

Center data and define model

```
df0 = df
df0$age = scale(df0$age, scale = FALSE)
df0$toxin = scale(df0$toxin, scale = FALSE)
df0$size = scale(df0$size, scale = FALSE)
```

$$size_i \sim \text{Normal}(\mu_i, \sigma)$$

$$\mu_i = a + b \times \text{toxin}_i + c \times \text{age}_i$$

```
rt_fit = ulam(alist(size ~ normal(mu, sigma),
  mu <- a + b*toxin + c*age,
  a ~ normal(0, 0.3),
  b ~ normal(0, 1),
  c ~ normal(0, 1),
  sigma ~ exponential(1)),
  data = df0, chains = 4, cores = 4)
```

Model fit

$$size_i \sim Normal(\mu_i, \sigma)$$

$$\mu_i = a + b \times toxin_i + c \times age_i$$

```
> precis(rt_fit, prob = 0.95)
      mean   sd  2.5% 97.5% rhat ess_bulk
a      0.00 0.22 -0.43  0.45    1  1679.38
b     -0.90 0.35 -1.60 -0.22    1   821.89
c      0.46 0.14  0.18  0.74    1   791.07
sigma  5.38 0.27  4.87  5.93    1  1225.56

> plot(precis(rt_fit, prob = 0.95))
```

