tp3.R

October 19, 2022

[1]:
```
#Importation de données
evans <- read.table("http://web1.sph.emory.edu/dkleinb/allDatasets/datasets/
 ↪evans.dat")
head(evans)
```

A data.frame: 6 × 12

	V1 <int>	V2 <int>	V3 <int>	V4 <int>	V5 <int>	V6 <int>	V7 <int>	V8 <int>	V9 <int>	V10 <int>	V11 <int>
1	21	0	0	56	270	0	0	80	138	0	0
2	31	0	0	43	159	1	0	74	128	0	0
3	51	1	1	56	201	1	1	112	164	1	1
4	71	0	1	64	179	1	0	100	200	1	1
5	74	0	0	49	243	1	0	82	145	0	0
6	91	0	0	46	252	1	0	88	142	0	0

[2]:
```
names(evans) <-␣
 ↪c("id","chd","cat","age","chl","smk","ecg","dbp","sbp","hpt","ch","cc")
head(evans)
```

A data.frame: 6 × 12

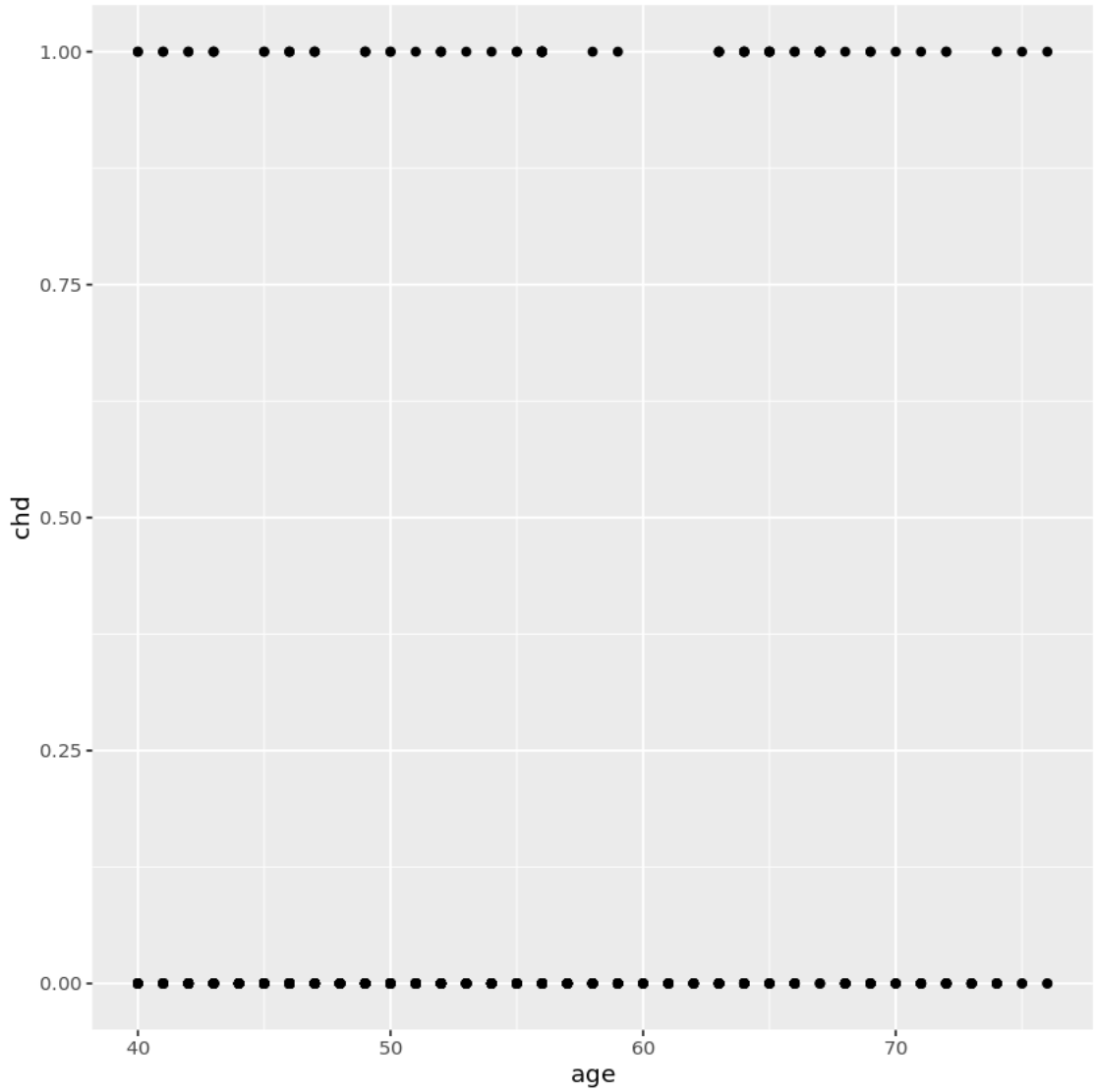
	id <int>	chd <int>	cat <int>	age <int>	chl <int>	smk <int>	ecg <int>	dbp <int>	sbp <int>	hpt <int>	ch <int>
1	21	0	0	56	270	0	0	80	138	0	0
2	31	0	0	43	159	1	0	74	128	0	0
3	51	1	1	56	201	1	1	112	164	1	1
4	71	0	1	64	179	1	0	100	200	1	1
5	74	0	0	49	243	1	0	82	145	0	0
6	91	0	0	46	252	1	0	88	142	0	0

