

```

library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.0 --
## v ggplot2 3.2.1    v purrr  0.3.3
## v tibble  2.1.3    v dplyr  0.8.3
## v tidyr   1.0.0    v stringr 1.4.0
## v readr   1.3.1    v forcats 0.4.0

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

library(brms)

## Loading required package: Rcpp
## Loading 'brms' package (version 2.12.0). Useful instructions
## can be found by typing help('brms'). A more detailed introduction
## to the package is available through vignette('brms_overview').

##
## Attaching package: 'brms'

## The following object is masked from 'package:stats':
##
##      ar

library(tidybayes)
library(cowplot)

##
## *****
## Note: As of version 1.0.0, cowplot does not change the
## default ggplot2 theme anymore. To recover the previous
## behavior, execute:
## theme_set(theme_cowplot())
## *****

library(multcomp)

## Loading required package: mvtnorm
## Loading required package: survival
##
## Attaching package: 'survival'

## The following object is masked from 'package:brms':
##
##      kidney

## Loading required package: TH.data
## Loading required package: MASS
##
## Attaching package: 'MASS'

```

```

## The following object is masked from 'package:dplyr':
##
##   select
##
## Attaching package: 'TH.data'
##
## The following object is masked from 'package:MASS':
##
##   geysler
dat <- read_tsv("data/functional_test_all_log_reg2.txt") %>% mutate(cage2 = paste(treatment, group, cage))

## Parsed with column specification:
## cols(
##   bee = col_character(),
##   treatment = col_character(),
##   group = col_character(),
##   cage = col_character(),
##   alive = col_double()
## )

controlDatChlor <- read_tsv("data/control_exp_functional_test_added_Chlorothalonil_2020.txt") %>% mutate(

## Parsed with column specification:
## cols(
##   bee = col_character(),
##   bee_cage = col_character(),
##   group = col_character(),
##   cage = col_character(),
##   cage2 = col_character(),
##   alive = col_double()
## )

controlDatFiltered <- read_tsv("data/control_exp_functional_test_filtered_microbiome_2020.txt") %>% mutate(

## Parsed with column specification:
## cols(
##   bee = col_character(),
##   bee_cage = col_character(),
##   group = col_character(),
##   cage = col_character(),
##   cage2 = col_character(),
##   alive = col_double()
## )

```

Tetracycline

```

priorsCage <- c(prior(student_t(3,0,2.5), class = "b"))
tet <- brm(alive ~ 0 + cage2 , data = filter(dat, treatment == "Tetracycline"), family= bernoulli(), com

## Compiling the C++ model
## Trying to compile a simple C file
## Running /usr/local/Cellar/r/3.6.1_1/lib/R/bin/R CMD SHLIB foo.c
## /usr/local/clang7/bin/clang -I"/usr/local/Cellar/r/3.6.1_1/lib/R/include" -DNDEBUG -I"/usr/local/1

```

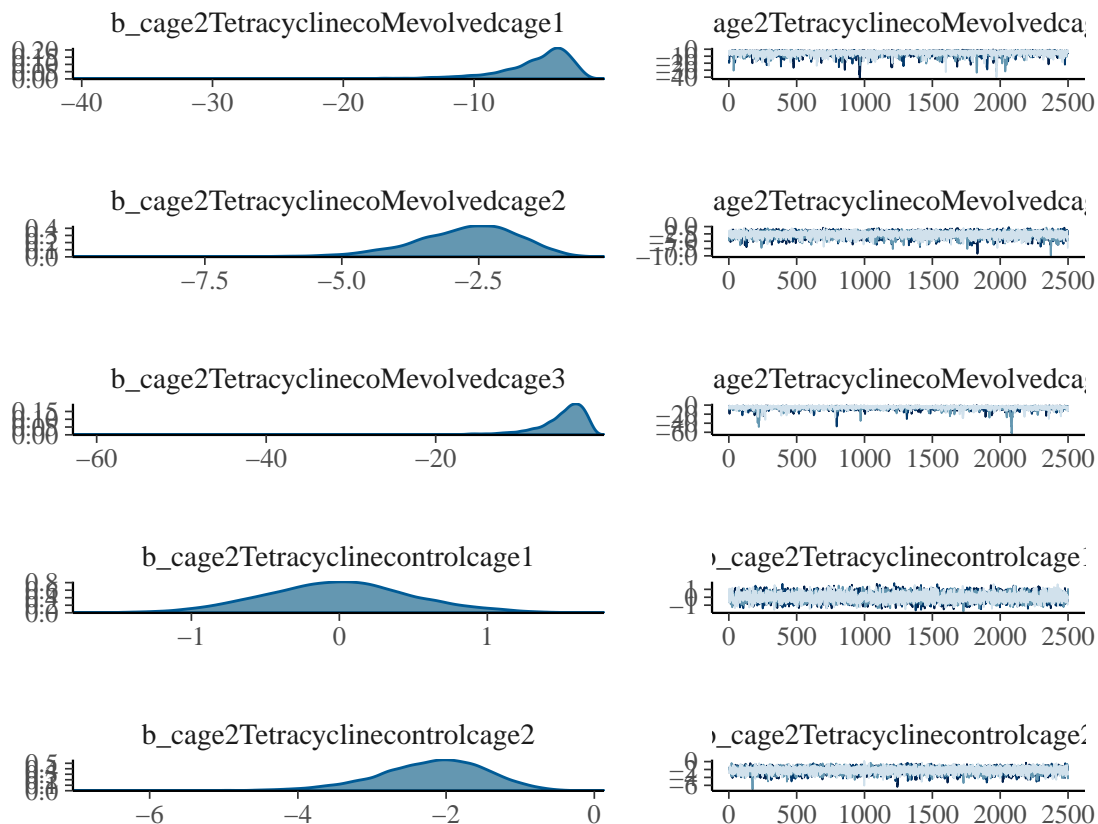
```

## In file included from <built-in>:1:
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:88:
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:1: error: unknow
## namespace Eigen {
## ^
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:16: error: expe
## namespace Eigen {
## ^
## ;
## In file included from <built-in>:1:
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:96:10: fatal error: 'complex' file no
## #include <complex>
## ^~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

