

Spatial clustering to define spatial scales and synthetic habitat covariates

```
# source("../functions/spatial_clustering.R")
source("../functions/data_processing.R")
library(ade4)
library(adegraphics)
library(sf)

covariates <- readRDS("covariates.rds")
```

Camera-level covariates

Let's establish clusters of similar cameras in terms of habitat in order to build a synthetic habitat covariate.

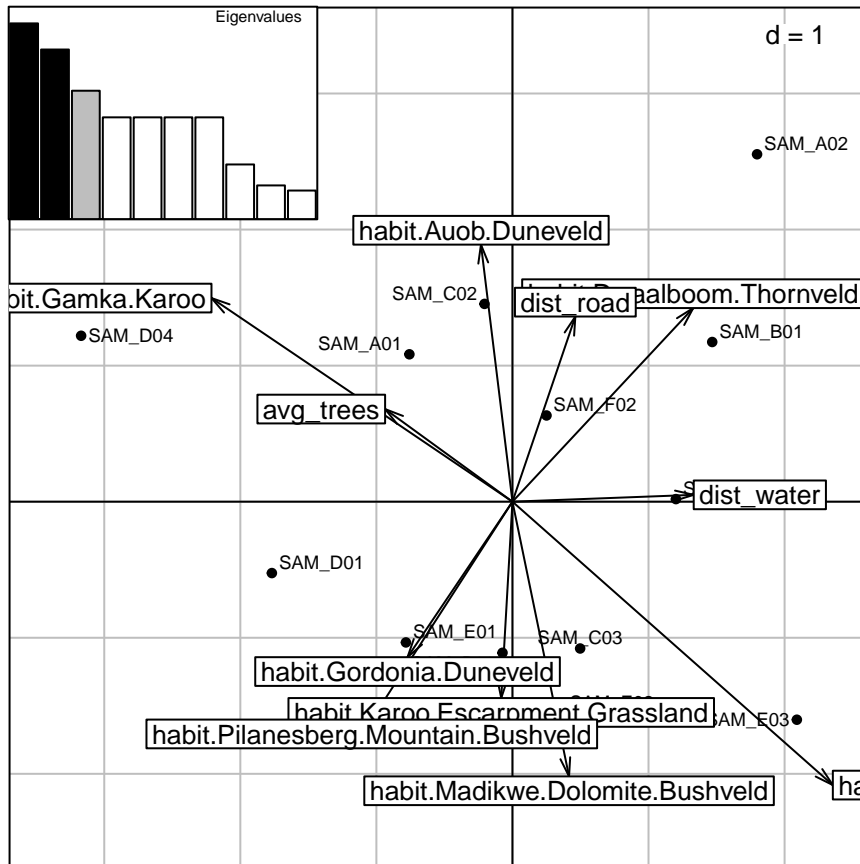
We perform a multivariate analysis on the data:

```
# Prepare data for mv analysis
cov.mva <- covariates %>% select(-code_loc) %>%
  st_drop_geometry() %>% remove_rownames() %>% column_to_rownames("site_ID")
cov.mva
```

##	avg_trees	habitat_mucina	dist_road	dist_water
## SAM_A01	2.8	Gamka Karoo	300	4079.598
## SAM_A02	14.5	Dwaalboom Thornveld	576	8815.168
## SAM_B01	14.5	Dwaalboom Thornveld	230	9455.907
## SAM_B02	4.2	Karoo Escarpment Grassland	80	4346.734
## SAM_B03	5.0	Pilanesberg Mountain Bushveld	65	2748.358
## SAM_C02	11.5	Auob Duneveld	280	4226.053
## SAM_C03	8.4	Gordonia Duneveld	10	9640.335
## SAM_D01	24.5	Gordonia Duneveld	40	2234.062
## SAM_D03	6.0	Dwaalboom Thornveld	10	7964.671
## SAM_D04	42.3	Gamka Karoo	34	2348.755
## SAM_E01	5.4	Gordonia Duneveld	58	2930.154
## SAM_E02	7.4	Madikwe Dolomite Bushveld	7	6382.672
## SAM_E03	4.0	Eastern Upper Karoo	22	9395.011
## SAM_F02	9.0	Dwaalboom Thornveld	150	3341.612

```
hillsmith <- dudi.hillsmith(cov.mva, scannf = FALSE, nf = 3)
```

```
scatter(hillsmith, plabels.optim = TRUE)
```

