Poisson Regression model Demo

趙友誠

2024-10-11

Table of contents

資料簡介 DoctorVisits Dataset from package AER

```
library(AER)
library(Hmisc)
library(ggplot2)
library(DataExplorer)
data(DoctorVisits)
str(DoctorVisits)
```

```
'data.frame':   5190 obs. of  12 variables:
 $ visits   : num  1 1 1 1 1 1 1 1 1 ...
 $ gender   : Factor w/ 2 levels "male","female": 2 2 1 1 1 2 2 2 2 1 ...
 $ age      : num  0.19 0.19 0.19 0.19 0.19 0.19 0.19 0.19 0.19 0.19 ...
 $ income   : num  0.55 0.45 0.9 0.15 0.45 0.35 0.55 0.15 0.65 0.15 ...
 $ illness  : num  1 1 3 1 2 5 4 3 2 1 ...
 $ reduced  : num  4 2 0 0 5 1 0 0 0 0 ...
 $ health   : num  1 1 0 0 1 9 2 6 5 0 ...
 $ private  : Factor w/ 2 levels "no","yes": 2 2 1 1 1 1 1 1 2 2 ...
 $ freepoor : Factor w/ 2 levels "no","yes": 1 1 1 1 1 1 1 1 1 1 ...
 $ freerepat: Factor w/ 2 levels "no","yes": 1 1 1 1 1 1 1 1 1 1 ...
 $ nchronic : Factor w/ 2 levels "no","yes": 1 1 1 1 2 2 1 1 1 1 ...
 $ lchronic : Factor w/ 2 levels "no","yes": 1 1 1 1 1 1 1 1 1 1 ...
```

Table 1: 變數解釋

變數	解釋	資料格式	備註
visits	過去兩週的看醫生 (諮詢) 的次數	num	counts:0~9
gender	性別	factor	1=male,2=female
age	年齡	num	years/100:0.19~0.72
income	年收入 (in 10,000 dollars)	num	income/10000:0.0~1.5

變數	解釋	資料格式	備註
illness	過去兩週不舒服的次數	num	counts:0~5
reduced	過去兩週因生病或受傷的休養天數	num	counts:0~14
health	GHQ-12 心理健康問卷分數 (越低代表心理狀態越健康)	num	0~12
private	有無私人醫療保險	factor	1=no,2=yes
freepoor	有無政府醫療保險 (低收)	factor	1=no,2=yes
freerepat	有無政府醫療保險 (退伍軍人、高齡、失能)	factor	1=no,2=yes
nchronic	有無不影響行動的慢性疾病	factor	1=no,2=yes
lchronic	有無限制行動的慢性疾病	factor	1=no,2=yes

```
latex(describe(DoctorVisits),title="",file="")
```

DoctorVisits
12 Variables 5190 Observations

visits

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
5190	0	10	0.489	0.3017	0.5154	0	0	0	0	0	1	2

Value	0	1	2	3	4	5	6	7	8	9
Frequency	4141	782	174	30	24	9	12	12	5	1
Proportion	0.798	0.151	0.034	0.006	0.005	0.002	0.002	0.002	0.001	0.000

For the frequency table, variable is rounded to the nearest 0

gender

n	missing	distinct
5190	0	2

Value	male	female
Frequency	2488	2702
Proportion	0.479	0.521

age

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
5190	0	12	0.978	0.4064	0.2258	0.19	0.19	0.22	0.32	0.62	0.72	0.72

Value	0.19	0.22	0.27	0.32	0.37	0.42	0.47	0.52	0.57	0.62	0.67	0.72
Frequency	752	1213	523	301	146	126	181	222	273	316	315	822
Proportion	0.145	0.234	0.101	0.058	0.028	0.024	0.035	0.043	0.053	0.061	0.061	0.158

For the frequency table, variable is rounded to the nearest 0

income

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
5190	0	14	0.983	0.5832	0.4085	0.15	0.25	0.25	0.55	0.90	1.10	1.30

Value	0.00	0.01	0.06	0.15	0.25	0.35	0.45	0.55	0.65	0.75	0.90	1.10	1.30	1.50
Frequency	79	35	80	249	1195	462	400	467	455	441	589	361	162	215
Proportion	0.015	0.007	0.015	0.048	0.230	0.089	0.077	0.090	0.088	0.085	0.113	0.070	0.031	0.041