```

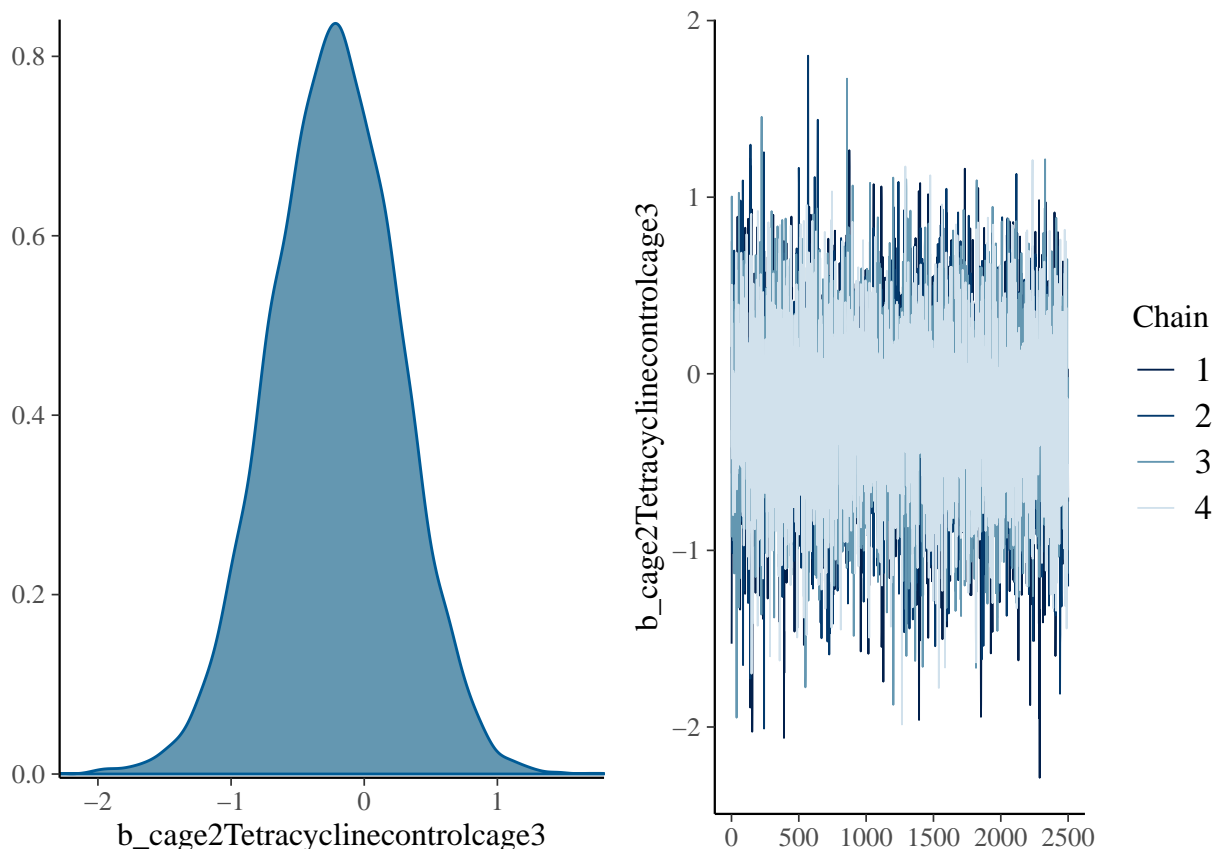
```
## Start sampling
```

```
plot(tet)
```



Chain

— 1
— 2
— 3
— 4



```
summary(tet)
```

```
## Family: bernoulli
## Links: mu = logit
## Formula: alive ~ 0 + cage2
## Data: filter(dat, treatment == "Tetracycline") (Number of observations: 100)
## Samples: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##           total post-warmup samples = 10000
##
## Population-Level Effects:
##
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
cage2TetracyclinecoMevolvedcage1	-5.55	3.60	-15.39	-1.84	1.00
cage2TetracyclinecoMevolvedcage2	-2.75	0.98	-4.93	-1.13	1.00
cage2TetracyclinecoMevolvedcage3	-5.39	3.98	-15.38	-1.61	1.00
cage2Tetracyclinecontrolcage1	-0.00	0.50	-0.97	1.01	1.00
cage2Tetracyclinecontrolcage2	-2.20	0.74	-3.81	-0.92	1.00
cage2Tetracyclinecontrolcage3	-0.23	0.48	-1.17	0.69	1.00

```
##
```

	Bulk_ESS	Tail_ESS
cage2TetracyclinecoMevolvedcage1	3616	2100
cage2TetracyclinecoMevolvedcage2	6752	4963
cage2TetracyclinecoMevolvedcage3	3127	1240
cage2Tetracyclinecontrolcage1	7063	5933
cage2Tetracyclinecontrolcage2	6637	4627
cage2Tetracyclinecontrolcage3	6364	5428

```
##
## Samples were drawn 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).
```

```
(hypTet <- hypothesis(tet, "cage2TetracyclinecoMevolvedcage1 + cage2TetracyclinecoMevolvedcage2 + cage2
```

```
## Hypothesis Tests for class b:
```

```
##               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
```

```
## 1 (cage2Tetracyclin... = 0   -11.25      5.6   -25.62    -4.31      NA
```

```
##   Post.Prob Star
```

```
## 1           NA   *
```

```
## ---
```

```
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
```

```
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
```

```
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
```

```
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

Chlorothalonil

```
chlor <- brm(alive ~ 0 + cage2, data = filter(dat, treatment == "Chlorothalonil"), family= bernoulli(),
```

```
## Compiling the C++ model
```

```
## recompiling to avoid crashing R session
```

```
## Trying to compile a simple C file
```

```
## Running /usr/local/Cellar/r/3.6.1_1/lib/R/bin/R CMD SHLIB foo.c
```

```
## /usr/local/clang7/bin/clang -I"/usr/local/Cellar/r/3.6.1_1/lib/R/include" -DNDEBUG -I"/usr/local/1
```

```
## In file included from <built-in>:1:
```

```
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E
```

```
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
```

```
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:88:
```

```
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:1: error: unknow
```

```
## namespace Eigen {
```

```
## ^
```

```
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:16: error: expect
```

```
## namespace Eigen {
```

```
## ^
```

```
## ;
```

```
## In file included from <built-in>:1:
```

```
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E
```

```
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
```

```
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:96:10: fatal error: 'complex' file no
```

```
## #include <complex>
```

