LSM

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Klasifikacija

- Predvideti zavisnu promenljivu
- Šta utiče na raspodelu zavisne promenljive?

$$Y_i|X_i : \begin{pmatrix} 0 & 1 \\ 1-\pi(X_i) & \pi(X_i) \end{pmatrix}$$

Regresiona funkcija je

$$E(Y_i|X_i) = \pi(X_i)$$

Zašto linearni model nije adekvatan?

1. Greške modela ne mogu se modelirati normalnom raspodelom, ili nekom drugom absolutno neprekidnom i smetričnom oko nule.
2. Disperzija grešaka modela nije konstantna. Važi: $D(Y_i|X_i) = \pi(X_i)(1 - \pi(X_i)) = D(\varepsilon_i)$.
3. Regresiona funkcija verovatnoća pa treba da bude zadovoljeno da je $\pi(X_i) \in [0, 1]$.

Transformacija modela

$$F^{-1}(\pi(X_i)) = X\beta$$

1. $F(x) = \Phi(x)$ PROBIT regresija
2. $F(x) = \frac{1}{1+e^{-x}}$ LOGISTIČKA regresija
3. $F(x) = 1 - e^{-e^x}$ LOG-VEJBULOVA regresija

Probit regresija

$$\Phi^{-1}(\pi(X_i)) = \beta_0^* + \beta_1^* X_i$$

Pretpostavimo da ispitujemo zavisnost temperature Y od vlažnosti vazduha X i da se proglašava vanredno stanje ukoliko temperatura pređe neki kritični nivo C. Neka je Y_c indikator vanrednog stanja. Pod pretpostavkom da je $Y_i = aX_i + b + \varepsilon_i$, gde $\{\varepsilon_i\}$ je Gausov beli shum, modeliranje $E(Y_c|X)$ se svodi na probit regresiju.

Parametri se mogu oceniti metodom maksimalne verodostojnosti.

Log – Vejbulova regresija

$$F_G^{-1}(\pi(X_i)) = \log(-\log(1-\pi(X_i))) = \beta_0 + \beta_1 X_1$$

zbog svoje asimetričnosti, se najčešće koristi za modelovanje malih i velikih verovatnoća uspeha

Parametri se mogu oceniti metodom maksimalne verodostojnosti.

Logistička regresija

$$F_L^{-1}(\pi(X_i)) = \log\left(\frac{\pi(X_i)}{1-\pi(X_i)}\right) = \beta_0 + \beta_1 X_i$$

$\lambda(p) = \log\left(\frac{p}{1-p}\right)$ logit transformacija

$\lambda(X_i) = \log\left(\frac{\pi(X_i)}{1-\pi(X_i)}\right)$

Količnik $\frac{\pi(X_i)}{1-\pi(X_i)}$ se naziva *kvota.*

Interpretacija kvote

Ocena parametara

Metod maksimalne verodostojnosti

$$l(\beta) = \sum_{i=1}^{n} \left(Y_i \log \left(\frac{\pi(X_i)}{1-\pi(X_i)} \right) + \log(1-\pi(X_i)) \right)$$
$$= \sum_{i=1}^{n} Y_i(\beta_0 + \beta_1 X_i) - \sum_{i=1}^{n} \log \left(1 + e^{\beta_0+\beta_1 X_i}\right)$$

Numerički se rešava sistem $\frac{\partial l(\beta)}{\partial \beta} = 0$

Ocenjena logit funkcija je

$$\hat{\lambda}(X) = \hat{\beta}_0 + \hat{\beta}_1 X$$

Ocena parametara

U opštem slučaju

$$\hat{\lambda}(X) = X\hat{\beta}$$

$\hat{\beta}$ ima normalnu $\mathcal{N}(\beta, I^{-1}(\beta))$ raspodelu kao ocena maksimalne verodostojnosti pa se mogu napraviti intervali poverenja za $\lambda(X)$ a zatim i za $\pi(X)$.

Testiranje značajnosti koeficijenta

Valdova statistika

$$Z = \frac{\hat{\beta}_i}{SE(\hat{\beta}_i)}$$

- test količnika verodostojnosti

$$2\log\left(\frac{L(\hat{\beta}_0, \hat{\beta}_1)}{L(\hat{\beta}_0)}\right) \sim \chi^2_1$$

$$2\log\left(\frac{L(\hat{\beta})}{L(\hat{\beta}_0)}\right) \sim \chi^2_q$$

broj koeficijenata za koje se pretpostavlja da su 0

Devijacija

- meri razliku između pretpostavljenog modela i saturiranog modela
- Definiše se sa $D_0 = 2(l(y, \hat{\theta}_s) - l(y, \hat{\beta}_0))$ gde je $\hat{\theta}_s$ ocena u saturiranom modelu
- $D = 2(l(y, \hat{\theta}_s) - l(y, \hat{\beta}))$
- $D_0 - D \sim \chi^2_q$

Slučaj grupisanih podataka

najčešće kad je neki prediktor kategorička promenljiva

Za svako X_i iz uzorka formiramo podskup koji čine oni elementi uzorka čija je nezavisna komponenta jednaka odabranom X_i.

Neka je m_j broj elemenata u j-toj podgrupi posmatranog uzorka, $j = 1, 2...J$.

