Practicals - Logistic and Poisson regression

Epidemiological methods in medical research 2023

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Exercise 1: The BCG study revisited

We will revisit the BCG study (exercise 2 of the previous practical) where we are interested in comparing the risk of leprosy between the BCG vaccinated and non BCG vaccinated subjects:

- subjects were grouped into 7 age intervals: 0-4, 5-9, 10-14, 15-19, 20-24, 25-29, 30-34 (in years) and we would like to adjust for age since it may confound the association between vaccination and leprosy.
- the non-vaccinated group will be composed of the whole population survey of 80,622 persons (`conall` in the dataset).

The purpose of this exercise is to compare 3 different approaches to quantify the vaccine effect and discuss the underlying statistical models. To focus on these objectives the code and software output is provided.

Here is a summary of the dataset:

```
bcg <- read.table("https://bozenne.github.io/doc/Teaching/bcg.txt",
                  header = TRUE)
bcg$age <- as.character(bcg$age)
bcg$status <- as.character(bcg$status)
bcg.r <- bcg[bcg$status %in% c("case","conall"),]

table227 <- xtabs(n~scar+status+age, data = bcg.r)
ftable(table227)
```

```
            age 00_04 05_09 10_14 15_19 20_24 25_29 30_34
scar status
0    case           1    11    28    16    20    36    47
     conall      7593  7143  5611  2208  2438  4356  5245
1    case           1    14    22    28    19    11     6
     conall     11719 10184  7561  8117  5588  1625  1234
```

Part I

A simple approach consists in evaluating the probability of contracting leprosy in each age and vaccination subgroup, and comparing them between vaccination subgroups.

1. Can you make sense of the following software output?
   Does it help to answer the research question?

```
table227.pc <- prop.table(table227, margin = c(1,3))
ftable(round(100*table227.pc,3))
```

```
            age   00_04  05_09  10_14  15_19  20_24  25_29  30_34
scar status
0    case         0.013  0.154  0.497  0.719  0.814  0.820  0.888
     conall      99.987 99.846 99.503 99.281 99.186 99.180 99.112
1    case         0.009  0.137  0.290  0.344  0.339  0.672  0.484
     conall      99.991 99.863 99.710 99.656 99.661 99.328 99.516
```

```
[1] "00_04" "05_09" "10_14" "15_19" "20_24" "25_29" "30_34"
```

2. Here is some more complicated R code.
   Can you understand what it is doing? (appendix A should help)
   Does it help to answer the research question?

```
age.groups <- dimnames(table227.pc)$age
age.groups
```

```
[1] "00_04" "05_09" "10_14" "15_19" "20_24" "25_29" "30_34"
```

```
library(exact2x2)
df.resI <- NULL
for(iAge in age.groups){
  iTab <- table227[,,iAge]
  iTest <- binomMeld.test(x1 = iTab["0","case"], n1 = sum(iTab["0",]),
                          x2 = iTab["1","case"], n2 = sum(iTab["1",]),
                          parmtype = "difference", conf.int = TRUE)
  df.resI <- rbind(df.resI,
                   data.frame(age = iAge,
                              estimate = unname(iTest$estimate),
                              lower = iTest$conf.int[1],
                              upper = iTest$conf.int[2],
                              p.value = iTest$p.value)
                   )
}
df.resI
```

```
    age      estimate        lower         upper    p.value
1 00_04 -4.635868e-05 -0.000685681  0.0003805052 1.00000000
2 05_09 -1.647831e-04 -0.001577776  0.0010614538 0.92819700
3 10_14 -2.064193e-03 -0.004522346  0.0002342452 0.07826868
4 15_19 -3.756553e-03 -0.008367311 -0.0002525178 0.03326422
5 20_24 -4.748075e-03 -0.009414869 -0.0009798127 0.01037704
6 25_29 -1.473005e-03 -0.006202971  0.0044151797 0.69509953
7 30_34 -4.042621e-03 -0.008441027  0.0021433379 0.20074780
```

