Delaware River PIT tag data analysis

Ben Letcher

2022-07-27

Note: the results shown here are preliminary and have not been officially reviewed by USGS, NYDEC or PA Fish and Boat

This notebook uses targets to manage running code and updating R objects. Targets sets up dependencies among specified objects and only re-runs code as necessary (when an upstream component gets updated). This can save run times for projects with models that take a while to run, like capture-mark-recapture models.

Data preparation and model running happens using targets and exploration of the data and model runs is below in this Markdown document.

'knit' the document to update all targets and the markdown exploration below.

'tar_make()' runs all the R scripts and functions specified in '_targets.R'. Only updated code or sections that are downstream from updated data are re-run.
'tar_read()' reads 'target' data into the global environment.

To set up a targets project, use use_targets()

This section (tar_make()) reruns the model

```
#  tar_watch(seconds = 10, outdated = FALSE, targets_only = TRUE)


# comment this out when knitting - get Latex error that it can't find the check mark the tar_make() use
#tar_make()

# tar_prune() # cleans unused data files
#tar_invalidate(everything())
#tar_invalidate(ends_with("ttt"))


#str(d)
```

Load data for analysis
Without a postscript, the data are for all fish (main and trib)

```
dRaw0 <- tar_read(dRaw0) #all data - including untagged
dRaw <- tar_read(dRaw) #all data for CMR models
d <- tar_read(target_d)
eh <- tar_read(target_eh)
```

Visualize the network - does not work with pdf output

```
#tar_visnetwork()
```

Which rivers (Water) riverN corresponds to

```
table(d$Water, d$riverN)
#>
#>                           1    2    3    4    5    6
#>   Balls Creek            41    0    0    0    0    0
#>   Cold Spring Creek       0   95    0    0    0    0
#>   Roods Creek             0    0  159    0    0    0
#>   Sands Creek             0    0    0  139    0    0
#>   Shehawken Creek         0    0    0    0   91    0
#>   West Br Delaware River  0    0    0    0    0 5634
```

Raw data summary tables

```
kable(data.frame(ftable(d$date)))
```

Var1	Freq
2018-05-07	110
2018-05-08	34
2018-05-09	48
2018-06-11	129
2018-06-12	99
2018-06-13	88
2018-07-16	212
2018-07-17	176
2018-07-18	142
2018-08-21	11
2018-09-17	21
2018-09-20	89
2018-10-22	85
2018-10-23	131
2018-10-24	129
2019-04-08	240
2019-04-10	129
2019-05-06	170
2019-05-07	91
2019-06-10	169
2019-06-11	129
2019-07-15	212
2019-07-16	312
2019-07-17	25
2019-08-12	131
2019-08-13	139
2019-08-14	186
2019-08-15	49
2019-09-16	108
2019-09-17	55

Var1	Freq
2019-09-18	293
2019-10-21	262
2019-10-22	31
2019-10-23	74
2020-07-16	146
2020-07-20	249
2020-07-21	29
2020-08-10	89
2020-08-11	41
2020-08-17	145
2020-08-20	110
2020-09-10	187
2020-09-14	252
2020-09-15	47
2020-10-13	368
2020-10-14	55
2020-10-15	132

```
#kable(data.frame(ftable(d$Water, d$riverN)))

#kable(data.frame(ftable(d$Water, d$riverN, d$date)))
kable(data.frame(ftable(d$species)))
```

Var1	Freq
brook trout	13
brown trout	5534
rainbow trout	611

```
### Number of unique tags
length(unique(d$tag))
#> [1] 4610
```

Group observations by month.
Luckily, sampling periods do not span months, so we can use month as a grouping variable for sampling occasion

```
kable(data.frame(ftable(d$dateYM)))
```

Var1	Freq
2018-05	192
2018-06	316
2018-07	530
2018-08	11
2018-09	110
2018-10	345
2019-04	369
2019-05	261

Var1	Freq
2019-06	298
2019-07	549
2019-08	505
2019-09	456
2019-10	367
2020-07	424
2020-08	385
2020-09	486
2020-10	555

Tag information

Grouped by Water (sampling area)

```
tagN <- d %>%
  group_by(tag, Water) %>%
  summarize(n = n()) %>%
  filter(tag != "") %>%
  arrange(desc(n))
#> `summarise()` has grouped output by 'tag'. You can override using the `.groups`
#> argument.

### Number of times individual fish were observed
table(tagN$n)
#>
#>    1    2    3    4    5    6    7    8    9
#> 3641  611  223   90   30   12    4    1    1

### Number of times individual fish were observed by river
(table(tagN$Water, tagN$n))
#>
#>                            1    2    3    4    5    6    7    8    9
#>   Balls Creek             30    4    1    0    0    0    0    0    0
#>   Cold Spring Creek       39    9    4    2    1    1    1    0    0
#>   Roods Creek             78   21    6    4    1    0    0    0    0
#>   Sands Creek             97   16    2    1    0    0    0    0    0
#>   Shehawken Creek         45   10    6    2    0    0    0    0    0
#>   West Br Delaware River 3352  551  204   81   28   11    3    1    1
```

Grouped by state

```
tagN_s <- d %>%
  group_by(tag, state) %>%
  summarize(n = n()) %>%
  filter(tag != "") %>%
  arrange(desc(n))
#> `summarise()` has grouped output by 'tag'. You can override using the `.groups`
#> argument.

### Number of times individual fish were observed
```

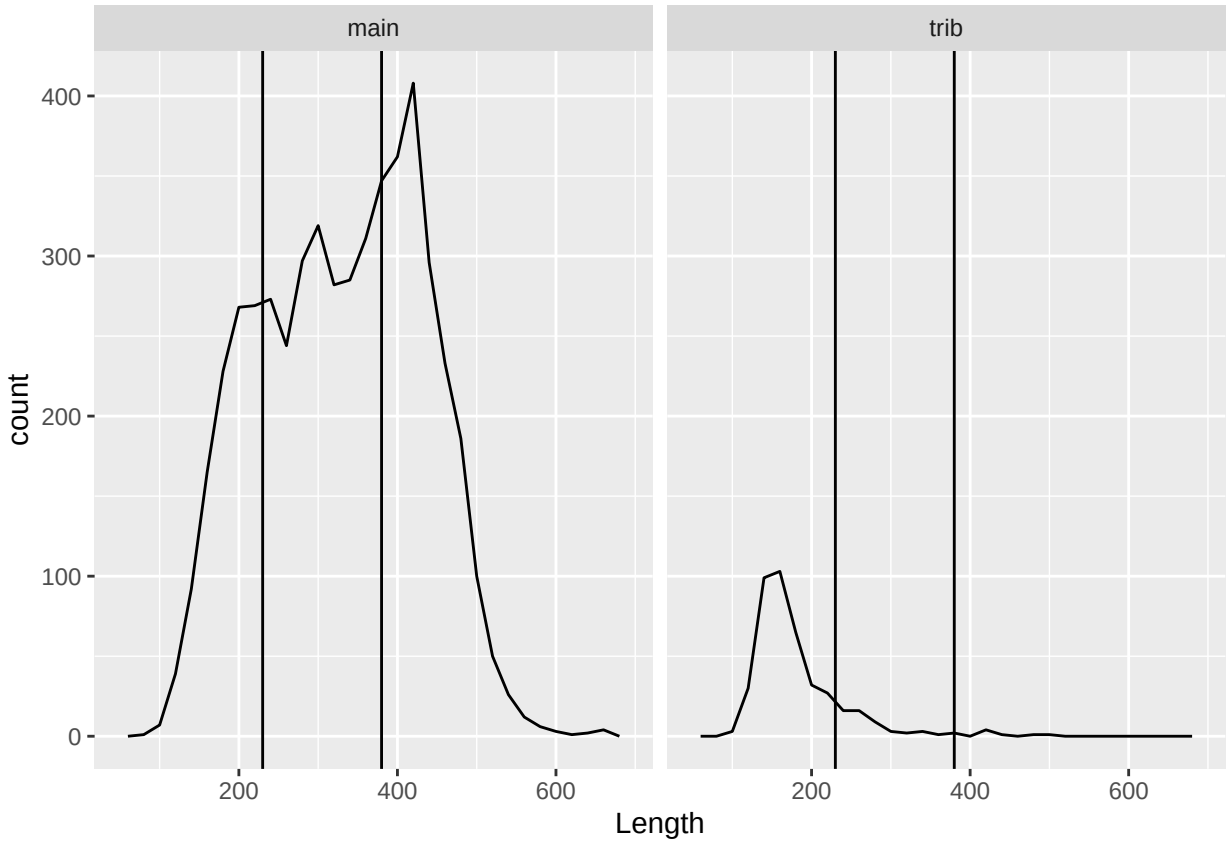
```
table(tagN_s$n)
#>
#>    1    2    3    4    5    6    7    9
#> 3949  640  170   57   23    9    2    1

### Number of times individual fish were observed by river
table(tagN_s$state, tagN_s$n)
#>
#>       1    2    3    4    5    6    7    9
#>   1  963   69    4    0    0    0    0    0
#>   2 1660  274   58   17    7    0    0    0
#>   3 1025  232   87   35   15    8    2    1
#>   4  264   59   15    5    1    1    0    0
#>   5   29    6    6    0    0    0    0    0
#>   6    8    0    0    0    0    0    0    0
```

Grouped by main/trib
this is what is used for the primary analysis

```
tagN_mt <- d %>%
  group_by(tag, mainTrib) %>%
  summarize(n = n()) %>%
  filter(tag != "") %>%
  arrange(desc(n))
#> `summarise()` has grouped output by 'tag'. You can override using the `.groups`
#> argument.

### Number of times individual fish were observed
table(tagN_mt$n)
#>
#>    1    2    3    4    5    6    7    8    9
#> 3641  611  223   90   30   12    4    1    1

### Number of times individual fish were observed by river
(table(tagN_mt$mainTrib, tagN_mt$n))
#>
#>          1    2    3    4    5    6    7    8    9
#>   main 3352  551  204   81   28   11    3    1    1
#>   trib  289   60   19    9    2    1    1    0    0
```

Basic summary plots of raw tagging data

```
ggplot(d %>% filter(species == "brown trout"), aes(Length)) +
  geom_freqpoly() +
  geom_vline(xintercept = c(tar_read(target_sizeCutoff1), tar_read(target_sizeCutoff2))) +
  facet_grid(~mainTrib)
#> `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
# dTame <- d %>%
#             select(Latitude, Longitude, tag, dateTime, species, Length, Weight) %>%
#             filter(tag != "", tag != "ad")
#
# write.csv(dTame, './dataOut/dTame.csv', row.names = FALSE)
```

Encounter histories

This is the data structure for the capture-recapture models. Each column is a sampling 'occasion' (here = month) and each row is an individual, where a '1' indicates capture and a '0' indicates not captured.

```
str(eh$eh)
#>  num [1:3673, 1:17] 1 1 1 1 1 1 1 1 1 1 ...
#>  - attr(*, "dimnames")=List of 2
#>   ..$ : NULL
#>   ..$ : chr [1:17] "date_2018-05" "date_2018-06" "date_2018-07" "date_2018-08" ...
kable(head(eh$eh,8))
```

date_2018-05	date_2018-06	date_2018-07	date_2018-08	date_2018-09	date_2018-10	date_2019-04	date_2019-05	date_2019-06	date_2019-07	date_2019-08	date_2019-09	date_2019-10	date_2020-07	date_2020-08	date_2020-09	date_2020-10
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

date	2018-05	2018-06	2018-07	2018-08	2018-09	2018-10	2019-04	2019-05	2019-06	2019-07	2019-08	2019-09	2019-10	2020-07	2020-08	2020-09	2020-10
	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

```
table(paste(eh$first, eh$last, sep="_"))
#>
#>  1_17 10_17 11_17 12_17 13_17 14_17 15_17 16_17  2_17  3_17  4_17  5_17  6_17
#>   173   360   295   264   257   297   246   291   264   373     8    62   231
#>  7_17  8_17  9_17
#>   233   130   189
```

Transitions
River size1 size2 size3
Main 1 2 3
Trib 4 5 6

There are very few transitions between main and trib and we can characterize size transitions better with a growth model - run phiT_pT models separately for main and trib

```
s <- eh$stateMatrix
s[s == 0] <- NA

s2 <- data.frame(s) %>%
  unite("all", sep = "", na.rm = TRUE, remove = TRUE) %>%
  #distinct() %>%
  arrange()

table(s2)
#> all
#>         1        11       111      1112       112      1122        12       122
#>       774        58         3         1         6         3        34        14
#>      1222       132         2        22       222      2222     22222      2223
#>         5         1      1097       185        46        17         7         4
#>     22233       223      2233     22333    223333   2233333  22333333        23
#>         2        25        10         6         2         1         1        53
#>       233      2333     23333    233333       253         3        32        33
#>        33         8         1         2         1       687         2       172
#>       333      3333     33333    333333   3333333 333333333         4        42
#>        71        32        12         7         2         1       182         1
#>        44       444      4444     44444    444444     44445   4444555      4445
#>        47        12         3         1         1         1         1         1
#>      4455        45       455      4555         5      5455        55       555
#>         2         2         2         2        17         1         1         2
#>       556         6        63
#>         1         6         1
```

Summary info for years and occasions

```
years <- colnames(eh$eh) %>%
  substr(6,9) %>%
  as.numeric()

months <- colnames(eh$eh) %>%
  substr(11,12) %>%
  as.numeric()

occs <- colnames(eh$eh)
```

Models

'phi' = apparent survival (probability of staying in the area = p(survival) + p(not moving out of area)).
'p' = probability of capture given that the fish is alive.

