

Experiment 2: Full Model Set and R Specification

Model	Formula	Rstan Code
m0b	$Y_i \sim \text{Beta}(p_i, \theta)$ $\text{logit}(p_i) = \alpha$ $\alpha \sim \text{Normal}(0, 1)$ $\theta \sim \text{HalfCauchy}(0, 1)$	<pre># Intercept Model m0b <- map2stan(alist(y ~ dbeta2(p, theta), logit(p) <- a, a ~ dnorm(0, 1), theta ~ dcauchy(0, 1)), data = dlist, constraints=list(theta="lower=0"), start=list(theta = 1), warmup=1000, iter=1e4, cores=2)</pre>
m1b	$Y_i \sim \text{Beta}(p_i, \theta)$ $\text{logit}(p_i) = \alpha_{\text{FISH}[i]}$ $\alpha_{\text{FISH}[i]} \sim \text{Normal}(0, 1)$ $\theta \sim \text{HalfCauchy}(0, 1)$	<pre># Fixed effects model: fish m1b <- map2stan(alist(y ~ dbeta2(p, theta), logit(p) <- a_fish[fish_id], a_fish[fish_id] ~ dnorm(0, 1), theta ~ dcauchy(0, 1)), data=dlist, constraints=list(theta="lower=0"), start=list(theta=1), warmup=1000 , iter=1e4, cores=2)</pre>

m2b

$$\begin{aligned}
 Y_i &\sim \text{Beta}(p_i, \theta) \\
 \text{logit}(p_i) &= \alpha_{\text{FISH}[i]} \\
 \alpha_{\text{FISH}[i]} &\sim \text{Normal}(\alpha, \sigma_{\text{FISH}}) \\
 \alpha &\sim \text{Normal}(0, 1) \\
 \sigma_{\text{FISH}} &\sim \text{HalfCauchy}(0, 1) \\
 \theta &\sim \text{HalfCauchy}(0, 1)
 \end{aligned}$$

m3b

$$\begin{aligned}
 Y_i &\sim \text{Beta}(p_i, \theta) \\
 \text{logit}(p_i) &= \alpha + \alpha_{\text{FISH}[i]} + \beta_{\text{TREATMENT}[i]} \\
 \alpha_{\text{FISH}[i]} &\sim \text{Normal}(0, \sigma_{\text{FISH}}) \\
 \alpha &\sim \text{Normal}(0, 1) \\
 \sigma_{\text{FISH}} &\sim \text{HalfCauchy}(0, 1) \\
 \beta_{\text{TREATMENT}} &\sim \text{Normal}(0, 1) \\
 \theta &\sim \text{HalfCauchy}(0, 1)
 \end{aligned}$$

```

# Varying intercepts: fish
m2b <- map2stan(
  alist(
    y ~ dbeta2(p, theta),
    logit(p) <- a_fish[fish_id],
    a_fish[fish_id] ~ dnorm(a, sigma_fish),
    a ~ dnorm(0, 1),
    sigma_fish ~ dcauchy(0, 1),
    theta ~ dcauchy(0, 1)
  ),
  data = dlist,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2 )

# varying intercepts for fish by (fixed) treatment effect
m3b <- map2stan(
  alist(
    y ~ dbeta2( p, theta ),
    logit(p) <- a + a_fish[fish_id] +
      b_treatment*treatment ,
    a_fish[fish_id] ~ dnorm(0, sigma_fish),
    a ~ dnorm(0, 1),
    b_treatment ~ dnorm(0, 1),
    theta ~ dcauchy(0, 1),
    sigma_fish ~ dcauchy(0, 1)
  ),
  data = dlist,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000 , iter=1e4, cores=2)

```

m4b

$$\begin{aligned}Y_i &\sim \text{Beta}(p_i, \theta) \\ \text{logit}(p_i) &= \alpha + \alpha_{\text{FISH}[i]} + \beta_{\text{TREATMENT}[i]} \\ \alpha_{\text{FISH}[i]} &\sim \text{Normal}(0, \sigma_{\text{FISH}}) \\ \beta_{\text{TREATMENT}[i]} &\sim \text{Normal}(0, \sigma_{\text{TREATMENT}}) \\ \alpha &\sim \text{Normal}(0, 1) \\ \sigma_{\text{FISH}} &\sim \text{HalfCauchy}(0, 1) \\ \sigma_{\text{TREATMENT}} &\sim \text{HalfCauchy}(0, 1) \\ \theta &\sim \text{Exp}(1)\end{aligned}$$

```
# Varying Intercepts: fish and treatment
m4b <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),
    # linear model
    logit(p) <- a + a_fish[fish_id] + b_treat[treatment],
    # adaptive priors
    a_fish[fish_id] ~ dnorm(0, sigma_fish),
    b_treat[treatment] ~ dnorm(0, sigma_treat),
    # fixed priors
    a ~ dnorm(0, 1),
    theta ~ dexp(1),
    sigma_fish ~ dcauchy(0,1),
    sigma_treat ~ dcauchy(0,1)
  ),
  data = dlist,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000 , iter=1e4 , cores=2 )
```

