LDA-HW2-al3998

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Question 1

1. Consider a marginal model for the log odds of moderate or severe onycholysis. Using GEE, set up a suitable model assuming linear trends. Use month as the time variable. Assume "exchangeable" correlation for the association among the repeated binary responses.

Model setup:

$E[Y_{ij}]$=μ_{ij} Link function: $log\mu_{ij}$ =η_{ij} = $\sum_{k=1}^{p} X_{ij}\beta_k$ Under poisson assumption: $Var(Y_{ij}) = \phi V(\mu_{ij}) = \phi\mu_{ij}$

The model I built is

$$\eta_{ij} = \beta_0 + \beta_1 Treatment_i + \beta_2 Month_{ij} + \beta_3 (Treatment_i * Month_{ij})$$

```
Call:
geeglm(formula = Response ~ Treatment * Month, family = binomial(link = "logit"),
    data = toenail1, id = Subject_ID, corstr = "exchangeable")

 Coefficients:
                 Estimate  Std.err   Wald Pr(>|W|)
(Intercept)      -0.58192  0.17206 11.439 0.000719 ***
Treatment1        0.00718  0.25949  0.001 0.977924
Month            -0.17128  0.03000 32.596 1.13e-08 ***
Treatment1:Month -0.07773  0.05411  2.064 0.150862
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = exchangeable
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)    1.088  0.5013
  Link = identity

Estimated Correlation Parameters:
      Estimate Std.err
alpha   0.4218  0.2119
Number of clusters:   294  Maximum cluster size: 7
```

Test if the treatment interaction term is required The null hypothesis is: β_3=0

```
     [,1] [,2] [,3] [,4]
[1,]    0    0    0    1
```

X2.stat	DF	Pr(>|X^2|)
2.063	1	0.1509

As we can see from the result,p-value is greater than 0.05 so that we fail to reject the null and we can remove the interaction terms.

I fit the model again as

$$\eta_{ij} = \beta_0 + \beta_1 Treatment_i + \beta_2 Month_{ij}$$

```
Call:
geeglm(formula = Response ~ Treatment + Month, family = binomial(link = "logit"),
    data = toenail1, id = Subject_ID, corstr = "exchangeable")

 Coefficients:
            Estimate Std.err  Wald Pr(>|W|)
(Intercept)  -0.6104  0.1777 11.80  0.00059 ***
Treatment1    0.0402  0.2532  0.03  0.87388
Month        -0.2051  0.0259 62.66  2.4e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = exchangeable
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     1.09   0.423
  Link = identity

Estimated Correlation Parameters:
      Estimate Std.err
alpha    0.424   0.182
Number of clusters:   294  Maximum cluster size: 7
```

2. Provide Interpretations for the coefficients in your model.

Interpretation:

	Estimate	Std.err	Wald	Pr(>|W|)
(Intercept)	-0.610	0.178	11.796	0.001
Treatment1	0.040	0.253	0.025	0.874
Month	-0.205	0.026	62.656	0.000

$$\eta_{ij} = -0.610 + 0.0402 Treatment - 0.2051 Month$$

- β_0:Log odds of moderate or severe onycholysis for oral treatment B at baseline month is -0.610
- β_1:Log odds ratio of moderate or severe onycholysis comparing treatment A to treatment B with month fixed is 0.0402

- β_2:Log odds ratio of moderate or severe onycholysis for 1 unit increase in month among treatment B is -0.2051

3. From the results of your analysis what conclusions do you draw about the effect of treatment on changes in the severity of onycholysis over time? Provide results that support your conclusions.

From the result above, we can recall the test of interaction terms for treatmet and month,at 0.05 significant level,the p-value is greater than 0.05 so that we fail to reject the null and can conclude that the effect of treatment in the severity of onycholysis will not change over time.

4.Try Different correlation structures. Is the analysis and inference sensitive to this choice?

