《统计学习》慕课

XXX

## 1 1

利用 R 中 DAAG 包中自带的 anesthetic 数据集建立 Logistic 回归模型。其中，取麻醉剂浓度 (conc) 为自变量 x，患者是否保持静止（nomove）为因变量 y，y 取 1 时表示患者静止，y 取 0 时表示患者有移动。利用 summary 函数对回归结果进行分析。需要上传程序代码。

```
library(DAAG)
head(anesthetic)
```

```
##   move conc   logconc nomove
## 1    0  1.0 0.0000000      1
## 2    1  1.2 0.1823216      0
## 3    0  1.4 0.3364722      1
## 4    1  1.4 0.3364722      0
## 5    1  1.2 0.1823216      0
## 6    0  2.5 0.9162907      1
```

```
cdplot(factor(nomove)~conc,data=anesthetic,main='条件密度图',ylab='病人移动',xlab='麻醉剂量')
```

条件密度图
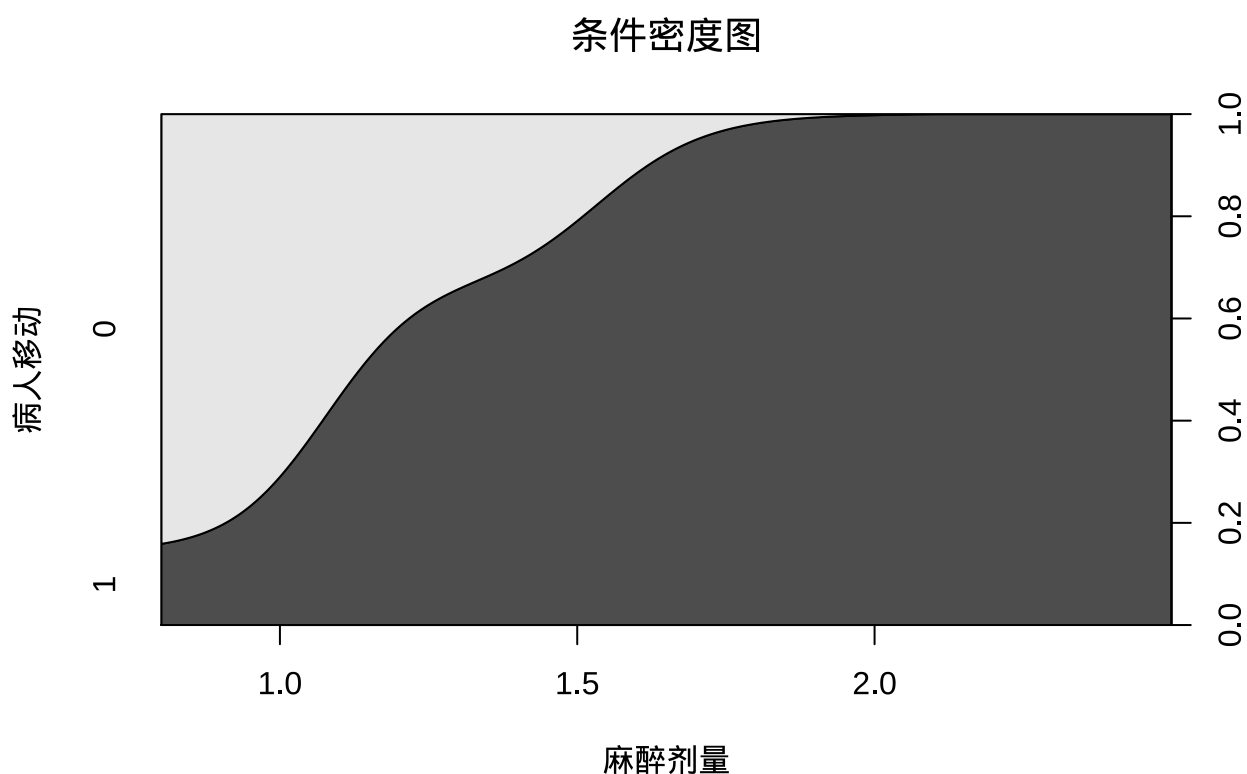
从图中可见，随着麻醉剂量加大，手术病人倾向于静止。下面利用 logistic 回归进行建模。

```
anes1=glm(nomove~conc,family=binomial(link='logit'),data=anesthetic)
summary(anes1)
```

```
## 
## Call:
## glm(formula = nomove ~ conc, family = binomial(link = "logit"),
##     data = anesthetic)
## 
## Deviance Residuals:
##     Min       1Q    Median       3Q       Max
## -1.76666  -0.74407  0.03413  0.68666  2.06900
## 
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -6.469      2.418   -2.675  0.00748 **
## conc           5.567      2.044    2.724  0.00645 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
```

```
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 41.455  on 29  degrees of freedom
## Residual deviance: 27.754  on 28  degrees of freedom
## AIC: 31.754
##
## Number of Fisher Scoring iterations: 5
```

