

Supplementary material

2025-08-01

```
library(here)
library(brms)
library(loo)
library(collapse)
library(data.table)
source(here::here("Scripts", "FelC-Plot-Fun.R"))
```

Summary of total captures

Number of individual pike caught

Captures = 5836

Sex distribution

```
##
##      f      m      u
## 2664 2509  663
```

Total length (cm)

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##    12.60   66.00   73.20   73.62   82.30   126.20    191
## SD = 16.10742
```

Weight (g)

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##     11.3  1787.5  2681.0  2983.5  3720.5  17000.0   3328
## SD = 1979.642
```

Summary of captures for pike that received an external tag

Number of pike tagged externally

captures = 4597

Sex distribution

##

f m u

2319 2183 95

Total length (cm)

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
##	28.00	67.00	74.00	75.16	83.00	121.00	9

SD = 13.60763

Weight (g)

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
##	184	1923	2765	3098	3790	17000	3025

SD = 1871.578

Summary of captures for telemetry pike

Number of pike tagged with acoustic tags

captures = 317

Tagged in February or March

captures = 300

Sex distribution

##

f m u

177 139 1

Total length (cm)

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	55.70	68.50	74.40	76.42	81.00	121.00

SD = 12.36162

Weight (g)

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
##	1388	2395	3174	3761	4368	15000	2

SD = 2111.102

	N	Mean	SD	Min	Max
Barthe_f	6	83.16667	17.319661	63.6	115.2
Barthe_m	5	62.10000	1.685230	61.2	65.1
Beek_m	2	67.35000	6.010408	63.1	71.6
DZB_f	31	88.59677	10.753030	69.6	110.5
DZB_m	9	72.96667	2.850439	68.9	77.4
DZB_u	1	84.10000	NaN	84.1	84.1
Duwenbeek_f	1	77.30000	NaN	77.3	77.3
Duwenbeek_m	5	68.00000	5.072968	60.1	72.2
GB_f	17	70.58235	12.929193	58.9	106.5
GB_m	12	68.28333	4.615356	59.1	74.8
NRB_f	27	81.02963	8.543275	65.6	96.6
NRB_m	9	69.75556	6.012510	60.5	76.2
P_f	26	81.91538	11.719409	67.5	110.0
P_m	12	66.73333	6.109655	58.6	79.1
Peene_f	14	73.44286	14.098484	56.4	106.4
Peene_m	11	64.26364	5.958401	56.3	73.5
S_f	27	87.92222	14.247411	64.0	121.0
S_m	24	73.48333	4.369227	61.6	81.5
Sehrowbach_f	5	83.10000	3.507136	79.0	87.0
Sehrowbach_m	8	67.63750	4.656466	61.5	76.1
WRB_f	22	78.29545	16.429140	55.7	120.6
WRB_m	42	71.05238	5.252699	58.2	82.4
WRB_u	1	74.10000	NaN	74.1	74.1

Mark recapture analysis

Time between capture and recapture

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.0     48.0   202.0   249.9   376.0   988.0
## [1] 228.7917
```

Pike captured at least twice

```
## [1] 666
```

Pike captured at least three times

```
## [1] 51
```

Pike for which length and sex data is available

```
## [1] 546
```

Summary of distances between captures (km)

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0000  0.5886   2.6012   5.0080   7.5496  58.6411
## SD = 6.247015
```

Recapture models

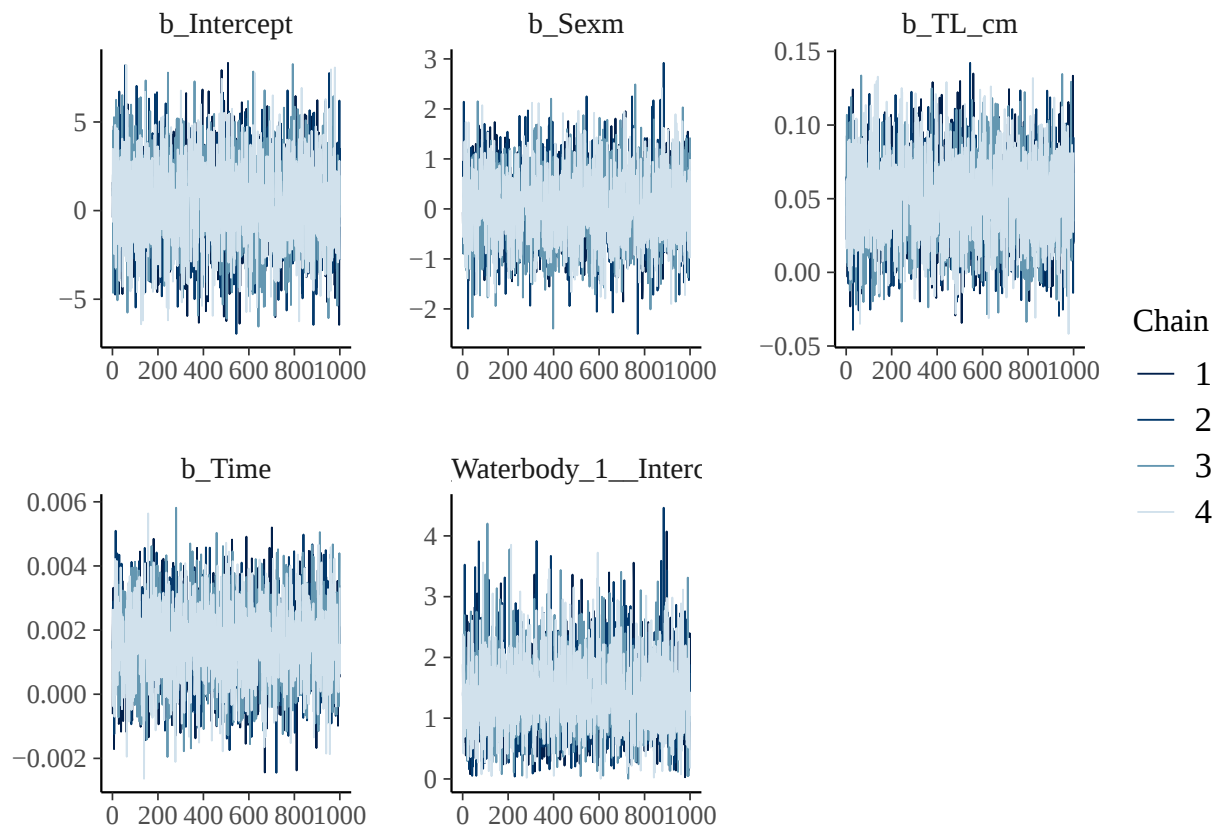
```
NITT=120000;THIN=100;BURN=20000
```

```
prior0<-get_prior(distance_km ~ Sex*TL_cm + Time + (1|Waterbody_1) , data=recap[-which(recap$Sex=="u")
prior1<-get_prior(distance_km ~ Sex+TL_cm + Time + (1|Waterbody_1), data=recap[-which(recap$Sex=="u")

fit0<-brm(data = recap[-which(recap$Sex=="u"),],
  family = gaussian(),
  formula = distance_km ~ Sex*TL_cm + Time + (1|Waterbody_1),
  prior = prior0,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit0 <- add_criterion(fit0, c("loo", "waic"))
fit1<-brm(data = recap[-which(recap$Sex=="u"),],
  family = gaussian(),
  formula = distance_km ~ Sex+TL_cm + Time + (1|Waterbody_1) ,
  prior = prior1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit1 <- add_criterion(fit1, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

