Generalized Linear Madness

EES 5891-03

Bayesian Statistical Methods

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Generalized Linear Models and Beyond

Generalized Linear Models

- Linear Models:

$$y \sim \text{Normal}(\mu, \sigma)$$
$$\mu = \alpha + \sum_i \beta_i x_i$$

- Polynomial models become linear models

$$y \sim \text{Normal}(\mu, \sigma)$$
$$\mu = \alpha + \sum_i \beta_i x^i$$

  - transform:

$$\begin{aligned} x_1 &= x \\ x_2 &= x^2 \\ &\dots \end{aligned}$$
$$\mu = \alpha + \sum_i \beta_i x_i$$

- Generalized Linear Models (GLMs)

$$y \sim F(\mu)$$
$$\text{Link}(\mu) = \alpha + \sum_i \beta_i x_i$$

  - F could be Poisson, Binomial, etc.
  - Link could be logit, log, etc.
- Generalized Additive Models (GAMs)

$$y \sim F(\mu)$$
$$\mu = \alpha + \sum_i f_i(x)$$

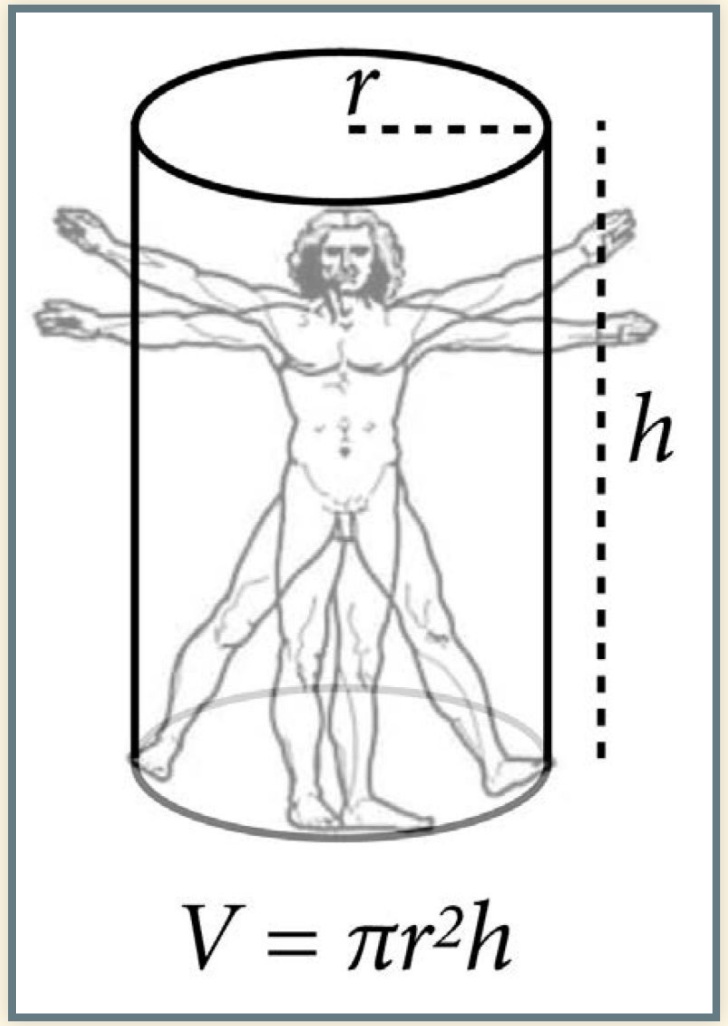
or

$$\mu = \alpha + \sum_i f_i(x_1, x_2, \dots)$$

Beyond Linearity

- Linear models are widely applicable
  - You can use them out of the box
  - `quap` and `ulam` automatically take a linear model specification (`alist`) and turn it into R or Stan code
- Scientific models
  - Model equations from scientific knowledge
  - They may not be linear
  - Often require custom (“bespoke”) programming
    - Stan programming language

Example: “Vitruvian Can”