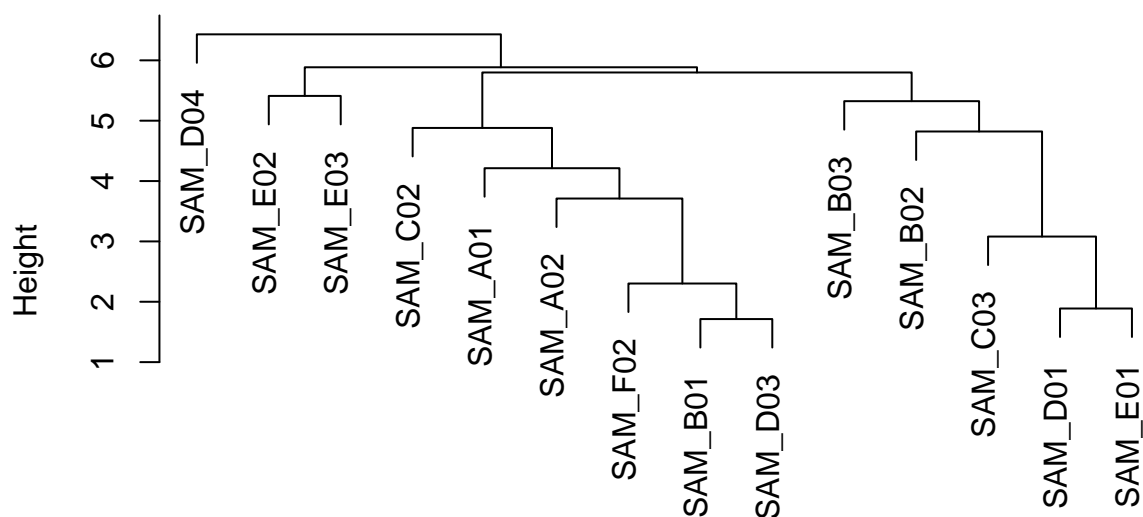


Then, we perform hierarchical clustering for habitat covariates at camera level to define the synthetic habitat covariate classes.

```
dist <- dist.dudi(hillsmith)

fit <- hclust(dist, method = "complete")
plot(fit)
```

