

Extinction risk from climate change: Biological and physical processes

March 25th, 2024

Load libraries and data

```
rm(list = ls())
root.dir = "C:/Users/mcu08001/Documents/1New Research/CC MetaRisk2/Analysis"

#Load Libraries
library(coda); library(ggplot2); library(rstan); library(bayesplot); library(
shinystan); library(loo); library(rstanarm); library(dplyr); library(ggpubr)

options(mc.cores = parallel::detectCores())
rstan_options(auto_write = FALSE)

#Load data
dataP<-read.table("MetaRisk2 aggthres 5.txt",header=T); attach(dataP)

## The following object is masked from package:base:
##
##      version

#other quantities
#betareg requires no 0s or 1s
koffset = 0.001 #the k that gives the best posterior predictive check
percent2 <- adj.percent
percent2[adj.percent == 0] = koffset;
percent2[adj.percent == 1] = 1 - koffset;
dataP$percent2 <- percent2;

data.use<-dataP; attach(data.use)

## The following object is masked _by_ .GlobalEnv:
##
##      percent2

## The following objects are masked from dataP:
##
##      Adaptation, adj.percent, Antarctic, Arctic, Author, ave.percent,
##      Climate.Mod, concat, Demography.LH, Disp.Mod, Dispersal, Earth.Sys,
##      Endemic, Fresh, Island, Land.Use.Change, max.percent, min.percent,
##      Model.Type, Mtn, N.Middle, Non.clim.threat, Other, Other.Habitat,
##      Physiology, Pop.diff, Pre.Ind.Rise, Region, S.Middle, Scenario,
```

```
##      Sp.int, Study, Taxa, Threatened, Time, Total.N, Tropics, version,
##      WtSp, Year, Year.Pred

## The following object is masked from package:base:
##
##      version

N = length(data.use$percent2)
n.Study <- length(unique(data.use$Study)) #number of studies
Studyint<-as.integer(unclass(factor(data.use$Study)))
phi = data.use$Total.N

#Load intercept model
load("2all_interc.rds")
mod.int<-mod
loo.mod.int<-loo.mod
```

Test for the overall effect of mechanisms

Here I tested if extinction predictions change based on adding all mechanisms.

```
#form matrix of factors
#create model matrix for coefficients
betamat <- data.frame(
  Intercept = rep(1,N),
  Dispersal = ifelse(data.use$Dispersal == "Y",1,0),
  Sp.int = ifelse(data.use$Sp.int == "Y",1,0),
  Physiology = ifelse(data.use$Physiology == "Y",1,0),
  Adaptation = ifelse(data.use$Adaptation == "Y",1,0),
  Pop.diff = ifelse(data.use$Pop.diff == "Y",1,0),
  Demography.LH = ifelse(data.use$Demography.LH == "Y",1,0),
  Earth.Sys = ifelse(data.use$Earth.Sys == "Y",1,0),
  Other.Habitat = ifelse(data.use$Other.Habitat == "Y",1,0))

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)

params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

# init.beta=rep(0,ncol(betamat)-1)
# init.fn<- function (chain_id) {
#   list(beta = c(-2.5,init.beta))
# }
#
# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#       chains = 3, warmup=7000, cores=3,iter=10000,
#       init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#
```

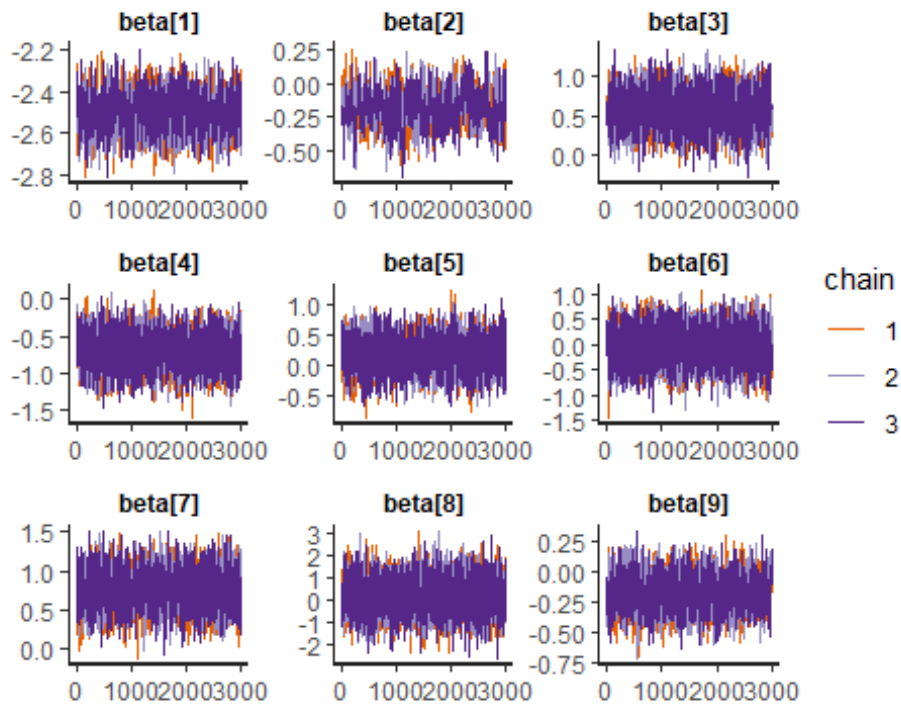
```

load("3allmechs.rds")#load("2disp.rds") #replace once run
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

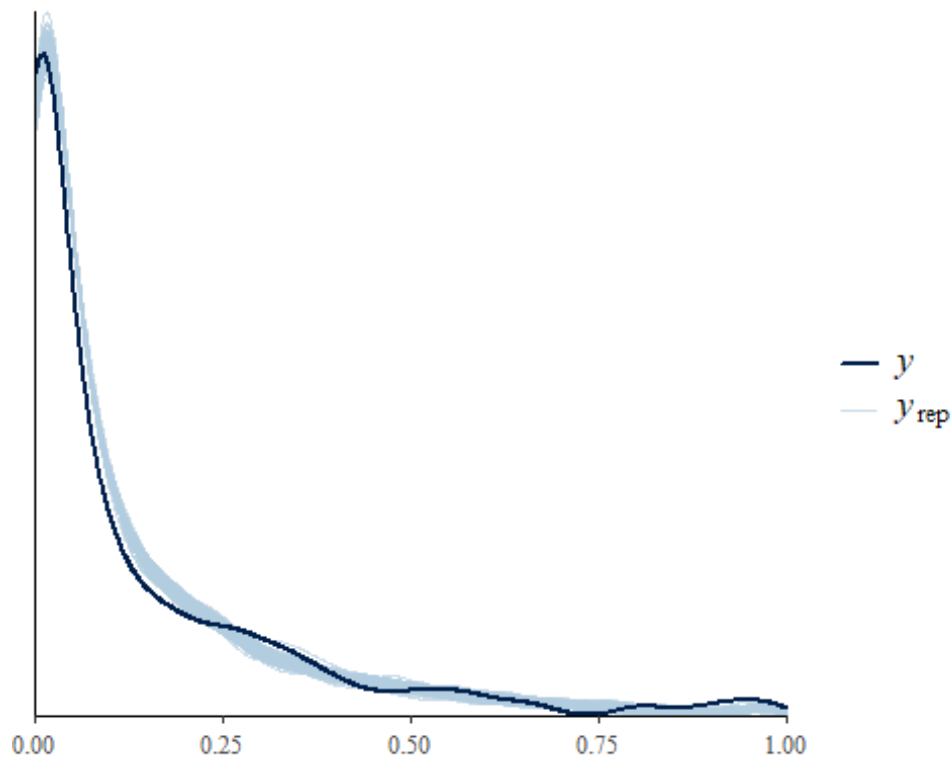
##              mean      se_mean      sd      2.5%      97.5%      n_eff
f
## beta[1] -2.49832275 0.002733730 0.08767882 -2.6685318 -2.32670632 1028.675
0
## beta[2] -0.17927810 0.006082637 0.13358386 -0.4512645  0.08324395  482.307
7
## beta[3]  0.57021608 0.004242309 0.21643997  0.1490208  0.99546485 2602.976
9
## beta[4] -0.69508947 0.004510538 0.22090556 -1.1354436 -0.27382868 2398.593
6
## beta[5]  0.18374189 0.005139278 0.26260149 -0.3358366  0.69727861 2610.899
8
## beta[6] -0.03520058 0.004532672 0.33066712 -0.6893540  0.62428032 5321.983
6
## beta[7]  0.76606114 0.005646052 0.22969788  0.3136622  1.21835088 1655.099
9
## beta[8]  0.24765985 0.013548023 0.75496559 -1.2307855  1.68387334 3105.292
3
## beta[9] -0.16647449 0.003744163 0.14119534 -0.4383269  0.11719039 1422.103
4
##              Rhat
## beta[1] 1.0038963
## beta[2] 1.0021249
## beta[3] 1.0016896
## beta[4] 1.0016993
## beta[5] 1.0002538
## beta[6] 1.0000357
## beta[7] 1.0013531
## beta[8] 0.9999919
## beta[9] 1.0016170

#checks
traceplot(mod,pars=params.to.monitor2,inc_warmup=FALSE)

```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo    7612.3   96.7
## p_loo        1986.5   25.0
## looic       -15224.5  193.5
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##               Count Pct.    Min. ESS
## (-Inf, 0.7]  (good)   1429  44.2%   125
##  (0.7, 1]   (bad)    1547  47.8%   <NA>
##  (1, Inf)   (very bad)  259   8.0%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model","Model including mechanisms"),
  LOOic = c(loo.mod.int$estimates[3],loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6],loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 1: Comparisons of L00ic without and
with all mechanisms", format = "markdown")
```

Table 1: Comparisons of L00ic without and with all mechanisms

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanisms	-15224.54	193.4992

```
L00ic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", L00ic.diff)

## Difference in L00ic = -10.77316
```

Test for effect of modeling dispersal

Here I tested if extinction predictions change based on whether species-specific dispersal was modeled. I predicted that extinction risks would not vary overall from the median, assuming that models that do not model dispersal explicitly model an overall mean value.