```
##      elpd_diff se_diff
## fit1  0.0      0.0
## fit0 -0.6      0.5
```



```
#### Model summary
```

```

## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: distance_km ~ Sex + TL_cm + Time + (1 | Waterbody_1)
## Data: recap[-which(recap$Sex == "u"), ] (Number of observations: 532)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Waterbody_1 (Number of levels: 20)
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)      1.39      0.60      0.34      2.73 1.00      4065      3966
##
## Regression Coefficients:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      0.50      2.39     -4.22      5.28 1.00      4169      3750
## Sexm           0.06      0.70     -1.29      1.42 1.00      3516      3856
## TL_cm          0.05      0.03     -0.01      0.11 1.00      4128      3686
## Time           0.00      0.00     -0.00      0.00 1.00      3972      3929
##
## Further Distributional Parameters:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma        6.17      0.19      5.81      6.57 1.00      4158      3878
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).

```

Connectivity and maximum horizontal displacement (MHD)

Numer of pike in the sample

```
## [1] 242
```

Sex distribution

```
## Sex
##   F   M
## 133 109
```

Individuals with two years of data

```
## [1] 128
```

Individuals with three years of data

```
## [1] 48
```

Connectivity during spawning

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##   1.00    2.00    5.00   12.56   17.00   87.00    599
## SD = 15.67527
```

Connectivity out of spawning

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##   1.000    1.000    3.000    9.454   13.000   63.000    633
## SD = 12.55801
```

MHD during spawning

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##   0.1414  5.1777  9.9260  11.7397  14.3520  57.6138    599
## SD = 9.615237
```

MHD out of spawning

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
##   0.1414  4.8640  9.1194  10.8575  13.6097  44.8010    633
## SD = 8.579201
```

Difference in Connectivity during and out of spawning

```
##
## Welch Two Sample t-test
##
## data: data$MHD_spawn_ext_km and data$MHD_out_ext_km
## t = 1.2864, df = 701.79, p-value = 0.1987
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.4642294  2.2285223
## sample estimates:
```

```
## mean of x mean of y
## 11.73966 10.85751
```

Difference in MHD during and out of spawning

```
##
## Welch Two Sample t-test
##
## data: data$MHD_spawn_ext_km and data$MHD_out_ext_km
## t = 1.2864, df = 701.79, p-value = 0.1987
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.4642294 2.2285223
## sample estimates:
## mean of x mean of y
## 11.73966 10.85751
```

Model: Connectivity during spawning

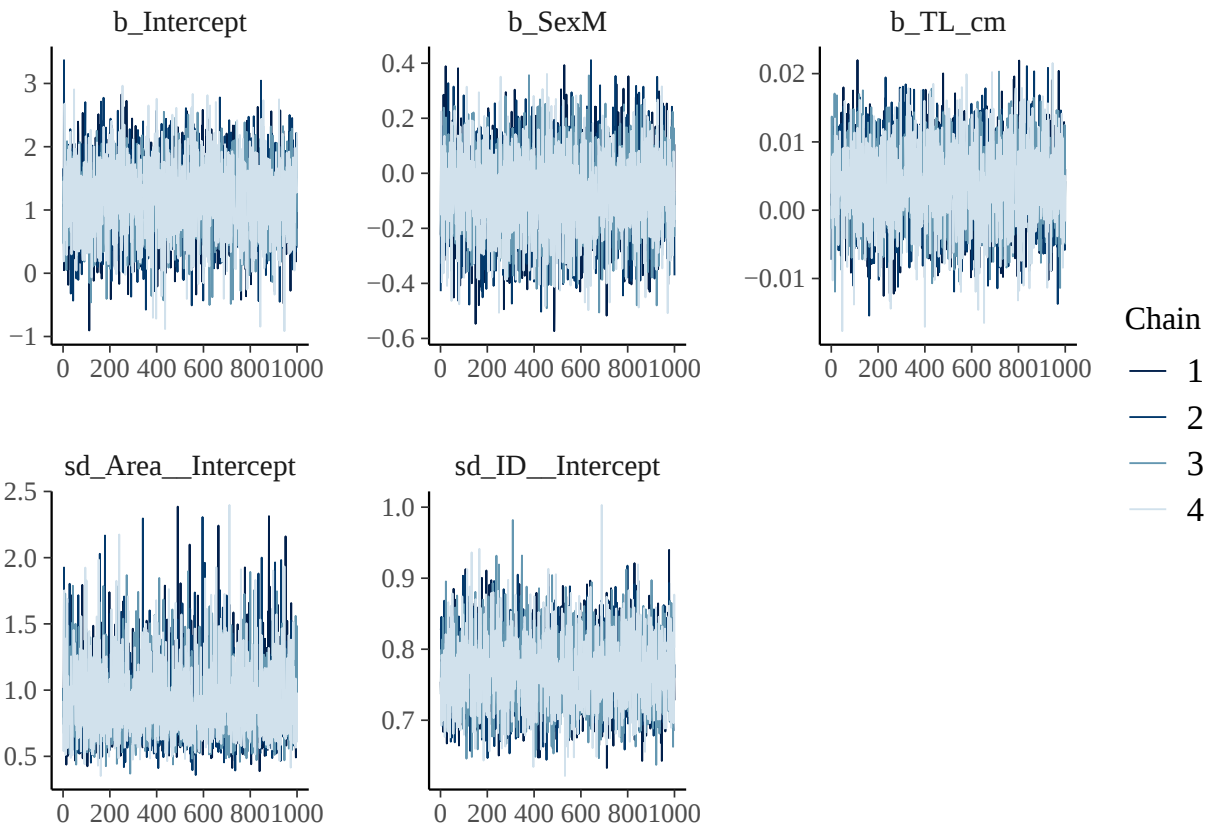
```
prior_ycon_spawn1<-get_prior(y_ConnectivityScore_Spawn.ext ~ Sex*TL_cm + (1|ID) + (1|Area), data=data,
prior_ycon_spawn2<-get_prior(y_ConnectivityScore_Spawn.ext ~ Sex+TL_cm + (1|ID) + (1|Area), data=data,

fit_ycon_spawn1<-brm(data = data,
  family = poisson(),
  formula = y_ConnectivityScore_Spawn.ext ~ Sex*TL_cm + (1|ID) + (1|Area),
  prior = prior_ycon_spawn1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_ycon_spawn1 <- add_criterion(fit_ycon_spawn1, c("loo", "waic"))

fit_ycon_spawn2<-brm(data = data,
  family = poisson(),
  formula = y_ConnectivityScore_Spawn.ext ~ Sex+TL_cm + (1|ID) + (1|Area),
  prior = prior_ycon_spawn2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_ycon_spawn2 <- add_criterion(fit_ycon_spawn2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

