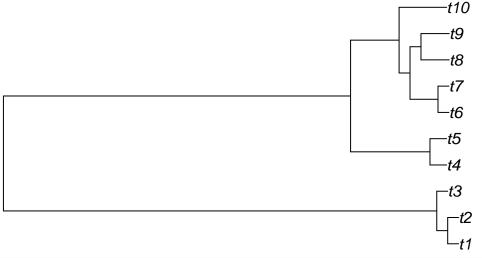
Comparing CLARITY, Omnibus Embedding and UASE

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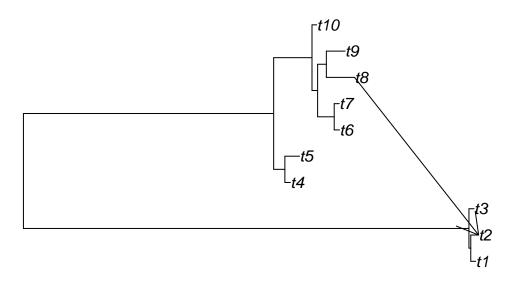
Data generation

We use the ClaritySim package to create the 'original' data generated according to some tree structure, which we will then scale and add a mixture to:



```
mixed <- mixCoalescent(original, fraction = 1, transform = TRUE)
mixture <- mixed$edges

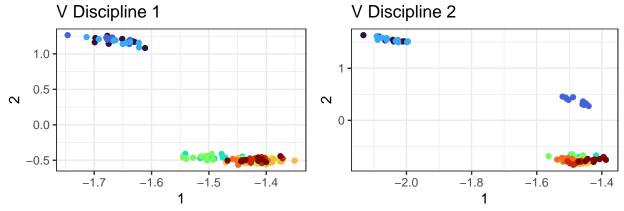
library(ape)
plot(mixed$tree)
edges(mixture[1], mixture[2], arrows = 1)</pre>
```

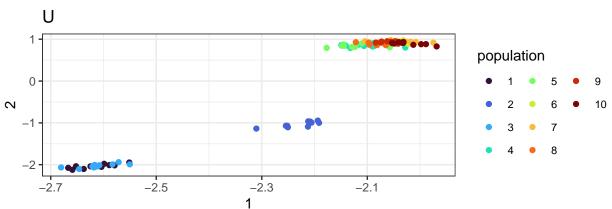


UASE

```
source("UASE.R")
groups <- original$A %*% 1:ncol(original$A)

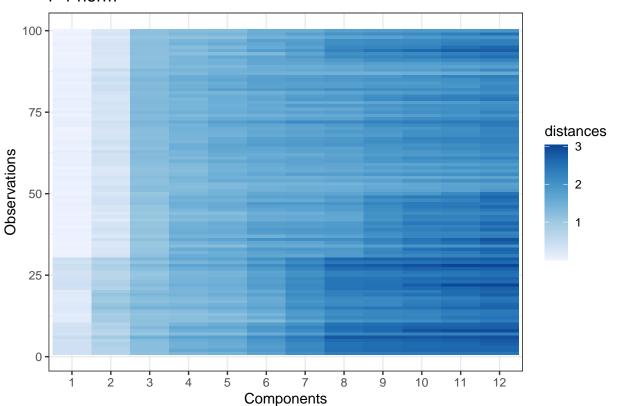
similarity <- cbind(original$Y, mixed$Y)
mix_UASE <- UASE(similarity, d = 12, groups)
plot_UASE(mix_UASE)</pre>
```