```
#form matrix of factors
betamat <- model.matrix(~Dispersal, data = data.use) #

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

init.beta=rep(0,ncol(betamat)-1)
init.fn<- function (chain_id) {
  list(beta = c(-2.5,init.beta))
}

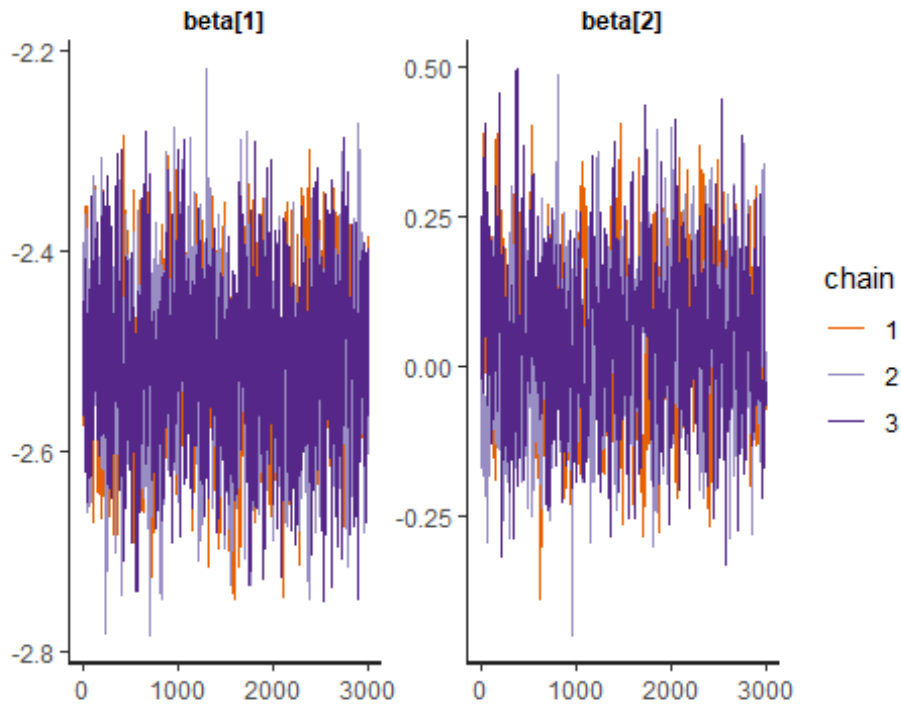
# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.t
o.monitor,
#          chains = 3, warmup=5000, cores=7,iter=8000,
#          init = init.fn, control=list(adapt_delta = 0.9, max_treedepth = 1
5))

load("2disp.rds")#load("2disp.rds") #replace once run
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

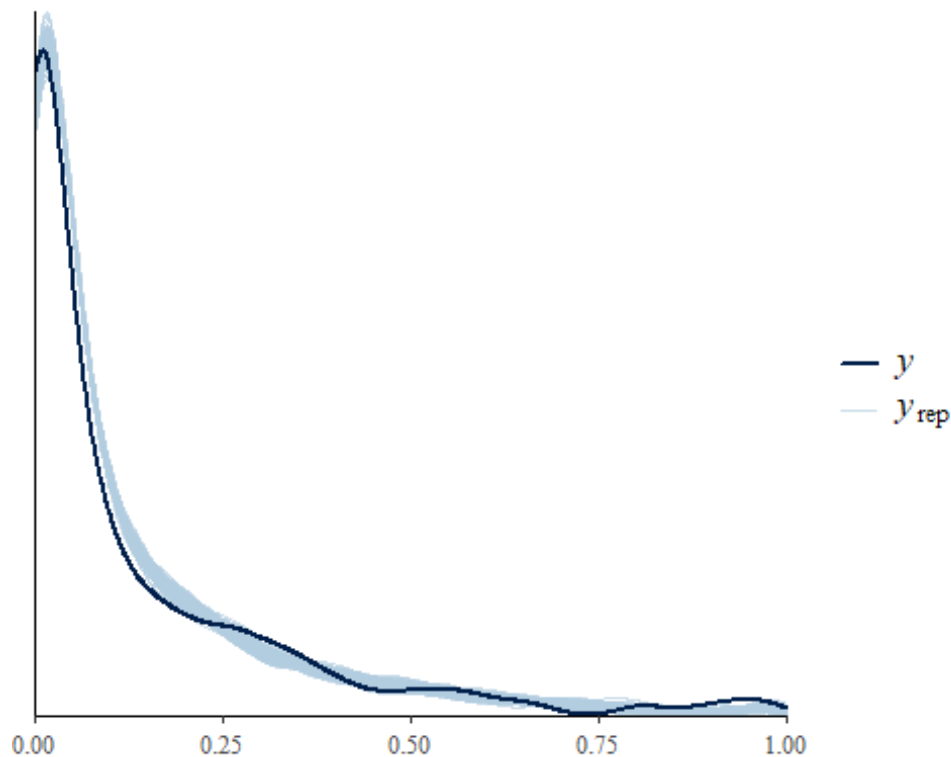
##           mean      se_mean      sd      2.5%      97.5%     n_eff
## beta[1] -2.51345235 0.002357712 0.07537208 -2.6591104 -2.3638673 1021.9732
## beta[2]  0.04655653 0.004855012 0.12127358 -0.1874777  0.2786506  623.9528
##           Rhat
```

```
## beta[1] 1.002395
## beta[2] 1.006386

#checks
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo    7604.5   96.6
## p_loo       1994.2   25.0
## looic      -15209.0  193.2
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##               Count Pct.    Min. ESS
## (-Inf, 0.7]  (good)   1419  43.9%   110
## (0.7, 1]    (bad)    1514  46.8%   <NA>
## (1, Inf)    (very bad) 302   9.3%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```



```
)
knitr::kable(table.data, caption = "Table 2: Comparisons of LOOic without and
with mechanism", format = "markdown")
```

Table 2: Comparisons of LOOic without and with mechanism

Model	LOOic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15209.00	193.2132

```
Looic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in LOOic =", Looic.diff)

## Difference in LOOic = 4.764411
```

Results

No support for the model (LOOic is higher). ## Effect of modeling species interactions
Here I tested if extinction predictions change based on if species interactions were included or not. I predicted that extinction risks would not vary overall from the median, assuming that models that do not model species interactions explicitly model an overall mean value.

```
#form matrix
betamat <- model.matrix(~Sp.int, data = data.use) # 1 - No, 2 - Some, 3 - Yes

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

# init.beta=rep(0,ncol(betamat)-1)
# init.fn<- function(chain_id) {
#   list(beta = c(-2.5,init.beta))
# }

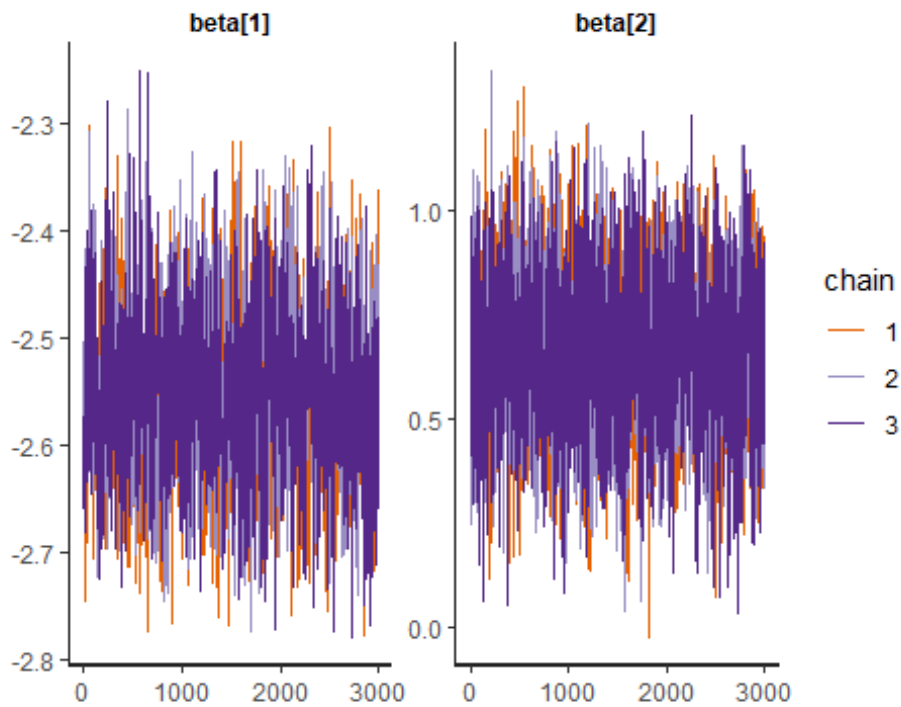
# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#         chains = 3, warmup=7000, cores=3,iter=10000,
#         init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#

load("2spint.rds")
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

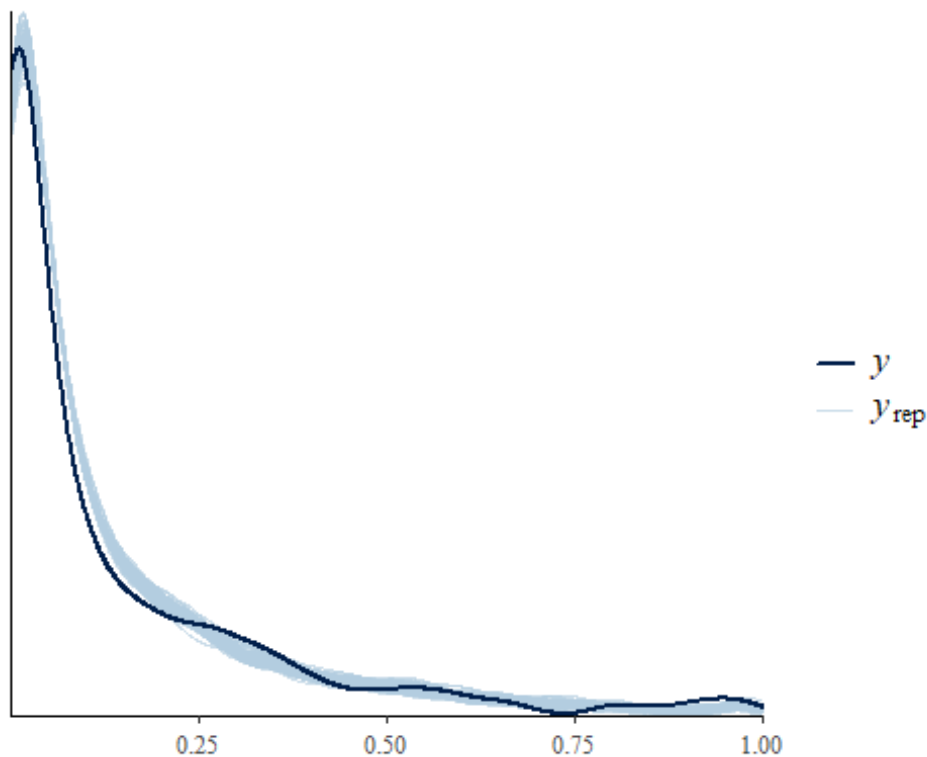
##           mean      se_mean      sd      2.5%      97.5%      n_eff
## beta[1] -2.5509373 0.002450317 0.07554138 -2.6970716 -2.399795  950.4417
## beta[2]  0.6576968 0.004200829 0.17854542  0.3055554  1.007170 1806.4561
```

```
##           Rhat
## beta[1] 1.007268
## beta[2] 1.001380

#checks
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo   7617.4   96.8
## p_loo      1981.1   25.0
## looic     -15234.8  193.6
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##               Count Pct.    Min. ESS
## (-Inf, 0.7]  (good)   1373  42.4%   111
##  (0.7, 1]    (bad)    1594  49.3%   <NA>
##  (1, Inf)    (very bad) 268   8.3%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 3: Comparisons of L00ic without and with mechanism", format = "markdown")
```

Table 3: Comparisons of L00ic without and with mechanism

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15234.83	193.5842

```
L00ic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", L00ic.diff)

## Difference in L00ic = -21.05881
```