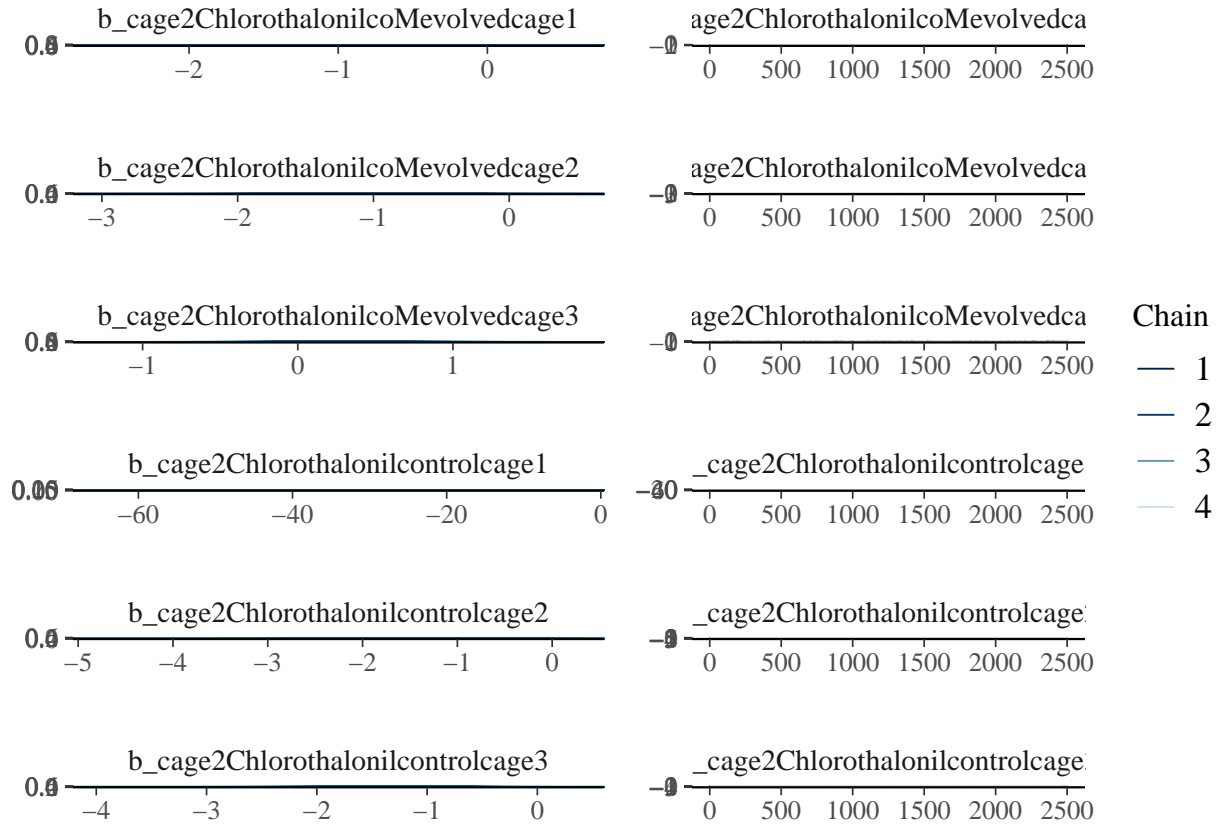
```
## ^~~~~~
```

```
## 3 errors generated.
```

```
## make: *** [foo.o] Error 1
```

```
## Start sampling
```

```
plot(chlor, N = 6, ask = F)
```



```
summary(chlor)
```

```
## Family: bernoulli
## Links: mu = logit
## Formula: alive ~ 0 + cage2
## Data: filter(dat, treatment == "Chlorothalonil") (Number of observations: 100)
## Samples: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##           total post-warmup samples = 10000
##
## Population-Level Effects:
##
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
## cage2ChlorothalonilcoMevolvedcage1	-0.86	0.49	-1.88	0.08	1.00
## cage2ChlorothalonilcoMevolvedcage2	-1.04	0.52	-2.12	-0.09	1.00
## cage2ChlorothalonilcoMevolvedcage3	0.32	0.46	-0.58	1.26	1.00
## cage2Chlorothalonilcontrolcage1	-4.77	3.63	-14.03	-1.05	1.00
## cage2Chlorothalonilcontrolcage2	-1.39	0.65	-2.75	-0.24	1.00
## cage2Chlorothalonilcontrolcage3	-1.34	0.57	-2.52	-0.33	1.00

```
##
```

	Bulk_ESS	Tail_ESS
## cage2ChlorothalonilcoMevolvedcage1	8701	6219
## cage2ChlorothalonilcoMevolvedcage2	7924	5450
## cage2ChlorothalonilcoMevolvedcage3	8888	6063
## cage2Chlorothalonilcontrolcage1	4422	1819
## cage2Chlorothalonilcontrolcage2	7798	6194
## cage2Chlorothalonilcontrolcage3	8867	5779

```
##
## Samples were drawn 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).
```

```
(hypChlor <- hypothesis(chlor, "cage2ChlorothalonilcoMevolvedcage1 + cage2ChlorothalonilcoMevolvedcage2
```

```
## Hypothesis Tests for class b:
```

```
##               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (cage2Chlorothalo... = 0      5.93      3.82      1.34      15.43      NA
##   Post.Prob Star
```

```
## 1      NA      *
```

```
## ---
```

```
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
```

```
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
```

```
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
```

```
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

Glyphosate

```
glyph <- brm(alive ~ 0 + cage2, data = filter(dat, treatment == "Glyphosate"), family= bernoulli(), con
```

```
## Compiling the C++ model
```

```
## recompiling to avoid crashing R session
```

```
## Trying to compile a simple C file
```

```
## Running /usr/local/Cellar/r/3.6.1_1/lib/R/bin/R CMD SHLIB foo.c
```

```
## /usr/local/clang7/bin/clang -I"/usr/local/Cellar/r/3.6.1_1/lib/R/include" -DNDEBUG -I"/usr/local/1
```

```
## In file included from <built-in>:1:
```

```
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E
```

```
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
```

```
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:88:
```

```
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:1: error: unknow
```

```
## namespace Eigen {
```

```
## ^
```

```
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:16: error: expe
```

```
## namespace Eigen {
```

```
## ^
```

```
## ;
```

```
## In file included from <built-in>:1:
```

```
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E
```

```
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
```

```
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:96:10: fatal error: 'complex' file no
```

```
## #include <complex>
```