Correlation structure:unstructured

```
Call:
geeglm(formula = Response ~ Treatment * Month, family = binomial(link = "logit"),
    data = toenail1, id = Subject_ID, corstr = "unstructured")

 Coefficients:
                 Estimate Std.err  Wald Pr(>|W|)
(Intercept)       -0.7396  0.1664 19.75  8.8e-06 ***
Treatment1         0.0373  0.2469  0.02    0.880
Month             -0.1319  0.0263 25.11  5.4e-07 ***
Treatment1:Month  -0.0896  0.0482  3.46    0.063 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = unstructured
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     1.04   0.334
  Link = identity

Estimated Correlation Parameters:
          Estimate Std.err
alpha.1:2    0.904  0.2983
alpha.1:3    0.712  0.2414
alpha.1:4    0.512  0.1885
alpha.1:5    0.247  0.1180
alpha.1:6    0.157  0.0927
alpha.1:7    0.131  0.0945
alpha.2:3    0.824  0.2737
alpha.2:4    0.608  0.2178
alpha.2:5    0.272  0.1248
alpha.2:6    0.238  0.1152
alpha.2:7    0.157  0.1027
alpha.3:4    0.789  0.2723
alpha.3:5    0.284  0.1278
```

```
alpha.3:6    0.215  0.1107
alpha.3:7    0.192  0.1135
alpha.4:5    0.368  0.1525
alpha.4:6    0.282  0.1297
alpha.4:7    0.250  0.1302
alpha.5:6    0.498  0.1989
alpha.5:7    0.475  0.2034
alpha.6:7    0.706  0.2607
Number of clusters:   294  Maximum cluster size: 7
```

Test if the treatment interaction term is required The null hypothesis is: β_3=0

```
     [,1] [,2] [,3] [,4]
[1,]    0    0    0    1
```

X2.stat	DF	Pr(>|Xˆ2|)
3.46	1	0.063

As we can see from the result, the p-value is greater than 0.05 so that when the correlation structure is unstructured,the analysis and inference are not sensitive to this choice.

Correlation structure:independence

```
Call:
geeglm(formula = Response ~ Treatment * Month, family = binomial(link = "logit"),
    data = toenail1, id = Subject_ID, corstr = "independence")

 Coefficients:
                  Estimate   Std.err  Wald Pr(>|W|)
(Intercept)      -0.556627  0.171171 10.57   0.0011 **
Treatment1       -0.000582  0.250848  0.00   0.9981
Month            -0.170308  0.029163 34.11  5.2e-09 ***
Treatment1:Month -0.067222  0.052116  1.66   0.1971
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = independence
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     1.04    0.39
Number of clusters:   294  Maximum cluster size: 7
```

Test if the treatment interaction term is required The null hypothesis is: β_3=0

```
     [,1] [,2] [,3] [,4]
[1,]    0    0    0    1
```

X2.stat	DF	Pr(>|Xˆ2|)
1.66	1	0.197

As we can see from the result, the p-value is greater than 0.05 so that when the correlation structure is independence,the analysis and inference are not sensitive to this choice.

Correlation structure:AR1

```
Call:
geeglm(formula = Response ~ Treatment * Month, family = binomial(link = "logit"),
    data = toenail1, id = Subject_ID, corstr = "ar1")

 Coefficients:
                 Estimate Std.err  Wald Pr(>|W|)
(Intercept)       -0.6441  0.1684 14.64  0.00013 ***
Treatment1         0.0691  0.2520  0.08  0.78409
Month             -0.1376  0.0274 25.27    5e-07 ***
Treatment1:Month  -0.0968  0.0517  3.51  0.06105 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = ar1
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     1.01   0.362
  Link = identity

Estimated Correlation Parameters:
      Estimate Std.err
alpha    0.687   0.135
Number of clusters:   294  Maximum cluster size: 7
```

Test if the treatment interaction term is required The null hypothesis is: β_3=0

```
     [,1] [,2] [,3] [,4]
[1,]    0    0    0    1
```

X2.stat	DF	Pr(>|Xˆ2|)
3.51	1	0.061

As we can see from the result, the p-value is greater than 0.05 so that when the correlation structure is independence,the analysis and inference are not sensitive to this choice.