Cluster Dendrogram



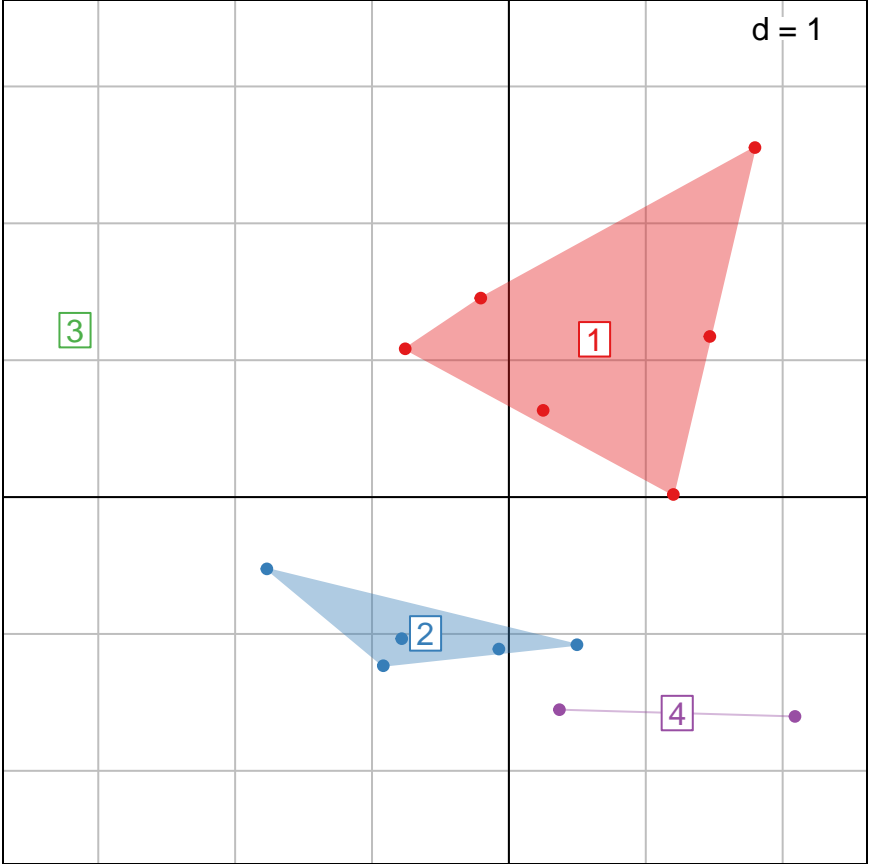
dist
hclust (*, "complete")

```
threshold <- 5.5

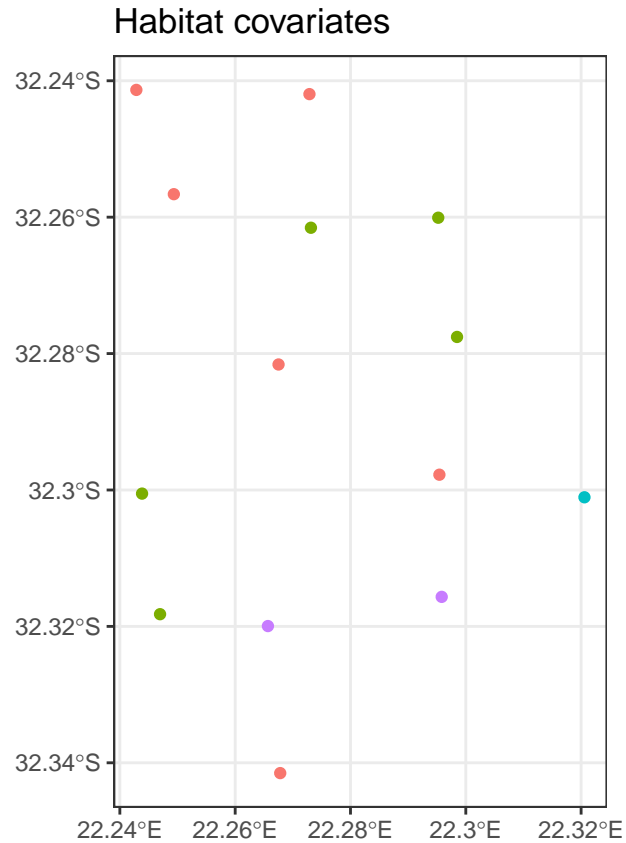
covcam <- cutree(fit, h = threshold)

f <- covcam[match(rownames(hillsmith$li), names(covcam))]
fact <- as.factor(f)

s.class(hillsmith$li, fac = fact,
        ellipse = 0, starSize = 0, chullSize = 1,
        col = TRUE)
```



Spatial visialisation of the habitat covariates associated with cameras:



Not constrained clustering

Now we build camera clusters based on distance to get different inference scales.

