InteractionExtension

```r
# reproducible R environments
library(groundhog)
```

Loaded 'groundhog' (version:2.2.0) using R-4.2.2

Tips and troubleshooting: https://groundhogR.com

```r
# dependencies
pkgs <- c(
  "dplyr",
  "ggplot2",
  "stringr",
  "ggcorrplot",
  "MASS",
  "Matrix"
)

# activate libraries
suppressMessages(groundhog.library(pkgs, "2023-03-01"))
```

```r
# create a sample sheet
meta <- data.frame(
  sampleID = paste0("Sample", seq(1,9)),
  river = paste0("River", rep(seq(1,3), each = 3)),
  site = rep(paste0("Site", c(1,2,3)), 3)
)

meta$river_site <- paste(meta$rive, ":", meta$site, sep = "")
meta
```

```
   sampleID  river  site    river_site
1  Sample1 River1 Site1 River1:Site1
2  Sample2 River1 Site2 River1:Site2
3  Sample3 River1 Site3 River1:Site3
4  Sample4 River2 Site1 River2:Site1
5  Sample5 River2 Site2 River2:Site2
6  Sample6 River2 Site3 River2:Site3
7  Sample7 River3 Site1 River3:Site1
8  Sample8 River3 Site2 River3:Site2
9  Sample9 River3 Site3 River3:Site3
```

Let's say there is a river-level correlation. This means:

- There should be correlation between columns 1-3, 4-6, and 7-9.

Let's assume there is a site-level correlation. For instance, perhaps a level of a contaminant is high near the source and decays as you move further down the rive (up in site number). This means:

- There should be a correlation between instances of Site1s, Site2s, and Site3s that is steadily decreasing.

```
meta$river_site
```

```
[1] "River1:Site1" "River1:Site2" "River1:Site3" "River2:Site1" "River2:Site2"
[6] "River2:Site3" "River3:Site1" "River3:Site2" "River3:Site3"
```

```r
sigma <- matrix(
  c(
    0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0,
    0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0,
    0.0, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0,
    0.0, 0.0, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0,
    0.0, 0.0, 0.0, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0,
    0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.0, 0.0, 0.0,
    0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.0, 0.0,
    0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.0,
    0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5
  ), 9,9
) %>% t

sigma %>% data.frame()
```

```
    X1  X2  X3  X4  X5  X6  X7  X8  X9
1 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
2 0.0 0.5 0.0 0.0 0.0 0.0 0.0 0.0 0.0
3 0.0 0.0 0.5 0.0 0.0 0.0 0.0 0.0 0.0
4 0.0 0.0 0.0 0.5 0.0 0.0 0.0 0.0 0.0
5 0.0 0.0 0.0 0.0 0.5 0.0 0.0 0.0 0.0
6 0.0 0.0 0.0 0.0 0.0 0.5 0.0 0.0 0.0
7 0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.0 0.0
8 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5 0.0
9 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.5
```

```r
(d <- Diagonal(n = 9, x = 0.5))
```

```
9 x 9 diagonal matrix of class "ddiMatrix"
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
 [1,]  0.5   .    .    .    .    .    .    .    .
 [2,]   .   0.5   .    .    .    .    .    .    .
 [3,]   .    .   0.5   .    .    .    .    .    .
 [4,]   .    .    .   0.5   .    .    .    .    .
 [5,]   .    .    .    .   0.5   .    .    .    .
 [6,]   .    .    .    .    .   0.5   .    .    .
 [7,]   .    .    .    .    .    .   0.5   .    .
 [8,]   .    .    .    .    .    .    .   0.5   .
 [9,]   .    .    .    .    .    .    .    .   0.5
```

```r
complexCorMatrix <- function(meta, effect1, effect2)
{

  n <- ncol(meta)

  effect1_levels <- unique(meta[, effect1$name])
  effect2_levels <- unique(meta[, effect2$name])

  interactions <- paste(meta[, effect1$name], ":",
      meta[, effect2$name], sep = "")

  n <- length(interactions)

  df <- data.frame(matrix(0, nrow = n, ncol = n))

  rownames(df) <- interactions
```

```r
  colnames(df) <- interactions

  # iterate through and add the cor conditionally
  for(i in 1:n){
    icol <- colnames(df)[i]

    for(j in 1:n){
      jcol <- rownames(df)[j]

      for(i in 1:length(effect1_levels)) {
        if(str_detect(icol, effect1_levels[i])) {
          df[jcol, icol] <- df[jcol, icol] + effect1$cors[i]
        }
      }

      for(i in 1:length(effect2_levels)) {
        if(str_detect(jcol, effect2_levels[i])) {
          df[jcol, icol] <- df[jcol, icol] + effect2$cors[i]
        }
      }

    }
  }


  df
}


x <- complexCorMatrix(meta,
  list(name = "river", cors = c(0.3, 0.4, 0.5)),
  list(name = "site", cors = c(0.2, 0.3, 0.4))
)

ggcorrplot(x, lab = TRUE, color = c("blue", "#00693e"))
```
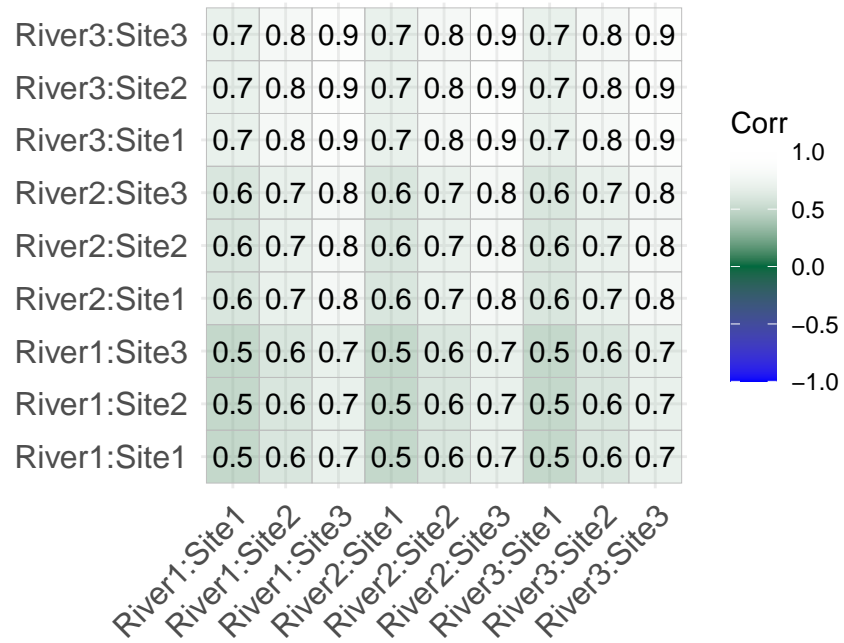
```
# for(s in c("one", "two", "three")) {
#   if(grep("o", s)) {
#     print("hello")
#   }
# }
```