U okviru svake podgrupe ocenimo $\pi(X_j) = P\{Y = 1|X_j\}$. Neka je n_j proj elemenata u podgrupi za koje je vrednost zavisne promenljive jednaka 1. Tada je $\hat{\pi}\{Y = 1|X_j\} = \frac{1}{1+e^{\hat{\beta}_0+\hat{\beta}_1 x_j}}$. Očekivan broj elemenata iz svake od grupa:

$$\hat{n}_j = m_j\hat{\pi}_j = m_j\frac{1}{1 + e^{\hat{\beta}_0+\hat{\beta}_1 x_j}}.$$

Pirsonovi reziduali

$$r_j = \frac{n_j - m_j\hat{\pi}_j}{\sqrt{m_j\hat{\pi}_j(1-\hat{\pi}_j)}} = \frac{n_j - \hat{n}_j}{\sqrt{\hat{n}_j(1-\frac{\hat{n}_j}{m_j})}}.$$

$$C = \sum_{j=1}^{J} r_j^2.$$

C ima približno χ^2_{J-2}. Kada se u modelu javlja $p+1$ ocenjen parametar onda C ima približno χ^2_{J-p-1} raspodelu

Reziduali devijacije

Rezidual devijacije, za $n_j - \hat{n}_j > 0$, je definisan sa:

$$d_j = \sqrt{2\left(n_j \ln \frac{n_j}{m_j \hat{\pi}_j} + (m_j - n_j) \ln \frac{m_j - n_j}{m_j(1 - \hat{\pi}_j)}\right)}$$

$$= \sqrt{2\left(n_j \ln \frac{n_j}{\hat{n}_j} + (m_j - n_j) \ln \frac{m_j - n_j}{m_j - \hat{n}_j}\right)}$$

Za $n_j - \hat{n}_j < 0$ za j-ti rezidual se uzima $-d_j$, u suprotnom nula.

Specijalni slučajevi:

za $n_j = 0$

$$d_j = -\sqrt{2m_j \left| \ln \frac{m_j}{m_j - \hat{n}_j} \right|},$$

dok je za $n_j = m_j$

$$d_j = \sqrt{2m_j \left| \ln \frac{m_j}{\hat{n}_j} \right|}.$$

Reziduali devijacije

Test statistika je

$$D = \sum_{j=1}^{J} d_j^2.$$

D ima približno χ^2_{J-2} raspodelu. Kada se u modelu javlja $p+1$ ocenjen parametar onda D ima približno χ^2_{J-p-1} raspodelu. Primetimo da je D zapravo devijacija modela.

Hosmer-Lemešov test

- Podaci se grupišu u g kategorija na osnovu sličnosti ocenjenih verovatnoća. Granice koje određuju grupu se dobijaju kao odgovarajući kvantili. Npr. prva grupa sadrži sve elemente za koje je ocenjena verovatnoća između 0 i 0.1, druga, od 0.1 do 0.2 itd. Statstika se pravi analogno Pirsonovoj u slučaju grupisanih podataka

$$C = \sum_{k=1}^{g} \frac{(o_k - M_k \bar{\pi}_k)^2}{M_k \bar{\pi}_k (1 - \bar{\pi}_k)},$$

gde je M_k broj elemenata u k-toj grupi, c_k je broj različitih elemenata u $k - toj$ grupi i $o_k = \sum_{j=1}^{c_k} Y_j$ i

$$\bar{\pi}_k = \sum_{j=1}^{c_k} \frac{m_j \hat{\pi}_k}{M_k}$$

Ukoliko je dobar model C ima χ^2_{g-2} raspodelu

Primer – babyfood

- disease: number with disease
- nondisease: number without disease
- sex: a factor with levels Boy Girl
- food: a factor with levels Bottle Breast Suppl

Primer – babyfood

```
library(faraway)
bolesti <- glm(cbind(disease, nondisease) ~ sex+food,
family=binomial,
babyfood)
summary(bolesti)
```

```
##
## Call:
## glm(formula = cbind(disease, nondisease) ~ sex + food, family = binomial,
##     data = babyfood)
##
## Deviance Residuals:
##       1        2        3        4        5        6
##  0.1096  -0.5052   0.1922  -0.1342   0.5896  -0.2284
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.6127     0.1124 -14.347  < 2e-16 ***
## sexGirl      -0.3126     0.1410  -2.216   0.0267 *
## foodBreast   -0.6693     0.1530  -4.374 1.22e-05 ***
## foodSuppl    -0.1725     0.2056  -0.839   0.4013
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 26.37529  on 5  degrees of freedom
## Residual deviance:  0.72192  on 2  degrees of freedom
## AIC: 40.24
##
## Number of Fisher Scoring iterations: 4
```

Primer – babyfood

```
bolestiSex <- glm(cbind(disease, nondisease) ~ sex,
family=binomial,
babyfood)
summary(bolestiSex)
```

```
##
## Call:
## glm(formula = cbind(disease, nondisease) ~ sex, family = binomial,
##     data = babyfood)
##
## Deviance Residuals:
##        1         2         3         4         5         6
##  2.32857  -0.03126  -2.41107   1.75294   1.04279  -2.34573
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.89991    0.08966 -21.190   <2e-16 ***
## sexGirl     -0.32613    0.14036  -2.323   0.0202 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 26.375  on 5  degrees of freedom
## Residual deviance: 20.899  on 4  degrees of freedom
## AIC: 56.417
##
## Number of Fisher Scoring iterations: 4
```

Primer – babyfood

```
bolestiFood <- glm(cbind(disease, nondisease) ~ food,
family=binomial,
babyfood)
summary(bolestiFood)
```

```
##
## Call:
## glm(formula = cbind(disease, nondisease) ~ food, family = binomial,
##     data = babyfood)
##
## Deviance Residuals:
##       1         2         3         4         5         6
##  1.16335   0.05492   1.08856  -1.32306  -0.05930  -1.18475
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.74676    0.09693 -18.022  < 2e-16 ***
## foodBreast  -0.67645    0.15281  -4.427 9.57e-06 ***
## foodSuppl   -0.17435    0.20531  -0.849    0.396
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 26.375  on 5  degrees of freedom
## Residual deviance:  5.699  on 3  degrees of freedom
## AIC: 43.217
##
## Number of Fisher Scoring iterations: 4
```

Primer – babyfood

```
anova(bolestiSex,bolesti,test="Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(disease, nondisease) ~ sex
## Model 2: cbind(disease, nondisease) ~ sex + food
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1         4    20.8992
## 2         2     0.7219  2   20.177 4.155e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Primer – babyfood