3. Here is the output from the same R code as before except that the argument `parmtype` has been changed to `"ratio"`.
   Does it change your appreciation of the vaccine efficacy?
   What property of the testing procedure do you notice?

```
    age  estimate      lower      upper    p.value
1 00_04 0.6479522 0.00827165 50.8580868 1.00000000
2 05_09 0.8928310 0.37676901  2.1720971 0.92819700
3 10_14 0.5842863 0.31889878  1.0578105 0.07826868
4 15_19 0.4778392 0.25028232  0.9440460 0.03326422
5 20_24 0.4164616 0.21071034  0.8206767 0.01037704
6 25_29 0.8202934 0.37734768  1.6425565 0.69509953
7 30_34 0.5448181 0.19061559  1.2730218 0.20074780
```

[Extra] Can you have perform a similar analysis with the `glm` function? (appendix A should help). What is the drawback of using `glm`?

Part II

A common analysis is to make a logistic model, using age as a covariate:

```
e.common <- glm(status=="case" ~ age + scar,
                family = binomial(link="logit"),
                weight = n,
                data = bcg.r)
summary(e.common)
```

	Estimate	Pr(>|z|)
(Intercept)	-8.880038	7.238979e-36
age05_09	2.623536	3.572990e-04
age10_14	3.583111	6.760471e-07
age15_19	3.824128	1.263355e-07
age20_24	3.900156	7.553260e-08
age25_29	4.155632	9.187360e-09
age30_34	4.157639	8.556965e-09

	Estimate	Pr(>|z|)
scar	-0.5470646	0.0001034434

4. What is the interpretation of each coefficient and corresponding p-values? In particular how would you explicit the vaccine effect?

5. Same questions with the following logistic model

```
e.common2 <- glm(status=="case" ~ 0 + age + scar,
                family = binomial(link="logit"),
                weight = n,
                data = bcg.r)
summary(e.common2)
```

	Estimate	Pr(>|z|)
age00_04	-8.880038	7.238979e-36
age05_09	-6.256502	6.277280e-195
age10_14	-5.296927	2.940433e-257
age15_19	-5.055910	1.366578e-175
age20_24	-4.979882	2.502577e-169
age25_29	-4.724406	8.390947e-222
age30_34	-4.722399	4.365121e-253

	Estimate	Pr(>|z|)
scar	-0.5470646	0.0001034434

6. Have a look at the following predicted values. Can you guess what they are? How would they look like for `e.common2`?
   Can you compute those values yourself based on the estimated coefficients?

```
data.frame(age = bcg.r$age[1:14],
           scar = bcg.r$scar[1:14],
           pred1 = predict(e.common, type = "link")[1:14],
           pred2 = predict(e.common, type = "response")[1:14])
```

```
     age scar  pred1   pred2              age scar  pred1   pred2
8  00_04    0 -8.880 0.00014          1 00_04    1 -9.427 0.00008
9  05_09    0 -6.257 0.00191          2 05_09    1 -6.804 0.00111
10 10_14    0 -5.297 0.00498          3 10_14    1 -5.844 0.00289
11 15_19    0 -5.056 0.00633          4 15_19    1 -5.603 0.00367
12 20_24    0 -4.980 0.00683          5 20_24    1 -5.527 0.00396
13 25_29    0 -4.724 0.00880          6 25_29    1 -5.271 0.00511
14 30_34    0 -4.722 0.00882          7 30_34    1 -5.269 0.00512
```

7. How would you assess the main modeling assumption based on the previous software outputs?

[Extra] The following R code fit a common effect model on the probability scale. Why is this model less reasonnable than the one using the odds scale? Why is it challenging for the software to estimate the model parameters? (this is why starting value are input to `glm`)

```
starting.values <- c(0.035,0.1,0.35,0.4,0.46,0.75,0.78,-0.03)/100
e.common3 <- glm(status=="case" ~ 0 + age + scar,
                 family = binomial(link="identity"),
                 weight = n,
                 data = bcg.r,
                 start = starting.values)
summary(e.common3)
```

```
             Estimate     Pr(>|z|)              Estimate  Pr(>|z|)
age00_04 0.0003547222 7.061058e-02    scar -0.0002939937 0.1500859
age05_09 0.0016196894 2.748984e-07
age10_14 0.0039166478 6.419051e-13
age15_19 0.0044351916 1.340900e-11
age20_24 0.0049835320 1.773590e-10
age25_29 0.0078678282 3.886355e-12
age30_34 0.0081484003 2.034830e-13
```

