

tulips

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tulips

reference: McElreath, Statistical Rethinking, chap 7, pp.209-239

```
library(rethinking)
library(ggplot2)
```

Tulips

data

```
## R code 7.18
data(tulips)
d <- tulips
str(d)
```

```
## 'data.frame': 27 obs. of 4 variables:
## $ bed : Factor w/ 3 levels "a","b","c": 1 1 1 1 1 1 1 1 1 2 ...
## $ water : int 1 1 1 2 2 2 3 3 3 1 ...
## $ shade : int 1 2 3 1 2 3 1 2 3 1 ...
## $ blooms: num 0 0 111 183.5 59.2 ...
```

map

```
# ## R code 7.19
# m7.6 <- map(
#   alist(
#     blooms ~ dnorm( mu , sigma ) ,
#     mu <- a + bW*water + bS*shade ,
#     a ~ dnorm( 0 , 100 ) ,
#     bW ~ dnorm( 0 , 100 ) ,
#     bS ~ dnorm( 0 , 100 ) ,
#     sigma ~ dunif( 0 , 100 )
#   ) ,
#   data=d )
# m7.7 <- map(
#   alist(
#     blooms ~ dnorm( mu , sigma ) ,
#     mu <- a + bW*water + bS*shade + bWS*water*shade ,
#     a ~ dnorm( 0 , 100 ) ,
#     bW ~ dnorm( 0 , 100 ) ,
#     bS ~ dnorm( 0 , 100 ) ,
#     bWS ~ dnorm( 0 , 100 ) ,
#     sigma ~ dunif( 0 , 100 )
```

```
# ),  
# data=d )
```

use Nelder-Mead

```
## R code 7.20  
m7.6 <- map(  
  alist(  
    blooms ~ dnorm( mu , sigma ) ,  
    mu <- a + bW*water + bS*shade ,  
    a ~ dnorm( 0 , 100 ) ,  
    bW ~ dnorm( 0 , 100 ) ,  
    bS ~ dnorm( 0 , 100 ) ,  
    sigma ~ dunif( 0 , 100 )  
  ) ,  
  data=d ,  
  method="Nelder-Mead" ,  
  control=list(maxit=1e4) )  
m7.7 <- map(  
  alist(  
    blooms ~ dnorm( mu , sigma ) ,  
    mu <- a + bW*water + bS*shade + bWS*water*shade ,  
    a ~ dnorm( 0 , 100 ) ,  
    bW ~ dnorm( 0 , 100 ) ,  
    bS ~ dnorm( 0 , 100 ) ,  
    bWS ~ dnorm( 0 , 100 ) ,  
    sigma ~ dunif( 0 , 100 )  
  ) ,  
  data=d ,  
  method="Nelder-Mead" ,  
  control=list(maxit=1e4) )
```

```
## R code 7.21  
coefstab(m7.6,m7.7)
```

```
##      m7.6    m7.7  
## a      53.50   95.46  
## bW     76.25   52.28  
## bS    -38.84  -44.09  
## sigma  57.41   48.24  
## bWS      NA    3.91  
## nobs    27     27
```

```
## R code 7.22  
compare( m7.6 , m7.7 )
```

```
##      WAIC pWAIC dWAIC weight    SE dSE  
## m7.6 306.1   5.4     0      1  9.03  NA  
## m7.7 317.1   9.1    11     0 14.16  6.74
```

center the data

```
## R code 7.23
d$shade.c <- d$shade - mean(d$shade)
d$water.c <- d$water - mean(d$water)

## R code 7.24
m7.8 <- map(
  alist(
    blooms ~ dnorm( mu , sigma ) ,
    mu <- a + bW*water.c + bS*shade.c ,
    a ~ dnorm( 130 , 100 ) ,
    bW ~ dnorm( 0 , 100 ) ,
    bS ~ dnorm( 0 , 100 ) ,
    sigma ~ dunif( 0 , 100 )
  ) ,
  data=d ,
  start=list(a=mean(d$blooms),bW=0,bS=0,sigma=sd(d$blooms)) )
m7.9 <- map(
  alist(
    blooms ~ dnorm( mu , sigma ) ,
    mu <- a + bW*water.c + bS*shade.c + bWS*water.c*shade.c ,
    a ~ dnorm( 130 , 100 ) ,
    bW ~ dnorm( 0 , 100 ) ,
    bS ~ dnorm( 0 , 100 ) ,
    bWS ~ dnorm( 0 , 100 ) ,
    sigma ~ dunif( 0 , 100 )
  ) ,
  data=d ,
  start=list(a=mean(d$blooms),bW=0,bS=0,bWS=0,sigma=sd(d$blooms)) )
coefTAB(m7.8,m7.9)
```

```
##      m7.8    m7.9
## a      129.00  129.01
## bW      74.22   74.96
## bS     -40.74  -41.14
## sigma   57.35   45.22
## bWS      NA   -51.87
## nobs     27     27
```

interpret parameters

```
## R code 7.25
k <- coef(m7.7)
k[1] + k[2]*2 + k[3]*2 + k[4]*2*2
```

```
##      a
## 127.4667
```

```
## R code 7.26
k <- coef(m7.9)
k[1] + k[2]*0 + k[3]*0 + k[4]*0*0
```

```
##      a
```

```
## 129.008
```

```
## R code 7.27
```

```
precis(m7.9)
```

```
##           Mean StdDev  5.5%  94.5%
## a      129.01   8.67 115.15 142.87
## bW      74.96  10.60  58.02  91.90
## bS     -41.14  10.60 -58.08 -24.20
## bWS    -51.87  12.95 -72.57 -31.18
## sigma  45.22   6.15  35.39  55.06
```