Vitruvian Can Model

- Height and Weight data set (from Chapter 4)

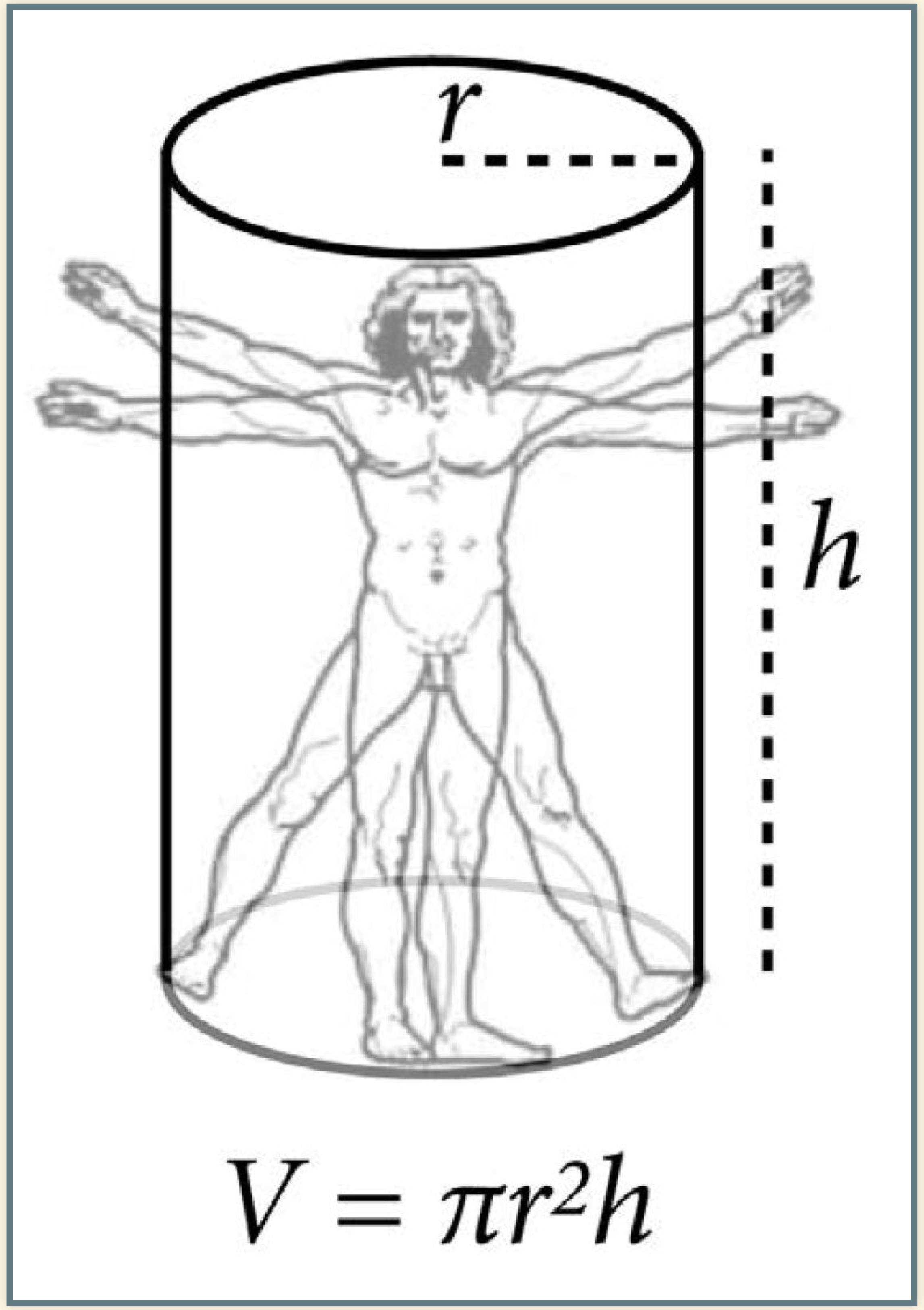
```
data(Howell1)
d <- Howell1

d <- d %>% mutate(h = height / mean(height),
                  w = weight / mean(weight))
```

