Tau specification analysis

Run on the cluster:

```
start <- Sys.time()</pre>
# function to generate the discrete data and covariates
# takes a RNG seed, sample size, number of predictors, lambda (root of the
# non-zero elements in the precision matrix), values to populate the
# extraneous covariate vector with, and boolean for whether the two groups
# should have the same covariance
# returns the continuous data, covariates, and true covariance matrix
generate_discrete <- function(n = 100, p = 10, lambda = 15,</pre>
                               cov1 = -0.1, cov2 = 0.1, same = T){
  # generating the precision matrix: Assume two discrete covariate levels, one
  # for each group
  Lam1 \leftarrow c(rep(lambda, 4), rep(0, p - 3))
  Lam2 \leftarrow c(rep(0, 4), rep(lambda, p - 3))
  # if same is true, the individuals in both groups will have the same
  # covariance matrix
  if (same) Lam2 <- Lam1
  # create covariance matrix for both groups
  Var1 <- solve(Lam1 %*% t(Lam1) + diag(rep(10, p + 1)))</pre>
  Var2 \leftarrow solve(Lam2 \%\% t(Lam2) + diag(rep(10, p + 1)))
  # create the extraneous covariate; individuals in group j have a covariate
  # vector of length p with cov_j as the only entry, j \in \{1,2\}
  Z \leftarrow matrix(c(rep(cov1, n %/% 2), rep(cov2, n %/% 2)), n, p)
  # create the data matrix; individuals in group j are generated from a MVN with
  # 0 mean vector and covariance matrix Var_j, j\in {1,2}
  X1 \leftarrow MASS::mvrnorm(n %/% 2, rep(0, p + 1), Var1)
  X2 \leftarrow MASS::mvrnorm(n %/% 2, rep(0, p + 1), Var2)
  data_mat <- rbind(X1, X2)</pre>
 return(list(data = data_mat, covts = Z, true_precision = list(solve(Var1), solve(Var2))))
}
library(covdepGE)
library(doRNG)
set.seed(1)
```

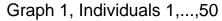
```
# number of trials and values of bandwidth to try
n_trials <- 1000
tau \leftarrow c(0.01, 0.05, 0.1, 0.5, 1, 5)
# grid of slab variance
sbsq_grid \leftarrow c(0.01, 0.05, 0.1, 0.5, 1, 3, 7, 10)
n_cores <- parallel::detectCores() - 1</pre>
print(paste("N cores:", n_cores))
doParallel::registerDoParallel(n_cores)
results <- foreach (j = 1:n_trials, .packages = "covdepGE") %dorng%{
  # generate the data
  cont <- generate_discrete()</pre>
  X <- cont$data</pre>
  Z <- cont$covts</pre>
  # list for storing the results from each bandwidth and the data
  bw_res <- vector("list", length(tau) + 1)</pre>
  bw_res[[1]] <- cont</pre>
  names(bw_res) <- c("data", tau)</pre>
  # loop over each of the bandwidths
  for (bandwidth in tau){
    bw_res[[as.character(bandwidth)]] <- tryCatch(</pre>
      covdepGE(X, Z, sbsq = sbsq_grid, CS = T, tau = bandwidth, kde = F, scale = F,
                elbo_tol = 1e-12, alpha_tol = 1e-12, max_iter = 1e2, warnings = F),
      error = function(msg) as.character(msg))
 }
  # save the final results
  bw res
doParallel::stopImplicitCluster()
Sys.time() - start
#save(results, file = "tau_specif_disc_indep_models.Rda")
library(ggplot2)
library(latex2exp)
library(covdepGE)
library(foreach)
load(paste0("C:/Users/jacob/OneDrive/Documents/TAMU/Research/An approximate ",
            "Bayesian approach to covariate dependent/covdepGE/dev/",
            "analyses_demos_experiments/hyperparameter_specification/",
            "tau specif disc indep models.Rda"))
n trials <- 1000
tau \leftarrow c(0.01, 0.05, 0.1, 0.5, 1, 5)
```

