(2^{nd}) Analyses for 2^{nd} draft

GCFR vs SWAFR manuscript

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```
# General programming
library(tidyverse)
library(here)  # for more reliable file paths
library(glue)  # better than paste()
library(magrittr)  # for %<>% & %$%

# GIS
library(raster)
library(rgdal)

# Analyses
library(canprot)  # for CLES
library(broom)  # to tidy model outputs

# Figures
library(cowplot)  # for panelling
library(ggfortify)  # for autoplot() of PCAs
```

```
# Environmental variable names in nice order
var_names <- c(
  "Elevation",
  "MAP",
  "PDQ",
  "Surface T",
  "NDVI",
  "CEC",
  "Clay",
  "Soil C",
  "pH"
)

# Preserve clean plotting environment
op <- par()

# Global ggplot2 theme settings
theme_set(theme_bw() + theme(
  strip.background = element_blank(),
  panel.grid = element_blank()
))
```

Preamble/outline

Here I layout (another) the "new", second incarnation of the analyses as discussed in August 2019, during the writing of the second draft of the manuscript.

To reiterate that manuscript, we hypothesise that the greater vascular plant species richness of the GCFR compared to that of the SWAFR is explained by the regions' difference in environmental heterogeneity.

The proposed "story" of questions for the analyses is as follows:

1. Is the GCFR more heterogeneous environmentally than the SWAFR, and does the scale of that heterogeneity differ to that of the SWAFR?
2. Do the regions differ w.r.t. the species richness of both HDS and QDS cells, and, for HDS cells' richness (S_{HDS}), does the explanatory power of mean QDS richness (S_{QDS}) and turnover (T_{QDS}) differ between the regions?
3. Does heterogeneity explain differences in richness and turnover between the regions?

1. Comparing regions' environmental heterogeneity

Is the GCFR more heterogeneous environmentally than the SWAFR, and does the scale of that heterogeneity differ to that of the SWAFR?

In order to determine which region is more environmentally heterogeneous, and what scales heterogeneity is most pronounced, we calculated environmental heterogeneity at various spatial scales. We treated environmental heterogeneity (EH) as the variance of twentieth, eighth- (EDS), quarter- (QDS) and half- (HDS) degree-squares' environmental conditions in tenth- (TDS), QDS, HDS and one-degree-squares (DS) respectively. More generally, for pixels X at some broad scale b, EH is based on the values of the N sub-pixels x_i at the finer scale f as follows:

$$EH(X_b) = \text{Var}(X_f) = \frac{1}{N}\sum_{i=1}^{N}(x_{f\,i} - \overline{x_f})^2.$$

For our purposes, EH is thus defined for the nine environmental variables X at the four spatial scales as follows:

$$EH(X_{\text{DS}}) = \text{Var}(X_{\text{HDS}}),$$

$$EH(X_{\text{HDS}}) = \text{Var}(X_{\text{QDS}})$$

$$EH(X_{\text{QDS}}) = \text{Var}(X_{\text{EDS}})$$

$$EH(X_{\text{TDS}}) = \text{Var}(X_{\frac{1}{20}\text{DS}})$$

...

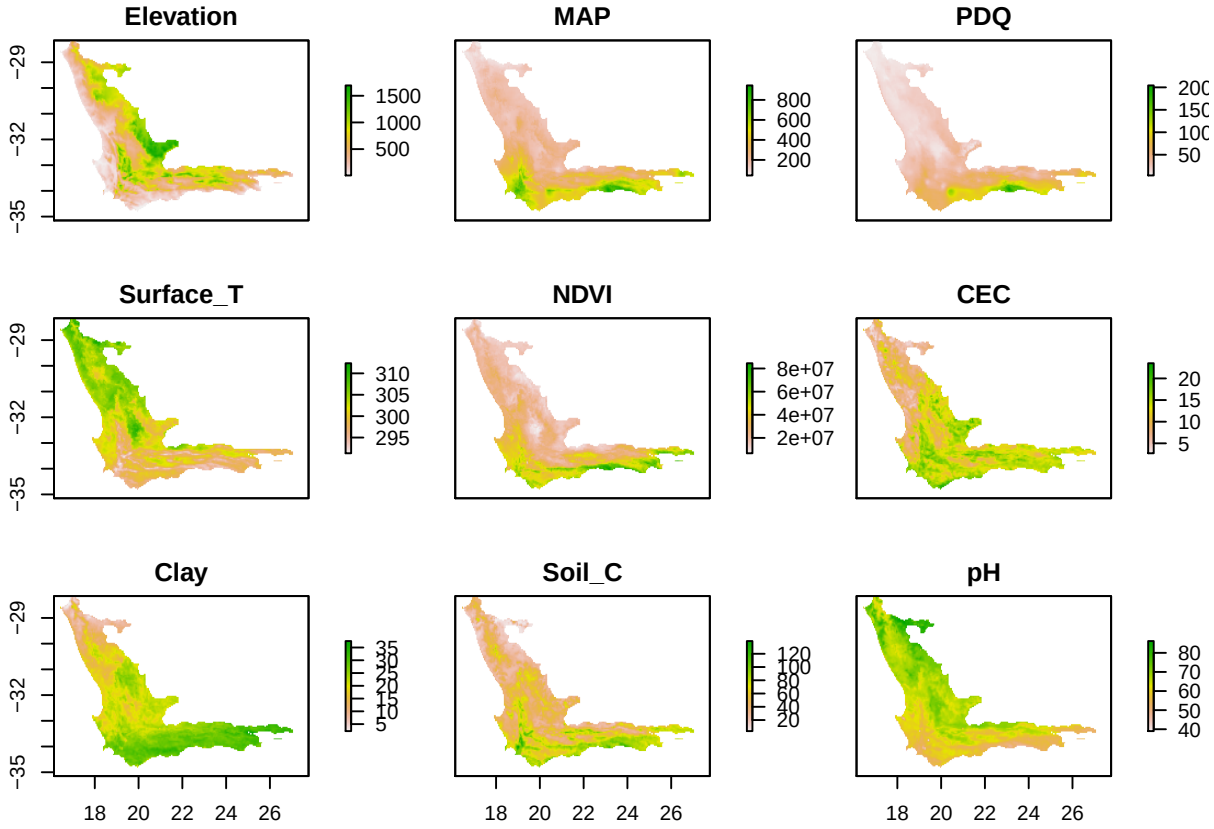
```
data_dir <- here("data/derived-data/May-2019")
GCFR_file_names  <- glue("{data_dir}/GCFR_{var_names}_masked2.tif")
SWAFR_file_names <- glue("{data_dir}/SWAFR_{var_names}_masked2.tif")
GCFR_variables  <- stack(GCFR_file_names)
SWAFR_variables <- stack(SWAFR_file_names)
names(GCFR_variables)  <- str_replace_all(var_names, " ", "_")
names(SWAFR_variables) <- str_replace_all(var_names, " ", "_")
GCFR_variables
```

```
## class      : RasterStack
## dimensions : 140, 220, 30800, 9  (nrow, ncol, ncell, nlayers)
## resolution : 0.05, 0.05  (x, y)
## extent     : 16.45, 27.45, -35.15, -28.15  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0
## names      :    Elevation,          MAP,          PDQ,    Surface_T,         NDVI,          CEC,
## min values : 6.366550e+00, 4.490771e+01, 3.845532e+00, 2.913266e+02, 6.709096e+06, 2.699161e+00,
## max values : 1.693627e+03, 9.445777e+02, 2.042740e+02, 3.123608e+02, 8.453450e+07, 2.350940e+01,
```

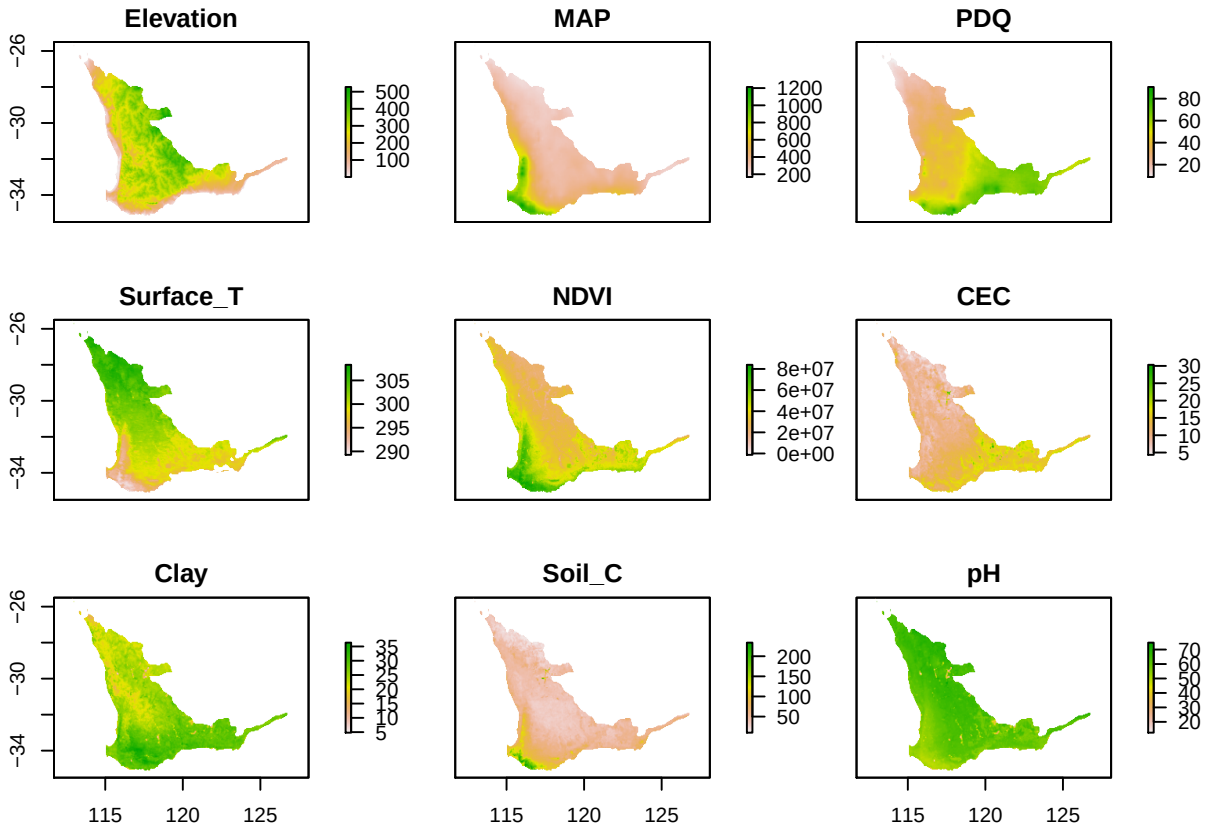
```
SWAFR_variables
```

```
## class       : RasterStack
## dimensions  : 200, 280, 56000, 9  (nrow, ncol, ncell, nlayers)
## resolution  : 0.05, 0.05  (x, y)
## extent      : 112.9, 126.9, -35.5, -25.5  (xmin, xmax, ymin, ymax)
## crs         : +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0
## names       :     Elevation,           MAP,           PDQ,     Surface_T,          NDVI,
## min values  :  4.407049e-01,  1.677904e+02,  8.773942e+00,  2.892730e+02, -1.272565e+06,  4.344898
## max values  :  5.276772e+02,  1.212685e+03,  9.061172e+01,  3.082984e+02,  8.391765e+07,  3.031978
```

```
par(mfrow = c(3, 3))
plot(GCFR_variables)
```




```
par(op)

par(mfrow = c(3, 3))
plot(SWAFR_variables)
```




```
par(op)
```

```
EDS_template_raster <- GCFR_variables$Elevation %>%
  aggregate(fact = 5) %>%  # aggregate up to QDS
  disaggregate(fact = 2)   # disaggregate down to EDS
GCFR_variables_EDS <- resample(
  GCFR_variables, EDS_template_raster,
  method = "bilinear"
)
GCFR_variables_EDS
```

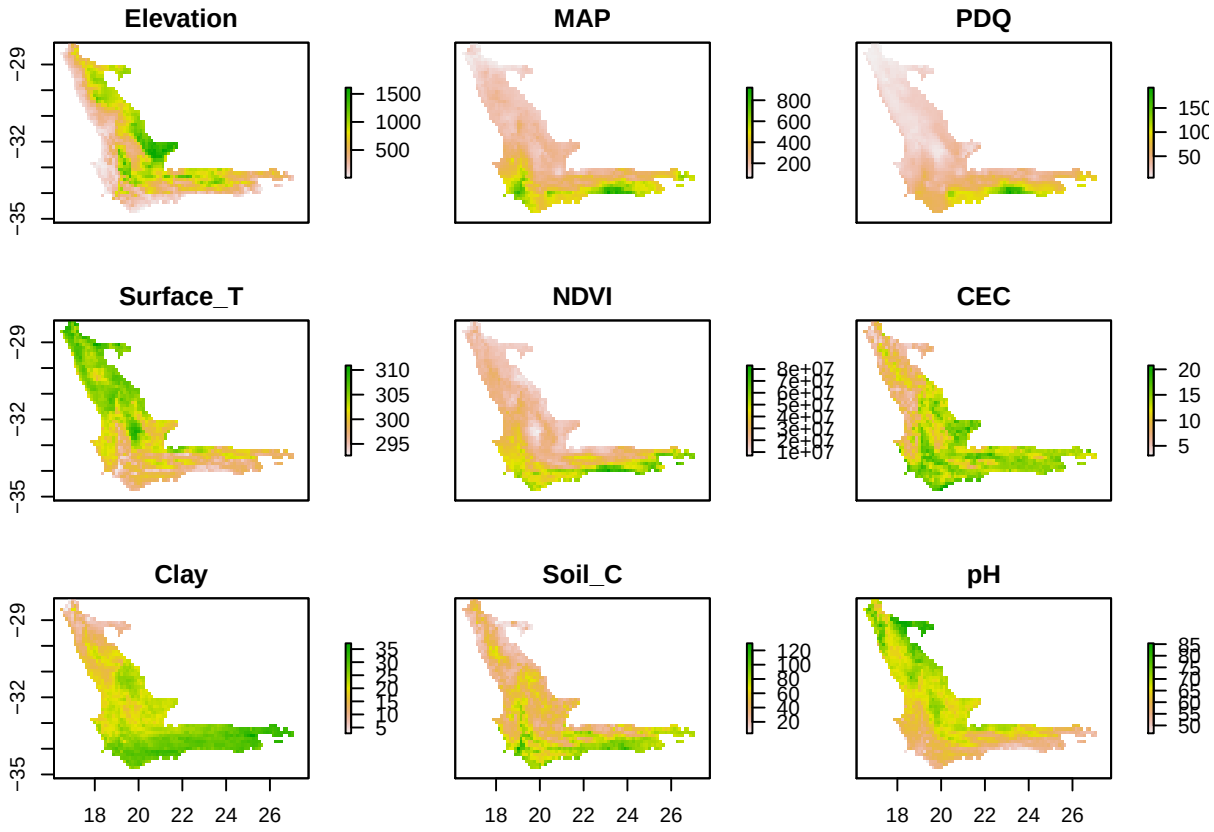
```
## class      : RasterBrick
## dimensions : 56, 88, 4928, 9  (nrow, ncol, ncell, nlayers)
## resolution : 0.125, 0.125  (x, y)
## extent     : 16.45, 27.45, -35.15, -28.15  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0
## source     : memory
## names      :    Elevation,          MAP,          PDQ,    Surface_T,          NDVI,          CEC,
## min values : 7.740328e+00, 6.333686e+01, 5.568253e+00, 2.926559e+02, 7.119721e+06, 3.109218e+00,
## max values : 1.611345e+03, 9.199011e+02, 1.921860e+02, 3.109162e+02, 8.301637e+07, 2.076085e+01,
```

```
EDS_template_raster <- SWAFR_variables$Elevation %>%
  aggregate(fact = 5) %>%
  disaggregate(fact = 2)
SWAFR_variables_EDS <- resample(
  SWAFR_variables, EDS_template_raster,
  method = "bilinear"
)
SWAFR_variables_EDS
```

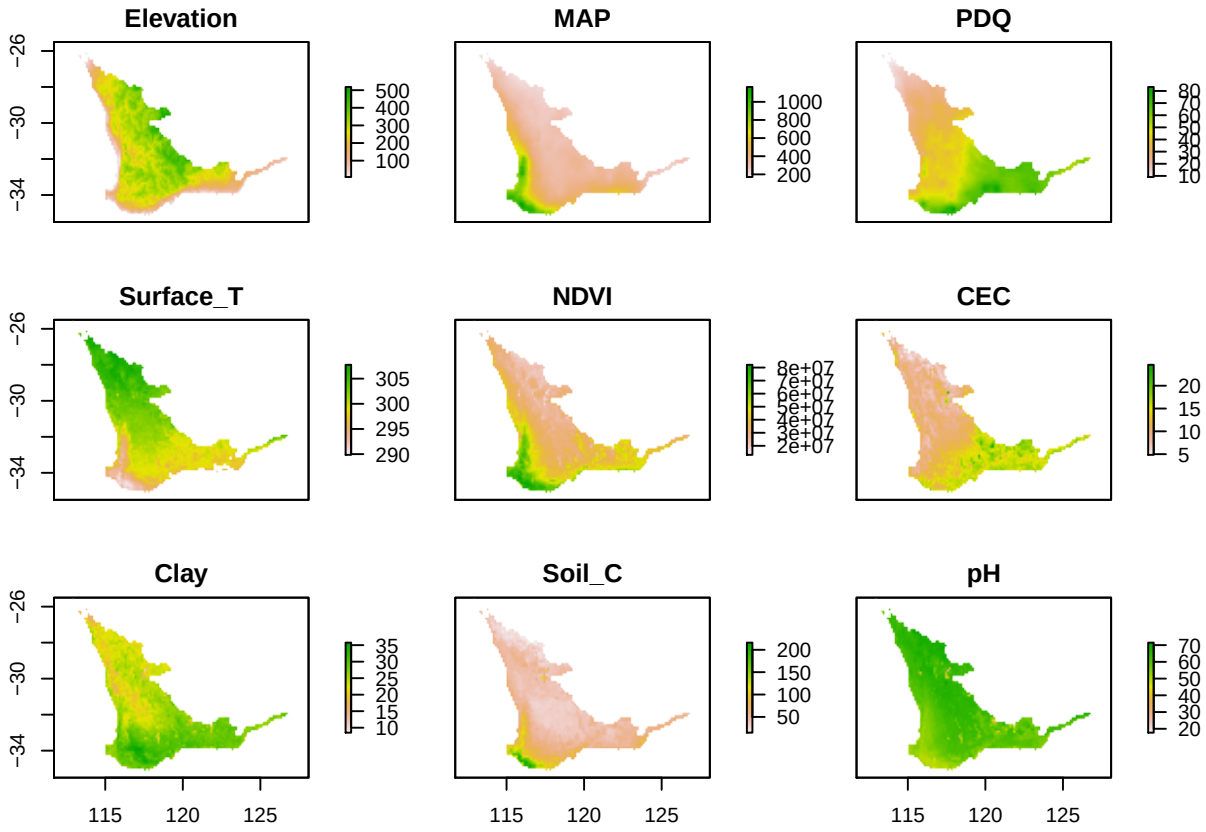
```
## class      : RasterBrick
## dimensions : 80, 112, 8960, 9  (nrow, ncol, ncell, nlayers)
## resolution : 0.125, 0.125  (x, y)
```

```
## extent     : 112.9, 126.9, -35.5, -25.5  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0
## source     : memory
## names      :    Elevation,          MAP,          PDQ,    Surface_T,          NDVI,          CEC,
## min values : 7.149977e+00, 1.708365e+02, 9.094913e+00, 2.898587e+02, 1.308367e+07, 4.849654e+00,
## max values : 5.180779e+02, 1.163782e+03, 8.326768e+01, 3.077511e+02, 8.209903e+07, 2.458403e+01,
```

```
par(mfrow = c(3, 3))
plot(GCFR_variables_EDS)
```



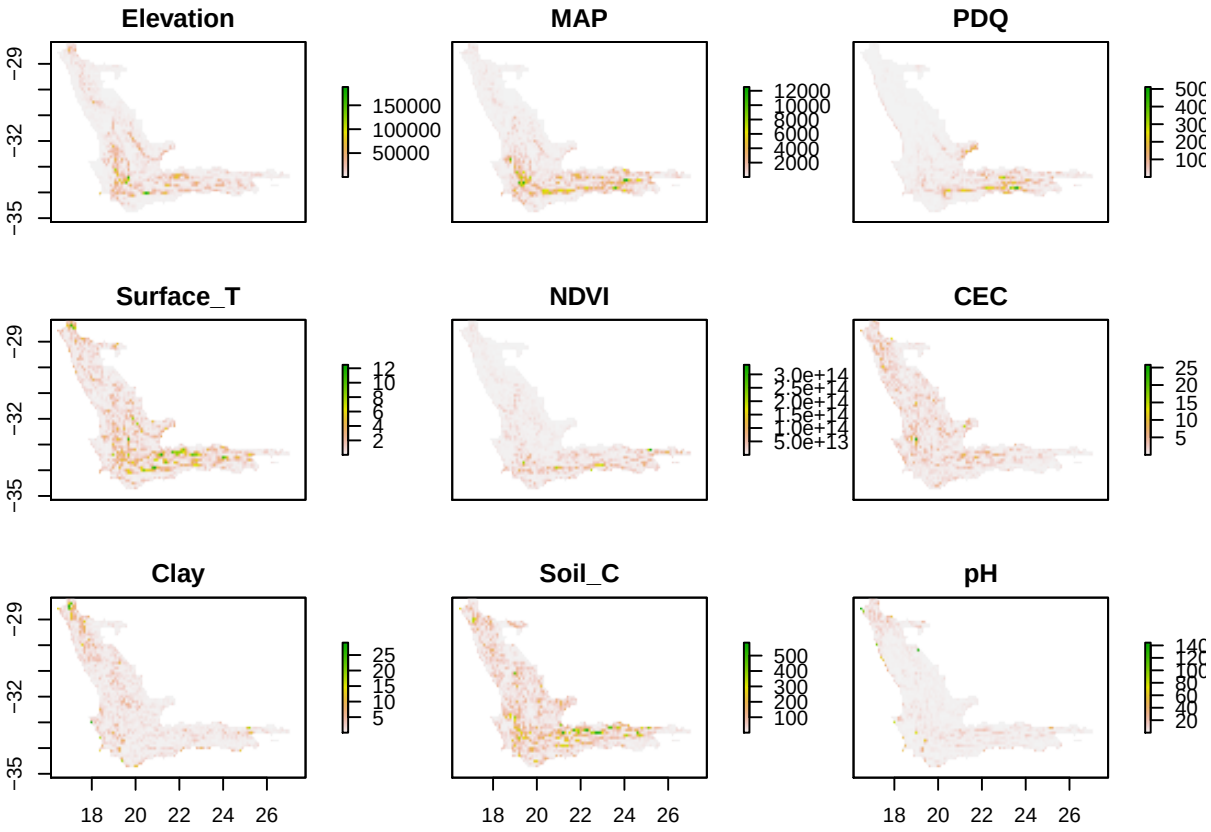