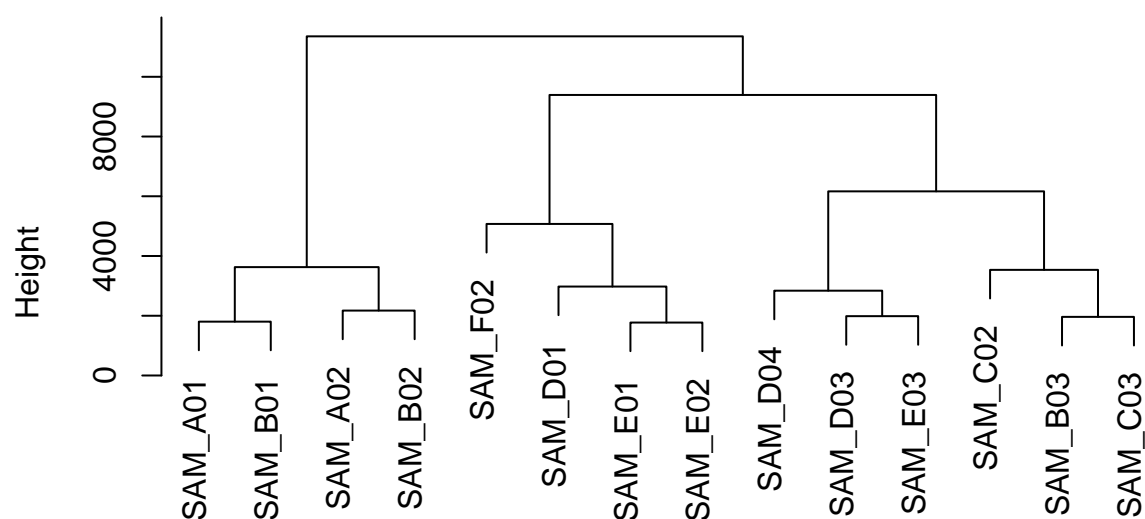
Sites clustering (get different scales)

```
clust <- covariates %>% dplyr::select(site_ID)

#distance matrix
distmat <- st_distance(clust)
rownames(distmat) <- clust$site_ID
colnames(distmat) <- clust$site_ID

#clustering
fit <- hclust(as.dist(distmat), method = "complete")
plot(fit)
```

