

TAP2 Factorial Design

Task One

Hypothesis

At follow-up participants' stress will be predicted by the programme to which they were assigned (trial_arm) but this effect will be moderated by their job role. Specifically, they predicted that the effect of trial_arm would be stronger in (1) medical roles compared to management and support worker roles; (2) management roles compared to support worker roles.

The design

As there are two independent variables that predict a dependent variable, a General Linear Model using a 2-way Factorial design will be fit.

Summary statistics

Initially summary statistics of both independent variables (trial group and job role) will be reported, including the means and confidence intervals. This will illustrate the initial relationship between the independent variables and the dependent variables. The means will demonstrate how stress scores differ across the groups and the confidence intervals will illustrate how much the scores vary. I will be looking directly to see if there are any obvious patterns, for example, are the means between the groups similar? are they dissimilar? Is there are groups that are vastly different to the others? This will allow an initial understanding of the data.

Furthermore, the means and confidence intervals will be plotted in order to visualize the data. This will allow a visual comparison of the means in each job role and in each trial group. I will be looking to see whether job groups vary in stress score, whether trial groups vary in stress scores and finally if stress scores vary between trial groups within a job role.

Fit the model

Use lm() function

The factorial model will then be fit using the lm() function. This function will be chosen as its a more flexible choice that allows analysis to obtain diagnostic plots (that you're not able to obtain using the aless() package). Furthermore, the lm() function does not affect the parameter estimates, meaning b is more accurate.

Set manual contrasts

The contrasts will then be manually set in order to compare groups in relation to the hypothesis. For example, for hypothesis 1: medical roles compared to management and support worker roles, contrasts will compare medical roles to non-medical roles (2/3,1/2,1/2). For hypothesis 2: management roles compared to support worker roles, contrast will compare management roles to support worker roles (1/2,-1/2).

Report overall model summary

The overall summary will then be reported for the model (including the trial group, job role and the interaction between the trial group and job role). This will show whether the interaction between both independent variables (trial group and job role) are statistically significant. If p<0.05 then the interaction effect is significant therefore supporting the hypothesis, if p>0.05 then the interaction effect is insignificant.

Report parameter estimates

The parameter estimates will then be reported in order to gain the raw effect sizes of the interactions between the effect of job role (for medical vs non medical and management vs support worker) on stress to see if scores are significantly different in for the trial groups (psycho-social and mindful). Within this data i will be looking to see if the interaction effects are statistically significant, if they are this will support the hypothesis. This will be formally tested using a simple effect analysis in order to solidify the understanding of the data.

Report the simple effects analysis

This will formally test the effect of role within each trial group separately and also test the effect of trial group within each role separately.

Report the effect sizes

The final part of fitting the model requires to test the effect sizes in order to gain information regarding how much the interaction effect explains the variance in the dependent variable (stress score). Omega squared will be reported rather than eta squared as omega squared is less biased.

Test assumptions

In order to test the assumptions of homogeneity, normality and linearity diagnostic plots will be produced. Homogeneity will be tested with the use of Residuals vs Fitted plot and Scale-Location plot. To assume homogeneity i will be looking for a straight line with a vertical spread of points along the x-axis, if there is a substantial curve of the line or the data shows a clear funnel shape this would suggest heteroscedasticity.

A Normal Q-Q plot will then be plotted to determine if the data set is well modeled by a normal distribution. I will be looking to see if the Q-Q plot is skewed or tailed as this would suggest the sample is not normally distributed, perhaps suggesting potential influential cases.

Finally cooks distance will be plotted in order to establish whether there are any influential cases or outliers. Here, i will be looking to see if any cases are above the threshold of 1 as this would suggest influential cases' outliers. If any outliers are identified a robust model will be fit in order to evaluate whether they have caused bias in the data set.

Robust Model

If there was any suggestion of bias in the Cooks distance measurement a robust model will be fit in order to understand whether it has caused bias in the OLS model. The summary statistics will report "the test for bias" if the p-values for this test is non-significant this will tell me that the bias in the OLS model is not problematic. Furthermore, the robust model parameters should have similar b estimates to the OLS and the significance should also remain similar. If not, this would suggest the OLS model has been biased.