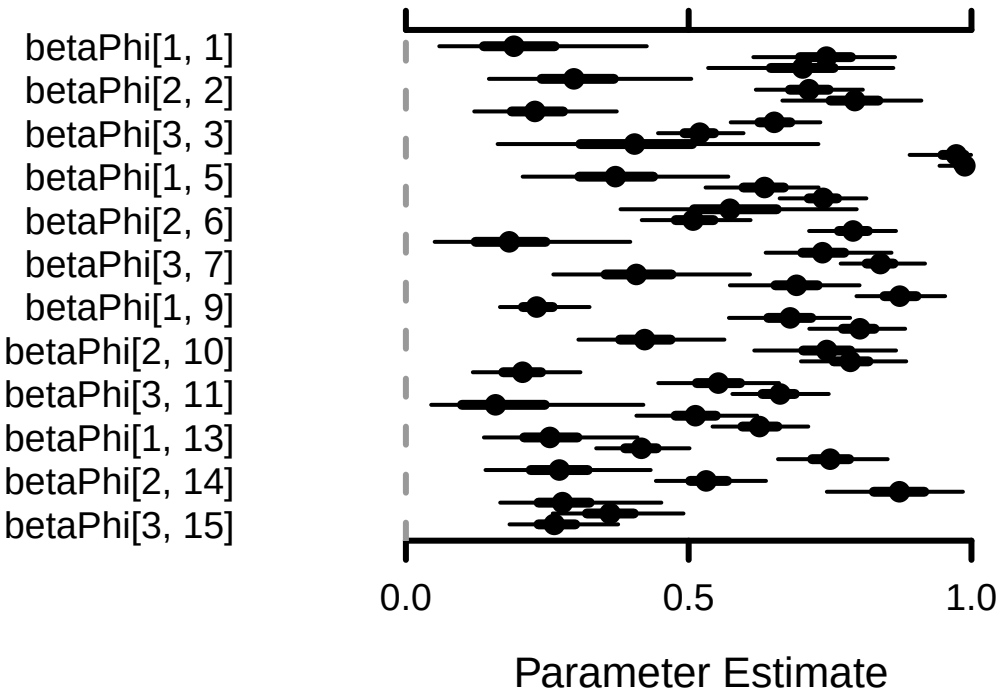
phiT_pT_main

Load data 'main' for analysis

```
#d_tt <- tar_read(target_d_trib)
eh_main <- tar_read(target_eh_main)

str(eh_main$eh)
#>  num [1:3388, 1:16] 1 1 1 1 1 1 1 1 1 1 ...
#>  - attr(*, "dimnames")=List of 2
#>   ..$ : NULL
#>   ..$ : chr [1:16] "date_2018-05" "date_2018-06" "date_2018-07" "date_2018-09" ...
#kable(eh_main$eh[1:8,1:10])

table(paste(eh_main$first, eh_main$last, sep="_"))
#>
#>  1_16 10_16 11_16 12_16 13_16 14_16 15_16  2_16  3_16  4_16  5_16  6_16  7_16
#>   173   242   244   238   297   246   291   264   313    51   216   233   130
#>  8_16  9_16
#>   189   261
```

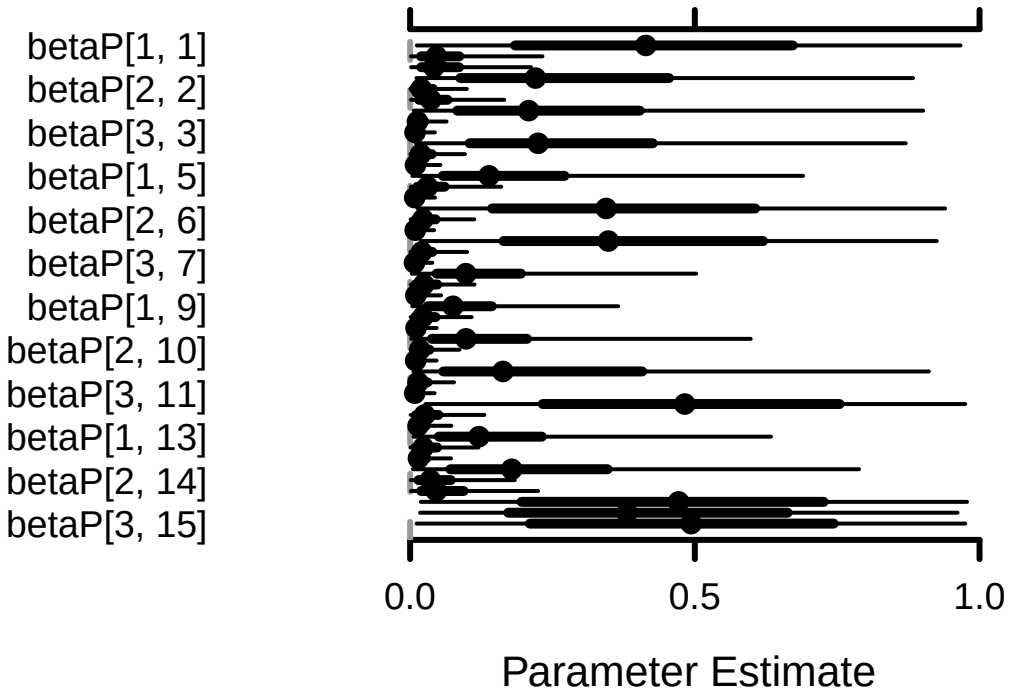
```
### Read the model run into global memory
if (tar_exist_objects(c("tt_modelOut_main"))) {
  mod_tt_main <- tar_read(tt_modelOut_main)

  MCMCplot(object = mod_tt_main$mcmc, params = "betaPhi")
  MCMCplot(object = mod_tt_main$mcmc, params = "betaP")

   priors <- rnorm(tar_read(tt_runData_main)$nIter * tar_read(tt_runData_main)$nChains, 0, 1/sqrt(.1))
   MCMCtrace(object = mod_tt_main$mcmc,
             ISB = FALSE,
             exact = TRUE,
             params = c("betaPhi[1, 1]", "betaPhi[2, 1]", "betaPhi[3, 1]",
                        "betaPhi[1, 2]", "betaPhi[2, 2]", "betaPhi[3, 2]"
                        #"betaPhi[1, 3]", "betaPhi[2, 3]", "betaPhi[3, 3]"
                        ),
```

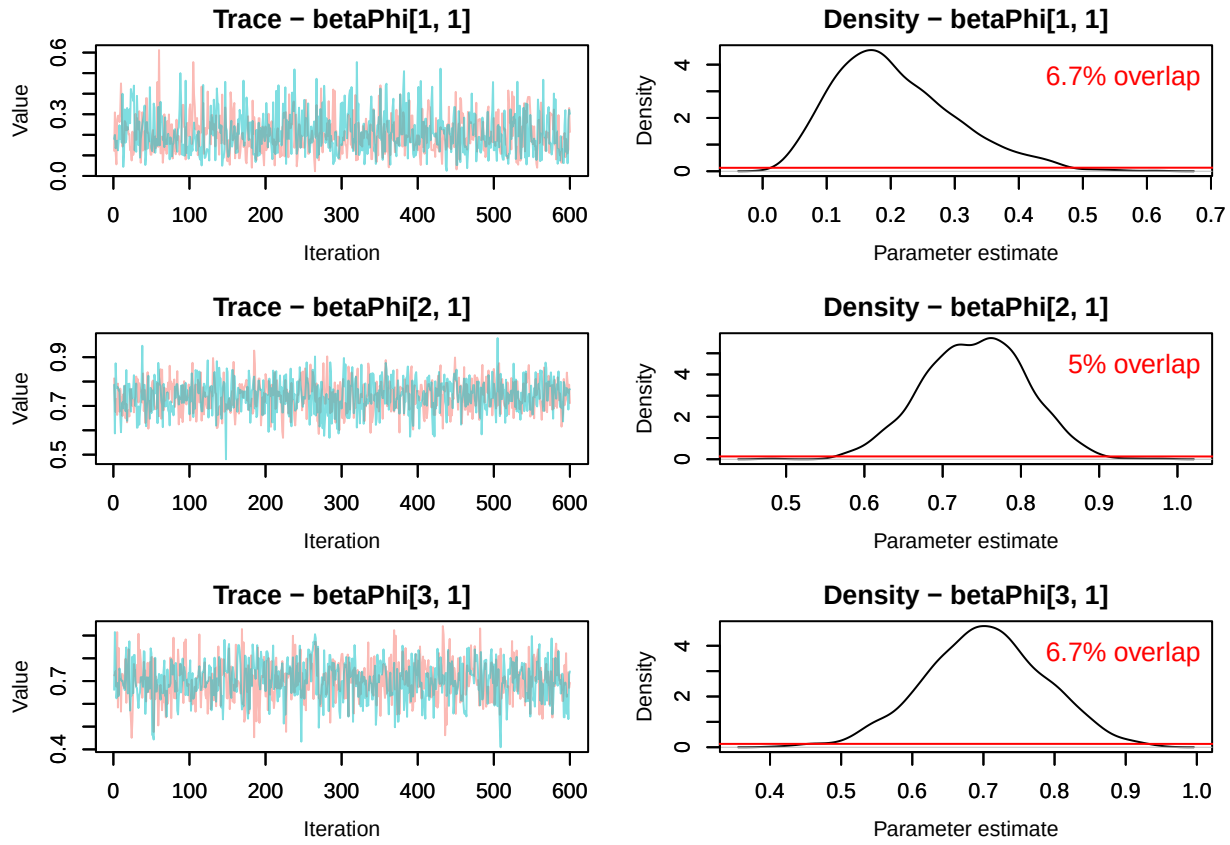
```
            pdf = FALSE,
            priors = priors
            )

      MCMCtrace(object = mod_tt_main$mcmc,
            ISB = FALSE,
            exact = TRUE,
            params = c("betaP[1, 1]", "betaP[2, 1]", "betaP[3, 1]",
                       "betaP[1, 2]", "betaP[2, 2]", "betaP[3, 2]"
                       #"betaP[1, 3]", "betaP[2, 3]", "betaP[3, 3]"
                       ),
            pdf = FALSE,
            priors = priors
            )

    modSummary_tt_main <- MCMCsummary(object = mod_tt_main$mcmc, round = 3) %>%
      rename(lo = '2.5%', med = '50%', hi = '97.5%')
}
```



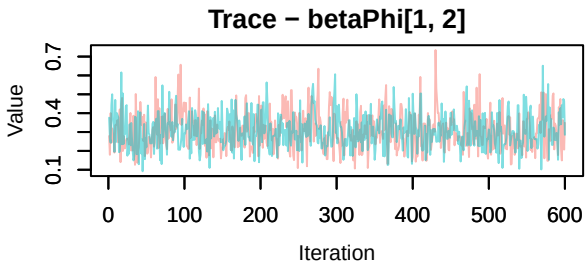

```
#> Warning in MCMCtrace(object = mod_tt_main$mcmc, ISB = FALSE, exact = TRUE, :
#> Only one prior specified for > 1 parameter. Using a single prior for all
#> parameters.
#> Warning in MCMCtrace(object = mod_tt_main$mcmc, ISB = FALSE, exact = TRUE, :
#> Number of samples in prior is greater than number of total or specified
#> iterations (for all chains) for specified parameter. Only last 1200 iterations
```

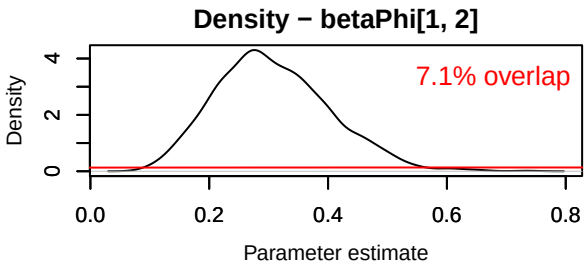
```
#> will be used.
```

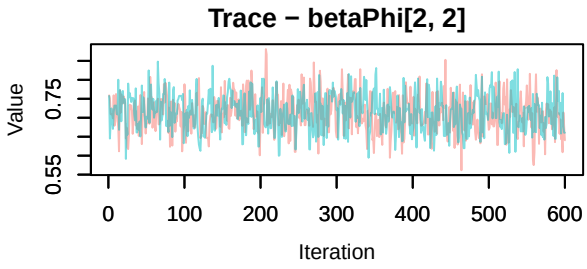

betaP[1, 1]
betaP[2, 2]
betaP[3, 3]
betaP[1, 5]
betaP[2, 6]
betaP[3, 7]
betaP[1, 9]
betaP[2, 10]
betaP[3, 11]
betaP[1, 13]
betaP[2, 14]
betaP[3, 15]
0.0
0.5
1.0
Parameter Estimate

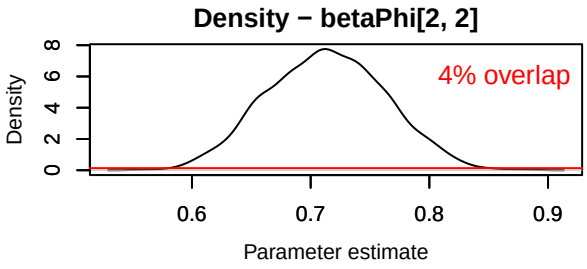


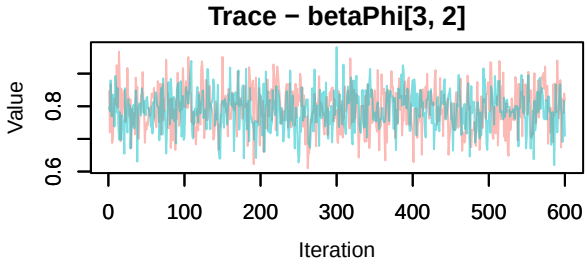

```
#> Warning in MCMCtrace(object = mod_tt_main$mcmc, ISB = FALSE, exact = TRUE, :
#> Only one prior specified for > 1 parameter. Using a single prior for all
#> parameters.
#> Warning in MCMCtrace(object = mod_tt_main$mcmc, ISB = FALSE, exact = TRUE, :
#> Number of samples in prior is greater than number of total or specified
#> iterations (for all chains) for specified parameter. Only last 1200 iterations
#> will be used.
```

