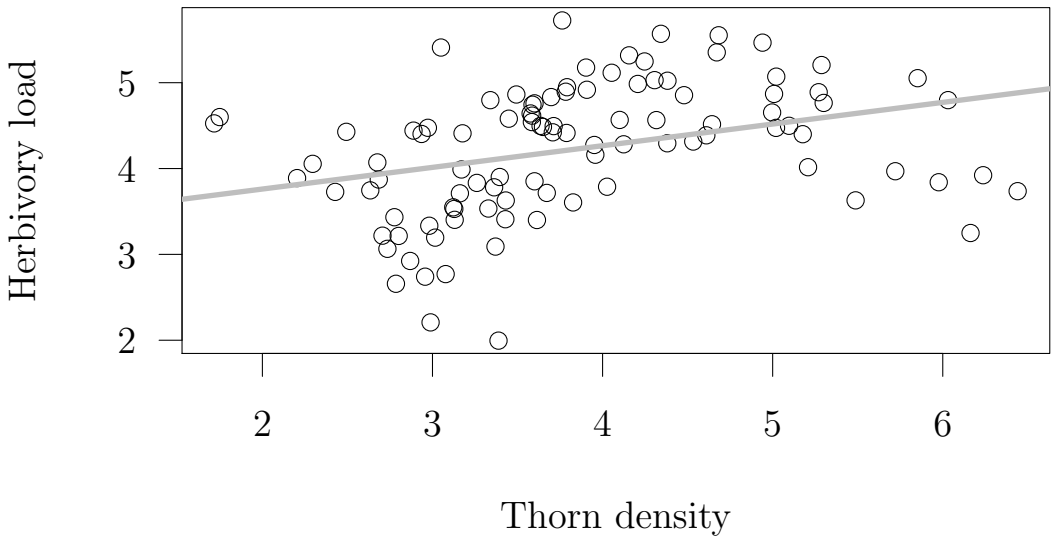
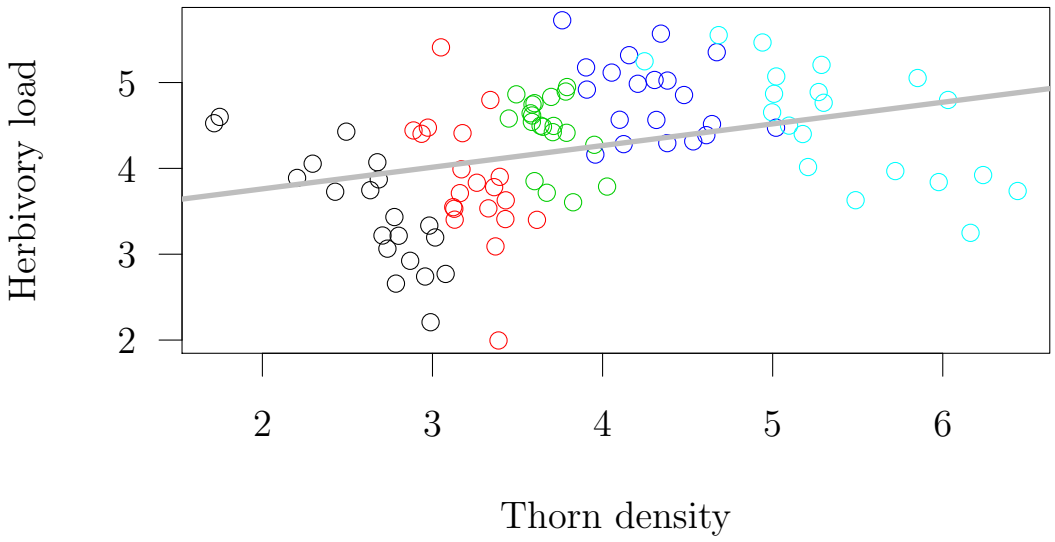
```
library(lme4)

## Loading required package:  Matrix

thorns <- read.table(file = "thorndata.txt", header=TRUE)
thornLMM <- lmer(response ~ predictor + (1|block), data = thorns)
setpar <- function()
{
par(las=1, cex=1.2)
}
```