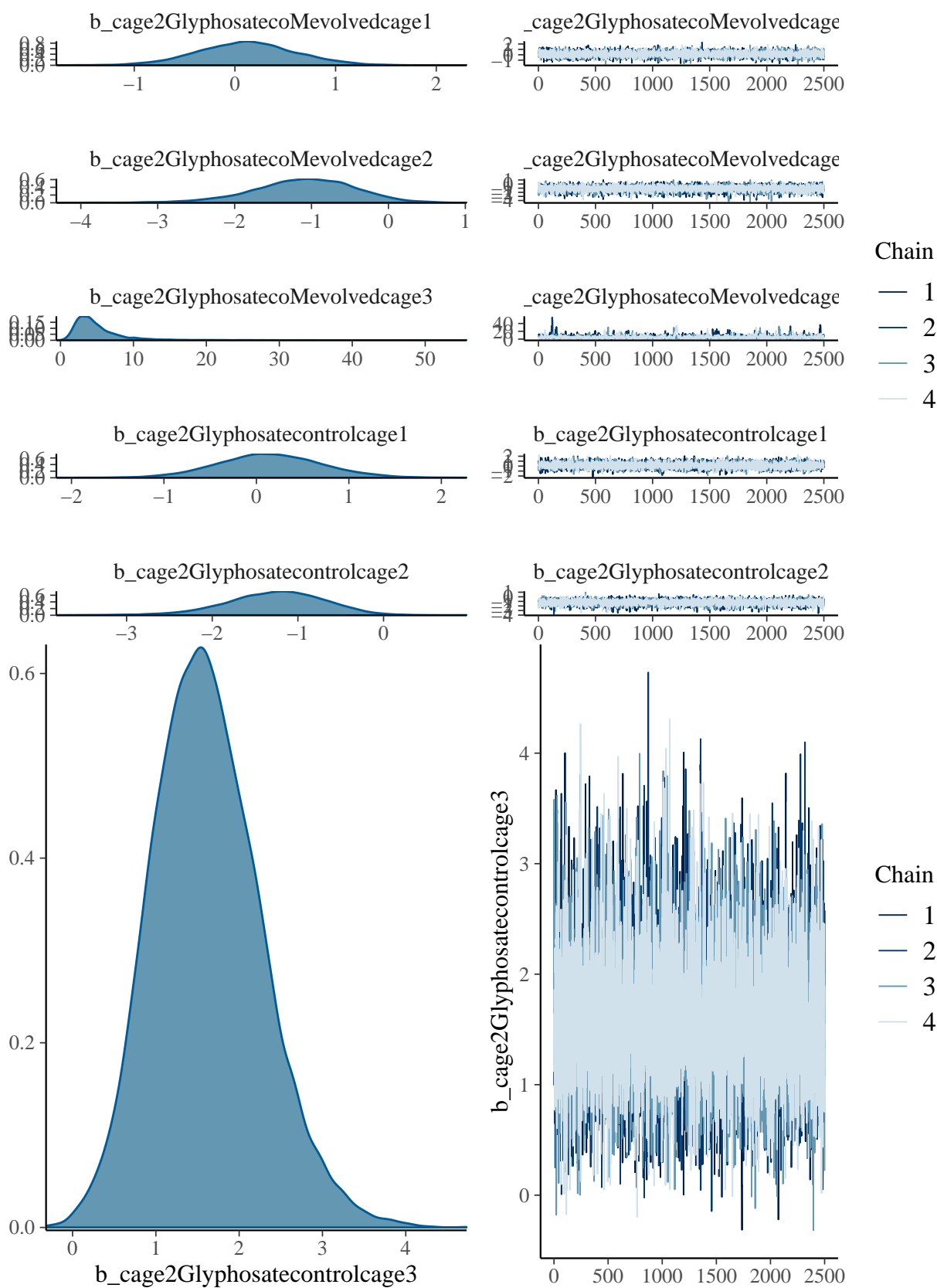
```
## ^~~~~~
```

```
## 3 errors generated.
```

```
## make: *** [foo.o] Error 1
```

```
## Start sampling
```

```
plot(glyph)
```




```
## Family: bernoulli
## Links: mu = logit
## Formula: alive ~ 0 + cage2
## Data: filter(dat, treatment == "Glyphosate") (Number of observations: 88)
## Samples: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
## total post-warmup samples = 10000
```

Population-Level Effects:

##		Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
##	cage2Glyphosatecoveolvedcage1	0.12	0.49	-0.84	1.08	1.00
##	cage2Glyphosatecoveolvedcage2	-1.10	0.66	-2.51	0.11	1.00
##	cage2Glyphosatecoveolvedcage3	5.06	3.76	1.32	14.68	1.00
##	cage2Glyphosatecontrolcage1	0.15	0.56	-0.94	1.26	1.00
##	cage2Glyphosatecontrolcage2	-1.26	0.57	-2.46	-0.22	1.00
##	cage2Glyphosatecontrolcage3	1.62	0.65	0.47	3.00	1.00

```
## Bulk_ESS Tail_ESS
```

##	cage2GlyphosatecoMevolvedcage1	9492	6725
##	cage2GlyphosatecoMevolvedcage2	9350	5759
##	cage2GlyphosatecoMevolvedcage3	3737	2049
##	cage2Glyphosatecontrolcage1	9145	6519
##	cage2Glyphosatecontrolcage2	9184	5173
##	cage2Glyphosatecontrolcage3	9552	5919

```
## Samples were drawn 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).
```

```
(hypGlyph <- hypothesis(glyph, "cage2GlyphosatecoMevolvedcage1 + cage2GlyphosatecoMevolvedcage2 + cage2
```

```
## Hypothesis Tests for class b:
```

##	Hypothesis	Estimate	Est.Error	CI.Lower	CI.Upper	Evid.Ratio
## 1	(cage2Glyphosatec... = 0	3.57	4	-1.38	13.43	NA
##	Post.Prob Star					
## 1	NA					

```
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
```

'*': For one-sided hypotheses, the posterior probability exceeds 95%;

```
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
```

```
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

Chlorothionil added control

```
chlorContr <- brm(alive ~ 0 + cage2, data = controlDatChlor, family= bernoulli(), control = list(adapt = 0))
```

Compiling the C++ model

