

## Códigos em R

```
#exemplo 1:
# x = dap
# y = altura
x<- c(5.9, 6.3, 7.0, 9.4, 12.0,
      12.5, 15.4, 17.0, 20.0, 23.0)
y<- c(8.1, 9.2, 8.7, 12.7, 13.2,
      12.4, 15.7, 17.0, 18.9, 20.1)
#diagrama de dispersao
plot(y ~ x, xlab="DAP",
      ylab="Altura")
# correlação
cor(y,x)

#ajuste da reta
mod1<- lm(y ~ x)
summary(mod1)
plot(y ~ x, xlab="DAP",
      ylab="Altura")
curve(coef(mod1)[1]+coef(mod1)[2]*x,x, add=T,
      lwd=2, col=2)
# diagnostico
plot(rstandard(mod1) ~ predict(mod1), ylim=c(-2,2),
      xlab="Valores preditos", ylab="Resíduos Padronizados")
abline(h=0)
plot(rstandard(mod1) ~ x, ylim=c(-2,2),
      xlab="DAP", ylab="Resíduos Padronizados")
abline(h=0)
```

```

# plantas
Ciclo<- c("Tardio", "Precoce")
Viresc<- c("Normal", "Virescente")
(plantas<- matrix(c(3470, 1030, 910, 290),
                  ncol=2, nrow=2))
colnames(plantas)<- Viresc
rownames(plantas)<- Ciclo
plantas
barplot(plantas, legend=T)
barplot(plantas, legend=T, beside=T)

```

```

plantas_col<- matrix(c(plantas[,1]/sum(plantas[,1])*100,
                      plantas[,2]/sum(plantas[,2])*100),
                    ncol=2, nrow=2)
colnames(plantas_col)<- Viresc
rownames(plantas_col)<- Ciclo
barplot(plantas_col, legend=T, beside=T)

```

```

# insetos
Sexo<- c("Macho", "Femea")
Armadilha<- c("Alaranjada", "Amarela")
(insetos<- matrix(c(246, 17, 458, 32),
                  ncol=2, nrow=2, byrow=T))
colnames(insetos)<- Sexo
rownames(insetos)<- Armadilha
insetos
barplot(insetos, legend=T)
barplot(insetos, legend=T, beside=T)
barplot(t(insetos), legend=T, beside=T)

```

```

# aves
(aves<- matrix(c(30, 20, 9,
                13, 22, 26),
              ncol=3, nrow=2, byrow=T))
colnames(aves)<-c("Arvores", "Arbusto", "Chao")
rownames(aves)<-c("Primavera", "Outono")
aves
aves2<- aves
aves2[1,]<- aves[1,]/sum(aves[1,])*100
aves2[2,]<- aves[2,]/sum(aves[2,])*100
aves2

```

```

barplot(aves2, legend=T, beside=T)
barplot(t(aves2), beside=T, legend=T)
chisq.test(aves)
(CCP<- sqrt(chisq.test(aves)$statistic/
(chisq.test(aves)$statistic+sum(aves))))
CCP/sqrt((2-1)/2)

```

```

Floresta<- rep(c("A", "B"), each=13)
diametro<- c(16, 50, 13, 8, 5,
            77, 93, 27, 57, 28, 24, 16, 49,
            38, 43, 32, 18, 47,
            33, 38, 27, 50, 34, 34, 31, 28)
require(lattice)
dotplot(diametro ~ Floresta, xlab="Floresta",
        ylab="Diâmetro")

```

```
progenie<- rep(c("A", "B", "C", "D", "E"),
              times=6)
volume<- c(212, 108, 63, 175, 133,
           206, 194, 77, 239, 106,
           224, 163, 100, 100, 185,
           289, 111, 99, 104, 136,
           324, 236, 68, 256, 147,
           219, 146, 76, 267, 210)
dotplot(volume ~ progenie, xlab="Progênio",
        ylab="Volume de madeira")
boxplot(volume ~ progenie, xlab="Progênio",
        ylab="Volume de madeira")
```