Bayes Factor

Bayes Factor will report the probability of the data given the alternative hypothesis relative to the probability of the data given the null. Bayes Factor will indicate whether i should change my beliefs about the alternative hypothesis. For example, a number above 3 is evidence to support the alternative hypothesis, but a value below 0.3 is evidence for the null hypothesis. Bayes Factor will be calculated for the individual effect of role, the effect of role and trial group and finally the combined effect of role and trial group. The effect i will focus on will be the effect of role and trial group as well as the combined effect as this relates directly to the hypothesis. These values will be used to form the final conclusion of the analysis.

Task Two

Description of the General Linear Model

The general linear model is a statistical technique that investigates the linear relationship between one dependent variable and one or more independent variable(s). The GLM is the foundation for several statistical tests including, ANOVA, Regressions analysis and correlation analysis. The formula for the General Linear Model is stated below:

$$Y_i = (\text{model})_i + e_i$$
$$\text{Outcome}_i = b_0 + b_1 \text{predictor}_{i1} + e_i$$

- Y stands for the dependent variable (the variable the model aims to predict)
- b_0 stands for the intercept (which is always constant)

- b_1 stands for a weight or a slope, otherwise referred to as the coefficient. This determines how much weight one variable contributes to the model.
- e stands for the error in the model.

The hypothesis:

At follow-up participants' stress will be predicted by the programme to which they were assigned (trial_arm) but this effect will be moderated by their job role. Specifically, they predicted that the effect of trial_arm would be stronger in (1) medical roles compared to management and support worker roles; (2) management roles compared to support worker roles.

Therefore, as the report has two independent variables, where trial is moderated by job role, that predicts one dependent variable (stress score), a 2-way factorial design is best suited. This design allows researchers to assess the interaction and allows the effects of a factor (trial group) to be estimated at several levels of another factor (job role). This will result in a conclusion that has fully investigated all possible combinations of the levels of the categorical predictors.

The equation for the factorial design

$$\text{stress}_i = b_0 + b_1 \text{trial}_i + b_2 \text{role}_i + b_3 \text{trial}_i \times \text{role}_i + e_i$$

The assumptions of the model

As the current model is a linear model there are three main assumptions that need to be met. The first is linearity and additivity, linearity is the assumption that the relationship between the dependent variable (stress score) and the independent variables (trial group and job role) is linear. This can be tested with the use of plots. Additivity is the assumption that when there are several independent variables in the model we assume that the combined effect of those variables are "additive", in other words that the effect of one variable adds to the effect of the other variable.

Secondly, the population errors are assumed to be "spherical". This is broken down into two conditions; population errors are assumed to have homoscedasticity and population errors are assumed to be independent/unrelated. The first condition means that the variance in errors is the same at all values of the predictors (trial and job role). The second condition relates to the assumption that errors should be un-influenced.

The last assumption is the normality of the sampling distribution, which refers to the assumption that the residuals of the model are normally distributed, or that the sampling distribution of the parameter is normally distributed.

Task Three

Preparing data for analysis.

Loaded packages

```
library(tidyverse)
library(ggfortify)
```

Loaded data and filtered tibble

```
mindful_tib <- here::here("data/tap_mindfulness.csv") %>%
  read_csv() %>%
  dplyr::mutate(
    role = forcats::as_factor(role) %>% forcats::fct_relevel("Medical", "Management", "Support workers"),
    trial_arm = forcats::as_factor(trial_arm)
  )

mindful_tib <- mindful_tib %>%
  dplyr::filter(time == "Follow-up")
```

Exploring data

Reporting the mean and confidence intervals of stress scores

```
mindful_tib %>%
  dplyr::group_by(role, trial_arm) %>%
  dplyr::summarize(
    mean = mean(stress, na.rm = TRUE),
    "95% CI lower" = mean_ci_normal(stress)$min,
    "95% CI upper" = mean_ci_normal(stress)$max
  ) %>%
  knitr::kable(digits = 2, caption = "Table 1: Summary statistics")
```