1 Régression logistique

chd = variable à expliquer binaire age = variable explicative

[7]:
```
#Présenter les données

#library(ggplot2)
#ggplot(data = evans) +
#    aes(x = age,
#        y = chd) +
#    geom_point()
```

```
plot(evans$age,evans$chd)
```

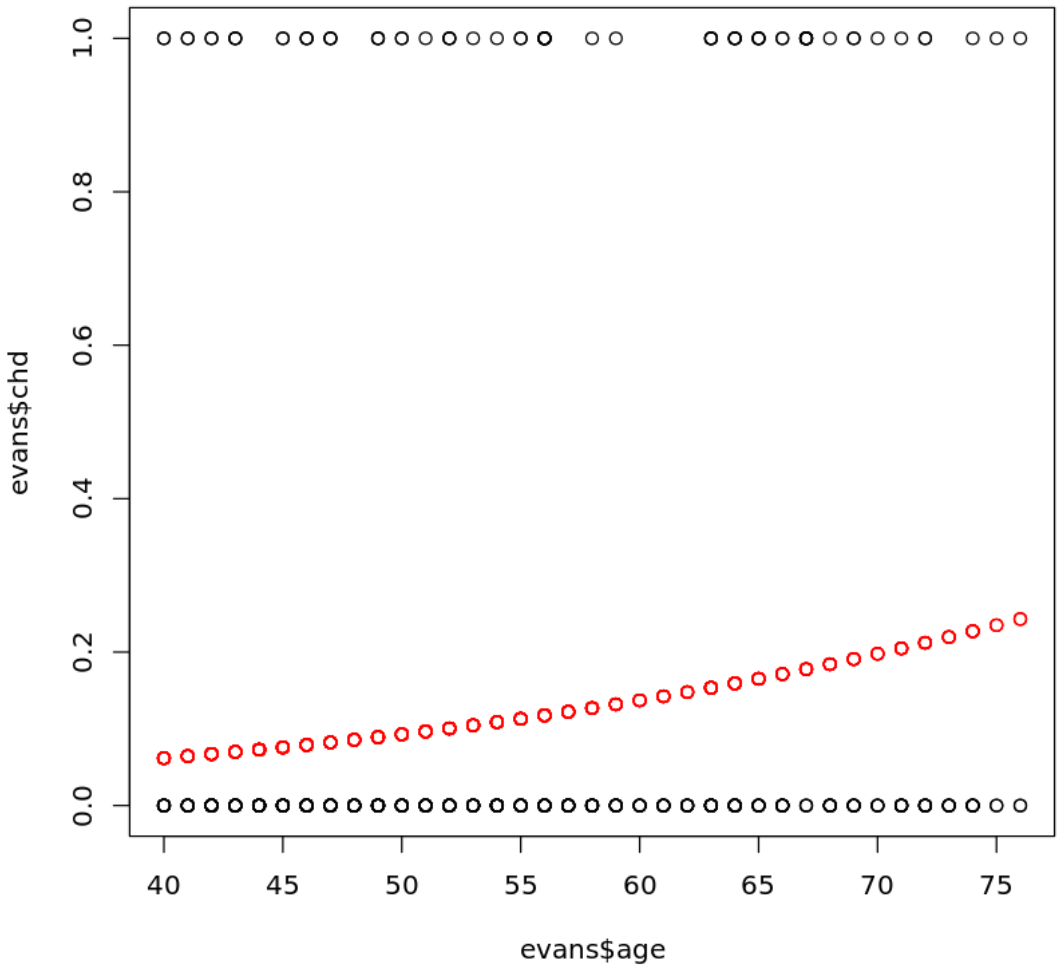


[8]:
```
myreg=glm(chd~age, data = evans, family=binomial(link=logit))
summary(myreg)
```