Part III

Another possible analysis is to model an interaction between age and vaccine:

```
e.full <- glm(status=="case" ~ age * scar,
              family = binomial(link="logit"),
              weight = n,
              data = bcg.r)
summary(e.full)
```

```
              Estimate     Pr(>|z|)                    Estimate  Pr(>|z|)
 (Intercept) -8.934982 4.094169e-19   scar            -0.4339847 0.7589523
 age05_09     2.458989 1.857212e-02   age05_09:scar    0.3204617 0.8275025
 age10_14     3.634702 3.556874e-04   age10_14:scar   -0.1054519 0.9417362
 age15_19     4.007728 1.014914e-04   age15_19:scar   -0.3082730 0.8314994
 age20_24     4.131781 5.550098e-05   age20_24:scar   -0.4467520 0.7580548
 age25_29     4.139192 4.461984e-05   age25_29:scar    0.2344074 0.8720925
 age30_34     4.220099 2.976596e-05   age30_34:scar   -0.1773891 0.9045692
```

8. What is the interpretation of each coefficient and corresponding p-values? In particular how would you explicit the vaccine effect?

9. Same questions with the following logistic model:

```
e.full2 <- glm(status=="case" ~ 0 + age + age:scar,
              family = binomial(link="logit"),
              weight = n,
              data = bcg.r)
summary(e.full2)
```

```
          Estimate      Pr(>|z|)                      Estimate   Pr(>|z|)
age00_04 -8.934982  4.094169e-19      age00_04:scar -0.4339847 0.75895232
age05_09 -6.475993 3.532959e-102      age05_09:scar -0.1135229 0.77828821
age10_14 -5.300280 3.119233e-172      age10_14:scar -0.5394366 0.05878419
age15_19 -4.927254  7.323866e-86      age15_19:scar -0.7422577 0.01819865
age20_24 -4.803201 1.552490e-101      age20_24:scar -0.8807367 0.00611894
age25_29 -4.795791 1.327620e-180      age25_29:scar -0.1995773 0.56376575
age30_34 -4.714883 3.389080e-227      age30_34:scar -0.6113738 0.15957550
```

10. Can you make sense of the following F-tests?

```
anova(e.full, test = "Chisq")
```

```
Analysis of Deviance Table

Model: binomial, link: logit

Response: status == "case"

Terms added sequentially (first to last)


         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                        27     3504.0
age       6  200.659        21     3303.3 < 2.2e-16 ***
scar      1   15.297        20     3288.0 9.187e-05 ***
age:scar  6    3.600        14     3284.4    0.7306
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(e.full2, test = "Chisq")
```

```
Analysis of Deviance Table

Model: binomial, link: logit

Response: status == "case"

Terms added sequentially (first to last)


         Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
NULL                        28     112126
age       7   108823        21       3303 < 2.2e-16 ***
age:scar  7       19        14       3284  0.008516 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

11. Discuss the pros and cons of each approach/parametrisation.
What would you report in a scientific article?

Exercise 2: The Bissau study revisited

In rural Guinea-Bissau, 5274 children under 7 months of age were visited two times at home, with an interval of approximately 6 months. Information about vaccination (BCG, DTP, measles vaccine) was collected at each visit and at second visit, death during follow-up was registered. Other children move away during follow-up or survive until the second visit ('censored'). The dataset `bissau.txt` contain the available information:

```
bissau <- read.table("https://bozenne.github.io/doc/Teaching/bissau.txt",
   header=TRUE)
str(bissau)
```

