factor_B_b3   5.0           0
## p_Factor_A_a1_Factor_B_b1_Factor_A_a2_Factor_B_b1   5.0           0
## p_Factor_A_a1_Factor_B_b1_Factor_A_a2_Factor_B_b2   5.0           0
## p_Factor_A_a1_Factor_B_b1_Factor_A_a2_Factor_B_b3   5.0           0
## p_Factor_A_a1_Factor_B_b1_Factor_A_a3_Factor_B_b1   5.0           0
## p_Factor_A_a1_Factor_B_b1_Factor_A_a3_Factor_B_b2   5.0           0
## p_Factor_A_a1_Factor_B_b1_Factor_A_a3_Factor_B_b3  86.9           1
## p_Factor_A_a1_Factor_B_b2_Factor_A_a1_Factor_B_b3   5.0           0
## p_Factor_A_a1_Factor_B_b2_Factor_A_a2_Factor_B_b1   5.0           0
## p_Factor_A_a1_Factor_B_b2_Factor_A_a2_Factor_B_b2   5.0           0
## p_Factor_A_a1_Factor_B_b2_Factor_A_a2_Factor_B_b3   5.0           0
## p_Factor_A_a1_Factor_B_b2_Factor_A_a3_Factor_B_b1   5.0           0
## p_Factor_A_a1_Factor_B_b2_Factor_A_a3_Factor_B_b2   5.0           0
## p_Factor_A_a1_Factor_B_b2_Factor_A_a3_Factor_B_b3  86.9           1
## p_Factor_A_a1_Factor_B_b3_Factor_A_a2_Factor_B_b1   5.0           0
## p_Factor_A_a1_Factor_B_b3_Factor_A_a2_Factor_B_b2   5.0           0
## p_Factor_A_a1_Factor_B_b3_Factor_A_a2_Factor_B_b3   5.0           0
## p_Factor_A_a1_Factor_B_b3_Factor_A_a3_Factor_B_b1   5.0           0
## p_Factor_A_a1_Factor_B_b3_Factor_A_a3_Factor_B_b2   5.0           0
## p_Factor_A_a1_Factor_B_b3_Factor_A_a3_Factor_B_b3  86.9           1
## p_Factor_A_a2_Factor_B_b1_Factor_A_a2_Factor_B_b2   5.0           0
## p_Factor_A_a2_Factor_B_b1_Factor_A_a2_Factor_B_b3   5.0           0
## p_Factor_A_a2_Factor_B_b1_Factor_A_a3_Factor_B_b1   5.0           0
## p_Factor_A_a2_Factor_B_b1_Factor_A_a3_Factor_B_b2   5.0           0
## p_Factor_A_a2_Factor_B_b1_Factor_A_a3_Factor_B_b3  86.9           1
## p_Factor_A_a2_Factor_B_b2_Factor_A_a2_Factor_B_b3   5.0           0
## p_Factor_A_a2_Factor_B_b2_Factor_A_a3_Factor_B_b1   5.0           0
## p_Factor_A_a2_Factor_B_b2_Factor_A_a3_Factor_B_b2   5.0           0
## p_Factor_A_a2_Factor_B_b2_Factor_A_a3_Factor_B_b3  86.9           1
## p_Factor_A_a2_Factor_B_b3_Factor_A_a3_Factor_B_b1   5.0           0
## p_Factor_A_a2_Factor_B_b3_Factor_A_a3_Factor_B_b2   5.0           0
## p_Factor_A_a2_Factor_B_b3_Factor_A_a3_Factor_B_b3  86.9           1
## p_Factor_A_a3_Factor_B_b1_Factor_A_a3_Factor_B_b2   5.0           0
## p_Factor_A_a3_Factor_B_b1_Factor_A_a3_Factor_B_b3  86.9           1
## p_Factor_A_a3_Factor_B_b2_Factor_A_a3_Factor_B_b3  86.9           1
```

We can check these against the analytic solution.

```
power_res <- power_twoway_between(design_result) #using default alpha level of .05
```

```
power_res$power_A
```

```
## [1] 0.4486306
```

```
power_res$power_B
```

```
## [1] 0.4486306
```

```
power_res$power_AB
```

```
## [1] 0.6434127
```

As we see, power is quite low with n = 20 per cell. Let’s examine how the power increases, as the sample size per condition increases.

```
plot_power(design_result, min_n = 20, max_n = 100)
```

Two by two ANOVA, within design

Potvin & Schutz (2000) simulate a wide range of repeated measure designs. The give an example of a 3x3 design, with the following correlation matrix:

Variances were set to 1 (so all covariance matrices in their simulations were identical). In this specific example, the white fields are related to the correlation for the A main effect (these cells have the same level for B, but different levels of A). The grey cells are related to the main effect of B (the cells have the same level of A, but different levels of B). Finally, the black cells are related to the AxB interaction (they have different levels of A and B). The diagonal (all

1. relate to cells with the same levels of A and B.

Potvin & Schulz (2000) examine power for 2x2 within ANOVA designs and develop approximations of the error variance. For a design with 2 within factors (A and B) these are:

For the main effect of A: $\sigma_e^2 = \sigma^2(1 - \overline{\rho}_A) + \sigma^2(q-1)(\overline{\rho}_B - \overline{\rho}_{AB})$

For the main effectof B: $\sigma_e^2 = \sigma^2(1 - \overline{\rho}_B) + \sigma^2(p-1)(\overline{\rho}_A - \overline{\rho}_{AB})$

For the interaction between A and B: $\sigma_e^2 = \sigma^2(1 - \rho_{\max}) - \sigma^2(\overline{\rho}_{\min} - \overline{\rho}_{AB})$

We first simulate a within subjects 2x2 ANOVA design.

```
mu = c(2,1,4,2)
n <- 20
sd <- 5
r <- c(
  0.8, 0.5, 0.4,
       0.4, 0.5,
            0.8
  )

design = "2w*2w"
labelnames = c("A", "a1", "a2", "B", "b1", "b2")
```

```
design_result <- ANOVA_design(design = design,
                              n = n,
                              mu = mu,
                              sd = sd,
                              r = r,
                              labelnames = labelnames)
```

```
# power_result_vig_4 <- ANOVA_power(design_result, nsims = nsims)
# power_result_vig_4$sim_data <- NULL
# power_result_vig_4$plot1 <- NULL
# power_result_vig_4$plot2 <- NULL
# saveRDS(power_result_vig_4, file = "vignettes/sim_data/power_result_vig_4.rds")
power_result_vig_4 <- readRDS(file = "vignettes/sim_data/power_result_vig_4.rds")
```

We can use the exact simulation as well.

```
ANOVA_exact(design_result = design_result)
```

```
## Power and Effect sizes for ANOVA tests
##     power partial_eta_squared cohen_f non_centrality
## A   26.92              0.0952  0.3244              2
## B   64.23              0.2400  0.5620              6
## A:B 26.92              0.0952  0.3244              2
##
## Power and Effect sizes for contrasts
##                        power effect_size
## p_A_a1_B_b1_A_a1_B_b2 26.92     -0.3162
## p_A_a1_B_b1_A_a2_B_b1 39.70      0.4000
## p_A_a1_B_b1_A_a2_B_b2  5.00      0.0000
## p_A_a1_B_b2_A_a2_B_b1 64.23      0.5477
## p_A_a1_B_b2_A_a2_B_b2 13.60      0.2000
## p_A_a2_B_b1_A_a2_B_b2 76.52     -0.6325
```

We see the 26.9 and 64.2, and 26.9 correspond to the results of the exact simulation.