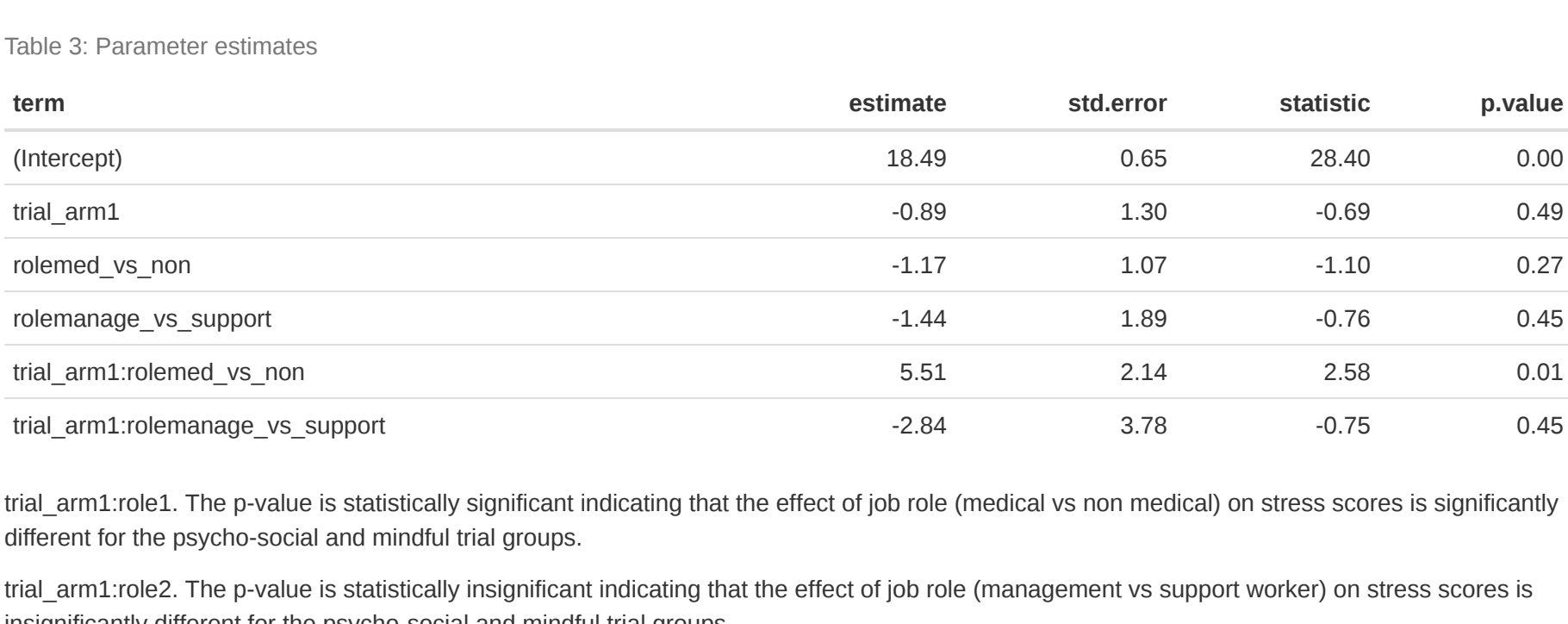
Table 1: Summary statistics

role	trial_arm	mean	95% CI lower	95% CI upper
Medical	Psychosocial information	21.55	20.18	22.93
Medical	Mindfulness	16.99	15.49	18.48
Management	Psychosocial information	17.64	12.23	23.04
Management	Mindfulness	20.00	13.26	26.74
Support workers	Psychosocial information	17.62	16.05	19.18
Support workers	Mindfulness	17.14	15.67	18.61

Note that the means of stress scores for the roles management and support worker under both trial groups are fairly similar. However, the mean stress score for medical roles differ by a large amount in each trial group.

Plot to visualize the means and confidence intervals of stress scores

```
ggplot2::ggplot(mindful_tib, aes(x = role, y = stress, colour = trial_arm)) +
  stat_summary(fun.data = "mean_ci_normal", geom = "pointinterval", position = position_dodge(width = 0.2)) +
  coord_cartesian(ylim = c(10,30)) +
  scale_y_continuous(breaks = 0:40) +
  labs(x = "Job profession", y = "Stress scores (0-42)", colour = "Trial group") +
  theme_minimal()
```



Note, the mean stress scores of those with a medical job role clearly differ in each trial group more so than that of the management and support worker groups. However, upon comparing the management and support worker groups, it appears that management role differs in stress score within trial groups more than the support worker role.

This initial relationships supports the hypothesis that the effect of trial group would be stronger in medical roles compared to non-medical roles and stronger in management roles compared to support worker roles.