Result

Overall model is better with species interactions (delta L00IC is negative). ## Effect of modeling physiology Here I tested if extinction predictions change based on if physiology was included or not. I predicted that extinction risks would not vary overall from the median, assuming that models that do not model physiology explicitly model an overall mean value.

```
betamat <- model.matrix(~Physiology, data = data.use) #

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

init.beta=rep(0,ncol(betamat)-1)
init.fn<- function (chain_id) {
  list(beta = c(-2.5,init.beta))
}

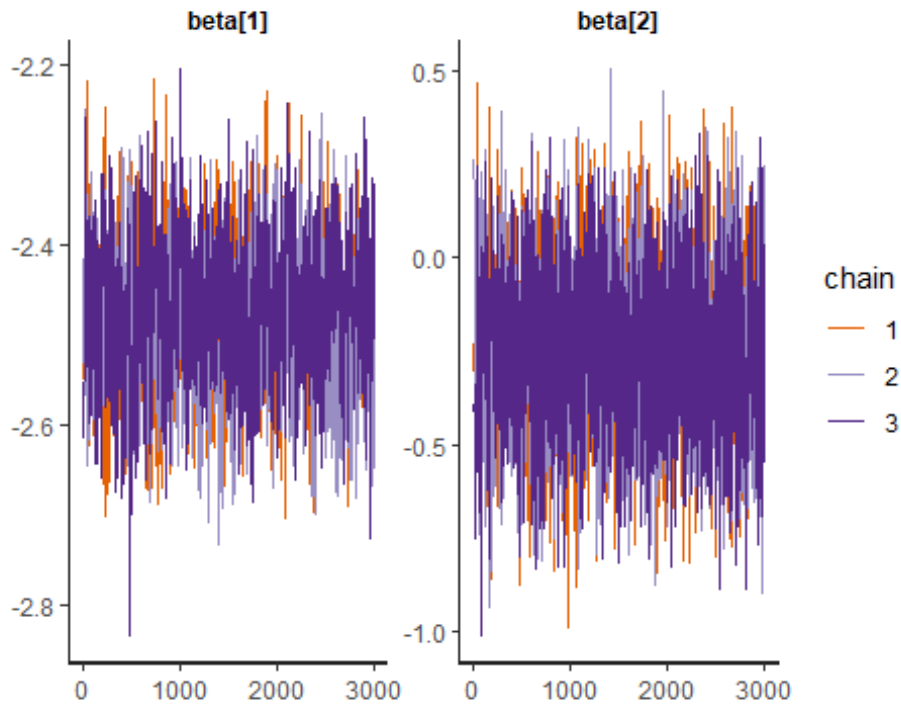
# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#          chains = 3, warmup=7000, cores=3,iter=10000,
#          init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#

load("2phys.rds")
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

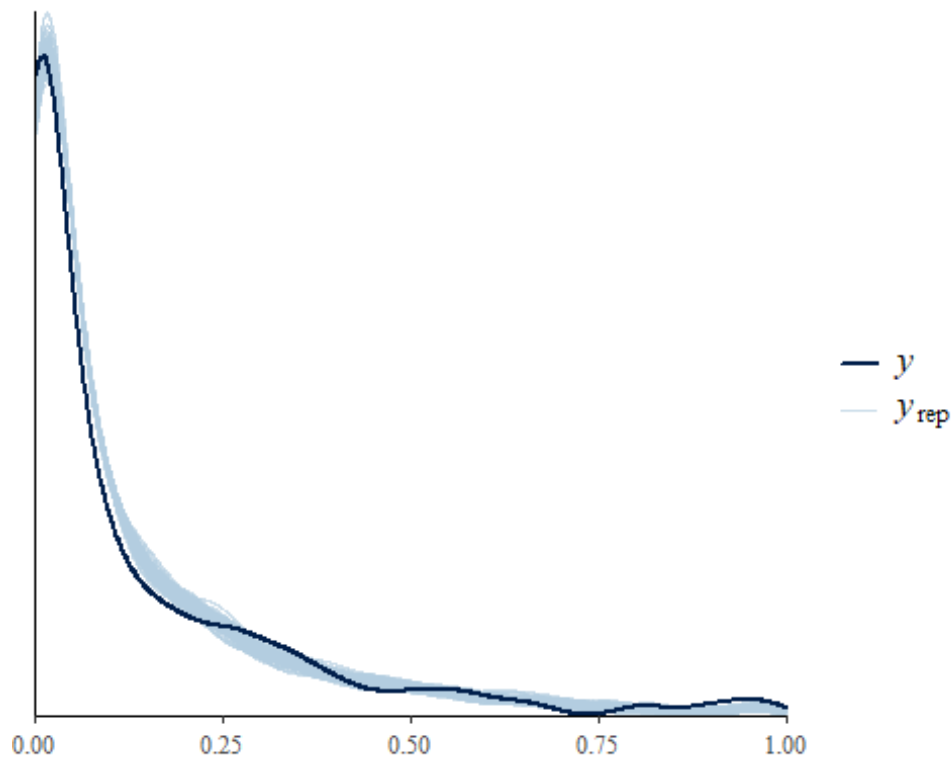
##           mean      se_mean      sd      2.5%      97.5%     n_eff
## beta[1] -2.4820191 0.002481308 0.07546208 -2.6279215 -2.3346343  924.9032
## beta[2] -0.2411791 0.004835885 0.20727066 -0.6552755  0.1529959 1837.0615
##           Rhat
```

```
## beta[1] 1.004280
## beta[2] 1.002053

#checks
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo    7606.0   96.7
## p_loo       1992.4   25.2
## looic      -15212.1 193.3
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                Count Pct.    Min. ESS
## (-Inf, 0.7]  (good)   1425  44.0%   132
##  (0.7, 1]   (bad)    1513  46.8%   <NA>
##  (1, Inf)   (very bad)  297   9.2%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 4: Comparisons of L00ic without and with mechanism", format = "markdown")
```

Table 4: Comparisons of L00ic without and with mechanism

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15212.08	193.3125

```
Looic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", Looic.diff)

## Difference in L00ic = 1.68942
```

Result

Overall model is worse with physiology (delta LOOIC is positive). ## Effect of modeling demography Here I tested if extinction predictions change based on if demography was included or not. I predicted that extinction risks would not vary overall from the median, assuming that models that do not model demography explicitly model an overall mean value.

```
betamat <- model.matrix(~Demography.LH)

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

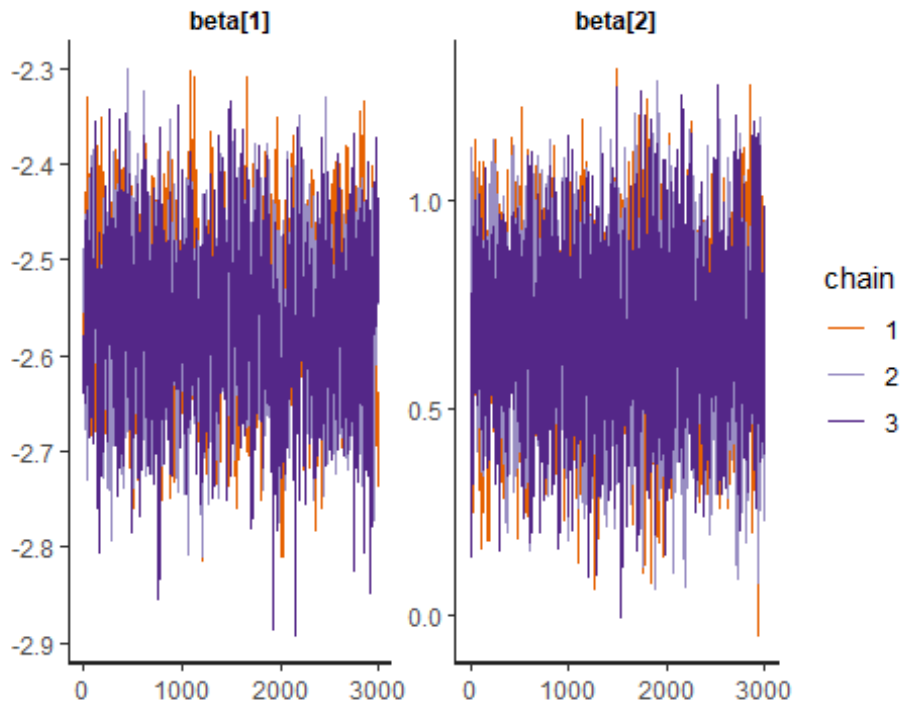
init.beta=rep(0,ncol(betamat)-1)
init.fn<- function (chain_id) {
  list(beta = c(-2.5,init.beta))
}

# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#          chains = 3, warmup=7000, cores=3,iter=10000,
#          init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#
load("2demo.rds")
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

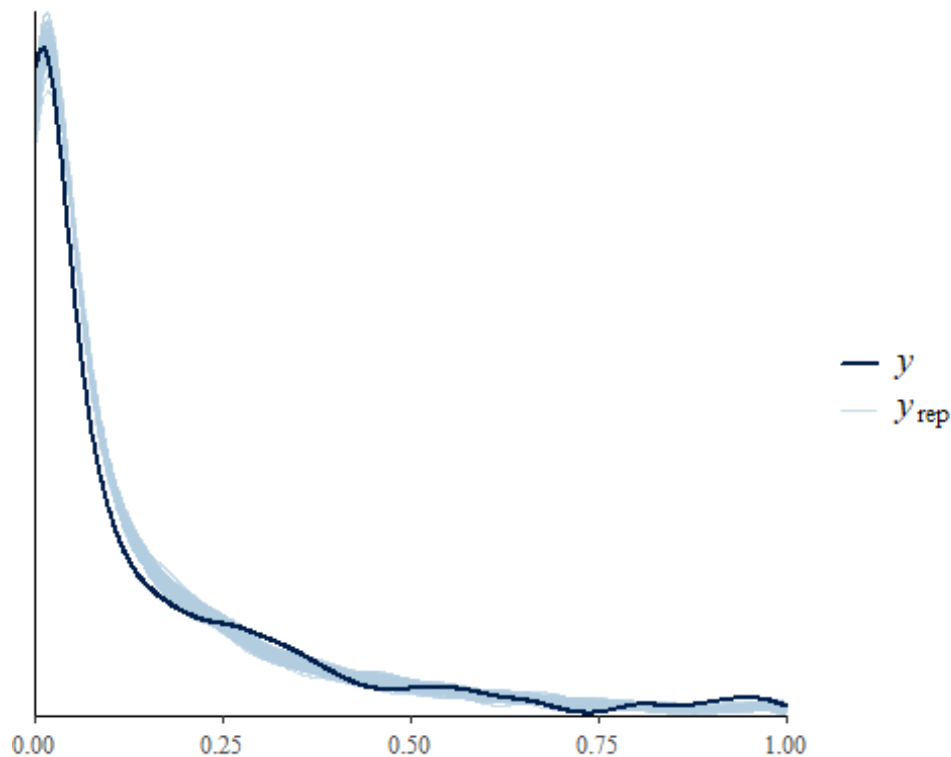
##           mean      se_mean      sd      2.5%      97.5%     n_eff
## beta[1] -2.5629363 0.002470222 0.07888965 -2.7171100 -2.409383 1019.925
## beta[2]  0.6815055 0.004476903 0.18817752  0.3106803  1.052866 1766.770
##           Rhat
```

```
## beta[1] 1.001379
## beta[2] 1.001775

#checks
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```

```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo   7612.6   96.8
## p_loo      1986.6   24.9
## looic     -15225.2 193.7
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##               Count Pct.    Min. ESS
## (-Inf, 0.7]  (good)   1401  43.3%   138
##  (0.7, 1]   (bad)    1573  48.6%   <NA>
##  (1, Inf)   (very bad)  261   8.1%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 5: Comparisons of L00ic without and
with mechanism", format = "markdown")
```

Table 5: Comparisons of L00ic without and with mechanism

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15225.24	193.6831

```
Looic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", Looic.diff)

## Difference in L00ic = -11.46957
```

Result

Overall model is better with demography (delta L00IC is negative). Extinction risks increase when demography is modeled. ## Effect of modeling population differentiation Here I tested if extinction predictions change based on if population differentiation was included or not. I predicted that extinction risks would decrease from the median, assuming that population differentiation indicates more adaptability in species than usually modeled.