For the frequency table, variable is rounded to the nearest 0

illness

n	missing	distinct	Info	Mean	Gmd
5190	0	6	0.934	1.432	1.481

Value	0	1	2	3	4	5
Frequency	1554	1638	946	542	274	236
Proportion	0.299	0.316	0.182	0.104	0.053	0.045

For the frequency table, variable is rounded to the nearest 0

reduced

```
     n   missing   distinct      Info      Mean       Gmd       .05       .10       .25       .50       .75       .90       .95
  5190         0         15     0.368    0.8618     1.592         0         0         0         0         0         2         7

Value          0     1     2     3     4     5     6     7     8     9    10    11    12    13
Frequency   4454   177   108    74    45    40    17    38    17     7    12     2     6     5
Proportion 0.858 0.034 0.021 0.014 0.009 0.008 0.003 0.007 0.003 0.001 0.002 0.000 0.001 0.001

Value         14
Frequency    188
Proportion 0.036

For the frequency table, variable is rounded to the nearest 0
```

health

```
     n   missing   distinct      Info      Mean       Gmd       .05       .10       .25       .50       .75       .90       .95
  5190         0         13     0.797     1.218     1.84         0         0         0         0         2         4         6

Value          0     1     2     3     4     5     6     7     8     9    10    11    12
Frequency   3026   823   446   273   187   132   104    61    42    32    21    24    19
Proportion 0.583 0.159 0.086 0.053 0.036 0.025 0.020 0.012 0.008 0.006 0.004 0.005 0.004

For the frequency table, variable is rounded to the nearest 0
```

private

```
     n   missing   distinct
  5190         0         2

Value         no   yes
Frequency   2892  2298
Proportion 0.557 0.443
```

freepoor

```
     n   missing   distinct
  5190         0         2

Value         no   yes
Frequency   4968   222
Proportion 0.957 0.043
```

freerepat

```
     n   missing   distinct
  5190         0         2

Value        no  yes
Frequency  4099 1091
Proportion 0.79 0.21
```

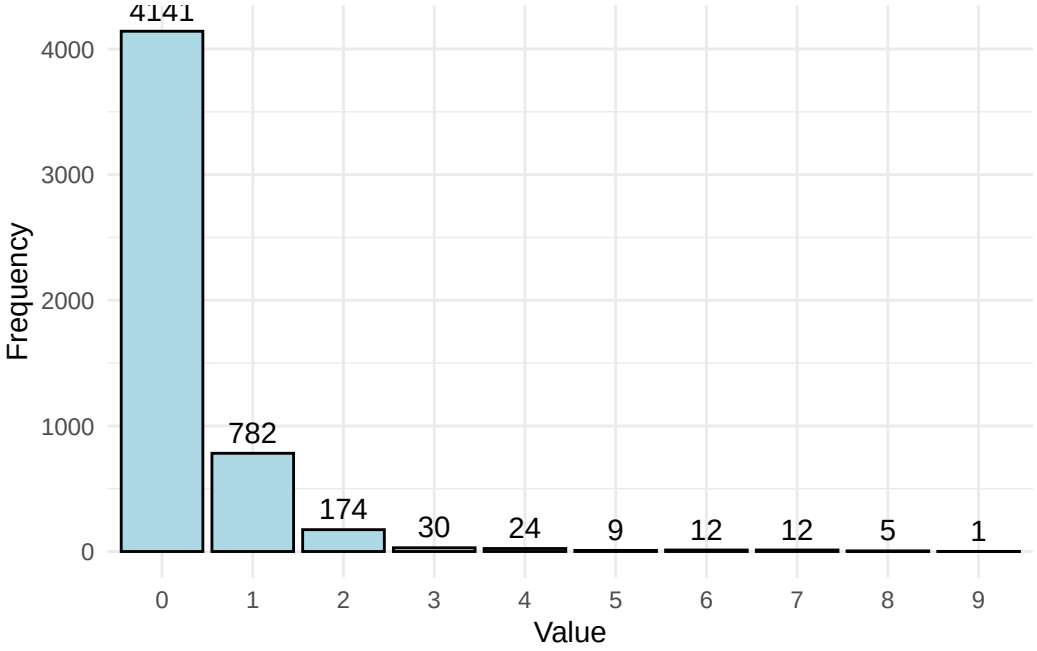
nchronic

```
     n   missing   distinct
  5190         0         2

Value         no   yes
Frequency   3098  2092
Proportion 0.597 0.403
```

lchronic

```
     n   missing   distinct
  5190         0         2

Value         no   yes
Frequency   4585   605
Proportion 0.883 0.117
```

```r
library(ggplot2)
mytable <- data.frame(table(DoctorVisits$visits))
ggplot(mytable, aes(x = factor(Var1), y = Freq)) +
  geom_bar(stat = "identity", fill = "lightblue", color = "black") +
  geom_text(aes(label = Freq), vjust = -0.5, hjust = 0.5) +  # 調整 vjust 和 hjust
  labs(x = "Value", y = "Frequency") +
  theme_minimal()
```