Fitting the GLM (Factorial design)

Setting manual contrasts

```
med_vs_non <- c(-2/3,1/3,1/3)
manage_vs_support <- c(0, -1/2, 1/2)
contrasts(mindful_tib$role) <- cbind(med_vs_non, manage_vs_support)
# alternate hypothesis, which makes sense as the effect of only job role is not the hypothesis being tested
mindful_lm <- lm(stress ~ trial_arm+role, data =mindful_tib)
```

Reporting the models statistics

Overall model summary

```
car::Anova(mindful_lm, type = 3) %>%
  knitr::kable(digits = 2, caption = "Table 2: Overall model summary")
```

Table 2: Overall model summary

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	57617.75	1	806.44	0.00
trial_arm	33.73	1	0.47	0.49
role	453.50	2	3.17	0.04
trial_arm:role	664.55	2	4.65	0.01
Residuals	37723.85	528	NA	NA

Note that the variable trial_arm:role, representing the F-statistic of the model, has a hugely significant p-value (p= 0.01) attached to the F-statistic (4.65), indicating that the effect of trial group influenced by the job role significantly predicts the dependent variable (stress score).

These values support the hypothesis that stress is predicted by the trial group moderated by job role.

Parameter estimates

```
brnom::tidy(mindful_lm) %>%
  knitr::kable(digits = 2, caption = "Table 3: Parameter estimates")
```

Table 3: Parameter estimates

term	estimate	std.error	statistic	p.value
(Intercept)	18.49	0.65	28.40	0.00
trial_arm1	-0.89	1.30	-0.69	0.49
rolemed_vs_non	-1.17	1.07	-1.10	0.27
rolemanage_vs_support	-1.44	1.89	-0.76	0.45
trial_arm:rolemed_vs_non	5.51	2.14	2.58	0.01
trial_arm:rolemanage_vs_support	-2.84	3.78	-0.75	0.45

trial_arm1:role1. The p-value is statistically significant indicating that the effect of job role (medical vs non medical) on stress scores is significantly different for the psycho-social and mindful trial groups.

trial_arm1:role2. The p-value is statistically insignificant indicating that the effect of job role (management vs support worker) on stress scores is insignificant different for the psycho-social and mindful trial groups.

Simple effects analysis

```
emmeans::joint_tests(mindful_lm, "role") %>%
  knitr::kable(digits = 2, caption = "Table 4: Simple effects analysis for job roles")
```

Table 4: Simple effects analysis for job roles

model term	role	df1	df2	F.ratio	p.value
trial_arm	Medical	1	528	20.80	0.00
trial_arm	Management	1	528	0.43	0.51
trial_arm	Support workers	1	528	0.18	0.67

Note p<0.001 for the medical job role. Suggesting a medical role has a significant effect on the dependent variable (stress score) within the trial groups (mindful and psycho-social).

p-value for the management role (p=0.51) and the support worker role (p=0.67) are both insignificant p>0.05 threshold. Suggesting that a management role and a support worker role has an insignificant effect on the dependent variable (stress score) within the trial group.

In summary it seems like the trial group (mindful and psycho-social) is more significant for the medical job role than for the management or support worker role. This supports the hypothesis that the effect of trial group will be stronger in medical roles vs non medical roles, as the medical role has a significant effect on stress and the non-medical roles (management and support worker) have insignificant effects on stress.

```
emmeans::joint_tests(mindful_lm, "trial_arm") %>%
  knitr::kable(digits = 2, caption = "Table 5: Simple effects analysis for trial groups")
```

Table 5: Simple effects analysis for trial groups

programme they were assigned moderated (by their job role) than under the null (stress will not be predicted by the programme moderated by their job role). Our beliefs that the role affects stress scores should increase by a value of about 1.15. A value of 1.15 is fairly weak evidence to accept the alternative hypothesis, which makes sense as the effect of only job role is not the hypothesis being tested.

Bayes factor for job role and trial_arm (trial group) is 30.56. Therefore, the data is 30.56 times more likely under the model that predicts stress scores from the job role and trial group than the model that predicts stress scores from job role alone. A value of 30.56 is a substantial change and strong evidence to accept the alternative hypothesis, this is of value as the effect of both factors is part of the hypothesis being tested.

Bayes factor for the combined effect of job role and trial_arm (trial group) (4.64). Suggests the data is 4.46 times more likely under the model that predicts stress scores from the combined effect of the job role and trial_arm (trial group) than under the model that predicts stress from the

Note the p-value for the psycho-social trial group (p= 0.0008). Suggesting the psycho-social group within all job roles has a significant effect p<0.001 on the dependent variable (stress score).

The p-value for the mindful trial group (p= 0.52). Suggesting the mindful group within all job roles has a insignificant effect p>0.05 on the dependent variable (stress score).

