Supplemental Material for
'Niche estimation above and below the species level'

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R code for comparing splitting, lumping, partial pooling, and phylogenetically-informed ecological niche models on a simulated dataset (*Box 3*)

This source code is archived in Zenodo (Rodríguez-Sánchez 2018) and can also be found at https://github.com/Pakillo/phyloENM-TREE.

Simulate taxa niches and phylogeny

Here we simulate (following Pearse *et al.* 2016) a group of phylogenetically related taxa with different sentivities to temperature, so that closely related taxa will have more similar niches.

```r
nspp <- 6
nsite <- 30


# simulate a phylogenetic tree
library(ape)
set.seed(6)
```

```r
phy <- rtree(n = nspp)
phy <- compute.brlen(phy, method = "Grafen", power = 0.5)
#plot(phy)


# standardize the phylogenetic covariance matrix to have determinant 1
Vphy <- vcv(phy)
Vphy.std <- Vphy/(det(Vphy)^(1/nspp))


# Perform a Cholesky decomposition of Vphy
iD <- t(chol(Vphy.std))


# Generate environmental site variable
env <- seq(0, 20, length.out = nsite)



## Set up species-specific regression coefficients as random effects


set.seed(79)


intercept <- iD %*% runif(nspp, -1, 2)
slope <- iD %*% runif(nspp, -0.4, 0.1)


intercept <- intercept[gtools::mixedorder(rownames(intercept)), ]
slope <- slope[gtools::mixedorder(rownames(slope)), ]


#intercept
#slope


## Calculate suitabilities for each taxa and site
```

```r
suitab <- rep(intercept, each = nsite)

suitab <- suitab + rep(slope, each = nsite) * rep(env, nspp)

suitab.error <- suitab + rnorm(nspp * nsite, mean = 0, sd = 1) #add some random 'error'

suitab.invlogit <- arm::invlogit(suitab)

suitab.error.invlogit <- arm::invlogit(suitab.error)


set.seed(114)


pres <- rbinom(length(suitab.error), size = 1, prob = suitab.error.invlogit)  # pres-abs


dat <- data.frame(taxa = paste("t", sort(rep(1:nspp, nsite)), sep = ""),

                  site = rep(1:nsite, nspp),

                  env = rep(env, nspp),

                  suitab.invlogit = suitab.invlogit,

                  presabs = pres)
```
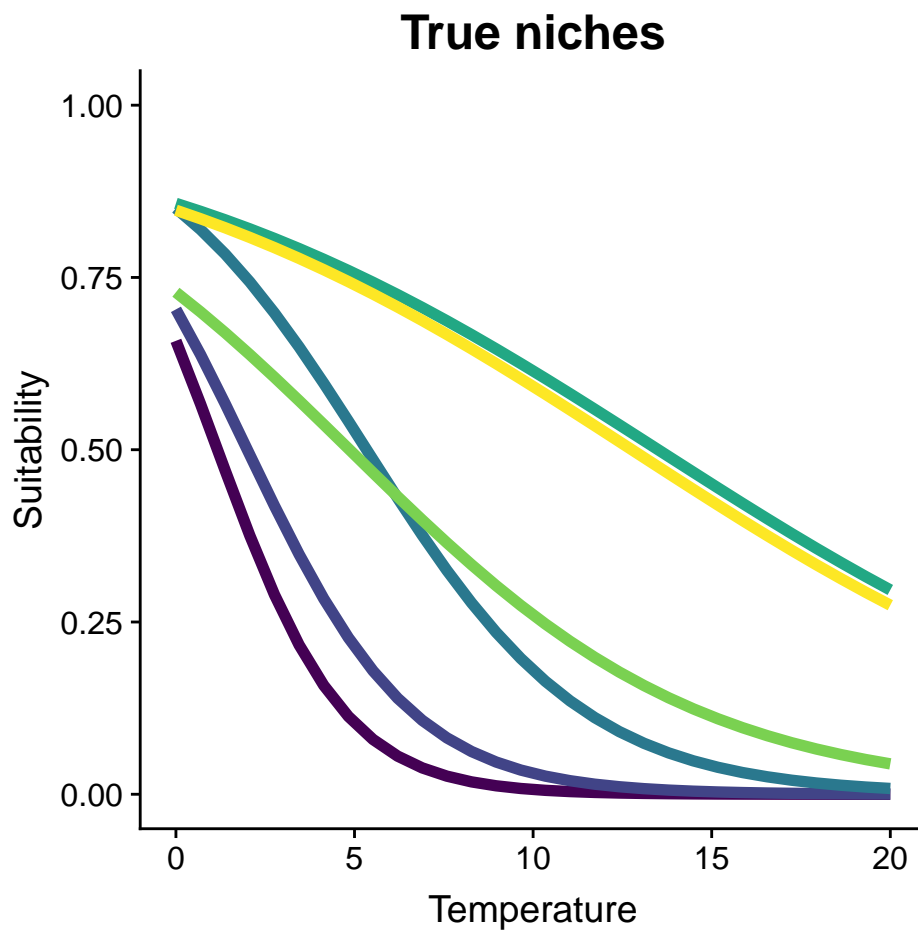
Plot simulated niches

```r
library(ggplot2)

library(cowplot)

library(viridis)



simul.niches <- ggplot(dat, aes(env, suitab.invlogit, colour = taxa)) +

  ylim(0, 1) +

  labs(x = "Temperature", y = "Suitability", title = "True niches") +

  geom_line(size = 2) +

  scale_color_viridis(discrete = TRUE) +

  theme(plot.title = element_text(size = 18)) +

  theme(legend.position = "none")
```

```
simul.niches
```