觀察變數分布建議使用 Hmisc::describe()。

```
sum(DoctorVisits$private=="yes" & DoctorVisits$freepoor=="yes" & DoctorVisits$freerepat=="yes")
```

```
[1] 0
```

```
sum(DoctorVisits$private=="yes" & DoctorVisits$freepoor=="yes")
```

```
[1] 0
```

```
sum(DoctorVisits$private=="yes" & DoctorVisits$freerepat=="yes")
```

```
[1] 0
```

```
sum(DoctorVisits$freepoor=="yes" & DoctorVisits$freerepat=="yes")
```

```
[1] 0
```

```
DoctorVisits$insurance <- as.factor(apply(DoctorVisits[,8:10], MARGIN = 1, function(row){
  return(ifelse(row[1]=="yes", "P",ifelse(row[2]=="yes", "GP", ifelse(row[3]=="yes", "GR", "N"))))
}))
DoctorVisits <- DoctorVisits[,c(1:7,13,11,12)]
sum(DoctorVisits$nchronic=="yes" & DoctorVisits$lchronic=="yes")
```

```
[1] 0
```

```
sum(DoctorVisits$lchronic=="yes")
```

```
[1] 605
```

```
sum(DoctorVisits$nchronic=="yes")
```

```
[1] 2092
```

```
sum(DoctorVisits$nchronic=="no" & DoctorVisits$lchronic=="no")
```

```
[1] 2493
```

```
DoctorVisits$chronDis <- as.factor(apply(DoctorVisits[,9:10], MARGIN = 1, function(row){
  return(ifelse(row[1]=="yes", "nch",ifelse(row[2]=="yes", "lch", "N")))
```

```
}))
DoctorVisits <- DoctorVisits[,c(1:8,11)]
```

將 private, freepoor, freerepat 三個變數合併成 insurance 類別變數:

P=private, GP=freepoor, GR=freerepat, N= 沒有保險

nchronic,lchronic 合併成 chronDis 類別變數:

nch= 有慢性疾病但不限制行動, lch= 有慢性疾病並且會限制行動, N= 沒有慢性疾病

建構模型

```
mydata <- model.matrix(~.*.-1, data = DoctorVisits[,-1])
mydata <- data.frame(visits = DoctorVisits$visits, mydata[,-1])
fullmodel <- glm(visits~.,data=mydata, family = poisson())
nullmodel <- glm(visits~1,data=mydata, family = poisson())
fit.step <- step(
  nullmodel,
  scope = list(lower = nullmodel,upper=fullmodel),
  direction = "both",k = log(5190), trace = FALSE)
cat("The number of variables selected is:",length(fit.step$coefficients)-1)
```

```
The number of variables selected is: 9
```

```
summary(fit.step)
```

```

Call:
glm(formula = visits ~ reduced + illness + illness.reduced +
    age + age.reduced + age.health + reduced.health + genderfemale +
    genderfemale.age, family = poisson(), data = mydata)

Coefficients:
                  Estimate Std. Error z value Pr(>|z|)
(Intercept)      -2.733401   0.106077 -25.768  < 2e-16 ***
reduced           0.243237   0.012260  19.839  < 2e-16 ***
illness           0.243573   0.021086  11.552  < 2e-16 ***
illness.reduced  -0.013430   0.002913  -4.610 4.03e-06 ***
age               1.428861   0.225245   6.344 2.24e-10 ***
age.reduced      -0.130323   0.021866  -5.960 2.52e-09 ***
age.health        0.128120   0.024048   5.328 9.95e-08 ***
reduced.health   -0.005169   0.001449  -3.569 0.000359 ***
genderfemale      0.601664   0.127675   4.712 2.45e-06 ***
genderfemale.age -0.920576   0.255766  -3.599 0.000319 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 5634.8  on 5189  degrees of freedom
Residual deviance: 4295.5  on 5180  degrees of freedom
AIC: 6647.1

Number of Fisher Scoring iterations: 6
```