Question 2

1. Set up a suitable GEE model for rate of skin cancers with Treatment and Year as covariates.

The model will be fitted as:

model set up

Y_{ij}=[0,1];$E[Y_{ij}]$=μ_{ij} Mean response model:$log(\mu_{ij}) = \eta_{ij}$ Under binomial assumption:$V(\mu_{ij}) = \mu_{ij}(1 - \mu_{ij})$

$$\eta_{ij} = \beta_0 + \beta_1 Treatment + \beta_2 Year + \beta_3 Treatment * Year$$

```
Call:
geeglm(formula = Y ~ Treatment * Year, family = poisson(link = "log"),
    data = skin, id = ID, corstr = "unstructured")

 Coefficients:
               Estimate  Std.err   Wald Pr(>|W|)
(Intercept)    -1.35953  0.12009 128.16   <2e-16 ***
Treatment1      0.04891  0.16353   0.09     0.76
Year           -0.00379  0.03232   0.01     0.91
Treatment1:Year  0.03271  0.04917   0.44     0.51
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = unstructured
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     2.67   0.394
  Link = identity

Estimated Correlation Parameters:
          Estimate Std.err
alpha.1:2    0.294  0.0862
alpha.1:3    0.328  0.1113
alpha.1:4    0.367  0.1284
alpha.1:5    0.419  0.2276
alpha.2:3    0.243  0.0565
alpha.2:4    0.232  0.0635
alpha.2:5    0.241  0.1113
alpha.3:4    0.741  0.4089
alpha.3:5    0.517  0.2039
alpha.4:5    0.507  0.2262
Number of clusters:   1683  Maximum cluster size: 5
```

Test if the interaction term is required: The null hypothesis is: β_3=0

```
  X2.stat DF Pr(>|X^2|)
1   0.443  1      0.506
```

We can see that the p-value is $0.506 > 0.05$,so that we fail to reject the null and we can remove the interaction term from the model.

Then I fit the model again as

$$\eta_{ij} = \beta_0 + \beta_1 Treatment + \beta_2 Year$$

```
Call:
geeglm(formula = Y ~ Treatment + Year, family = poisson(link = "log"),
    data = skin, id = ID, corstr = "unstructured")

 Coefficients:
            Estimate Std.err   Wald Pr(>|W|)
(Intercept)  -1.4020  0.1069 172.03   <2e-16 ***
Treatment1    0.1297  0.1052   1.52     0.22
Year          0.0134  0.0250   0.29     0.59
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = unstructured
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     2.68   0.401
  Link = identity

Estimated Correlation Parameters:
          Estimate Std.err
alpha.1:2    0.295  0.0871
alpha.1:3    0.329  0.1120
alpha.1:4    0.365  0.1282
alpha.1:5    0.415  0.2248
alpha.2:3    0.242  0.0565
alpha.2:4    0.231  0.0630
alpha.2:5    0.237  0.1091
alpha.3:4    0.743  0.4147
alpha.3:5    0.513  0.2052
alpha.4:5    0.504  0.2297
Number of clusters:   1683  Maximum cluster size: 5
```

	Estimate	Std.err	Wald	Pr(>|W|)
(Intercept)	-1.402	0.107	172.031	0.000
Treatment1	0.130	0.105	1.521	0.218
Year	0.013	0.025	0.286	0.593

2. Provide Interpretations for the coefficients in your model.

- β_0: the log rate of having non-melanoma skin cancers in placebo group at baseline is -1.402.
- β_1: the log rate ratio of having non-melanoma skin cancer between carotene group and placebo group with year fixed is 0.130.

- β_2: the log rate ratio of having non-melanoma skin cancer with one unit increase in years of follow-up for placebo group will be 0.013.

3. From the results of your analysis what conclusions do you draw about the effect of beta carotene on the rate of skin cancers? Provide results that support your conclusions.

At 0.05 significant level, the treatment is not significant when adjusted year, we conclude that effect of beta carotene on the rate of skin cancers is not sufficient.