```
'data.frame':        5274 obs. of  8 variables:
 $ id       : int  1 2 3 4 5 6 7 8 9 10 ...
 $ fuptime  : int  65 161 166 166 161 161 166 166 166 166 ...
 $ fupstatus: chr  "dead" "censored" "censored" "censored" ...
 $ bcg      : chr  "yes" "yes" "no" "yes" ...
 $ dtp      : int  1 2 0 0 0 0 2 1 2 2 ...
 $ age      : int  182 125 69 96 131 26 129 90 119 146 ...
 $ agem     : int  5 4 2 3 4 0 4 2 3 4 ...
 $ dtpany   : logi  TRUE TRUE FALSE FALSE FALSE FALSE ...
```

We already analyzed this dataset in Practical 1: we looked at the marginal risk, odds, and rate of death in each vaccination group and compare them between groups. We would now like account for age in the analysis of the effects of DTP and BCG on the mortality. To this end we will use a Poisson regression model, under the strong assumption that the mortality is constant over the follow-up time.

1. Fit a Poisson regression model for survival with follow-up time as the time variable (i.e., using `log(fuptime)` as offset), including bcg and agem as categorical covariates. How is BCG vaccination associated with the mortality rate?

2. Estimate the effect of any dose of DTP, using the created variable dtpany, adjusted only for agem as a categorical variable.

3. Now, also adjust for bcg. What happened? Can you explain?

4. Is there an interaction between DTP and bcg?

Appendix A: Comparing proportions of events between two groups

Consider only the first age group:

```
table227.age2 <- table227[,,"05_09"]
table227.age2
```

```
    status
scar   case conall
   0     11   7143
   1     14  10184
```

Difference

We can test the difference in proportion of infection between the groups using

```
library(exact2x2)
test.age2 <- binomMeld.test(x1 = table227.age2["0","case"],
                            n1 = sum(table227.age2["0",]),
                            x2 = table227.age2["1","case"],
                            n2 = sum(table227.age2["1",]),
                            parmtype = "difference", conf.int = TRUE)
test.age2
```

```

        melded binomial test for difference

data:  sample 1:(11/7154), sample 2:(14/10198)
proportion 1 = 0.0015376, proportion 2 = 0.0013728, p-value = 0.9282
alternative hypothesis: true difference is not equal to 0
95 percent confidence interval:
 -0.001577776  0.001061454
sample estimates:
difference (p2-p1)
     -0.0001647831
```

The results can be extract from the object `test.age2` doing:

```
data.frame(estimate = unname(test.age2$estimate),
           lower = test.age2$conf.int[1],
           upper = test.age2$conf.int[2],
           p.value = test.age2$p.value)
```

```
       estimate        lower       upper  p.value
1 -0.0001647831 -0.001577776 0.001061454 0.928197
```

An alternative implementation uses a binomial model with an identity link:

```
e.glm_diff <- glm(status=="case" ~ scar,
                  family = binomial(link="identity"),
                  weight = n,
                  data = bcg.r[bcg.r$age=="05_09",])
summary(e.glm_diff)$coef
```

```
                 Estimate   Std. Error    z value   Pr(>|z|)
(Intercept)  0.0015376013 0.0004632477  3.3191776 0.00090283
scar        -0.0001647831 0.0005907876 -0.2789211 0.78030537
```

Estimates are identical but p-value and confidence intervals will differ in small samples as the `glm` function rely on more crude approximation for quantifying the uncertainty compared to `binomMeld.test`.

Ratio

We can test the ratio between the proportion of infection in the two groups using

```
binomMeld.test(x1 = table227.age2["0","case"],
               n1 = sum(table227.age2["0",]),
               x2 = table227.age2["1","case"],
               n2 = sum(table227.age2["1",]),
               parmtype = "ratio", conf.int = TRUE)
```

```
        melded binomial test for ratio

data:  sample 1:(11/7154), sample 2:(14/10198)
proportion 1 = 0.0015376, proportion 2 = 0.0013728, p-value = 0.9282
alternative hypothesis: true ratio is not equal to 1
95 percent confidence interval:
 0.376769 2.172097
sample estimates:
ratio (p2/p1)
     0.892831
```

An alternative implmentation uses a binomial model with a log link:

```
e.glm_ratio <- glm(status=="case" ~ scar,
                  family = binomial(link="log"),
                  weight = n,
                  data = bcg.r[bcg.r$age=="05_09",])
cbind(RR = exp(coef(e.glm_ratio)),summary(e.glm_ratio)$coef)
```