```
par(op)

par(mfrow = c(3, 3))
plot(SWAFR_variables_EDS)
```



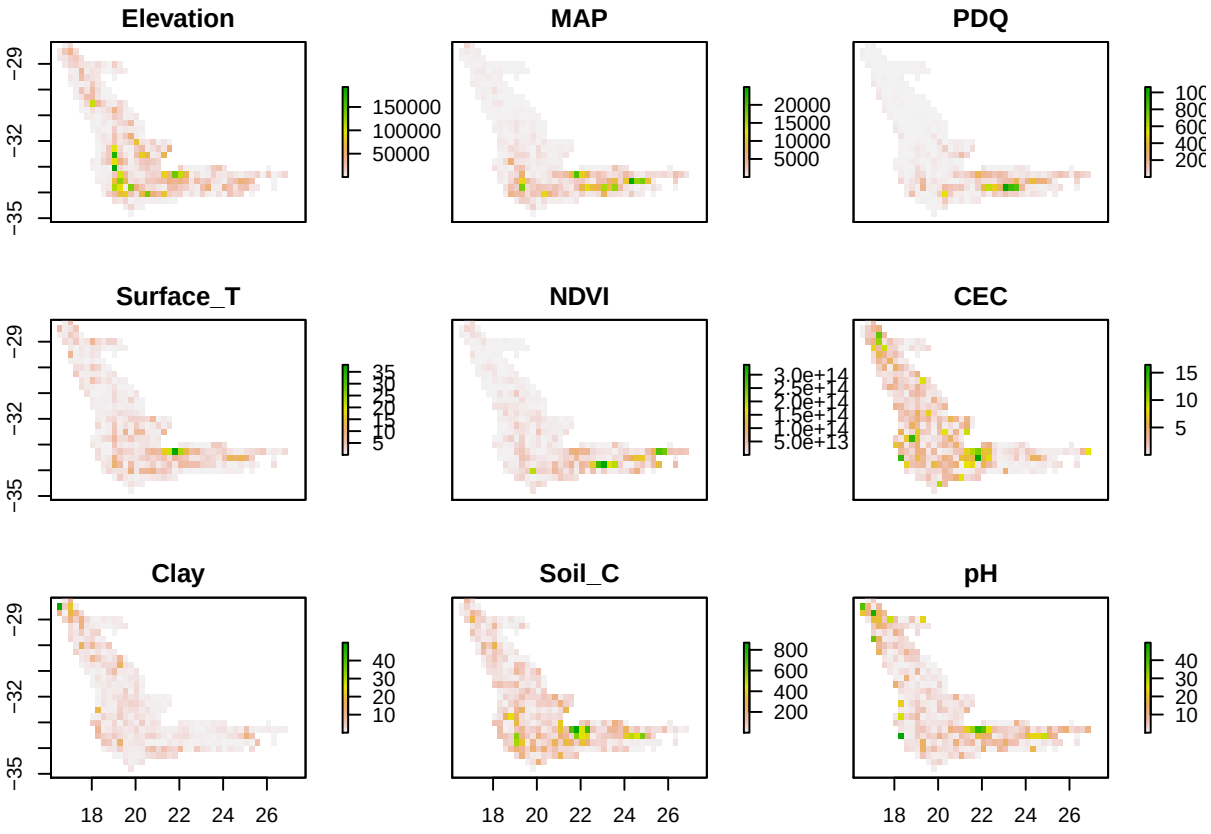

```
par(op)
```

```
scales <- c(1, 2, 4)

GCFR_heterogeneity <- map(scales,
  ~ GCFR_variables_EDS %>%
    aggregate(fact = .x) %>%
    aggregate(fun = var)
)
names(GCFR_heterogeneity) <- c("QDS", "HDS", "DS")
GCFR_heterogeneity %<>% {c(point1 = aggregate(GCFR_variables, fun = var), .)}

SWAFR_heterogeneity <- map(scales,
  ~ SWAFR_variables_EDS %>%
    aggregate(fact = .x) %>%
    aggregate(fun = var)
)
names(SWAFR_heterogeneity) <- c("QDS", "HDS", "DS")
SWAFR_heterogeneity %<>% {c(point1 = aggregate(SWAFR_variables, fun = var), .)}
```

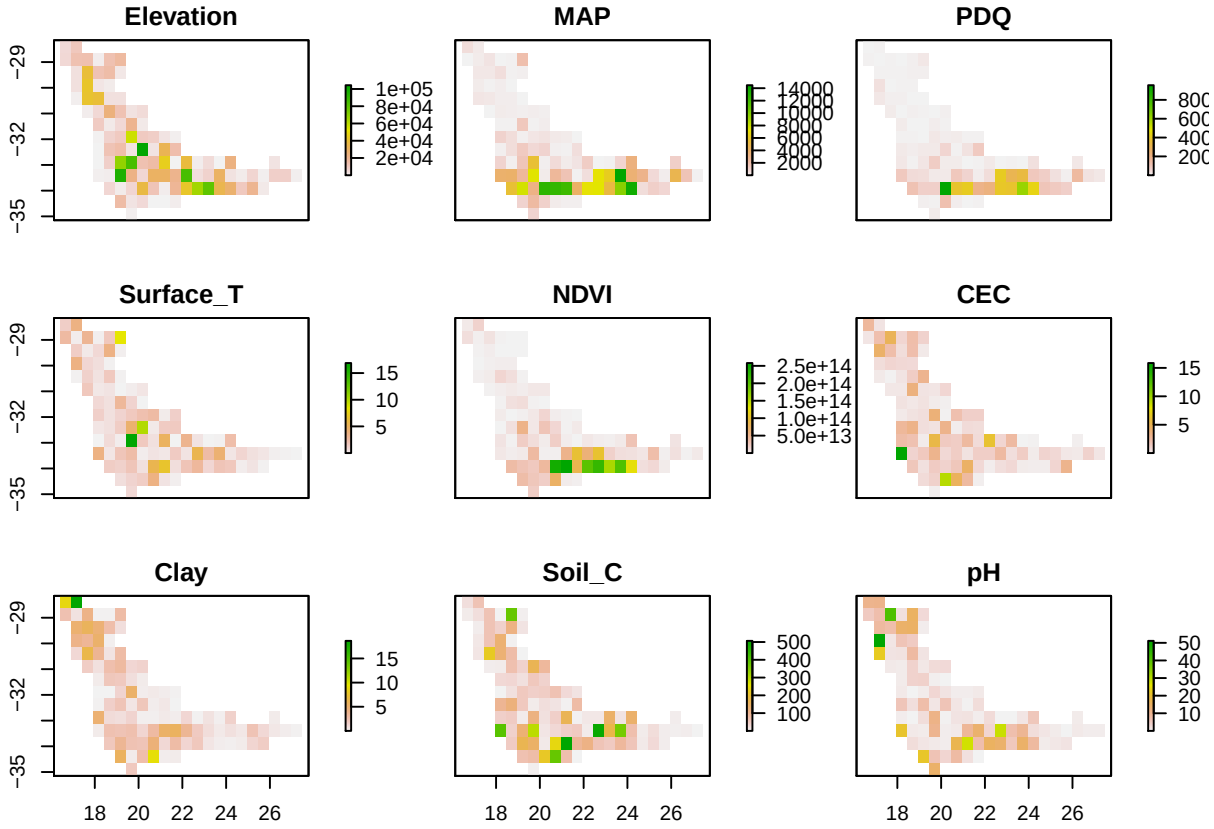
```
par(mfrow = c(3, 3))
plot(GCFR_heterogeneity$point1)
```



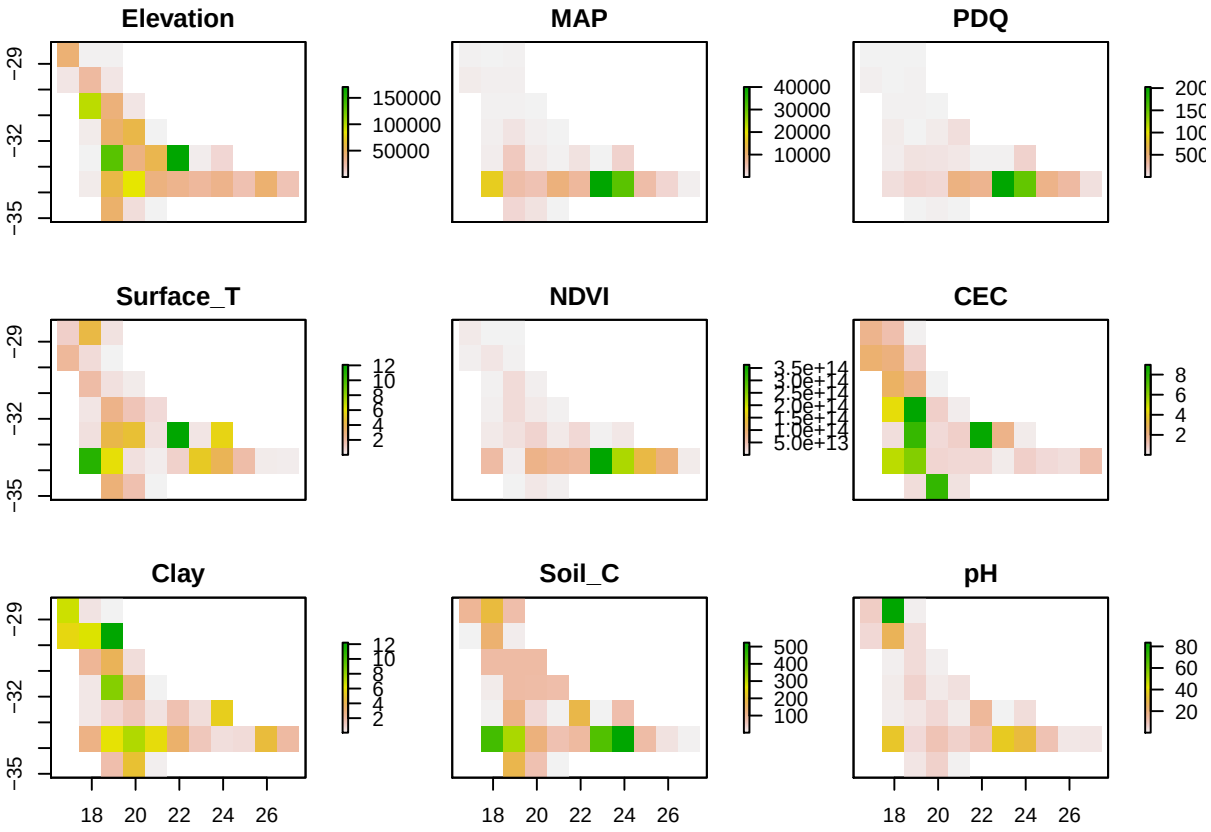

```
par(op)

par(mfrow = c(3, 3))
plot(GCFR_heterogeneity$QDS)
```



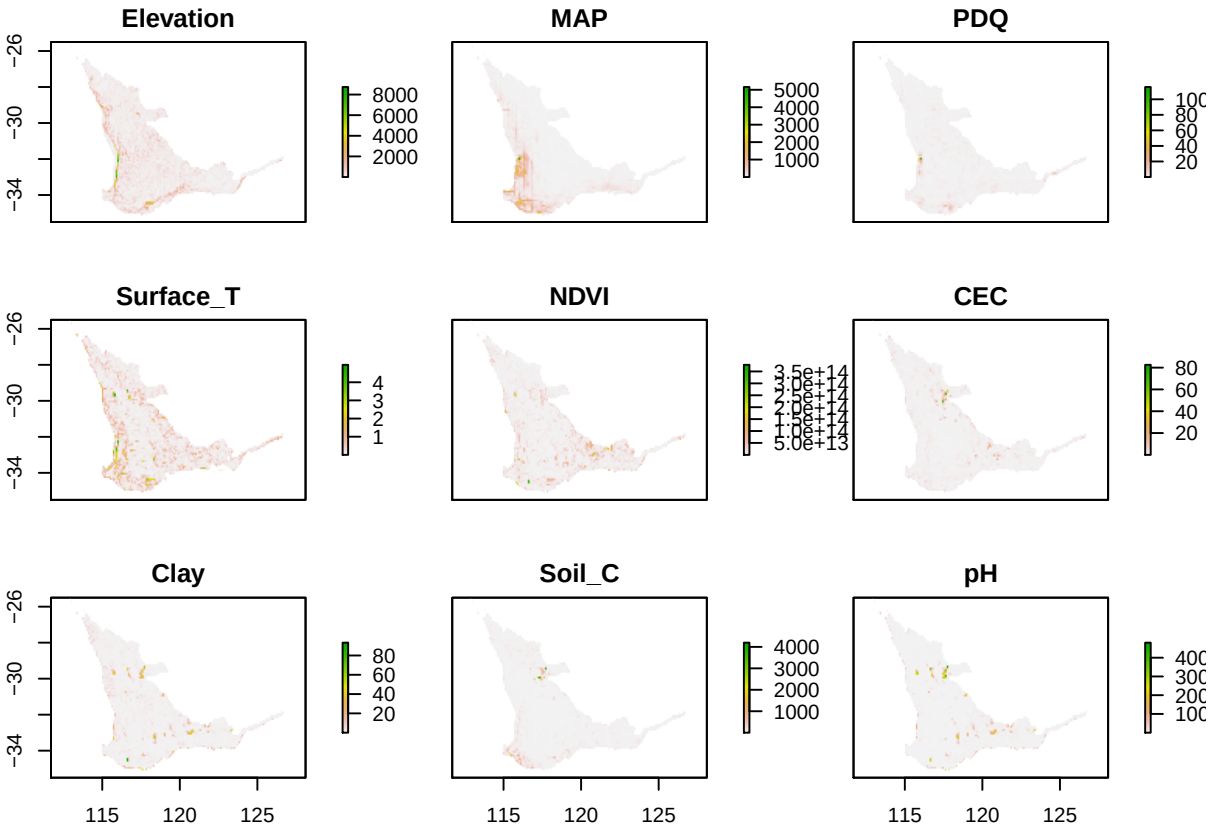
```
par(op)

par(mfrow = c(3, 3))
plot(GCFR_heterogeneity$HDS)
```



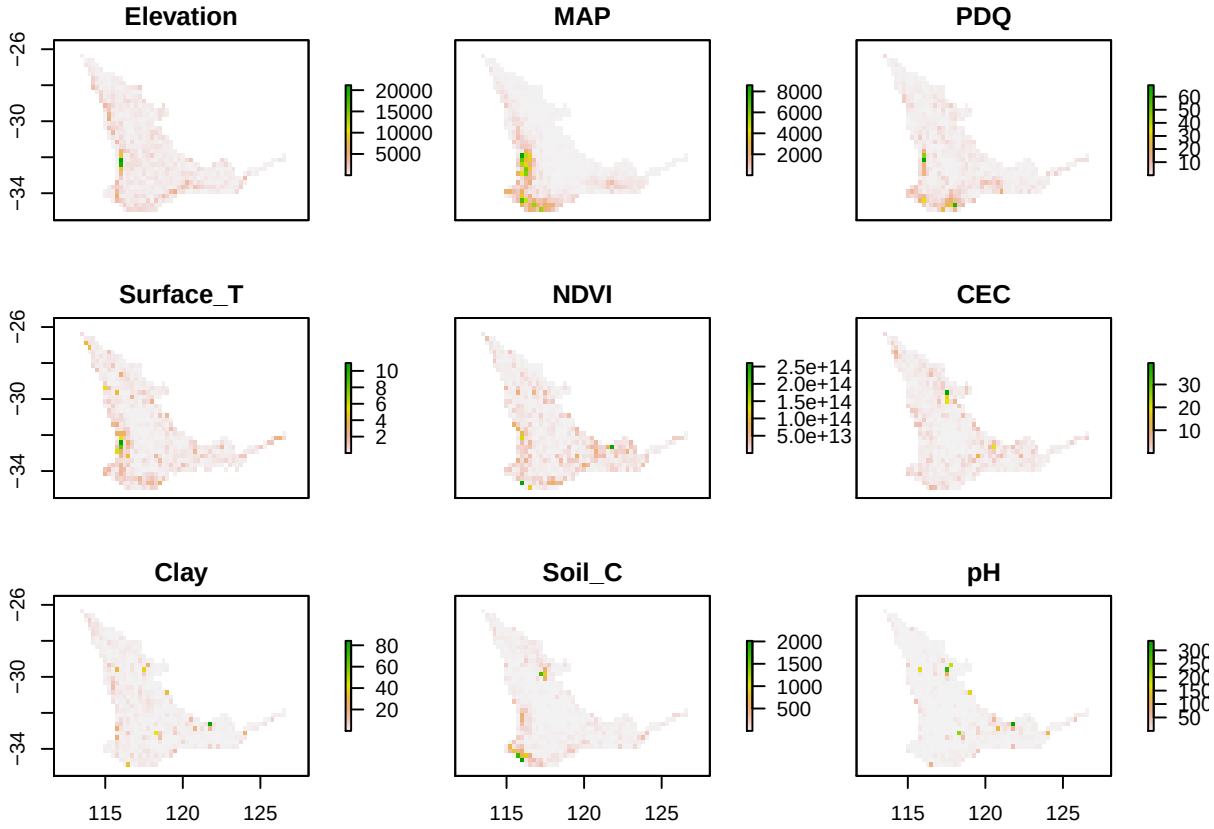

```
par(op)

par(mfrow = c(3, 3))
plot(GCFR_heterogeneity$DS)
```



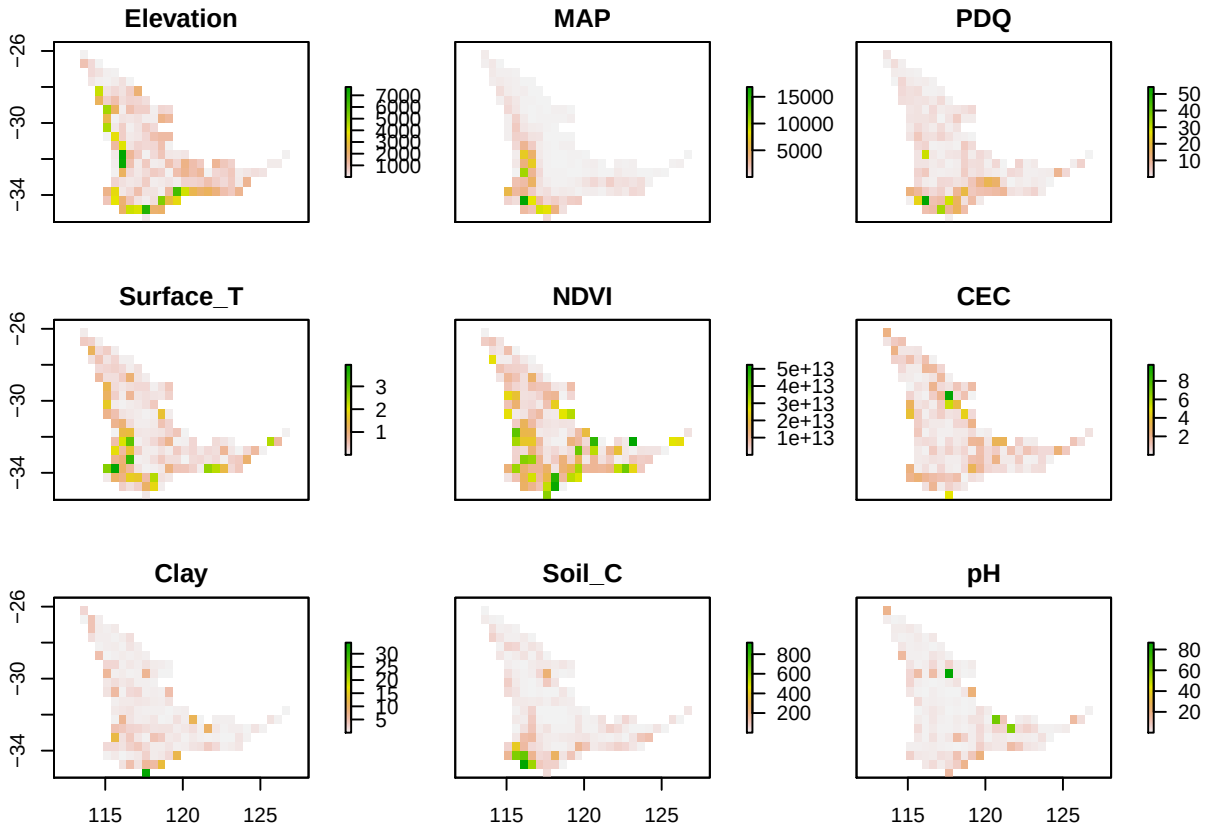