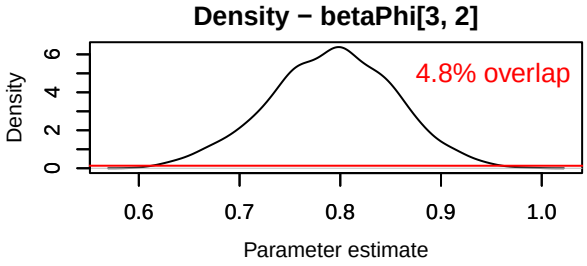

Trace − betaPhi[1, 2]
Value
0.1
0.4
0.7
0
100
200
300
400
500
600
Iteration

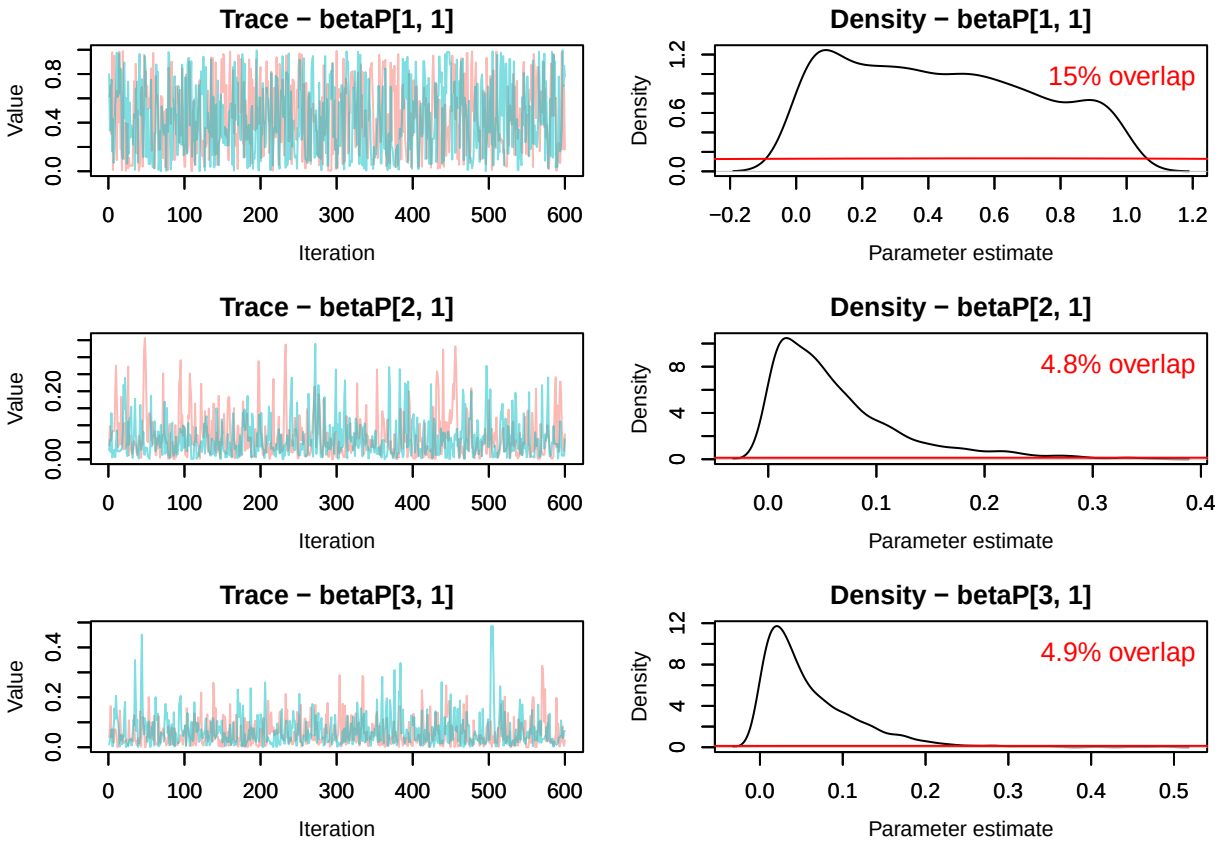

Density − betaPhi[1, 2]
Density
0
2
4
7.1% overlap
0.0
0.2
0.4
0.6
0.8
Parameter estimate

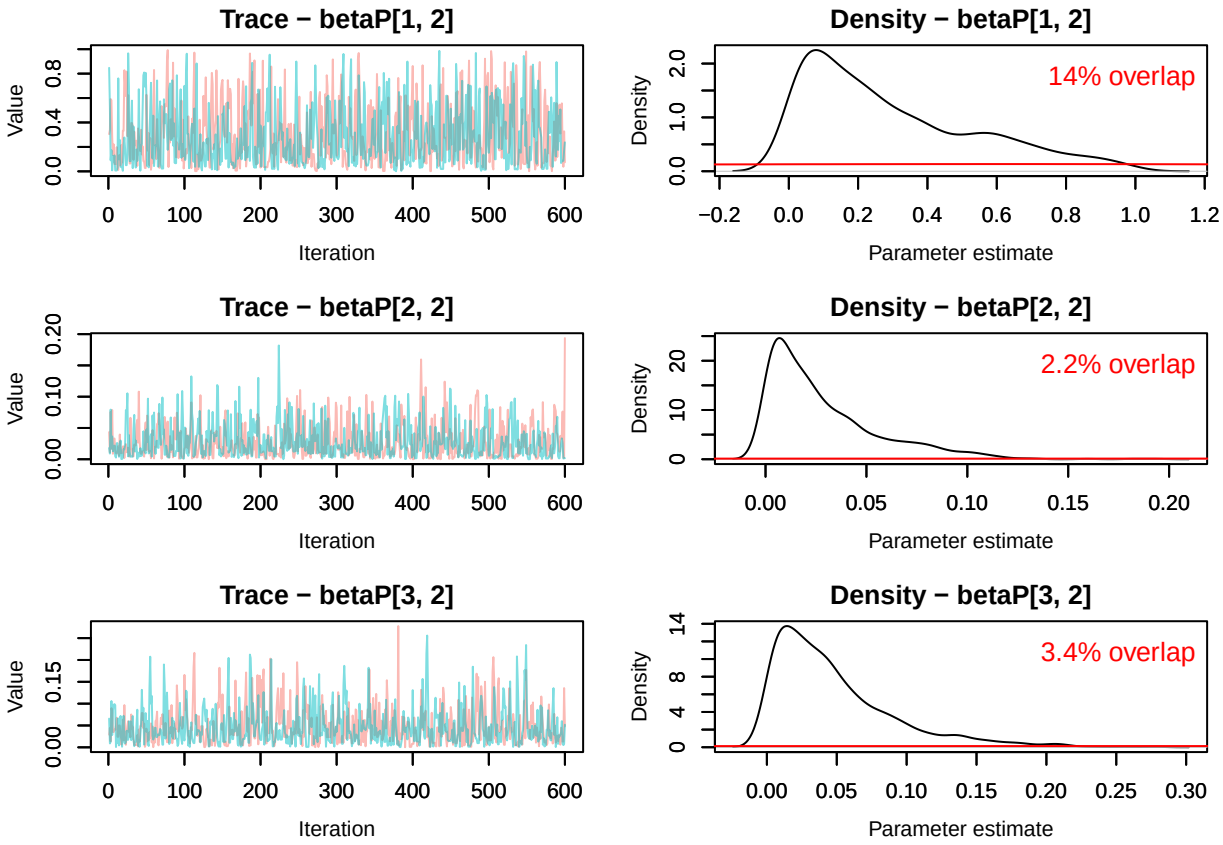

Trace − betaPhi[2, 2]
Value
0.55
0.75
0
100
200
300
400
500
600
Iteration


Density − betaPhi[2, 2]
Density
0
2
4
6
8
4% overlap
0.6
0.7
0.8
0.9
Parameter estimate


Trace − betaPhi[3, 2]
Value
0.6
0.8
0
100
200
300
400
500
600
Iteration


Density − betaPhi[3, 2]
Density
0
2
4
6
4.8% overlap
0.6
0.7
0.8
0.9
1.0
Parameter estimate


Trace − betaP[1, 1]
Value
Iteration
Density − betaP[1, 1]
15% overlap
Density
Parameter estimate
Trace − betaP[2, 1]
Value
Iteration
Density − betaP[2, 1]
4.8% overlap
Density
Parameter estimate
Trace − betaP[3, 1]
Value
Iteration
Density − betaP[3, 1]
4.9% overlap
Density
Parameter estimate

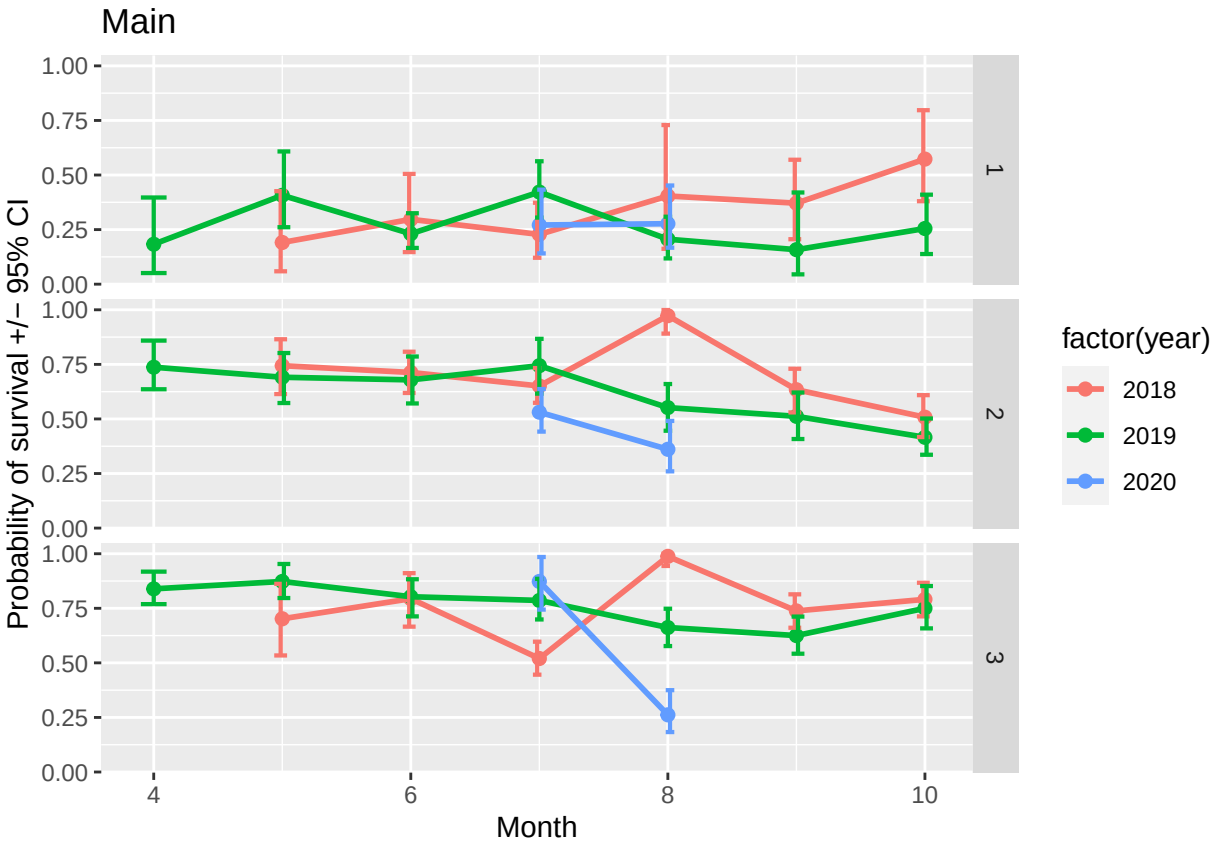


Main, phi, p and psi

```
nS <- mod_tt_main$myConstants$nStates
nT <- mod_tt_main$myConstants$T

phi_tt_main <- modSummary_tt_main %>%
  filter(substr(row.names(modSummary_tt_main), 1, 7) == "betaPhi") %>%
  add_column(data.frame(state = 1:nS, dateYM = rep(1:(nT - 1), each = nS))) %>%
  mutate(year = years[dateYM],
         month = months[dateYM],
         river = "main")

p_tt_main <- modSummary_tt_main %>%
  filter(substr(row.names(modSummary_tt_main), 1, 6) == "betaP[") %>%
  add_column(data.frame(state = 1:nS, dateYM = rep(1:(nT - 1), each = nS))) %>%
  mutate(year = years[dateYM],
         month = months[dateYM],
         river = "main")

psi_tt_main <- modSummary_tt_main %>%
  filter(substr(row.names(modSummary_tt_main), 1, 3) == "psi") %>%
  add_column(data.frame(stateFrom = 1:nS, stateTo = rep(1:nS, each = nS), dateYM = rep(1:(nT - 1), ea
  mutate(year = years[dateYM],
         month = months[dateYM],
```