- Model people as cylinders

$$\begin{aligned} V &= \pi r^2 h \\ r &= ph \\ V &= \pi (ph)^2 h = \pi p^2 h^3 \\ W &= kV = k\pi p^2 h^3 \end{aligned}$$

  - V = volume
  - W = weight

- This is clearly *not* a linear model



Statistical Model

$$
\begin{aligned}
W &\sim \text{Log-Normal}(\mu, \sigma) \\
\exp(\mu) &= \pi k p^2 h^3 \\
k &\sim \textit{some prior} \\
p &\sim \textit{some prior} \\
\sigma &\sim \text{Exponential}(1)
\end{aligned}
$$

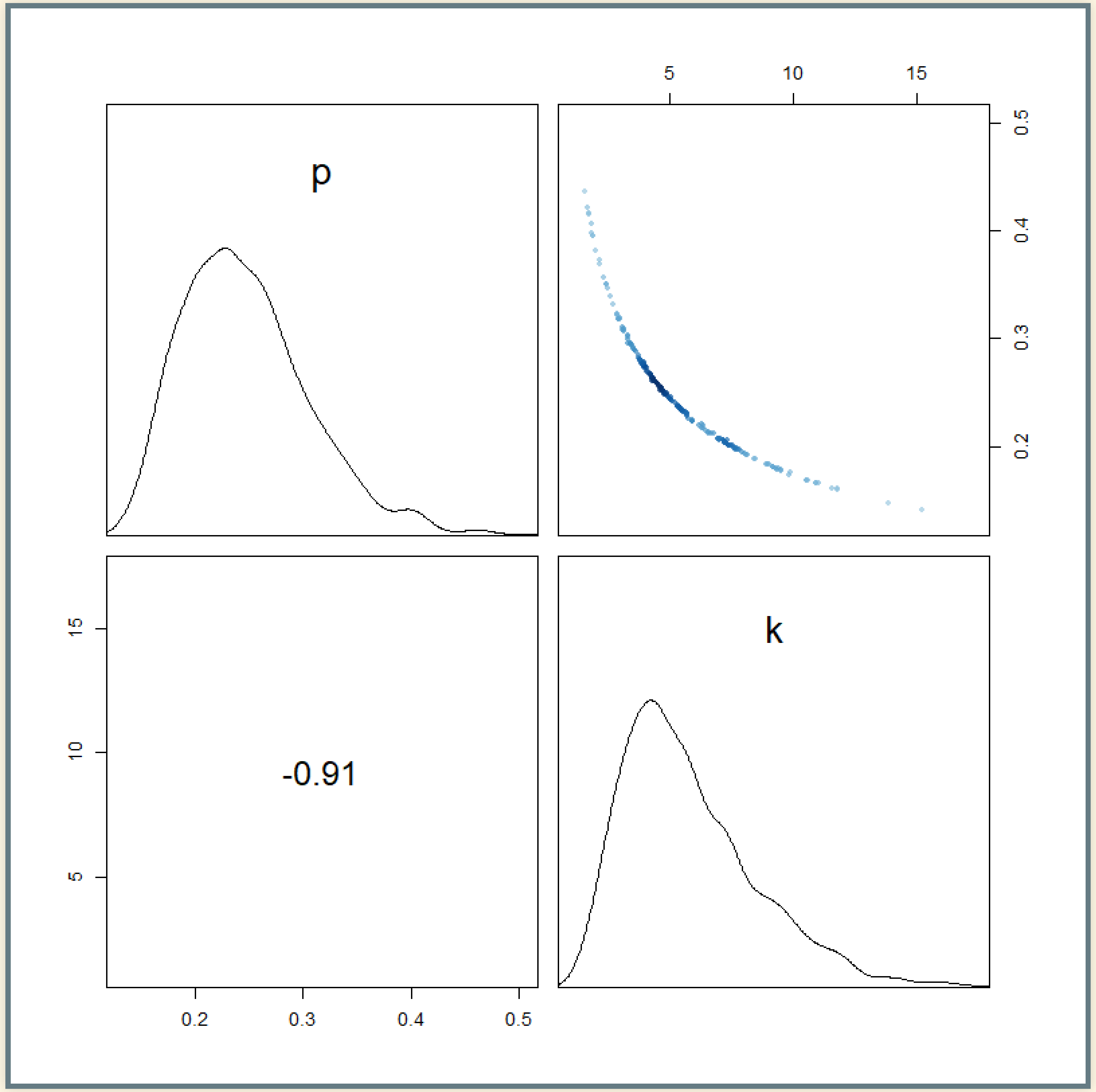
```
mdl <- ulam(
  alist(
    w ~ dlnorm(mu, sigma),
    exp(mu) <- 3.14159265 * k * p^2 * h^3,
    p ~ dbeta(2, 18),
    k ~ dexp(0.5),
    sigma ~ dexp(1)
  ), data = d, chains = 4, cores = 4
)
```

```
precis(mdl, digits = 2)
```