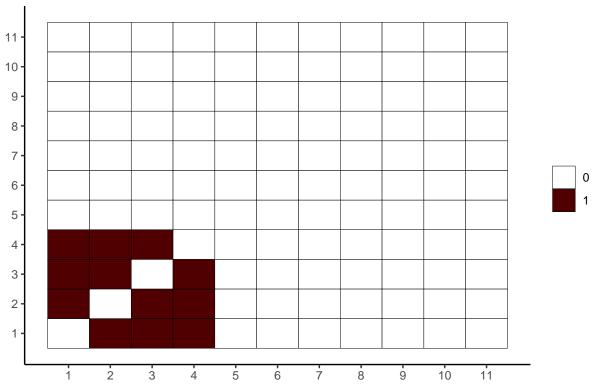
```
names(results) <- paste("Trial", 1:n_trials)</pre>
# get all of the models
mods <- lapply(results, `[`, as.character(tau))</pre>
# look at the ELBO
elbo <- lapply(lapply(mods, lapply, `[[`, "model_details"), lapply, `[[`, "ELBO")
ELBO vec <- unlist(elbo)</pre>
length(ELBO_vec[ELBO_vec < -5e4])</pre>
## [1] 39
length(ELBO_vec[ELBO_vec > -5e4])
## [1] 5961
summary(ELBO_vec[ELBO_vec < -5e4])</pre>
##
         Min.
                 1st Qu.
                             Median
                                           Mean
                                                    3rd Qu.
## -1.196e+30 -9.991e+21 -1.801e+14 -9.201e+28 -6.970e+11 -3.394e+07
summary(ELBO_vec[ELBO_vec > -5e4])
##
      Min. 1st Qu. Median
                              Mean 3rd Qu.
## -48756 -46733 -46246 -46242 -45778 -44023
# filter out the models that blew up
elbo_stable <- lapply(elbo, function(elbo) elbo > -5e4)
mods_unstable <- lapply(1:n_trials, function(trial_ind) mods[[trial_ind]][!elbo_stable[[trial_ind]]])</pre>
names(mods_unstable) <- names(results)</pre>
# analyze the models that blew up
# filter out those of length 0
mods_unstable0 <- mods_unstable[lapply(mods_unstable, length) != 0]</pre>
# look at the mu distribution for those that blew up
summary(abs(unlist(lapply(mods_unstable0, lapply, `[[`, "mu_matrices"))))
        Min.
               1st Qu.
                          Median
                                       Mean
                                              3rd Qu.
## 0.000e+00 0.000e+00 0.000e+00 6.459e+09 0.000e+00 3.765e+12
# visualize the unique graphs for a model that blew up
sapply(lapply(mods_unstable0, lapply, `[[`, "model_details"), lapply, `[[`, "ELBO")
##
        Trial 229 Trial 354
                                 Trial 369
                                               Trial 576
                                                              Trial 590
## 0.01 -33938355 -3.91362e+25 -1.196089e+30 -1.800523e+14 -6.9703e+11
## 0.05 -33938355 -3.91362e+25 -1.196089e+30 -1.800523e+14 -6.9703e+11
```

```
## 0.1 -33938321 -3.913618e+25 -1.196089e+30 -1.800522e+14 -697029895098
##
        Trial 630 Trial 643
                                Trial 651
                                              Trial 657
                                                            Trial 785
## 0.01 -579954449 -2.30788e+12 -1.470452e+12 -9.991491e+21 -23181925136
## 0.05 -579954449 -2.30788e+12 -1.470452e+12 -9.991491e+21 -23181925136
## 0.1 -579954165 -2.307865e+12 -1.470452e+12 -9.991488e+21 -23181911382
##
        Trial 797
                     Trial 840
                                   Trial 856
## 0.01 -1.453983e+25 -1.968497e+15 -4.106954e+18
## 0.05 -1.453983e+25 -1.968497e+15 -4.106954e+18
## 0.1 -1.453983e+25 -1.968497e+15 -4.106952e+18
```

plot(mods_unstable0[["Trial 369"]]\$`0.01`, title_sum = T)

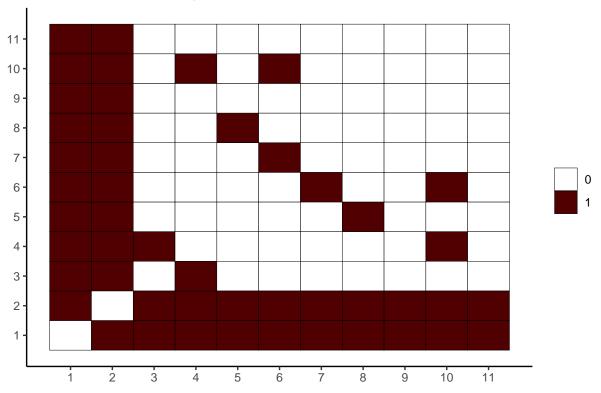
[[1]]





