Tutorial for Bioregionalization R package

`virtual_sp` is a dataset simulated that comes with the package. This dataset relies on the response curve of virtual species to a virtual raster. The virtual raster contains 10000 cells and was simulated using `gstat` R package. See here for details.

Based on this layer, the `virtualspecies` R package (Leroy et al. 2015) was used to simulate the response curve of 100 virtual species. A Gaussian curve was used. The mean and standard deviation of the response function was varying among species, such as some of them are more or less generalists/specialists.

For every species in every cell, we could derive a suitability index. Species with suitability index inferior to 0.15 were arbitrarily set absent.

```
# Import virtual dataset
data("virtual_sp")
```

The first step is to convert the data.frame into a contingency table.

```
sp_mat <- contingency(sp_df, "sp", "site", "pa", binary = TRUE)
```

We then need to project the network.

```
sp_proj <- project_network(sp_mat, similarity = "simpson")
sp_proj <- sp_proj[, c("id1", "id2", "simpson")]

# write.table(sp_proj[, c("id1", "id2", "simpson")], "OSLOM2/vignette.txt",
#             row.names = FALSE)
```

Running OSLOM (under Linux distribution).

Here: ./oslom_undir -r 10 -seed 1000 -t 0.5 -cp 0.5 -f vignette.txt -w

Converting the OSLOM .tp file into a list.

```
res <- readLines("OSLOM2/vignette.txt_oslo_files/tp")
oslom_vignette <- oslom_output(res, sp_mat)
length(unique(oslom_vignette$bioregion))
```

```
## [1] 2
```

Function to compute zscores.

Example with CA analysis and k-means clustering.

```
CA_res <- CA_cluster(sp_mat)
```

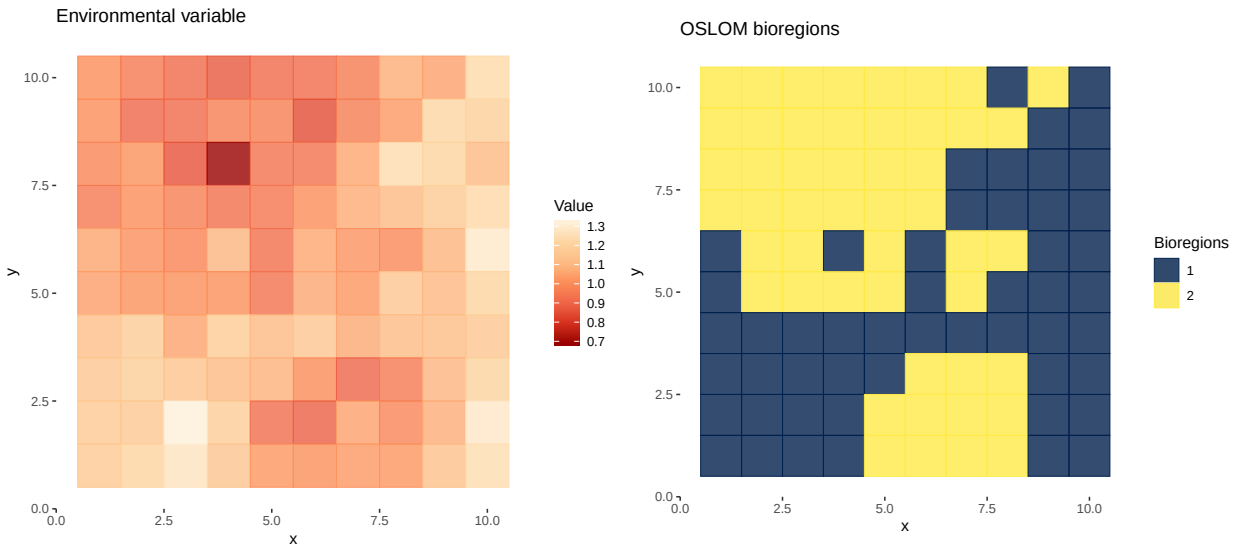
Projection on a map.

```
plot_grid(
  # Plot of environmental values
  sp_df %>%
    distinct(site, .keep_all = TRUE) %>%
```

```
  ggplot(aes(x, y)) +
  geom_tile(aes(fill = sim1, color = sim1),
            alpha = 0.8, width = 1, height = 1) +
  scale_color_distiller("Value", palette = "OrRd") +
  scale_fill_distiller("Value", palette = "OrRd") +
  coord_equal() +
  labs(title = "Environmental variable") +
  theme(panel.background = element_rect(fill = "transparent",colour = NA)),

# Plot of bioregions
sp_df %>%
  left_join(oslom_vignette, by = "site") %>%
  distinct(site, .keep_all = TRUE) %>%
  ggplot(aes(x, y)) +
  geom_tile(aes(fill = as.factor(bioregion), color = as.factor(bioregion)),
            alpha = 0.8, width = 1, height = 1) +
  scale_color_viridis_d("Bioregions", option = "E") +
  scale_fill_viridis_d("Bioregions", option = "E") +
  coord_equal() +
  labs(title = "OSLOM bioregions") +
  theme(panel.background = element_rect(fill = "transparent",colour = NA)),

nrow = 1)
```




```
# With sf
# res_map <- sp_df %>%
#   left_join(oslom_vignette, by = "site") %>%
#   st_as_sf(coords = c("x", "y")) %>%
#   group_by(bioregion) %>%
#   summarise()
#
# ggplot(res_map) +
#   geom_sf(aes(fill = as.factor(bioregion), color = as.factor(bioregion))) +
#   scale_fill_viridis_d("Bioregions") +
#   scale_color_viridis_d("Bioregions") +
#   labs(x = "Longitude", y = "Latitude")
```