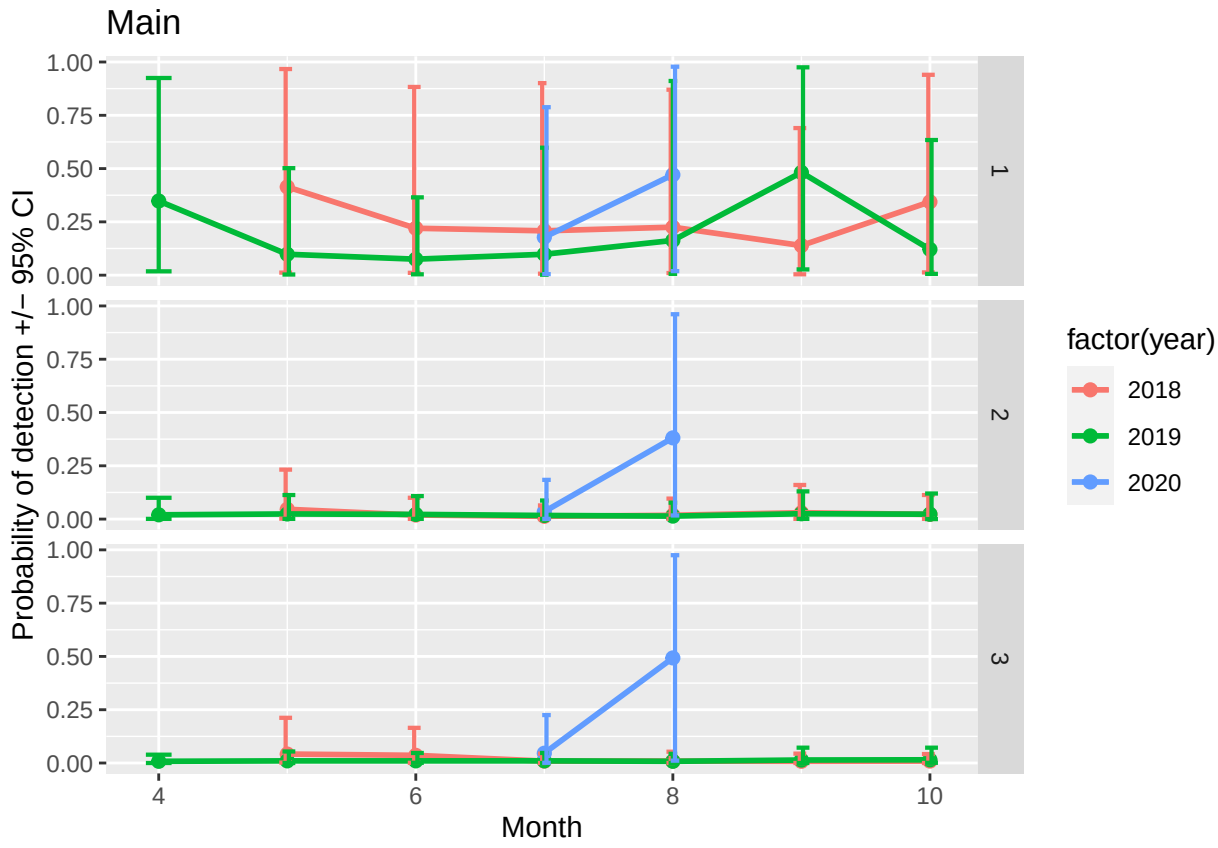
```
           river = "main")
```

```
#phi
ggplot(phi_tt_main, aes(month, med, color = factor(year))) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = lo, ymax = hi),
                width = 0.2,
                position = position_dodge(0.05),
                size = 0.75) +
  ylab("Probability of survival +/- 95% CI") +
  xlab("Month") +
  ggtitle("Main") +
  facet_grid(rows = vars(state))
```

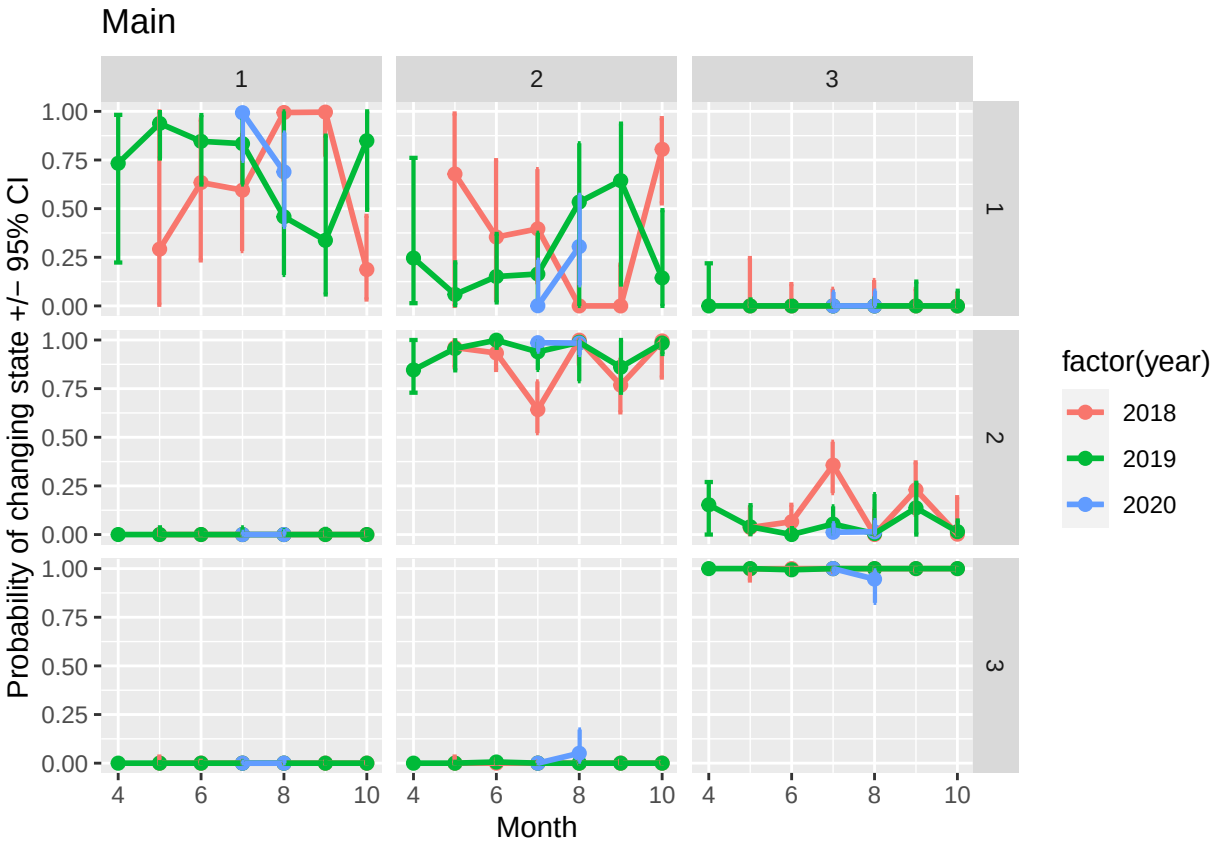



```
# p
ggplot(p_tt_main, aes(month, med, color = factor(year))) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = lo, ymax = hi),
                width = 0.2,
                position = position_dodge(0.05),
                size = 0.75) +
  ylab("Probability of detection +/- 95% CI") +
```

```
  xlab("Month") +
  ggtitle("Main") +
  facet_grid(rows = vars(state))
```




```
#psi
ggplot(psi_tt_main, aes(month, med, color = factor(year))) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = lo, ymax = hi),
                width = 0.2,
                position = position_dodge(0.03),
                size = 0.75) +
  ylab("Probability of changing state +/- 95% CI") +
  xlab("Month") +
  ggtitle("Main") +
  facet_grid(rows = vars(stateFrom),
             cols = vars(stateTo))
```



phiT_pT_trib

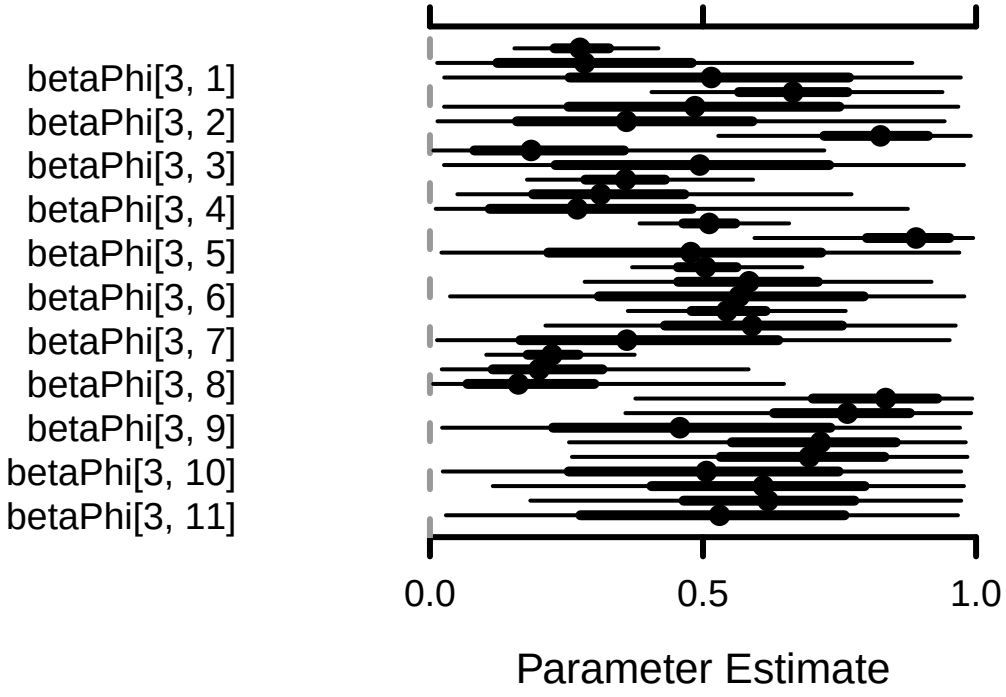
Load data 'trib' for analysis

```
#d_tt <- tar_read(target_d_trib)
eh_trib <- tar_read(target_eh_trib)

str(eh_trib$eh)
#>  num [1:288, 1:12] 1 1 1 1 1 1 1 1 1 1 ...
#>  - attr(*, "dimnames")=List of 2
#>   ..$ : NULL
#>   ..$ : chr [1:12] "date_2018-07" "date_2018-08" "date_2018-09" "date_2018-10" ...
#kable(eh_trib$eh[1:8,1:10])

table(paste(eh_trib$first, eh_trib$last, sep="_"))
#>
#> 1_12 2_12 3_12 4_12 5_12 6_12 7_12 8_12
#>   60    8   12   15  100   53   20   20
```

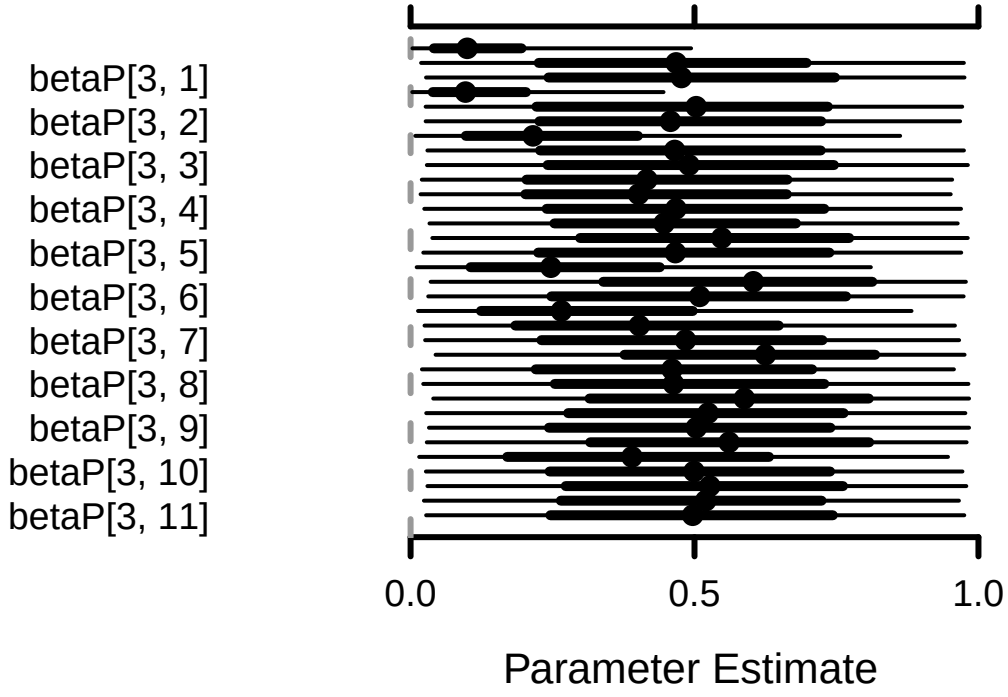
Plot trib model estimates

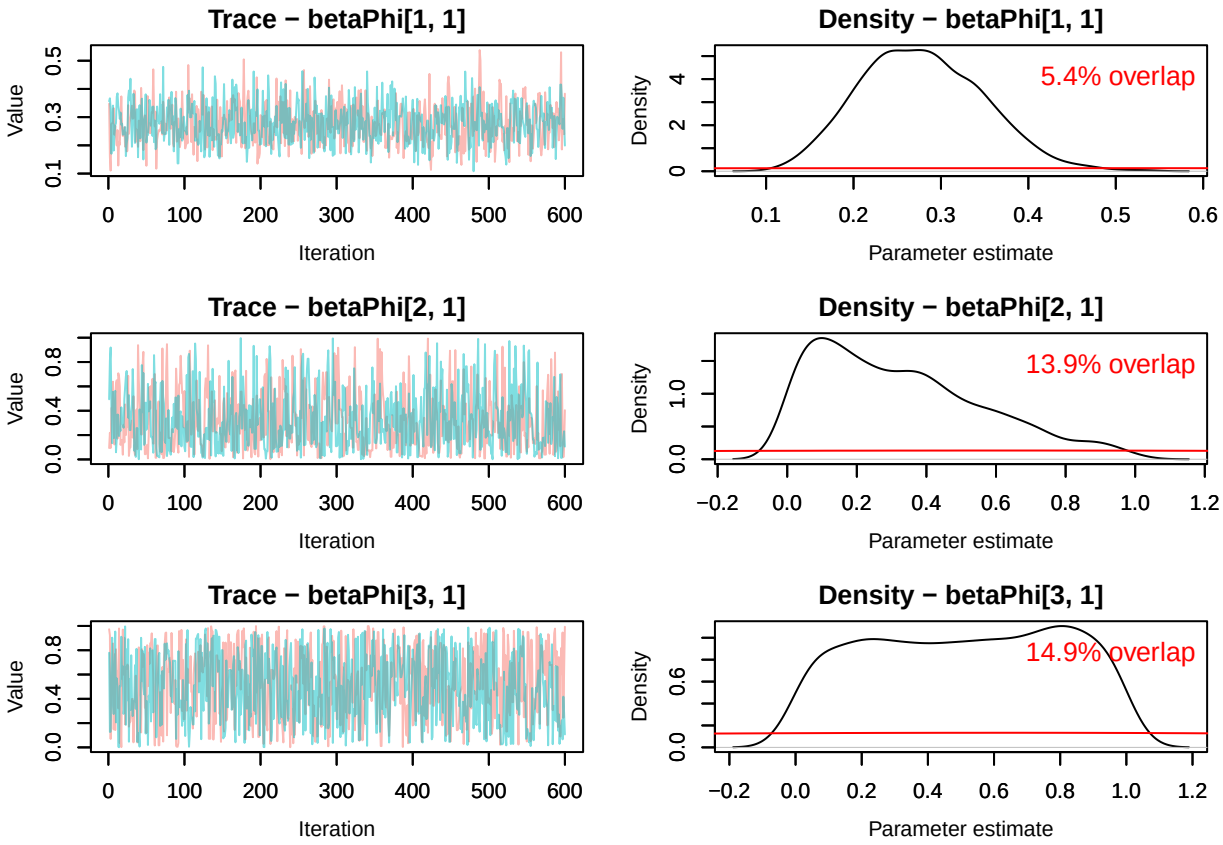
```
### Read the model run into global memory
if (tar_exist_objects(c("tt_modelOut_trib"))) {
  mod_tt_trib <- tar_read(tt_modelOut_trib)
```