tryptich

```
## R code 7.28
```

```
# make a plot window with three panels in a single row
```

```
par(mfrow=c(1,3)) # 1 row, 3 columns
```

```
# loop over values of water.c and plot predictions
```

```
shade.seq <- -1:1
```

```
for ( w in -1:1 ) {
```

```
  dt <- d[d$water.c==w,]
```

```
  plot( blooms ~ shade.c , data=dt , col=rangi2 ,  
        main=paste("water.c =",w) , xaxp=c(-1,1,2) , ylim=c(0,362) ,  
        xlab="shade (centered)" )
```

```
  mu <- link( m7.9 , data=data.frame(water.c=w,shade.c=shade.seq) )
```

```
  mu.mean <- apply( mu , 2 , mean )
```

```
  mu.PI <- apply( mu , 2 , PI , prob=0.97 )
```

```
  lines( shade.seq , mu.mean )
```

```
  lines( shade.seq , mu.PI[1,] , lty=2 )
```

```
  lines( shade.seq , mu.PI[2,] , lty=2 )
```

```
}
```

```
## [ 100 / 1000 ]
```

```
[ 200 / 1000 ]
```

```
[ 300 / 1000 ]
```

```
[ 400 / 1000 ]
```

```
[ 500 / 1000 ]
```

```
[ 600 / 1000 ]
```

```
[ 700 / 1000 ]
```

```
[ 800 / 1000 ]
```

```
[ 900 / 1000 ]
```

```
[ 1000 / 1000 ]
```

```
## [ 100 / 1000 ]
```

```
[ 200 / 1000 ]
```

```
[ 300 / 1000 ]
```

```
[ 400 / 1000 ]
```

```
[ 500 / 1000 ]
```

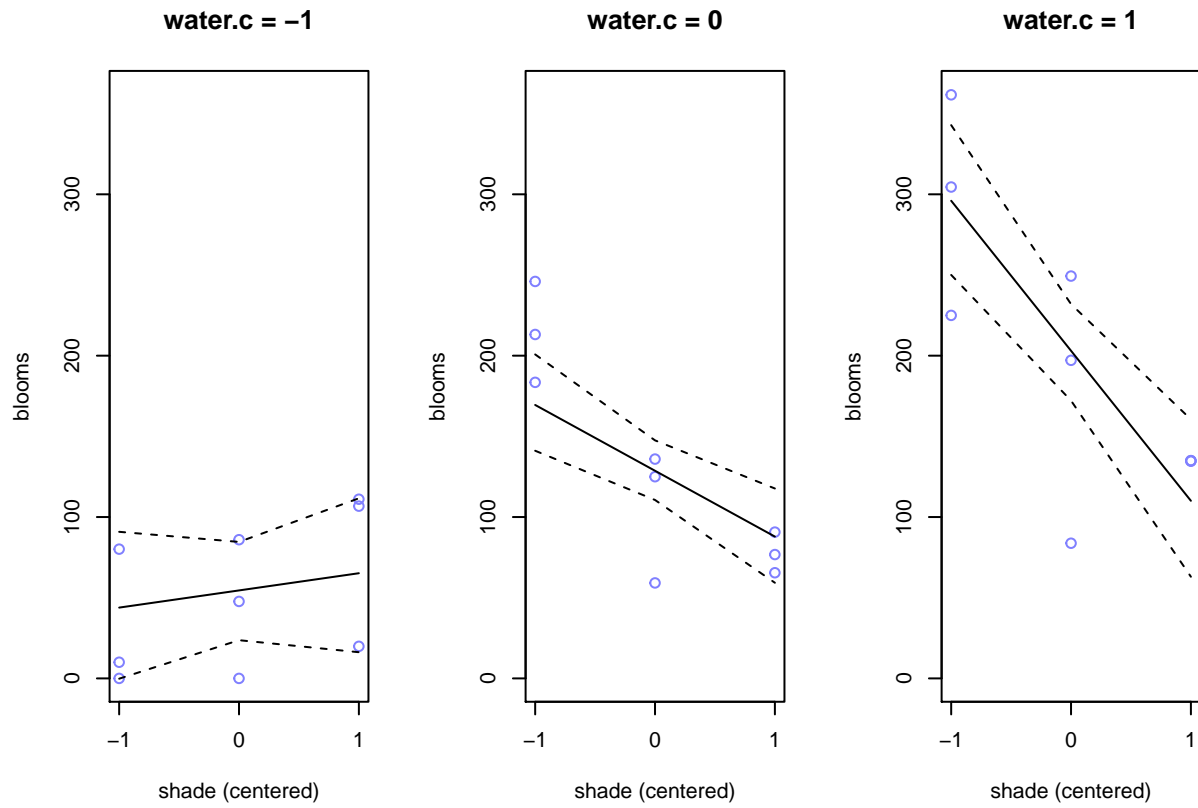
```
[ 600 / 1000 ]
```

```
[ 700 / 1000 ]
```

```
[ 800 / 1000 ]
```

```
[ 900 / 1000 ]
```

```
[ 1000 / 1000 ]
```



```
## [ 100 / 1000 ]
[ 200 / 1000 ]
[ 300 / 1000 ]
[ 400 / 1000 ]
[ 500 / 1000 ]
[ 600 / 1000 ]
[ 700 / 1000 ]
[ 800 / 1000 ]
[ 900 / 1000 ]
[ 1000 / 1000 ]
```