Table 2: fitted model

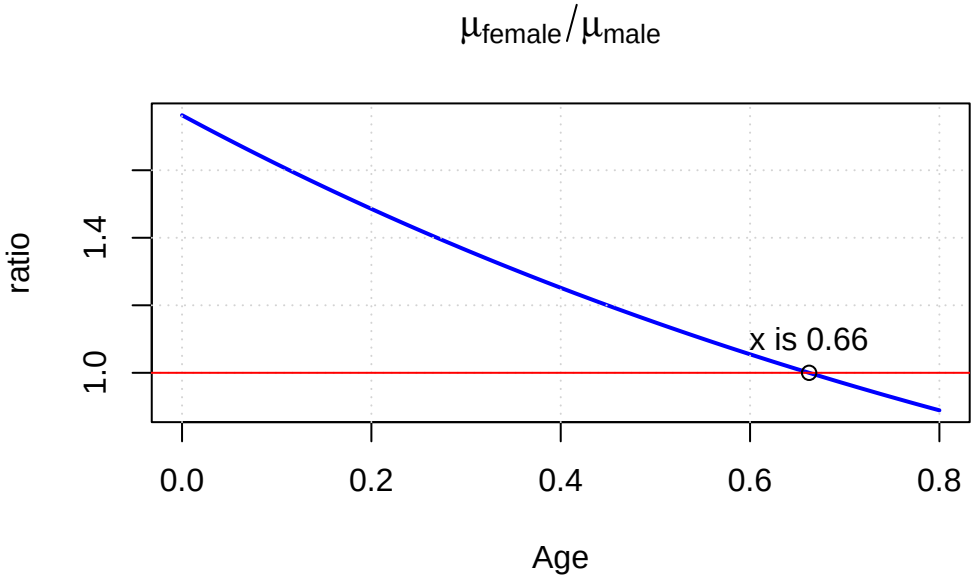
	Coefficients	Std Error	Z value	P value	Significance
(Intercept)	−2.816	0.107	−26.350	0.000	***
illness	0.241	0.021	11.257	0.000	***
genderfemale	0.567	0.128	4.437	0.000	***
age	1.603	0.224	7.146	0.000	***
reduced	0.236	0.012	19.123	0.000	***
health	0.065	0.013	4.988	0.000	***
illness.reduced	−0.013	0.003	−4.506	0.000	***
age.reduced	−0.115	0.021	−5.366	0.000	***
reduced.health	−0.005	0.001	−3.515	0.000	***
genderfemale.age	−0.856	0.256	−3.344	0.001	**

按照慣例做法，將未選中的主效應項加入模型:

發現加入 health 會使得 age.health 與 health 不顯著，因此傾向保留主效應。

```
oldformula <- fit.step$formula
newformula <- update(oldformula, .~.-age.health+health)
fit.step <- glm(newformula, data = mydata, family = poisson())
output <- summary(fit.step)$coefficients
output <- data.frame(
  coef = round(output[,1],3),
  sd = round(output[,2],3),
  z = round(output[,3],3),
  pvalue = round(output[,4],3)
)
output$sig <- sapply(output$pvalue, function(p) {
  ifelse(p < 0.001,"***",ifelse(p < 0.01,"**",ifelse(p < 0.05,"*","")))
})
colnames(output) <- c("Coefficients", "Std Error", "Z value", "P value", "Significance")
output <- output[c(1,3,8,5,2,10,4,6,7,9),]
latex(output, title="",file="",caption = "fitted model")
```

```
x <- seq(0, 0.8, by = 0.001)
curve(expr = exp(0.567 - 0.856 * x), from = 0, to = 0.8,
      xlab = "Age", ylab = "ratio",
      col = "blue", lwd = 2, main = expression(mu[female] / mu[male]))
grid()
abline(h=1, col="red")
points(x = 0.567/0.856, y = 1, col="black")
text(x = 0.567/0.856, y = 1.1,paste0("x is ",round(0.567/0.856,2)))
```



check for overdispersion

estimation of dispersion parameter

```
# Deviance Method
dispersion_deviance <- sum(resid(fit.step, type = "deviance")^2)/fit.step$df.residual
cat("estimated dispersion by deviance:", dispersion_deviance)
```

```
estimated dispersion by deviance: 0.8298426
```

```
# Pearson Method
dispersion_pearson <- sum(resid(fit.step, type = "pearson")^2)/fit.step$df.residual
cat("estimated dispersion by pearson:", dispersion_pearson)
```

```
estimated dispersion by pearson: 1.312561
```