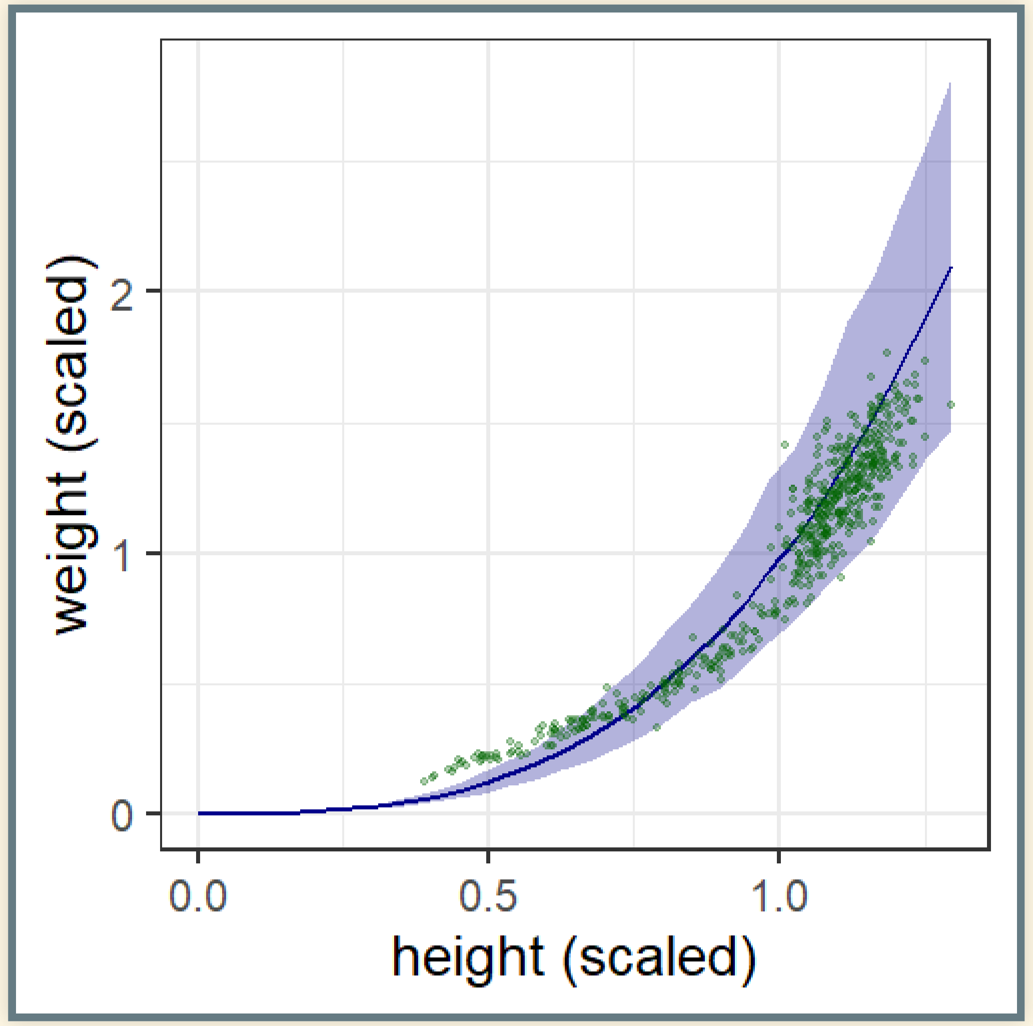
```
##        mean   sd 5.5% 94.5% n_eff Rhat4
## p      0.25 0.06 0.17  0.35   499  1.01
## k      5.81 2.70 2.47 10.92   570  1.00
## sigma  0.21 0.01 0.20  0.22   770  1.01
```