True niches

Plot phylogeny

```r
library(ggtree)


phylog <- ggplot(phy) +
  geom_tree(size = 2, colour = "grey70") +
  geom_tree(size = 2, aes(color = label)) +
  scale_color_viridis(discrete = "TRUE") +
  theme(legend.position = "none",
        axis.title = element_blank(),
```
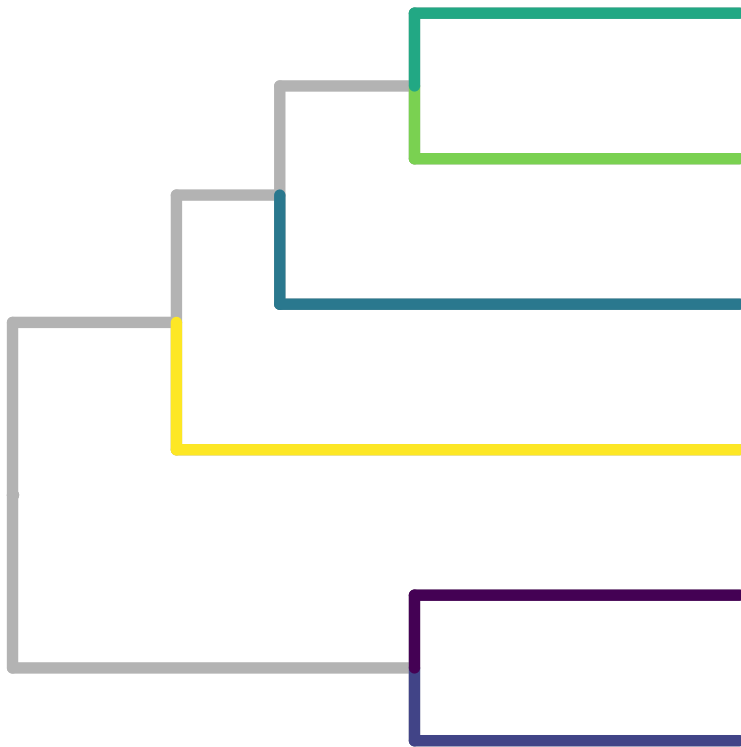
```
        axis.text = element_blank(),

        axis.ticks = element_blank(),

        axis.line = element_blank()) +

  labs(title = "Phylogeny") +

  theme(plot.title = element_text(size = 18)) +

  theme(plot.margin = unit(c(0.2,1,1,1), "cm"))


phylog
```