```
anova(bolestiFood,bolesti,test="Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(disease, nondisease) ~ food
## Model 2: cbind(disease, nondisease) ~ sex + food
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1         3     5.6990
## 2         2     0.7219  1   4.9771  0.02569 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
 b1=data.frame(Bolest=rep(1,77),Sex=rep("Boy",77),Food=rep("Bottle",77))
 b2=data.frame(Bolest=rep(0,381),Sex=rep("Boy",381),Food=rep("Bottle",381))
b3=data.frame(Bolest=rep(1,19),Sex=rep("Boy",19),Food=rep("Supl",19))
b4=data.frame(Bolest=rep(0,128),Sex=rep("Boy",128),Food=rep("Supl",128))
b5=data.frame(Bolest=rep(1,47),Sex=rep("Boy",47),Food=rep("Breast",47))
b6=data.frame(Bolest=rep(0,447),Sex=rep("Boy",447),Food=rep("Breast",447))
b7=data.frame(Bolest=rep(1,48),Sex=rep("Girl",48),Food=rep("Bottle",48))
b8=data.frame(Bolest=rep(0,336),Sex=rep("Girl",336),Food=rep("Bottle",336))
b9=data.frame(Bolest=rep(1,16),Sex=rep("Girl",16),Food=rep("Supl",16))
b10=data.frame(Bolest=rep(0,111),Sex=rep("Girl",111),Food=rep("Supl",111))
b11=data.frame(Bolest=rep(1,31),Sex=rep("Girl",31),Food=rep("Breast",31))
b12=data.frame(Bolest=rep(0,433),Sex=rep("Girl",433),Food=rep("Breast",433))
babyfood1=rbind(b1,b2,b3,b4,b5,b6,b7,b8,b9,b10,b11,b12)

babyfood1$Food=factor(babyfood1$Food)
babyfood1$Sex=factor(babyfood1$Sex)
babyfood1$Bolest=factor(babyfood1$Boles)
summary(babyfood1)
```

```
##  Bolest     Sex           Food
##  0:1836   Boy :1099   Bottle:842
##  1: 238   Girl: 975   Supl  :274
##                       Breast:958
```

```r
bolestiN <- glm(Bolest ~ Sex+Food,
family=binomial,
babyfood1)
summary(bolestiN)
```

```
##
## Call:
## glm(formula = Bolest ~ Sex + Food, family = binomial, data = babyfood1)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.6030  -0.5218  -0.4409  -0.3795   2.3094
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.6127     0.1124 -14.347  < 2e-16 ***
## SexGirl      -0.3126     0.1410  -2.216   0.0267 *
## FoodSupl     -0.1725     0.2056  -0.839   0.4013
## FoodBreast   -0.6693     0.1530  -4.374 1.22e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1478.1  on 2073  degrees of freedom
## Residual deviance: 1452.4  on 2070  degrees of freedom
```

Da li je odabrani model zadovoljavajući?

```
D=sum(residuals.glm(bolesti,c("deviance"))^2)
D
```

```
## [1] 0.7219218
```

```
C=sum(residuals.glm(bolesti,c("pearson"))^2)
pchisq(D,df=6-4,lower.tail = FALSE)
```

```
## [1] 0.6970062
```

```
pchisq(C,df=6-4,lower.tail = FALSE)
```

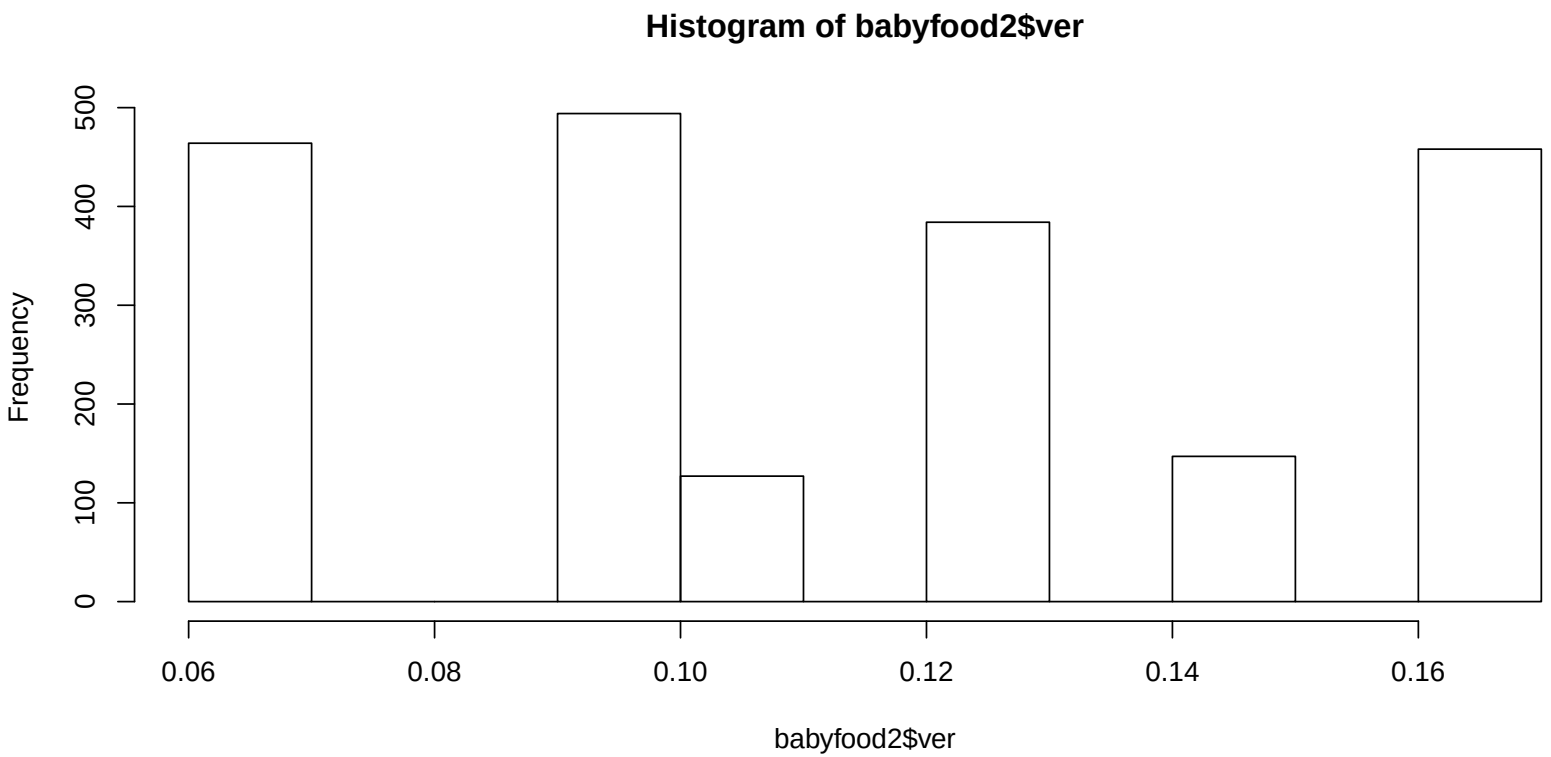
```
## [1] 0.6944444
```

Ovu analizu ne smemo da primenimo u slučaju da podaci nisu grupisani.

Klasifikacija

$$Y_i = \begin{cases} 0, & \hat{p}_i < C \\ 1, & \hat{p}_i \geq C \end{cases}$$