```
## recompiling to avoid crashing R session
```

```
## Trying to compile a simple C file
```

```
## Running /usr/local/Cellar/r/3.6.1_1/lib/R/bin/R CMD SHLIB foo.c
```

```
## /usr/local/clang7/bin/clang -I"/usr/local/Cellar/r/3.6.1_1/lib/R/include" -DNDEBUG -I"/usr/local/l
```

```
## In file included from <built-in>:1:
```

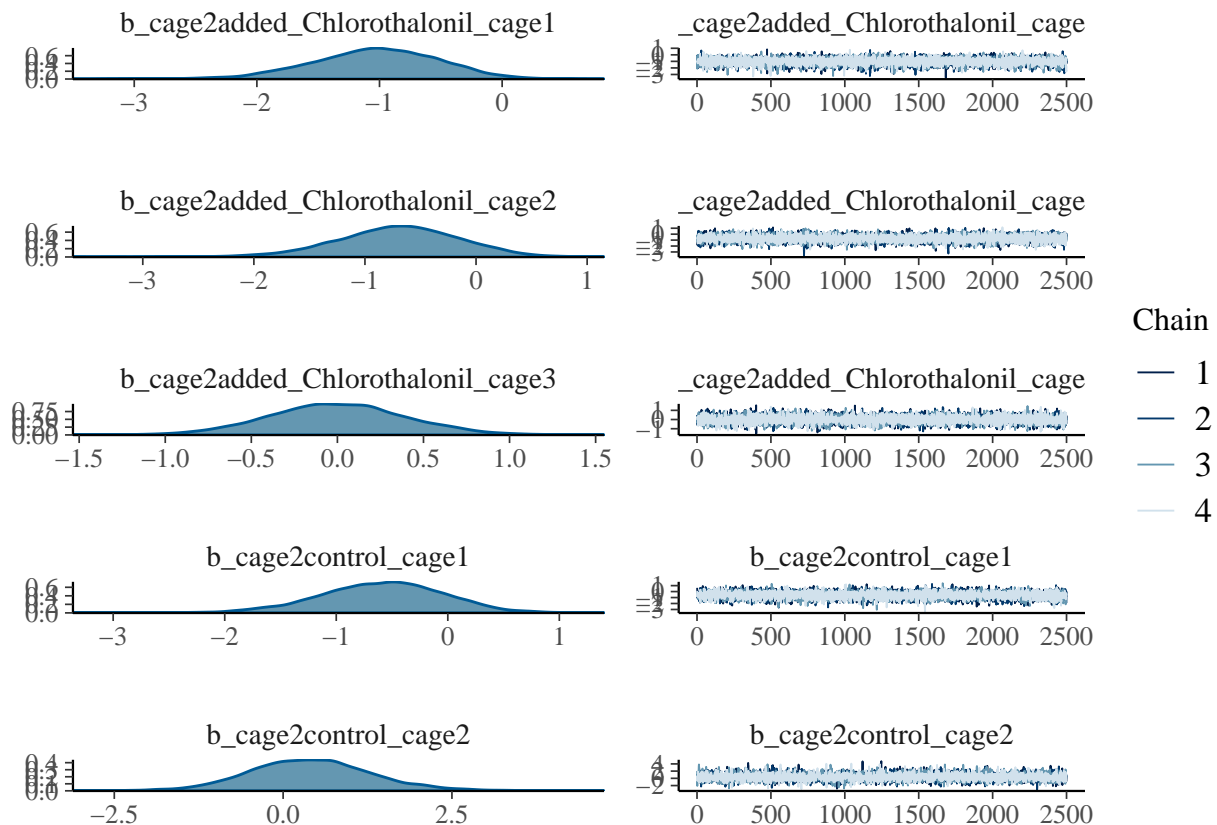
```

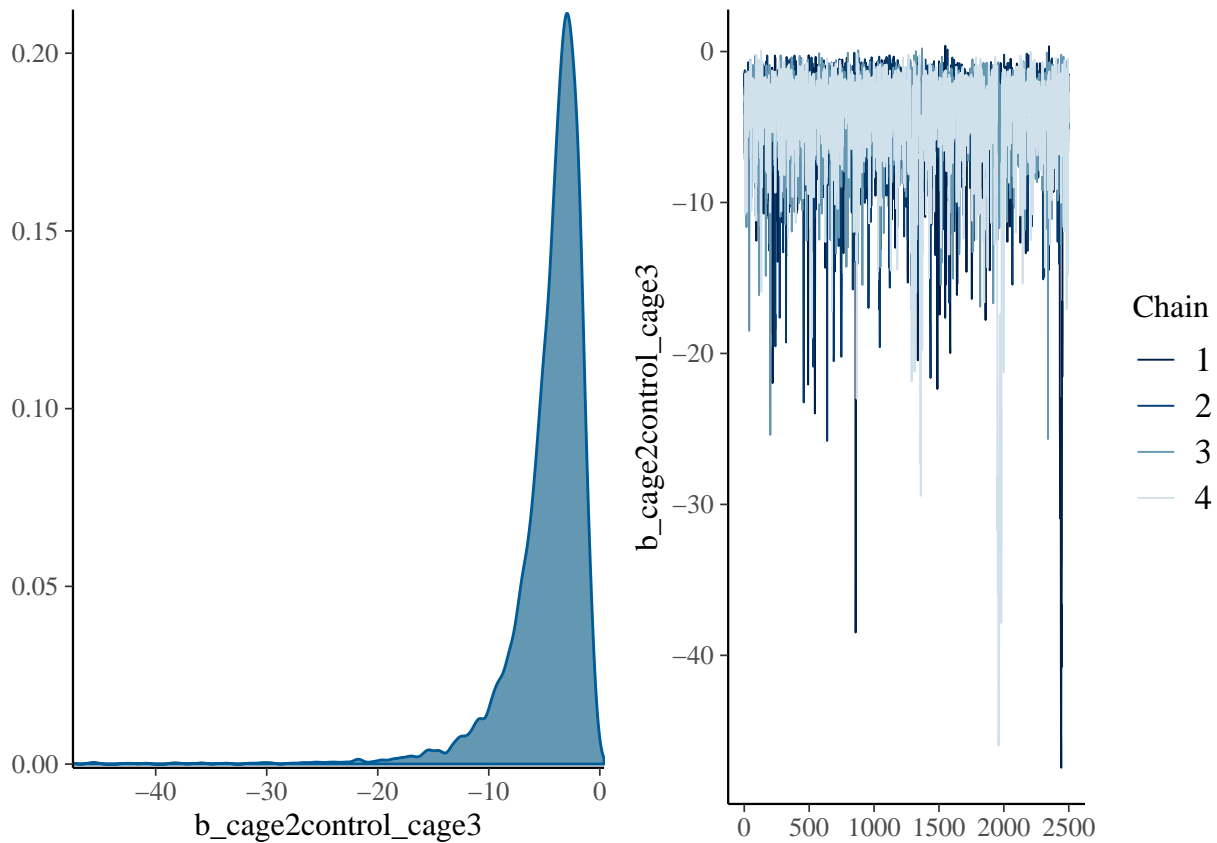
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:88:
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:1: error: unknow
## namespace Eigen {
## ^
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:16: error: expe
## namespace Eigen {
##           ^
##           ;
## In file included from <built-in>:1:
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/E:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:96:10: fatal error: 'complex' file no
## #include <complex>
##           ~~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