Phylogeny

Splitting

Here we fit independent binomial generalized linear models (GLM) to each taxon.

```
split <- ggplot(dat, aes(env, presabs, colour = taxa)) +

  ylim(0, 1) +

  labs(x = "Temperature", y = "Suitability", title = "Splitting (GLM)") +

  geom_smooth(method = "glm", method.args = list(family = "binomial"), se = FALSE, size = 2)

  scale_color_viridis(discrete = TRUE) +

  theme(plot.title = element_text(size = 18)) +

  theme(legend.position = "none")


split
```
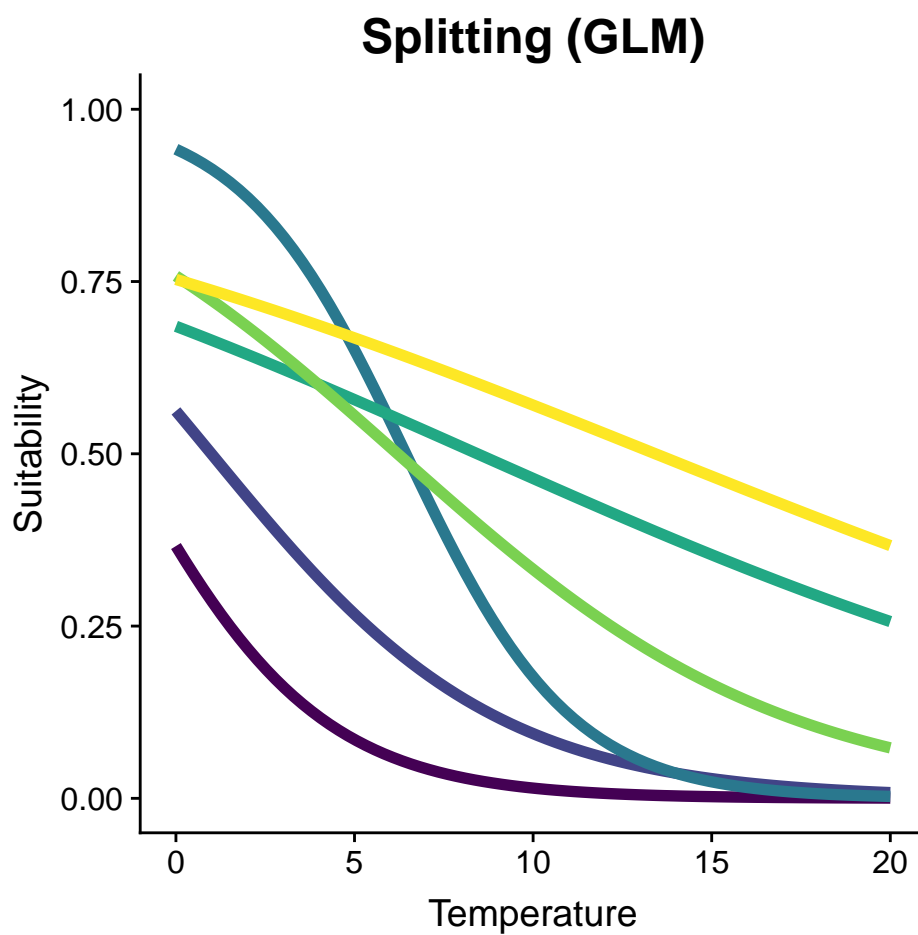