```
predictBolestiN <-predict(bolestiN, type = 'response')
babyfood2=cbind(babyfood1,ver=predictBolestiN,prognoza=(predictBolestiN>=0.5))
hist(babyfood2$ver)
```



C iz skupa $\{0.5, 0.15, 0.1\}$

```
##
##       FALSE
##    0   1836
##    1    238
```

```
##
##       FALSE TRUE
##    0   1455  381
##    1    161   77
```

```
##
##       FALSE TRUE
##    0    880  956
##    1     78  160
```

Koje C je adekvatno?

$St.:Pr.$	0	1
0	a	b
1	c	d

tačnost klasifikacije je $A = \frac{a+d}{a+b+c+d}$

TNR (true negative rates) - specifičnost $TNR = \frac{a}{a+b}$

FPR $FPR = 1 - TNR$

TPR (true positive rates) - senzitivnost $TPR = \frac{d}{c+d}$

PPV (positive predictive value) $PPV = \frac{d}{b+d}$

F_1 skor $F_1 = 2\frac{PPV \cdot TPR}{PPV+TPR}$

ROC kriva

Zavisnost sezitivnosti od FPR (1- specifičnost) , kad se C menja

Najbolja je u gornjem levom uglu grafika koja odgovara savršenom klasifikatoru Ukoliko želimo da poredimo dva klasifikatora (modela) možemo koristiti i površinu ispod krive (AUC). Što je veća površina bolja je prediktivna moć modela.

Površina (koja ima oblik Vilkokson-Manove statistike) predstavlja ocenu verovatnoće da će ocenjena verovatnoća uspeha (na osnovu koje se donosi odluka o klasifikaciji) biti veća u slučaju da slučajno odabrani element uzorka dolazi iz pozitivne klase, nego ukoliko dolazi iz negativne klase.

Površina nam zapravo govori koliko dobro ovaj model razdvaja klase, i kako ne zavisi od praga, češće se koristi za poređenje modela.

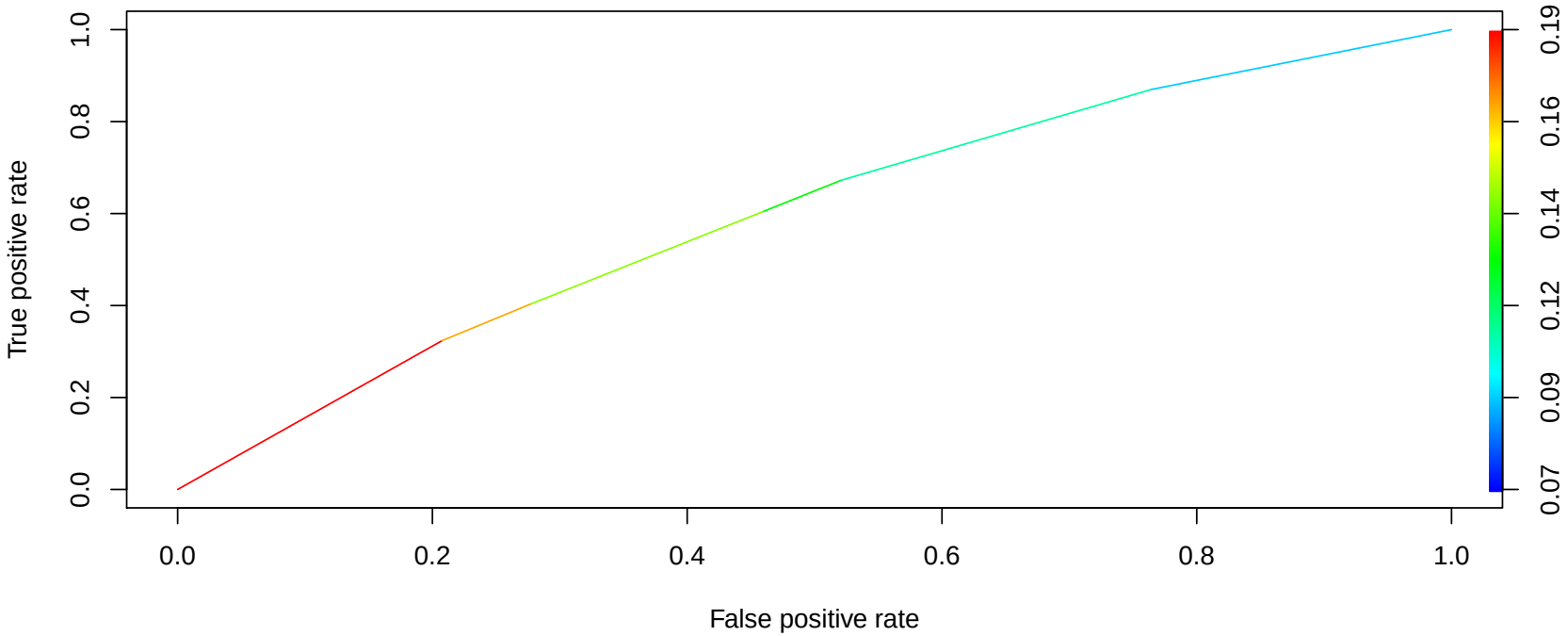
Mera 2*AUC-1 se naziva Đinijev koeficijent.

Još jedna mera koja se često koristi je

$$KS = \sup_{C} TPR(C) - FPR(C)$$

Veća vrednost ove statistike upućuje na bolji klasifikator.

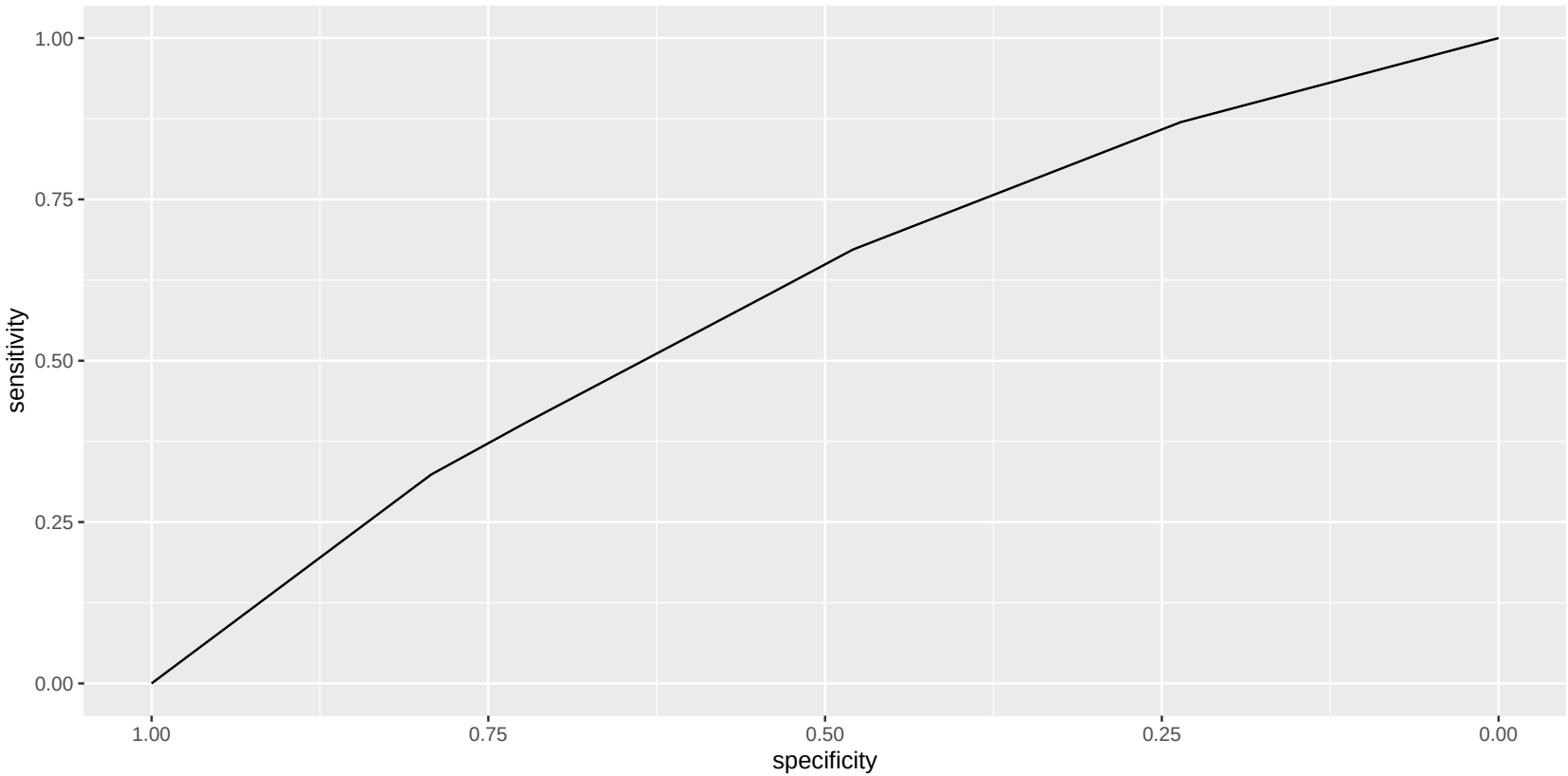
```r
library(ROCR)
ROCRpred <- prediction(predictBolestiN, babyfood1$Bolest)
ROCRperf <- performance(ROCRpred, 'tpr','fpr')

