

# plants

Chris Parrish

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plants

reference:

- McElreath, Statistical Rethinking, chap 5, pp.119-164

## plants

### Post-treatment bias

```
library(rethinking)
library(ggplot2)
library(cowplot)
theme_set(theme_gray())
```

### data

```
## R code 5.41
# number of plants
N <- 100

# simulate initial heights
h0 <- rnorm(N,10,2)

# assign treatments and simulate fungus and growth
treatment <- rep( 0:1 , each=N/2 )
fungus <- rbinom( N , size=1 , prob=0.5 - treatment*0.4 )
h1 <- h0 + rnorm(N, 5 - 3*fungus)

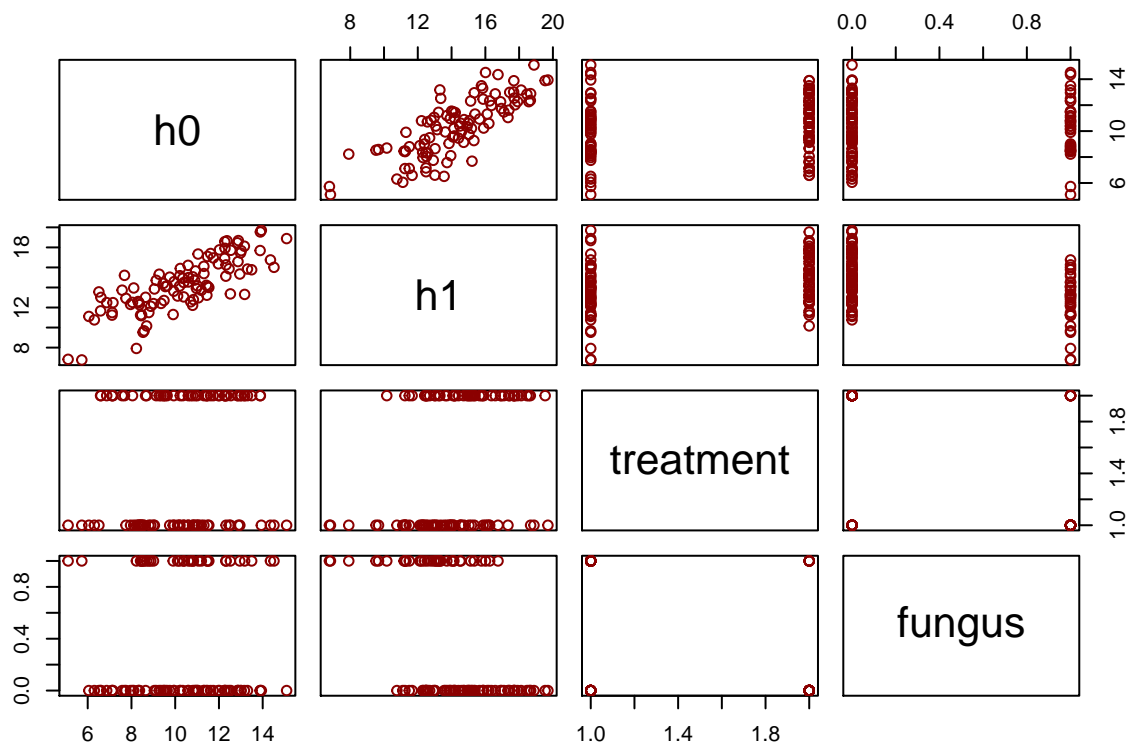
# compose a clean data frame
d <- data.frame( h0=h0 , h1=h1 , treatment=treatment , fungus=fungus )
```