```
betamat <- model.matrix(~Pop.diff)

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

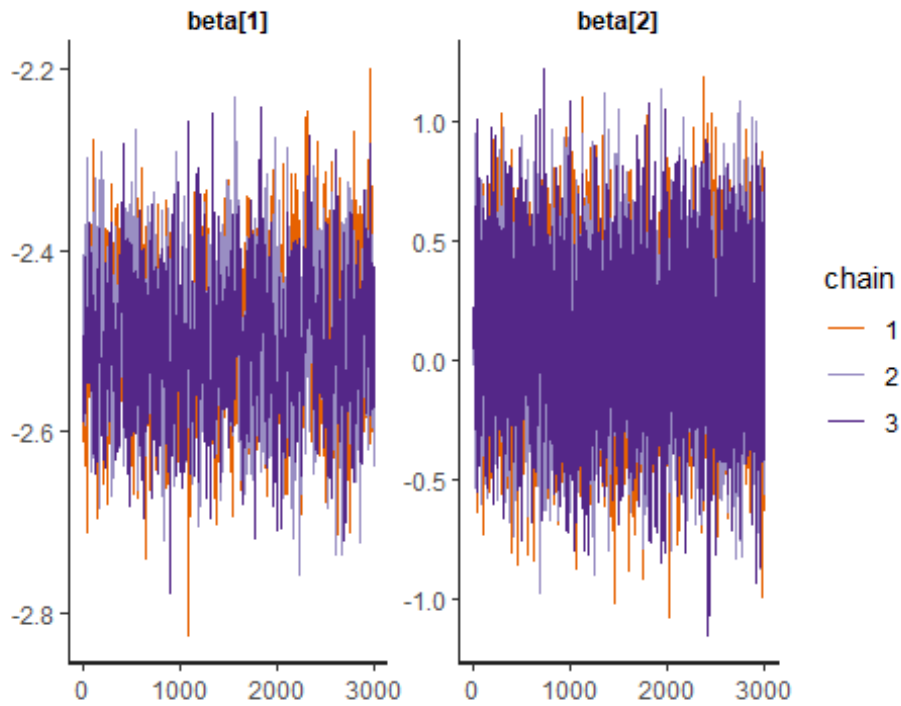
init.beta=rep(0,ncol(betamat)-1)
init.fn<- function (chain_id) {
  list(beta = c(-2.5,init.beta))
}

# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#       chains = 3, warmup=7000, cores=3,iter=10000,
#       init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#
load("2pdiff.rds")
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

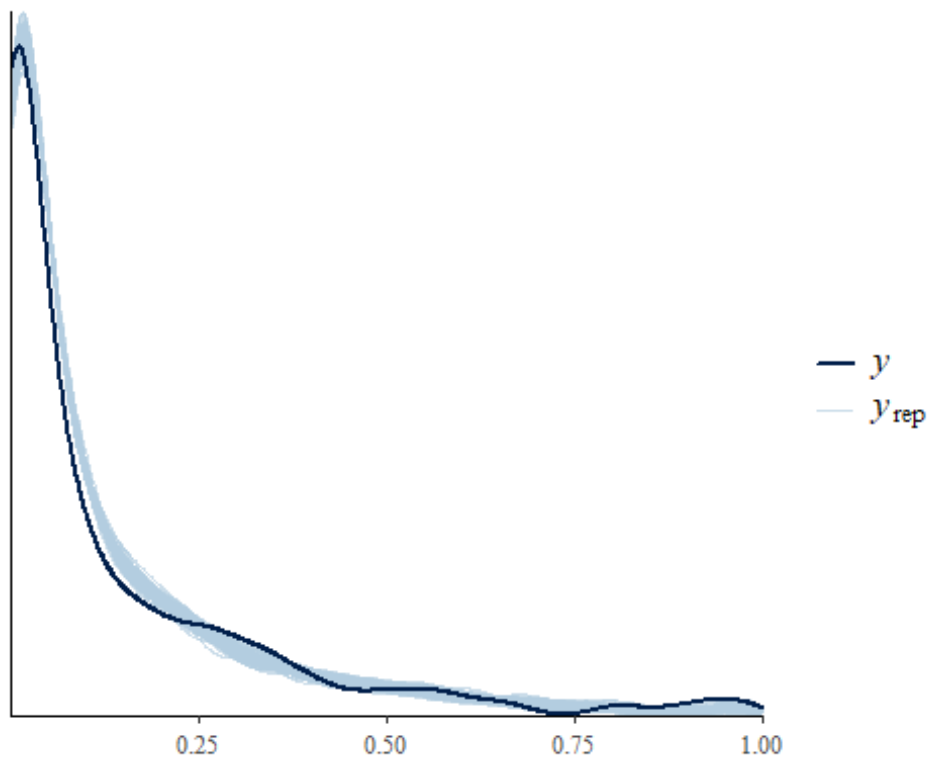
##           mean      se_mean      sd      2.5%      97.5%      n_eff
## beta[1] -2.49845651 0.002441750 0.07473787 -2.6396638 -2.3494908  936.8698
## beta[2]  0.09185001 0.004529495 0.32213222 -0.5294159  0.7286732 5057.8837
##           Rhat
```

```
## beta[1] 1.005086
## beta[2] 1.000413

#checks
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo   7606.6   96.9
## p_loo      1992.5   25.5
## looic      -15213.1 193.7
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##                Count Pct.    Min. ESS
## (-Inf, 0.7]  (good)   1392  43.0%   127
##  (0.7, 1]   (bad)    1565  48.4%   <NA>
##  (1, Inf)   (very bad)  278   8.6%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 6: Comparisons of L00ic without and with mechanism", format = "markdown")
```

Table 6: Comparisons of L00ic without and with mechanism

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15213.15	193.7395

```
Looic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", Looic.diff)

## Difference in L00ic = 0.6236441
```

Result

Overall model is worse with population differentiation (delta LOOIC is positive). ## Effect of modeling adaptation Here I tested if extinction predictions change based on if adaptation was included or not. I predicted that extinction risks would decrease from the median, assuming that adaptation indicates more adaptability in species than usually modeled.

```
betamat <- model.matrix(~Adaptation)

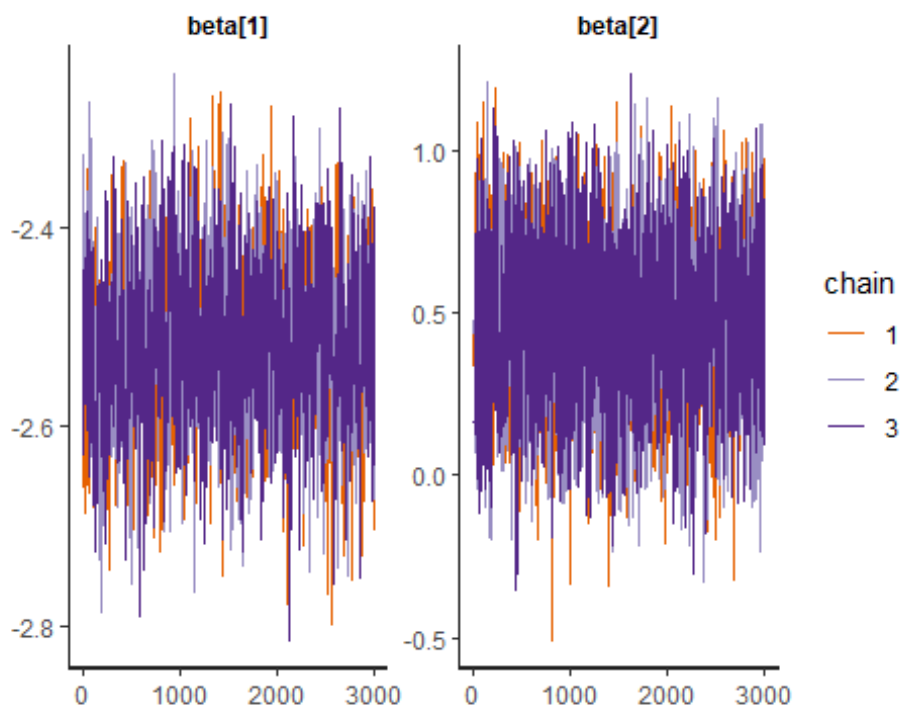
stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

init.beta=rep(0,ncol(betamat)-1)
init.fn<- function (chain_id) {
  list(beta = c(-2.5,init.beta))
}

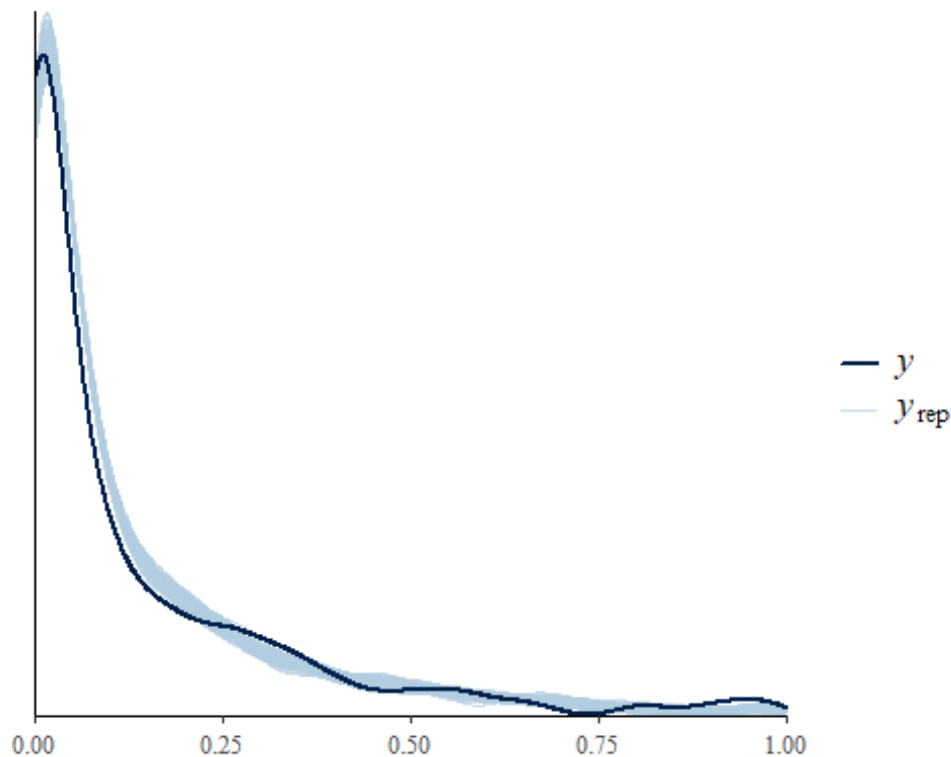
# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#          chains = 3, warmup=7000, cores=3,iter=10000,
#          init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#
load("2adapt.rds")
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

##              mean      se_mean      sd      2.5%      97.5%      n_eff
## beta[1] -2.519886 0.002626487 0.0765695 -2.67391951 -2.3735273 849.887
## beta[2]  0.465504 0.005502585 0.2310354  0.00594716  0.9178168 1762.883
##              Rhat
## beta[1] 1.001604
## beta[2] 1.000348
```

```
#checks  
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(  
  stan.data$percent,  
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],  
  fun = 'dens_overlay'  
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo  7605.1   96.8
## p_loo     1993.4   25.4
## looic     -15210.3 193.6
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##               Count Pct.    Min. ESS
## (-Inf, 0.7]  (good)   1438  44.5%   121
##  (0.7, 1]   (bad)    1535  47.4%   <NA>
##  (1, Inf)   (very bad)  262   8.1%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 7: Comparisons of L00ic without and with mechanism", format = "markdown")
```

Table 7: Comparisons of L00ic without and with mechanism

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15210.27	193.6141

```
Looic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", Looic.diff)

## Difference in L00ic = 3.497617
```

Result

Overall model is worse with adaptation (delta LOOIC is positive). However, there is a suggestion that extinction risks increase with adaptation. ## Effect of modeling habitat Here I tested if extinction predictions change based on if non-climate habitat variation was included or not. I predicted that extinction risks would increase from the median, assuming that habitat variation would reduce ranges more than just climate alone and thus increase risks.