得到 intercept 和 conc 的系数为-6.47 和 5.57，由此可见麻醉剂量超过 1.16(6.47/5.57) 时，病人静止概率超过 50%。

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2 2

使用 R 中的 iris 数据集，利用 Kmeans 算法对其进行聚类，选择聚类簇数 k=3，并对聚类结果进行简单的分析和说明。需要上传程序代码。（备注：可以参考 11.6 节课程内容）

```
library(factoextra)
newiris<-iris
newiris$Species<-NULL# 对训练数据去掉分类标记，如果不去掉因为有这类无法聚类的文本，会报错
iris1<-kmeans(newiris,3)# 分类模型训练
fitted(iris1)# 查看具体分类情况
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1     5.175758    3.624242     1.472727   0.2727273
## 2     4.738095    2.904762     1.790476   0.3523810
## 2     4.738095    2.904762     1.790476   0.3523810
## 2     4.738095    2.904762     1.790476   0.3523810
## 1     5.175758    3.624242     1.472727   0.2727273
## 1     5.175758    3.624242     1.472727   0.2727273
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```

```r
table(iris$Species,iris1$cluster)# 查看分类概括
```

```
##
##                 1   2   3
##   setosa       33  17   0
##   versicolor    0   4  46
##   virginica     0   0  50
```

```r
# 聚类结果可视化
plot(newiris[c("Sepal.Length", "Sepal.Width")], col = iris1$cluster, pch = as.integer(iris$Species
points(iris1$centers[,c("Sepal.Length", "Sepal.Width")], col = 1:3, pch = 8, cex=2)# 标记聚类中心
```
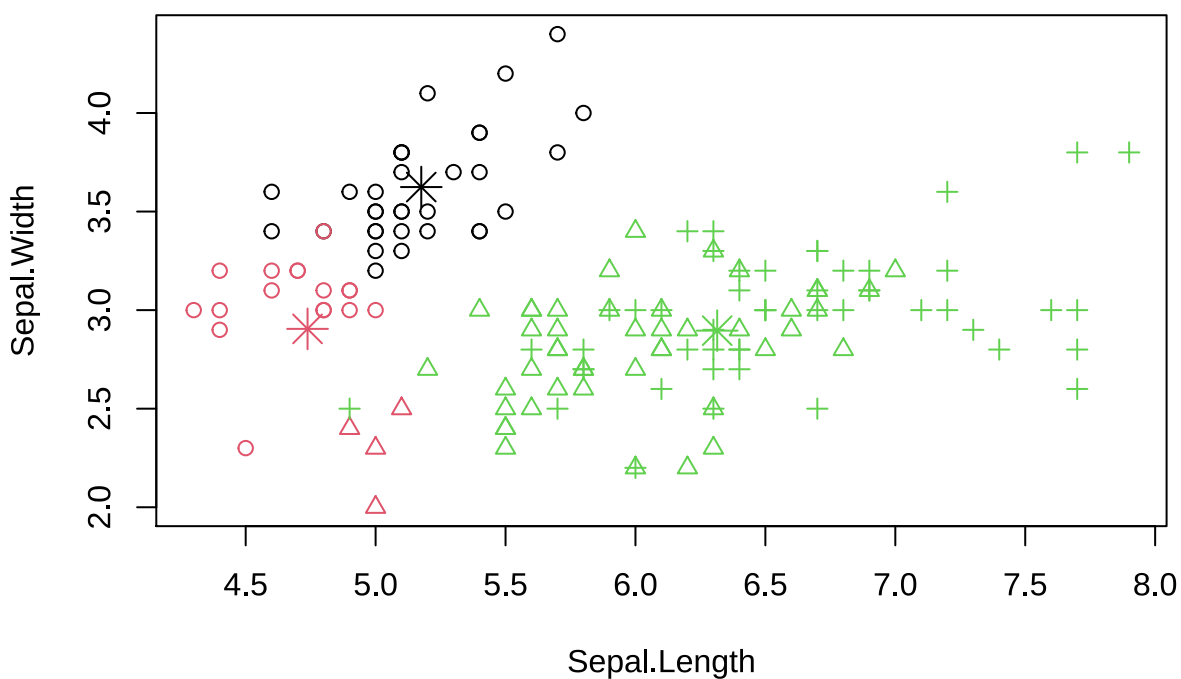
从输出结果看，setosa 花成功聚为 1 类（图中左上角的红 o）；而 versicolor 花和 virginica 有 16 个分错交叉，但主体部分区分的还比较明显。