Lumping

Here we fit a single binomial generalized linear model (GLM) to all taxa together.

```r
lump <- ggplot(dat, aes(env, presabs)) +
  ylim(0, 1) +
  labs(x = "Temperature", y = "Suitability", title = "Lumping (GLM)") +
  geom_smooth(method = "glm", method.args = list(family = "binomial"), se = FALSE, size = 3,
              colour = "black") +
  # for comparison with real niches:
  geom_line(aes(env, suitab.invlogit, colour = taxa), size = 2, alpha = 0.2) +
  scale_color_viridis(discrete = TRUE, guide = guide_legend(override.aes = list(alpha = 1)))
  theme(plot.title = element_text(size = 18)) +
  theme(legend.position = "none")

lump
```
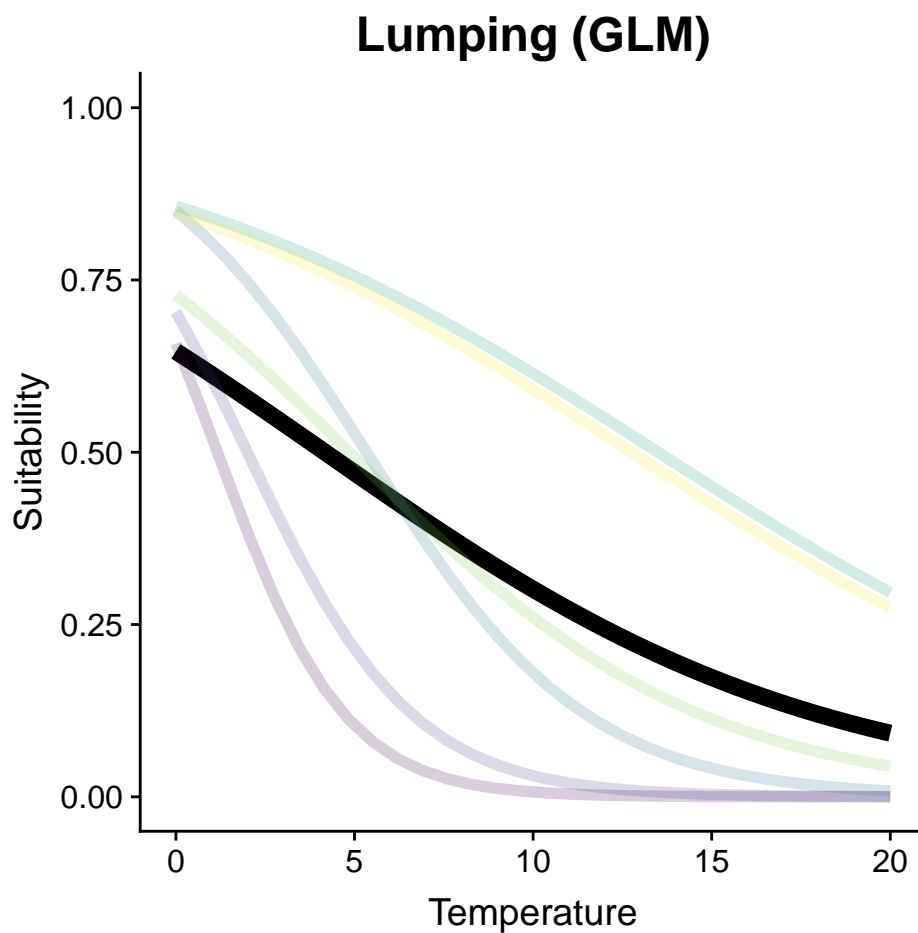
Pooling (GLMM)

Here we fit a mixed effects model (GLMM) with varying intercepts and slopes, so that there is partial pooling among taxa.

```r
library(lme4)


mixed <- glmer(presabs ~ env + (1 + env | taxa), data = dat, family = binomial)
# summary(mixed)
# coef(mixed)
dat$mixedpred <- fitted(mixed, newdata = dat, type = "response")


mixedfig <- ggplot(dat, aes(env, mixedpred, colour = taxa)) +
  ylim(0, 1) +
  labs(x = "Temperature", y = "Suitability", title = "Pooling (GLMM)") +
  geom_line(size = 2) +
  scale_color_viridis(discrete = TRUE) +
  theme(plot.title = element_text(size = 18)) +
  theme(legend.position = "none")


mixedfig
```
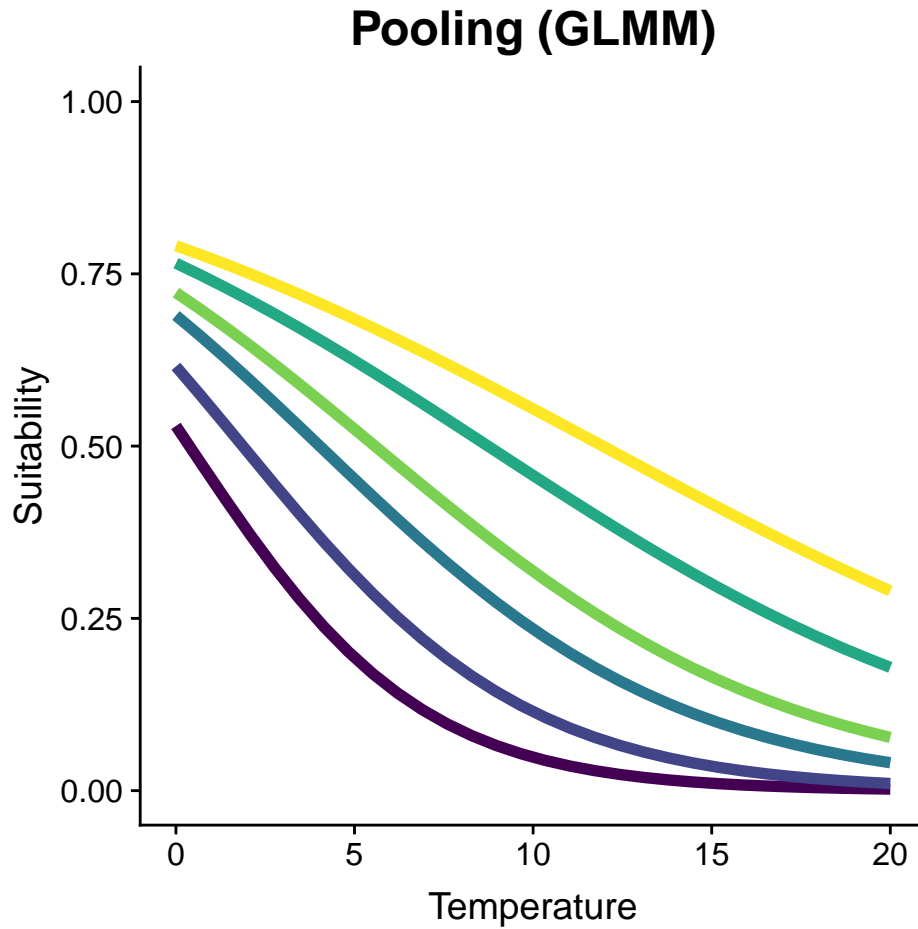
Pooling (GLMM)