```
betamat <- model.matrix(~Other.Habitat)

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

init.beta=rep(0,ncol(betamat)-1)
init.fn<- function (chain_id) {
  list(beta = c(-2.5,init.beta))
}

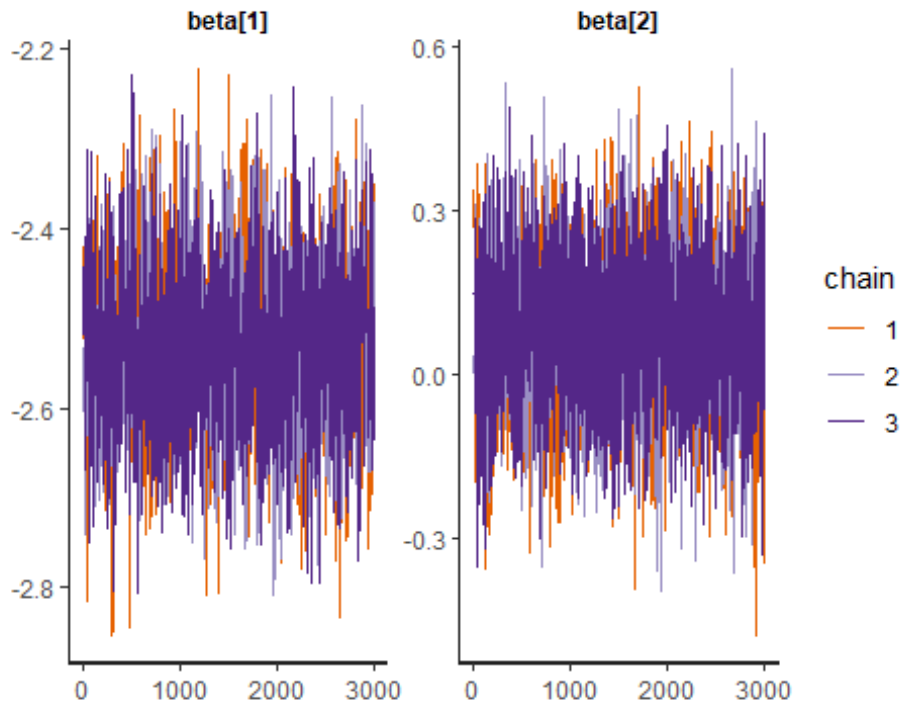
# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#       chains = 3, warmup=7000, cores=3,iter=10000,
#       init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#
load("2habitat.rds")
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

##           mean      se_mean      sd      2.5%      97.5%     n_eff
## beta[1] -2.52947317 0.002738102 0.08875661 -2.7036858 -2.3566572 1050.757
## beta[2]  0.07480421 0.003515232 0.13082793 -0.1876801  0.3310826 1385.138
##           Rhat
```

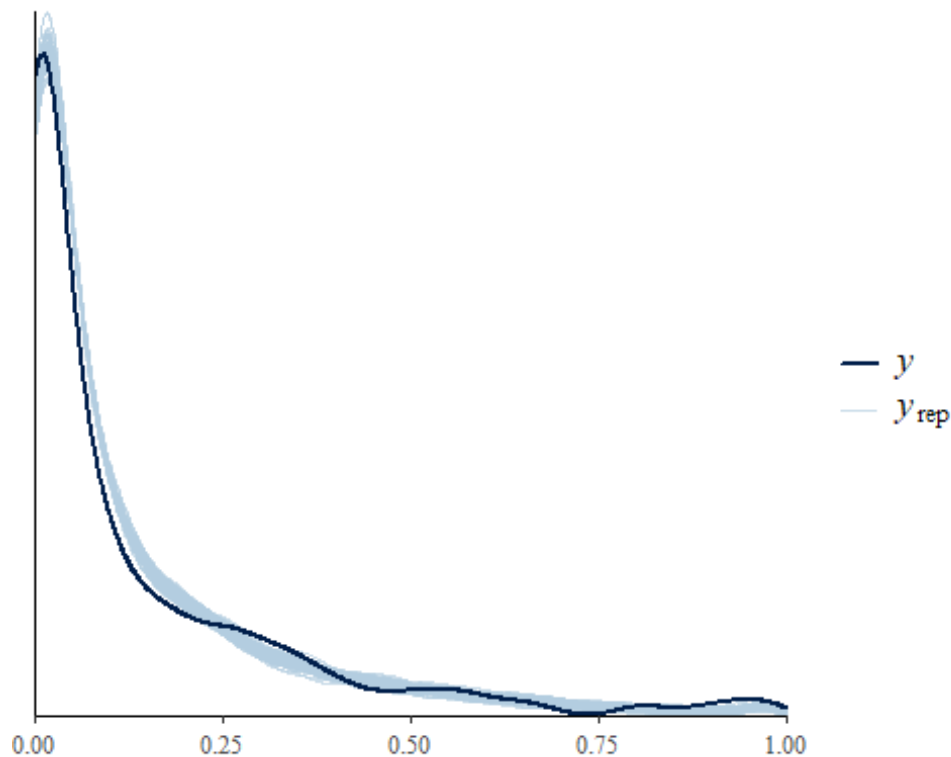


```
## beta[1] 1.000932
## beta[2] 1.000215

#checks
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo   7607.3   96.6
## p_loo      1991.1   25.0
## looic     -15214.6 193.2
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##               Count Pct.    Min. ESS
## (-Inf, 0.7] (good)   1394 43.1%   117
## (0.7, 1]   (bad)    1568 48.5%   <NA>
## (1, Inf)   (very bad) 273  8.4%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 8: Comparisons of L00ic without and with mechanism", format = "markdown")
```

Table 8: Comparisons of L00ic without and with mechanism

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15214.60	193.2276

```
L00ic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", L00ic.diff)

## Difference in L00ic = -0.8351962
```

Result

Overall model is better with habitat (delta LOOIC is negative). However, the effect is not borne out by credible intervals of the contrast.

Effect of modeling Earth systems

Here I tested if extinction predictions change based on if Earth systems models were included or not. I predicted that extinction risks would not affect model outcomes.

```
betamat <- model.matrix(~Earth.Sys)

stan.data<-list(N = N, percent = data.use$percent2, betamat = betamat, phi =
phi, S = n.Study, P = ncol(betamat), Study = Studyint)
params.to.monitor=c("beta","y_rep","stu","sigma_stu", "eta","log_lik")

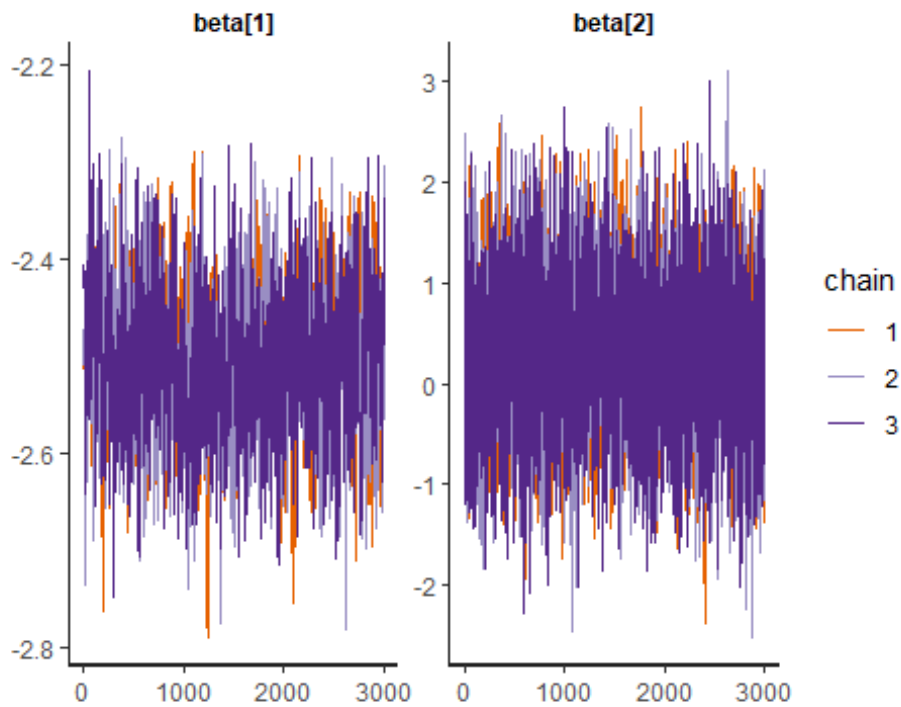
init.beta=rep(0,ncol(betamat)-1)
init.fn<- function (chain_id) {
  list(beta = c(-2.5,init.beta))
}

# mod=stan(file="MetaRisk2 RSTAN beta mat.stan",data=stan.data,pars=params.to
.monitor,
#          chains = 3, warmup=7000, cores=3,iter=10000,
#          init = init.fn, save_warmup = FALSE, control=list(adapt_delta = 0.
9, max_treedepth = 15))#
load("2earth.rds")
params.to.monitor2=c("beta")#
sumx = summary(mod,probs=c(.025,0.975), digits=4, pars=params.to.monitor2)
sumx$summary

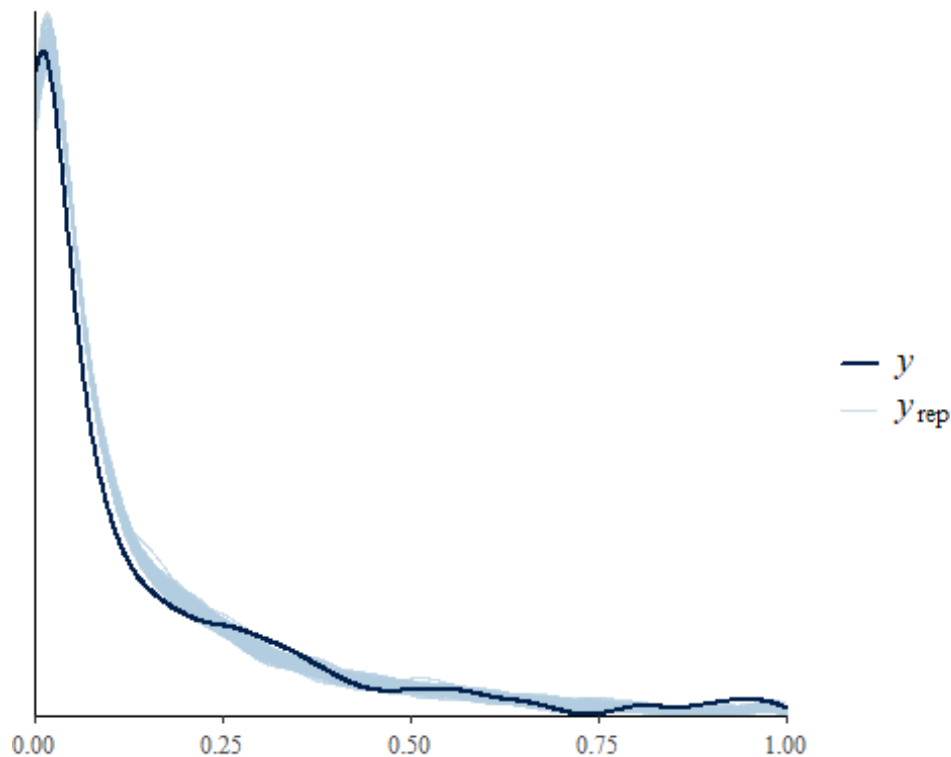
##           mean      se_mean      sd      2.5%      97.5%      n_eff
## beta[1] -2.5040802 0.002739317 0.07488736 -2.648257 -2.355702   747.3643
## beta[2]  0.3189709 0.014656238 0.76119787 -1.162564  1.838785 2697.4296
```