```
                     RR   Estimate Std. Error     z value     Pr(>|z|)
(Intercept) 0.001537601 -6.4775316  0.3012794 -21.5000784 1.55425e-102
scar        0.892831036 -0.1133579  0.4026162  -0.2815533  7.78286e-01
```

Note that the p-values for `binomMeld.test` do not dependent on how the groups are compared (difference, ratio, odds ratio). This is not true for `glm`.

Appendix B: Parametrisation

All greek letters denote estimates (usually they are denoted with hat, e.g. $\hat{\theta}$ but it is omitted here for lisibility).

Part I	model (probability scale)		testing procedure		
strata	non-exposed	exposed	risk difference	risk ratio	p-value
0-4	$\alpha_1 = 0.013\%$	$\beta_1 = 0.009\%$	$\beta_1 - \alpha_1 = -0.005\%$	$\frac{\beta_1}{\alpha_1} = 0.648$	1
5-9	$\alpha_2 = 0.154\%$	$\beta_2 = 0.137\%$	$\beta_2 - \alpha_2 = -0.016\%$	$\frac{\beta_2}{\alpha_2} = 0.893$	0.928
10-14	$\alpha_3 = 0.497\%$	$\beta_3 = 0.290\%$	$\beta_3 - \alpha_3 = -0.206\%$	$\frac{\beta_3}{\alpha_3} = 0.584$	0.078
15-19	$\alpha_4 = 0.719\%$	$\beta_4 = 0.344\%$	$\beta_4 - \alpha_4 = -0.376\%$	$\frac{\beta_4}{\alpha_4} = 0.478$	0.033
20-24	$\alpha_5 = 0.814\%$	$\beta_5 = 0.339\%$	$\beta_5 - \alpha_5 = -0.745\%$	$\frac{\beta_5}{\alpha_5} = 0.416$	0.010
25-29	$\alpha_6 = 0.820\%$	$\beta_6 = 0.672\%$	$\beta_6 - \alpha_6 = -0.147\%$	$\frac{\beta_6}{\alpha_6} = 0.820$	0.695
30-34	$\alpha_7 = 0.888\%$	$\beta_7 = 0.484\%$	$\beta_7 - \alpha_7 = -0.404\%$	$\frac{\beta_7}{\alpha_7} = 0.545$	0.201

Part II 4	model (odds scale)		model (probability scale)		risk
strata	non-exposed	exposed	non-exposed	exposed	ratio
0-4	$e^{\alpha} = 0.014\%$	$e^{\alpha}e^{\beta} = 0.008\%$	$\frac{1}{1+e^{-\alpha}} = 0.014\%$	$\frac{1}{1+e^{-\alpha-\beta}} = 0.008\%$	0.571
5-9	$e^{\alpha}e^{\gamma_1} = 0.192\%$	$e^{\alpha}e^{\gamma_1}e^{\beta} = 0.111\%$	$\frac{1}{1+e^{-\alpha-\gamma_1}} = 0.191\%$	$\frac{1}{1+e^{-\alpha-\gamma_1-\beta}} = 0.111\%$	0.581
10-14	$e^{\alpha}e^{\gamma_2} = 0.501\%$	$e^{\alpha}e^{\gamma_2}e^{\beta} = 0.290\%$	$\frac{1}{1+e^{-\alpha-\gamma_2}} = 0.498\%$	$\frac{1}{1+e^{-\alpha-\gamma_2-\beta}} = 0.289\%$	0.580
15-19	$e^{\alpha}e^{\gamma_3} = 0.637\%$	$e^{\alpha}e^{\gamma_3}e^{\beta} = 0.269\%$	$\frac{1}{1+e^{-\alpha-\gamma_3}} = 0.633\%$	$\frac{1}{1+e^{-\alpha-\gamma_3-\beta}} = 0.367\%$	0.580