```
par(op)

par(mfrow = c(3, 3))
plot(SWAFR_heterogeneity$point1)
```



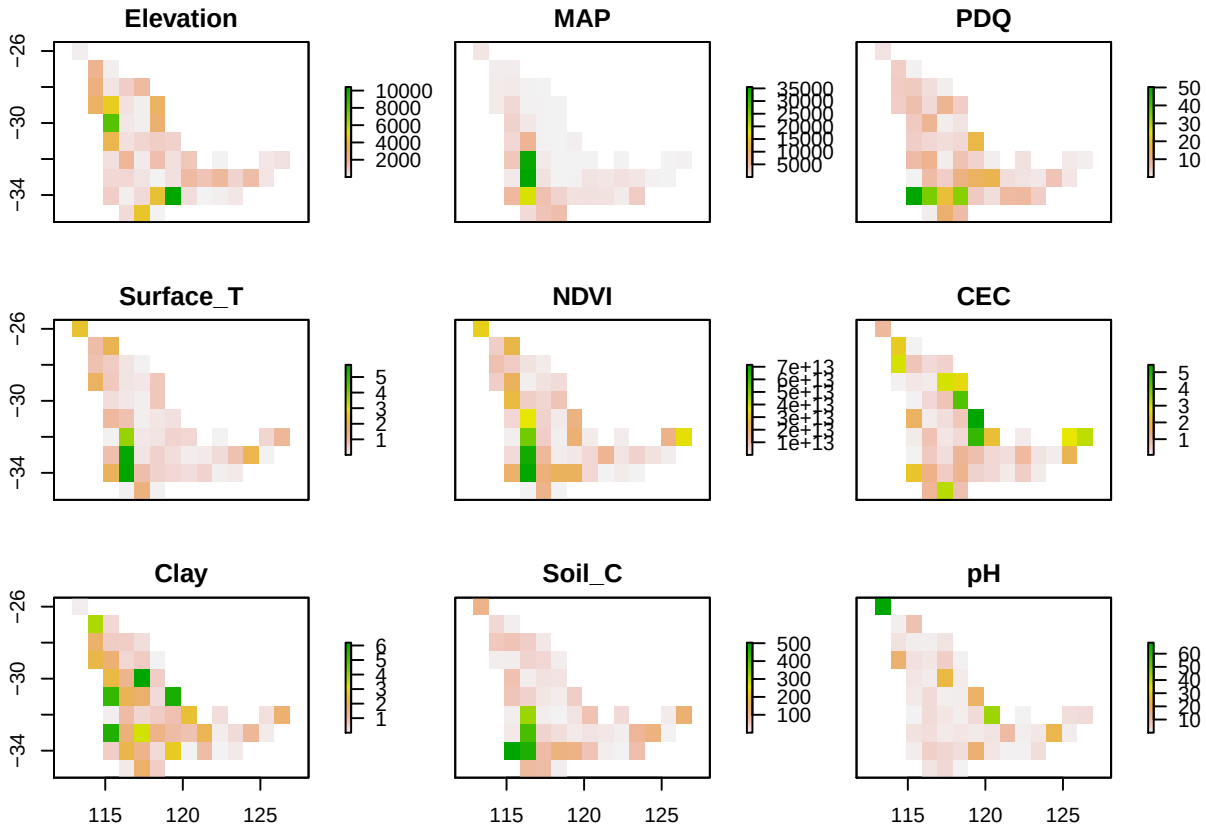
```
par(op)

par(mfrow = c(3, 3))
plot(SWAFR_heterogeneity$QDS)
```




```
par(op)

par(mfrow = c(3, 3))
plot(SWAFR_heterogeneity$HDS)
```




```
par(op)

par(mfrow = c(3, 3))
plot(SWAFR_heterogeneity$DS)
```



```r
par(op)
```

```r
# Join regions' datasets
heterogeneity <- map2(GCFR_heterogeneity, SWAFR_heterogeneity,
  ~ na.exclude(rbind(
    cbind(region = "GCFR",  as.data.frame(log10(.x))),
    cbind(region = "SWAFR", as.data.frame(log10(.y)))
  ))
)
```

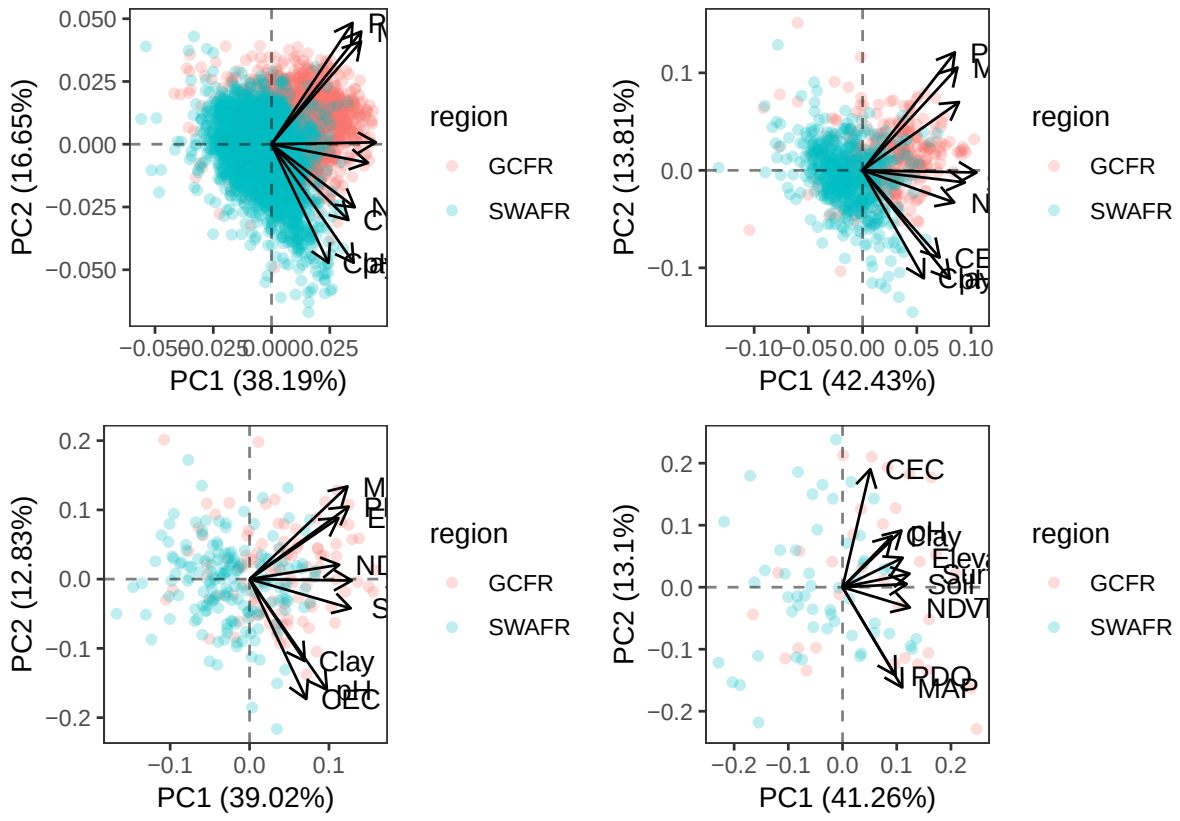
```r
heterogeneity_PCAs <- map(heterogeneity,
  ~ prcomp(
    .x[, -1],
    center = TRUE,
    scale. = TRUE
  )
)
map(heterogeneity_PCAs, summary)
```

```
## $point1
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5    PC6
## Standard deviation     1.8539 1.2243 0.89661 0.86925 0.75606 0.7470
## Proportion of Variance 0.3819 0.1665 0.08932 0.08396 0.06351 0.0620
## Cumulative Proportion  0.3819 0.5484 0.63775 0.72171 0.78522 0.8472
##                           PC7     PC8     PC9
## Standard deviation     0.73289 0.66832 0.62552
## Proportion of Variance 0.05968 0.04963 0.04347
## Cumulative Proportion  0.90690 0.95653 1.00000
##
## $QDS
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5     PC6
## Standard deviation     1.9543 1.1147 0.90436 0.88177 0.80313 0.71216
## Proportion of Variance 0.4244 0.1381 0.09087 0.08639 0.07167 0.05635
## Cumulative Proportion  0.4244 0.5624 0.65327 0.73966 0.81133 0.86768
##                           PC7     PC8     PC9
## Standard deviation     0.66146 0.62594 0.60128
## Proportion of Variance 0.04861 0.04353 0.04017
## Cumulative Proportion  0.91630 0.95983 1.00000
##
## $HDS
## Importance of components:
##                           PC1    PC2    PC3     PC4     PC5     PC6    PC7
## Standard deviation     1.8740 1.0746 0.9850 0.90862 0.82854 0.76507 0.7099
## Proportion of Variance 0.3902 0.1283 0.1078 0.09173 0.07628 0.06504 0.0560
## Cumulative Proportion  0.3902 0.5185 0.6263 0.71808 0.79435 0.85939 0.9154
##                           PC8    PC9
## Standard deviation     0.65867 0.5724
## Proportion of Variance 0.04821 0.0364
## Cumulative Proportion  0.96360 1.0000
##
## $DS
## Importance of components:
##                           PC1    PC2    PC3     PC4     PC5     PC6    PC7
## Standard deviation     1.9271 1.0859 0.9999 0.91028 0.79126 0.73452 0.6469
## Proportion of Variance 0.4126 0.1310 0.1111 0.09207 0.06957 0.05995 0.0465
## Cumulative Proportion  0.4126 0.5437 0.6547 0.74681 0.81637 0.87632 0.9228
```

```
##                             PC8     PC9
## Standard deviation     0.62256 0.55410
## Proportion of Variance 0.04306 0.03411
## Cumulative Proportion  0.96589 1.00000
```

```
# Force PC1 scores to be positive if all vars rotations are negative
heterogeneity_PCAs %<>% map(function(PCA) {
  if (all(PCA$rotation[, 1] <= 0)) {
    message("Multiplying this one by -1")
    PCA$rotation[, 1] %<>% multiply_by(-1)
    PCA$x[, 1]        %<>% multiply_by(-1)
  }
  PCA
})
```

```
plot_grid(plotlist = map2(
  .x = heterogeneity_PCAs,
  .y = heterogeneity,
  .f =
    ~ autoplot(.x, data = .y, colour = "region",
      alpha = 0.25,
      loadings       = TRUE, loadings.colour      = "black",
      loadings.label = TRUE, loadings.label.colour = "black",
      loadings.label.hjust = -0.25
    ) +
    ggtitle(unique(.y$scale)) +
    geom_hline(yintercept = 0, linetype = "dashed", alpha = 0.5) +
    geom_vline(xintercept = 0, linetype = "dashed", alpha = 0.5)
))
```




```
PC1s <- map(heterogeneity_PCAs, ~tibble(PC1 = .x$x[, 1]))
heterogeneity %<>% map2(PC1s, ~cbind(.x, .y))
```

```
CLES_results <- map2_dfr(
  .x = heterogeneity %>%
    map(filter, region == "GCFR") %>%
    map(dplyr::select, -region),
  .y = heterogeneity %>%
    map(filter, region == "SWAFR") %>%
    map(dplyr::select, -region),
  .id = "scale",  # for every spatial scale,
  ~ map2_df(
    .x = .x,
    .y = .y,
    .id = "variable",  # for every variable in each region,
    ~ tibble(
      CLES_value = CLES(.y, .x),  # calculate the CLES,
      U_test = wilcox.test(.x, .y, conf.int = TRUE) %>%  # & Mann-Whitney U-test
        tidy() %>%
        list()
    )
  )
)
CLES_results %<>% mutate(
  variable = factor(variable, levels = var_names %>%
    str_replace_all(" ", "_") %>%
    c("PC1")
  ),
  scale = case_when(
    scale == "point1" ~ 0.10,
    scale == "QDS"    ~ 0.25,
    scale == "HDS"    ~ 0.50,
    scale == "DS"     ~ 1.00
  ),
  diff  = map_dbl(U_test, "estimate"),
  P_U   = map_dbl(U_test, "p.value"),
  U_low = map_dbl(U_test, "conf.low"),
  U_upp = map_dbl(U_test, "conf.high")
)
CLES_results
```

```
## # A tibble: 40 x 8
##    scale variable  CLES_value U_test            diff       P_U  U_low U_upp
##    <dbl> <fct>          <dbl> <list>           <dbl>     <dbl>  <dbl> <dbl>
##  1   0.1 Elevation      0.908 <tibble [1 x 7~ 1.24   0.        1.20   1.27
##  2   0.1 MAP            0.776 <tibble [1 x 7~ 0.927  1.57e-249 0.879  0.976
##  3   0.1 PDQ            0.801 <tibble [1 x 7~ 0.937  2.97e-296 0.891  0.983
##  4   0.1 Surface_T      0.744 <tibble [1 x 7~ 0.648  2.41e-196 0.609  0.687
##  5   0.1 NDVI           0.537 <tibble [1 x 7~ 0.0919 6.81e-  6 0.0520 0.132
##  6   0.1 CEC            0.646 <tibble [1 x 7~ 0.322  4.31e- 71 0.288  0.356
##  7   0.1 Clay           0.570 <tibble [1 x 7~ 0.151  1.02e- 17 0.117  0.185
##  8   0.1 Soil_C         0.693 <tibble [1 x 7~ 0.514  3.24e-123 0.475  0.554
##  9   0.1 pH             0.641 <tibble [1 x 7~ 0.386  2.39e- 66 0.344  0.428
## 10   0.1 PC1            0.819 <tibble [1 x 7~ 2.09   0.        2.00   2.18
## # ... with 30 more rows
```

```
CLES_models <- CLES_results %>%
  split(.$variable) %>%
  map(~lm(CLES_value ~ scale, .x))
CLES_models$Elevation
```

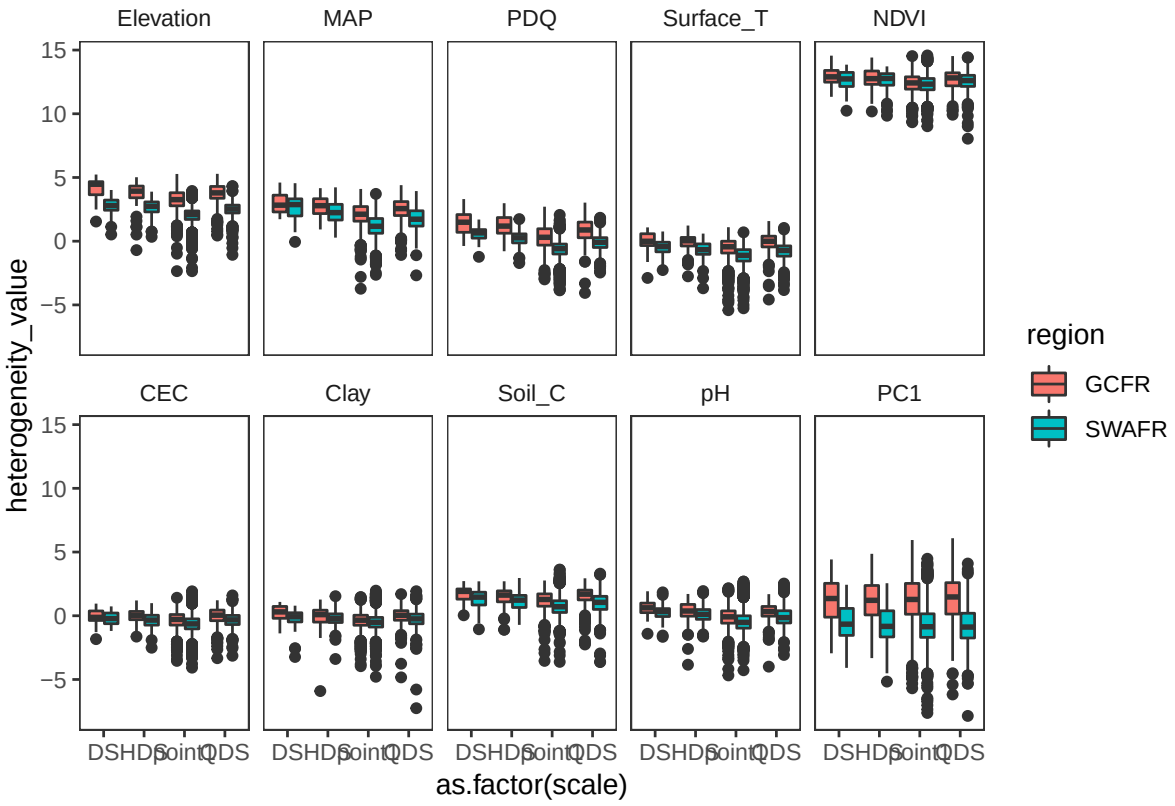
```
##
```

```
## Call:
## lm(formula = CLES_value ~ scale, data = .x)
##
## Coefficients:
## (Intercept)        scale
##     0.90749     -0.02919
```

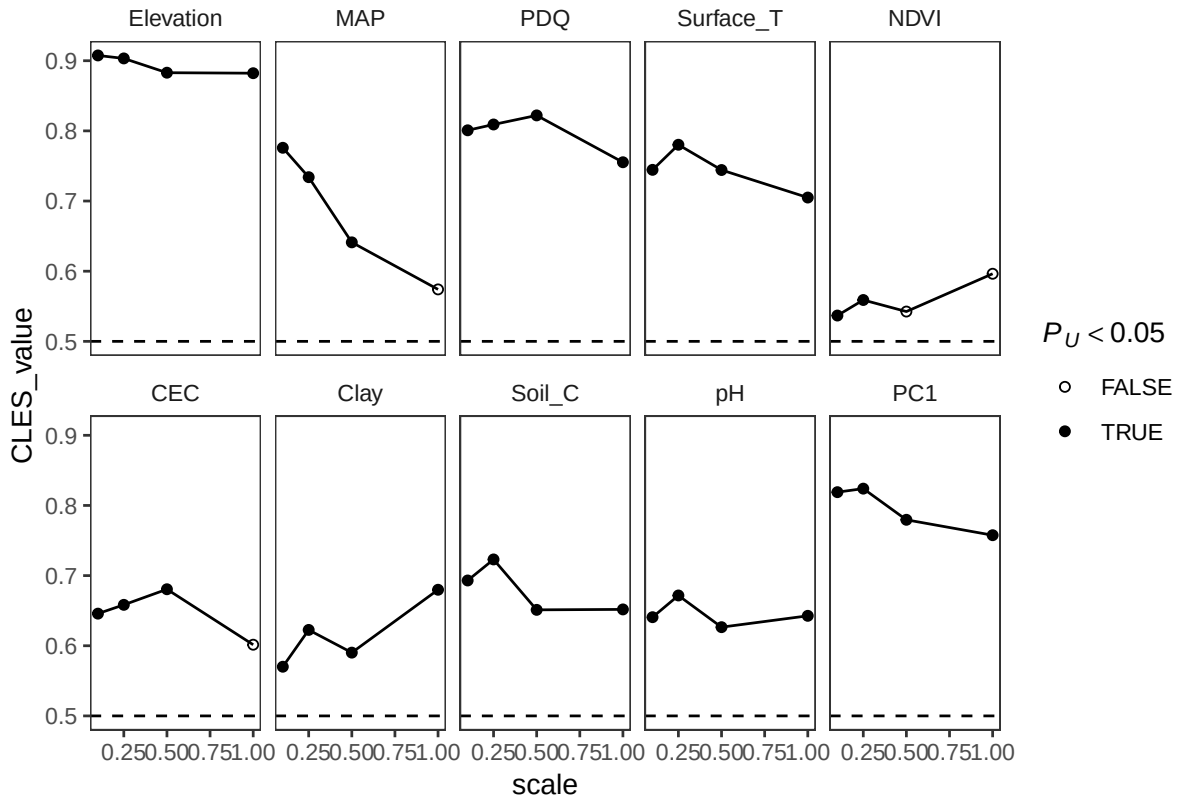
```
# Summarise those models
CLES_model_summaries <- CLES_models %>%
  map_df(.id = "variable", tidy) %>%
  filter(term != "(Intercept)") %>%
  mutate(sig = case_when(
    p.value <= 0.05 ~ "*",
    p.value <= 0.10 ~ ".",
    TRUE            ~ " "
  )) %>%
  mutate(variable = factor(variable, levels = var_names %>%
     str_replace_all(" ", "_") %>%
     c("PC1")
  )) %>%
  mutate_if(is.numeric, round, digits = 3) %>%
  dplyr::select(variable, estimate, p.value, sig)
CLES_model_summaries
```