```
##           Rhat
## beta[1] 1.003790
## beta[2] 1.001719

#checks
traceplot(mod, pars=params.to.monitor2, inc_warmup=FALSE)
```



```
pp_check(
  stan.data$percent,
  rstan::extract(mod, par = 'y_rep')$y_rep[1:100, ],
  fun = 'dens_overlay'
)
```



```
#calculate loo
# log_lik_1 <- extract_log_lik(mod, merge_chains = FALSE)
# r_eff <- relative_eff(exp(log_lik_1), cores = 6)
# loo.mod <- loo(log_lik_1, r_eff = r_eff, cores = 6)
loo.mod #

##
## Computed from 9000 by 3235 log-likelihood matrix.
##
##           Estimate      SE
## elpd_loo   7604.2   96.6
## p_loo      1994.2   25.1
## looic     -15208.3 193.2
## -----
## MCSE of elpd_loo is NA.
##
## Pareto k diagnostic values:
##               Count Pct.    Min. ESS
## (-Inf, 0.7] (good)   1395  43.1%   140
##  (0.7, 1]  (bad)    1562  48.3%   <NA>
##  (1, Inf) (very bad)  278   8.6%   <NA>
## See help('pareto-k-diagnostic') for details.

table.data<-data.frame(
  Model = c("Intercept-only model", "Model including mechanism"),
  LOOic = c(loo.mod.int$estimates[3], loo.mod$estimates[3]),
  SE = c(loo.mod.int$estimates[6], loo.mod$estimates[6])
)
```

```
)
knitr::kable(table.data, caption = "Table 9: Comparisons of L00ic without and
with mechanism", format = "markdown")
```

Table 9: Comparisons of L00ic without and with mechanism

Model	L00ic	SE
Intercept-only model	-15213.77	193.3243
Model including mechanism	-15208.33	193.1726

```
Looic.diff = loo.mod$estimates[3] - loo.mod.int$estimates[3]
cat("Difference in L00ic =", Looic.diff)

## Difference in L00ic = 5.443511
```

Result

Overall model is worse with Earth systems (delta LOOIC is positive). ##Compile results and create figures

```
n.total <- nrow(data.use) #total N

#use common median threat
posterior2=as.data.frame(mod.int)
grand.mean = posterior2[["mu"]]
grand.mean.pred <- invlogit(quantile(grand.mean, probs = c(0.025, 0.5, 0.975)
))

#####
*****

load("2disp.rds") #replace with load("2disp.rds") when done
mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Threatened == "Y")/n.total #prop of yes
p.n <- sum(data.use$Threatened == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]] + posterior[["beta[2]"]])
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(
  "r.mean.1" = r.mean.1,
  "beta.N" = beta.N,
  "beta.Y" = beta.Y,
  "beta.vs.r.mean.n" = beta.vs.r.mean.n,
  "beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975),na.rm
=TRUE))
```

```

threat.vals <- data.frame(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],
  beta.N = pred.1[2,2],
  beta.N.hi = pred.1[3,2],
  beta.Y.lo = pred.1[1,3],
  beta.Y = pred.1[2,3],
  beta.Y.hi = pred.1[3,3],
  beta.N.mean.lo = pred.1[1,4],
  beta.N.mean = pred.1[2,4],
  beta.N.mean.hi = pred.1[3,4],
  beta.Y.mean.lo = pred.1[1,5],
  beta.Y.mean = pred.1[2,5],
  beta.Y.mean.hi = pred.1[3,5]
)

#####
load("2spint.rds")
mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Threatened == "Y")/n.total #prop of yes
p.n <- sum(data.use$Threatened == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]] + posterior[["beta[2]"]])
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(
  "r.mean.1" = r.mean.1,
  "beta.N" = beta.N,
  "beta.Y" = beta.Y,
  "beta.vs.r.mean.n" = beta.vs.r.mean.n,
  "beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975), na.rm
=TRUE))

threat.vals[2,] <- data.frame(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],
  beta.N = pred.1[2,2],
  beta.N.hi = pred.1[3,2],
  beta.Y.lo = pred.1[1,3],
  beta.Y = pred.1[2,3],
  beta.Y.hi = pred.1[3,3],
  beta.N.mean.lo = pred.1[1,4],
  beta.N.mean = pred.1[2,4],

```

```

    beta.N.mean.hi = pred.1[3,4],
    beta.Y.mean.lo = pred.1[1,5],
    beta.Y.mean = pred.1[2,5],
    beta.Y.mean.hi = pred.1[3,5]
)

#####

load("2phys.rds")
mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Non.clim.threat == "Y")/n.total #prop of yes
p.n <- sum(data.use$Non.clim.threat == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]] + posterior[["beta[2]"]])
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(
  "r.mean.1" = r.mean.1,
  "beta.N" = beta.N,
  "beta.Y" = beta.Y,
  "beta.vs.r.mean.n" = beta.vs.r.mean.n,
  "beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975), na.rm
=TRUE))

threat.vals[3,] <- cbind(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],
  beta.N = pred.1[2,2],
  beta.N.hi = pred.1[3,2],
  beta.Y.lo = pred.1[1,3],
  beta.Y = pred.1[2,3],
  beta.Y.hi = pred.1[3,3],
  beta.N.mean.lo = pred.1[1,4],
  beta.N.mean = pred.1[2,4],
  beta.N.mean.hi = pred.1[3,4],
  beta.Y.mean.lo = pred.1[1,5],
  beta.Y.mean = pred.1[2,5],
  beta.Y.mean.hi = pred.1[3,5]
)
#####

load("2demo.rds")

```



```

mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Land.Use.Change == "Y")/n.total #prop of yes
p.n <- sum(data.use$Land.Use.Change == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]] + posterior[["beta[2]"]])
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(
  "r.mean.1" = r.mean.1,
  "beta.N" = beta.N,
  "beta.Y" = beta.Y,
  "beta.vs.r.mean.n" = beta.vs.r.mean.n,
  "beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975), na.rm
=TRUE))

threat.vals[4,]<- cbind(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],
  beta.N = pred.1[2,2],
  beta.N.hi = pred.1[3,2],
  beta.Y.lo = pred.1[1,3],
  beta.Y = pred.1[2,3],
  beta.Y.hi = pred.1[3,3],
  beta.N.mean.lo = pred.1[1,4],
  beta.N.mean = pred.1[2,4],
  beta.N.mean.hi = pred.1[3,4],
  beta.Y.mean.lo = pred.1[1,5],
  beta.Y.mean = pred.1[2,5],
  beta.Y.mean.hi = pred.1[3,5]
)
#*****
*****
load("2pdiff.rds")
mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Land.Use.Change == "Y")/n.total #prop of yes
p.n <- sum(data.use$Land.Use.Change == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]] + posterior[["beta[2]"]])
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(

```

```

"r.mean.1" = r.mean.1,
"beta.N" = beta.N,
"beta.Y" = beta.Y,
"beta.vs.r.mean.n" = beta.vs.r.mean.n,
"beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975), na.rm
=TRUE))

threat.vals[5,]<- cbind(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],
  beta.N = pred.1[2,2],
  beta.N.hi = pred.1[3,2],
  beta.Y.lo = pred.1[1,3],
  beta.Y = pred.1[2,3],
  beta.Y.hi = pred.1[3,3],
  beta.N.mean.lo = pred.1[1,4],
  beta.N.mean = pred.1[2,4],
  beta.N.mean.hi = pred.1[3,4],
  beta.Y.mean.lo = pred.1[1,5],
  beta.Y.mean = pred.1[2,5],
  beta.Y.mean.hi = pred.1[3,5]
)
#*****
#*****
#*
load("2adapt.rds")
mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Land.Use.Change == "Y")/n.total #prop of yes
p.n <- sum(data.use$Land.Use.Change == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]]) + posterior[["beta[2]"]]
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(
"r.mean.1" = r.mean.1,
"beta.N" = beta.N,
"beta.Y" = beta.Y,
"beta.vs.r.mean.n" = beta.vs.r.mean.n,
"beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975), na.rm
=TRUE))

threat.vals[6,]<- cbind(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],

```

```

beta.N = pred.1[2,2],
beta.N.hi = pred.1[3,2],
beta.Y.lo = pred.1[1,3],
beta.Y = pred.1[2,3],
beta.Y.hi = pred.1[3,3],
beta.N.mean.lo = pred.1[1,4],
beta.N.mean = pred.1[2,4],
beta.N.mean.hi = pred.1[3,4],
beta.Y.mean.lo = pred.1[1,5],
beta.Y.mean = pred.1[2,5],
beta.Y.mean.hi = pred.1[3,5]
)
#####
#####
#
load("2habitat.rds")
mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Land.Use.Change == "Y")/n.total #prop of yes
p.n <- sum(data.use$Land.Use.Change == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]]) + posterior[["beta[2]"]])
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(
  "r.mean.1" = r.mean.1,
  "beta.N" = beta.N,
  "beta.Y" = beta.Y,
  "beta.vs.r.mean.n" = beta.vs.r.mean.n,
  "beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975), na.rm
=TRUE))

threat.vals[7,]<- cbind(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],
  beta.N = pred.1[2,2],
  beta.N.hi = pred.1[3,2],
  beta.Y.lo = pred.1[1,3],
  beta.Y = pred.1[2,3],
  beta.Y.hi = pred.1[3,3],
  beta.N.mean.lo = pred.1[1,4],
  beta.N.mean = pred.1[2,4],
  beta.N.mean.hi = pred.1[3,4],
  beta.Y.mean.lo = pred.1[1,5],
  beta.Y.mean = pred.1[2,5],
  beta.Y.mean.hi = pred.1[3,5])

```

```

)
#*****
#
load("2earth.rds")
mod.a <- mod
posterior <- as.data.frame(mod.a)
p.y <- sum(data.use$Land.Use.Change == "Y")/n.total #prop of yes
p.n <- sum(data.use$Land.Use.Change == "N")/n.total #prop of nos
beta.Y = invlogit(posterior[["beta[1]"]]) + posterior[["beta[2]"]])
beta.N = invlogit(posterior[["beta[1]"]])
#r.mean.1 = p.n * beta.N + p.y * beta.Y
r.mean.1 = invlogit(grand.mean)
beta.vs.r.mean.n = (beta.N) - (r.mean.1)
beta.vs.r.mean.y = (beta.Y) - (r.mean.1)

param.vals.1 <- data.frame(
  "r.mean.1" = r.mean.1,
  "beta.N" = beta.N,
  "beta.Y" = beta.Y,
  "beta.vs.r.mean.n" = beta.vs.r.mean.n,
  "beta.vs.r.mean.y" = beta.vs.r.mean.y
)
pred.1 = (apply(param.vals.1, 2, quantile, probs = c(0.025, 0.5, 0.975),na.rm
=TRUE))

threat.vals[8,]<- cbind(overall.mean = pred.1[2,1],
  beta.N.lo = pred.1[1,2],
  beta.N = pred.1[2,2],
  beta.N.hi = pred.1[3,2],
  beta.Y.lo = pred.1[1,3],
  beta.Y = pred.1[2,3],
  beta.Y.hi = pred.1[3,3],
  beta.N.mean.lo = pred.1[1,4],
  beta.N.mean = pred.1[2,4],
  beta.N.mean.hi = pred.1[3,4],
  beta.Y.mean.lo = pred.1[1,5],
  beta.Y.mean = pred.1[2,5],
  beta.Y.mean.hi = pred.1[3,5]
)
#*****
#
threat.vals$threat = c("Dispersal", "Species Interactions", "Physiology", "Dem
ography", "Population differentiation", "Adaptation", "Habitat", "Earth syste
ms")