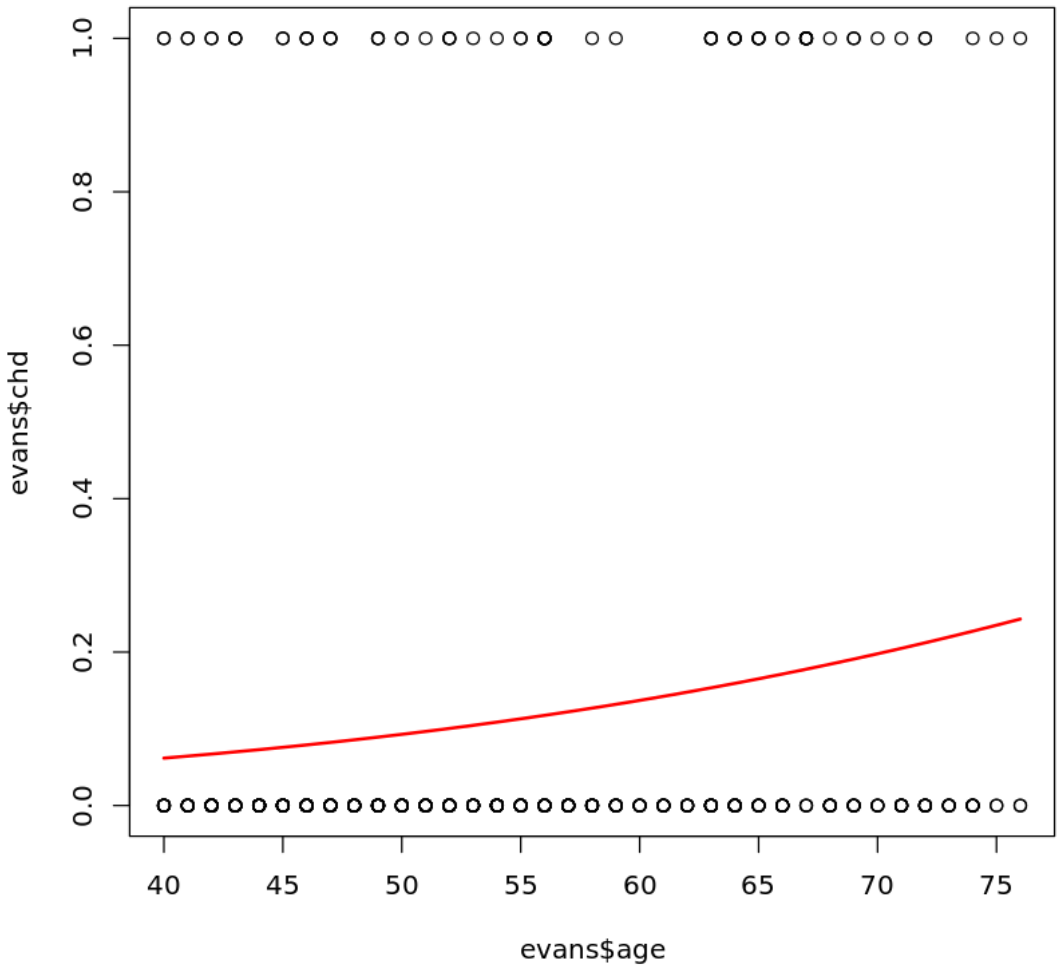
```
Call:
glm(formula = chd ~ age, family = binomial(link = logit), data = evans)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.7579  -0.5170  -0.4464  -0.3929   2.3518
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.47833    0.75610  -5.923 3.16e-09 ***
age          0.04445    0.01315   3.381 0.000723 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 438.56  on 608  degrees of freedom
Residual deviance: 427.22  on 607  degrees of freedom
AIC: 431.22

Number of Fisher Scoring iterations: 5
```