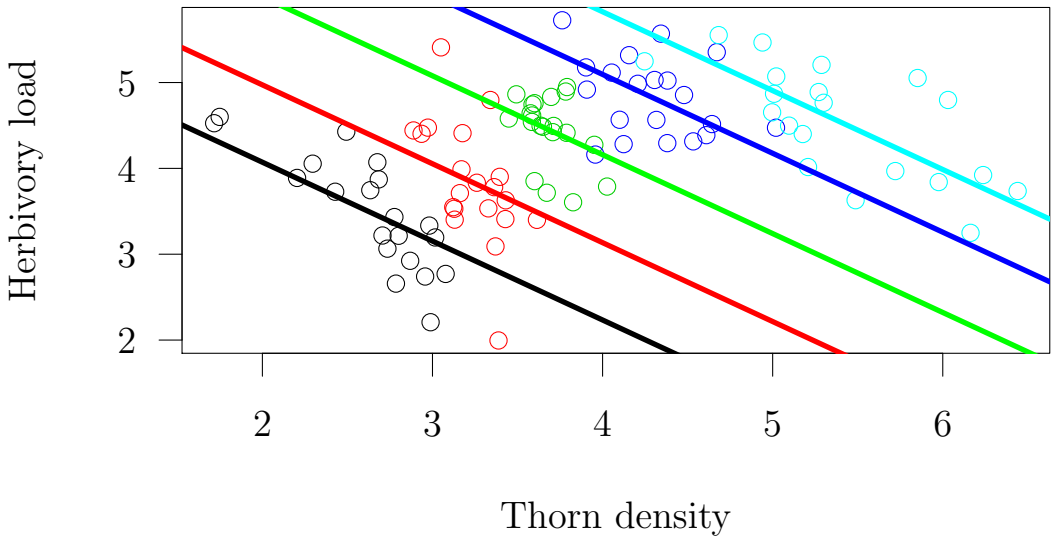
```
setpar()
plot(thorns$response, x=thorns$predictor, ylab = "Herbivory load", xlab= "Thorn densi
abline(lm(response~ predictor, data=thorns), lwd=5, col="gray")#this is a shortcut t
```



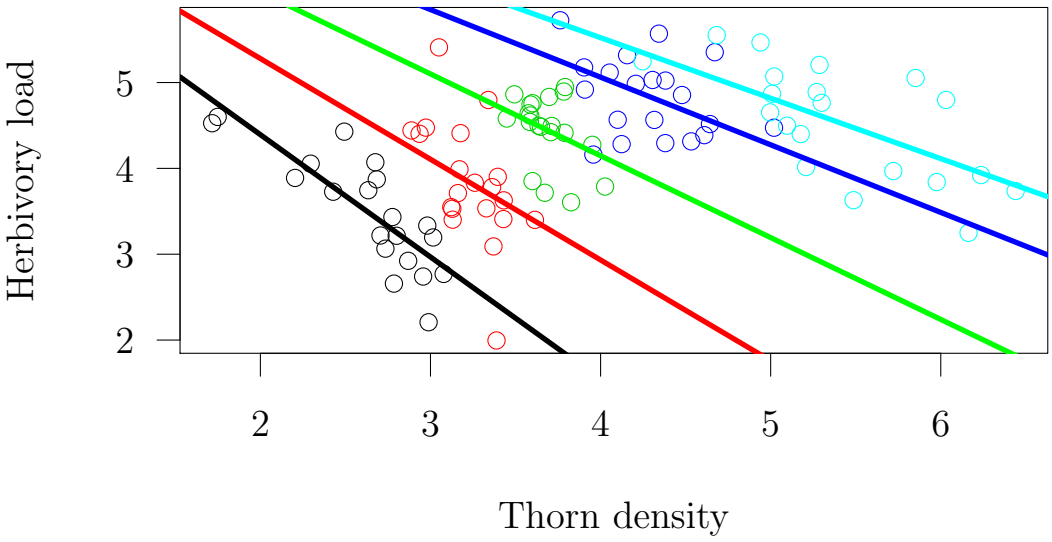

```
setpar()
plot(thorns$predictor, thorns$response, col=thorns$block, ylab = "Herbivory load", xl
abline(lm(response~ predictor, data=thorns), lwd=5, col="gray")
```




```
setpar()
plot(thorns$predictor, thorns$response, col=thorns$block, ylab = "Herbivory load", xl
slp <- fixef(thornLMM)[2]
inter <- fixef(thornLMM)[1]
re <- ranef(thornLMM)$block[,1]

abline(a = inter+re[1], b=slp, lwd=5)
abline(a = inter+re[2], b=slp, lwd=5, col="red")
abline(a = inter+re[3], b=slp, lwd=5, col="green")
abline(a = inter+re[4], b=slp, lwd=5, col="blue")
abline(a = inter+re[5], b=slp, lwd=5, col="cyan")
```




```
setpar()
plot(thorns$predictor, thorns$response, col=thorns$block, ylab = "Herbivory load", xl
thornLMM2 <- lmer(response ~ 1 + predictor + (1+predictor|block), data=thorns)

## singular fit

slp <- fixef(thornLMM2)[2]
inter <- fixef(thornLMM2)[1]
reint <- ranef(thornLMM2)$block[,1]
resl <- ranef(thornLMM2)$block[,2]

abline(a = inter+reint[1], b=slp+resl[1], lwd=5)
abline(a = inter+reint[2], b=slp+resl[2], lwd=5, col="red")
abline(a = inter+reint[3], b=slp+resl[3], lwd=5, col="green")
abline(a = inter+reint[4], b=slp+resl[4], lwd=5, col="blue")
abline(a = inter+reint[5], b=slp+resl[5], lwd=5, col="cyan")
```


Herbivory load
5
4
3
2
2
3
4
5
6
Thorn density