plot(ROCRperf, colorize = TRUE)
```



```r
library(pROC)
g <- roc(babyfood2$Bolest ~ babyfood2$ver, data = babyfood2)
auc(g)
```

```
## Area under the curve: 0.598
```

```r
ggroc(g)
```



KS statistika

```
tpr <- coords(g, g$thresholds, input="thr", ret="tpr", transpose = FALSE)
fpr <- coords(g, g$thresholds, input="thr", ret="fpr", transpose = FALSE)

tpr-fpr
```

```
## [1] 0.0000000 0.1055867 0.1515717 0.1448024 0.1261282 0.1160131 0.0000000
```

```
max(tpr-fpr)
```

```
## [1] 0.1515717
```

Optimlni prag

```
coords(g,'best',best.method=c("youden"),ret='threshold')
```

```
## [1] 0.1009679
```

```
coords(g,'best',best.method=c("closest.topleft"),ret='threshold')
```

```
## [1] 0.1182937
```

```
coords(g,'best',best.method=c("youden"),
       ret=c('threshold',"1-specificity",'sensitivity'))
```

```
##     threshold 1-specificity   sensitivity
##     0.1009679     0.5206972     0.6722689
```

```
coords(g,'best',best.method=c("closest.topleft"),
       ret=c('threshold',"1-specificity",
             'sensitivity'))
```

```
##     threshold 1-specificity   sensitivity
##     0.1182937     0.4602397     0.6050420
```

Primer - upis na fakultet