```
## # A tibble: 10 x 4
##    variable  estimate p.value sig
##    <fct>        <dbl>   <dbl> <chr>
##  1 Elevation   -0.029   0.135 " "
##  2 MAP         -0.224   0.028 *
##  3 PDQ         -0.055   0.26  " "
##  4 Surface_T   -0.062   0.207 " "
##  5 NDVI         0.059   0.134 " "
##  6 CEC         -0.054   0.361 " "
##  7 Clay         0.104   0.143 " "
##  8 Soil_C      -0.065   0.27  " "
##  9 pH          -0.013   0.729 " "
## 10 PC1         -0.076   0.059 .
```

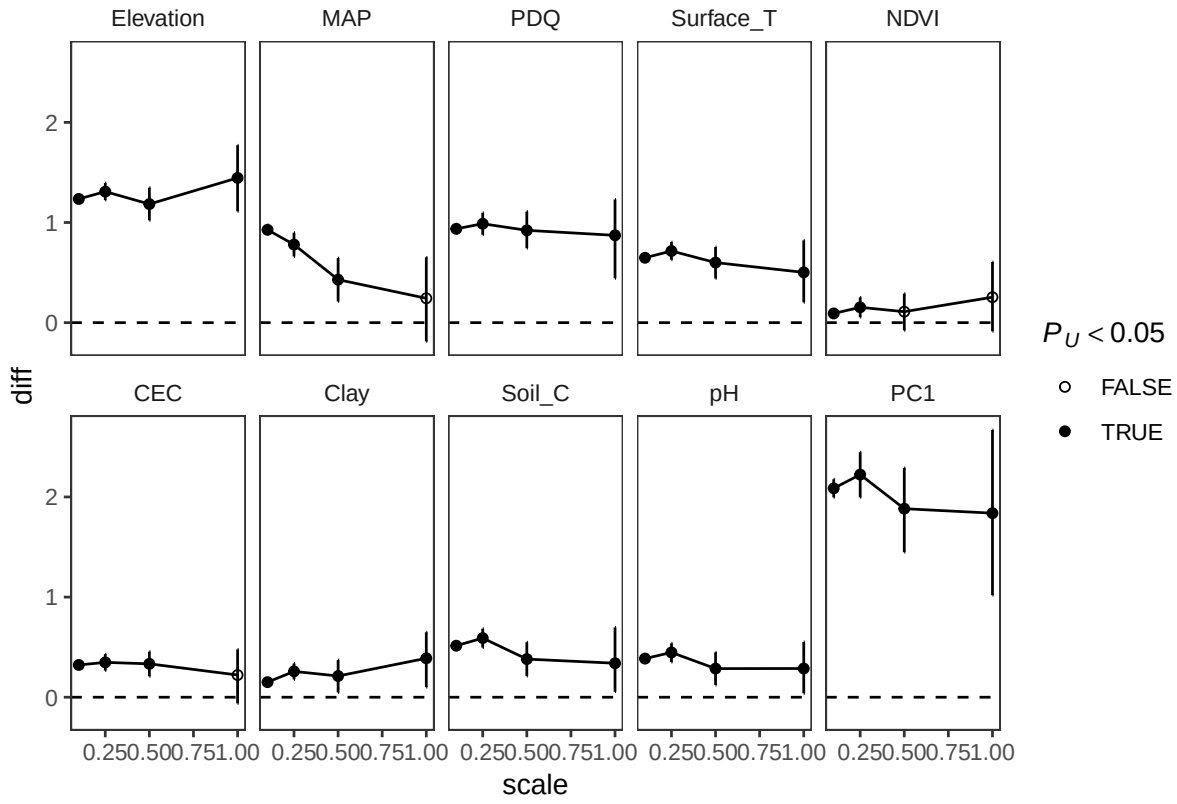
```
heterogeneity %>%  #heterogeneity_df %>%
  bind_rows(.id = "scale") %>%
  gather(
    variable, heterogeneity_value,
    -region, -scale#, -lon, -lat
  ) %>%
  mutate(variable = factor(variable, levels = var_names %>%
    str_replace_all(" ", "_") %>%
    c("PC1")
  )) %>%
  ggplot(aes(as.factor(scale), heterogeneity_value, fill = region)) +
    geom_boxplot() +
    facet_wrap(~variable, nrow = 2)
```




```
ggplot(CLES_results) +
  aes(scale, CLES_value, group = variable) +
  geom_hline(yintercept = 0.5, lty = "dashed") +
  geom_line() +
  geom_point(aes(shape = P_U < 0.05)) +
  scale_shape_manual(name = bquote(italic("P"["U"]) < 0.05), values = c(1, 19)) +
  facet_wrap(~variable, nrow = 2)
```




```
ggplot(CLES_results) +
  aes(scale, diff, group = variable) +
  geom_hline(yintercept = 0.0, lty = "dashed") +
  geom_line() +
  geom_errorbar(aes(ymin = U_low, ymax = U_upp), width = 0) +
  geom_point(aes(shape = P_U < 0.05)) +
  scale_shape_manual(name = bquote(italic("P"["U"]) < 0.05), values = c(1, 19)) +
  facet_wrap(~variable, nrow = 2)
```



2. Comparing & decomposing regions' species richness

```
# Assign a variable to the global environment,
# not simply the parent environment (as with <<-),
# with the same name
assign_global <- function(x) {
  assign(
    x     = deparse(substitute(x)),
    value = x,
    envir = .GlobalEnv
  )
}

# Read in and assign all polygon objects to global environment
import_region_polygons <- function(borders_dir =
                                     here("data/derived-data/borders")) {

  # GCFR ----------------------------------------------------------------------

  GCFR_border          <- readOGR(glue("{borders_dir}/GCFR_border"))
  GCFR_border_buffered <- readOGR(glue("{borders_dir}/GCFR_border_buffered"))
  GCFR_box             <- readOGR(glue("{borders_dir}/GCFR_box"))
  GCFR_QDS             <- readOGR(glue("{borders_dir}/GCFR_QDS"))
  assign_global(GCFR_border)
  assign_global(GCFR_border_buffered)
  assign_global(GCFR_box)
  assign_global(GCFR_QDS)

  # SWAFR ---------------------------------------------------------------------
```

```
  SWAFR_border          <- readOGR(glue("{borders_dir}/SWBP_Mike-Cramer"))
  SWAFR_border_buffered <- readOGR(glue("{borders_dir}/SWAFR_border_buffered"))
  SWAFR_box             <- readOGR(glue("{borders_dir}/SWAFR_box"))
  SWAFR_QDS             <- readOGR(glue("{borders_dir}/SWAFR_QDS"))
  assign_global(SWAFR_border)
  assign_global(SWAFR_border_buffered)
  assign_global(SWAFR_box)
  assign_global(SWAFR_QDS)

  # FIXME: Why are these shapefile imports throwing non-fatal errors/warnings?
  # TODO: Add GIS-std-checkers here too
}

# Include lon/lat when converting from Raster* to data.frame
raster2df <- function(r) {
  lon_lat <- xyFromCell(r, 1:ncell(r))
  colnames(lon_lat) <- c("lon", "lat")
  df <- as.data.frame(log10(r))
  df <- cbind(lon_lat, df)
  df
}
```

```
import_region_polygons()
```

```
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\GCFR_border", layer: "LA_CUR
## with 2 features
## It has 1 fields
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\GCFR_border_buffered", layer
## with 1 features
## It has 1 fields
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\GCFR_box", layer: "value"
## with 1 features
## It has 1 fields
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\GCFR_QDS", layer: "areakm2"
## with 1920 features
## It has 4 fields
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\SWBP_Mike-Cramer", layer: "S
## with 1 features
## It has 1 fields
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\SWAFR_border_buffered", laye
## with 1 features
## It has 1 fields
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\SWAFR_box", layer: "value"
## with 1 features
## It has 1 fields
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\user\Desktop\Cape-vs-SWA\data\derived-data\borders\SWAFR_QDS", layer: "areakm2"
## with 2464 features
## It has 4 fields
```

```
Larsen_grid <- rbind(GCFR_QDS, SWAFR_QDS)
Larsen_grid$hdgc <- str_remove(Larsen_grid$qdgc, ".$")
```

```
Larsen_grid$dgc  <- str_remove(Larsen_grid$hdgc, ".$")
```

```
heterogeneity_w_coords <- map2(GCFR_heterogeneity, SWAFR_heterogeneity,
  ~ na.exclude(rbind(
    cbind(region = "GCFR",  raster2df(.x)),
    cbind(region = "SWAFR", raster2df(.y))
  ))
)
heterogeneity <- map2(heterogeneity, heterogeneity_w_coords, full_join)

heterogeneity$QDS$QDS <- heterogeneity$QDS %$%
  SpatialPoints(
    coords      = data.frame(x = lon, y = lat),
    proj4string = crs(Larsen_grid)
  ) %over%
  Larsen_grid %>%
  pull(qdgc)

heterogeneity$HDS$HDS <- heterogeneity$HDS %$%
  SpatialPoints(
    coords      = data.frame(x = lon, y = lat),
    proj4string = crs(Larsen_grid)
  ) %over%
  Larsen_grid %>%
  pull(hdgc)

heterogeneity$DS$DS <- heterogeneity$DS %$%
  SpatialPoints(
    coords      = data.frame(x = lon, y = lat),
    proj4string = crs(Larsen_grid)
  ) %over%
  Larsen_grid %>%
  pull(dgc)
```

```
GCFR_species_occ <- read_rds(here(
  "data/derived-data/flora",
  "trimmed_GCFR_clean_flora_spdf_species"
))
SWAFR_species_occ <- read_rds(here(
  "data/derived-data/flora",
  "trimmed_SWAFR_clean_flora_spdf_species"
))
species_occ <- rbind(GCFR_species_occ, SWAFR_species_occ)

species_occ$QDS <- species_occ %over%
  Larsen_grid %>%
  pull(qdgc)
species_occ@data$QDS %<>% as.character()
species_occ$HDS <- str_remove(species_occ$QDS, ".$")
species_occ$DS  <- str_remove(species_occ$HDS, ".$")

QDS_richness <- species_occ@data %>%
  group_by(QDS) %>%
  summarise(QDS_richness = length(unique(species)))
mean_QDS_richness <- QDS_richness %>%
  mutate(HDS = str_remove(QDS, ".$")) %>%
  group_by(HDS) %>%
  summarise(mean_QDS_richness = mean(QDS_richness))
```

```r
HDS_richness <- species_occ@data %>%
  group_by(HDS) %>%
  summarise(HDS_richness = length(unique(species)))
mean_HDS_richness <- HDS_richness %>%
  mutate(DS = str_remove(HDS, ".$")) %>%
  group_by(DS) %>%
  summarise(mean_HDS_richness = mean(HDS_richness))
mean_QDS_richness2 <- QDS_richness %>%
  mutate(DS = str_remove(QDS, ".{2}$")) %>%
  group_by(DS) %>%
  summarise(mean_QDS_richness2 = mean(QDS_richness))
DS_richness <- species_occ@data %>%
  group_by(DS) %>%
  summarise(DS_richness = length(unique(species)))

data <- heterogeneity[-1]
data$QDS %<>%
  as_tibble() %>%
  full_join(QDS_richness) %>%
  na.exclude()
data$HDS %<>%
  as_tibble() %>%
  full_join(mean_QDS_richness) %>%
  full_join(HDS_richness) %>%
  na.exclude() %>%
  mutate(
    QDS_turnover      = HDS_richness - mean_QDS_richness,
    QDS_turnover_prop = QDS_turnover / HDS_richness
  )
data$DS %<>%
  as_tibble() %>%
  full_join(mean_HDS_richness) %>%
  full_join(mean_QDS_richness2) %>%
  full_join(DS_richness) %>%
  na.exclude() %>%
  mutate(
    HDS_turnover       = DS_richness - mean_HDS_richness,
    HDS_turnover2      = DS_richness - mean_QDS_richness2,
    HDS_turnover_prop  = HDS_turnover/DS_richness,
    HDS_turnover2_prop = HDS_turnover2/DS_richness
  )
```

```r
m1 <- lm(QDS_richness ~ PC1, data$QDS)
m2 <- lm(log(QDS_richness) ~ PC1, data$QDS)
m3 <- lm(log10(QDS_richness) ~ PC1, data$QDS)
AIC(m1, m2, m3)
```

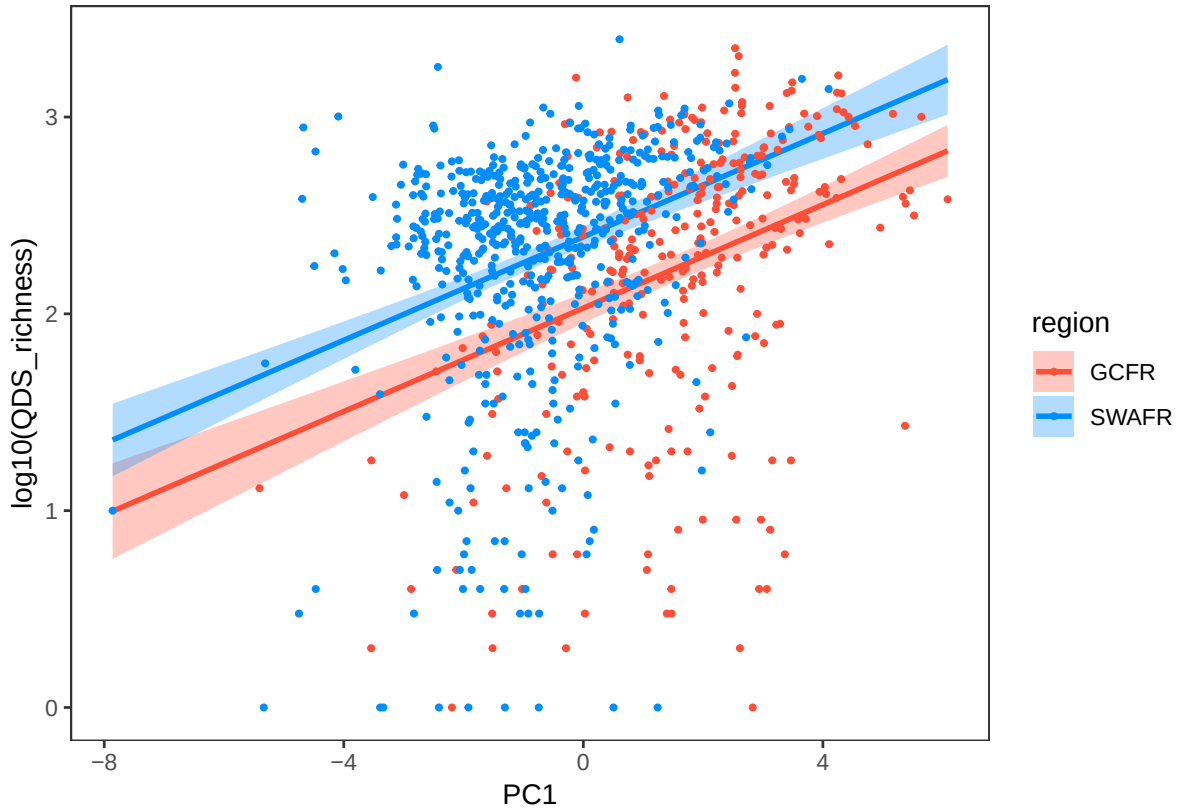
```
##    df       AIC
## m1  3 12595.318
## m2  3  3137.526
## m3  3  1664.625
```

```r
# Choose m3
m4 <- lm(log10(QDS_richness) ~ PC1 + region, data$QDS)
m5 <- lm(log10(QDS_richness) ~ PC1 * region, data$QDS)
AIC(m3, m4, m5)
```

```
##    df      AIC
## m3  3 1664.625
```

```
## m4  4 1617.737
## m5  5 1614.166
```

```
# Choose m4
visreg::visreg(m4,
  xvar = "PC1", by = "region", overlay = TRUE,
  gg = TRUE
)
```



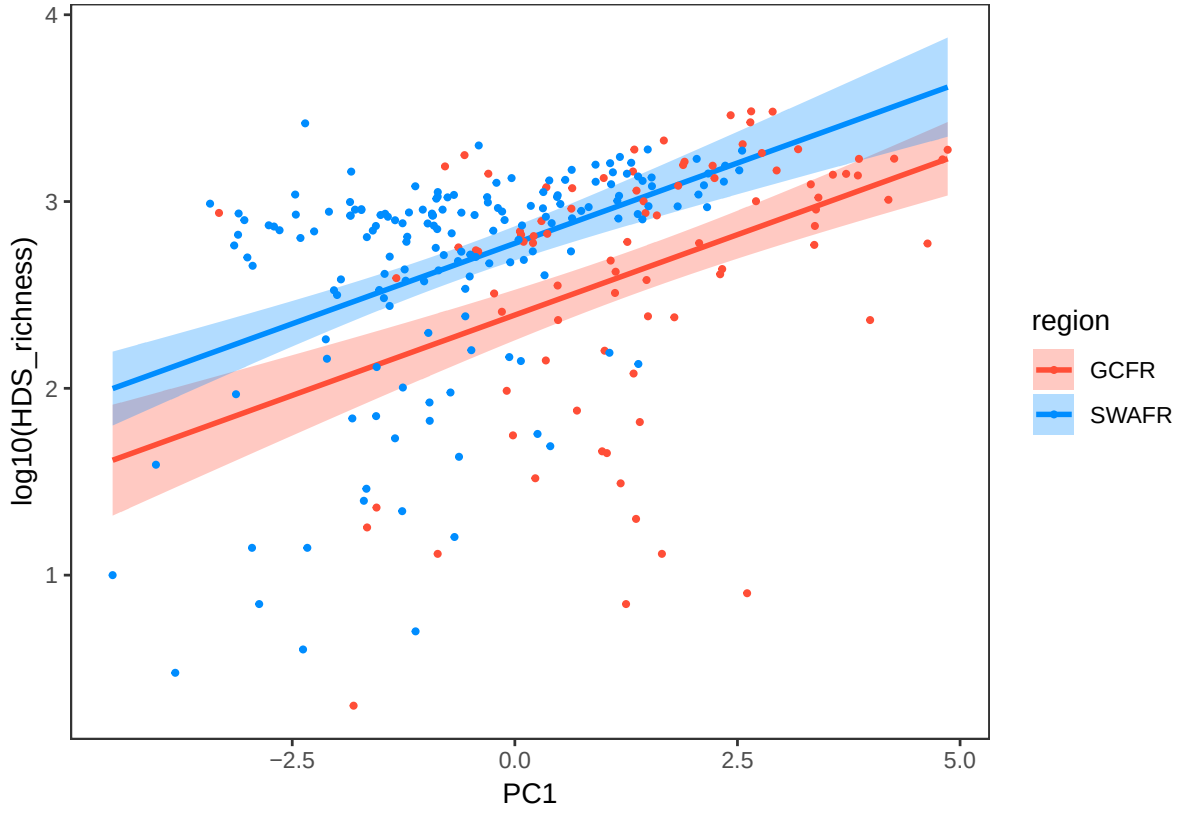

```
#ggplot(data$QDS, aes(PC1, QDS_richness)) +
#  geom_smooth(method = lm, formula = y ~ x + colour) +
#  geom_point(aes(colour = region)) +
#  scale_y_log10()

m1 <- lm(HDS_richness ~ PC1, data$HDS)
m2 <- lm(log(HDS_richness) ~ PC1, data$HDS)
m3 <- lm(log10(HDS_richness) ~ PC1, data$HDS)
AIC(m1, m2, m3)
```

```
##    df       AIC
## m1  3 3886.3993
## m2  3  868.9062
## m3  3  448.5538
```

```
# Choose m3
m4 <- lm(log10(HDS_richness) ~ PC1 + region, data$HDS)
m5 <- lm(log10(HDS_richness) ~ PC1 * region, data$HDS)
AIC(m3, m4, m5)
```

```
##    df      AIC
## m3  3 448.5538
## m4  4 432.2665
## m5  5 434.2659
```

```
# Choose m4
visreg::visreg(m4,
  xvar = "PC1", by = "region", overlay = TRUE,
  gg = TRUE
)
```




```
#ggplot(data$HDS, aes(PC1, HDS_richness, colour = region)) +
#  geom_smooth(method = lm, formula = y ~ x) +
#  geom_point() +
#  scale_y_log10()

m1 <- lm(DS_richness ~ PC1, data$DS)
m2 <- lm(log(DS_richness) ~ PC1, data$DS)
m3 <- lm(log10(DS_richness) ~ PC1, data$DS)
AIC(m1, m2, m3)
```

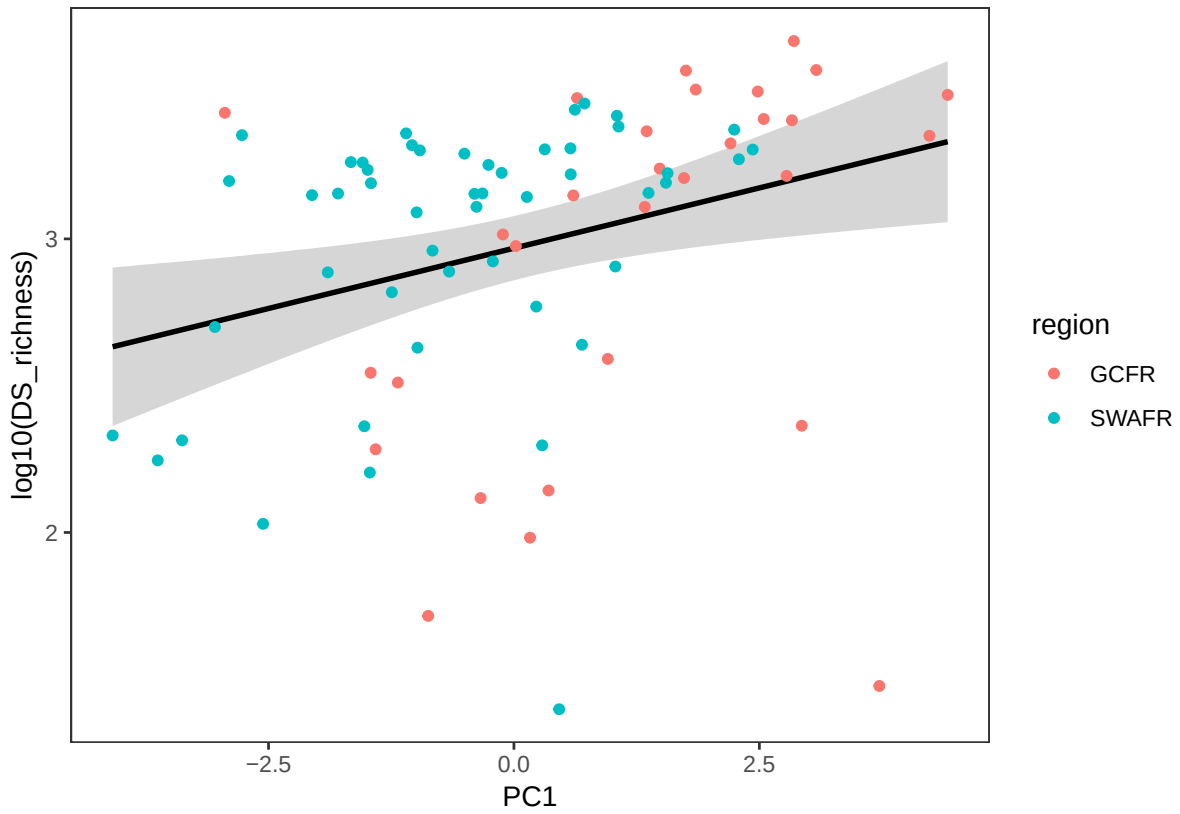
```
##    df       AIC
## m1  3 1325.0771
## m2  3  250.3610
## m3  3  116.9159
```