##	elpd_diff	se_diff
## fit_ycon_spawn2	0.0	0.0
## fit_ycon_spawn1	-11.4	5.6



Model summary

```

## Family: poisson
## Links: mu = log
## Formula: y_ConnectivityScore_Spawn.ext ~ Sex + TL_cm + (1 | ID) + (1 | Area)
## Data: data (Number of observations: 369)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.91 0.28 0.52 1.57 1.00 3741 3933
##
## ~ID (Number of levels: 223)
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.77 0.05 0.68 0.87 1.00 3892 4065
##
## Regression Coefficients:
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept 1.15 0.57 0.06 2.25 1.00 3946 3904
## SexM -0.08 0.15 -0.38 0.22 1.00 3903 3856
## TL_cm 0.00 0.01 -0.01 0.01 1.00 3804 3891
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).

```

Intra-class correlation coefficient

```
## [1] "Repeatability = 0.07, [0, 0.19], p = 0.011356626404264"
```

Correlation between years

```

##
## Pearson's product-moment correlation
##
## data: data$next_con_spawn and data$y_ConnectivityScore_Spawn.ext
## t = 7.3221, df = 143, p-value = 1.626e-11
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.3926037 0.6314521
## sample estimates:
## cor
## 0.5221936

```

Model: Connectivity out of spawning

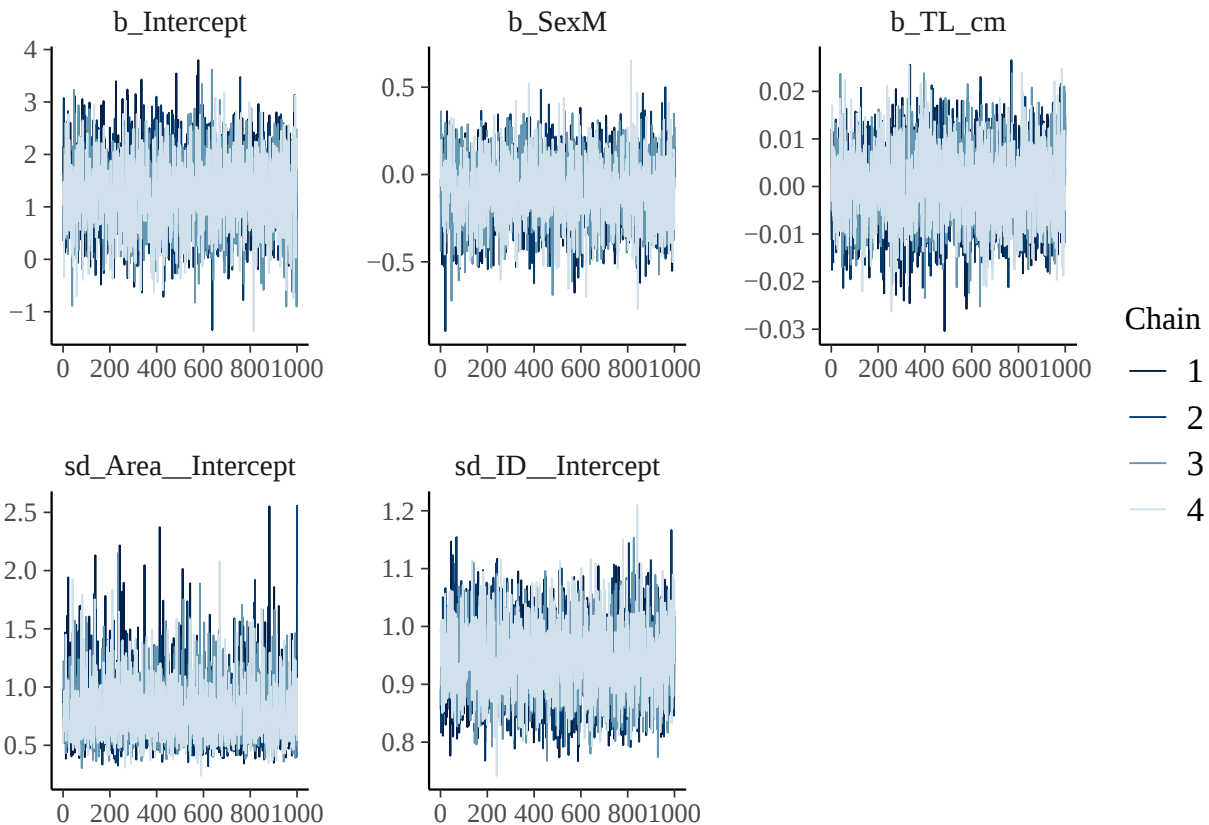
```
prior_ycon_Out1<-get_prior(y_ConnectivityScore_Out.ext ~ Sex*TL_cm + (1|ID) + (1|Area), data=data, fam
prior_ycon_Out2<-get_prior(y_ConnectivityScore_Out.ext ~ Sex+TL_cm + (1|ID) + (1|Area), data=data, fam

fit_ycon_Out1<-brm(data = data,
  family = poisson(),
  formula = y_ConnectivityScore_Out.ext ~ Sex*TL_cm + (1|ID) + (1|Area),
  prior = prior_ycon_Out1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_ycon_Out1 <- add_criterion(fit_ycon_Out1, c("loo", "waic"))

fit_ycon_Out2<-brm(data = data,
  family = poisson(),
  formula = y_ConnectivityScore_Out.ext ~ Sex+TL_cm + (1|ID) + (1|Area),
  prior = prior_ycon_Out2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_ycon_Out2 <- add_criterion(fit_ycon_Out2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

##		elpd_diff	se_diff
##	fit_ycon_Out2	0.0	0.0
##	fit_ycon_Out1	-1.1	4.1



Model summary