[[2]]

Graph 2, Individuals 51,...,100

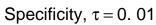


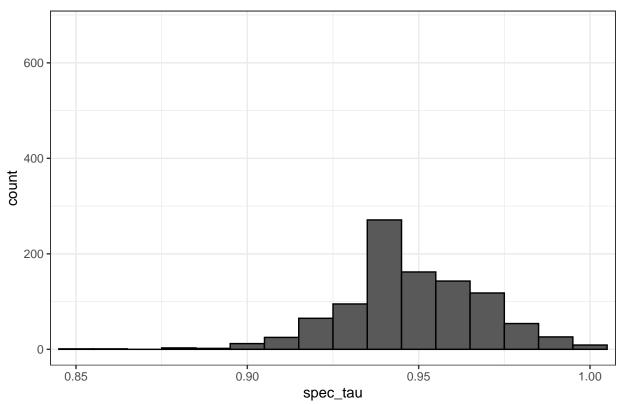
```
# filter out the trials with instability
mods_stable <- mods[setdiff(names(mods), names(mods_unstable0))]
length(mods_stable)</pre>
```

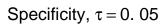
[1] 987

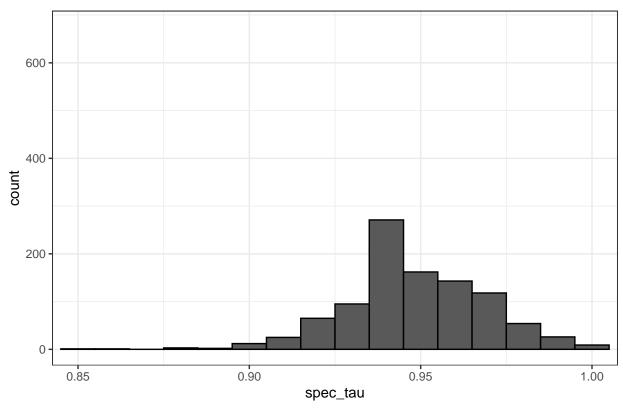
```
# get the true precision structure
true_prec <- results$`Trial 1`$data$true_precision[[1]]</pre>
true_graph <- (true_prec != 0) * 1</pre>
true_graph <- true_graph - diag(diag(true_graph))</pre>
# find the true number of 0's and 1's in one graph and across all structures
n <- nrow(results$`Trial 1`$data$data)</pre>
true1_graph <- sum(true_graph == 1)</pre>
true0_graph <- sum(true_graph == 0)</pre>
true1_tot <- true1_graph * n</pre>
true0_tot <- true0_graph * n</pre>
# find the estimated graphs for each model
mod_graphs <- lapply(mods_stable, lapply, `[[`, "graphs")</pre>
# find the true 1's and 0's for each
true_pos <- lapply(</pre>
  mod_graphs, lapply, function(model) sum(sapply(
    model, function(graph) sum(graph == 1 & true_graph == 1))))
```

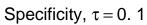
```
true_neg <- lapply(</pre>
  mod_graphs, lapply, function(model) sum(sapply(
    model, function(graph) sum(graph == 0 & true_graph == 0))))
true_pos_and_neg <- foreach(trial_ind = 1:length(true_pos)) %do% {</pre>
  res <- as.list(mapply(sum, true_pos[[trial_ind]], true_neg[[trial_ind]]))
  names(res) <- as.character(tau)</pre>
  res
names(true_pos_and_neg) <- names(true_pos)</pre>
# find sensitivity, specificity, and accuracy for each model
sens <- lapply(true_pos, lapply, `/`, true1_tot)</pre>
spec <- lapply(true_neg, lapply, `/`, true0_tot)</pre>
accu <- lapply(true_pos_and_neg, lapply, `/`, true1_tot + true0_tot)</pre>
# get the summary of all of the sensitivities
summary(unlist(sens))
##
      Min. 1st Qu. Median
                                Mean 3rd Qu.
                                                 Max.
##
         1
                  1
                          1
                                   1
min_spec <- round(min(unlist(spec)), 2)</pre>
max_spec <- max(unlist(spec))</pre>
# get visualizations and summaries for each of the specificities and accuracies
for (bandwidth in as.character(tau)){
  cat("\n\nSpecificity results for tau =", bandwidth, "\n\nWeights: ")
  print(unique(as.numeric(results\texts\textstyle{Trial 1}[[bandwidth]]\textstyle{\textstyle{Weights}})))
  cat("\n")
  # get all of the specificities for the specified bandwidth
  spec_tau <- sapply(spec, `[[`, bandwidth)</pre>
  # visualize the specificities
  plot <- ggplot() + geom_histogram(aes(x = spec_tau), binwidth = 0.01, color = "black") +</pre>
    coord_cartesian(xlim = c(min_spec, max_spec), ylim = c(0, 675)) +
    ggtitle(TeX(paste0("Specificity, $\\tau = $", bandwidth))) + theme_bw() +
    theme(plot.title = element text(hjust = 0.5))
  print(plot)
  print(summary(spec_tau))
  cat("\n", rep("-", 80), sep = "")
}
##
## Specificity results for tau = 0.01
## Weights: [1] 2 0
```