```
# Choose m3 (m2, but marginally, so m3 for consistency)
m4 <- lm(log10(DS_richness) ~ PC1 + region, data$DS)
m5 <- lm(log10(DS_richness) ~ PC1 * region, data$DS)
AIC(m3, m4, m5)
```

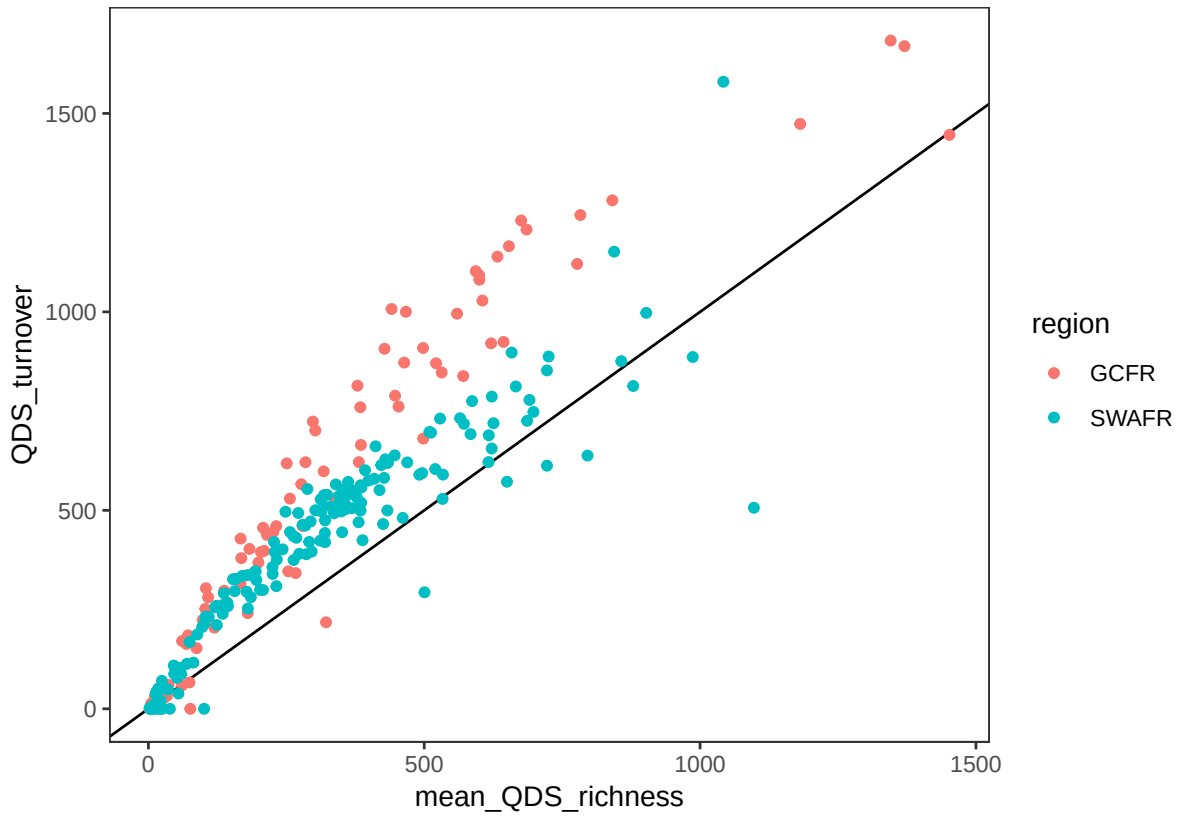
```
##    df      AIC
## m3  3 116.9159
## m4  4 115.3485
## m5  5 117.2877
```

```
# Choose m3 still
ggplot(data$DS, aes(PC1, log10(DS_richness))) +
```

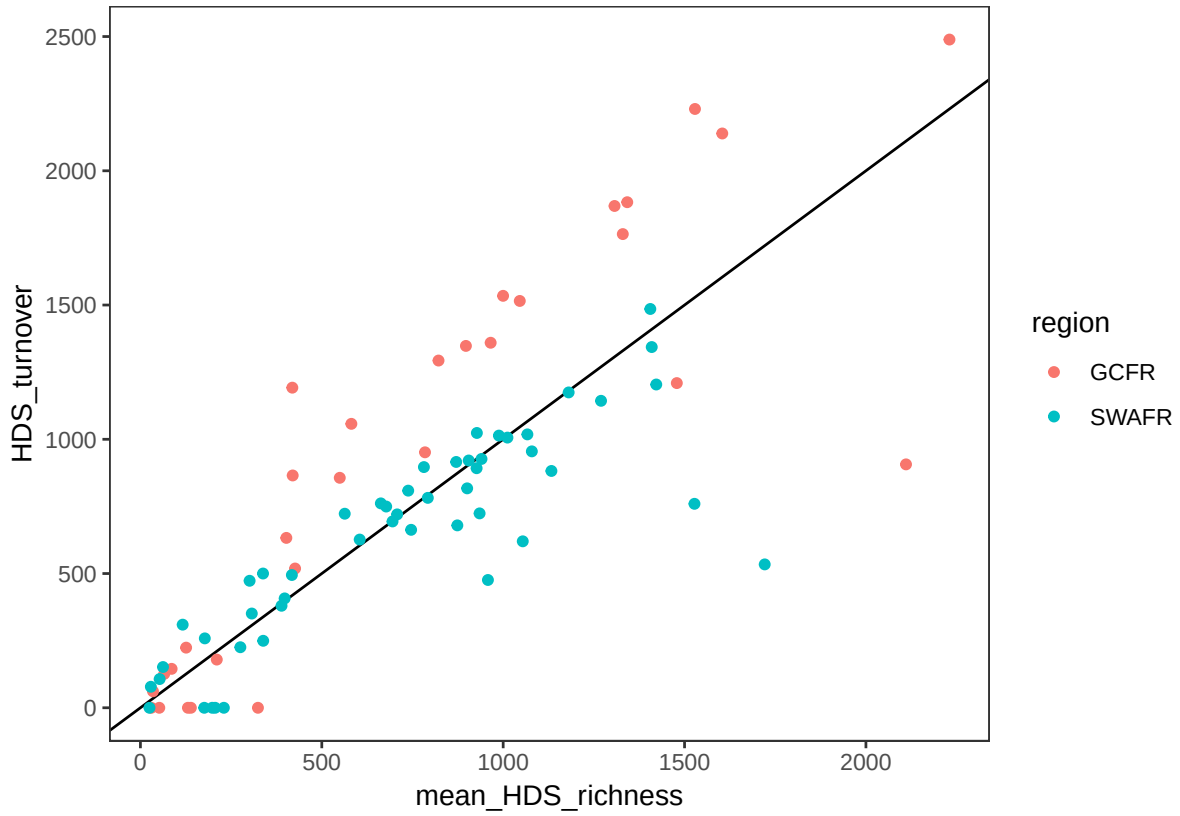
```
  geom_smooth(method = lm, colour = "black") +
  geom_point(aes(colour = region))
```



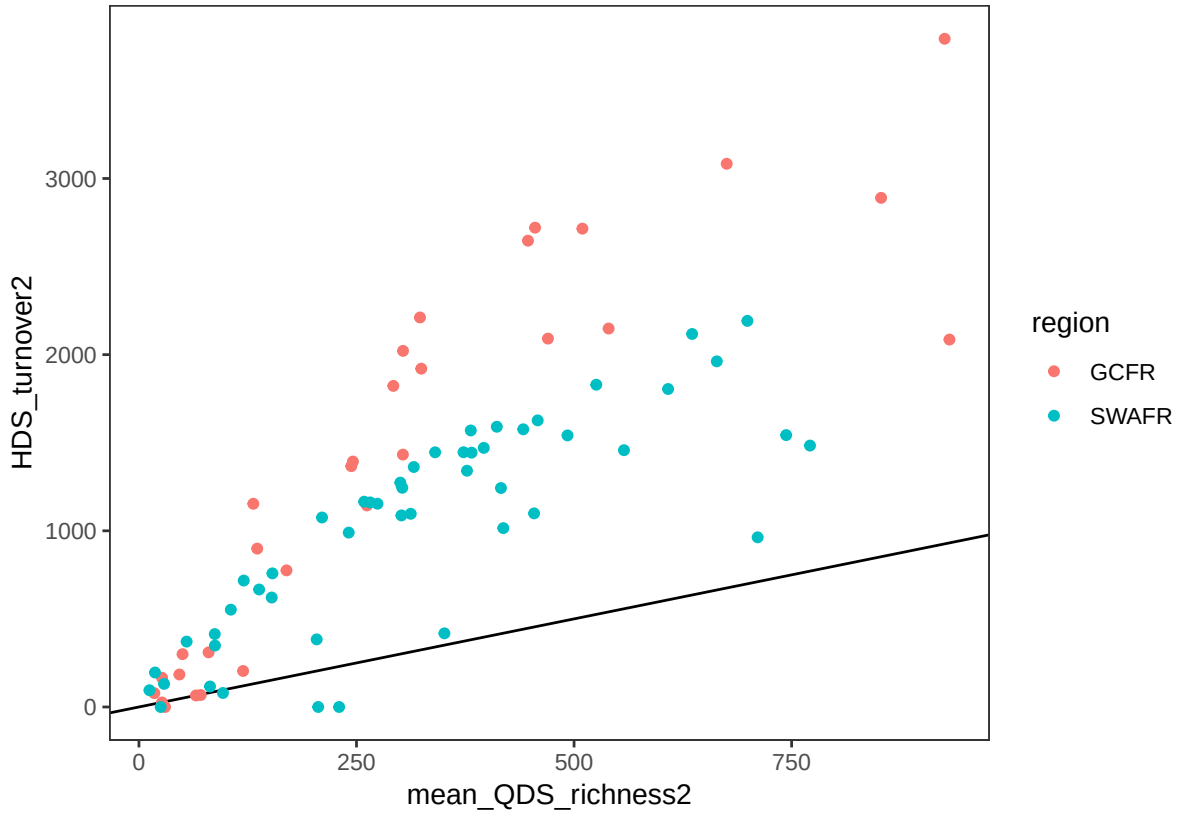

```
ggplot(data$HDS, aes(mean_QDS_richness, QDS_turnover, colour = region)) +
  geom_abline(intercept = 0, slope = 1) +
  geom_point()
```



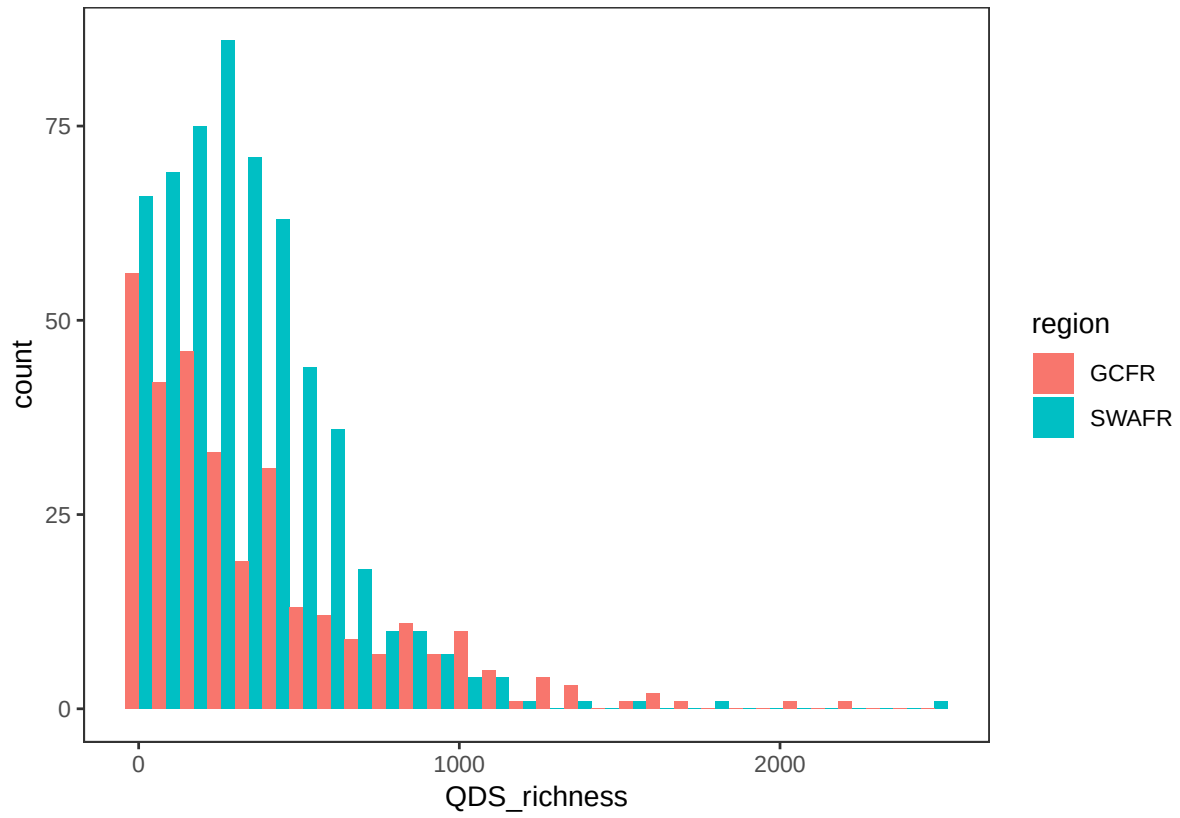

```
ggplot(data$DS, aes(mean_HDS_richness, HDS_turnover, colour = region)) +
  geom_abline(intercept = 0, slope = 1) +
  geom_point()
```



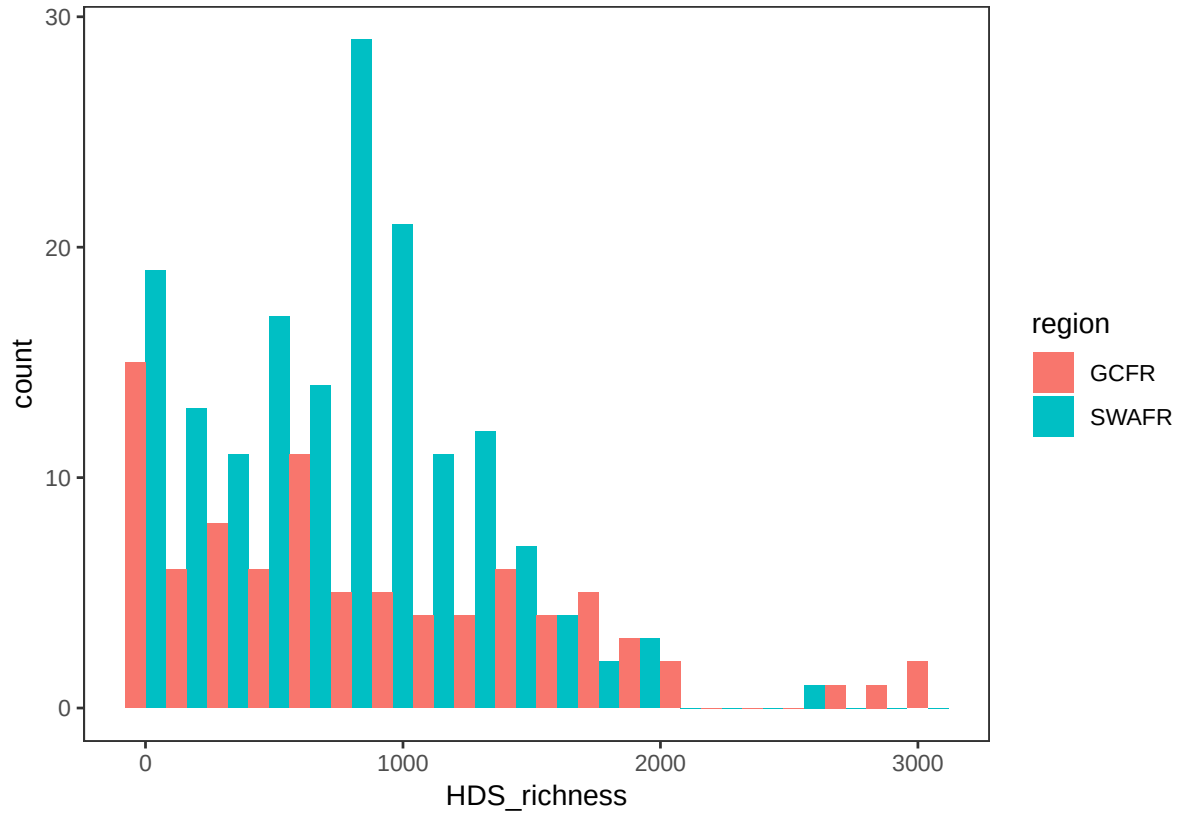
```
ggplot(data$DS, aes(mean_QDS_richness2, HDS_turnover2, colour = region)) +
  geom_abline(intercept = 0, slope = 1) +
  geom_point()
```



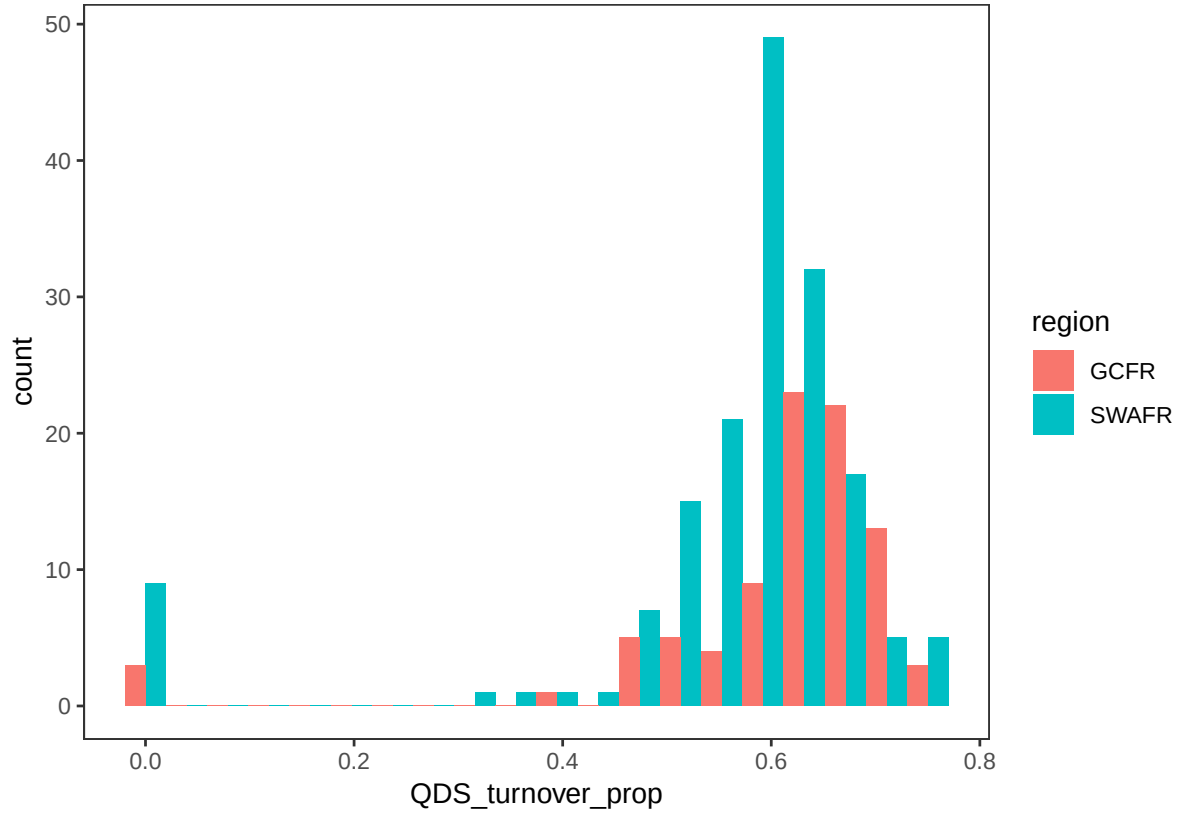

