

Let us get back on the Titanic dataset,

```
1 loc_fichier = "http://freakonometrics.free.fr/titanic.RData"
2 download.file(loc_fichier, "titanic.RData")
3 load("titanic.RData")
4 base = base[!is.na(base$Age),]
```

On consider two variables, the age x (the continuous one) and the survivor indicator y (the qualitative one)

```
1 X = base$Age
2 Y = base$Survived
```

It looks like the age might be a valid explanatory variable in the logistic regression,

```
1 summary(glm(Survived~Age, data=base, family=binomial))
2
3 Coefficients:
4             Estimate Std. Error z value Pr(>|z|)
5 (Intercept) -0.05672    0.17358  -0.327   0.7438
6 Age         -0.01096    0.00533  -2.057   0.0397 *
7 ---
8 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
9
10 (Dispersion parameter for binomial family taken to be 1)
11
12 Null deviance: 964.52 on 713 degrees of freedom
13 Residual deviance: 960.23 on 712 degrees of freedom
14 AIC: 964.23
```

The significance test here has a p-value just below 4%. Actually, one can relate it with the value of the deviance (the null deviance and the residual deviance). Recall that $D = 2 \log \frac{\hat{L}}{\hat{L}_0}$ while $D_0 = 2 \log \frac{\hat{L}}{\bar{L}}$. Under the assumption that x is worthless, $D_0 - D$ tends to a χ^2 distribution with 1 degree of freedom. And we can compute the p-value of that likelihood ratio test,

```
1 1-pchisq(964.52-960.23,1)
2 [1] 0.03833717
```

(which is consistent with a Gaussian test). But if we consider a nonlinear transformation

```
1 summary(glm(Survived~bs(Age), data=base, family=binomial))
2
3 Coefficients:
4             Estimate Std. Error z value Pr(>|z|)
5 (Intercept)   0.8648    0.3460   2.500 0.012433 *
6 bs(Age)1     -3.6772    1.0458  -3.516 0.000438 ***
7 bs(Age)2      1.7430    1.1068   1.575 0.115299
8 bs(Age)3     -3.9251    1.4544  -2.699 0.006961 **
9 ---
10 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
11
```

```

12 (Dispersion parameter for binomial family taken to be 1)
13
14 Null deviance: 964.52 on 713 degrees of freedom
15 Residual deviance: 948.69 on 710 degrees of freedom

```

which seems to be “more significant”

```

1 1-pchisq(964.52-948.69,3)
2 [1] 0.001228712

```

So it looks like the variable x is interesting here.

To visualize the non-null correlation, one can consider the condition distribution of x given y=1, and compare it with the condition distribution of x given y=0,

```

1 ks.test(X[Y==0],X[Y==1])
2
3      Two-sample Kolmogorov-Smirnov test
4
5 data:  X[Y == 0] and X[Y == 1]
6 D = 0.088777, p-value = 0.1324
7 alternative hypothesis: two-sided

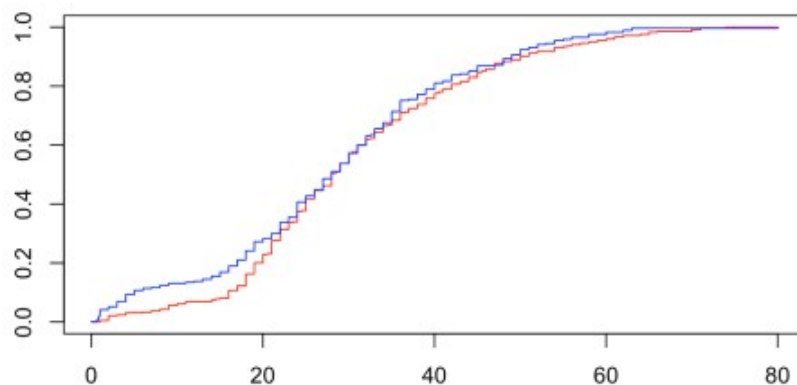
```

i.e. with a p-value above 10%, the two distributions are not significantly different.

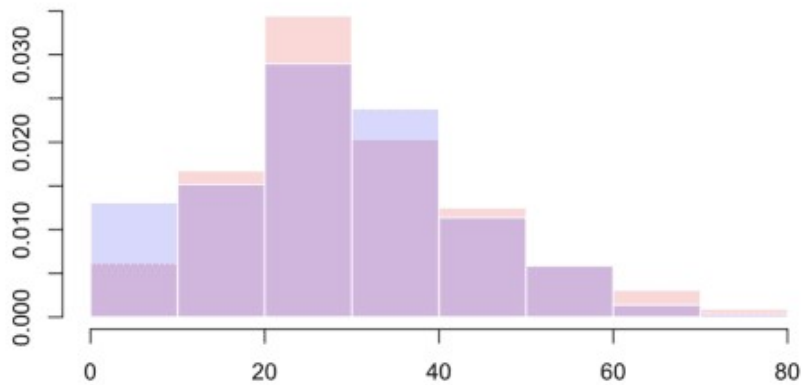
```

1 F0 = function(x) mean(X[Y==0]<=x)
2 F1 = function(x) mean(X[Y==1]<=x)
3 vx = seq(0,80,by=.1)
4 vy0 = Vectorize(F0)(vx)
5 vy1 = Vectorize(F1)(vx)
6 plot(vx,vy0,col="red",type="s")
7 lines(vx,vy1,col="blue",type="s")

```



(we can also look at the density, but it looks like that there is not much to see)



An alternative is discretize variable x and to use Pearson's independence test,

```

1 k=5
2 LV = quantile(X, (0:k)/k)
3 LV[1] = 0
4 Xc = cut(X, LV)
5 table(Xc, Y)
6
7      Y
7 Xc    0  1
8 (0,19] 85 79
9 (19,25] 92 45
10 (25,31.8] 77 50
11 (31.8,41] 81 63
12 (41,80] 89 53
13 chisq.test(table(Xc, Y))
14
15      Pearson's Chi-squared test
16
17 data:  table(Xc, Y)
18 X-squared = 8.6155, df = 4, p-value = 0.07146

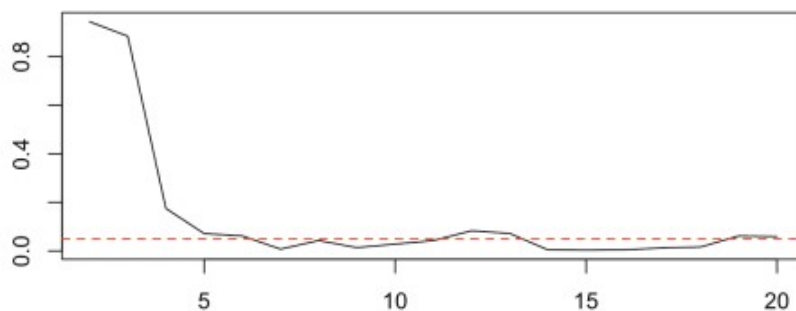
```

The p-value is here 7%, with five categories for the age. And actually, we can compare the p-value

```

1 pvalue = function(k=5) {
2   LV = quantile(X, (0:k)/k)
3   LV[1] = 0
4   Xc = cut(X, LV)
5   chisq.test(table(Xc, Y))$p.value}
6 vk = 2:20
7 vp = Vectorize(pvalue)(vk)
8 plot(vk, vp, type="l")
9 abline(h=.05, col="red", lty=2)

```



which gives a p-value close to 5%, as soon as we have enough categories....