```
## Family: poisson
## Links: mu = log
## Formula: y_ConnectivityScore_Out.ext ~ Sex + TL_cm + (1 | ID) + (1 | Area)
## Data: data (Number of observations: 335)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.79 0.26 0.43 1.42 1.00 4092 3974
##
## ~ID (Number of levels: 198)
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 0.94 0.06 0.82 1.07 1.00 3978 3637
##
## Regression Coefficients:
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept 1.29 0.69 -0.02 2.64 1.00 3772 3847
## SexM -0.10 0.18 -0.45 0.25 1.00 3739 3889
## TL_cm 0.00 0.01 -0.01 0.02 1.00 3893 4027
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
rpcon_ext<-rptR::rpt(y_ConnectivityScore_Out.ext ~ Sex+TL_cm + (1|ID) + (1|Area), grname = c("ID"), da
npermut = 0, adjusted = FALSE)
saveRDS(rpcon_ext,here::here("Models","Repeat_connectivity_Outspawning.rds"))
```

Intra-class correlation coefficient

```
## [1] "Repeatability = 0.19, [0.08, 0.37], p = 3.45924799028703e-06"
```

Correlation among years

```
##
## Pearson's product-moment correlation
##
## data: data$next_con_out and data$y_ConnectivityScore_Out.ext
## t = 11.503, df = 134, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.6087878 0.7805959
## sample estimates:
## cor
## 0.7048848
```

Model: MHD during spawning

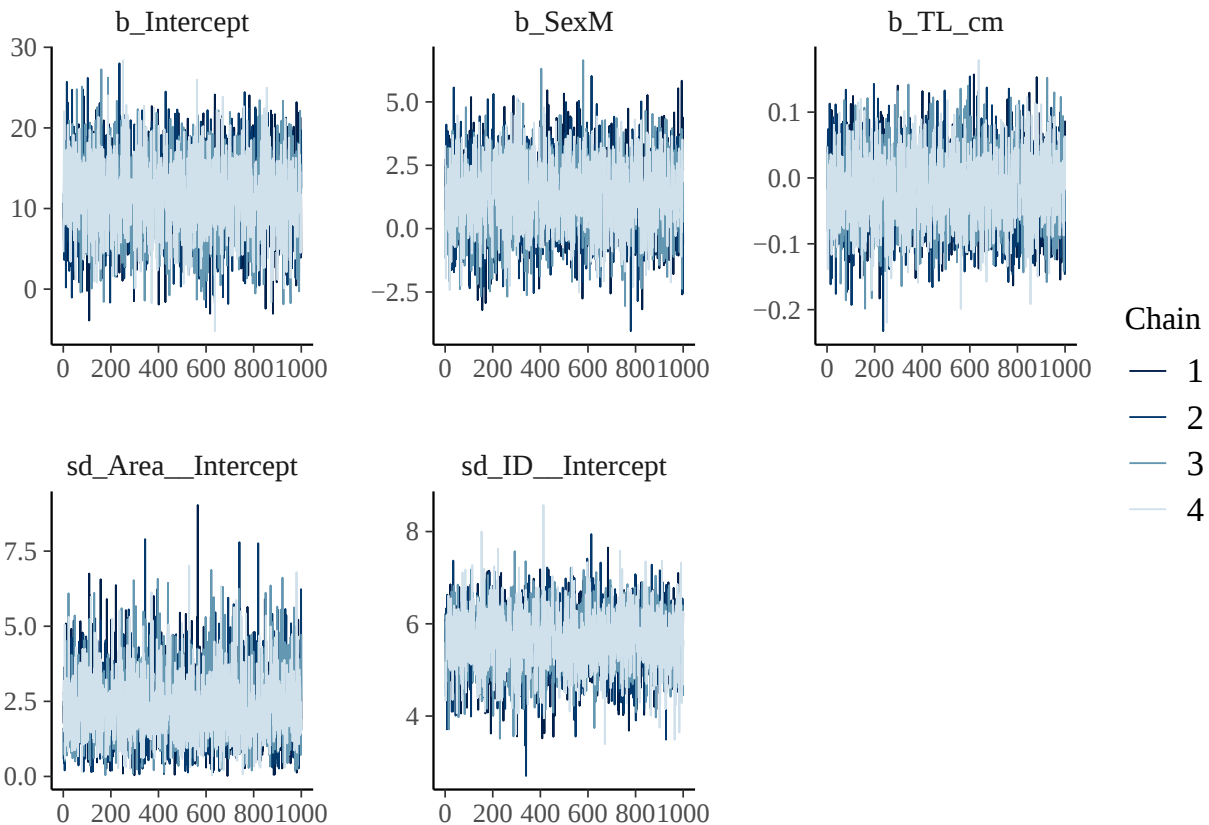
```
prior_yMHD_spawn1<-get_prior(MHD_spawn_ext_km ~ Sex*TL_cm + (1|ID) + (1|Area), data=data, family=gaussian)
prior_yMHD_spawn2<-get_prior(MHD_spawn_ext_km ~ Sex+TL_cm + (1|ID) + (1|Area), data=data, family=gaussian)

fit_yMHD_spawn1<-brm(data = data,
  family = gaussian(),
  formula = MHD_spawn_ext_km ~ Sex*TL_cm + (1|ID) + (1|Area),
  prior = prior_yMHD_spawn1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_yMHD_spawn1 <- add_criterion(fit_yMHD_spawn1, c("loo", "waic"))

fit_yMHD_spawn2<-brm(data = data,
  family = gaussian(),
  formula = MHD_spawn_ext_km ~ Sex+TL_cm + (1|ID) + (1|Area),
  prior = prior_yMHD_spawn2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_yMHD_spawn2 <- add_criterion(fit_yMHD_spawn2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

##		elpd_diff	se_diff
##	fit_yMHD_spawn2	0.0	0.0
##	fit_yMHD_spawn1	-0.1	1.5



Model summary

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: MHD_spawn_ext_km ~ Sex + TL_cm + (1 | ID) + (1 | Area)
## Data: data (Number of observations: 369)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 2.32 1.11 0.48 5.00 1.00 4073 3776
##
## ~ID (Number of levels: 223)
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept) 5.63 0.63 4.35 6.82 1.00 4278 4006
##
## Regression Coefficients:
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept 11.47 4.71 2.17 20.60 1.00 3985 4102
## SexM 1.28 1.40 -1.45 3.96 1.00 4064 3751
## TL_cm -0.02 0.05 -0.12 0.09 1.00 4029 3715
##
## Further Distributional Parameters:
## Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma 7.53 0.41 6.79 8.40 1.00 3859 4101
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

```
rpMHD_spawn<-readRDS(here::here("Models","Repeat_MHD_spawning.rds"))
print(paste0("Repeatability = ", round(rpMHD_spawn[["R"]], digits=2), ", ", ["", round(rpMHD_spawn[["CI_em
```

Intra-class correlation coefficient

```
## [1] "Repeatability = 0.35, [0.2, 0.48], p = 6.36362435093178e-08"
```