Cluster Dendrogram



```
as.dist(distmat)
hclust (*, "complete")
```

```
# Threshold
threshold.coarse <- 6000
threshold.fine <- 2500

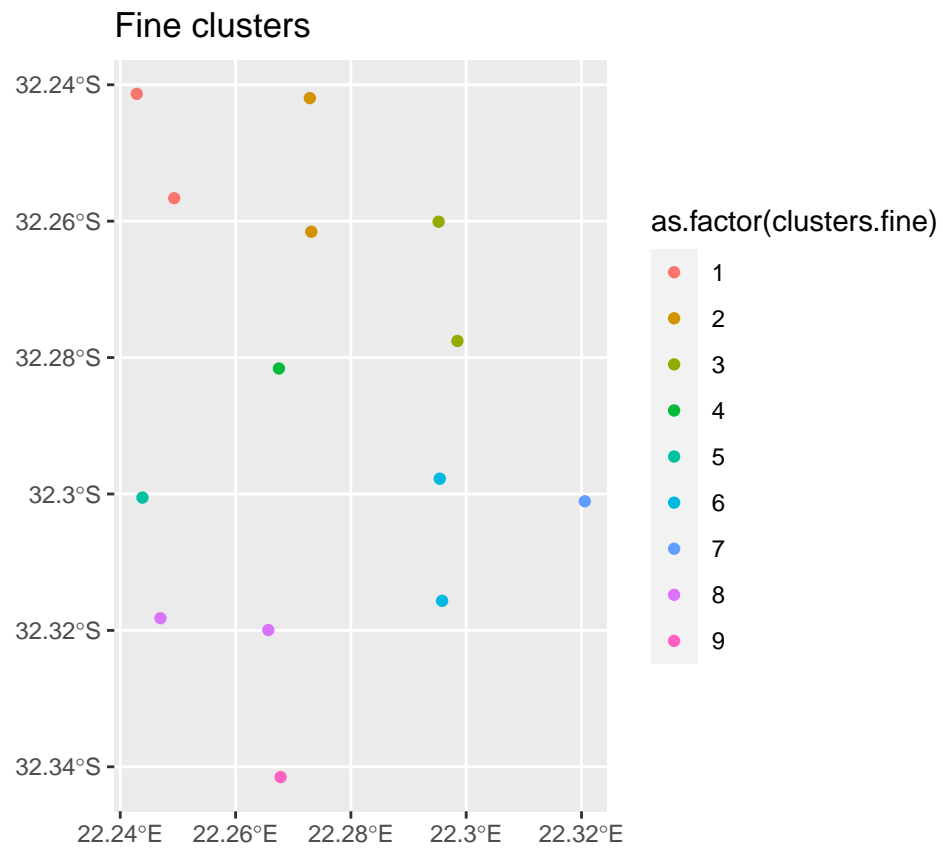
# Tree cutting
clusters.coarse <- cutree(fit, h = threshold.coarse)

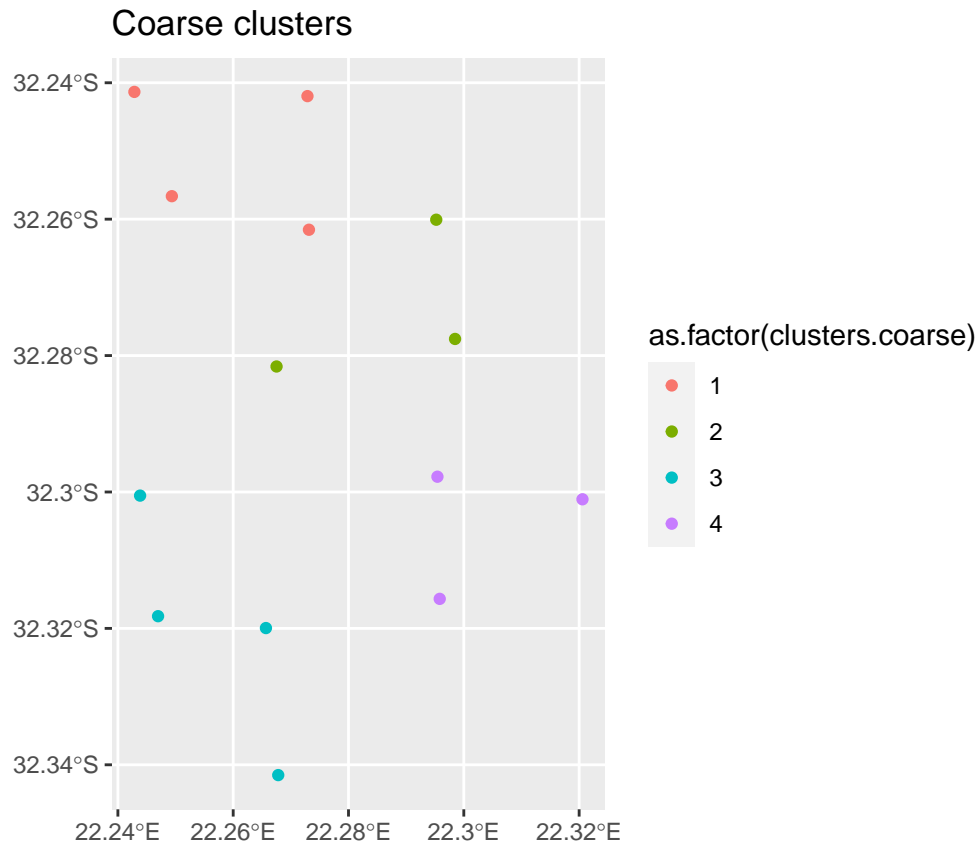
clusters.fine <- cutree(fit, h = threshold.fine)

# Plotting
tab <- data.frame(clusters.coarse) %>% rownames_to_column("site_ID")
tab2 <- data.frame(clusters.fine) %>% rownames_to_column("site_ID")
tab <- tab %>% left_join(tab2, by = "site_ID")

clust <- clust %>% left_join(tab, by = "site_ID")
```

Result:





Sites covariates

Replace the original camera-level covariate by mean/new factor level.

```
cov <- covariates %>% left_join(tab, by = "site_ID")

cov.fine <- cov %>% st_drop_geometry() %>% group_by(clusters.fine) %>%
  summarise(mean_road = mean(dist_road),
            mean_trees = mean(avg_trees),
            mean_water = mean(dist_water),
            habitat_mucina = as.factor(paste(unique(habitat_mucina), collapse = "."))) %>%
  mutate(clusters.fine = paste0("SAM", clusters.fine)) %>%
  column_to_rownames("clusters.fine")
cov.fine
```

	mean_road	mean_trees	mean_water	habitat_mucina
## SAM1	265.0	8.65	6767.753	
## SAM2	328.0	9.35	6580.951	
## SAM3	37.5	6.70	6194.346	
## SAM4	280.0	11.50	4226.053	
## SAM5	40.0	24.50	2234.062	
## SAM6	16.0	5.00	8679.841	
## SAM7	34.0	42.30	2348.755	
## SAM8	32.5	6.40	4656.413	
## SAM9	150.0	9.00	3341.612	
##				habitat_mucina


```

## SAM1          Gamka Karoo.Dwaalboom Thornveld
## SAM2 Dwaalboom Thornveld.Karoo Escarpment Grassland
## SAM3 Pilanesberg Mountain Bushveld.Gordonia Duneveld
## SAM4          Auob Duneveld
## SAM5          Gordonia Duneveld
## SAM6          Dwaalboom Thornveld.Eastern Upper Karoo
## SAM7          Gamka Karoo
## SAM8          Gordonia Duneveld.Madikwe Dolomite Bushveld
## SAM9          Dwaalboom Thornveld

cov.coarse <- cov %>% st_drop_geometry() %>% group_by(clusters.coarse) %>%
  summarise(mean_road = mean(dist_road),
            mean_trees = mean(avg_trees),
            mean_water = mean(dist_water),
            habitat_mucina = as.factor(paste(unique(habitat_mucina), collapse = "."))) %>%
  mutate(clusters.coarse = paste0("SAM", clusters.coarse)) %>%
  column_to_rownames("clusters.coarse")
cov.coarse

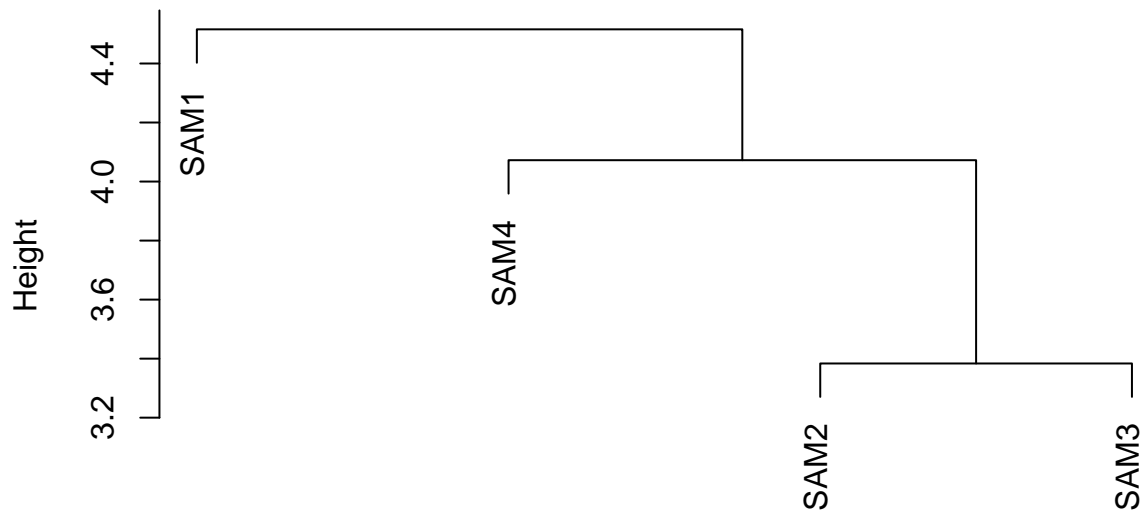
##      mean_road mean_trees mean_water
## SAM1  296.5000    9.00000   6674.352
## SAM2  118.3333    8.30000   5538.248
## SAM3   63.7500   11.57500   3722.125
## SAM4   22.0000   17.43333   6569.479
##
##                               habitat_mucina
## SAM1      Gamka Karoo.Dwaalboom Thornveld.Karoo Escarpment Grassland
## SAM2  Pilanesberg Mountain Bushveld.Auob Duneveld.Gordonia Duneveld
## SAM3  Gordonia Duneveld.Madikwe Dolomite Bushveld.Dwaalboom Thornveld
## SAM4          Dwaalboom Thornveld.Gamka Karoo.Eastern Upper Karoo

hillsmith.coarse <- dudi.hillsmith(cov.coarse, nf = 2, scannf = FALSE)
dist.cov.coarse <- dist.dudi(hillsmith.coarse)

fit.coarse <- hclust(dist.cov.coarse, method = "complete")
plot(fit.coarse)