- Log-normal distribution ensures that $W > 0$
- μ is the mean of $\log(W)$
- Choosing priors
  - People are a lot less wide than tall, so
    - $r < h/2$
    - $p < 0.5$
    - Prior: $p \sim \text{Beta}(2, 18)$
      - Mean = $2/(2 + 18) = 0.1$
  - k is density (weight / volume)
    - Prior: $k \sim \text{Exponential}(0.5)$

Model Results



```
pairs(mdl, pars = c("p", "k"))
```



```
new_data <- tibble(h = seq(0, max(d$h), length.out = 30))
w_sim <- predicted_draws(mdl, new_data, value = "w_pred") %>%
  group_by(.row) %>%
  summarize(h = head(h, 1), w = mean(w_pred),
            PI = list(set_names(PI(w_pred), c("min", "max")))) %>%
  unnest_wider(PI)
ggplot(w_sim, aes(x = h, y = w)) +
  geom_line(size = 1, color = "darkblue") +
  geom_ribbon(aes(ymin = min, ymax = max), fill = "darkblue",
              alpha = 0.3) +
  geom_point(data = d, size = 1, alpha = 0.3, color = "darkgreen")
        +
  labs(x = "height (scaled)", y = "weight (scaled)")
```

Alternate Formulation

- Our model is

$$
\begin{aligned}
W &\sim \text{Log-Normal}(\mu, \sigma) \\
\exp(\mu) &= \pi k p^2 h^3
\end{aligned}
$$

- But we could also write it

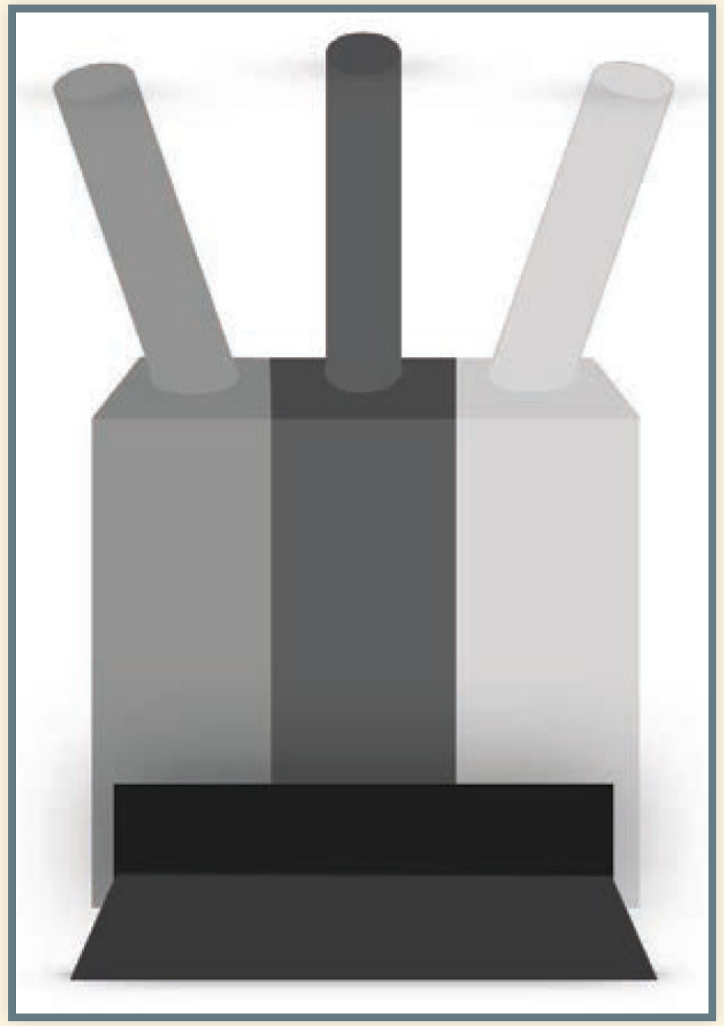
$$
\begin{aligned}
\log(W) &\sim \text{Normal}(\mu, \sigma) \\
\mu &= \log(\pi k p^2 h^3) \\
&= \log(\pi) + \log(k) + 2\log(p) + 3\log(h)
\end{aligned}
$$