4. Repeat the above analysis adjusting for skin type, age, and the count of the number of previous skin cancers. What conclusions do you draw about the effect of beta carotene on the adjusted rate of skin cancers?

```
Call:
geeglm(formula = Y ~ Treatment + Year + Age + Skin + Exposure,
    family = poisson(link = "log"), data = skin, id = ID, corstr = "unstructured")

 Coefficients:
            Estimate  Std.err   Wald Pr(>|W|)
(Intercept) -3.06545  0.32970  86.45   <2e-16 ***
Treatment1   0.11595  0.09772   1.41   0.2354
Year         0.01637  0.02469   0.44   0.5072
Age          0.01527  0.00513   8.88   0.0029 **
Skin1        0.18398  0.10808   2.90   0.0887 .
Exposure     0.13806  0.01016 184.49   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = unstructured
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     1.64  0.0776
  Link = identity

Estimated Correlation Parameters:
          Estimate Std.err
alpha.1:2    0.164  0.0353
alpha.1:3    0.178  0.0365
alpha.1:4    0.199  0.0572
alpha.1:5    0.186  0.0513
alpha.2:3    0.197  0.0479
alpha.2:4    0.181  0.0436
alpha.2:5    0.150  0.0457
alpha.3:4    0.317  0.0884
alpha.3:5    0.312  0.0773
alpha.4:5    0.245  0.0686
Number of clusters:   1683  Maximum cluster size: 5
```

I fit the model as:

$$\eta_{ij} = \beta_0 + \beta_1 Treatment + \beta_2 Year + \beta_3 Age + \beta_4 Skin_1 + \beta_5 Exposure$$

null hypothesis: β_1=0

estimate	std.error	statistic	p.value	beta0	df	lwr	upr
0.116	0.098	1.41	0.235	0	1	-0.076	0.307

The p-value equals to 0.235 which is greater than 0.05,so that we fail to reject the null and conclude that there is no difference in log rate ratios between carotene gorup and placebo group when adjusting for skin type, age, and the count of the number of previous skin cancers.

5.Try Different correlation structures.Is the analysis and inference sensitive to this choice?

For model in part 1) Correlation structure:AR1

```
Call:
geeglm(formula = Y ~ Treatment + Year, family = poisson(link = "log"),
    data = skin, id = ID, corstr = "ar1")

 Coefficients:
            Estimate  Std.err   Wald Pr(>|W|)
(Intercept) -1.37639  0.11040 155.43   <2e-16 ***
Treatment1   0.15365  0.11098   1.92     0.17
Year         0.00605  0.02453   0.06     0.81
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = ar1
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     2.63   0.384
  Link = identity

Estimated Correlation Parameters:
      Estimate Std.err
alpha    0.545   0.111
Number of clusters:   1683  Maximum cluster size: 5
```

	Estimate	Std.err	Wald	Pr(>|W|)
(Intercept)	-1.376	0.110	155.430	0.000
Treatment1	0.154	0.111	1.917	0.166
Year	0.006	0.025	0.061	0.805

Correlation structure:exchangable

```
Call:
geeglm(formula = Y ~ Treatment + Year, family = poisson(link = "log"),
    data = skin, id = ID, corstr = "exchangable")

 Coefficients:
            Estimate Std.err   Wald Pr(>|W|)
(Intercept)  -1.4123  0.1080 171.10   <2e-16 ***
Treatment1    0.1478  0.1094   1.83     0.18
Year          0.0173  0.0247   0.49     0.48
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = exchangeable ar1 unstructured userdefined fixed
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     2.65   0.374
  Link = identity

Estimated Correlation Parameters:
      Estimate Std.err
alpha    0.378   0.111
Number of clusters:   1683  Maximum cluster size: 5
```

	Estimate	Std.err	Wald	Pr(>|W|)
(Intercept)	-1.412	0.108	171.095	0.000
Treatment1	0.148	0.109	1.825	0.177
Year	0.017	0.025	0.492	0.483

I change the correlation structures of the model in part 1) and we can see that the coefficients are similar with the former model.So that the analysis and inference is not sensitive to this choice.

For model in part 4) Correlation structure:AR1

```
Call:
geeglm(formula = Y ~ Treatment + Year + Age + Skin + Exposure,
    family = poisson(link = "log"), data = skin, id = ID, corstr = "ar1")

 Coefficients:
            Estimate  Std.err   Wald Pr(>|W|)
(Intercept) -3.02093  0.32857  84.53   <2e-16 ***
Treatment1   0.12808  0.10083   1.61   0.2040
Year         0.01056  0.02508   0.18   0.6737
Age          0.01494  0.00511   8.53   0.0035 **
Skin1        0.15284  0.11232   1.85   0.1736
Exposure     0.13915  0.01065 170.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Correlation structure = ar1
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     1.64  0.0788
  Link = identity

Estimated Correlation Parameters:
      Estimate Std.err
alpha    0.294  0.0328
Number of clusters:   1683  Maximum cluster size: 5
```