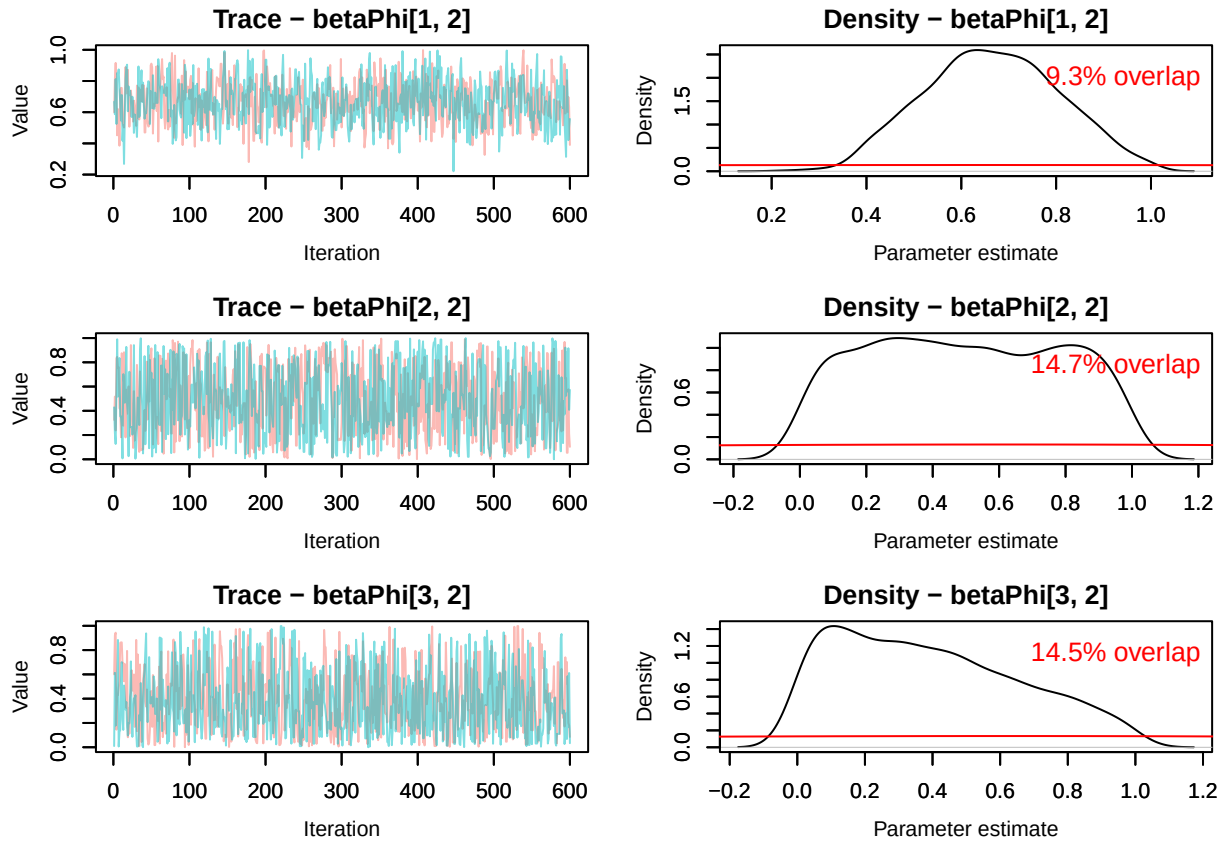
```
  MCMCplot(object = mod_tt_trib$mcmc, params = "betaPhi")
  MCMCplot(object = mod_tt_trib$mcmc, params = "betaP")

   MCMCtrace(object = mod_tt_trib$mcmc,
             ISB = FALSE,
             exact = TRUE,
             params = c("betaPhi[1, 1]", "betaPhi[2, 1]", "betaPhi[3, 1]",
                        "betaPhi[1, 2]", "betaPhi[2, 2]", "betaPhi[3, 2]",
                        "betaPhi[1, 3]", "betaPhi[2, 3]", "betaPhi[3, 3]"),
             pdf = FALSE,
             priors = priors
             )

    MCMCtrace(object = mod_tt_trib$mcmc,
           ISB = FALSE,
           exact = TRUE,
           params = c("betaP[1, 1]", "betaP[2, 1]", "betaP[3, 1]",
                      "betaP[1, 2]", "betaP[2, 2]", "betaP[3, 2]",
                      "betaP[1, 3]", "betaP[2, 3]", "betaP[3, 3]"),
           pdf = FALSE,
           priors = priors
           )

    modSummary_tt_trib <- MCMCsummary(object = mod_tt_trib$mcmc, round = 3) %>%
      rename(lo = '2.5%', med = '50%', hi = '97.5%')
}
```



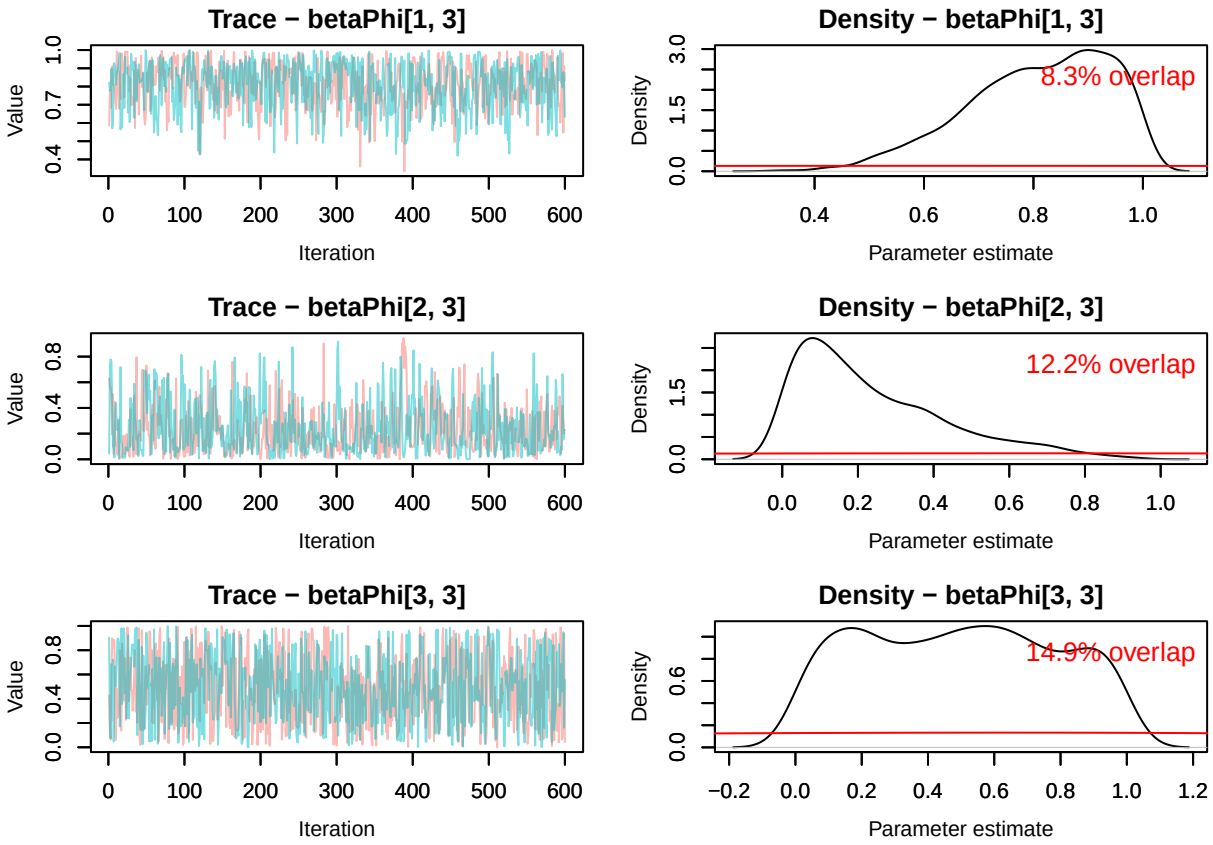

```
#> Warning in MCMCtrace(object = mod_tt_trib$mcmc, ISB = FALSE, exact = TRUE, :
#> Only one prior specified for > 1 parameter. Using a single prior for all
#> parameters.
#> Warning in MCMCtrace(object = mod_tt_trib$mcmc, ISB = FALSE, exact = TRUE, :
#> Number of samples in prior is greater than number of total or specified
#> iterations (for all chains) for specified parameter. Only last 1200 iterations
#> will be used.
```

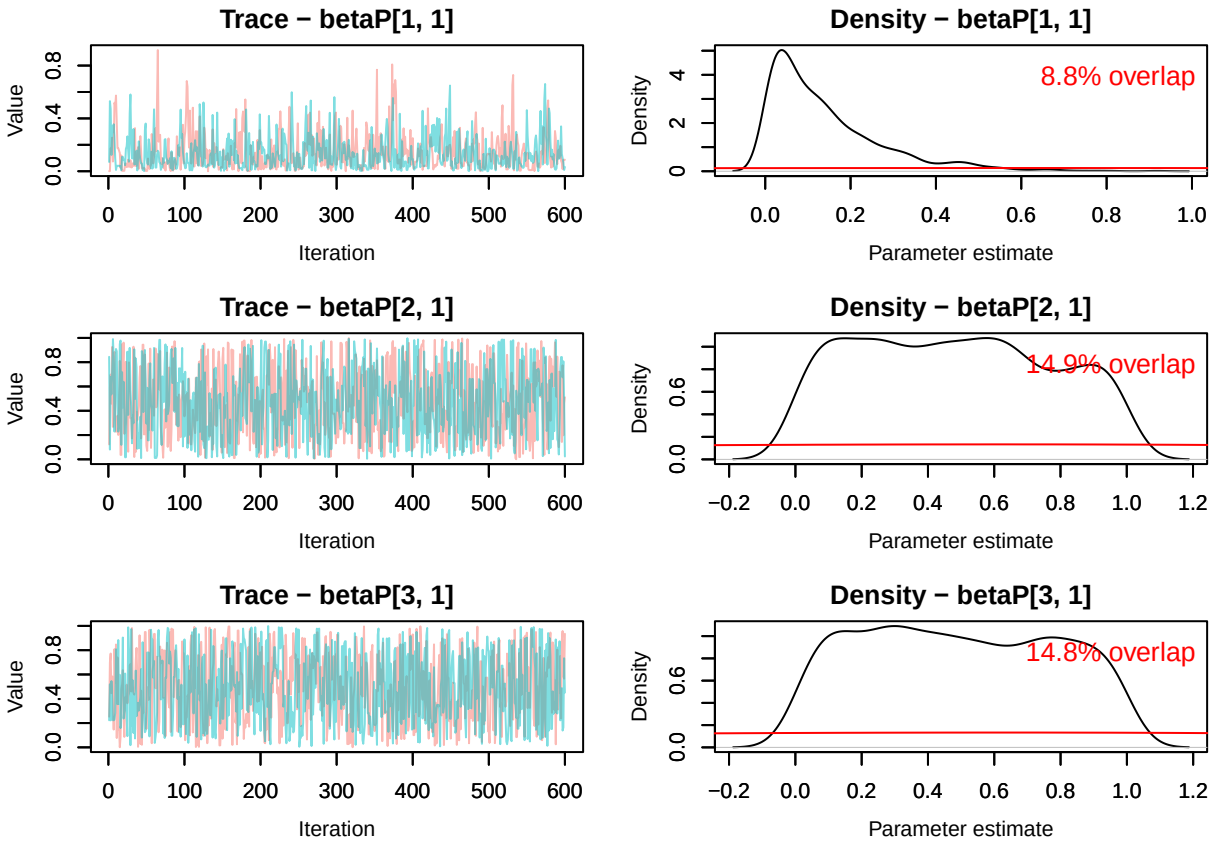

betaP[3, 1]
betaP[3, 2]
betaP[3, 3]
betaP[3, 4]
betaP[3, 5]
betaP[3, 6]
betaP[3, 7]
betaP[3, 8]
betaP[3, 9]
betaP[3, 10]
betaP[3, 11]
0.0
0.5
1.0
Parameter Estimate