which turns it into a linear regression.

Latent-Variable Models

Hidden Minds & Observed Behavior

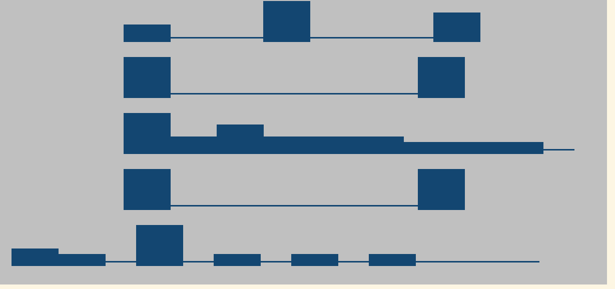
- Identifying children’s decision-making strategies
  - “Choice box” has three colored tubes
    - When a ball is dropped into a tube, a toy comes out of the box.
  - Experiment: Groups of 5 children
    - Subject sees four other children use the choice box
    - 3 children choose the same color (**majority color**)
    - 1 child chooses another color (**minority color**)
    - The third color is unused
  - Which color does the subject choose?



Data

```
data(Boxes)
precis(Boxes, digits = 2)
```

```
## 'data.frame': 629 obs. of 5 variables:
##                 mean   sd 5.5% 94.5%      histogram
## y               2.12 0.73    1     3
## gender          1.51 0.50    1     2
## age             8.03 2.50    5    13
## majority_first  0.48 0.50    0     1
## culture         3.75 1.96    1     8
```



- `y`: Which color did they choose?
  1. Unchosen color
  2. Majority color
  3. Minority color
- `majority_first`: Was the majority color chosen before the minority color?

```
table(Boxes$y) / length(Boxes$y)
```

```
##
##         1         2         3
## 0.2114467 0.4562798 0.3322734
```

- 45% of children chose the color that the majority of the four children chose.
- Does this mean that 45% of the children used a strategy of following the majority choice?
- Simulation:
  - Half of the children always choose the majority color (2).
  - The other half choose at random.

```
N <- 30
set.seed(163)
y1 <- sample(1:3, size = N/2, replace = TRUE)
y2 <- rep(2, N/2)
y <- sample(c(y1, y2))
table(y) / N
```

```
## y
##         1         2         3
## 0.1666667 0.6666667 0.1666667
```

  - 2/3 of the children choose the majority color, but only half of them are actually following the majority.