Correlation among years

```
##
## Pearson's product-moment correlation
##
## data: data$next_MHD_spawn and data$MHD_spawn_ext_km
## t = 5.846, df = 143, p-value = 3.271e-08
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2974833 0.5619710
## sample estimates:
## cor
## 0.4391948
```

Model: MHD out of spawning

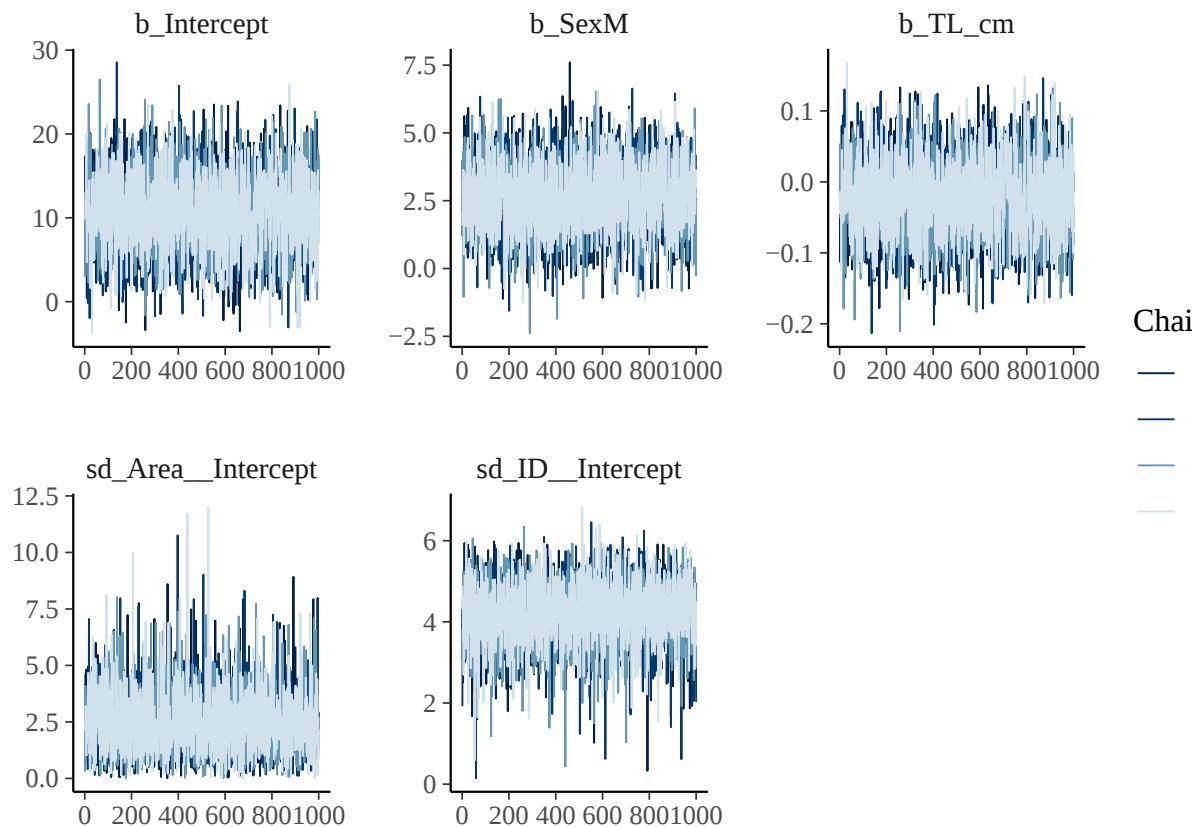
```
prior_yMHD_out1<-get_prior(MHD_out_ext_km ~ Sex*TL_cm + (1|ID) + (1|Area), data=data, family=gaussian())
prior_yMHD_out2<-get_prior(MHD_out_ext_km ~ Sex+TL_cm + (1|ID) + (1|Area), data=data, family=gaussian())

fit_yMHD_out1<-brm(data = data,
  family = gaussian(),
  formula = MHD_out_ext_km ~ Sex*TL_cm + (1|ID)+(1|Area),
  prior = prior_yMHD_out1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_yMHD_out1 <- add_criterion(fit_yMHD_out1, c("loo", "waic"))

fit_yMHD_out2<-brm(data = data,
  family = gaussian(),
  formula = MHD_out_ext_km ~ Sex+TL_cm + (1|ID)+(1|Area),
  prior = prior_yMHD_out2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)
fit_yMHD_out2 <- add_criterion(fit_yMHD_out2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

##		elpd_diff	se_diff
##	fit_yMHD_out1	0.0	0.0
##	fit_yMHD_out2	-0.2	1.0



Model validation

```
summary(fit_yMHD_out2)
```

Model summary

```
## Family: gaussian
## Links: mu = identity; sigma = identity
## Formula: MHD_out_ext_km ~ Sex + TL_cm + (1 | ID) + (1 | Area)
## Data: data (Number of observations: 335)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    2.41      1.34    0.39    5.56 1.00    4156    3965
##
## ~ID (Number of levels: 198)
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    4.21      0.76    2.59    5.57 1.00    3676    3809
##
## Regression Coefficients:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    10.80      4.51    1.74   19.57 1.00    3918    3707
## SexM          2.61      1.25    0.20    5.02 1.00    3717    3716
## TL_cm        -0.02      0.05   -0.13    0.08 1.00    3891    3941
##
## Further Distributional Parameters:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sigma       7.10      0.41    6.35    7.97 1.00    3990    3897
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Intra-class correlation coefficient

```
## [1] "Repeatability = 0.26, [0.1, 0.39], p = 0.000240426056684529"
```

Correlation among years

```
##
## Pearson's product-moment correlation
##
## data: data$next_MHD_out and data$MHD_out_ext_km
## t = 5.5774, df = 134, p-value = 1.297e-07
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.2866709 0.5613733
## sample estimates:
##      cor
## 0.4340578
```