```
mydata <- read.csv("https://stats.idre.ucla.edu/stat/data/binary.csv")

mydata$rank <- factor(mydata$rank)
mylogit <- glm(admit ~ gre + gpa + rank, data = mydata, family = "binomial")
summary(mylogit)
```

```
##
## Call:
## glm(formula = admit ~ gre + gpa + rank, family = "binomial",
##     data = mydata)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.6268  -0.8662  -0.6388   1.1490   2.0790
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.989979   1.139951  -3.500 0.000465 ***
## gre          0.002264   0.001094   2.070 0.038465 *
## gpa          0.804038   0.331819   2.423 0.015388 *
## rank2       -0.675443   0.316490  -2.134 0.032829 *
## rank3       -1.340204   0.345306  -3.881 0.000104 ***
## rank4       -1.551464   0.417832  -3.713 0.000205 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98  on 399  degrees of freedom
## Residual deviance: 458.52  on 394  degrees of freedom
## AIC: 470.52
```

```r
mylogit1 <- glm(admit ~ gre  + rank, data = mydata, family = "binomial")
summary(mylogit1)
```

```
##
## Call:
## glm(formula = admit ~ gre + rank, family = "binomial", data = mydata)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5199  -0.8715  -0.6588   1.1775   2.1113
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.802365   0.672982  -2.678 0.007402 **
## gre          0.003224   0.001019   3.163 0.001562 **
## rank2       -0.721737   0.313033  -2.306 0.021132 *
## rank3       -1.291305   0.340775  -3.789 0.000151 ***
## rank4       -1.602054   0.414932  -3.861 0.000113 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98  on 399  degrees of freedom
## Residual deviance: 464.53  on 395  degrees of freedom
## AIC: 474.53
##
## Number of Fisher Scoring iterations: 4
```

```r
anova(mylogit1,mylogit,test = "Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: admit ~ gre + rank
```

```r
mylogit2 <- glm(admit ~ gre  +gpa, data = mydata, family = "binomial")
summary(mylogit2)
```

```
##
## Call:
## glm(formula = admit ~ gre + gpa, family = "binomial", data = mydata)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.2730  -0.8988  -0.7206   1.3013   2.0620
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -4.949378   1.075093  -4.604 4.15e-06 ***
## gre          0.002691   0.001057   2.544   0.0109 *
## gpa          0.754687   0.319586   2.361   0.0182 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 499.98  on 399  degrees of freedom
## Residual deviance: 480.34  on 397  degrees of freedom
## AIC: 486.34
##
## Number of Fisher Scoring iterations: 4
```

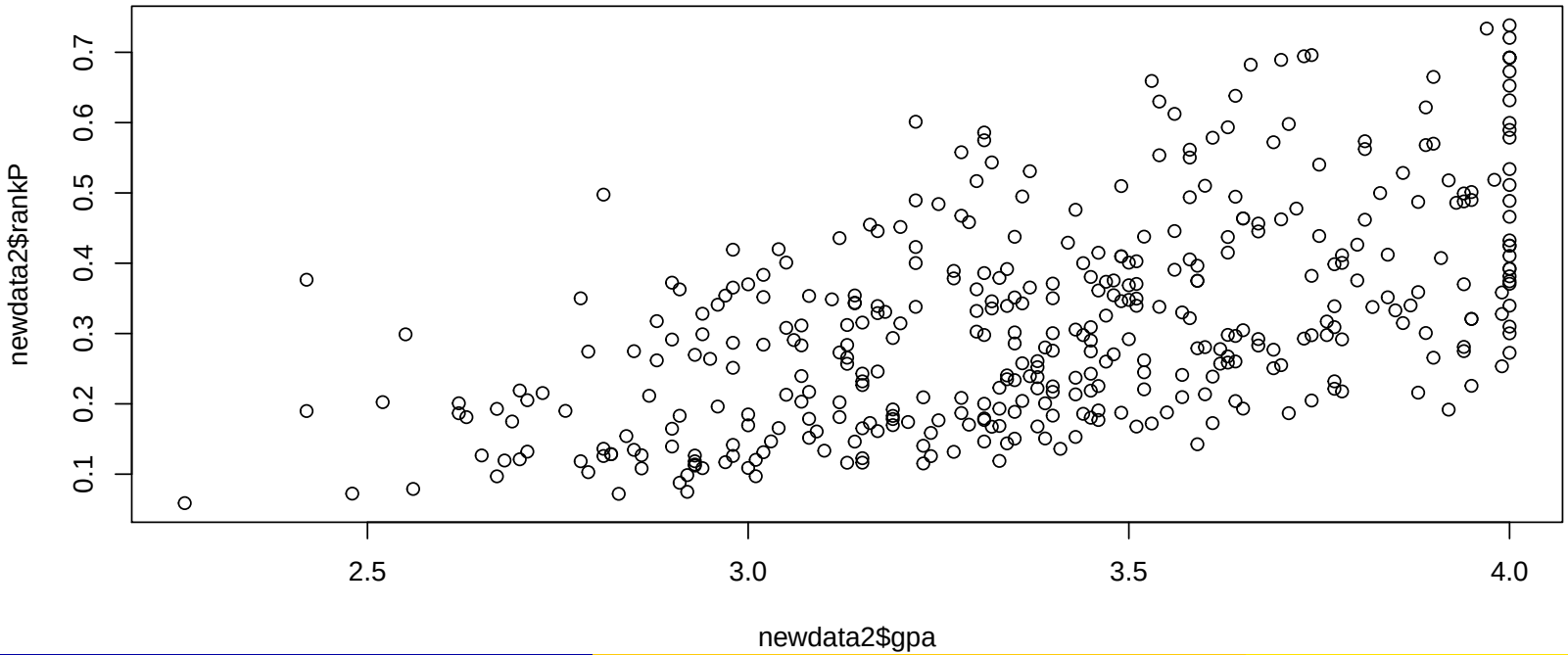
```r
anova(mylogit2,mylogit,test = "Chi")
```

```
## Analysis of Deviance Table
##
## Model 1: admit ~ gre + gpa
## Model 2: admit ~ gre + gpa + rank
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
```

