

# clustering-update

```
trait_groups_pam <- cluster::pam(x = trait_gower_daisy,  
                                k = 7,  
                                metric = "euclidean")  
  
pam_clusters <- trait_groups_pam$clustering %>%  
  enframe() %>%  
  rename(cluster = value) %>%  
  mutate(cluster = factor(cluster))  
  
pairwise.perm.manova(trait_gower_daisy, fact = pam_clusters$cluster)
```

Pairwise comparisons using permutation MANOVAs on a distance matrix

data: trait\_gower\_daisy by pam\_clusters\$cluster  
999 permutations

|   | 1      | 2      | 3      | 4      | 5      | 6      |
|---|--------|--------|--------|--------|--------|--------|
| 2 | 0.0030 | -      | -      | -      | -      | -      |
| 3 | 0.0035 | 0.0030 | -      | -      | -      | -      |
| 4 | 0.0360 | 0.0030 | 0.0030 | -      | -      | -      |
| 5 | 0.0315 | 0.0030 | 0.0035 | 0.0327 | -      | -      |
| 6 | 0.0045 | 0.0035 | 0.0030 | 0.0035 | 0.0070 | -      |
| 7 | 0.0360 | 0.0030 | 0.0045 | 0.0332 | 0.0327 | 0.0035 |

P value adjustment method: fdr

```
trait_groups_pam <- cluster::pam(x = trait_gower_daisy,  
                                k = 8,  
                                metric = "euclidean")
```

```

pam_clusters <- trait_groups_pam$clustering %>%
  enframe() %>%
  rename(cluster = value) %>%
  mutate(cluster = factor(cluster))

pairwise.perm.manova(trait_gower_daisy, fact = pam_clusters$cluster)

```

Pairwise comparisons using permutation MANOVAs on a distance matrix

data: trait\_gower\_daisy by pam\_clusters\$cluster  
 999 permutations

|   | 1      | 2      | 3      | 4      | 5      | 6      | 7      |
|---|--------|--------|--------|--------|--------|--------|--------|
| 2 | 0.0047 | -      | -      | -      | -      | -      | -      |
| 3 | 0.0264 | 0.0056 | -      | -      | -      | -      | -      |
| 4 | 0.0070 | 0.0047 | 0.0395 | -      | -      | -      | -      |
| 5 | 0.0158 | 0.0047 | 0.0320 | 0.0056 | -      | -      | -      |
| 6 | 0.0056 | 0.0070 | 0.0149 | 0.0047 | 0.0047 | -      | -      |
| 7 | 0.0140 | 0.0056 | 0.0467 | 0.0086 | 0.0414 | 0.0047 | -      |
| 8 | 0.0691 | 0.0247 | 0.1000 | 0.0320 | 0.0691 | 0.0320 | 0.0691 |

P value adjustment method: fdr