```
ggplot(data$QDS, aes(QDS_richness, fill = region)) +
  geom_histogram(bins = 30, position = "dodge")
```



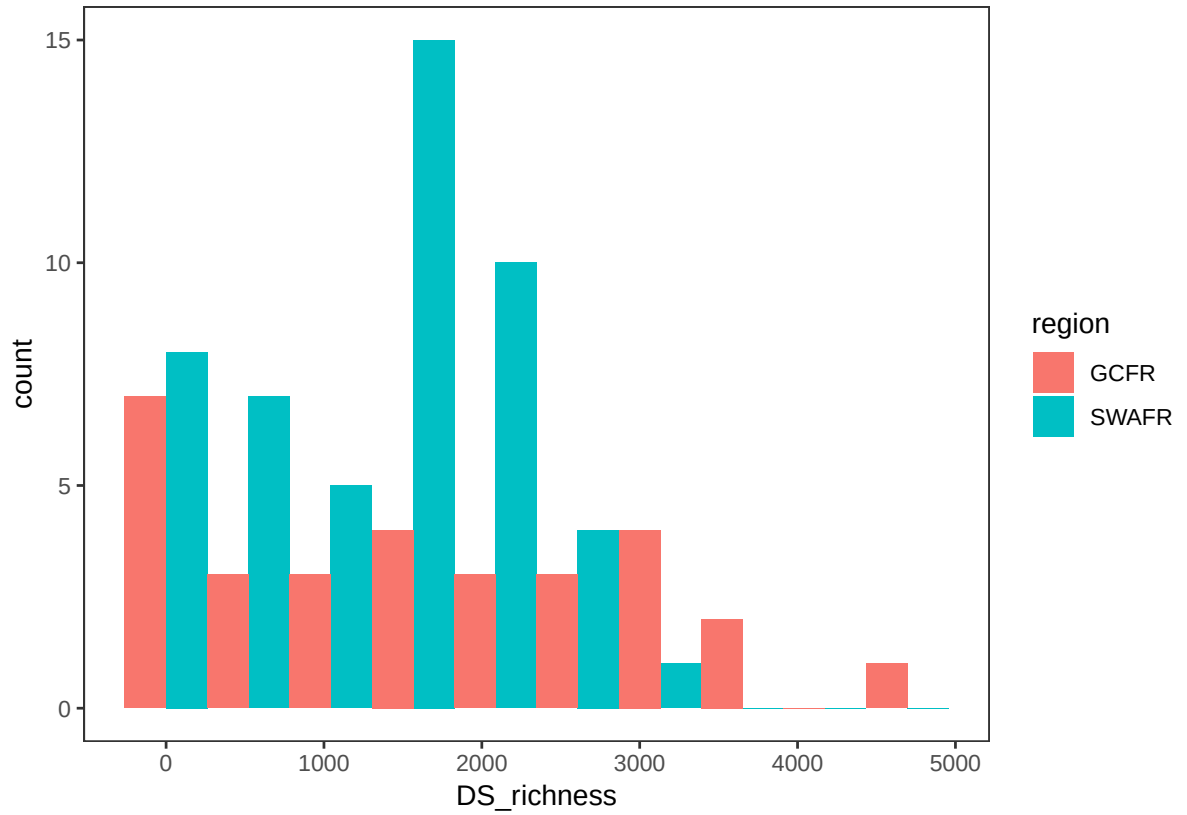

```
ggplot(data$HDS, aes(HDS_richness, fill = region)) +
  geom_histogram(bins = 20, position = "dodge")
```



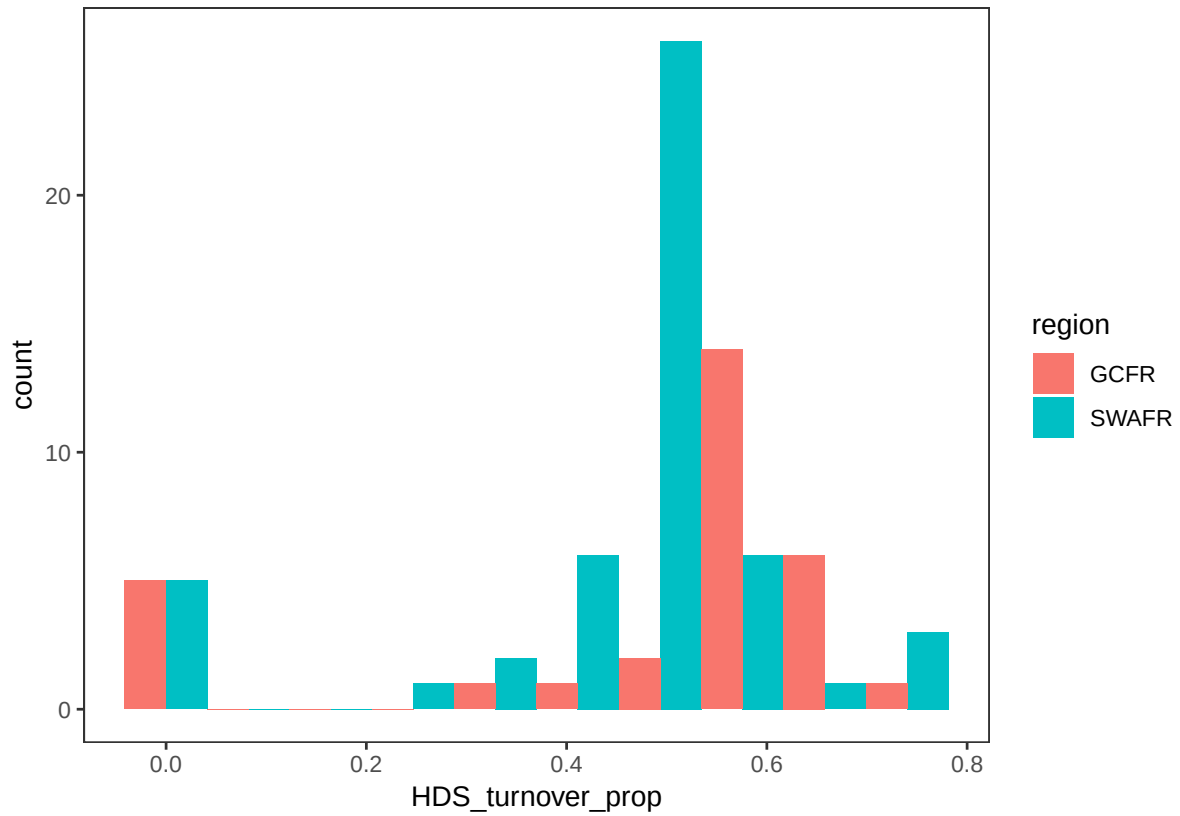

```
ggplot(data$HDS, aes(QDS_turnover_prop, fill = region)) +
  geom_histogram(bins = 20, position = "dodge")
```



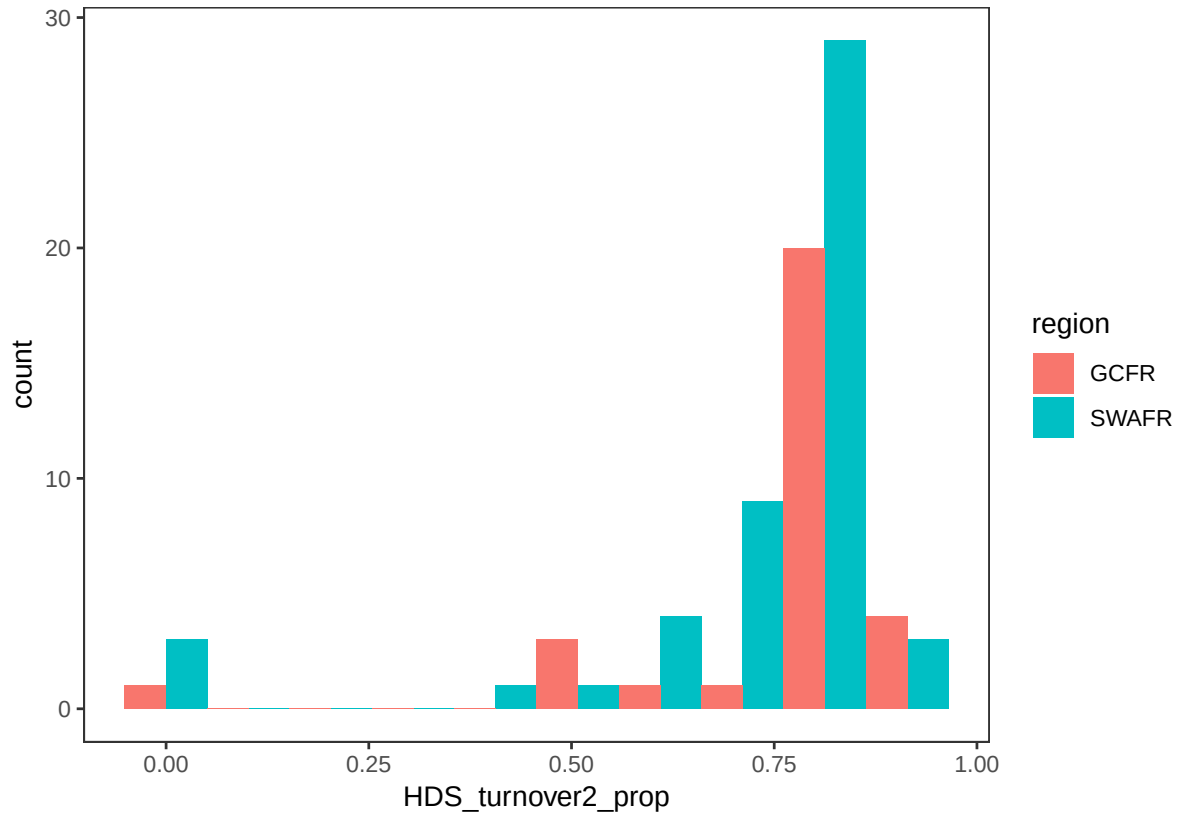

```
ggplot(data$DS, aes(DS_richness, fill = region)) +
  geom_histogram(bins = 10, position = "dodge")
```



```
ggplot(data$DS, aes(HDS_turnover_prop, fill = region)) +
  geom_histogram(bins = 10, position = "dodge")
```




```
ggplot(data$DS, aes(HDS_turnover2_prop, fill = region)) +
  geom_histogram(bins = 10, position = "dodge")
```




```
wilcox.test(QDS_richness ~ region, data$QDS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  QDS_richness by region
## W = 86760, p-value = 0.4572
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(HDS_richness ~ region, data$HDS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  HDS_richness by region
## W = 7522.5, p-value = 0.5791
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(DS_richness  ~ region, data$DS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  DS_richness by region
## W = 833, p-value = 0.4123
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(QDS_turnover       ~ region, data$HDS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  QDS_turnover by region
## W = 8024.5, p-value = 0.143
```

```
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(QDS_turnover_prop  ~ region, data$HDS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  QDS_turnover_prop by region
## W = 9787.5, p-value = 3.144e-06
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(HDS_turnover       ~ region, data$DS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  HDS_turnover by region
## W = 919.5, p-value = 0.09273
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(HDS_turnover_prop  ~ region, data$DS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  HDS_turnover_prop by region
## W = 1024.5, p-value = 0.006417
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(HDS_turnover2_prop ~ region, data$DS)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  HDS_turnover2_prop by region
## W = 1014.5, p-value = 0.008695
## alternative hypothesis: true location shift is not equal to 0
```

```
#data %>%
#  bind_rows(.id = "scale")
```

3. Environmental heterogeneity as an explanation of species richness

3.1. Univariate models

```
predictor_names <- c(str_replace_all(var_names, " ", "_"), "PC1")

models_non_region <- map(predictor_names,
  ~lm(paste("QDS_richness ~", .x), data$QDS)
)
names(models_non_region) <- predictor_names
models_add_region <- map(predictor_names,
  ~lm(paste("QDS_richness ~", .x, "+ region"), data$QDS)
)
names(models_add_region) <- predictor_names
models_int_region <- map(predictor_names,
  ~lm(paste("QDS_richness ~", .x, "* region"), data$QDS)
)
names(models_int_region) <- predictor_names
```

```
knitr::kable(pmap_dfr(
  .l  = list(models_non_region, models_add_region, models_int_region),
  .id = "variable",
  .f  = ~ AIC(..1, ..2, ..3) %>%
    mutate(
      model_rank = 1:3,
      model_type = c(" ", "+", "x")[model_rank],
      delta_AIC  = AIC - min(AIC),
      best_model = (model_rank == min(model_rank[delta_AIC < 2]))
    ) %>%
    filter(best_model) %>%
    dplyr::select(-df, -AIC, -model_rank, -best_model)
))
```

variable	model_type	delta_AIC
Elevation	x	0.0000000
MAP	x	0.0000000
PDQ	+	0.3187415
Surface_T	x	0.0000000
NDVI	x	0.0000000
CEC		1.6508805
Clay		0.0000000
Soil_C	x	0.0000000
pH		0.7960374
PC1	x	0.0000000

```
models_non_region <- map(predictor_names,
  ~lm(paste("HDS_richness ~", .x), data$HDS)
)
names(models_non_region) <- predictor_names
models_add_region <- map(predictor_names,
  ~lm(paste("HDS_richness ~", .x, "+ region"), data$HDS)
)
names(models_add_region) <- predictor_names
models_int_region <- map(predictor_names,
  ~lm(paste("HDS_richness ~", .x, "* region"), data$HDS)
)
names(models_int_region) <- predictor_names
pmap_dfr(
  .l  = list(models_non_region, models_add_region, models_int_region),
  .id = "variable",
  .f  = ~ AIC(..1, ..2, ..3) %>%
    mutate(
      model_rank = 1:3,
      model_type = c(" ", "+", "x")[model_rank],
      delta_AIC  = AIC - min(AIC),
      best_model = (model_rank == min(model_rank[delta_AIC < 2]))
    ) %>%
    filter(best_model) %>%
    dplyr::select(-df, -AIC, -model_rank, -best_model)
)
```

```
##     variable model_type  delta_AIC
## 1  Elevation            0.00000000
## 2        MAP            0.00000000
## 3        PDQ            1.13704138
## 4  Surface_T            0.00000000
```

```
## 5       NDVI            0.00000000
## 6        CEC            0.73543867
## 7       Clay            0.00000000
## 8     Soil_C            0.00000000
## 9         pH            0.06957038
## 10       PC1          + 0.00000000
```

```
models_non_region <- map(predictor_names,
  ~lm(glue("DS_richness ~", .x), data$DS)
)
names(models_non_region) <- predictor_names
models_add_region <- map(predictor_names,
  ~lm(paste("DS_richness ~", .x, "+ region"), data$DS)
)
names(models_add_region) <- predictor_names
models_int_region <- map(predictor_names,
  ~lm(paste("DS_richness ~", .x, "* region"), data$DS)
)
names(models_int_region) <- predictor_names
pmap_dfr(
  .l  = list(models_non_region, models_add_region, models_int_region),
  .id = "variable",
  .f  = ~ AIC(..1, ..2, ..3) %>%
    mutate(
      model_rank = 1:3,
      model_type = c(" ", "+", "x")[model_rank],
      delta_AIC  = AIC - min(AIC),
      best_model = (model_rank == min(model_rank[delta_AIC < 2]))
    ) %>%
    filter(best_model) %>%
    dplyr::select(-df, -AIC, -model_rank, -best_model)
)
```

```
##     variable model_type delta_AIC
## 1  Elevation            0.0000000
## 2        MAP            0.0000000
## 3        PDQ            0.0000000
## 4  Surface_T            0.0000000
## 5       NDVI            0.0000000
## 6        CEC            0.2467964
## 7       Clay            0.0000000
## 8     Soil_C            0.0000000
## 9         pH            0.0000000
## 10       PC1            0.0000000
```

3.2. Multivariate models

...

```
full_formula <- predictor_names[predictor_names != "PC1"] %>%
  {c(., paste(., "* region"))} %>%
  paste(collapse = " + ")

m_QDS_richness <- lm(glue("QDS_richness ~ {full_formula}"), data$QDS)
m_HDS_richness <- lm(glue("HDS_richness ~ {full_formula}"), data$HDS)
m_DS_richness  <- lm(glue("DS_richness ~ {full_formula}"), data$DS)

m_QDS_richness %<>% step(direction = "backward", trace = 0)
m_HDS_richness %<>% step(direction = "backward", trace = 0)
m_DS_richness  %<>% step(direction = "backward", trace = 0)
```

```r
# Reparameterise models to {*}:regionGCFR & {*}:regionSWAFR
# a.o.t. {*}*region, so that the figure of the effects actually represents
# each region, not the baseline (GCFR) and "relative SWAFR"
# (and that would cause inconsistencies too when their is no interaction with
# region term for a roughness variable).
reparameterise <- function(m) {
  response <- colnames(m$model)[[1]]
  data <- data %$% {
    if      (response == "QDS_richness") QDS
    else if (response == "HDS_richness") HDS
    else if (response == "DS_richness")  DS
  }
  preds_w_interactions <- m %$%
    coefficients %>%
    names() %>%
    magrittr::extract(str_which(., ":regionSWAFR"))
  reparameterisation <- preds_w_interactions %<>%
    str_remove(":regionSWAFR") %>%
    {glue("-{.}")} %>%
    paste(collapse = " ")
  update(m,
    formula = glue(". ~ . {reparameterisation}"),
    data    = data
  )
}
# Test:
#   a <- m_HDS_richness
#   b <- reparameterise(m_HDS_richness)
#   AIC(a, b) # same model! :)
m_QDS_richness %<>% reparameterise()
m_HDS_richness %<>% reparameterise()
m_DS_richness  %<>% reparameterise()
```

```r
models <- list(
  QDS_richness = m_QDS_richness,
  HDS_richness = m_HDS_richness,
  DS_richness  = m_DS_richness
)
models_summary <- models %>%
  map_df(.id = "response", tidy, conf.int = TRUE) %>%
  dplyr::select(-std.error, -statistic) %>%
  filter(term != "(Intercept)")

models_R2 <- models %>%
  map_df(.id = "response", glance) %>%
  dplyr::select(response, adj.r.squared)

models_summary %<>% full_join(models_R2)

glance(m_QDS_richness)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value    df logLik    AIC
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl> <int>  <dbl>  <dbl>
## 1     0.233         0.221  282.      18.9 1.46e-41    15 -6226. 12484.
## # ... with 3 more variables: BIC <dbl>, deviance <dbl>, df.residual <int>
```

```r
glance(m_HDS_richness)
```

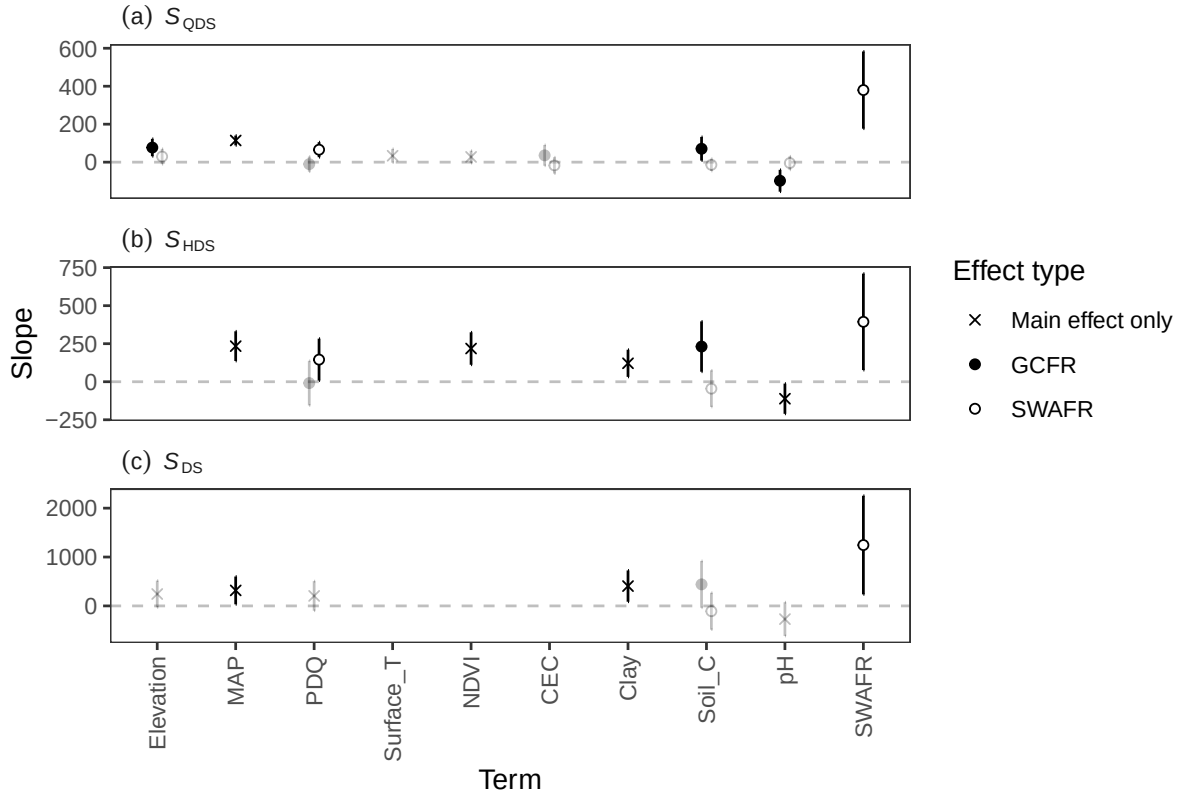
```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value    df logLik   AIC   BIC
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl> <int>  <dbl> <dbl> <dbl>
## 1     0.350         0.325  490.      14.4 1.20e-18    10 -1913. 3849. 3887.
## # ... with 2 more variables: deviance <dbl>, df.residual <int>
```