$$\begin{aligned}
 Y_i &\sim \text{Beta}(p_i, \theta) \\
 \text{logit}(p_i) &= \beta_{1\text{FISH}[i]} \text{Light}_i + \beta_{2\text{FISH}[i]} \text{Dark}_i \\
 \begin{bmatrix} \beta_{1\text{FISH}} \\ \beta_{2\text{FISH}} \end{bmatrix} &\sim \text{MVNormal}\left(\begin{bmatrix} \alpha \\ \beta_1 \\ \beta_2 \end{bmatrix}, S\right) \\
 \beta_1 &\sim \text{Normal}(0, 1) \\
 \beta_2 &\sim \text{Normal}(0, 1) \\
 \sigma_{\text{FISH}} &\sim \text{Exp}(1) \\
 \theta &\sim \text{HalfCauchy}(0, 1) \\
 \rho_{\text{FISH}} &\sim \text{LKJcorr}(2)
 \end{aligned}$$

```

mb1bNC <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),

    # linear model
    logit(p) <- (b_light + bl_fish[fish_id])*light +
      (b_dark + bd_fish[fish_id])*dark,

    # adaptive non-centered priors
    c(bl_fish, bd_fish)[fish_id] ~ dmvmnormNC(sigma_fish,
      Rho_fish),

    # fixed priors
    c(b_light, b_dark) ~ dnorm(0,1),
    theta ~ dcauchy(0,1),
    sigma_fish ~ dexp(1),
    Rho_fish ~ dlkjcorr(2)
  ),
  # data
  data = dlist,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)

```

mB1 (begin bar-
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pare)

$$\begin{aligned} Y_i &\sim \text{Beta}(p_i, \theta) \\ \text{logit}(p_i) &= \alpha_{\text{FISH}[i]} + \beta_{\text{TREATMENT}[i]} \\ \begin{bmatrix} \alpha_{\text{FISH}} \\ \beta_{\text{FISH}} \end{bmatrix} &\sim \text{MVNormal}\left(\begin{bmatrix} \alpha \\ \beta \end{bmatrix}, S\right) \\ \mathbf{S} &= \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} R \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} \\ \alpha &\sim \text{Normal}(0, 1) \\ \beta &\sim \text{Normal}(0, 1) \\ \sigma_{\text{FISH}} &\sim \text{Exp}(1) \\ \theta &\sim \text{HalfCauchy}(0, 1) \\ \rho_{\text{FISH}} &\sim \text{LKJCorr}(2) \end{aligned}$$

```
mB1 <- map2stan(  
  alist(  
    #likelihood  
    y ~ dbeta2( p, theta ),  
  
    # linear model  
    logit(p) <- a_fish[fish_id] + b_treatment*treatment ,  
  
    # adaptive NON-CENTERED priors  
    a_fish[fish_id] ~ dmvmnormNC(sigma_fish, Rho_fish),  
  
    # fixed priors  
    b_treatment ~ dnorm(0,1),  
    theta ~ dcauchy(0,1),  
    sigma_fish ~ dexp(1),  
    Rho_fish ~ dlkjcorr(2)  
  ),  
  # data  
  data = dlistB,  
  constraints=list(theta="lower=0"),  
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)
```

$$\begin{aligned}
Y_i &\sim \text{Beta}(p_i, \theta) \\
\text{logit}(p_i) &= \alpha_{\text{FISH}[i]} + \beta_{\text{FISH}[i]} \text{Treatment} \\
\begin{bmatrix} \alpha_{\text{FISH}} \\ \beta_{\text{FISH}} \end{bmatrix} &\sim \text{MVNormal}\left(\begin{bmatrix} \alpha \\ \beta \end{bmatrix}, S\right) \\
\mathbf{S} &= \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} R \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} \\
\alpha &\sim \text{Normal}(0, 1) \\
\beta &\sim \text{Normal}(0, 1) \\
\sigma_{\text{FISH}} &\sim \text{Exp}(1) \\
\theta &\sim \text{HalfCauchy}(0, 1) \\
\rho_{\text{FISH}} &\sim \text{LKJCorr}(2)
\end{aligned}$$

```

mB2 <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),

    # linear model
    logit(p) <- a_fish[fish_id] + (b_treatment +
    b_fish[fish_id])*treatment ,

    # adaptive NON-CENTERED priors
    c(a_fish, b_fish)[fish_id] ~ dmvmnormNC(sigma_fish,
    Rho_fish),

    # fixed priors
    b_treatment ~ dnorm(0,1),
    theta ~ dcauchy(0,1),
    sigma_fish ~ dexp(1),
    Rho_fish ~ dlkjcorr(2)
  ),
  # data
  data = dlistB,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)