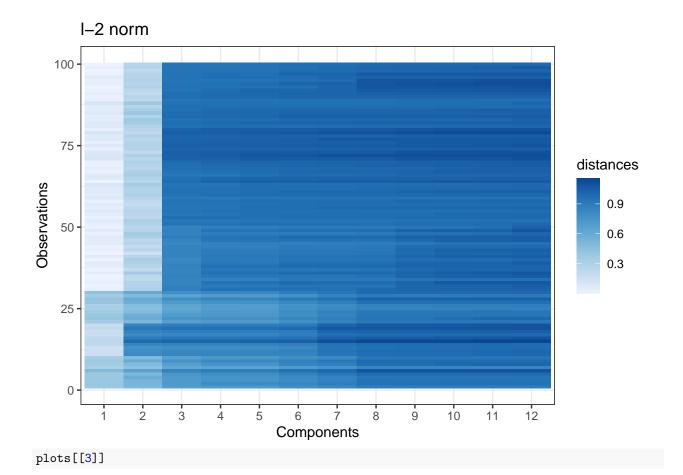


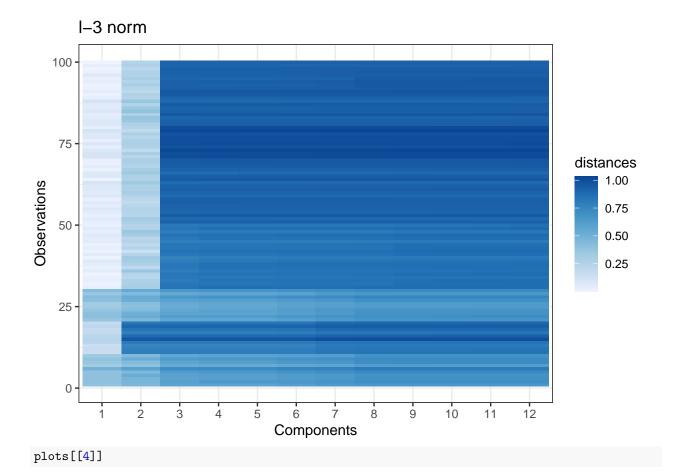
```
source("distances.R")
library(hrbrthemes)
1 <- 5
plots <- list()</pre>
for (i in 1:1){
  distances <- apply(as.matrix(1:12, nrow = 1), MARGIN = 1, FUN = function(ii){
    distance_moved(mix_UASE$right, d = ii, l = i, scale = FALSE)
  })
  distance_plot <- expand.grid( Components = as.factor(1:12), Observations = 1:nrow(distances))</pre>
  distance_plot$distances <- c(t(distances))</pre>
  distance_plot <- as_tibble(distance_plot)</pre>
  plots[[i]] \leftarrow ggplot(distance_plot, aes(x = Components))+
    geom_tile(aes(y = Observations, fill = distances)) +
    scale_fill_distiller(direction = 1) +
    labs(title = paste("l-", i, " norm", sep = ""))
}
plots[[1]]
```

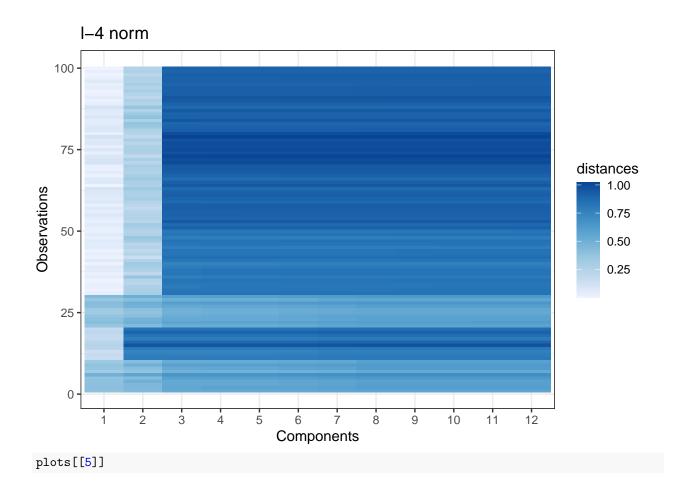
I-1 norm

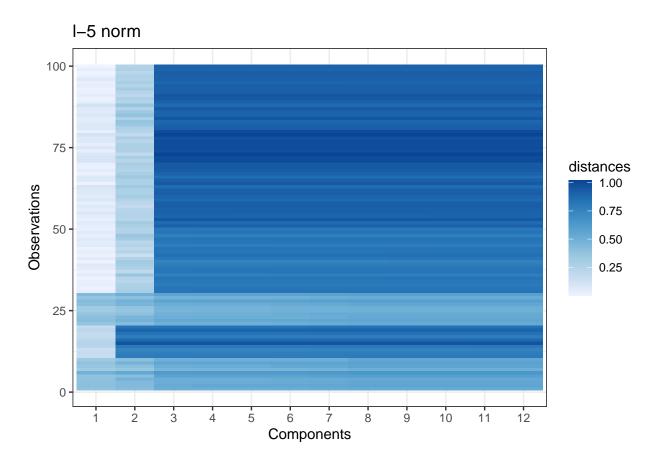


plots[[2]]