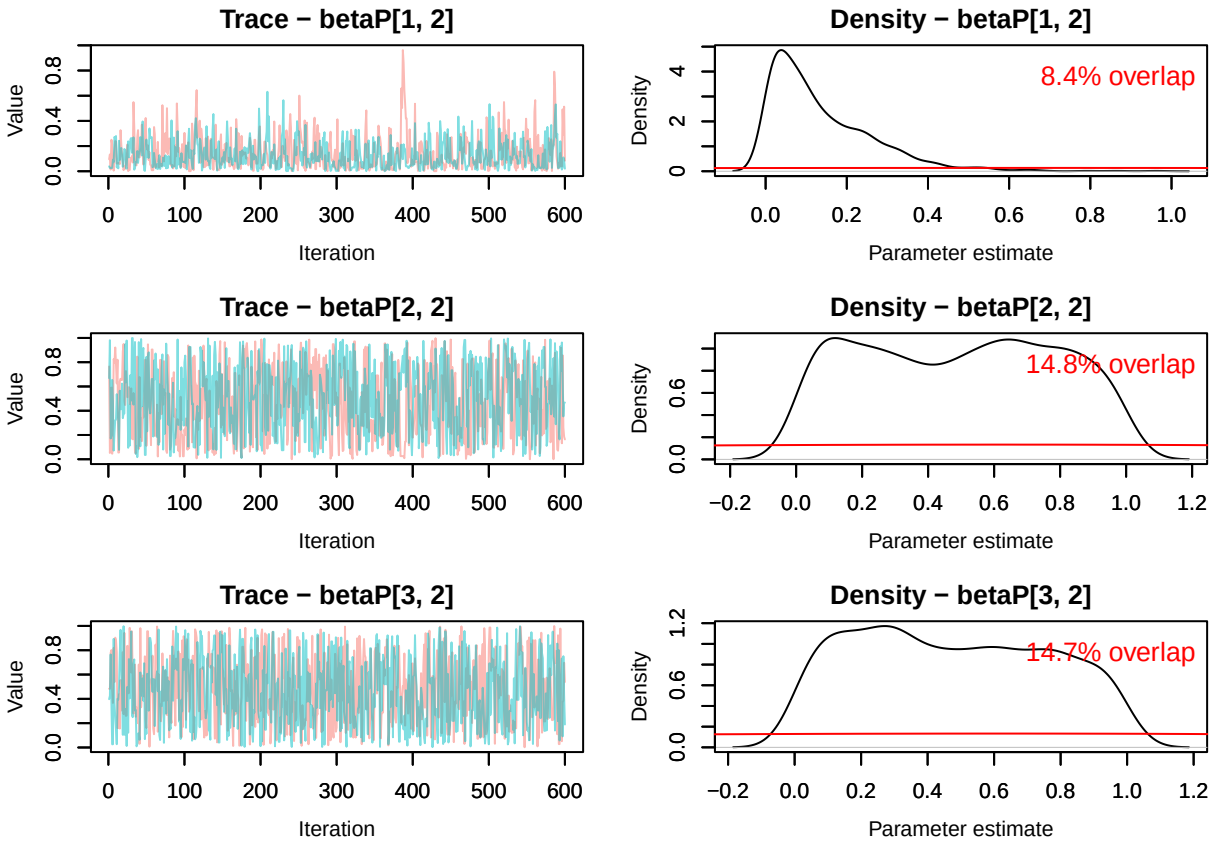

Trace − betaPhi[1, 1]
Value
Iteration
Density − betaPhi[1, 1]
Density
5.4% overlap
Parameter estimate
Trace − betaPhi[2, 1]
Value
Iteration
Density − betaPhi[2, 1]
Density
13.9% overlap
Parameter estimate
Trace − betaPhi[3, 1]
Value
Iteration
Density − betaPhi[3, 1]
Density
14.9% overlap
Parameter estimate

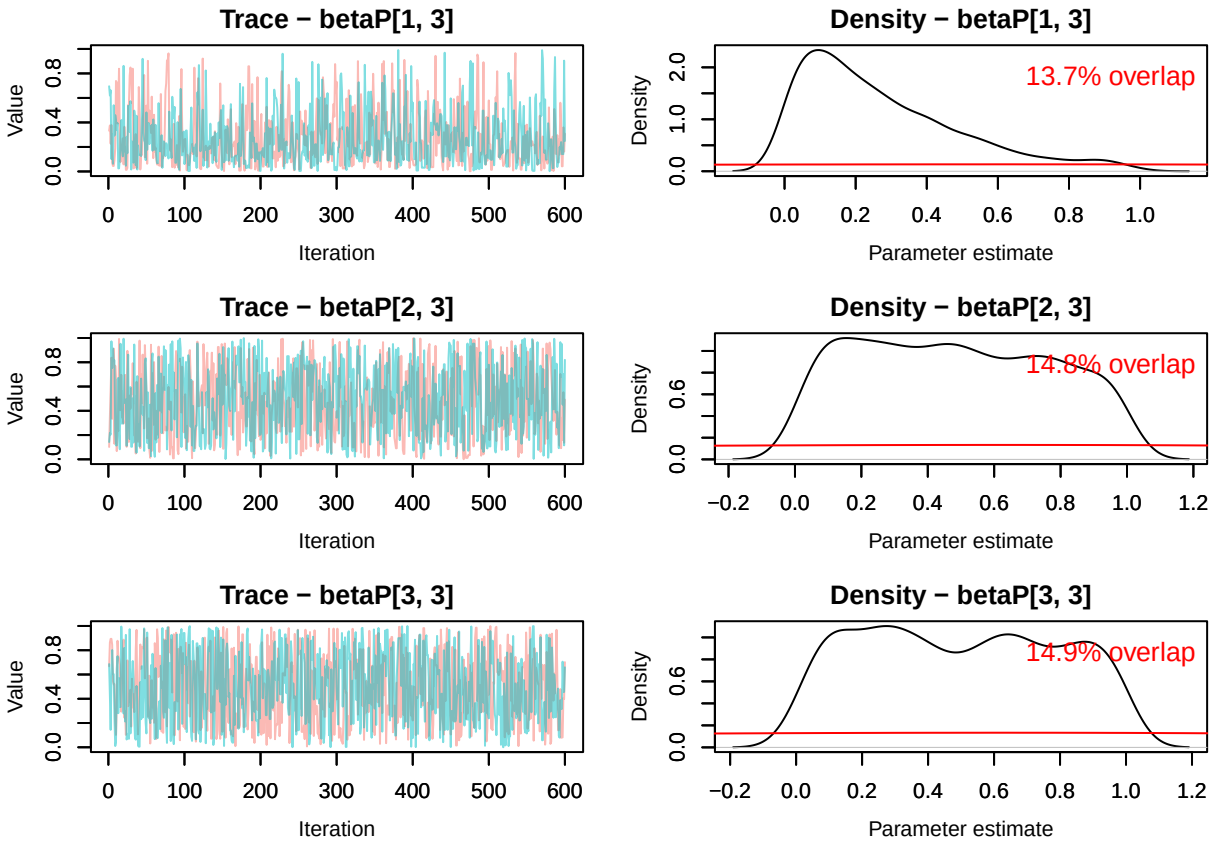



```
#> Warning in MCMCtrace(object = mod_tt_trib$mcmc, ISB = FALSE, exact = TRUE, :
#> Only one prior specified for > 1 parameter. Using a single prior for all
#> parameters.
#> Warning in MCMCtrace(object = mod_tt_trib$mcmc, ISB = FALSE, exact = TRUE, :
#> Number of samples in prior is greater than number of total or specified
#> iterations (for all chains) for specified parameter. Only last 1200 iterations
#> will be used.
```


Trace − betaPhi[1, 3]
Value
Iteration
Density − betaPhi[1, 3]
Density
8.3% overlap
Parameter estimate
Trace − betaPhi[2, 3]
Value
Iteration
Density − betaPhi[2, 3]
Density
12.2% overlap
Parameter estimate
Trace − betaPhi[3, 3]
Value
Iteration
Density − betaPhi[3, 3]
Density
14.9% overlap
Parameter estimate

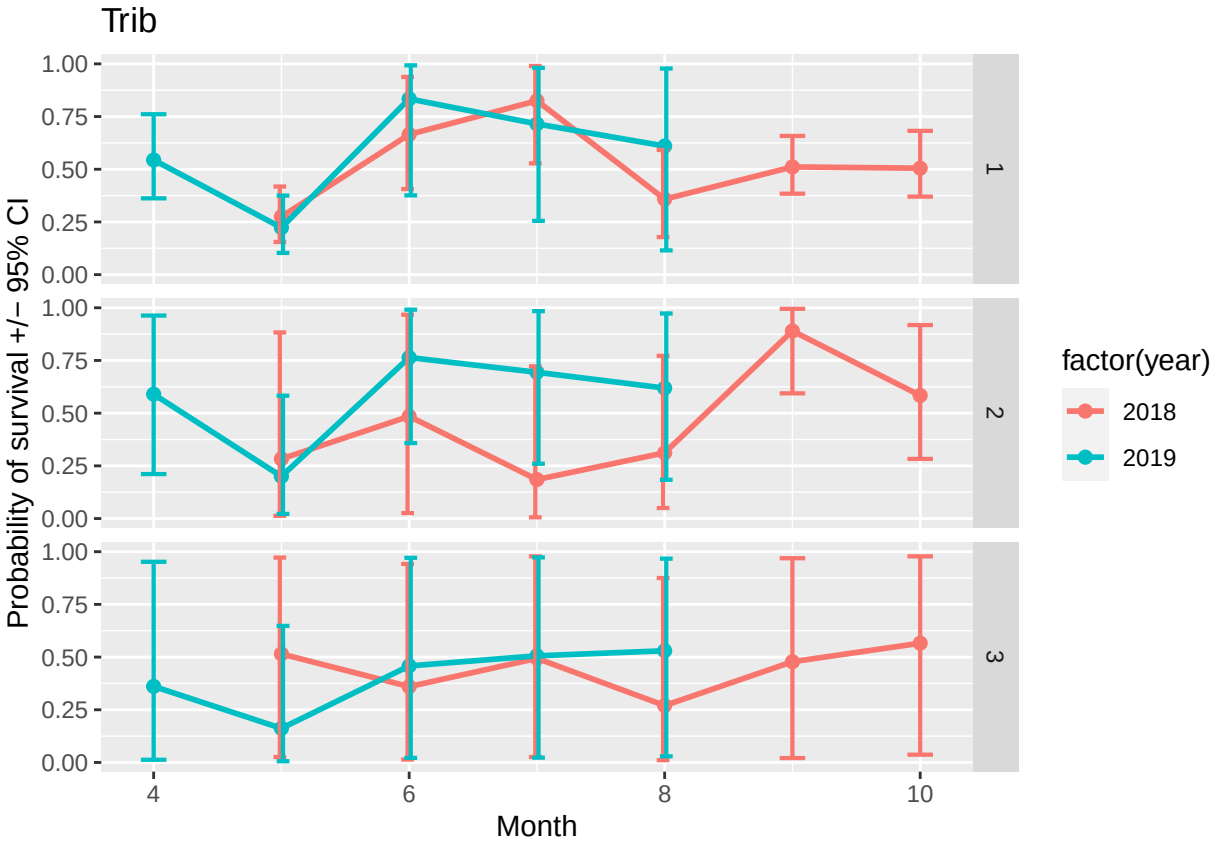

Trace − betaP[1, 1]
Value
Iteration
Density − betaP[1, 1]
Density
Parameter estimate
8.8% overlap
Trace − betaP[2, 1]
Value
Iteration
Density − betaP[2, 1]
Density
Parameter estimate
14.9% overlap
Trace − betaP[3, 1]
Value
Iteration
Density − betaP[3, 1]
Density
Parameter estimate
14.8% overlap


Trace − betaP[1, 2]
Value
Iteration
Density − betaP[1, 2]
Density
Parameter estimate
8.4% overlap
Trace − betaP[2, 2]
Value
Iteration
Density − betaP[2, 2]
Density
Parameter estimate
14.8% overlap
Trace − betaP[3, 2]
Value
Iteration
Density − betaP[3, 2]
Density
Parameter estimate
14.7% overlap