Effect sizes

```
car::Anova(mindful_lm, type = 3) %>%
  effects::omega_squared(, ci = 0.95) %>%
  knitr::kable(digits = 4, caption = "Table 6: Effect sizes (Omega squared)")
```

Table 6: Effect sizes (Omega squared)

(2) management roles compared to support worker roles.

However, the parameter estimates for management vs support worker do not support hypothesis (2). As there is no statistical significance to the difference in stress scores for both of the job roles (management and support worker).

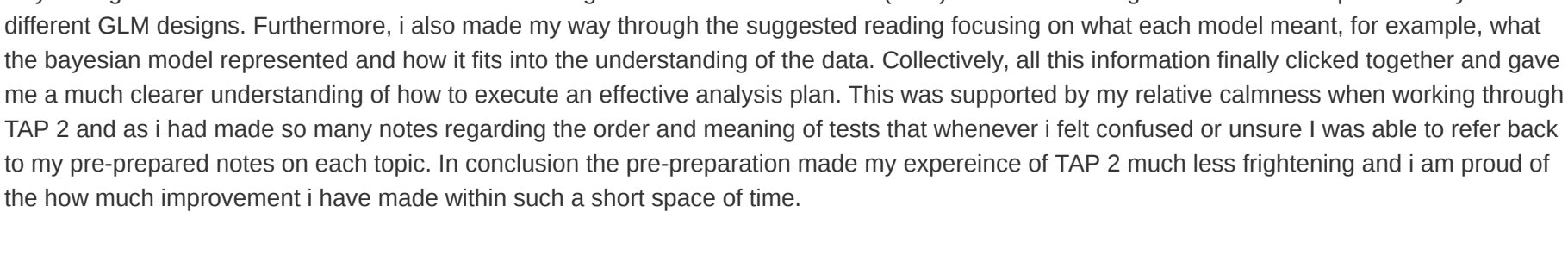
The simple effects analysis further supports this as *p*-value show that the support worker role and the management role has an insignificant effect on stress. Therefore suggesting that there's little statistical significance that the management role, moderated by trial group, has a larger effect on stress compared to the support worker role, as both effects are insignificant.

Reflective statement

Note the omega squared values for trial_arm (0.001) shows that the job role explains 0.1% of the variance in the dependent variable (stress score). The omega squared values for role (0.008) shows that the job role explains 0.8% of the variance in the dependent variable (stress score).

The omega squared values for trial_arm x role interaction (0.0135) explains 1.4% of the variance in the dependent variable (stress score).

Testing assumptions



Interpreting Residual vs Fitted and Scale-Location graphs.

(Residuals vs Fitted) The line lies flat along 0. The vertical spread of points are similar as you move along the x-axis. Therefore, the residuals show homogeneity.

(Scale-Location) The vertical spread of points are similar as you move along the x-axis. Also showing homogeneity.

Interpreting Normal Q-Q plot

The plots on the Q-Q plot only deviate slightly from the lines at the extremes. Potentially suggesting a slightly tailed Q-Q plot, however this is not drastic enough to violate normality. Therefore, we can assume the normality.

Interpreting Cooks distance

Cases 97, 101 and 201 have larger cooks distance values compared to the other plots. However, these values are below the value of 0.1 and does not surpass the threshold of 1. Therefore, cooks distance plot does not show any influential cases or outliers.

Bayes Factor

```
role_bf <- Bayesfactor::lmbf(formula = stress~ role, data = mindful_tib)
trial_bf <- Bayesfactor::lmbf(stress~ role + trial_arm, data = mindful_tib)
int_bf <- Bayesfactor::lmbf(formula = stress~ role + trial_arm + role:trial_arm, data = mindful_tib)
role_bf
```

```
## Bayes factor analysis
## -----
## [1] role : 1.154869 ±0.62%
##
## Against denominator:
## Intercept only
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
trial_bf/role_bf
```

```
## Bayes factor analysis
## -----
## [1] role + trial_arm : 32.72878 ±5.43%
##
## Against denominator:
## stress ~ role
## ---
## Bayes factor type: BFlinearModel, JZS
```

```
int_bf/trial_bf
```

```
## Bayes factor analysis
## -----
## [1] role + trial_arm + role:trial_arm : 4.453829 ±6.07%
##
## Against denominator:
## stress ~ role + trial_arm
## ---
## Bayes factor type: BFlinearModel, JZS
```

Bayes factor for role (1.15), suggests the data are 1.15 times more likely under the alternative hypothesis (stress will be predicted by the programme) than under the null hypothesis (stress will not be predicted by the programme moderated by their job role). Our beliefs that the role affects stress scores should increase by a factor of about 1.15. A value of 1.15 is fairly weak evidence to accept the alternate hypothesis, which makes sense as the effect of only job role is not the hypothesis being tested.