```r
newdata1 <- with(mydata, data.frame(gre = mean(gre), gpa = mean(gpa), rank = factor(1:4)))
newdata1$rankP <- predict(mylogit, newdata = newdata1, type = "response")
newdata1
```

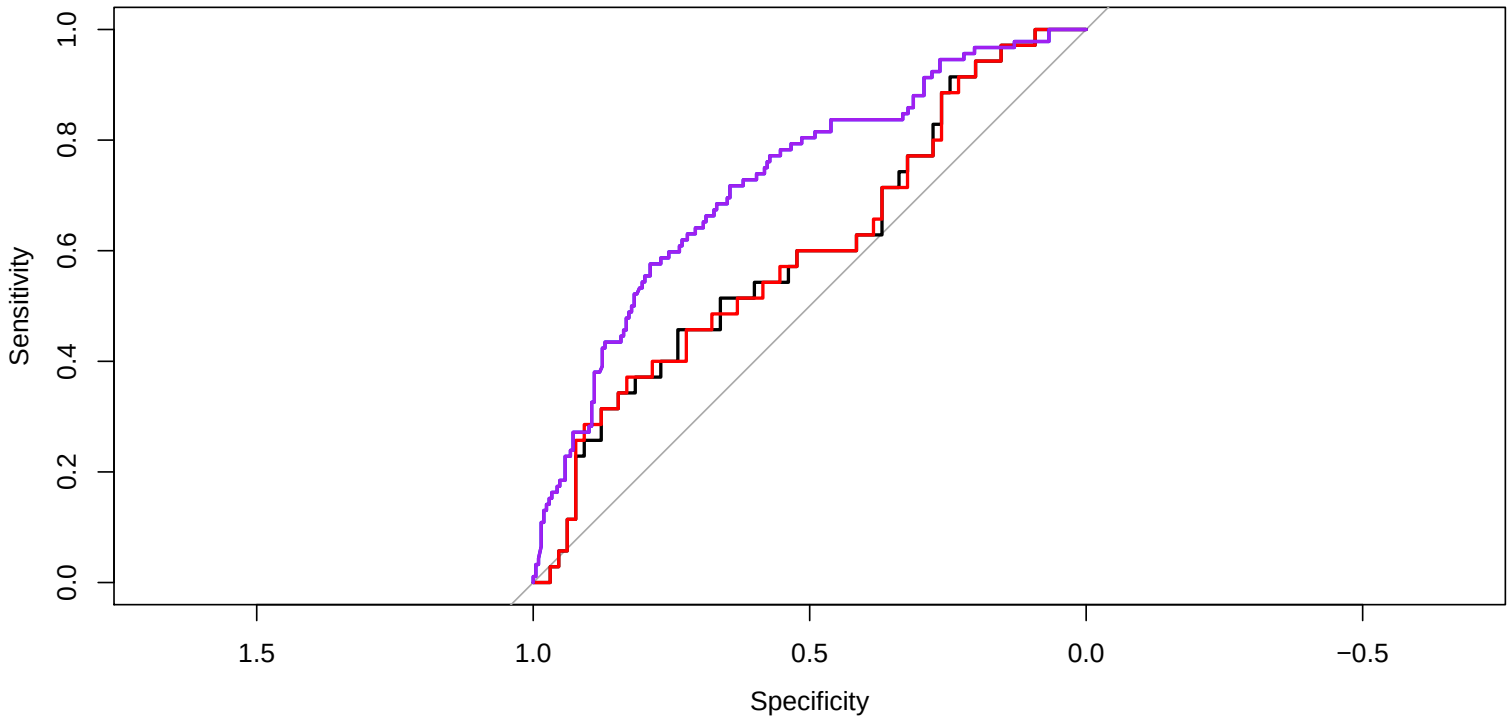
```
##     gre    gpa rank     rankP
## 1 587.7 3.3899    1 0.5166016
## 2 587.7 3.3899    2 0.3522846
## 3 587.7 3.3899    3 0.2186120
## 4 587.7 3.3899    4 0.1846684
```

```r
newdata2 <- mydata
newdata2$rankP <- predict(mylogit, newdata = newdata2, type = "response")
plot(newdata2$gpa,newdata2$rankP)
```



```r
mydataTr<-mydata[1:300,]

mydataTrPr<-mydata[1:300,]

mydataTest<-mydata[301:400,]

mydataTestPr<-mydata[301:400,]


mylogitTr <- glm(admit ~ gre + gpa + rank, data = mydataTr, family = "binomial")

mylogitTrPr <- glm(admit ~ gre + gpa + rank, data = mydataTrPr, family =binomial(link='probit'))


mydataTr$rankP <- predict(mylogitTr, newdata = mydataTr, type = "response")
mydataTest$rankP <- predict(mylogitTr, newdata = mydataTest, type = "response")
mydataTestPr$rankP <- predict(mylogitTrPr, newdata = mydataTest, type = "response")


mydataTrPr$rankP <- predict(mylogitTr, newdata = mydataTr, type = "response")
```

```
g <- roc(mydataTest$admit ~ mydataTest$rankP, data = mydataTest)
plot(g)
gPr <- roc(mydataTestPr$admit ~ mydataTestPr$rankP, data = mydataTest)
plot(gPr,add=TRUE,col='red')

gTr <- roc(mydataTr$admit ~ mydataTr$rankP, data = mydataTr)
plot(gTr,add=TRUE,col='blue')
gTrPr <- roc(mydataTrPr$admit ~ mydataTrPr$rankP, data = mydataTr)
plot(gTrPr,add=TRUE,col='purple')
```



```
auc(gTr)
```

```
## Area under the curve: 0.7258
```

```
auc(gTrPr)
```

```
## Area under the curve: 0.7258
```

```
coords(gTr,'best',best.method=c("closest.topleft"), ret=c("thr"))
```

```
## Warning in coords.roc(gTr, "best", best.method = c("closest.topleft"), ret
## = c("thr")): An upcoming version of pROC will set the 'transpose' argument
## to FALSE by default. Set transpose = TRUE explicitly to keep the current
## behavior, or transpose = FALSE to adopt the new one and silence this
## warning. Type help(coords_transpose) for additional information.
```