Among year site fidelity, and area re-use

Model: Site fidelity among year

Between areas

```
indices$fidelity_area<-as.numeric(indices$fidelity_area)
prior_fidelity_area1<-get_prior(fidelity_area ~ Sex*TL_cm+ (1|Area) + (1|ID), data=indices, family=bernoulli)
prior_fidelity_area2<-get_prior(fidelity_area ~ Sex+TL_cm + (1|Area) + (1|ID), data=indices, family=bernoulli)

fit_fidelity_area1<-brm(data = indices,
  family = bernoulli(),
  formula = fidelity_area ~ Sex*TL_cm + (1|Area) + (1|ID),
  prior = prior_fidelity_area1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

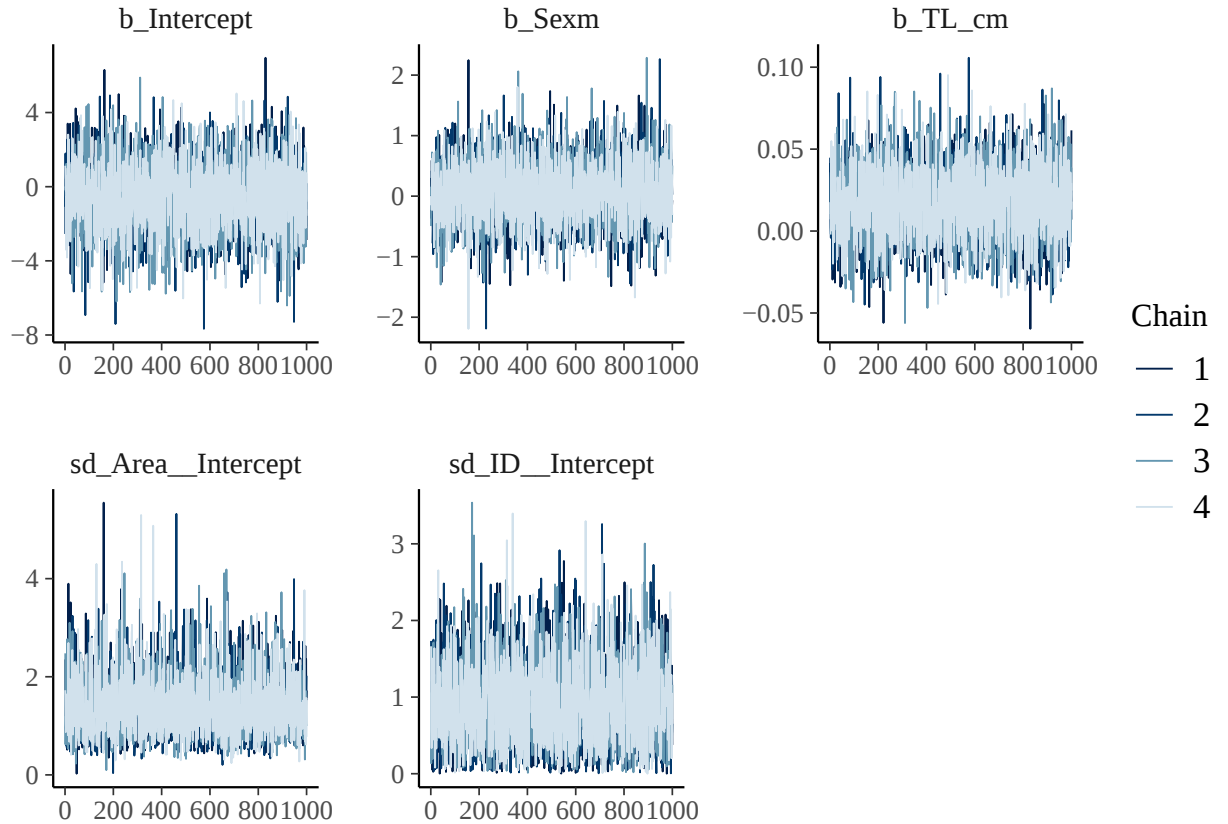
fit_fidelity_area1 <- add_criterion(fit_fidelity_area1, c("loo", "waic"))

fit_fidelity_area2<-brm(data = indices,
  family = bernoulli(),
  formula = fidelity_area ~ Sex+TL_cm + (1|Area) + (1|ID),
  prior = prior_fidelity_area2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

fit_fidelity_area2 <- add_criterion(fit_fidelity_area2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

```
##               elpd_diff se_diff
## fit_fidelity_area2  0.0         0.0
## fit_fidelity_area1 -0.8         0.3
```



```
summary(fit_fidelity_area2)
```

Model summary

```
## Family: bernoulli
## Links: mu = logit
## Formula: fidelity_area ~ Sex + TL_cm + (1 | Area) + (1 | ID)
## Data: indices (Number of observations: 217)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    1.37     0.59    0.53    2.82 1.00    4061    4143
##
## ~ID (Number of levels: 146)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.95     0.53    0.08    2.08 1.00    4202    3882
##
## Regression Coefficients:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept    -0.53     1.77   -3.96    3.05 1.00    4025    3928
## Sexm          0.07     0.49   -0.87    1.06 1.00    4048    3974
## TL_cm         0.02     0.02   -0.02    0.06 1.00    4002    3850
```

```
##  
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS  
## and Tail_ESS are effective sample size measures, and Rhat is the potential  
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Between receivers

```
indices$fidelity<-as.numeric(indices$fidelity)
prior_fidelity1<-get_prior(fidelity ~ Sex*TL_cm+ (1|Area) + (1|ID), data=indices, family=bernoulli())
prior_fidelity2<-get_prior(fidelity ~ Sex+TL_cm + (1|Area) + (1|ID), data=indices, family=bernoulli())

fit_fidelity1<-brm(data = indices,
  family = bernoulli(),
  formula = fidelity ~ Sex*TL_cm + (1|Area) + (1|ID),
  prior = prior_fidelity1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

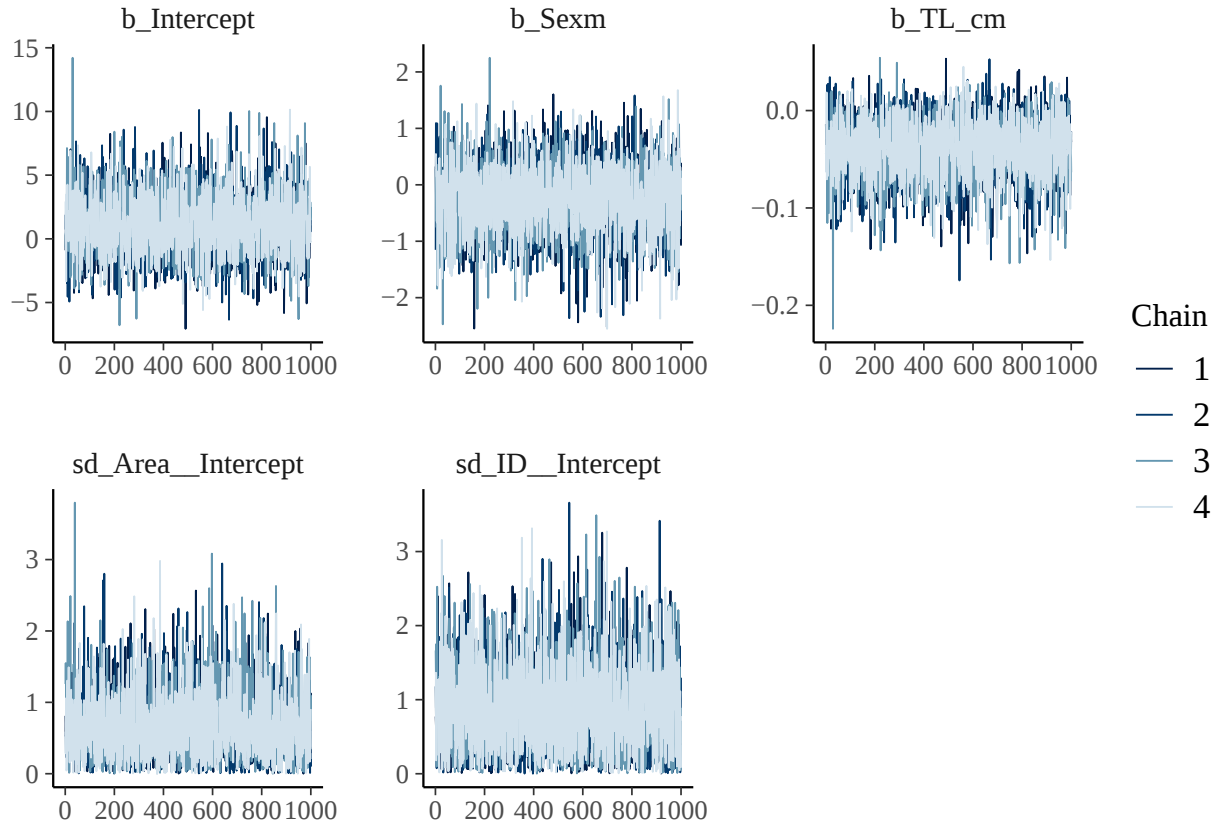
fit_fidelity1 <- add_criterion(fit_fidelity1, c("loo", "waic"))

fit_fidelity2<-brm(data = indices,
  family = bernoulli(),
  formula = fidelity ~ Sex+TL_cm + (1|Area) + (1|ID),
  prior = prior_fidelity2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

fit_fidelity2 <- add_criterion(fit_fidelity2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