Phylogenetic pooling (PGLMM)

Here we fit a phylogenetic generalized linear model (PGLMM) with varying intercepts and slopes, so that closely related taxa tend to have more similar niches.

```r
inv.phylo <- MCMCglmm::inverseA(phy, nodes = "TIPS", scale = TRUE)
A <- solve(inv.phylo$Ainv)
rownames(A) <- rownames(inv.phylo$Ainv)


library(brms)


pglmm <- brm(
  presabs ~ env + (1 + env | taxa),
```

```r
  data = dat,
  family = bernoulli(),
  cov_ranef = list(taxa = A),
  prior = c(
    prior(normal(0, 3), "b"),
    prior(normal(0, 3), "Intercept"),
    prior(student_t(3, 0, 3), "sd")),  # sd of group random effect
  chains = 3, cores = 3, iter = 2000,
  control = list(adapt_delta = 0.96)
)



# summary(pglmm)
# plot(pglmm)
# coef(pglmm)
# pp_check(pglmm)


dat$pglmm <- fitted(pglmm, newdata = dat, scale = "response")[,1]
```

```r
pglmmfig <- ggplot(dat, aes(env, pglmm, colour = taxa)) +
  ylim(0, 1) +
  labs(x = "Temperature", y = "Suitability", title = "Phylogenetic Pooling (PGLMM)") +
  geom_line(size = 2) +
  scale_color_viridis(discrete = TRUE) +
  theme(plot.title = element_text(size = 18)) +
  theme(legend.position = "none")


pglmmfig
```