Bayes factor for job role and trial_arm (trial group) is 30.56. Therefore, the data is 30.56 times more likely under the model that predicts stress score from the job role and trial group than the model that predicts stress scores from job role alone. A value of 30.56 is a substantial change and strong evidence to accept the alternative hypothesis, this is of value as the effect of both factors is part of the hypothesis being tested.

Bayes factor for the combined effect of job role and trial_arm (trial group) (4.64). Suggests the data are 4.64 times more likely under the model that predicts stress scores from the combined effect of the job role and trial_arm (trial group) than under the model that predicts stress from the main effects of job role and trial_arm (trial group). As this is an increase from the Bayes Factor of 30.56 this is strong evidence to accept the alternate hypothesis, which again makes sense as the interaction between both factors was the main hypothesis of this report.

In summary, a large Bayes factor of approximately 30.56 for the combined effect of trial group and job role is a strong evidence to support the initial hypothesis that stress will be predicted by the programme (trial_arm) moderated by their job role.

Conclusion

The aim of the report was to test the following hypothesis:

At follow-up participants' stress will be predicted by the programme to which they were assigned (trial_arm) but this effect will be moderated by their job role.

This section of the hypothesis is supported by the model summary as the p-values suggest that the effect of trial group influenced by the job role significantly predicts the dependent variable (stress). Furthermore, Bayes Factor of 30.56, discussed in the previous section, for the model including trial group and job role is evidence to accept the hypothesis.

Specifically, they predicted that the effect of trial_arm would be stronger in (1) medical roles compared to management and support worker roles

The reported model parameter estimates suggested that the effect of job role (medical vs management and support worker) is significantly different for each trial group (psycho-social and mindful). This supports hypothesis (1) as the values shows the effect of job role (medical vs non medical) on stress is different within the trial groups.

The simple effect analysis further supports this as the p-values for the medical role has a significant effect on stress but the p-values for management and support worker do not. Therefore suggesting medical roles have a stronger effect.

(2) management roles compared to support worker roles.

However, the parameter estimates for management vs support worker do not support hypothesis (2). As there is no statistical significance to the difference in stress scores for both of the job roles (management and support worker).

The simple effects analysis further supports this as p-value show that the support worker role and the management role has an insignificant effect on stress. Therefore suggesting that there is little statistical significance that the management role, moderated by trial group, has a larger effect on stress compared to the support worker role, as both effects are insignificant.

Reflective statement

The first challenge I faced at the beginning of this TAP was setting the levels for the categorical factors. I looked at the overview section for discov 13 in order to get a grasp, but since i hadn't set levels since discov 1 I found it difficult to get my head round it. I decided to go back to discov 1 and refresh my memory on the basics of setting levels for factors. I finally got a grasp of the code using forcats, but for some reason it still was not working. I looked through my codes to decipher what the issue was, eventually it clicked that i had tried to create the levels before i had downloaded the data file. Thankfully, this was an easy issue to fix and once the data was re-ordered i was able to continue to combat the rest of the report. As i spent some time trying to decipher why the code was not working, ordering the code tactfully has now become a rule of thumb in order to avoid unnecessary error messages in the future.

Another challenge i faced during the last TAP was how to order the analysis. For example, in TAP 1 the clarity of my analysis plan represented how i felt about the contents contained. In order to avoid feeling lost during TAP 2 i thoroughly went through each piece of material available. I made me way through each tutorial at least once and went through the more recent tutorials (9-14) now times making notes on each step necessary for different GLM designs. Furthermore, i also made my way through the suggested reading, focusing on what each model mean, for example, what the bayesian model represented and how it fits into the understanding of the data. Collectively, all this information finally clicked together and gave me a much clearer understanding of how to execute an effective analysis plan. This was supported by my relative calmness when working through TAP 2 and as i had made so many notes regarding the order and meaning of tests that whenever i felt confused or unsure i was able to refer back to my pre-prepared notes on each topic. In conclusion the pre-preparation made my experience of TAP 2 much less frightening and i am proud of the how much improvement i have made within such a short space of time.