```
## [1] 0.2950917
```

```
coords(g,x=0.3277611, ret=c("tpr","fpr"),input="thr")
```

```
## Warning in coords.roc(g, x = 0.3277611, ret = c("tpr", "fpr"), input =
## "thr"): An upcoming version of pROC will set the 'transpose' argument
## to FALSE by default. Set transpose = TRUE explicitly to keep the current
## behavior, or transpose = FALSE to adopt the new one and silence this
## warning. Type help(coords_transpose) for additional information.
```

```
##       tpr       fpr
## 0.5428571 0.4307692
```

domaći: uporediti ovaj model sa modelom bez nekog od prediktora prediktora

Uopšteni linearni modeli

Ovi modeli se sastoje od sledećih komponenti:

- linearna kombinacija koeficijenata modela

$$\eta_j = X_j^T \beta \text{ odnosno } \eta_j = \beta_0 + \sum_{i=1}^{p} X_{j_i} \beta_i$$

- "link" funkcije koja predstavlja transforamciju koju treba primeniti na funkciju srednje vrednosti zavisne promenljive (regresionu funkciju), da bi se ta transformisana promenljiva mogla opisati linearnim modelom, odnosno za $\mu_j = EY_j$ i za link funkciju g važi

$$g(\mu_j) = \eta_j$$

- disperizija zavisne promenljive se može predstaviti u obliku

$$D(Y_j) = CV(\mu_j).$$

Eksponencijalnoj familiji sa raspršenjem (rasejanjem) pripadaju sve raspodele za koje se funkcija gustine (zakon raspodele) mozhe prikazati u obliku:

$$f(y,\theta) = e^{\frac{c(\theta)^T T(y) - d(\theta) + S(y)}{\phi(\tau)}}$$

Parametar τ se naziva parametrom raspršenja. Kada je $\phi(\tau)$ poznato radi se o klasičnoj eksponencijalnoj familiji raspodela.

Ukoliko je $T(y) = y$ i $c(\theta) = \theta$ kažemo da se radi o raspodeli u kanonskom obliku}. Tada je

$$EY = -d'(\theta) = \mu$$
$$DY = d''(\theta)\phi(\tau) = V(\mu)\phi(\tau).$$

Najčešće je $\phi(\tau) = a\tau$ i u slučaju uopštenog linearnog modela podrazumevamo da je $f(y_i) = e^{\frac{y_i\theta_i - d(\theta_i)}{a_i\tau} + c(y_i, a_i\tau)}$.

Primeri

- logistička regresija
- Puasonova regresija
- ...

Odabir link funkcije

Ukoliko je link funkcija odabrana tako da je za kanonski parametar $\theta = \eta$ onda takvu funkciju nazivamo kanonskom link funkcijom

Prednost odabira kanonske link funkcije je što je tada $X^T Y$ dovoljna statistika za β jer je

$$L(y, \theta) = e^{\frac{\sum_{i=1}^{n} y_i x_i^T \beta - d(x_i^T \beta) - S(y_i)}{\phi(\tau)}}$$

ML ocena

$$l(y,\beta,\tau) = \sum \frac{y_i x_i^T \beta - d(x_i^T \beta)}{a_i \tau} + \sum c(a_i \tau, y_i)$$

$$\frac{\partial l(y,\beta,\tau)}{\partial \beta} = \sum \frac{x_i (y_i - d\dot{t}(x_i^T \beta))}{\tau a_i} = 0$$

$$\frac{\partial^2 l(y,\beta,\tau)}{\partial \beta \partial \beta^T} = -\sum \frac{x_i x_i^T d\dot{t}\dot{t}(x_i^T \beta)}{\tau a_i} \leq 0$$

drugi oblik se može dobiti korišćenjem

$$\frac{\partial l(y,\beta,\tau)}{\partial \beta} = \frac{\partial}{\partial \theta}\frac{\partial \theta}{\partial \mu}\frac{\partial \mu}{\partial \eta}\frac{\partial \eta}{\partial \beta}$$

Asimptotska svojstva ML ocene

- asimptotska normalnost kao posledica MLE ocene u regularnom slučaju;
- može se iskoristiti Valdova statistika definisana kao u slučaju logisičke regresije;
- jedna od mera kvaliteta modela je i *devijacija* odnosno "mera odstupanja pretpostavljenog modela od zasićenog modela." Definiše se sa $D = 2\tau(l(y, \hat{\theta}_s) - l(y, \hat{\theta}))$ gde je $\hat{\theta}_s$ ocena nepoznatih parametara u zasićenom modelu.

Ukoliko je τ *poznato* onda se razlika devijacija koristi za testiranje značajnosti koeficijenata modela.

Ukoliko je H_0 : da su nekih k koeficijenata u modelu 0, onda $\frac{(D_0-D_1)}{\tau}$ ima χ^2_{p+1-k}. Ponekad se $\frac{D}{\tau}$ naziva skaliranom devijacijom.

Kada je τ nepoznato, može se oceniti sa $\hat{\tau} = \frac{1}{n-p-1}\sum_{i=1}^{n}\frac{(y_i-\hat{\mu}_i)^2}{a_i V(\hat{\mu}_i)}$ (suma kvadrata Pirsonovih reziduala). Tada za testiranje značajnosti koeficijenata možemo koristiti statistiku

$$\frac{\frac{1}{p+1-k}(D_0 - D_1)}{\hat{\tau}}$$

koja ukoliko je nulta hipoteza tačna ima $F_{p+1-k,n-p-1}$.

Reziduali modela

- Pirsonovi $\frac{y_i - \hat{\mu}_i}{\sqrt{a_i V(\hat{\mu}_i)}}$
- reziduali devijacije $d_i = sign(y_i - \hat{\mu}_i)\sqrt{D(y_i, \hat{\mu}_i)}$ gde je $D(y_i, \hat{\mu}_i) = \frac{2}{a_i}\Big((y_i(\theta(y_i) - \theta(\hat{\mu}_i))) - (d(\theta(y_i)) - d(\theta(\hat{\mu}_i)))\Big)$