20-24	$e^{\alpha}e^{\gamma_4} = 0.687\%$	$e^{\alpha}e^{\gamma_4}e^{\beta} = 0.398\%$	$\frac{1}{1+e^{-\alpha-\gamma_4}} = 0.683\%$	$\frac{1}{1+e^{-\alpha-\gamma_4-\beta}} = 0.396\%$	0.580
25-29	$e^{\alpha}e^{\gamma_5} = 0.888\%$	$e^{\alpha}e^{\gamma_5}e^{\beta} = 0.514\%$	$\frac{1}{1+e^{-\alpha-\gamma_5}} = 0.880\%$	$\frac{1}{1+e^{-\alpha-\gamma_5-\beta}} = 0.511\%$	0.581
30-34	$e^{\alpha}e^{\gamma_6} = 0.889\%$	$e^{\alpha}e^{\gamma_6}e^{\beta} = 0.515\%$	$\frac{1}{1+e^{-\alpha-\gamma_6}} = 0.882\%$	$\frac{1}{1+e^{-\alpha-\gamma_6-\beta}} = 0.512\%$	0.580

Testing procedure: $\beta = -0.547$, p.value$= 0.0001$

Part II 5	model (odds scale)		model (probability scale)		risk
strata	non-exposed	exposed	non-exposed	exposed	ratio
0-4	$e^{\alpha_1} = 0.014\%$	$e^{\alpha_1}e^{\beta} = 0.008\%$	$\frac{1}{1+e^{-\alpha_1}} = 0.014\%$	$\frac{1}{1+e^{-\alpha_1}e^{-\beta}} = 0.008\%$	0.571
5-9	$e^{\alpha_2} = 0.192\%$	$e^{\alpha_2}e^{\beta} = 0.111\%$	$\frac{1}{1+e^{-\alpha_2}} = 0.191\%$	$\frac{1}{1+e^{-\alpha_2}e^{-\beta}} = 0.111\%$	0.581
10-14	$e^{\alpha_3} = 0.501\%$	$e^{\alpha_3}e^{\beta} = 0.290\%$	$\frac{1}{1+e^{-\alpha_3}} = 0.498\%$	$\frac{1}{1+e^{-\alpha_3}e^{-\beta}} = 0.289\%$	0.580
15-19	$e^{\alpha_4} = 0.637\%$	$e^{\alpha_4}e^{\beta} = 0.269\%$	$\frac{1}{1+e^{-\alpha_4}} = 0.633\%$	$\frac{1}{1+e^{-\alpha_4}e^{-\beta}} = 0.367\%$	0.580
20-24	$e^{\alpha_5} = 0.687\%$	$e^{\alpha_5}e^{\beta} = 0.398\%$	$\frac{1}{1+e^{-\alpha_5}} = 0.683\%$	$\frac{1}{1+e^{-\alpha_5}e^{-\beta}} = 0.396\%$	0.580
25-29	$e^{\alpha_6} = 0.888\%$	$e^{\alpha_6}e^{\beta} = 0.514\%$	$\frac{1}{1+e^{-\alpha_6}} = 0.880\%$	$\frac{1}{1+e^{-\alpha_6}e^{-\beta}} = 0.511\%$	0.581
30-34	$e^{\alpha_7} = 0.889\%$	$e^{\alpha_7}e^{\beta} = 0.515\%$	$\frac{1}{1+e^{-\alpha_7}} = 0.882\%$	$\frac{1}{1+e^{-\alpha_7}e^{-\beta}} = 0.512\%$	0.580

Testing procedure: $\beta = -0.547$, p.value$= 0.0001$

Part III 8	model (odds scale)		model (probability scale)		
strata	non-exposed	exposed	non-exposed	exposed	p-value
0-4	$e^{\alpha} = 0.013\%$	$e^{\alpha}e^{\gamma} = 0.009\%$	$\frac{1}{1+e^{-\alpha}} = 0.013\%$	$\frac{1}{1+e^{-\alpha}e^{-\gamma}} = 0.009\%$	0.759
5-9	$e^{\alpha}e^{\beta_1} = 0.154\%$	$e^{\alpha}e^{\beta_1}e^{\gamma}e^{\delta_1} = 0.137\%$	$\frac{1}{1+e^{-\alpha-\beta_1}} = 0.154\%$	$\frac{1}{1+e^{-\alpha-\beta_1-\gamma-\delta_1}} = 0.137\%$	0.778
10-14	$e^{\alpha}e^{\beta_2} = 0.499\%$	$e^{\alpha}e^{\beta_2}e^{\gamma}e^{\delta_2} = 0.291\%$	$\frac{1}{1+e^{-\alpha-\beta_2}} = 0.497\%$	$\frac{1}{1+e^{-\alpha-\beta_2-\gamma-\delta_2}} = 0.290\%$	0.059