```

mB3

$$Y_i \sim \text{Beta}(p_i, \theta)$$
$$\text{logit}(p_i) = \alpha_{\text{FISH}[i]} + \beta_1 \text{Light} + \beta_2 \text{Dark}$$
$$\alpha_{\text{FISH}[i]} \sim \text{Normal}(0, \sigma_{\text{FISH}})$$
$$\alpha \sim \text{Normal}(0, 1)$$
$$(\beta_1, \beta_2) \sim \text{Normal}(0, 1)$$
$$\sigma_{\text{FISH}} \sim \text{Exp}(1)$$
$$\theta \sim \text{HalfCauchy}(0, 1)$$

```
mB3 <- map2stan(  
  alist(  
    #likelihood  
    y ~ dbeta2( p, theta ),  
  
    # linear model  
    logit(p) <- a_fish[fish_id] + b_light*light +  
    b_dark*dark ,  
  
    # adaptive NON-CENTERED priors  
    a_fish[fish_id] ~ dnorm(0, sigma_fish),  
  
    # fixed priors  
    c(b_light, b_dark) ~ dnorm(0,1),  
    theta ~ dcauchy(0,1),  
    sigma_fish ~ dexp(1)  
  ),  
  # data  
  data = dlistB,  
  constraints=list(theta="lower=0"),  
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)
```

$$\begin{aligned}
 Y_i &\sim \text{Beta}(p_i, \theta) \\
 \text{logit}(p_i) &= \alpha_{\text{FISH}[i]} + \beta_{2\text{FISH}[i]} \text{Light}_i + \beta_{2\text{FISH}[i]} \text{Dark}_i \\
 \begin{bmatrix} \alpha_{\text{FISH}} \\ \beta_{1\text{FISH}} \\ \beta_{2\text{FISH}} \end{bmatrix} &\sim \text{MVNormal}\left(\begin{bmatrix} \alpha \\ \beta_1 \\ \beta_2 \end{bmatrix}, S\right) \\
 \alpha &\sim \text{Normal}(0, 1) \\
 (\beta_1, \beta_2) &\sim \text{Normal}(0, 1) \\
 \sigma_{\text{FISH}} &\sim \text{Exp}(1) \\
 \theta &\sim \text{HalfCauchy}(0, 1) \\
 \rho_{\text{FISH}} &\sim \text{LKJCorr}(2)
 \end{aligned}$$

```

# varying intercepts and slopes by fish and treatment
mB4 <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),

    # linear model
    logit(p) <- a_fish[fish_id] +
      (b_light+ bl_fish[fish_id])*light +
      (b_dark + bd_fish[fish_id])*dark ,

    # adaptive NON-CENTERED priors
    c(a_fish, bl_fish, bd_fish)[fish_id] ~
      dmvmnormNC(sigma_fish, Rho_fish),

    # fixed priors
    c(b_light, b_dark) ~ dnorm(0,1),
    theta ~ dcauchy(0,1),
    sigma_fish ~ dexp(1),
    Rho_fish ~ dlkjcorr(2)
  ),
  # data
  data = dlistB,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)

```


$$\begin{aligned}
Y_i &\sim \text{Beta}(p_i, \theta) \\
\text{logit}(p_i) &= \alpha_{\text{FISH}[i]} + \beta_{\text{BARBELS}[i]} \\
[\alpha_{\text{FISH}}] &\sim \text{MVNormal}\left([\alpha], S\right) \\
(\beta_{\text{BARBELS}[i]}) &\sim \text{Normal}(0, 1) \\
\sigma_{\text{FISH}} &\sim \text{Exp}(1) \\
\theta &\sim \text{HalfCauchy}(0, 1) \\
\rho_{\text{FISH}} &\sim \text{LKJCorr}(2)
\end{aligned}$$

```

# Adding barbels as a fixed effect
mB5 <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),

    # linear model
    logit(p) <- a_fish[fish_id] + b_barbels*barbels ,

    # adaptive NON-CENTERED priors
    a_fish[fish_id] ~ dmvmnormNC(sigma_fish, Rho_fish),

    # fixed priors
    b_barbels ~ dnorm(0,1),
    theta ~ dcauchy(0,1),
    sigma_fish ~ dexp(1),
    Rho_fish ~ dlkjcorr(2)
  ),
  # data
  data = dlistB,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)