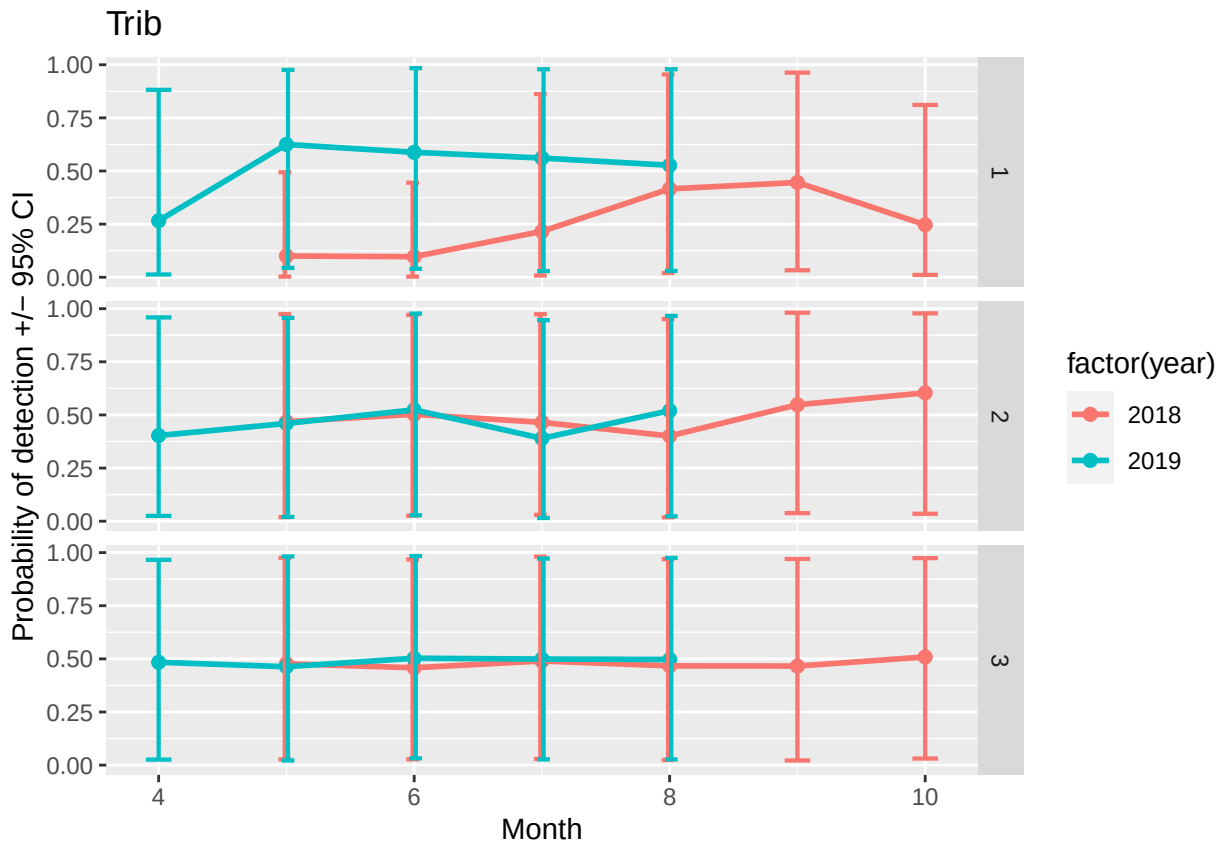



```
nS <- mod_tt_trib$myConstants$nStates
nT <- mod_tt_trib$myConstants$T

phi_tt_trib <- modSummary_tt_trib %>%
  filter(substr(row.names(modSummary_tt_trib), 1, 7) == "betaPhi") %>%
  add_column(data.frame(state = 1:nS, dateYM = rep(1:(nT - 1), each = nS))) %>%
  mutate(year = years[dateYM],
         month = months[dateYM],
         river = "trib")

p_tt_trib <- modSummary_tt_trib %>%
  filter(substr(row.names(modSummary_tt_trib), 1, 6) == "betaP[") %>%
  add_column(data.frame(state = 1:nS, dateYM = rep(1:(nT - 1), each = nS))) %>%
  mutate(year = years[dateYM],
         month = months[dateYM],
         river = "trib")

psi_tt_trib <- modSummary_tt_trib %>%
  filter(substr(row.names(modSummary_tt_trib), 1, 3) == "psi") %>%
  add_column(data.frame(stateFrom = 1:nS, stateTo = rep(1:nS, each = nS), dateYM = rep(1:(nT - 1), ea
  mutate(year = years[dateYM],
         month = months[dateYM],
         river = "trib")
```

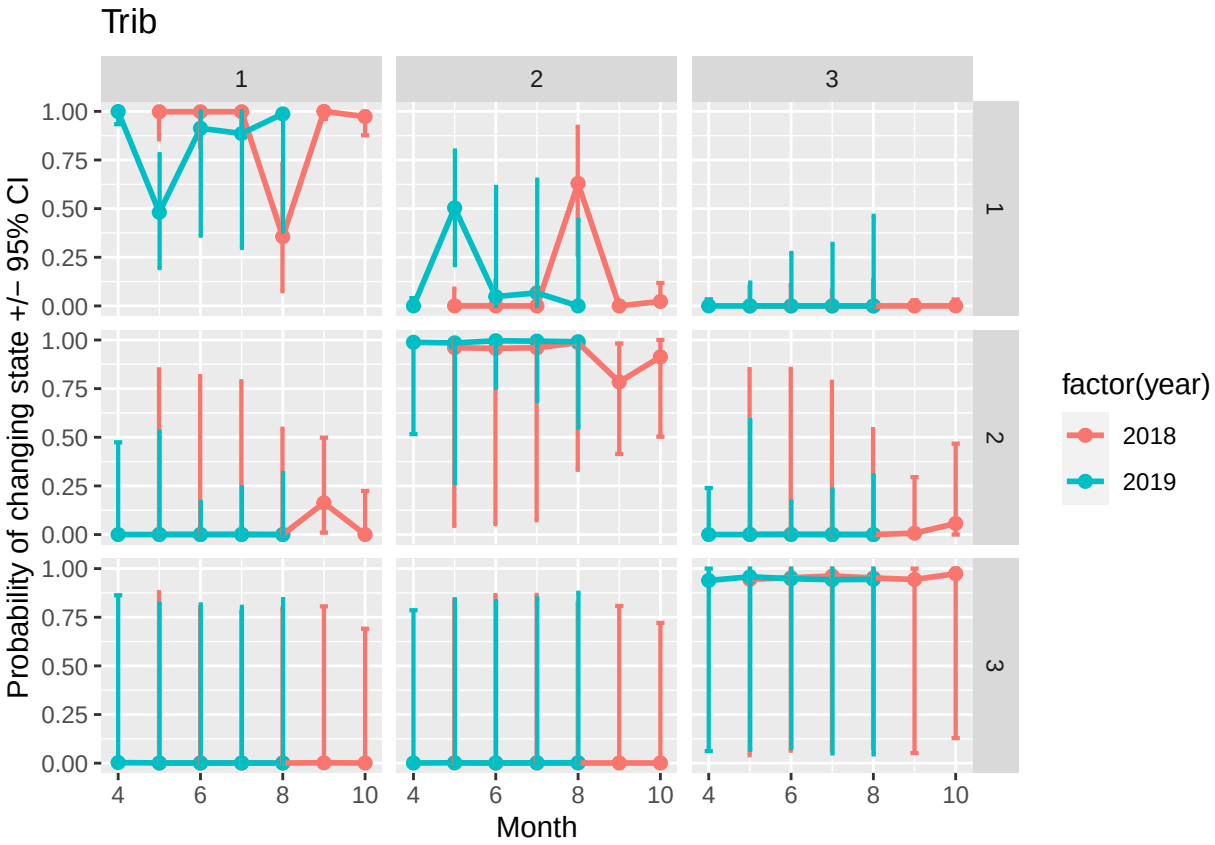
```
#phi
ggplot(phi_tt_trib, aes(month, med, color = factor(year))) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = lo, ymax = hi),
                width = 0.2,
                position = position_dodge(0.05),
                size = 0.75) +
  ylab("Probability of survival +/- 95% CI") +
  xlab("Month") +
  ggtitle("Trib") +
  facet_grid(rows = vars(state))
```




```
# p
ggplot(p_tt_trib, aes(month, med, color = factor(year))) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = lo, ymax = hi),
                width = 0.2,
                position = position_dodge(0.05),
                size = 0.75) +
  ylab("Probability of detection +/- 95% CI") +
  xlab("Month") +
  ggtitle("Trib") +
  facet_grid(rows = vars(state))
```



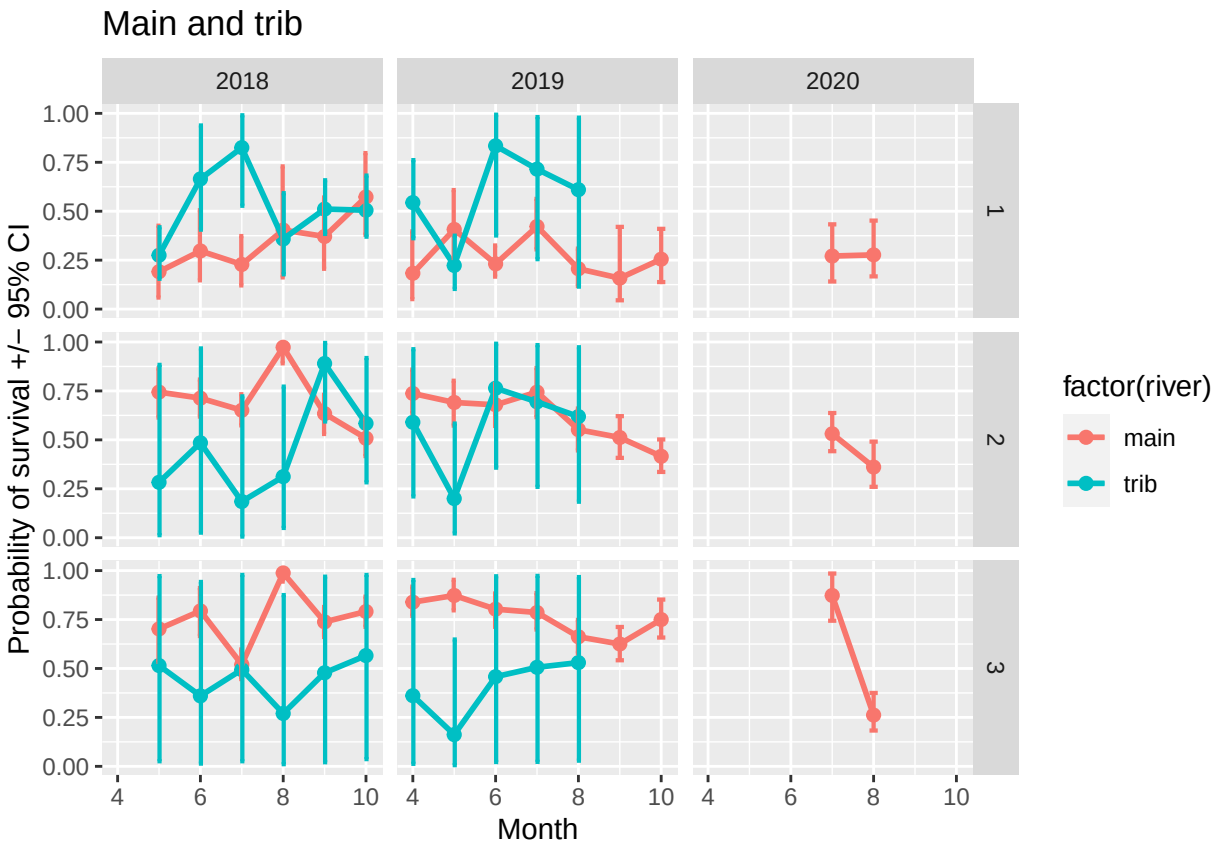

```
#psi
ggplot(psi_tt_trib, aes(month, med, color = factor(year))) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = lo, ymax = hi),
                width = 0.2,
                position = position_dodge(0.03),
                size = 0.75) +
  ylab("Probability of changing state +/- 95% CI") +
  xlab("Month") +
  ggtitle("Trib") +
  facet_grid(rows = vars(stateFrom),
             cols = vars(stateTo))
```



Combine main and trib estimates

```
phi_tt_mainTrib <- add_row(phi_tt_main, phi_tt_trib)
psi_tt_mainTrib <- add_row(psi_tt_main, psi_tt_trib)
```

```
ggplot(phi_tt_mainTrib, aes(month, med, color = factor(river))) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = lo, ymax = hi),
                width = 0.2,
                position = position_dodge(0.05),
                size = 0.75) +
  ylab("Probability of survival +/- 95% CI") +
  xlab("Month") +
  ggtitle("Main and trib") +
  facet_grid(rows = vars(state),
             cols = vars(year))
```



Calculate means for broad comparisons

```
  # Overall means across occasions
# Main
  (
    phi_tt_main_means <- phi_tt_main %>%
    group_by(state) %>%
    summarise(meanPhi = mean(mean),
              sdPhi = sd(mean),
              meanLo = mean(lo),
              meanMed = mean(med),
              meanHi = mean(hi)) %>%
    mutate(river = "main") %>%
    ungroup()
  )
#> # A tibble: 3 x 7
#>   state meanPhi sdPhi meanLo meanMed meanHi river
#>   <int>   <dbl> <dbl>  <dbl>   <dbl>  <dbl> <chr>
#> 1     1   0.306 0.113  0.164   0.298  0.488 main
#> 2     2   0.630 0.152  0.529   0.630  0.731 main
#> 3     3   0.734 0.170  0.643   0.734  0.824 main

  (
    psi_tt_main_means <- psi_tt_main %>%
```

```
    group_by(stateFrom, stateTo) %>%
    summarise(meanPhi = mean(mean),
              sdPhi = sd(mean),
              meanLo = mean(lo),
              meanMed = mean(med),
              meanHi = mean(hi)) %>%
    mutate(river = "main") %>%
    ungroup()
    )
#> `summarise()` has grouped output by 'stateFrom'. You can override using the
#> `.groups` argument.
#> # A tibble: 9 x 8
#>   stateFrom stateTo meanPhi    sdPhi   meanLo meanMed meanHi river
#>       <int>   <int>   <dbl>    <dbl>    <dbl>   <dbl>  <dbl> <chr>
#> 1         1       1 0.692   0.238    0.404     0.692  0.933  main
#> 2         1       2 0.299   0.236    0.0639    0.299  0.582  main
#> 3         1       3 0.00973 0.00660  0         0      0.0953 main
#> 4         2       1 0.0022  0.00142  0         0      0.0201 main
#> 5         2       2 0.914   0.0970   0.815     0.923  0.977  main
#> 6         2       3 0.0834  0.0973   0.0229    0.0747 0.183  main
#> 7         3       1 0.00133 0.000900 0         0      0.0107 main
#> 8         3       2 0.00573 0.0154   0.000533  0.0038 0.0238 main
#> 9         3       3 0.993   0.0157   0.971     0.996  0.999  main

# Trib
  (
    phi_tt_trib_means <- phi_tt_trib %>%
    group_by(state) %>%
    summarise(meanPhi = mean(mean),
              sdPhi = sd(mean),
              meanLo = mean(lo),
              meanMed = mean(med),
              meanHi = mean(hi)) %>%
    mutate(river = "trib") %>%
    ungroup()
    )
#> # A tibble: 3 x 7
#>   state meanPhi sdPhi meanLo meanMed meanHi river
#>   <int>   <dbl> <dbl>  <dbl>   <dbl>  <dbl> <chr>
#> 1     1   0.545 0.194 0.294    0.551  0.761 trib
#> 2     2   0.518 0.211 0.182    0.510  0.886 trib
#> 3     3   0.440 0.102 0.0207   0.427  0.930 trib

  (psi_tt_trib_means <- psi_tt_trib %>%
    group_by(stateFrom, stateTo) %>%
    summarise(meanPhi = mean(mean),
              sdPhi = sd(mean),
              meanLo = mean(lo),
              meanMed = mean(med),
              meanHi = mean(hi)) %>%
    mutate(river = "trib") %>%
    ungroup()
    )
```