Phylogenetic Pooling (PGLMM)
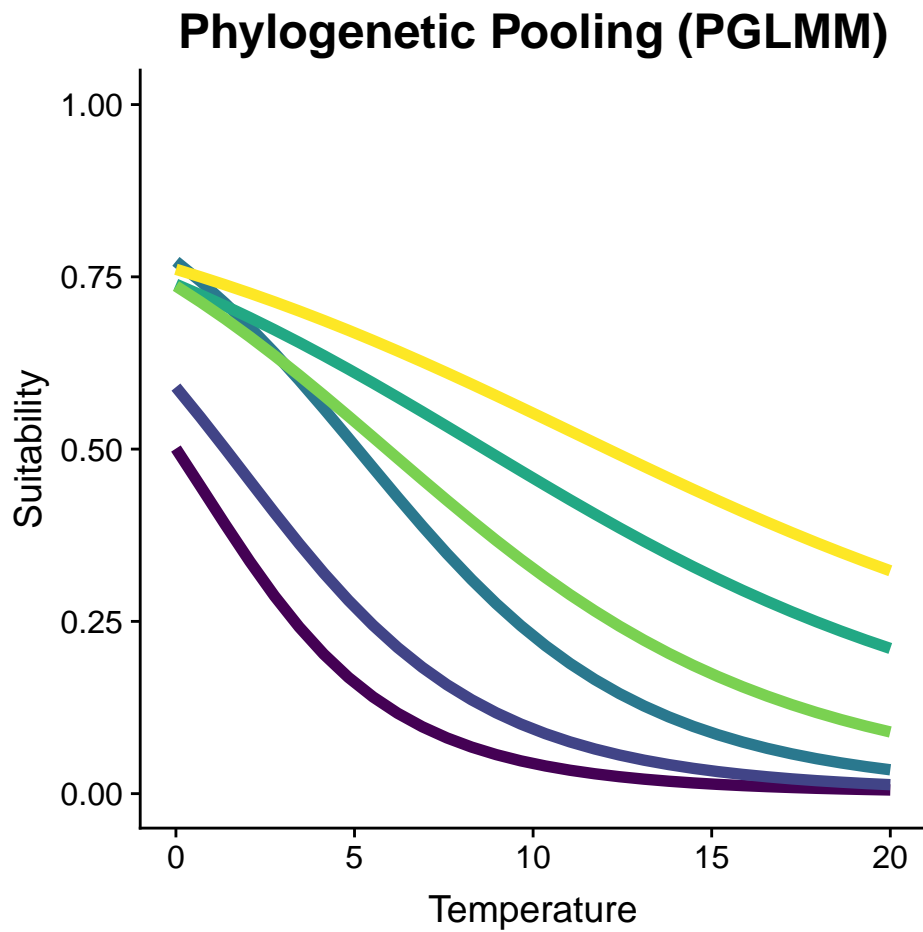
Combined figure

```
figure <- plot_grid(simul.niches, phylog,

                    split, lump,

                    mixedfig, pglmmfig,

                    nrow = 3, ncol = 2)


#figure


save_plot(paste0("FigureBox3", ".pdf"), figure, base_height = 11, base_width = 9)
```

References and software used

Bates, Douglas, Martin Mächler, Ben Bolker, and Steve Walker. 2015. "Fitting Linear Mixed-Effects Models Using lme4." Journal of Statistical Software 67 (1): 1–48. doi:10.18637/jss.v067.i01.

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Hadfield, Jarrod D. 2010. "MCMC Methods for Multi-Response Generalized Linear Mixed Models: The MCMCglmm R Package." Journal of Statistical Software 33 (2): 1–22. http://www.jstatsoft.org/v33/i02/.

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Wickham, Hadley. 2009. Ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York. http://ggplot2.org.

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Xie, Yihui. 2018. Knitr: A General-Purpose Package for Dynamic Report Generation in R. https://yihui.name/knitr/.

Yu, Guangchuang, David Smith, Huachen Zhu, Yi Guan, and Tommy Tsan-Yuk Lam. 2017. "Ggtree: An R Package for Visualization and Annotation of Phylogenetic Trees with Their Covariates and Other Associated Data." Methods in Ecology and Evolution. doi:10.1111/2041-210X.12628.