## Start sampling

```

```
plot(chlorContr)
```





```
summary(chlorContr)
```

```
## Family: bernoulli
## Links: mu = logit
## Formula: alive ~ 0 + cage2
## Data: controlDatChlor (Number of observations: 86)
## Samples: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##           total post-warmup samples = 10000
##
## Population-Level Effects:
##               Estimate Est.Error 1-95% CI u-95% CI Rhat
## cage2added_Chlorothalonil_cage1   -1.03    0.52   -2.09   -0.08 1.00
## cage2added_Chlorothalonil_cage2   -0.70    0.55   -1.83    0.33 1.00
## cage2added_Chlorothalonil_cage3    0.00    0.40   -0.78    0.79 1.00
## cage2control_cage1                -0.59    0.56   -1.73    0.45 1.00
## cage2control_cage2                 0.41    0.91   -1.31    2.29 1.00
## cage2control_cage3                -4.57    3.63  -13.25   -0.92 1.00
##               Bulk_ESS Tail_ESS
## cage2added_Chlorothalonil_cage1   8779   6282
## cage2added_Chlorothalonil_cage2   7560   6204
## cage2added_Chlorothalonil_cage3   7911   6639
## cage2control_cage1                8458   6319
## cage2control_cage2                8025   6055
## cage2control_cage3                3094   1398
##
## Samples were drawn 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).
(hypChlorContr <- hypothesis(chlorContr, "cage2added_Chlorothalonil_cage1 + cage2added_Chlorothalonil_cage2")

## Hypothesis Tests for class b:
##               Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (cage2added_Chlor... = 0    -1.96      2.09    -6.16     1.99         NA
##   Post.Prob Star
## 1              NA
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