```r
glance(m_DS_richness)
```

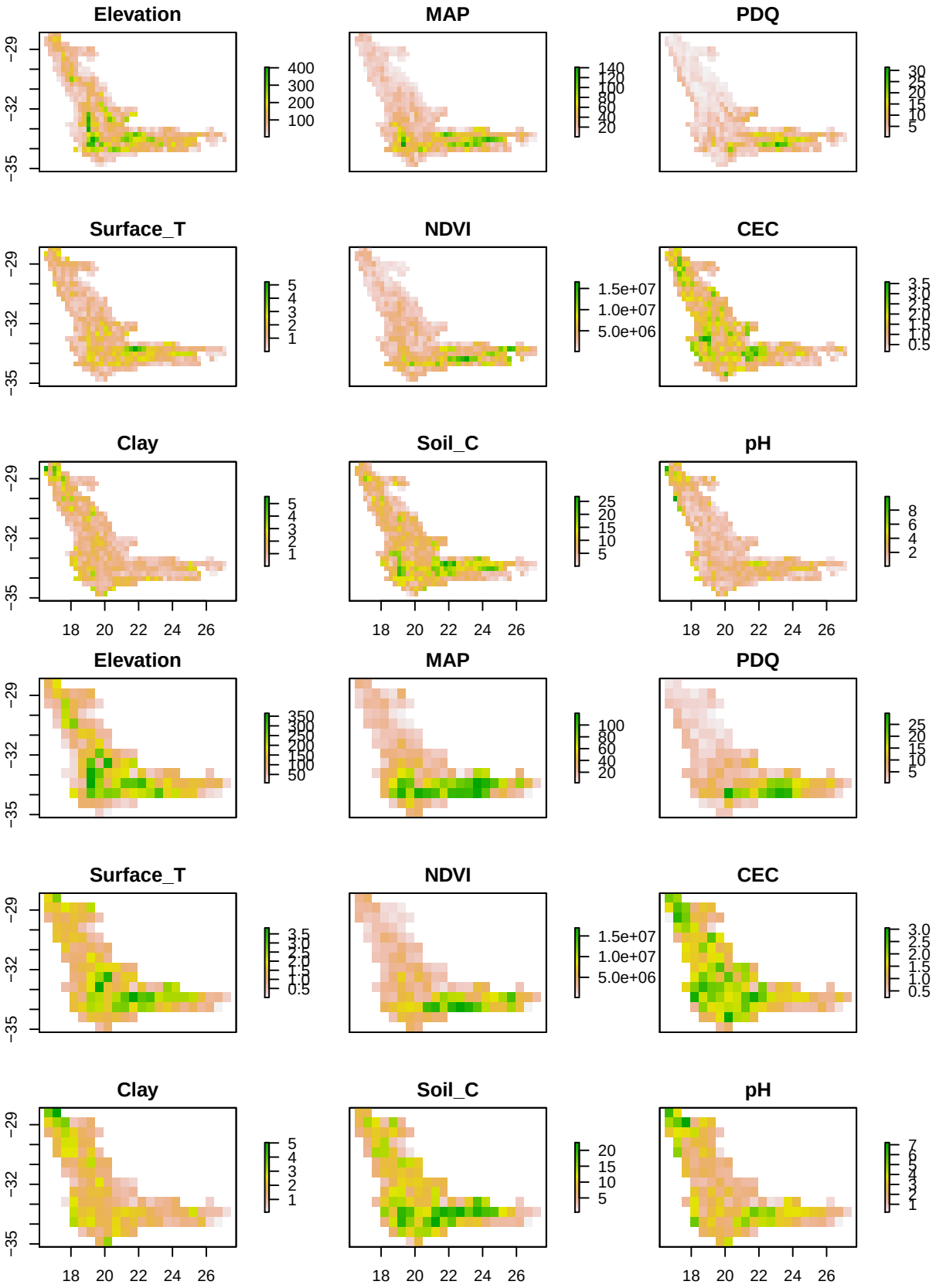
```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df logLik   AIC   BIC
##       <dbl>         <dbl> <dbl>     <dbl>   <dbl> <int>  <dbl> <dbl> <dbl>
## 1     0.392         0.323  856.      5.72 1.29e-5     9  -649. 1318. 1342.
## # ... with 2 more variables: deviance <dbl>, df.residual <int>
```

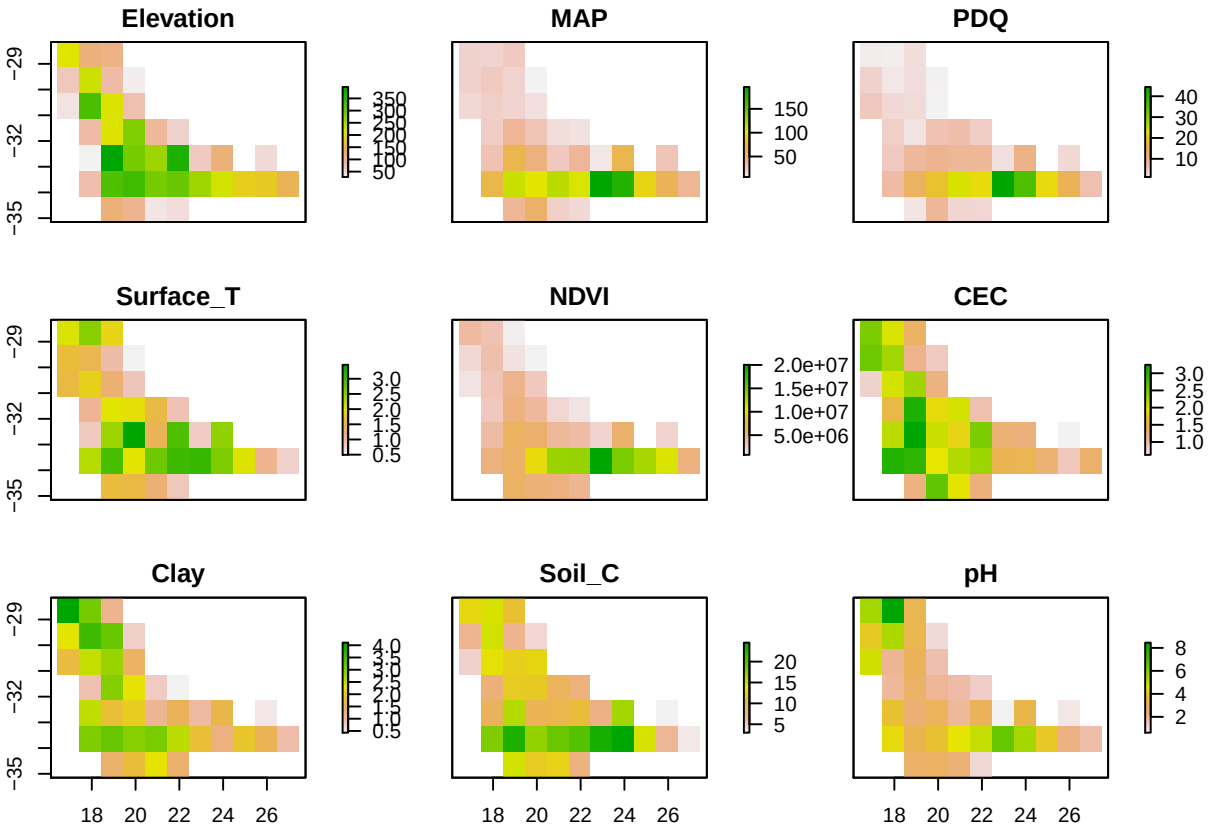
```r
models_summary_for_plot <- models_summary %>%
  mutate(
    response = case_when(
      response == "QDS_richness" ~ "(a)~~italic(S)[QDS]",
      response == "HDS_richness" ~ "(b)~~italic(S)[HDS]",
      response == "DS_richness"  ~ "(c)~~italic(S)[DS]"
    ),
    region =
      case_when(
        str_detect(term, "regionSWAFR") ~ "SWAFR",
        str_detect(term, "regionGCFR")  ~ "GCFR",
        TRUE                            ~ "Main effect only"
      ) %>%
      factor(levels = c("Main effect only", "GCFR", "SWAFR")),
    term = term %>%
      str_replace_all("\\.", " ") %>%
      str_remove_all("regionSWAFR:") %>%
      str_remove_all("regionGCFR:") %>%
      str_replace_all("regionSWAFR", "SWAFR") %>%
      factor(levels = c(str_replace_all(var_names, " ", "_"), "SWAFR")),
    sig = (p.value < 0.05)
  )
ggplot(models_summary_for_plot) +
  aes(
    term, estimate,
    fill = region, group = region, shape = region,
    alpha = sig
  ) +
  geom_hline(yintercept = 0, linetype = "dashed", colour = "grey75") +
  geom_errorbar(
    aes(ymin = conf.low, ymax = conf.high),
    position = position_dodge(width = 0.25),
    width = 0
  ) +
  geom_point(position = position_dodge(width = 0.25)) +
  labs(x = "Term", y = "Slope") +
  scale_fill_manual(values = c(NA, "black", "white")) +
  scale_shape_manual(values = c(4, 21, 21)) +
  scale_alpha_manual(values = c(0.25, 1)) +
  facet_wrap(~response, nrow = 3, scales = "free_y", labeller = label_parsed) +
  guides(
    fill = FALSE,
    shape = guide_legend(
```

```
      title = "Effect type",
      override.aes = list(fill = c(NA, "black", "white"))
    ),
    alpha = FALSE
  ) +
  theme(
    axis.text.x  = element_text(angle = 90, hjust = 1, vjust = 0.5),
    strip.text.x = element_text(angle =  0, hjust = 0)
  )
```



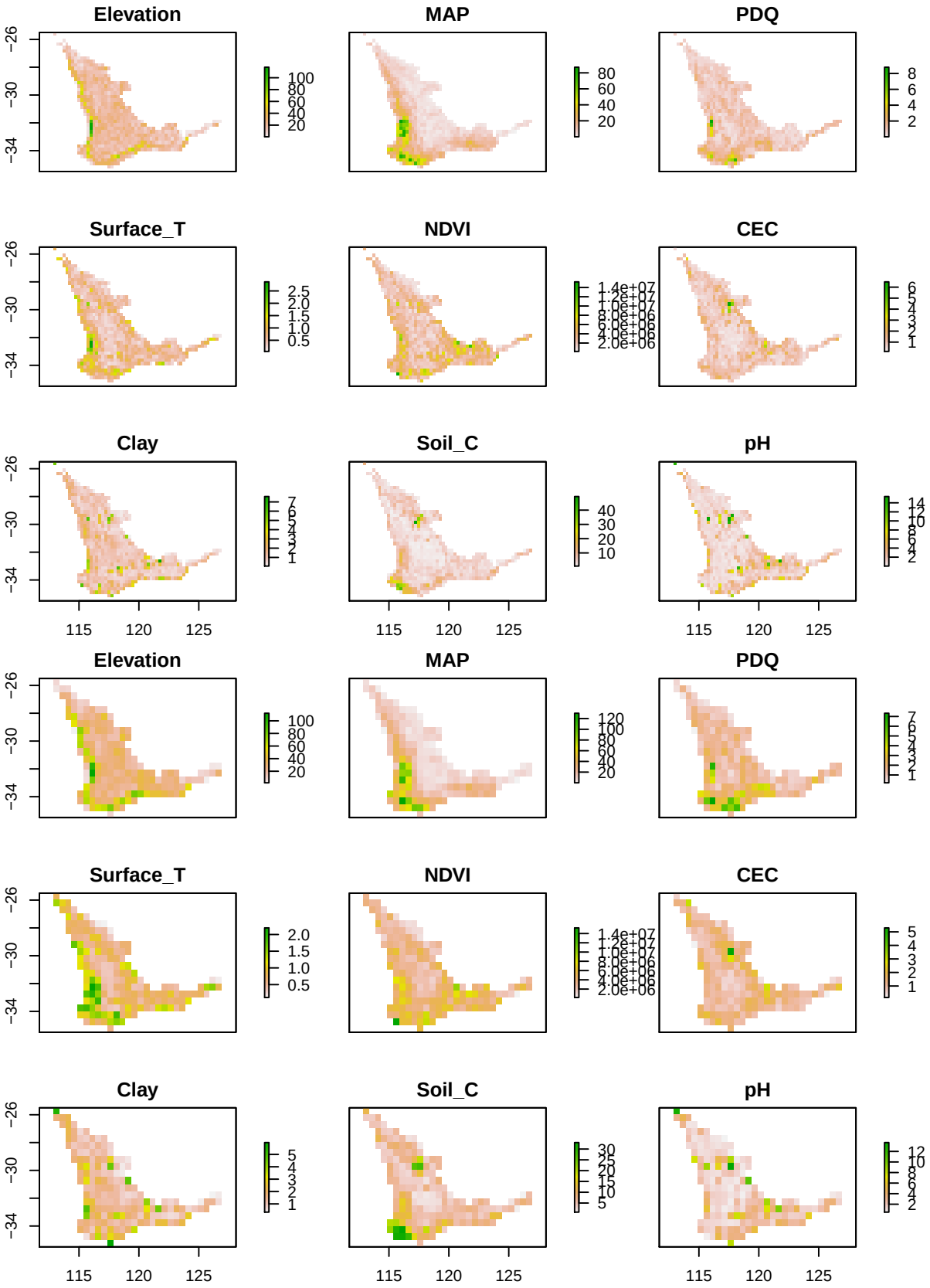

```
GCFR_heterogeneity2 <- list(
  QDS = aggregate(GCFR_variables, fact =  5, fun = sd),
  HDS = aggregate(GCFR_variables, fact = 10, fun = sd),
  DS  = aggregate(GCFR_variables, fact = 20, fun = sd)
)
map(GCFR_heterogeneity2, plot)
```

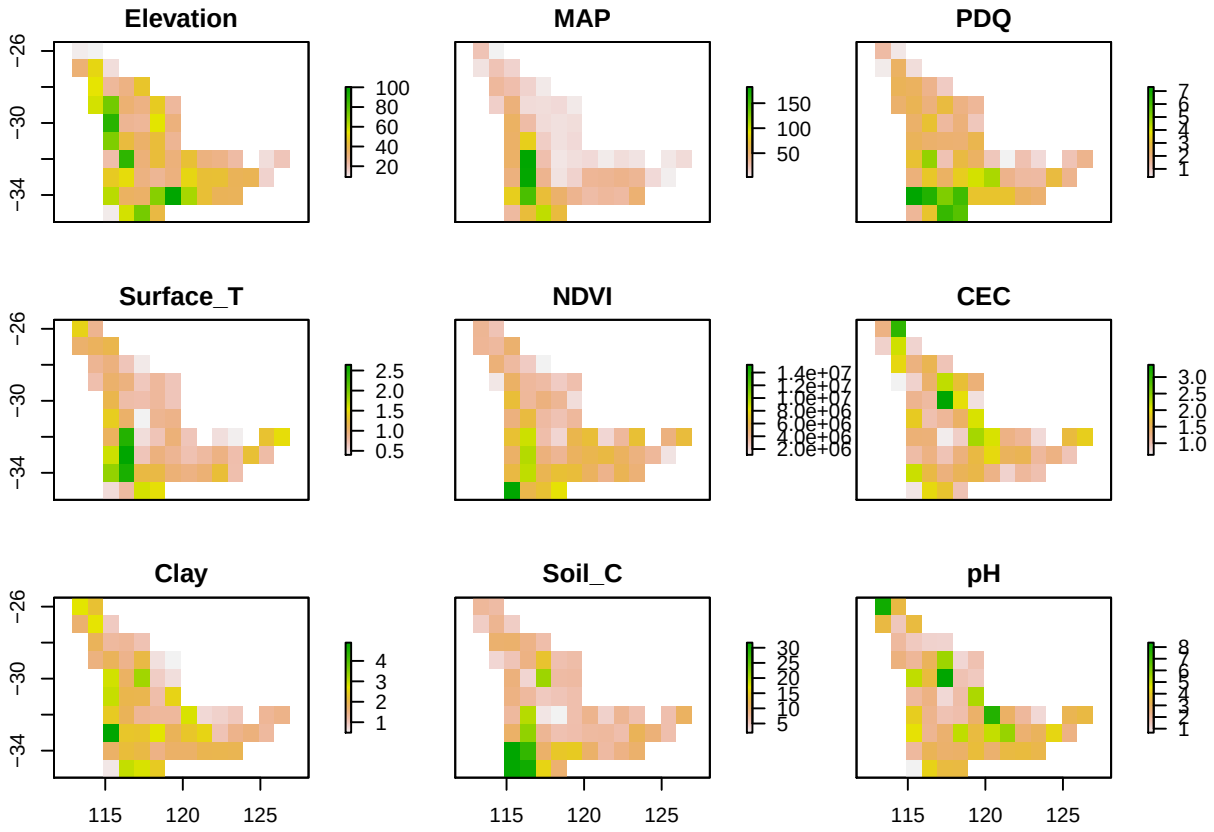

Elevation
MAP
PDQ
Surface_T
NDVI
CEC
Clay
Soil_C
pH
Elevation
MAP
PDQ
Surface_T
NDVI
CEC
Clay
Soil_C
pH




```
## $QDS
## NULL
##
## $HDS
## NULL
##
## $DS
## NULL
```

```
SWAFR_heterogeneity2 <- list(
  QDS = aggregate(SWAFR_variables, fact =  5, fun = sd),
  HDS = aggregate(SWAFR_variables, fact = 10, fun = sd),
  DS  = aggregate(SWAFR_variables, fact = 20, fun = sd)
)
map(SWAFR_heterogeneity2, plot)
```


Elevation
MAP
PDQ
Surface_T
NDVI
CEC
Clay
Soil_C
pH
Elevation
MAP
PDQ
Surface_T
NDVI
CEC
Clay
Soil_C
pH
−26
−30
−34
115
120
125



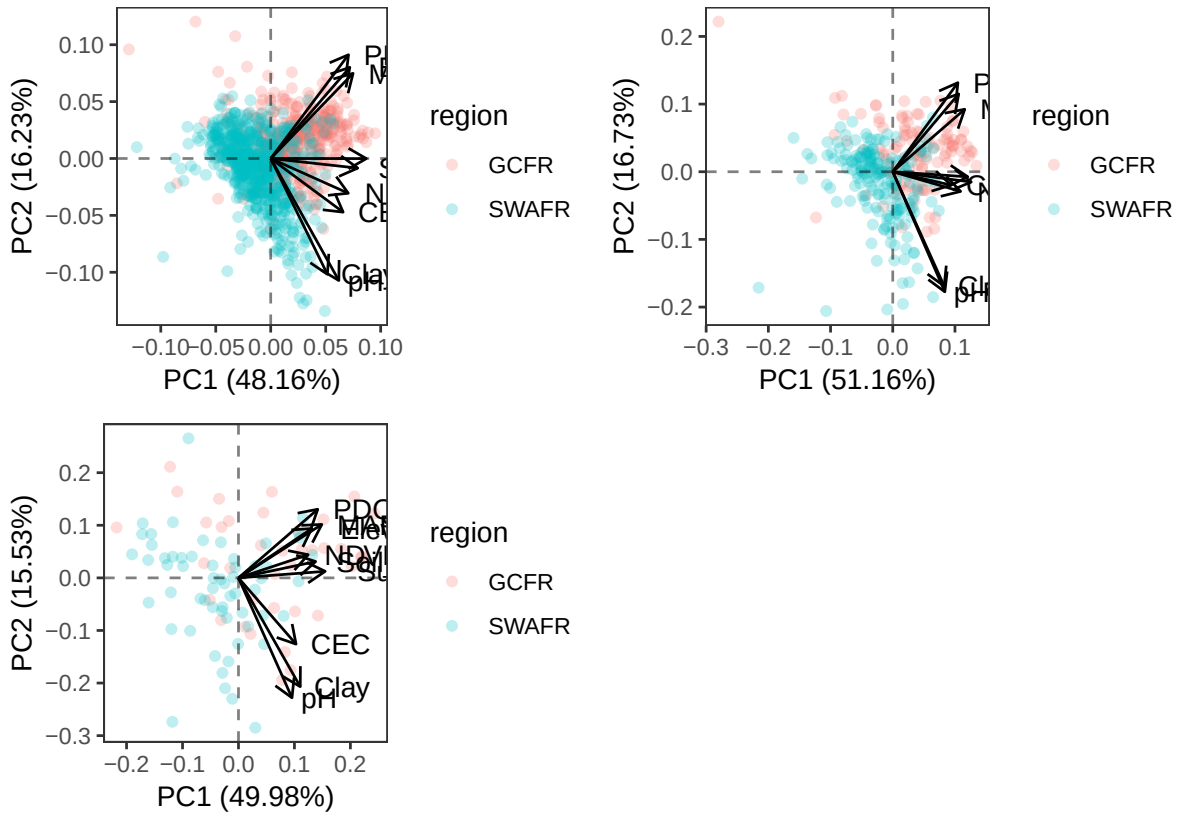

```
## $QDS
## NULL
##
## $HDS
## NULL
##
## $DS
## NULL
```

```
# Join regions' datasets
heterogeneity2 <- map2(GCFR_heterogeneity2, SWAFR_heterogeneity2,
  ~ na.exclude(rbind(
    cbind(region = "GCFR",  as.data.frame(log10(.x))),
    cbind(region = "SWAFR", as.data.frame(log10(.y)))
  ))
)
heterogeneity2_PCAs <- map(heterogeneity2,
  ~prcomp(.x[, -1], center = TRUE, scale. = TRUE)
)
map(heterogeneity2_PCAs, summary)
```

```
## $QDS
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5     PC6
## Standard deviation     2.0820 1.2085 0.86871 0.80698 0.72347 0.63164
## Proportion of Variance 0.4816 0.1623 0.08385 0.07236 0.05816 0.04433
## Cumulative Proportion  0.4816 0.6439 0.72774 0.80009 0.85825 0.90258
##                           PC7     PC8    PC9
## Standard deviation     0.59160 0.54606 0.4781
## Proportion of Variance 0.03889 0.03313 0.0254
## Cumulative Proportion  0.94147 0.97460 1.0000
##
```