Details on computation environment

```
## - Session info ---------------------------------------------------------
##   setting  value
##   version  R version 3.5.1 (2018-07-02)
##   os       Windows 7 x64 SP 1
##   system   x86_64, mingw32
##   ui       RTerm
##   language (EN)
##   collate  English_United Kingdom.1252
##   ctype    English_United Kingdom.1252
##   tz       Europe/Paris
##   date     2018-10-25
##
## - Packages -------------------------------------------------------------
##   package      * version  date        lib source
##   abind          1.4-5    2016-07-21 [1] CRAN (R 3.5.0)
##   ape          * 5.2      2018-09-24 [1] CRAN (R 3.5.1)
##   arm            1.10-1   2018-04-13 [1] CRAN (R 3.5.1)
##   assertthat     0.2.0    2017-04-11 [1] CRAN (R 3.5.0)
##   backports      1.1.2    2017-12-13 [1] CRAN (R 3.5.0)
##   base64enc      0.1-3    2015-07-28 [1] CRAN (R 3.5.0)
##   bayesplot      1.6.0    2018-08-02 [1] CRAN (R 3.5.1)
##   bindr          0.1.1    2018-03-13 [1] CRAN (R 3.5.0)
```

```
## bindrcpp          0.2.2     2018-03-29 [1] CRAN (R 3.5.0)
## bridgesampling    0.6-0     2018-10-21 [1] CRAN (R 3.5.1)
## brms            * 2.6.0     2018-10-23 [1] CRAN (R 3.5.1)
## Brobdingnag       1.2-6     2018-08-13 [1] CRAN (R 3.5.1)
## callr             3.0.0     2018-08-24 [1] CRAN (R 3.5.1)
## cli               1.0.1     2018-09-25 [1] CRAN (R 3.5.1)
## coda              0.19-2    2018-10-08 [1] CRAN (R 3.5.1)
## codetools         0.2-15    2016-10-05 [2] CRAN (R 3.5.1)
## colorspace        1.3-2     2016-12-14 [1] CRAN (R 3.5.0)
## colourpicker      1.0       2017-09-27 [1] CRAN (R 3.5.0)
## corpcor           1.6.9     2017-04-01 [1] CRAN (R 3.5.0)
## cowplot         * 0.9.3     2018-07-15 [1] CRAN (R 3.5.1)
## crayon            1.3.4     2017-09-16 [1] CRAN (R 3.5.0)
## crosstalk         1.0.0     2016-12-21 [1] CRAN (R 3.5.0)
## cubature          1.4       2018-06-13 [1] CRAN (R 3.5.1)
## debugme           1.1.0     2017-10-22 [1] CRAN (R 3.5.0)
## digest            0.6.18    2018-10-10 [1] CRAN (R 3.5.1)
## dplyr             0.7.7     2018-10-16 [1] CRAN (R 3.5.1)
## DT                0.4       2018-01-30 [1] CRAN (R 3.5.0)
## dygraphs          1.1.1.6   2018-07-11 [1] CRAN (R 3.5.1)
## evaluate          0.12      2018-10-09 [1] CRAN (R 3.5.1)
## ggplot2         * 3.0.0     2018-07-03 [1] CRAN (R 3.5.1)
## ggridges          0.5.1     2018-09-27 [1] CRAN (R 3.5.1)
## ggtree          * 1.4.20    2018-03-10 [1] Bioconductor
## glue              1.3.0     2018-07-17 [1] CRAN (R 3.5.1)
## gridExtra         2.3       2017-09-09 [1] CRAN (R 3.5.0)
## gtable            0.2.0     2016-02-26 [1] CRAN (R 3.5.0)
## gtools            3.8.1     2018-06-26 [1] CRAN (R 3.5.0)
## htmltools         0.3.6     2017-04-28 [1] CRAN (R 3.5.0)
## htmlwidgets       1.3       2018-09-30 [1] CRAN (R 3.5.1)
```

```