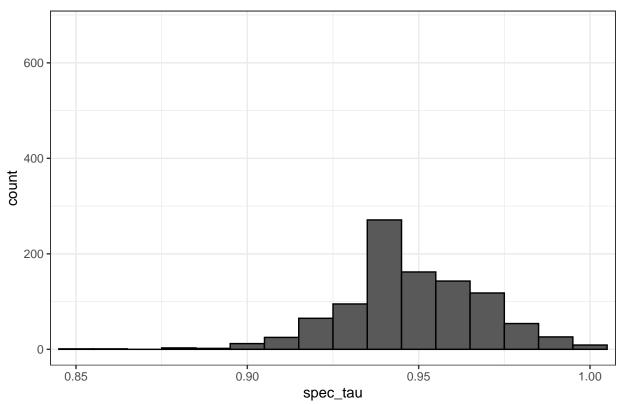


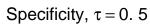


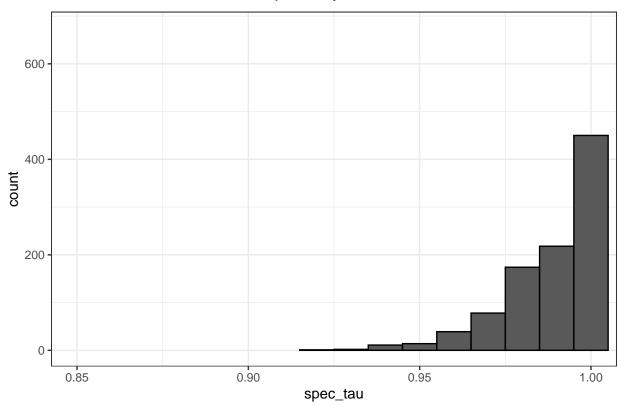




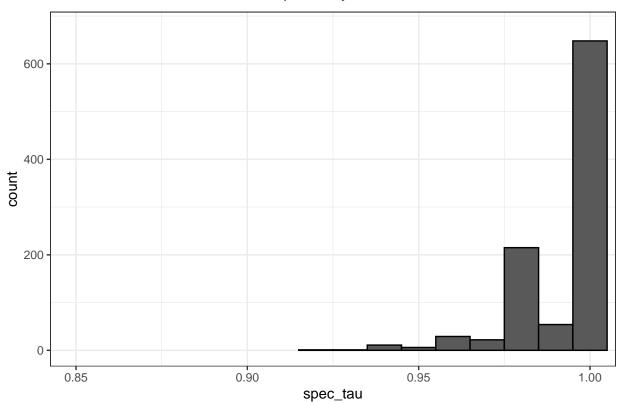


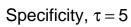


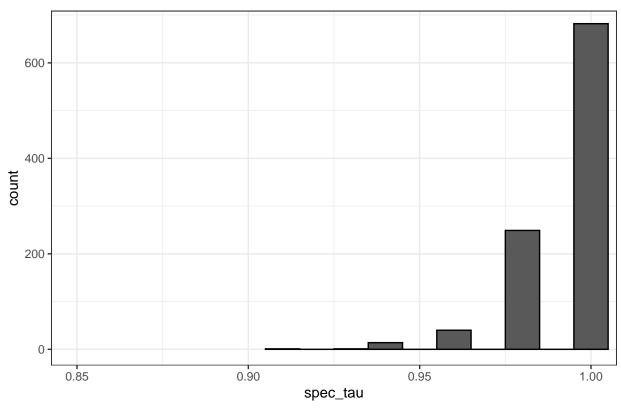




Specificity, $\tau = 1$







```
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## 0.9083 0.9817 1.0000 0.9929 1.0000 1.0000
##
```