Making a Model

- We want to identify the strategies children are using,
  - We don't know what's going on in their heads.
  - We only know which colors they choose, not why.
- Possible strategies:
  1. Follow the majority
  2. Follow the minority
  3. Maverick (choose the unused color)
  4. Random choice
  5. Follow the first color chosen
- Each strategy has a *prior* for the choices (1, 2, or 3)
- Develop a posterior probability for each strategy

- The probability of choosing color y is

$$\Pr(y) = \sum_{s=1}^{5} p_s \Pr(y|s),$$

  where s indicates the strategy, p_s is the probability of using strategy s.
- **Simplex:** The probabilities of the 5 strategies form a vector $(p_1, p_2, p_3, p_4, p_5)$, where they add up to 1.
- **Dirichlet prior:** for $(p_1, p_2, p_3, p_4, p_5)$.

$$p \sim \text{Dirichlet}([4, 4, 4, 4, 4])$$

  The p's don't have to be the same, but each has the same probability to be larger or smaller
  - Larger numbers instead of 4 would raise the probability for all the p's being equal.

Coding the Model

$$y \sim \text{Categorical}(\theta)$$

$$\theta_j = \sum s = 1^5 p_s \text{Pr}(j|s) \quad \text{for } j = 1 \ldots 3$$

$$p \sim \text{Dirichlet}([4, 4, 4, 4, 4])$$

- This is a complicated model
  - Can't use `ulam` or `quap`
  - Code it directly in Stan

```
data("Boxes_model")
cat(Boxes_model)
```

```
##
## data{
##     int N;
##     int y[N];
##     int majority_first[N];
## }
## parameters{
##     simplex[5] p;
## }
## model{
##     vector[5] phi;
##
##     // prior
##     p ~ dirichlet( rep_vector(4,5) );
##
##     // probability of data
##     for ( i in 1:N ) {
##         if ( y[i]==2 ) phi[1]=1; else phi[1]=0; // majority
##         if ( y[i]==3 ) phi[2]=1; else phi[2]=0; // minority
##         if ( y[i]==1 ) phi[3]=1; else phi[3]=0; // maverick
##         phi[4]=1.0/3.0;                         // random
##         if ( majority_first[i]==1 )             // follow first
##             if ( y[i]==2 ) phi[5]=1; else phi[5]=0;
##         else
##             if ( y[i]==3 ) phi[5]=1; else phi[5]=0;
##
##         // compute log( p_s * Pr(y_i|s )
##         for ( j in 1:5 ) phi[j] = log(p[j]) + log(phi[j]);
##         // compute average log-probability of y_i
##         target += log_sum_exp( phi );
##     }
## }
```