15-19	$e^{\alpha}e^{\beta_3} = 0.725\%$	$e^{\alpha}e^{\beta_3}e^{\gamma}e^{\delta_3} = 0.345\%$	$\frac{1}{1+e^{-\alpha-\beta_3}} = 0.719\%$	$\frac{1}{1+e^{-\alpha-\beta_3-\gamma-\delta_3}} = 0.344\%$	0.018
20-24	$e^{\alpha}e^{\beta_4} = 0.820\%$	$e^{\alpha}e^{\beta_4}e^{\gamma}e^{\delta_4} = 0.340\%$	$\frac{1}{1+e^{-\alpha-\beta_4}} = 0.814\%$	$\frac{1}{1+e^{-\alpha-\beta_4-\gamma-\delta_4}} = 0.339\%$	0.006
25-29	$e^{\alpha}e^{\beta_5} = 0.826\%$	$e^{\alpha}e^{\beta_5}e^{\gamma}e^{\delta_5} = 0.677\%$	$\frac{1}{1+e^{-\alpha-\beta_5}} = 0.820\%$	$\frac{1}{1+e^{-\alpha-\beta_5-\gamma-\delta_5}} = 0.672\%$	0.564
30-34	$e^{\alpha}e^{\beta_6} = 0.886\%$	$e^{\alpha}e^{\beta_6}e^{\gamma}e^{\delta_6} = 0.486\%$	$\frac{1}{1+e^{-\alpha-\beta_6}} = 0.888\%$	$\frac{1}{1+e^{-\alpha-\beta_6-\gamma-\delta_6}} = 0.484\%$	0.160

Testing procedure: $(\gamma, \gamma+\delta_1, \gamma+\delta_2, \gamma+\delta_3, \gamma+\delta_4, \gamma+\delta_5, \gamma+\delta_6)$ vs. 0

Part III 9	model (odds scale)		model (probability scale)		
strata	non-exposed	exposed	non-exposed	exposed	p-value
0-4	$e^{\alpha_1} = 0.013\%$	$e^{\alpha_1}e^{\beta_1} = 0.009\%$	$\frac{1}{1+e^{-\alpha_1}} = 0.013\%$	$\frac{1}{1+e^{-\alpha_1}e^{-\beta_1}} = 0.009\%$	0.759
5-9	$e^{\alpha_2} = 0.154\%$	$e^{\alpha_2}e^{\beta_2} = 0.137\%$	$\frac{1}{1+e^{-\alpha_2}} = 0.154\%$	$\frac{1}{1+e^{-\alpha_2}e^{-\beta_2}} = 0.137\%$	0.778
10-14	$e^{\alpha_3} = 0.499\%$	$e^{\alpha_3}e^{\beta_3} = 0.291\%$	$\frac{1}{1+e^{-\alpha_3}} = 0.497\%$	$\frac{1}{1+e^{-\alpha_3}e^{-\beta_3}} = 0.290\%$	0.059
15-19	$e^{\alpha_4} = 0.725\%$	$e^{\alpha_4}e^{\beta_4} = 0.345\%$	$\frac{1}{1+e^{-\alpha_4}} = 0.719\%$	$\frac{1}{1+e^{-\alpha_4}e^{-\beta_4}} = 0.344\%$	0.018
20-24	$e^{\alpha_5} = 0.820\%$	$e^{\alpha_5}e^{\beta_5} = 0.340\%$	$\frac{1}{1+e^{-\alpha_5}} = 0.814\%$	$\frac{1}{1+e^{-\alpha_5}e^{-\beta_5}} = 0.339\%$	0.006
25-29	$e^{\alpha_6} = 0.826\%$	$e^{\alpha_6}e^{\beta_6} = 0.677\%$	$\frac{1}{1+e^{-\alpha_6}} = 0.820\%$	$\frac{1}{1+e^{-\alpha_6}e^{-\beta_6}} = 0.672\%$	0.564
30-34	$e^{\alpha_7} = 0.886\%$	$e^{\alpha_7}e^{\beta_7} = 0.486\%$	$\frac{1}{1+e^{-\alpha_7}} = 0.888\%$	$\frac{1}{1+e^{-\alpha_7}e^{-\beta_7}} = 0.484\%$	0.160

Testing procedure: $(\beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \beta_6, \beta_7)$ vs. 0