## httpuv         1.4.5     2018-07-19 [1] CRAN (R 3.5.1)
## igraph         1.2.2     2018-07-27 [1] CRAN (R 3.5.1)
## inline         0.3.15    2018-05-18 [1] CRAN (R 3.5.0)
## jsonlite       1.5       2017-06-01 [1] CRAN (R 3.5.0)
## knitr          1.20      2018-02-20 [1] CRAN (R 3.5.1)
## labeling       0.3       2014-08-23 [1] CRAN (R 3.5.0)
## later          0.7.5     2018-09-18 [1] CRAN (R 3.5.1)
## lattice        0.20-35   2017-03-25 [1] CRAN (R 3.5.1)
## lazyeval       0.2.1     2017-10-29 [1] CRAN (R 3.5.0)
## lme4         * 1.1-18-1  2018-08-17 [1] CRAN (R 3.5.1)
## loo            2.0.0     2018-04-11 [1] CRAN (R 3.5.0)
## magrittr       1.5       2014-11-22 [1] CRAN (R 3.5.0)
## markdown       0.8       2017-04-20 [1] CRAN (R 3.5.0)
## MASS           7.3-51    2018-10-16 [1] CRAN (R 3.5.1)
## Matrix       * 1.2-14    2018-04-13 [1] CRAN (R 3.5.0)
## matrixStats    0.54.0    2018-07-23 [1] CRAN (R 3.5.1)
## MCMCglmm       2.26      2018-07-03 [1] CRAN (R 3.5.1)
## mime           0.6       2018-10-05 [1] CRAN (R 3.5.1)
## miniUI         0.1.1.1   2018-05-18 [1] CRAN (R 3.5.0)
## minqa          1.2.4     2014-10-09 [1] CRAN (R 3.5.0)
## munsell        0.5.0     2018-06-12 [1] CRAN (R 3.5.1)
## mvtnorm        1.0-8     2018-05-31 [1] CRAN (R 3.5.0)
## nlme           3.1-137   2018-04-07 [1] CRAN (R 3.5.1)
## nloptr         1.2.1     2018-10-03 [1] CRAN (R 3.5.1)
## pillar         1.3.0     2018-07-14 [1] CRAN (R 3.5.1)
## pkgbuild       1.0.2     2018-10-16 [1] CRAN (R 3.5.1)
## pkgconfig      2.0.2     2018-08-16 [1] CRAN (R 3.5.1)
## plyr           1.8.4     2016-06-08 [1] CRAN (R 3.5.0)
## prettyunits    1.0.2     2015-07-13 [1] CRAN (R 3.5.0)
## processx       3.2.0     2018-08-16 [1] CRAN (R 3.5.1)
```

```
##   promises        1.0.1    2018-04-13 [1] CRAN (R 3.5.0)
##   ps              1.2.0    2018-10-16 [1] CRAN (R 3.5.1)
##   purrr           0.2.5    2018-05-29 [1] CRAN (R 3.5.1)
##   R6              2.3.0    2018-10-04 [1] CRAN (R 3.5.1)
##   Rcpp          * 0.12.19  2018-10-01 [1] CRAN (R 3.5.1)
##   reshape2        1.4.3    2017-12-11 [1] CRAN (R 3.5.1)
##   rlang           0.3.0    2018-10-22 [1] CRAN (R 3.5.1)
##   rmarkdown       1.10     2018-06-11 [1] CRAN (R 3.5.1)
##   rprojroot       1.3-2    2018-01-03 [1] CRAN (R 3.5.0)
##   rsconnect       0.8.8    2018-03-09 [1] CRAN (R 3.5.0)
##   rstan           2.18.1   2018-10-16 [1] CRAN (R 3.5.1)
##   rstantools      1.5.1    2018-08-22 [1] CRAN (R 3.5.1)
##   scales          1.0.0    2018-08-09 [1] CRAN (R 3.5.1)
##   sessioninfo     1.1.0    2018-09-25 [1] CRAN (R 3.5.1)
##   shiny           1.1.0    2018-05-17 [1] CRAN (R 3.5.1)
##   shinyjs         1.0      2018-01-08 [1] CRAN (R 3.5.0)
##   shinystan       2.5.0    2018-05-01 [1] CRAN (R 3.5.0)
##   shinythemes     1.1.1    2016-10-12 [1] CRAN (R 3.5.0)
##   StanHeaders     2.18.0   2018-10-07 [1] CRAN (R 3.5.1)
##   stringi         1.2.4    2018-07-20 [1] CRAN (R 3.5.1)
##   stringr         1.3.1    2018-05-10 [1] CRAN (R 3.5.0)
##   tensorA         0.36.1   2018-07-29 [1] CRAN (R 3.5.1)
##   threejs         0.3.1    2017-08-13 [1] CRAN (R 3.5.0)
##   tibble          1.4.2    2018-01-22 [1] CRAN (R 3.5.0)
##   tidyr           0.8.1    2018-05-18 [1] CRAN (R 3.5.1)
##   tidyselect      0.2.5    2018-10-11 [1] CRAN (R 3.5.1)
##   viridis       * 0.5.1    2018-03-29 [1] CRAN (R 3.5.0)
##   viridisLite   * 0.3.0    2018-02-01 [1] CRAN (R 3.5.0)
##   withr           2.1.2    2018-03-15 [1] CRAN (R 3.5.0)
##   xtable          1.8-3    2018-08-29 [1] CRAN (R 3.5.1)
```

```
## xts              0.11-1   2018-09-12 [1] CRAN (R 3.5.1)
## yaml             2.2.0    2018-07-25 [1] CRAN (R 3.5.1)
## zoo              1.8-4    2018-09-19 [1] CRAN (R 3.5.1)
##
## [1] C:/Users/FRS/Documents/R/win-library/3.5
## [2] C:/R/R-3.5.1/library
```