```

$$\begin{aligned}
 Y_i &\sim \text{Beta}(p_i, \theta) \\
 \text{logit}(p_i) &= \alpha_{\text{FISH}[i]} + \beta_{\text{BARBELS}[i]} + \beta_{\text{TREATMENT}[i]} \\
 [\alpha_{\text{FISH}}] &\sim \text{MVNormal}([\alpha], S) \\
 (\beta_{\text{BARBELS}[i]}, \beta_{\text{TREATMENT}[i]}) &\sim \text{Normal}(0, 1) \\
 \sigma_{\text{FISH}} &\sim \text{Exp}(1) \\
 \theta &\sim \text{HalfCauchy}(0, 1) \\
 \rho_{\text{FISH}} &\sim \text{LKJCorr}(2)
 \end{aligned}$$

```

# Adding barbels and treatment as fixed effects
mB6 <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),

    # linear model
    logit(p) <- a_fish[fish_id] + b_barbels*barbels +
    b_treatment*treatment,

    # adaptive NON-CENTERED priors
    a_fish[fish_id] ~ dmvnormNC(sigma_fish, Rho_fish),

    # fixed priors
    c(b_barbels, b_treatment) ~ dnorm(0,1),
    theta ~ dcauchy(0,1),
    sigma_fish ~ dexp(1),
    Rho_fish ~ dlkjcorr(2)
  ),
  # data
  data = dlistB,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)

```

$$\begin{aligned}
Y_i &\sim \text{Beta}(p_i, \theta) \\
\text{logit}(p_i) &= \alpha_{\text{FISH}[i]} + \beta_{1\text{TREATMENT}[i]} \text{Barbels}_i \\
\begin{bmatrix} \alpha_{\text{FISH}} \\ \beta_{\text{TREATMENT}} \end{bmatrix} &\sim \text{MVNormal}\left(\begin{bmatrix} \alpha \\ \beta \end{bmatrix}, S\right) \\
\mathbf{S} &= \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} R \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} \\
\beta_1 &\sim \text{Normal}(0, 1) \\
(\sigma_{\text{TREATMENT}}, \sigma_{\text{FISH}}) &\sim \text{Exp}(1) \\
\theta &\sim \text{HalfCauchy}(0, 1) \\
\rho_{\text{FISH}} &\sim \text{LKJCorr}(2)
\end{aligned}$$

```

# Allowing barbel effect slope to vary with treatment
mB7 <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),

    # linear model
    logit(p) <- a_fish[fish_id] + (b_barbels +
      b_treatment[treatment])*barbels ,

    # adaptive NON-CENTERED priors
    a_fish[fish_id] ~ dmvnormNC(sigma_fish, Rho_fish),
    b_treatment[treatment] ~
      dmvnormNC(sigma_treatment, Rho_treatment),

    # fixed priors
    b_barbels ~ dnorm(0,1),
    theta ~ dcauchy(0,1),
    c(sigma_fish, sigma_treatment) ~ dexp(1),
    c(Rho_fish, Rho_treatment) ~ dlkjcorr(2)
  ),
  # data
  data = dlistB,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)

```

$$\begin{aligned}
Y_i &\sim \text{Beta}(p_i, \theta) \\
\text{logit}(p_i) &= \alpha_{\text{FISH}[i]} + \beta_{\text{FISH}[i]} \text{Barbels}_i \\
\begin{bmatrix} \alpha_{\text{FISH}} \\ \beta_{\text{FISH}} \end{bmatrix} &\sim \text{MVNormal}\left(\begin{bmatrix} \alpha \\ \beta \end{bmatrix}, S\right) \\
\mathbf{S} &= \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} R \begin{pmatrix} \sigma_\alpha & 0 \\ 0 & \sigma_\beta \end{pmatrix} \\
\beta &\sim \text{Normal}(0, 1) \\
\sigma_{\text{FISH}} &\sim \text{Exp}(1) \\
\theta &\sim \text{HalfCauchy}(0, 1) \\
\rho_{\text{FISH}} &\sim \text{LKJCorr}(2)
\end{aligned}$$

```

# Allowing barbel effect slope to vary with fish
mB8 <- map2stan(
  alist(
    #likelihood
    y ~ dbeta2( p, theta ),

    # linear model
    logit(p) <- a_fish[fish_id] + (b_barbels +
    b_fish[fish_id])*barbels ,

    # adaptive NON-CENTERED priors
    c(a_fish, b_fish)[fish_id] ~
    dmvmnormNC(sigma_fish, Rho_fish),

    # fixed priors
    b_barbels ~ dnorm(0,1),
    theta ~ dcauchy(0,1),
    sigma_fish ~ dexp(1),
    Rho_fish ~ dlkjcorr(2)
  ),
  # data
  data = dlistB,
  constraints=list(theta="lower=0"),
  start=list(theta=1), warmup=1000, iter=1e4, cores=2)

```