## exploratory data analysis

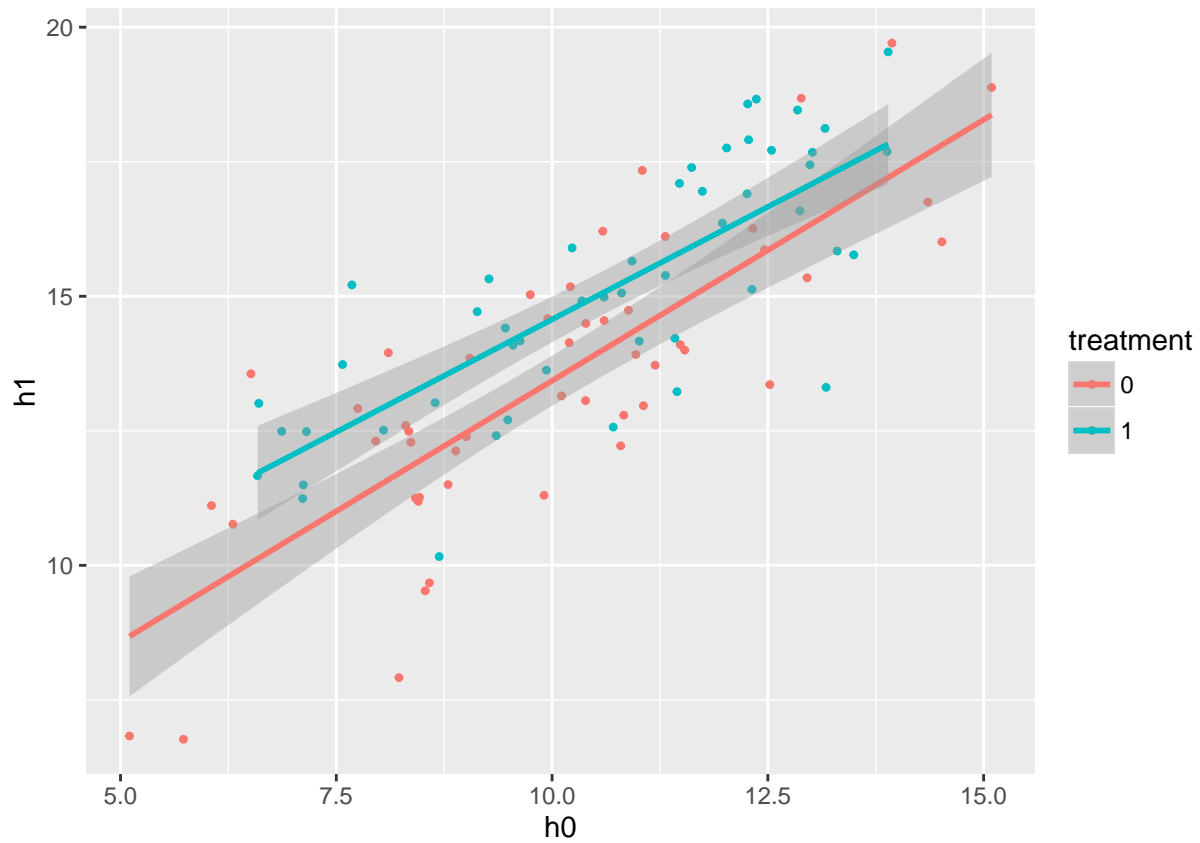
```
d2 <- d
d2$treatment <- factor(d2$treatment)
str(d2)
```

```
## 'data.frame': 100 obs. of 4 variables:
## $ h0 : num 11.54 13.94 8.8 5.1 8.37 ...
## $ h1 : num 14 19.7 11.5 6.83 12.29 ...
## $ treatment: Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
## $ fungus : int 1 0 1 1 0 1 0 1 1 1 ...
```

```
pairs(d2, col="darkred")
```



```
ggplot(d2, aes(h0, h1, color = treatment)) +
  geom_point(shape = 20) +
  geom_smooth(method = "lm")
```



## map

```
## R code 5.42
m5.13 <- map(
  alist(
    h1 ~ dnorm(mu,sigma),
    mu <- a + bh*h0 + bt*treatment + bf*fungus,
    a ~ dnorm(0,100),
    c(bh,bt,bf) ~ dnorm(0,10),
    sigma ~ dunif(0,10)
  ),
  data=d,
  start = list(a = 0))
precis(m5.13)
```

```
##      Mean StdDev  5.5% 94.5%
## a      5.30  0.50  4.50  6.10
## bh     0.96  0.05  0.89  1.04
## bt    -0.11  0.24 -0.49  0.27
## bf    -2.66  0.25 -3.05 -2.27
## sigma  1.03  0.07  0.91  1.14
```