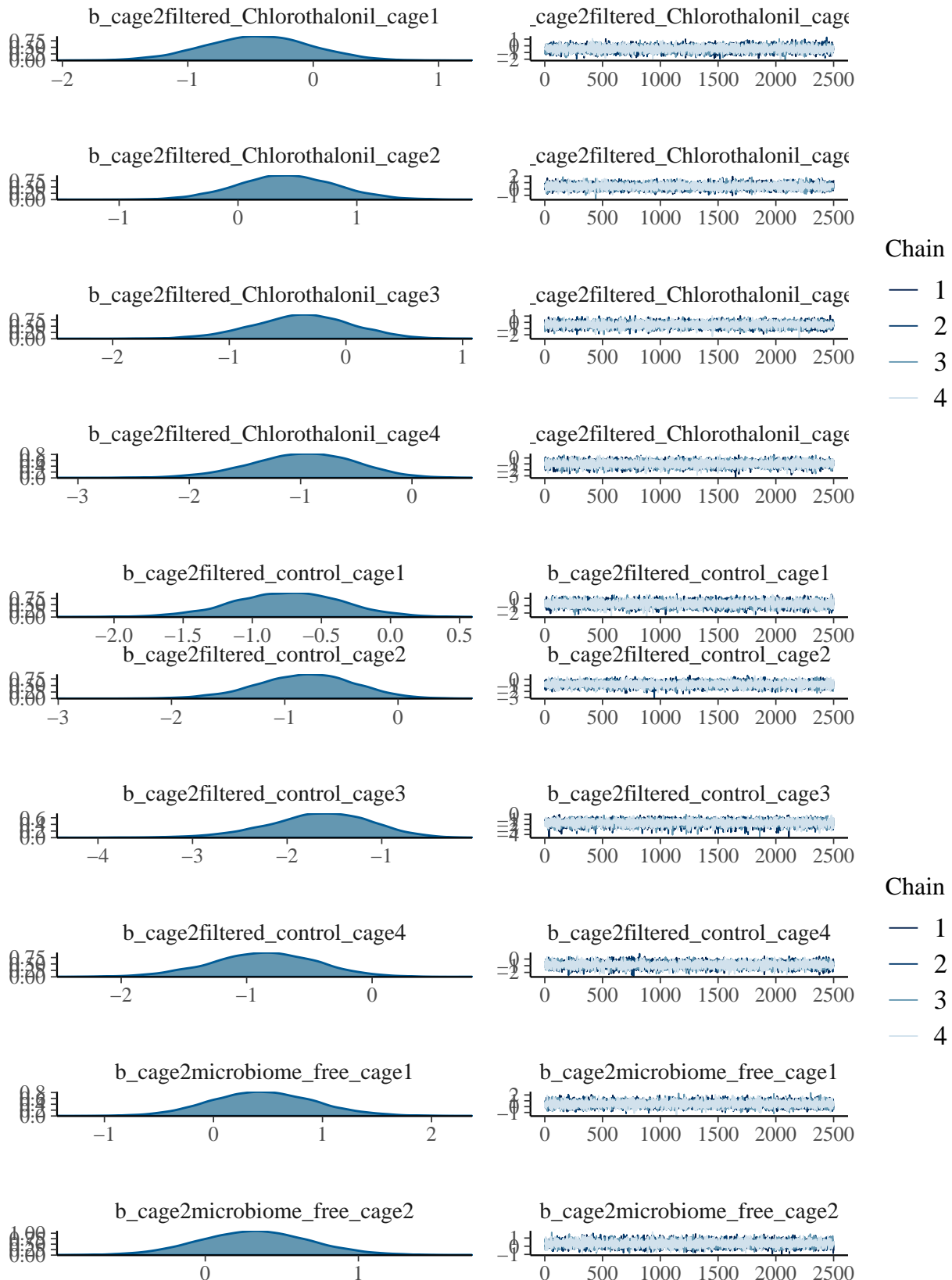
Filtered microbiome added control

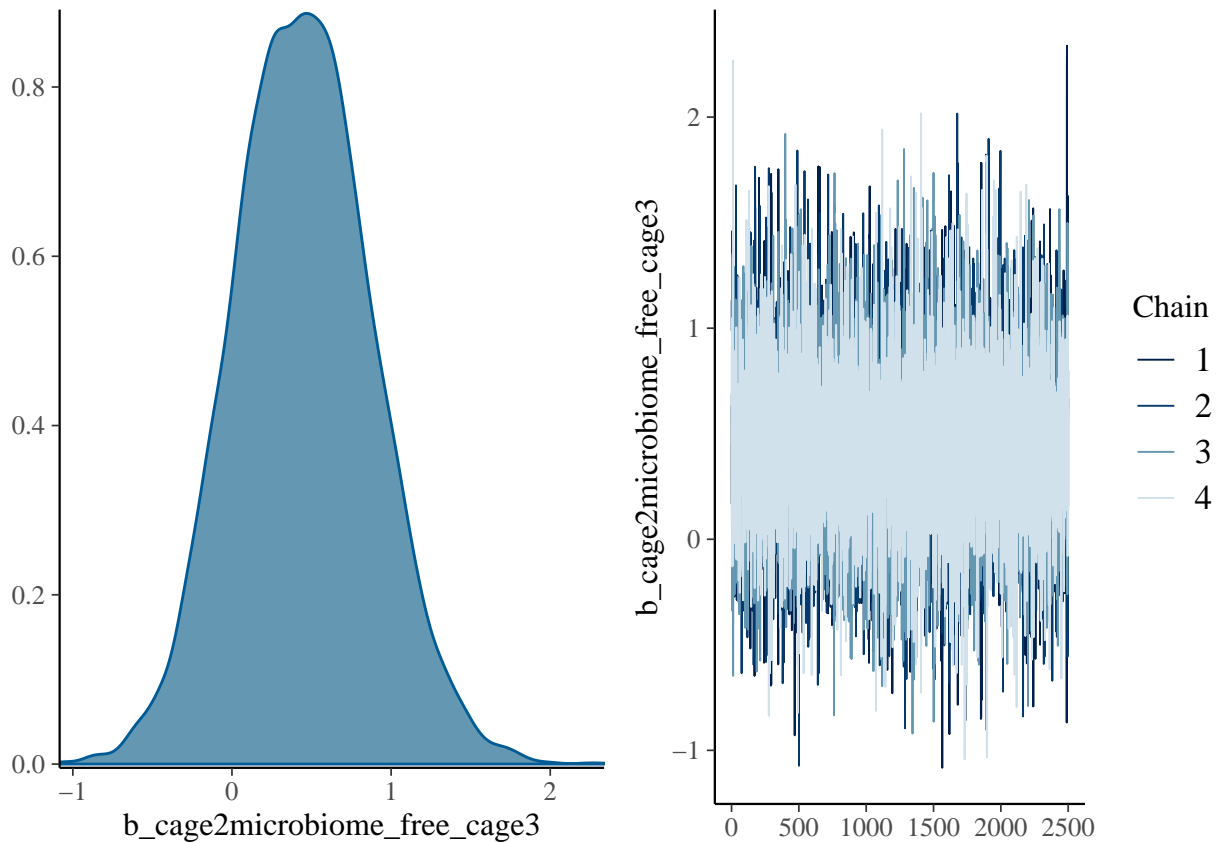
```
chlorContrFiltered <- brm(alive ~ 0 + cage2, data = controlDatFiltered, family= bernoulli(), control = 1)

## Compiling the C++ model
## recompiling to avoid crashing R session
## Trying to compile a simple C file
## Running /usr/local/Cellar/r/3.6.1_1/lib/R/bin/R CMD SHLIB foo.c
## /usr/local/clang7/bin/clang -I"/usr/local/Cellar/r/3.6.1_1/lib/R/include" -DNDEBUG -I"/usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/Eigen" -c /usr/local/Cellar/r/3.6.1_1/lib/R/bin/R CMD SHLIB foo.c
## In file included from <built-in>:1:
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/Eigen:1:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:88:
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:1: error: unknown namespace Eigen {
## namespace Eigen {
## ^
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/src/Core/util/Macros.h:613:16: error: expected ';'
## namespace Eigen {
## ^
## ;
## In file included from <built-in>:1:
## In file included from /usr/local/lib/R/3.6/site-library/StanHeaders/include/stan/math/prim/mat/fun/Eigen:1:
## In file included from /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Dense:1:
## /usr/local/lib/R/3.6/site-library/RcppEigen/include/Eigen/Core:96:10: fatal error: 'complex' file not found
## #include <complex>
## ^~~~~~
## 3 errors generated.
## make: *** [foo.o] Error 1

## Start sampling
```

```
plot(chlorContrFiltered)
```





```
summary(chlorContrFiltered)
```

```
## Family: bernoulli
## Links: mu = logit
## Formula: alive ~ 0 + cage2
## Data: controlDatFiltered (Number of observations: 270)
## Samples: 4 chains, each with iter = 5000; warmup = 2500; thin = 1;
##           total post-warmup samples = 10000
##
## Population-Level Effects:
##
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Rhat
## cage2filtered_Chlorothalonil_cage1	-0.44	0.43	-1.29	0.38	1.00
## cage2filtered_Chlorothalonil_cage2	0.41	0.41	-0.39	1.23	1.00
## cage2filtered_Chlorothalonil_cage3	-0.37	0.43	-1.24	0.45	1.00
## cage2filtered_Chlorothalonil_cage4	-0.98	0.48	-1.97	-0.09	1.00
## cage2filtered_control_cage1	-0.75	0.40	-1.57	0.04	1.00
## cage2filtered_control_cage2	-0.81	0.43	-1.69	-0.00	1.00
## cage2filtered_control_cage3	-1.66	0.56	-2.85	-0.66	1.00
## cage2filtered_control_cage4	-0.87	0.43	-1.73	-0.05	1.00
## cage2microbiome_free_cage1	0.46	0.48	-0.46	1.43	1.00
## cage2microbiome_free_cage2	0.33	0.37	-0.38	1.05	1.00
## cage2microbiome_free_cage3	0.45	0.43	-0.36	1.32	1.00