```
##           elpd_diff se_diff
## fit_fidelity2  0.0       0.0
## fit_fidelity1 -1.1       0.6
```



Model fit

```
summary(fit_fidelity2)
```

Model summary

```
## Family: bernoulli
## Links: mu = logit
## Formula: fidelity ~ Sex + TL_cm + (1 | Area) + (1 | ID)
## Data: indices (Number of observations: 217)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.68    0.44    0.04    1.74 1.00    4278    3933
##
## ~ID (Number of levels: 146)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.92    0.56    0.05    2.16 1.00    3984    3851
##
## Regression Coefficients:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      1.27     2.28   -3.20    5.75 1.00    3750    3889
## Sexm           -0.25     0.58   -1.43    0.87 1.00    3915    3833
## TL_cm          -0.04     0.03   -0.10    0.02 1.00    3800    3702
```

```
##  
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS  
## and Tail_ESS are effective sample size measures, and Rhat is the potential  
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Model: Indice of site re-use among year

Between area

```
prior_soren_area1<-get_prior(Sorensen_area ~ Sex*TL_cm+ (1|Area) + (1|ID), data=indices, family=Beta())
prior_soren_area2<-get_prior(Sorensen_area ~ Sex+TL_cm + (1|Area) + (1|ID), data=indices, family=Beta())

fit_soren_area1<-brm(data = indices,
  family = Beta(),
  formula = Sorensen_area ~ Sex*TL_cm + (1|Area) + (1|ID),
  prior = prior_soren_area1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

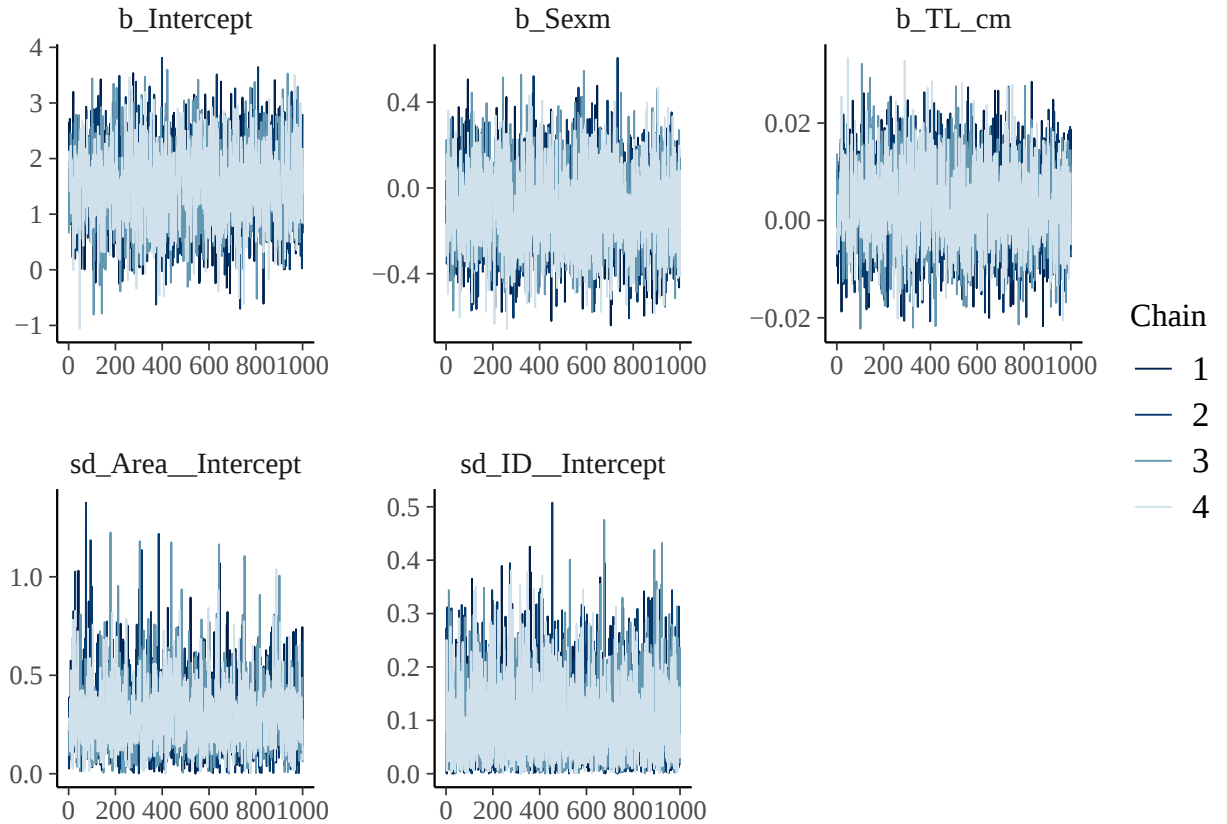
fit_soren_area1 <- add_criterion(fit_soren_area1, c("loo", "waic"))

fit_soren_area2<-brm(data = indices,
  family = Beta(),
  formula = Sorensen_area ~ Sex+TL_cm + (1|Area) + (1|ID),
  prior = prior_soren_area2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

fit_soren_area2 <- add_criterion(fit_soren_area2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