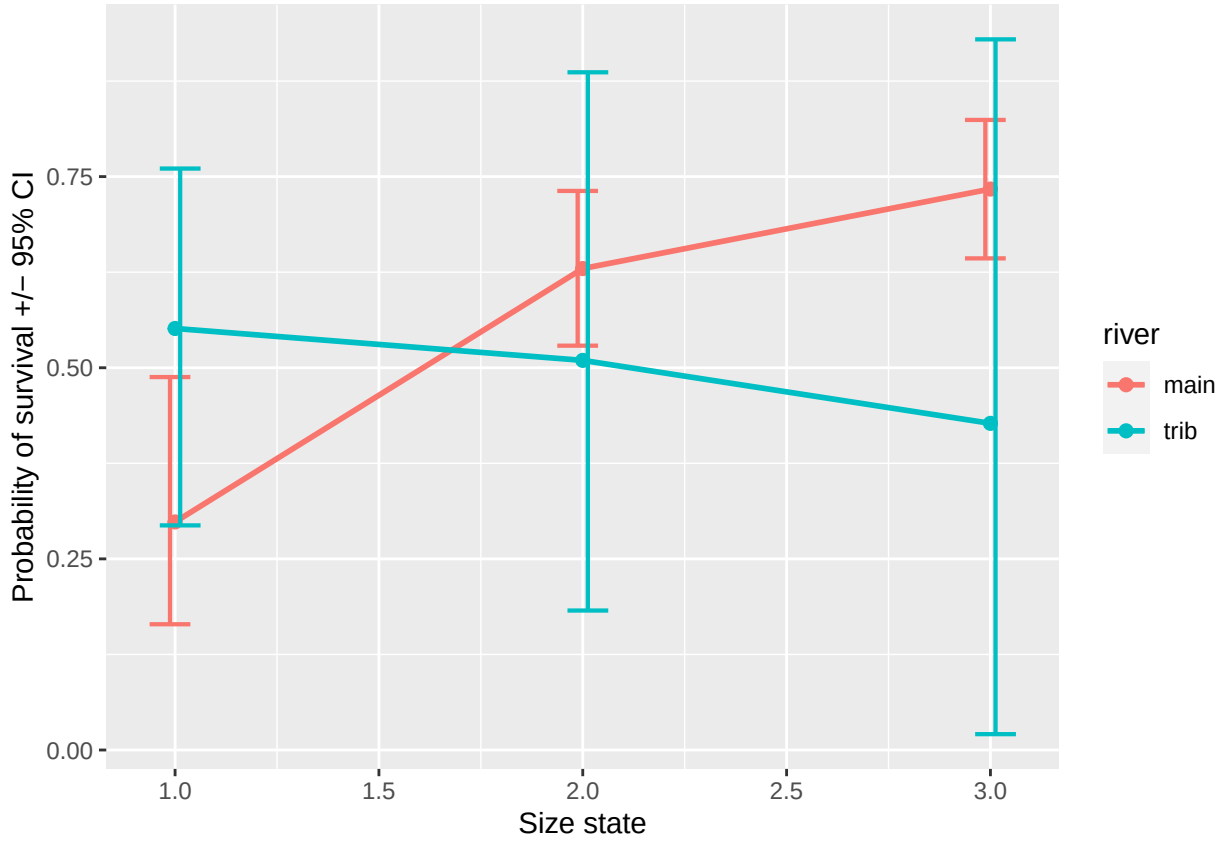
```
#> `summarise()` has grouped output by 'stateFrom'. You can override using the
#> `.groups` argument.
#> # A tibble: 9 x 8
#>   stateFrom stateTo meanPhi  sdPhi   meanLo meanMed meanHi river
#>       <int>   <int>   <dbl>  <dbl>    <dbl>   <dbl>  <dbl> <chr>
#> 1         1       1  0.845  0.217  0.602    0.872    0.955 trib
#> 2         1       2  0.139  0.215  0.0428   0.116    0.356 trib
#> 3         1       3  0.0155 0.0149 0        0        0.153 trib
#> 4         2       1  0.0674 0.0499 0.000909 0.0151   0.495 trib
#> 5         2       2  0.871  0.0705 0.381    0.956    0.998 trib
#> 6         2       3  0.0622 0.0364 0        0.00618  0.484 trib
#> 7         3       1  0.0994 0.0117 0        0.00127  0.809 trib
#> 8         3       2  0.105  0.0130 0        0.00136  0.828 trib
#> 9         3       3  0.796  0.0192 0.0665   0.951    1     trib
```

Combine mean main and trib estimates

```
phi_tt_mainTrib_means <- add_row(phi_tt_main_means, phi_tt_trib_means)
psi_tt_mainTrib_means <- add_row(psi_tt_main_means, psi_tt_trib_means)
```

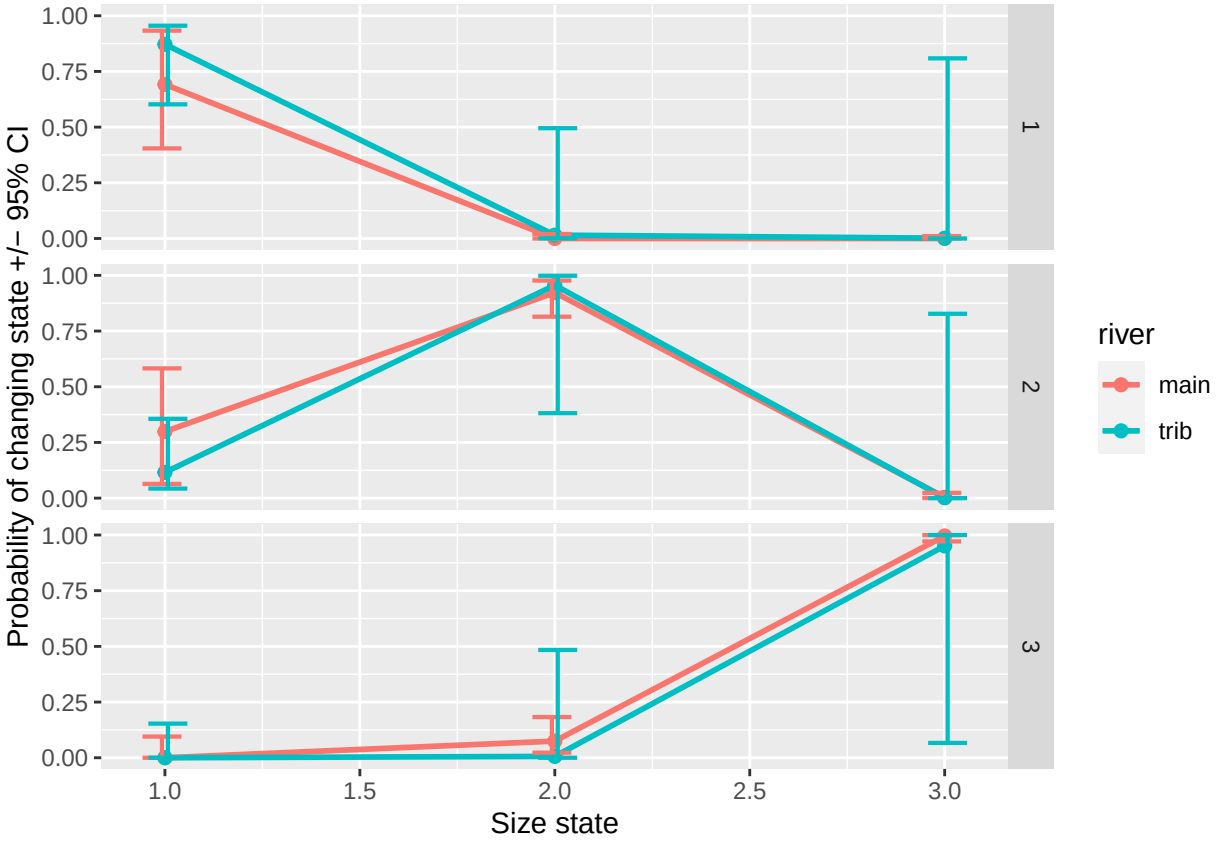
Probability of survival for each size state

```
ggplot(phi_tt_mainTrib_means, aes(state, meanMed, color = river)) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = meanLo, ymax = meanHi),
                width = 0.2,
                position = position_dodge(0.05),
                size = 0.75) +
  ylab("Probability of survival +/- 95% CI") +
  xlab("Size state")
```



Probability of changing state. 'From' size states are on the x-axis, 'to' size states are in the rows of the facets

```
ggplot(psi_tt_mainTrib_means, aes(stateFrom, meanMed, color = river)) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  geom_errorbar(aes(ymin = meanLo, ymax = meanHi),
                width = 0.2,
                position = position_dodge(0.03),
                size = 0.75) +
  ylab("Probability of changing state +/- 95% CI") +
  xlab("Size state") +
  facet_grid(rows = vars(stateTo))
```



Matrix model

```
# mMain <- matrix(
#   c()
# )
```

phiT_pT_psiT

Main and trib modelled together

```
### Read the model run into global memory
# if (tar_exist_objects(c("ttt_modelOut"))) {
#   mod_ttt <- tar_read(ttt_modelOut)
#
#   #MCMCplot(object = mod$mcmc)
#
#   modSummary_ttt <- MCMCsummary(object = mod_ttt$mcmc, round = 3)
# }
#kable(modSummary %>%
#        add_column(data.frame(year = rep(years[1:15], 2), dateYM = rep(occs[1:15], 2)) )


#  d %>%
#  summarize(unique(data.frame(dateYM, occ)))
```

```
# nS <- tar_read(ttt_nStates)
# nT <- tar_read(ttt_myConstants)$T
#
# modSummaryPhi_ttt <- modSummary_ttt %>%
#   filter(substr(row.names(modSummary), 1, 10) == "betaPhiOut") %>%
#   add_column(data.frame(state = 1:nS, dateYM = rep(1:(nT - 1), each = nS))) %>%
#   mutate(mainTrib = ifelse(state < 4, "Main", "Trib"),
#          size = paste0("Size", (state - 1) %% 3 + 1))
#
# ggplot(modSummaryPhi_ttt, aes(dateYM, mean)) +
#   geom_point() +
#   geom_line() +
#   facet_grid(mainTrib ~ size)
#
#
# # modSummaryYears <- modSummary %>%
# #   filter(substr(row.names(modSummary), 1, 3) == "betaPhiout") %>%
# #   add_column(data.frame(year = years[1:15], dateYM = occs[1:15], occ = 1:15)) %>%
# #   group_by(year) %>%
# #   mutate(maxSampPerYear = occ == max(occ))
# #
# # kable(
# #   modSummaryYears %>%
# #   group_by(year) %>%
# #   filter(!maxSampPerYear) %>%
# #   summarize(phiProd = prod(mean),
# #             dateRange = range(dateYM)) %>%
# #     as.data.frame()
# # )
#   MCMCplot(object = mod$mcmc, params = "betaPhiRiverOut")
#
#   priors <- rnorm(tar_read(ttt_runData)$nIter * tar_read(ttt_runData)$nChains, 0, 1/sqrt(.1))
#   MCMCtrace(object = mod$mcmc,
#             #ISB = FALSE,
#             #exact = TRUE,
#             params = c("betaPhiRiverOut"),
#             pdf = FALSE,
#             priors = priors
#             )
#
#     MCMCtrace(object = mod$mcmc,
#             #ISB = FALSE,
#             #exact = TRUE,
#             params = c("betaPhiOut"),
#             pdf = FALSE,
#             priors = priors
#             )
```

```
#create data frame for summarizing p results

# modSummaryYearsP <- modSummary %>%
#   filter(substr(row.names(modSummary), 1, 2) == "p[") %>%
#   add_column(data.frame(year = years[1:15], dateYM = occs[1:15], occ = 1:15)) %>%
```

```
#   group_by(year) %>%
#   mutate(maxSampPerYear = occ == max(occ))
#
# kable(
#   modSummaryYearsP %>%
#   group_by(year) %>%
#   summarize(pMean = mean(mean),
#             dateRange = range(dateYM))
#   )
```

```
# # modSummaryYearsP <- modSummary %>%
# #   filter(substr(row.names(modSummary), 1, 2) == "p[") %>%
# #   add_column(data.frame(year = years[1:15], dateYM = occs[1:15], occ = 1:15)) %>%
# #   group_by(year) %>%
# #   mutate(maxSampPerYear = occ == max(occ))
#
# modSummaryPsi_ttt <- modSummary_ttt %>%
#   filter(substr(row.names(modSummary_ttt), 1, 3) == "psi") %>%
#   add_column(data.frame(state = 1:nS, state2 = rep(1:nS, each = nS), dateYM = rep(1:(nT - 1), each =
#   mutate(mainTrib = ifelse(state < 4, "Main", "Trib"),
#          size = paste0("Size", (state - 1) %% 3 + 1))
#
# ggplot(modSummaryPsi_ttt, aes(dateYM, mean, color = factor(state2))) +
#   geom_point() +
#   facet_grid(mainTrib ~ size)
#
```