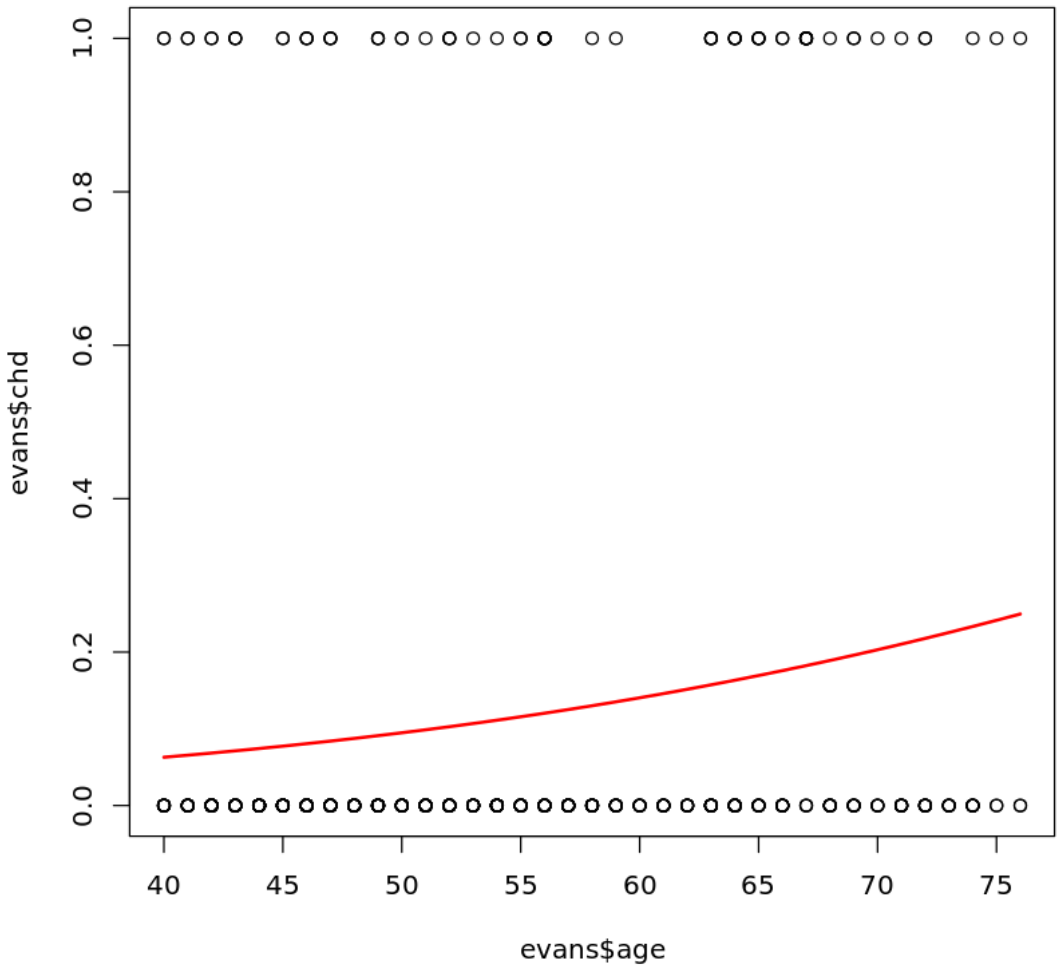
[16]:
```r
#logit(E(chd)) = 0,044 age -4,48

logit_ypredit=0.044* evans$age -4.48
ypredit=exp(logit_ypredit)/(1+ exp(logit_ypredit)) # transfo inverse de logit

plot(evans$age,evans$chd)
points(evans$age,ypredit, col="red")
```



[17]:
```
plot(evans$age,evans$chd)
o=order(evans$age)
points(evans$age[o],ypredit[o], col="red", type="l", lwd=2)
```