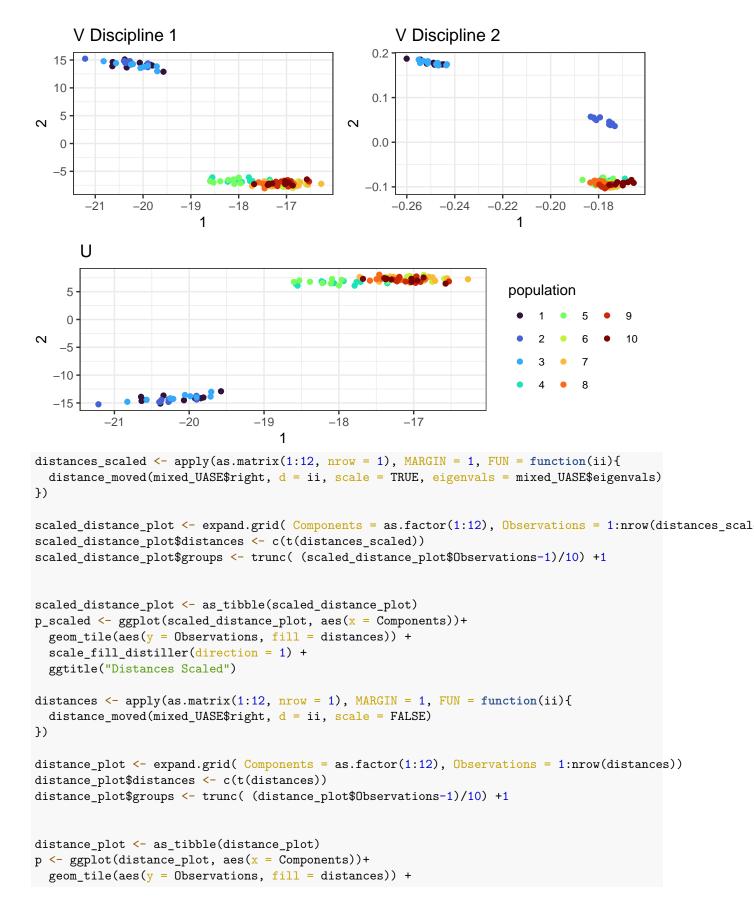






On different scales

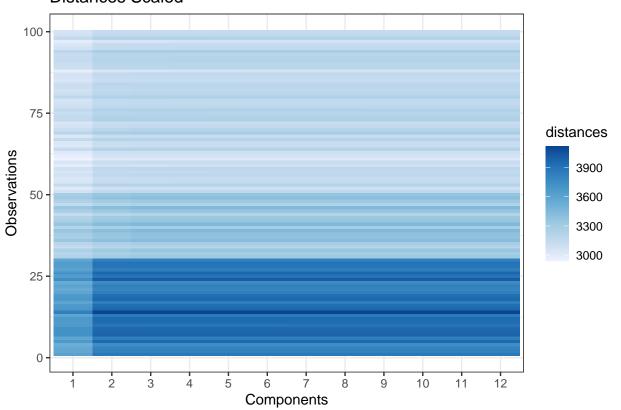
```
test<- original
test$Y<- test$Y * 100
similarity <- cbind(test$Y, mixed$Y)
mixed_UASE<-UASE(similarity, d = 12, groups)
plot_UASE(mixed_UASE)</pre>
```



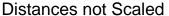
```
scale_fill_distiller(direction = 1) +
ggtitle("Distances not Scaled")

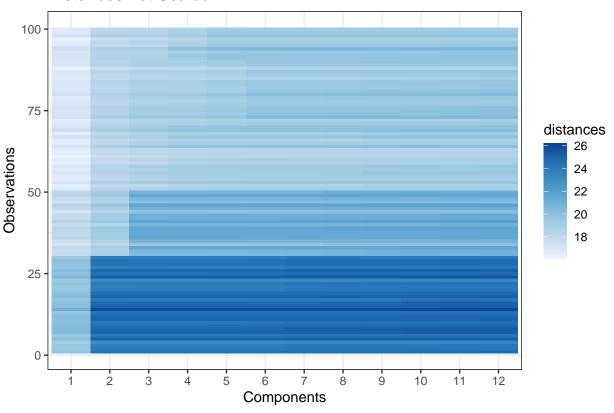
p_scaled
```

Distances Scaled



р





Omnibus

Use the graphstats package to compute omnibus embedding:

```
library(graphstats)
omni <- svd(gs.omni(original$Y, mixed$Y))</pre>
pcs <- 2
omni_plot <- omni$u[,1:pcs] %>% as_tibble()
## Warning: The `x` argument of `as_tibble.matrix()` must have unique column names if
## `.name_repair` is omitted as of tibble 2.0.0.
## i Using compatibility `.name_repair`.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
colnames(omni_plot) <- as.character(1:pcs)</pre>
omni_plot <- cbind( omni_plot,groups = as.factor(groups), discipline = rep(c(1,2), each = nrow(omni_plo
ggplot(omni_plot, aes(x = 1, y = 2)) +
 geom_point(aes(colour = groups)) +
 facet_wrap(~discipline) +
  scale_color_viridis_d(option = "turbo")
```