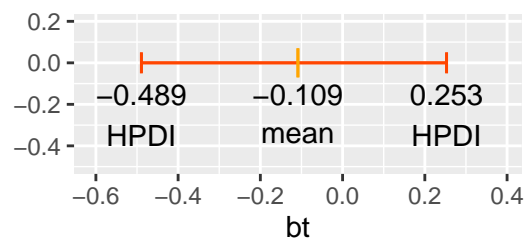
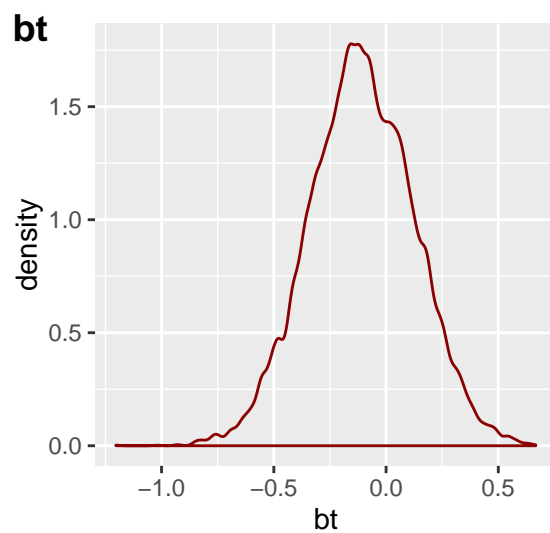
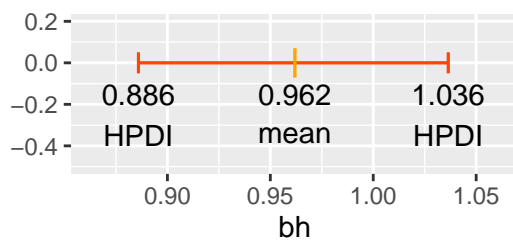
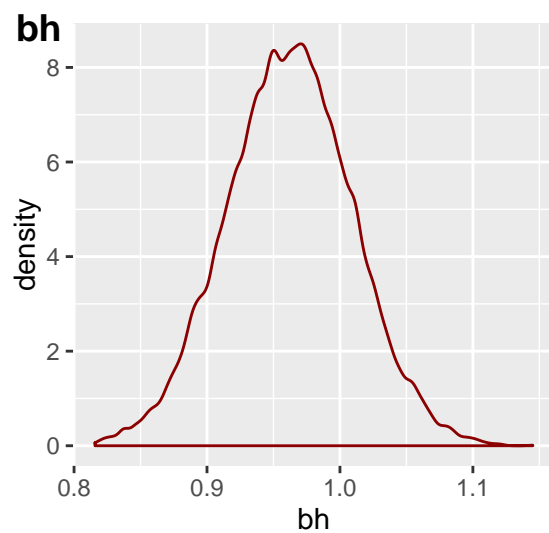
## parameter distributions

### plot parameter distributions

```
# extract samples
post <- extract.samples( m5.13 )
str(post)

## 'data.frame': 10000 obs. of 5 variables:
## $ a : num 5.2 4.9 4.94 4.66 5.38 ...
## $ bh : num 1.02 1.014 0.979 0.988 0.922 ...
## $ bt : num -0.8449 -0.2283 0.0113 0.2676 0.5442 ...
## $ bf : num -3.1 -2.55 -2.47 -1.96 -2.5 ...
## $ sigma: num 1.114 0.871 1.113 0.933 1.251 ...

# plot each parameter distribution
bh.plot <- parameter.dist(parameter = "bh", values = post$bh)
bt.plot <- parameter.dist(parameter = "bt", values = post$bt)
# display parameter distributions
plot_grid(bh.plot, bt.plot,
          labels=c("bh", "bt"), ncol = 2, nrow = 1)
```



## map

```
## R code 5.43
m5.14 <- map(
  alist(
    h1 ~ dnorm(mu, sigma),
```

```

      mu <- a + bh*h0 + bt*treatment,
      a ~ dnorm(0,100),
      c(bh,bt) ~ dnorm(0,10),
      sigma ~ dunif(0,10)
    ),
    data=d,
    start = list(a = 0))
precis(m5.14)

```

```

##      Mean StdDev 5.5% 94.5%
## a      4.35   0.72 3.20  5.51
## bh     0.91   0.07 0.80  1.02
## bt     1.09   0.31 0.61  1.58
## sigma 1.51   0.11 1.34  1.68

```

### plot parameter distributions

```

# extract samples
post <- extract.samples( m5.14 )
str(post)

## 'data.frame':   10000 obs. of  4 variables:
## $ a      : num  5.3 3.64 4.97 5.38 3.89 ...
## $ bh     : num  0.798 0.99 0.858 0.811 0.934 ...
## $ bt     : num  0.855 0.821 1.136 1.029 1.206 ...
## $ sigma : num  1.75 1.44 1.42 1.4 1.62 ...

# plot each parameter distribution
a.plot <- parameter.dist(parameter = "a", values = post$a)
bh.plot <- parameter.dist(parameter = "bh", values = post$bh)
bt.plot <- parameter.dist(parameter = "bt", values = post$bt)
sigma.plot <- parameter.dist(parameter = "sigma", values = post$sigma)
# display parameter distributions
plot_grid(a.plot, bh.plot, bt.plot, sigma.plot,
          labels=c("a", "bh", "bt", "sigma"), ncol = 2, nrow = 2)

```