save(threat.vals,file ="Mech traits results.rds")

```

```
threat.vals.r <- threat.vals
threat.vals.r[,1:13] <- round((threat.vals.r[,1:13]), digits = 4)
knitr::kable(threat.vals.r, caption = "Table 10: Extinction risk by mechanistic traits and difference from mean, with 95% credible intervals", format = "markdown", font = 5)
```

Table 10: Extinction risk by mechanistic traits and difference from mean, with 95% credible intervals

overall. mean	beta. N.lo	bet a.N	beta. N.hi	beta. Y.lo	bet a.Y	beta. Y.hi	beta.N. mean.lo	beta.N. mean	beta.N. mean.hi	beta.Y. mean.lo	beta.Y. mean	beta.Y. mean.hi	threat
0.076	0.06 54	0.0 749	0.08 60	0.06 16	0.0 784	0.09 93	-0.0157	- 0.0010	0.0139	-0.0177	0.0023	0.0254	Dispersal
0.076	0.06 31	0.0 723	0.08 32	0.09 57	0.1 309	0.17 61	-0.0178	- 0.0035	0.0112	0.0177	0.0551	0.1003	Species Interactions
0.076	0.06 74	0.0 770	0.08 83	0.04 16	0.0 616	0.08 93	-0.0134	0.0012	0.0164	-0.0371	- 0.0140	0.0152	Physiology
0.076	0.06 20	0.0 715	0.08 25	0.09 56	0.1 319	0.18 10	-0.0191	- 0.0044	0.0104	0.0183	0.0560	0.1065	Demography
0.076	0.06 66	0.0 759	0.08 71	0.04 59	0.0 822	0.14 67	-0.0140	0.0000	0.0153	-0.0320	0.0063	0.0710	Population differentiation
0.076	0.06 45	0.0 745	0.08 52	0.07 44	0.1 138	0.16 83	-0.0161	- 0.0013	0.0129	-0.0032	0.0379	0.0934	Adaptation
0.076	0.06 28	0.0 738	0.08 65	0.06 41	0.0 791	0.09 72	-0.0177	- 0.0021	0.0144	-0.0147	0.0032	0.0235	Habitat
0.076	0.06 61	0.0 756	0.08 66	0.02 53	0.1 007	0.33 75	-0.0150	- 0.0003	0.0143	-0.0516	0.0250	0.2615	Earth systems

#arrange in increasing order#

```
threat.vals$threat = with (threat.vals, reorder(threat, beta.Y))
```

#Figures

```
Fig1a<-ggplot(data = threat.vals)+
  geom_vline(xintercept=grand.mean.pred[2]) +
  geom_errorbar(aes(y = threat, xmin = beta.Y.lo, xmax = beta.Y.hi), width =
0) +
  geom_point(stat = "identity", aes(y = threat, x = beta.Y), color = "#416788",
size = 3, shape = 15) +
  xlab("Pre-industrial rise \n in temperature (C)") + xlim(c(0,.35)) +
  theme_classic()+
  theme(axis.title.y = element_blank(),axis.title=element_text(size=14),axis.
text = element_text(size=12))+
  guides(size=F)
```

Warning: The ``<scale>`` argument of ``guides()`` cannot be `FALSE`. Use "none" instead as

of ggplot2 3.3.4.

This warning is displayed once every 8 hours.

Call ``lifecycle::last_lifecycle_warnings()`` to see where this warning was generated.

Fig1a

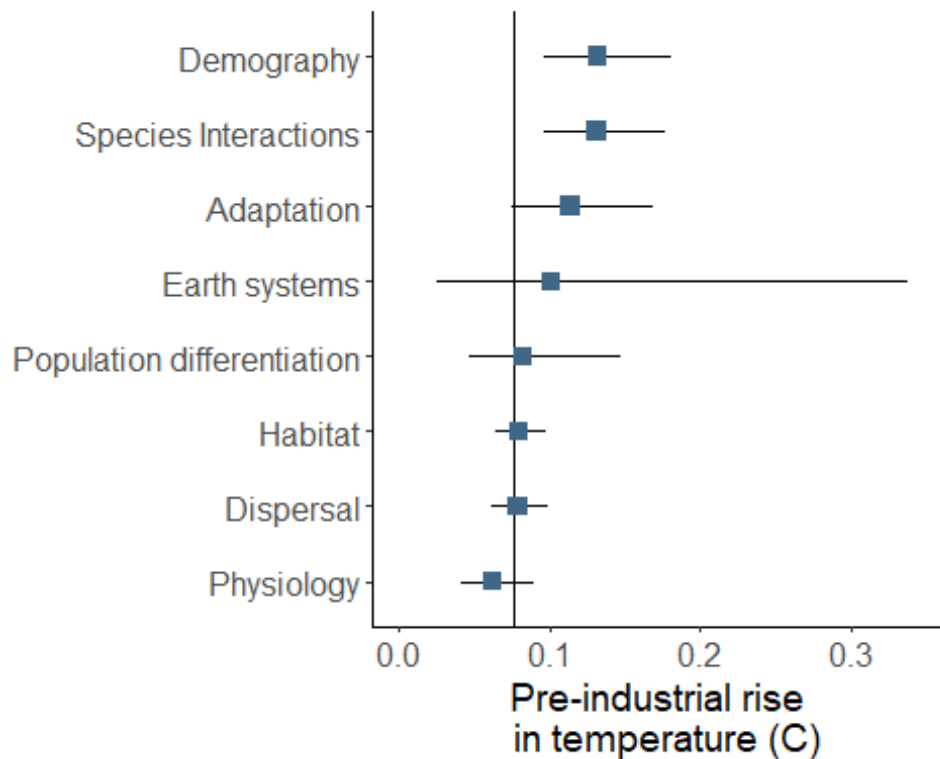


Fig. 1. Predicted extinction risk based on various mechanistic assumptions.

```
#Differences from zero
glob.mean.over <- rep("n",nrow(threat.vals))
glob.mean.over[threat.vals$beta.Y.mean > 0 & threat.vals$beta.Y.mean.lo > 0]
= "y"
glob.mean.over[threat.vals$beta.Y.mean < 0 & threat.vals$beta.Y.mean.hi < 0]
= "y"
threat.vals$glob.mean.over <- glob.mean.over

Fig1b <- ggplot(data = threat.vals)+
  geom_vline(xintercept=0) +
  geom_errorbar(aes(y = threat, xmin = beta.Y.mean.lo, xmax = beta.Y.mean.hi)
, width = 0) +
  geom_point(stat = "identity", aes(y = threat, x = beta.Y.mean, color = glob
.mean.over), size = 3, shape = 15) +
  scale_color_manual(values=c('grey','#5B507A'))+
  xlab("Percent difference \n from global mean") + xlim(c(-.15,.3)) +
  theme_classic()+
  theme(axis.title.y = element_blank(),axis.ticks.y = element_blank(),axis.li
ne.y = element_blank(),axis.text.y = element_blank(),
        axis.title=element_text(size=14),axis.text = element_text(size=12),le
gend.position = "none")+
  guides(size=F)
Fig1b
```

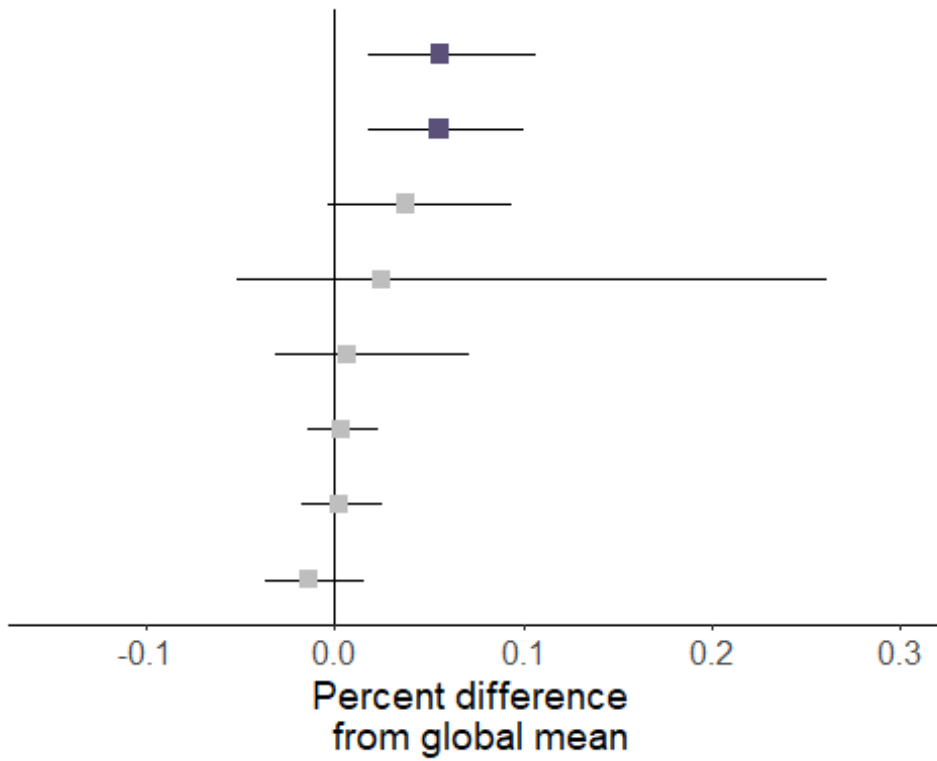


Fig. 2. Predicted extinction risk based on various mechanistic assumptions.

```
ggarrange(Fig1a, NULL, Fig1b, ncol=3, widths = c(4,.4, 2))
```

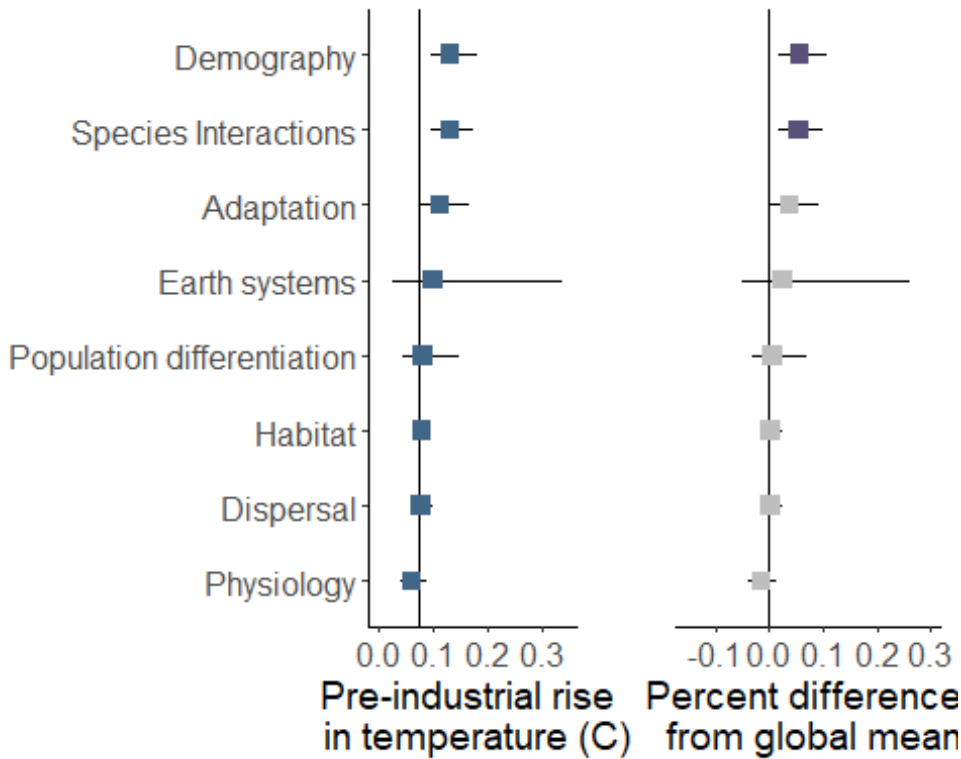


Fig. 3. Predicted extinction risk based on various mechanistic assumptions.