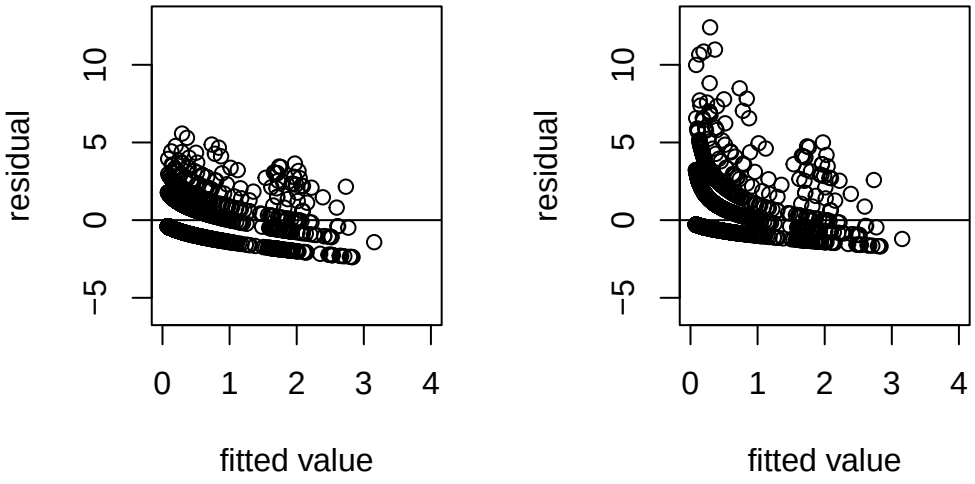
residual analysis

```
# 檢查 pearson residual 的變異數是否有等於 1
cat("Variance of Pearson residual:",var(resid(fit.step, type = "pearson")))
```

```
Variance of Pearson residual: 1.310178
```

```
# 殘差圖 (記得依 fitted value 大小排序)
par(mfrow = c(1, 2))
plot(sort(fit.step$fitted.values),
     resid(fit.step, type = "deviance")[order(fit.step$fitted.values, decreasing = FALSE)],
     main="Fig 2.1 Deviance resudual plot", ylab = "residual", xlab="fitted value",
     ylim = c(-6,13), xlim=c(0,4))
abline(0,0)
plot(sort(fit.step$fitted.values),
     resid(fit.step, type = "pearson")[order(fit.step$fitted.values, decreasing = FALSE)],
     main="Fig 2.2 Pearson resudual plot", ylab = "residual", xlab="fitted value",
     ylim = c(-6,13), xlim=c(0,4))
abline(0,0)
```

Fig 2.1 Deviance resudual pl **Fig 2.2 Pearson resudual pl**



dispersion test

```
dispersiontest(fit.step,alternative = "greater",
               trafo = 1)
```

```
    Overdispersion test

data:  fit.step
z = 6.6542, p-value = 1.424e-11
alternative hypothesis: true alpha is greater than 0
sample estimates:
    alpha
0.3801358
```

```
dispersiontest(fit.step,alternative = "greater",
               trafo = function(mu) mu)
```

```
    Overdispersion test

data:  fit.step
z = 6.6542, p-value = 1.424e-11
alternative hypothesis: true alpha is greater than 0
sample estimates:
    alpha
0.3801358
```

```
dispersiontest(fit.step,alternative = "greater",
               trafo = 2)
```

```
    Overdispersion test

data:  fit.step
z = 8.4562, p-value < 2.2e-16
alternative hypothesis: true alpha is greater than 0
```

```
sample estimates:
   alpha
1.008399
```

```
dispersiontest(fit.step,alternative = "greater",
               trafo = function(mu) mu^2)
```

```

    Overdispersion test

data:  fit.step
z = 8.4562, p-value < 2.2e-16
alternative hypothesis: true alpha is greater than 0
sample estimates:
   alpha
1.008399
```

```
dispersiontest(fit.step,alternative = "greater")
```

```

    Overdispersion test

data:  fit.step
z = 6.6542, p-value = 1.424e-11
alternative hypothesis: true dispersion is greater than 1
sample estimates:
dispersion
  1.380136
```

```
dispersiontest(fit.step,alternative = "two.sided")
```

```

    Dispersion test

data:  fit.step
z = 6.6542, p-value = 2.848e-11
alternative hypothesis: true dispersion is not equal to 1
sample estimates:
dispersion
  1.380136
```

```
dispersiontest(fit.step,alternative = "less")
```

```

    Underdispersion test

data:  fit.step
z = 6.6542, p-value = 1
alternative hypothesis: true dispersion is less than 1
sample estimates:
dispersion
  1.380136
```