```
## Bulk_ESS Tail_ESS
## cage2filtered_Chlorothalonil_cage1 12652 7964
## cage2filtered_Chlorothalonil_cage2 13918 7700
## cage2filtered_Chlorothalonil_cage3 13033 6630
## cage2filtered_Chlorothalonil_cage4 13971 7635
```

```
## cage2filtered_control_cage1          13502      7074
## cage2filtered_control_cage2          13957      6849
## cage2filtered_control_cage3          12085      6311
## cage2filtered_control_cage4          12128      7056
## cage2microbiome_free_cage1           12682      6808
## cage2microbiome_free_cage2           11562      7187
## cage2microbiome_free_cage3           13984      6876
##
## Samples were drawn 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).

(hypChlorContrFiltered <- hypothesis(chlorContrFiltered, "cage2filtered_Chlorothalonil_cage1 + cage2fil

## Hypothesis Tests for class b:
##              Hypothesis Estimate Est.Error CI.Lower CI.Upper Evid.Ratio
## 1 (cage2filtered_Ch... = 0      2.71      1.27      0.25      5.2          NA
##   Post.Prob Star
## 1          NA      *
## ---
## 'CI': 90%-CI for one-sided and 95%-CI for two-sided hypotheses.
## '*': For one-sided hypotheses, the posterior probability exceeds 95%;
## for two-sided hypotheses, the value tested against lies outside the 95%-CI.
## Posterior probabilities of point hypotheses assume equal prior probabilities.
```

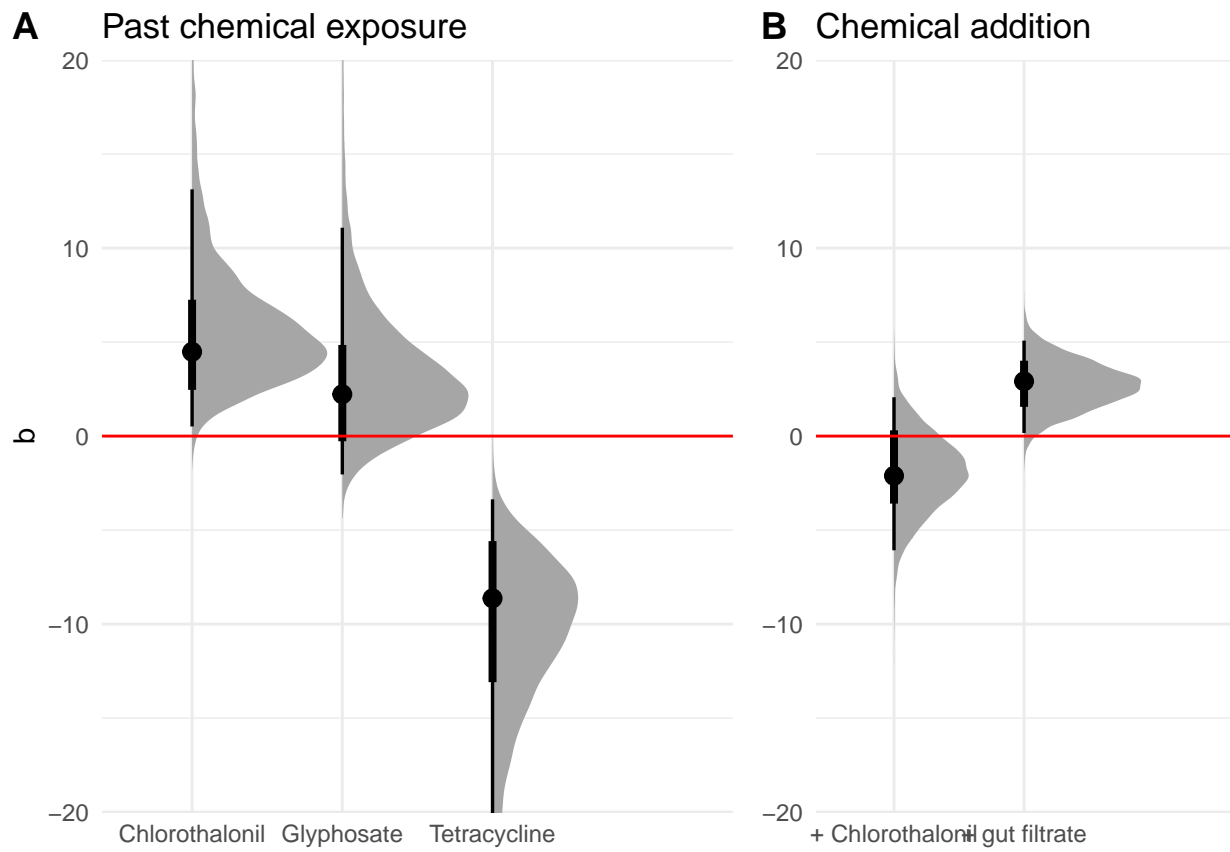
Plot results

```
get_variables(tet)

## [1] "b_cage2TetracyclinecoMevolvedcage1" "b_cage2TetracyclinecoMevolvedcage2"
## [3] "b_cage2TetracyclinecoMevolvedcage3" "b_cage2Tetracyclinecontrolcage1"
## [5] "b_cage2Tetracyclinecontrolcage2"    "b_cage2Tetracyclinecontrolcage3"
## [7] "lp__"                                "accept_stat__"
## [9] "stepsize__"                          "treedepth__"
## [11] "n_leapfrog__"                         "divergent__"
## [13] "energy__"

p1 <- tibble("Chlorothalonil" = hypChlor$samples[,1], "Tetracycline" = hypTet$samples[,1], "Glyphosate"
p2 <- tibble("+ Chlorothalonil" = hypChlorContr$samples[,1], "+ gut filtrate" = hypChlorContrFiltered$s

plot_grid(p1, p2, nrow = 1, rel_widths = c(3,2), labels = c("A", "B"))
```



```
ggsave("plots/brms.pdf", width = 6, height = 3)
```