	Estimate	Std.err	Wald	Pr(>|W|)
(Intercept)	-3.021	0.329	84.532	0.000
Treatment1	0.128	0.101	1.613	0.204
Year	0.011	0.025	0.177	0.674
Age	0.015	0.005	8.534	0.003
Skin1	0.153	0.112	1.852	0.174
Exposure	0.139	0.011	170.786	0.000

estimate	std.error	statistic	p.value	beta0	df	lwr	upr
0.128	0.101	1.61	0.204	0	1	-0.07	0.326

Correlation structure:exchangable

```
Call:
geeglm(formula = Y ~ Treatment + Year + Age + Skin + Exposure,
    family = poisson(link = "log"), data = skin, id = ID, corstr = "exchangable")

 Coefficients:
            Estimate  Std.err   Wald Pr(>|W|)
(Intercept) -3.04458  0.33263  83.78   <2e-16 ***
Treatment1   0.12357  0.09941   1.55   0.2139
Year         0.01759  0.02521   0.49   0.4854
Age          0.01496  0.00525   8.12   0.0044 **
Skin1        0.16191  0.11079   2.14   0.1439
Exposure     0.13899  0.01055 173.42   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation structure = exchangeable ar1 unstructured userdefined fixed
Estimated Scale Parameters:

            Estimate Std.err
(Intercept)     1.64  0.0769
  Link = identity

Estimated Correlation Parameters:
```

```
      Estimate Std.err
alpha    0.209  0.0262
Number of clusters:   1683  Maximum cluster size: 5
```

	Estimate	Std.err	Wald	Pr(>|W|)
(Intercept)	-3.045	0.333	83.777	0.000
Treatment1	0.124	0.099	1.545	0.214
Year	0.018	0.025	0.487	0.485
Age	0.015	0.005	8.122	0.004
Skin1	0.162	0.111	2.136	0.144
Exposure	0.139	0.011	173.419	0.000

estimate	std.error	statistic	p.value	beta0	df	lwr	upr
0.124	0.099	1.54	0.214	0	1	-0.071	0.318

I change the correlation structures of the model in part 4) and we can see that the p-value is still larger than 0.05 and the coefficients are similar with the former model.So that the analysis and inference is not sensitive to this choice.

6.Do you need to account for overdisperion.Comment

for model in part 1) and part 4) H0: $\phi = 1$ I do the z-test to check the overdispersion $z_{stat} = (\hat{\phi} - 1)/SD_{\phi}$

```
[1] 1.49e-05
```

```
[1] 1.11e-16
```

For both the model in part 1) and part 4),the p-value is less than 0.05 at 0.05 significant level,so that we reject the null and conclude that we need to account for the overdispersion.