```
#ggsave("Metarisk2_mech.png",width=8,height=6,unit="in",dpi="print")
```

```
threat.YN<-data.frame(
  threat = c("Dispersal - N","Dispersal - Y","Sp. Int. - N","Sp. Int. - Y","P
hysiology - N","Physiology - Y","Demography - N","Demography - Y","Pop. diff.
- N","Pop. diff. - Y","Adaptation - N","Adaptation - Y","Habitat - N","Habita
t - Y","Earth systems - N","Earth systems - Y"),
  YN = rep(c("N","Y"),8),
  beta = c(threat.vals$beta.N[1],threat.vals$beta.Y[1],threat.vals$beta.N[2],
threat.vals$beta.Y[2],threat.vals$beta.N[3],threat.vals$beta.Y[3],threat.vals
$beta.N[4],threat.vals$beta.Y[4],threat.vals$beta.N[5],threat.vals$beta.Y[5],
threat.vals$beta.N[6],threat.vals$beta.Y[6],threat.vals$beta.N[7],threat.vals
$beta.Y[7],threat.vals$beta.N[8],threat.vals$beta.Y[8]),
  beta.lo = c(threat.vals$beta.N.lo[1],threat.vals$beta.Y.lo[1],threat.vals$
beta.N.lo[2],threat.vals$beta.Y.lo[2],threat.vals$beta.N.lo[3],threat.vals$be
ta.Y.lo[3],threat.vals$beta.N.lo[4],threat.vals$beta.Y.lo[4],threat.vals$beta
.N.lo[5],threat.vals$beta.Y.lo[5],threat.vals$beta.N.lo[6],threat.vals$beta.Y
.lo[6],threat.vals$beta.N.lo[7],threat.vals$beta.Y.lo[7],threat.vals$beta.N.l
o[8],threat.vals$beta.Y.lo[8]),
  beta.hi = c(threat.vals$beta.N.hi[1],threat.vals$beta.Y.hi[1],threat.vals
$beta.N.hi[2],threat.vals$beta.Y.hi[2],threat.vals$beta.N.hi[3],threat.vals$b
eta.Y.hi[3],threat.vals$beta.N.hi[4],threat.vals$beta.Y.hi[4],threat.vals$bet
a.N.hi[5],threat.vals$beta.Y.hi[5],threat.vals$beta.N.hi[6],threat.vals$beta.
Y.hi[6],threat.vals$beta.N.hi[7],threat.vals$beta.Y.hi[7],threat.vals$beta.N.
hi[8],threat.vals$beta.Y.hi[8])
```



```

)

#set colors
boolColors <- as.character(c("N"="#416788", "Y"="#8cb369"))
boolScale <- scale_colour_manual(name="YN", values=boolColors)

#Figures
Fig2<-ggplot(data = threat.YN)+
  geom_vline(xintercept=grand.mean.pred[2]) +
  geom_errorbar(aes(y = threat, xmin = beta.lo, xmax = beta.hi), width = 0) +
  geom_point(stat = "identity", aes(y = threat, x = beta, color = YN), size =
3, shape = 15) +
  xlab("Pre-industrial rise \n in temperature (C)") + xlim(c(0,.35)) +
  theme_classic() + boolScale +
  theme(axis.title.y = element_blank(),axis.title=element_text(size=14),axis.
text = element_text(size=12))+
  guides(color = guide_legend(""))
Fig2

```

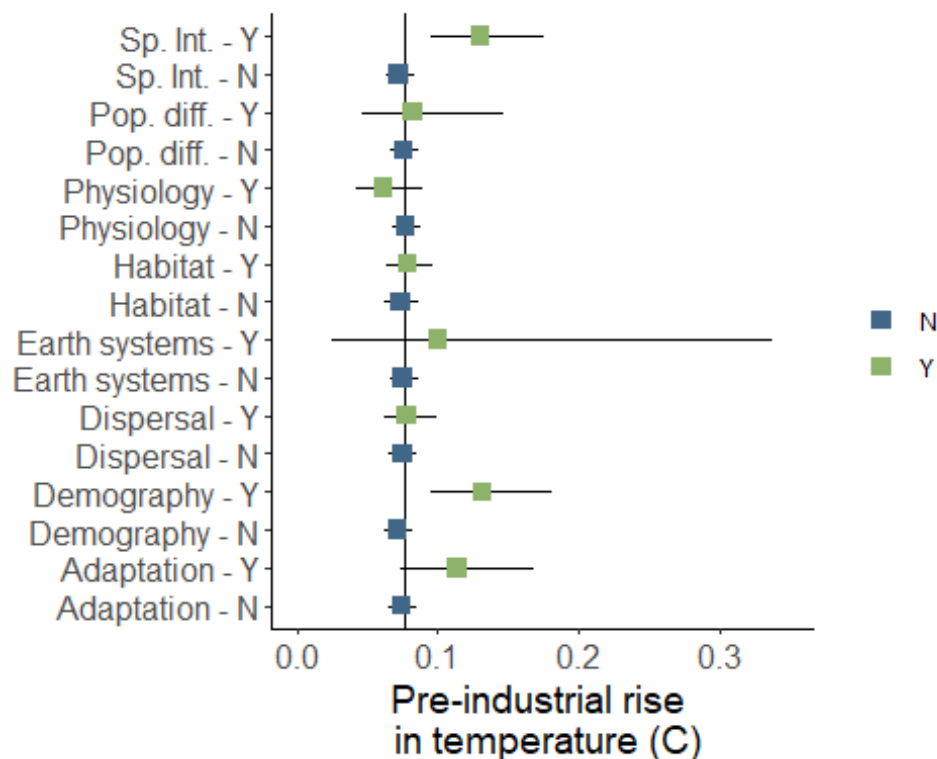


Fig. 4. Predicted extinction risk based on various mechanistic assumptions.

```

#ggsave("Metarisk2_mech_YN.png",width=8,height=6,unit="in",dpi="print")

#catalog sample sizes
N.1.st<-length(unique(dataP$Study[dataP$Dispersal == "Y"]))
N.1.mod<-length((dataP$Study[dataP$Dispersal == "Y"]))

```

```

N.2.st<-length(unique(dataP$Study[dataP$Sp.int == "Y"]))
N.2.mod<-length((dataP$Study[dataP$Sp.int == "Y"]))

N.3.st<-length(unique(dataP$Study[dataP$Physiology == "Y"]))
N.3.mod<-length((dataP$Study[dataP$Physiology == "Y"]))

N.4.st<-length(unique(dataP$Study[dataP$Demography.LH == "Y"]))
N.4.mod<-length((dataP$Study[dataP$Demography.LH == "Y"]))

N.5.st<-length(unique(dataP$Study[dataP$Pop.diff == "Y"]))
N.5.mod<-length((dataP$Study[dataP$Pop.diff == "Y"]))

N.6.st<-length(unique(dataP$Study[dataP$Adaptation == "Y"]))
N.6.mod<-length((dataP$Study[dataP$Adaptation == "Y"]))

N.7.st<-length(unique(dataP$Study[dataP$Other.Habitat == "Y"]))
N.7.mod<-length((dataP$Study[dataP$Other.Habitat == "Y"]))

N.8.st<-length(unique(dataP$Study[dataP$Earth.Sys == "Y"]))
N.8.mod<-length((dataP$Study[dataP$Earth.Sys == "Y"]))

table.data<-data.frame(
  Factor = threat.vals$threat,
  Studies = c(N.1.st,N.2.st,N.3.st,N.4.st,N.5.st,N.6.st,N.7.st,N.8.st),
  Models = c(N.1.mod,N.2.mod,N.3.mod,N.4.mod,N.5.mod,N.6.mod,N.7.mod,N.8.mod)
)
knitr::kable(table.data, caption = "Table 2: Number of studies and models for
each factor", format = "markdown")

```

Table 11: Number of studies and models for each factor

Factor	Studies	Models
Dispersal	64	431
Species Interactions	43	248
Physiology	39	260
Demography	51	337
Population differentiation	9	43
Adaptation	18	121
Habitat	171	1199
Earth systems	5	16

Conclusion

Studies that included species-specific demography, species interactions, and xx predicted higher extinction risks. # Variation explained

```

#After Gelman 2019 R2 for Bayesian
#
#Load model and beta matrix - check if mu is modeled separately
load("3allmechs.rds")
posterior=as.data.frame(mod);

betamat <- data.frame(
  Intercept = rep(1,N),
  Dispersal = ifelse(data.use$Dispersal == "Y",1,0),
  Sp.int = ifelse(data.use$Sp.int == "Y",1,0),
  Physiology = ifelse(data.use$Physiology == "Y",1,0),
  Adaptation = ifelse(data.use$Adaptation == "Y",1,0),
  Pop.diff = ifelse(data.use$Pop.diff == "Y",1,0),
  Demography.LH = ifelse(data.use$Demography.LH == "Y",1,0),
  Earth.Sys = ifelse(data.use$Earth.Sys == "Y",1,0),
  Other.Habitat = ifelse(data.use$Other.Habitat == "Y",1,0))

#Variables and matrices
S = 9000; #samples
K = ncol(betamat); #factors
p.mat <- as.matrix(posterior[,1:K])
y = dataP$percent2
y.mat = t(matrix(rep(y,S), nrow = N, ncol = S))
y.mean <- mean(y)

#Calculate y.pred for fixed effects only
y.pred <- matrix(rep(NA, N*S), nrow = S, ncol = N)
theta <- y.pred
for (i in 1:N) {
  theta[,i] = invlogit(p.mat %*% t(betamat[i,]))#rows = samples, cols = i
  y.pred[,i] = (theta[,i] * data.use$Total.N[i])/(theta[,i] * data.use$Total.N[i] + (1-theta[,i]) * data.use$Total.N[i])
}

#Calcluate residual variance
res.f = y.mat - y.pred
RSS.f = rowSums((res.f)^2)
res.v.f = 1/(N -1) * RSS.f

#Calculate fit variance
pred.v.f = 1/(N-1) * rowSums((y.pred)^2)

#Calculate R2
R2.v.f = pred.v.f/(pred.v.f + res.v.f)
cat("fixed effects R2 = ", quantile(R2.v.f,probs = c(0.025, 0.5, 0.975),na.rm = T))

## fixed effects R2 = 0.07282294 0.09797332 0.1291702

```

```

#Total model With random effects
y.pred.c <-(as.matrix(posterior[, (K+1):(N+K)])) #calculated in STAN, with all
RE and weightings

#Calculate residual variance
res.c = y.mat - y.pred.c
RSS.c = rowSums((res.c)^2)
res.v.c = 1/(N-1) * RSS.c

#Calculate fit variance

pred.v.c = 1/(N-1) * rowSums(y.pred.c^2)

#Calculate full model R2
R2.v.c = pred.v.c/(pred.v.c + res.v.c)
print(" ")
## [1] " "

cat("Overall model R2 = ", quantile(R2.v.c, probs = c(0.025, 0.5, 0.975), na.rm
= T))

## Overall model R2 = 0.7661777 0.7866636 0.8064059

```