```
##               elpd_diff se_diff
## fit_soren_area2  0.0         0.0
## fit_soren_area1 -0.8         0.5
```



Model fit

```
summary(fit_soren_area2)
```

Model summary

```
## Family: beta
## Links: mu = logit; phi = identity
## Formula: Sorensen_area ~ Sex + TL_cm + (1 | Area) + (1 | ID)
## Data: indices (Number of observations: 217)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.29    0.16    0.04    0.68 1.00    3923    3761
##
## ~ID (Number of levels: 146)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.10    0.08    0.00    0.28 1.00    3967    3833
##
## Regression Coefficients:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      1.52     0.68    0.19    2.83 1.00    3708    3951
## Sexm           -0.09     0.19   -0.45    0.28 1.00    3956    3547
## TL_cm          0.00     0.01   -0.01    0.02 1.00    3683    3978
```

```
##
## Further Distributional Parameters:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi      1.77      0.20      1.41      2.18 1.00      3831      4069
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Between receiver

```
prior_soren1<-get_prior(Sorensen ~ Sex*TL_cm+ (1|Area) + (1|ID), data=indices, family=Beta())
prior_soren2<-get_prior(Sorensen ~ Sex+TL_cm + (1|Area) + (1|ID), data=indices, family=Beta())

fit_soren1<-brm(data = indices,
  family = Beta(),
  formula = Sorensen ~ Sex*TL_cm + (1|Area) + (1|ID),
  prior = prior_soren1,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

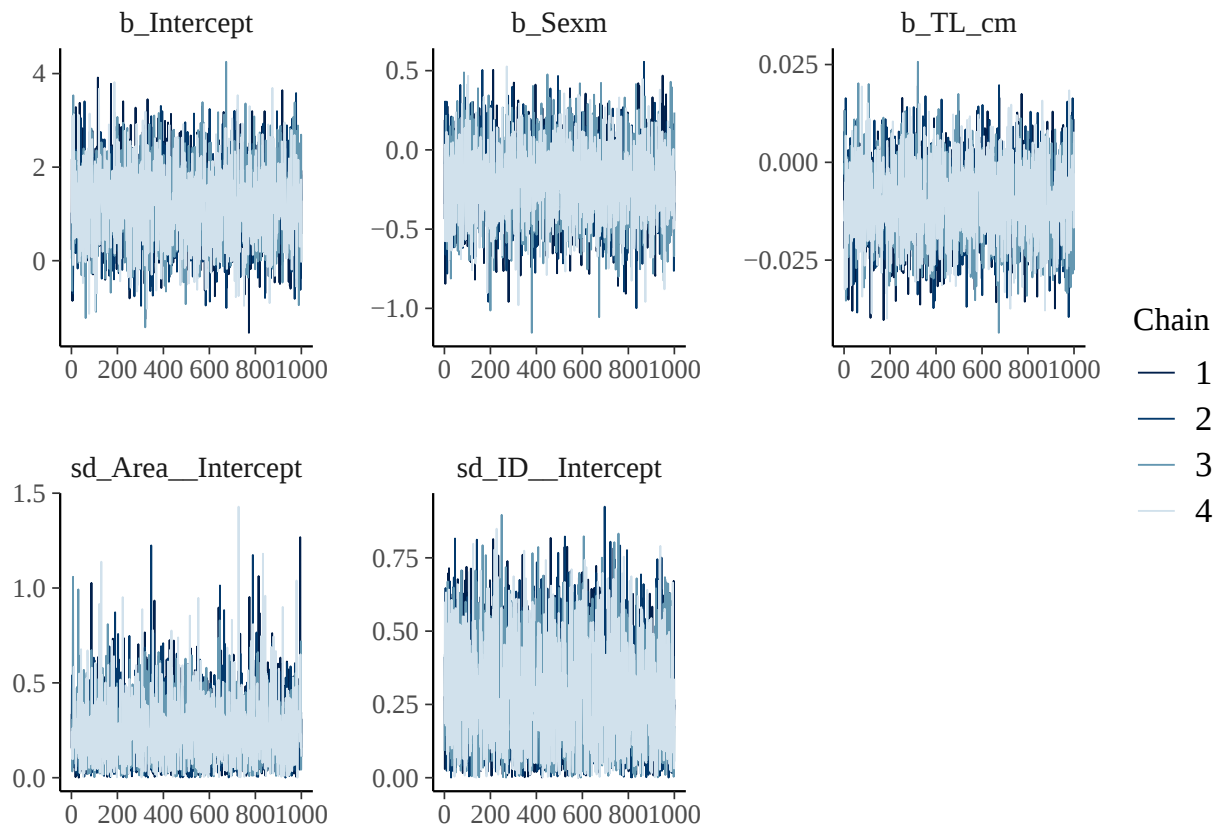
fit_soren1 <- add_criterion(fit_soren1, c("loo", "waic"))

fit_soren2<-brm(data = indices,
  family = Beta(),
  formula = Sorensen ~ Sex+TL_cm + (1|Area) + (1|ID),
  prior = prior_soren2,
  iter = NITT, warmup = BURN, thin=THIN, chains = 4, cores=4)

fit_soren2 <- add_criterion(fit_soren2, c("loo", "waic"))
```

Difference in expected log pointwise predictive density (ELPD)

```
##          elpd_diff se_diff
## fit_soren2  0.0        0.0
## fit_soren1 -0.7        1.1
```



Model fit

```
summary(fit_soren2)
```

Model summary

```
## Family: beta
## Links: mu = logit; phi = identity
## Formula: Sorensen ~ Sex + TL_cm + (1 | Area) + (1 | ID)
## Data: indices (Number of observations: 217)
## Draws: 4 chains, each with iter = 120000; warmup = 20000; thin = 100;
## total post-warmup draws = 4000
##
## Multilevel Hyperparameters:
## ~Area (Number of levels: 11)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.25    0.17    0.02    0.63 1.00    4082    3932
##
## ~ID (Number of levels: 146)
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## sd(Intercept)    0.28    0.18    0.02    0.67 1.00    3981    3957
##
## Regression Coefficients:
##      Estimate Est.Error 1-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## Intercept      1.25     0.79   -0.31    2.80 1.00    3758    3774
## Sexm           -0.21     0.23   -0.66    0.26 1.00    4055    3922
## TL_cm          -0.01     0.01   -0.03    0.01 1.00    3662    3525
```

```

##
## Further Distributional Parameters:
##      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
## phi      1.17      0.12      0.96      1.45 1.00      3903      4097
##
## Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).

```