Running the Model

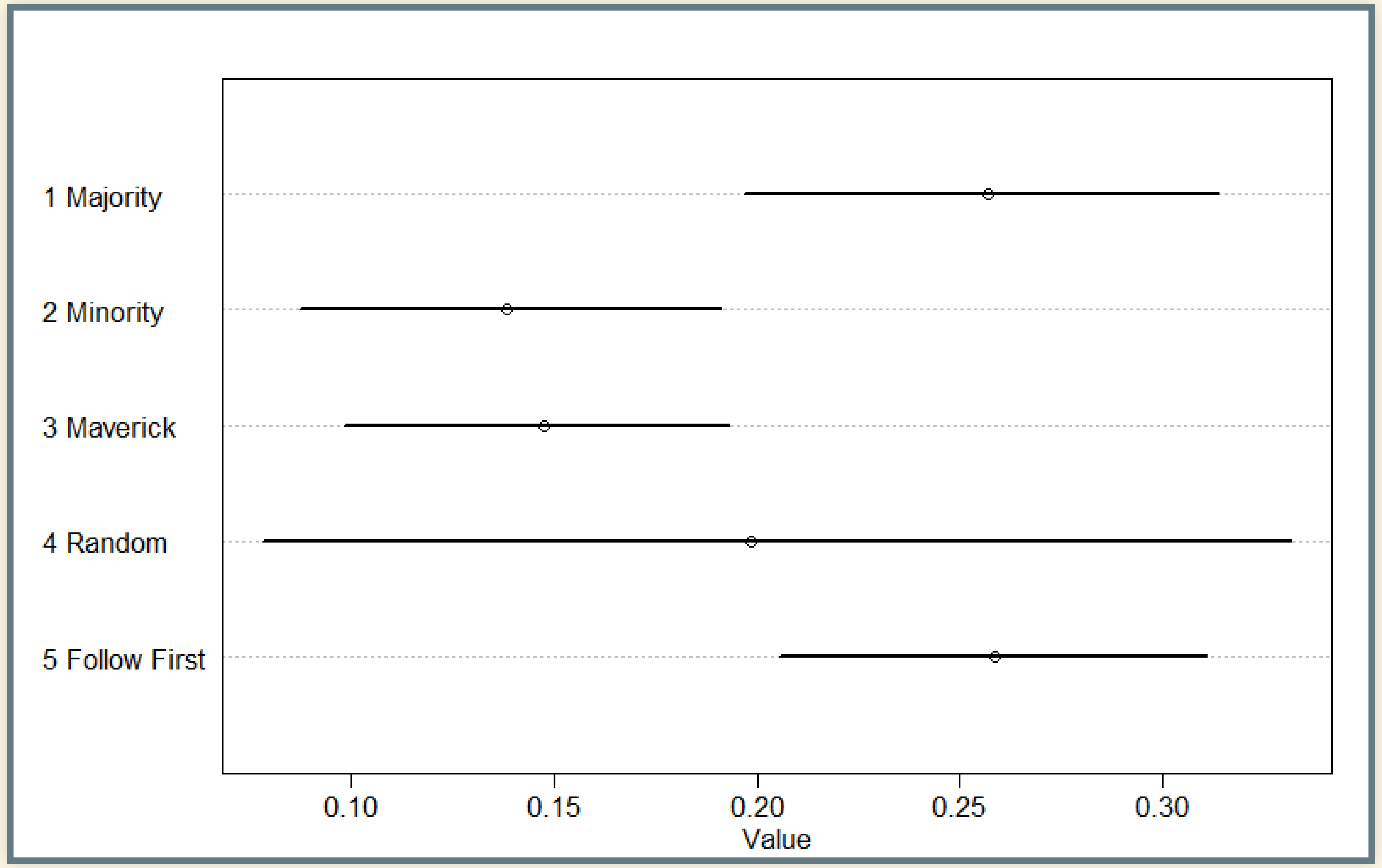
```
dat_list <- list(
  N = nrow(Boxes),
  y = Boxes$y,
  majority_first = Boxes$majority_first
)
```

```
mdl_box <- stan(model_code = Boxes_model, data = dat_list,
                chains = 4, cores = 4)
```

```
mdl_box
```

```
## Inference for Stan model: rt_cmdstanr_82e68937d1e417e265d6739ef917f4e6-
202211290539-1-4b9fa0.
## 4 chains, each with iter=1000; warmup=500; thin=1;
## post-warmup draws per chain=500, total post-warmup draws=2000.
##
##          mean se_mean   sd    2.5%     25%     50%     75%   97.5% n_eff Rhat
## p[1]    0.26    0.00 0.04    0.18    0.23    0.26    0.28    0.33   555 1.01
## p[2]    0.14    0.00 0.03    0.07    0.12    0.14    0.16    0.20   543 1.00
## p[3]    0.15    0.00 0.03    0.08    0.13    0.15    0.17    0.20   562 1.00
## p[4]    0.20    0.00 0.08    0.06    0.14    0.19    0.25    0.36   433 1.00
## p[5]    0.26    0.00 0.03    0.19    0.24    0.26    0.28    0.32  1554 1.00
## lp__ -667.21    0.06 1.54 -671.17 -667.98 -666.85 -666.06 -665.34   602 1.00
##
## Samples were drawn using NUTS(diag_e) at Tue Nov 29 5:39:48 AM 2022.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

```
p_labels <- c("1 Majority", "2 Minority", "3 Maverick", "4
        Random", "5 Follow First")
plot(precis(mdl_box, 2), labels = p_labels)
```


1 Majority
2 Minority
3 Maverick
4 Random
5 Follow First
Value