```

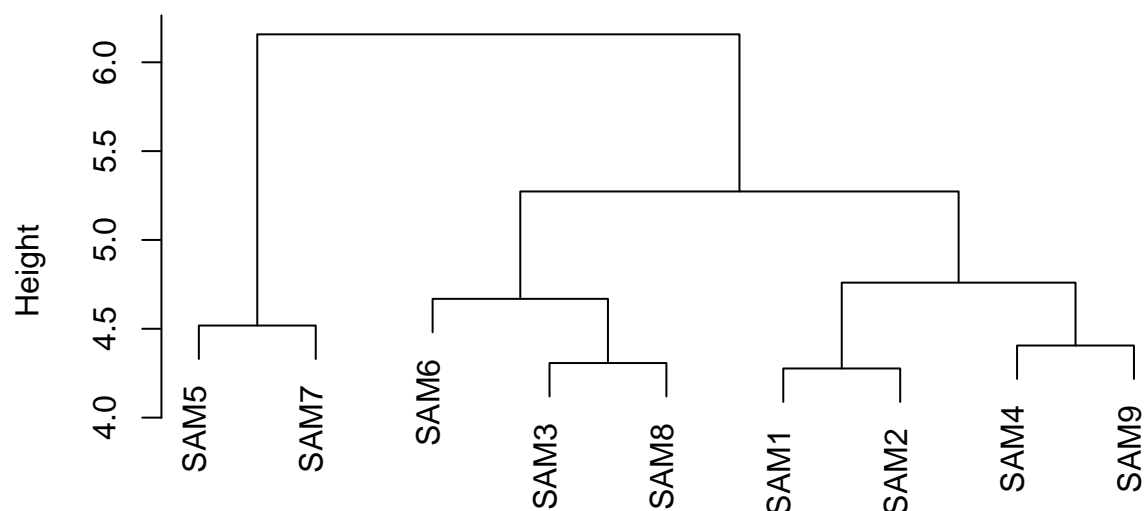
Cluster Dendrogram



```
dist.cov.coarse  
hclust (*, "complete")
```

```
threshold.coarse <- 3.8  
cov.coarse <- cutree(fit.coarse, h = threshold.coarse)  
  
hillsmith.fine <- dudi.hillsmith(cov.fine, nf = 3, scannf = FALSE)  
dist.cov.fine <- dist.dudi(hillsmith.fine)  
  
fit.fine <- hclust(dist.cov.fine, method = "complete")  
plot(fit.fine)
```

Cluster Dendrogram



```
dist.cov.fine
hclust (*, "complete")
```

```
threshold.fine <- 5
cov.fine <- cutree(fit.fine, h = threshold.fine)
```

Final cluster covariates:

```
cov.coarse
```

```
## SAM1 SAM2 SAM3 SAM4
##    1    2    2    3
```

```
cov.fine
```

```
## SAM1 SAM2 SAM3 SAM4 SAM5 SAM6 SAM7 SAM8 SAM9
##    1    1    2    1    3    2    3    2    1
```