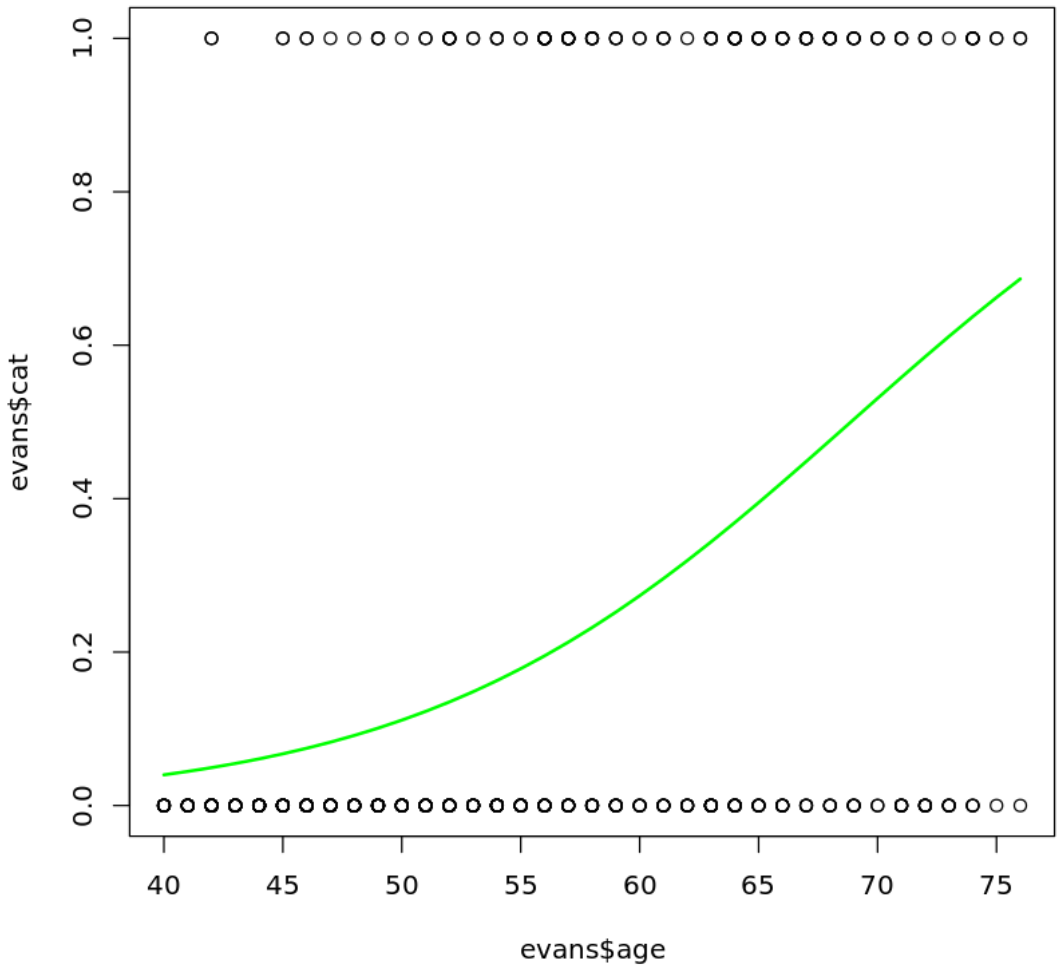
[18]:
```
#Méthode plus simple

plot(evans$age,evans$chd)
myreg=glm(evans$chd~evans$age, family=binomial(link=logit))
ypredit=myreg$fitted
o=order(evans$age)
points(evans$age[o],ypredit[o], col="red", type="l", lwd=2)
```



L'augmentation d'age augment la probabilité de la maladie.Pour le cas de:

cat = variable à expliquer binaire age = variable explicative

[25]:
```
plot(evans$age,evans$cat)
myreg=glm(cat~age, data = evans, family=binomial(link=logit))
ypredit=myreg$fitted
o=order(evans$age)
points(evans$age[o],ypredit[o], col="green", type="l", lwd=2)
```



[ ]:
```
chd = variable à expliquer binaire
age, chl, smk, ecg et hpt  = variables explicatives
```

[24]:
```
#age, chl, smk, ecg et hpt sont les variables de contrôle et chd variable␣
 ↪binaire à expliqeur.

myreg = glm(chd~age+smk+hpt, data = evans, family=binomial(link=logit))
summary(myreg)
```

```
Call:
glm(formula = chd ~ age + smk + hpt, family = binomial(link = logit),
    data = evans)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9746  -0.5451  -0.4168  -0.3296   2.6239

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.37565    0.84445  -6.366 1.94e-10 ***
age          0.04368    0.01373   3.182  0.00146 **
smk          0.83567    0.30138   2.773  0.00556 **
hpt          0.72221    0.26613   2.714  0.00665 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 438.56  on 608  degrees of freedom
Residual deviance: 411.13  on 605  degrees of freedom
AIC: 419.13

Number of Fisher Scoring iterations: 5
```

2 D’ou notre fonction: Y = 0,72 * hpt + 0,83 * smk + 0,04 * age - 5,37