Appendix

```
options(tinytex.verbose = TRUE)
knitr::opts_chunk$set(echo = FALSE, message = FALSE, warning = FALSE, comment = "")
library(tidyverse)
library(gee)  # for gee()
library(lme4)
library(data.table)
library(geepack)
library(doBy)
## Question 1
# load original data
toenail1 <- read.table("toenail.txt", header = T) %>%
as_tibble() %>%
mutate(Treatment = as.factor(Treatment))
# GEE Model 1:
```

```r
# - interaction with Treatment
gee1 = geeglm(Response ~ Treatment * Month, data = toenail1, family = "binomial"(link = "logit"), id = S
summary(gee1)
L <- matrix(0,ncol=4,nrow=1) # ncol = number of coeffcients in the model, nrow = number of tests
L[1,4]  <-1
L
q1 = esticon(gee1,L=L,joint.test = TRUE)
q1 %>%
knitr::kable()
# GEE Model 2:
gee2 = geeglm(Response ~ Treatment + Month, data = toenail1, family = "binomial"(link = "logit"), id = S
summary(gee2)
sum_1 = summary(gee2)
sum_1$coefficients %>%
  knitr::kable()
gee3 = geeglm(Response ~ Treatment*Month, data = toenail1, family = "binomial"(link = "logit"), id = Sub
summary(gee3)
L <- matrix(0,ncol=4,nrow=1) # ncol = number of coeffcients in the model, nrow = number of tests
L[1,4]  <-1
L
q1_un = esticon(gee3,L=L,joint.test = TRUE)
q1_un %>%
knitr::kable()
gee4 = geeglm(Response ~ Treatment*Month, data = toenail1, family = "binomial"(link = "logit"), id = Sub
summary(gee4)
L <- matrix(0,ncol=4,nrow=1) # ncol = number of coeffcients in the model, nrow = number of tests
L[1,4]  <-1
L
q1_in = esticon(gee4,L=L,joint.test = TRUE)
q1_in %>%
  knitr::kable()
gee5 = geeglm(Response ~ Treatment*Month, data = toenail1, family = "binomial"(link = "logit"), id = Sub
summary(gee5)
L <- matrix(0,ncol=4,nrow=1) # ncol = number of coeffcients in the model, nrow = number of tests
L[1,4]  <-1
L
q1_ar = esticon(gee5,L=L,joint.test = TRUE)
q1_ar %>%
knitr::kable()
## Question 2
# load data
skin <- read.table("skin.txt", header = F)
colnames(skin) = c("ID", "Center", "Age", "Skin", "Gender", "Exposure", "Y", "Treatment", "Year")
skin = skin %>%
  as_tibble() %>%
  mutate(Skin = as.factor(Skin),
         Gender = as.factor(Gender),
         Treatment = as.factor(Treatment))
gee_q2 = geeglm(Y ~ Treatment*Year, data = skin, family = "poisson"(link = "log"), id = ID, corstr = "un
summary(gee_q2)
L_1 = matrix(0, ncol = 4, nrow = 1)
L_1[1,4] <- 1
esticon(gee_q2, L = L_1, joint.test = T)
```

```r
gee_q2_final = geeglm(Y ~ Treatment+Year, data = skin, family = "poisson"(link = "log"), id = ID, corsti
summary(gee_q2_final)
# Coefficients
gee_q2_sum = summary(gee_q2_final)
gee_q2_sum$coefficients %>% knitr::kable()
gee_q2_4 = geeglm(Y ~ Treatment + Year + Age + Skin + Exposure, data = skin, family = "poisson"(link =
summary(gee_q2_4)
L3 = c(0,1,0,0,0,0)
q2_4= esticon(gee_q2_4,L=L3)
q2_4 %>%
knitr::kable()
gee_q2_ar = geeglm(Y ~ Treatment + Year, data = skin, family = "poisson"(link = "log"), id = ID, corstr
summary(gee_q2_ar)
gee_q2_sum1 = summary(gee_q2_ar)
gee_q2_sum1$coefficients %>% knitr::kable()
gee_q2_ex = geeglm(Y ~ Treatment + Year, data = skin, family = "poisson"(link = "log"), id = ID, corstr
summary(gee_q2_ex)
gee_q2_sum2 = summary(gee_q2_ex)
gee_q2_sum2$coefficients %>% knitr::kable()
gee_q2_4_ar = geeglm(Y ~ Treatment+ Year + Age + Skin + Exposure, data = skin, family = "poisson"(link
summary(gee_q2_4_ar)
L6 = c(0,1,0,0,0,0)
q2_6 = esticon(gee_q2_4_ar,L=L6)
gee_q2_sum3 = summary(gee_q2_4_ar)
gee_q2_sum3$coefficients %>% knitr::kable()
q2_6 %>%
  knitr::kable()
gee_q2_4_ex = geeglm(Y ~ Treatment+ Year + Age + Skin + Exposure, data = skin, family = "poisson"(link
summary(gee_q2_4_ex)
L7 = c(0,1,0,0,0,0)
q2_7 = esticon(gee_q2_4_ex,L=L7)
gee_q2_sum4 = summary(gee_q2_4_ex)
gee_q2_sum4$coefficients %>% knitr::kable()
q2_7 %>%
  knitr::kable()
#z-test#
z_stat_1 = (summary(gee_q2_final)$dispersion[,1]-1)/summary(gee_q2_final)$dispersion[,2]
1-pnorm(z_stat_1)
#z-test#
z_stat_4 = (summary(gee_q2_4)$dispersion[,1]-1)/summary(gee_q2_4)$dispersion[,2]
1-pnorm(z_stat_4)
```