```
## $HDS
## Importance of components:
##                            PC1    PC2     PC3     PC4     PC5     PC6
## Standard deviation     2.1457 1.2270 0.89003 0.76637 0.66199 0.60262
## Proportion of Variance 0.5116 0.1673 0.08802 0.06526 0.04869 0.04035
## Cumulative Proportion  0.5116 0.6788 0.76687 0.83212 0.88082 0.92117
##                            PC7     PC8     PC9
## Standard deviation     0.5450 0.49093 0.41413
## Proportion of Variance 0.0330 0.02678 0.01906
## Cumulative Proportion  0.9542 0.98094 1.00000
##
## $DS
## Importance of components:
##                            PC1    PC2    PC3    PC4     PC5    PC6     PC7
## Standard deviation     2.1210 1.1822 0.9973 0.8469 0.63505 0.6206 0.50295
## Proportion of Variance 0.4999 0.1553 0.1105 0.0797 0.04481 0.0428 0.02811
## Cumulative Proportion  0.4999 0.6551 0.7657 0.8454 0.89016 0.9330 0.96106
##                            PC8     PC9
## Standard deviation     0.47383 0.35484
## Proportion of Variance 0.02495 0.01399
## Cumulative Proportion  0.98601 1.00000
```

```
# Force PC1 scores to be positive if all vars rotations are negative
heterogeneity2_PCAs %<>% map(function(PCA) {
  if (all(PCA$rotation[, 1] <= 0)) {
    message("Multiplying this one by -1")
    PCA$rotation[, 1] %<>% multiply_by(-1)
    PCA$x[, 1]        %<>% multiply_by(-1)
  }
  PCA
})
plot_grid(plotlist = map2(
  .x = heterogeneity2_PCAs,
  .y = heterogeneity2,
  .f =
    ~ autoplot(.x, data = .y, colour = "region",
      alpha = 0.25,
      loadings       = TRUE, loadings.colour      = "black",
      loadings.label = TRUE, loadings.label.colour = "black",
      loadings.label.hjust = -0.25
    ) +
    ggtitle(unique(.y$scale)) +
    geom_hline(yintercept = 0, linetype = "dashed", alpha = 0.5) +
    geom_vline(xintercept = 0, linetype = "dashed", alpha = 0.5)
))
```




```
PC1s2 <- map(heterogeneity2_PCAs, ~tibble(PC1 = .x$x[, 1]))
heterogeneity2 %<>% map2(PC1s2, ~cbind(.x, .y))
CLES2_results <- map2_dfr(
  .x = heterogeneity2 %>%
    map(filter, region == "GCFR") %>%
    map(dplyr::select, -region),
  .y = heterogeneity2 %>%
    map(filter, region == "SWAFR") %>%
    map(dplyr::select, -region),
  .id = "scale",  # for every spatial scale,
  ~ map2_df(
    .x = .x,
    .y = .y,
    .id = "variable",  # for every variable in each region,
    ~ tibble(
      CLES_value = CLES(.y, .x),  # calculate the CLES,
      U_test = wilcox.test(.x, .y, conf.int = TRUE) %>%  # & Mann-Whitney U-test
        tidy() %>%
        list()
    )
  )
)
CLES2_results %<>% mutate(
  variable = factor(variable, levels = var_names %>%
    str_replace_all(" ", "_") %>%
    c("PC1")
  ),
  scale = case_when(
    scale == "point1" ~ 0.10,
    scale == "QDS"    ~ 0.25,
    scale == "HDS"    ~ 0.50,
```

```
    scale == "DS"     ~ 1.00
  ),
  diff  = map_dbl(U_test, "estimate"),
  P_U   = map_dbl(U_test, "p.value"),
  U_low = map_dbl(U_test, "conf.low"),
  U_upp = map_dbl(U_test, "conf.high")
)
CLES2_results
```

```
## # A tibble: 30 x 8
##    scale variable  CLES_value U_test          diff       P_U   U_low  U_upp
##    <dbl> <fct>          <dbl> <list>         <dbl>     <dbl>   <dbl>  <dbl>
##  1  0.25 Elevation      0.930 <tibble [1 x~ 0.652  8.05e-114 0.613   0.690
##  2  0.25 MAP            0.760 <tibble [1 x~ 0.415  5.90e- 43 0.363   0.467
##  3  0.25 PDQ            0.854 <tibble [1 x~ 0.504  5.74e- 78 0.458   0.551
##  4  0.25 Surface_T      0.809 <tibble [1 x~ 0.327  6.02e- 60 0.293   0.361
##  5  0.25 NDVI           0.545 <tibble [1 x~ 0.0460 1.85e-  2 0.00748 0.0844
##  6  0.25 CEC            0.689 <tibble [1 x~ 0.157  1.93e- 23 0.128   0.186
##  7  0.25 Clay           0.597 <tibble [1 x~ 0.0827 2.76e-  7 0.0522  0.113
##  8  0.25 Soil_C         0.726 <tibble [1 x~ 0.252  6.53e- 33 0.214   0.288
##  9  0.25 pH             0.655 <tibble [1 x~ 0.179  3.02e- 16 0.139   0.219
## 10  0.25 PC1            0.826 <tibble [1 x~ 2.38   2.06e- 66 2.15    2.60
## # ... with 20 more rows
```

```
CLES2_models <- CLES2_results %>%
  split(.$variable) %>%
  map(~lm(CLES_value ~ scale, .x))
CLES2_models$Elevation
```

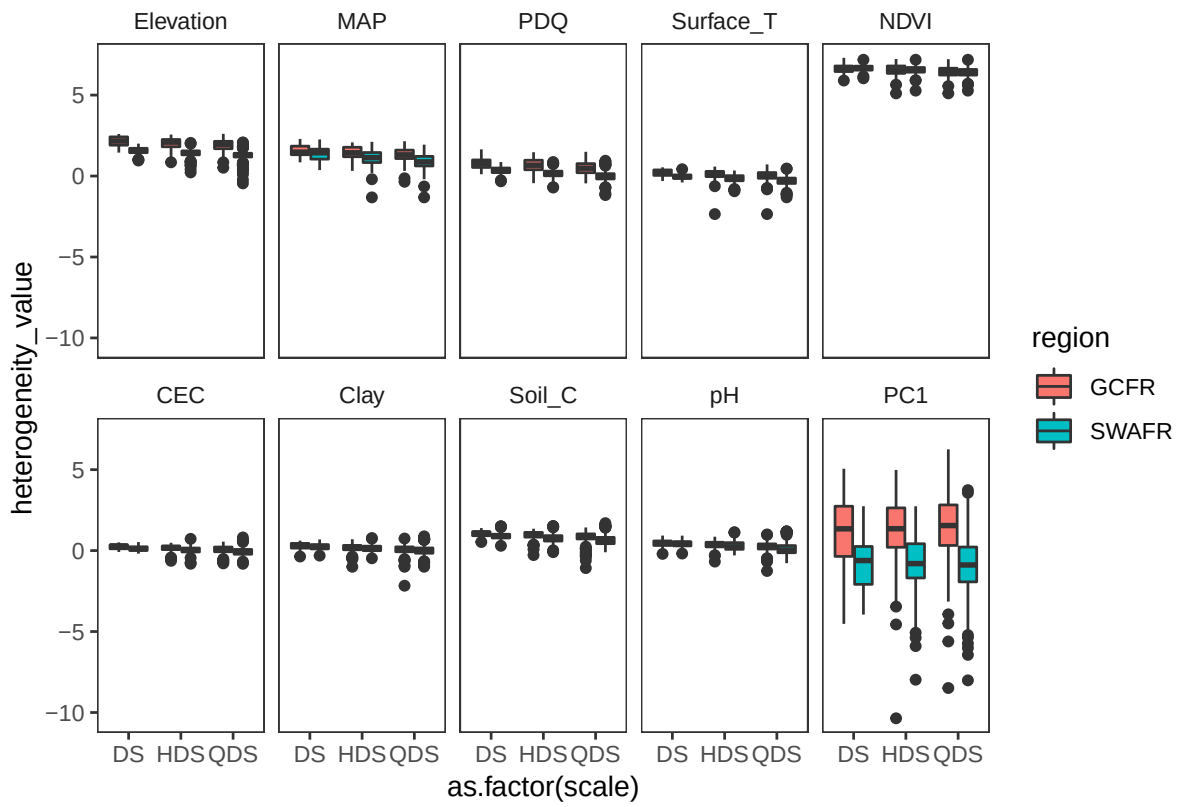
```
##
## Call:
## lm(formula = CLES_value ~ scale, data = .x)
##
## Coefficients:
## (Intercept)        scale
##     0.92611     -0.01698
```

```
# Summarise those models
CLES2_model_summaries <- CLES2_models %>%
  map_df(.id = "variable", tidy) %>%
  filter(term != "(Intercept)") %>%
  mutate(sig = case_when(
    p.value <= 0.05 ~ "*",
    p.value <= 0.10 ~ ".",
    TRUE            ~ " "
  )) %>%
  mutate(variable = factor(variable, levels = var_names %>%
     str_replace_all(" ", "_") %>%
     c("PC1")
  )) %>%
  mutate_if(is.numeric, round, digits = 3) %>%
  dplyr::select(variable, estimate, p.value, sig)
CLES2_model_summaries
```

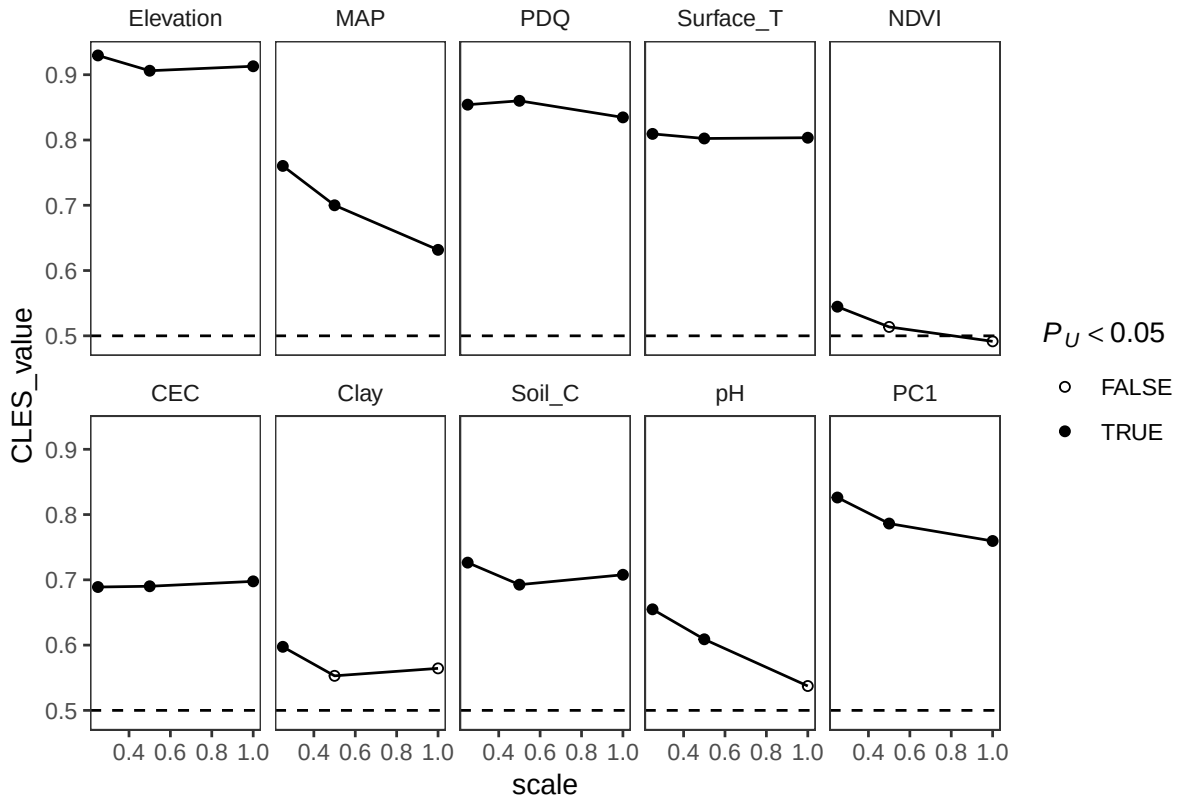
```
## # A tibble: 10 x 4
##    variable  estimate p.value sig
##    <fct>        <dbl>   <dbl> <chr>
##  1 Elevation   -0.017   0.638 " "
##  2 MAP         -0.166   0.098 .
##  3 PDQ         -0.03    0.355 " "
```

```
##  4 Surface_T   -0.006   0.553 " "
##  5 NDVI        -0.067   0.183 " "
##  6 CEC          0.012   0.134 " "
##  7 Clay        -0.034   0.614 " "
##  8 Soil_C      -0.017   0.75  " "
##  9 pH          -0.155   0.041 *
## 10 PC1         -0.084   0.194 " "
```

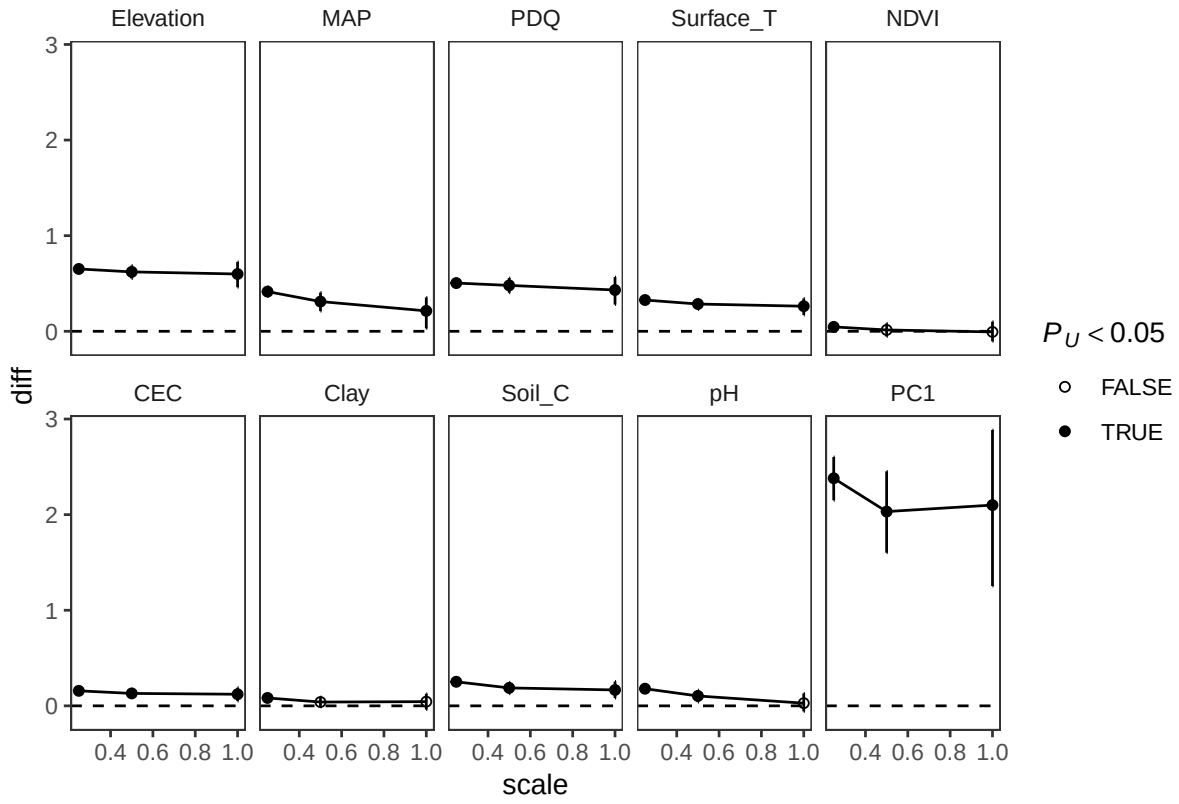
```
heterogeneity2 %>%  #heterogeneity_df %>%
  bind_rows(.id = "scale") %>%
  gather(
    variable, heterogeneity_value,
    -region, -scale#, -lon, -lat
  ) %>%
  mutate(variable = factor(variable, levels = var_names %>%
    str_replace_all(" ", "_") %>%
    c("PC1")
  )) %>%
  ggplot(aes(as.factor(scale), heterogeneity_value, fill = region)) +
    geom_boxplot() +
    facet_wrap(~variable, nrow = 2)
```




```
ggplot(CLES2_results) +
  aes(scale, CLES_value, group = variable) +
  geom_hline(yintercept = 0.5, lty = "dashed") +
  geom_line() +
  geom_point(aes(shape = P_U < 0.05)) +
  scale_shape_manual(name = bquote(italic("P"["U"]) < 0.05), values = c(1, 19)) +
  facet_wrap(~variable, nrow = 2)
```




```
ggplot(CLES2_results) +
  aes(scale, diff, group = variable) +
  geom_hline(yintercept = 0.0, lty = "dashed") +
  geom_line() +
  geom_errorbar(aes(ymin = U_low, ymax = U_upp), width = 0) +
  geom_point(aes(shape = P_U < 0.05)) +
  scale_shape_manual(name = bquote(italic("P"["U"]) < 0.05), values = c(1, 19)) +
  facet_wrap(~variable, nrow = 2)
```




```
heterogeneity2_w_coords <- map2(GCFR_heterogeneity2, SWAFR_heterogeneity2,
  ~ na.exclude(rbind(
    cbind(region = "GCFR",  raster2df(.x)),
    cbind(region = "SWAFR", raster2df(.y))
  ))
)
heterogeneity2 <- map2(heterogeneity2, heterogeneity2_w_coords, full_join)

heterogeneity2$QDS$QDS <- heterogeneity2$QDS %$%
  SpatialPoints(
    coords      = data.frame(x = lon, y = lat),
    proj4string = crs(Larsen_grid)
  ) %over%
  Larsen_grid %>%
  pull(qdgc)

heterogeneity2$HDS$HDS <- heterogeneity2$HDS %$%
  SpatialPoints(
    coords      = data.frame(x = lon, y = lat),
    proj4string = crs(Larsen_grid)
  ) %over%
  Larsen_grid %>%
  pull(hdgc)

heterogeneity2$DS$DS <- heterogeneity2$DS %$%
  SpatialPoints(
    coords      = data.frame(x = lon, y = lat),
    proj4string = crs(Larsen_grid)
  ) %over%
  Larsen_grid %>%
  pull(dgc)
```

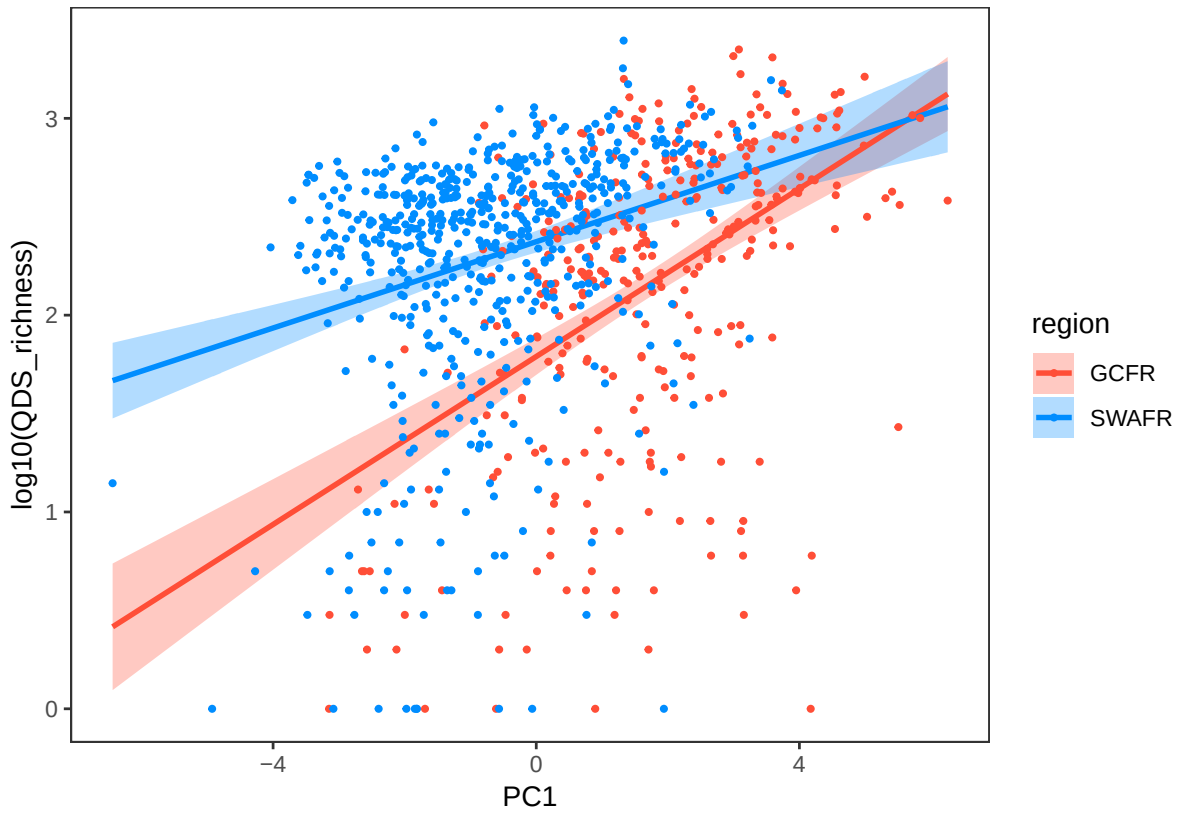
```r
data2 <- heterogeneity2
data2$QDS %<>%
  as_tibble() %>%
  full_join(QDS_richness) %>%
  na.exclude()
data2$HDS %<>%
  as_tibble() %>%
  full_join(mean_QDS_richness) %>%
  full_join(HDS_richness) %>%
  na.exclude() %>%
  mutate(
    QDS_turnover      = HDS_richness - mean_QDS_richness,
    QDS_turnover_prop = QDS_turnover / HDS_richness
  )
data2$DS %<>%
  as_tibble() %>%
  full_join(mean_HDS_richness) %>%
  full_join(mean_QDS_richness2) %>%
  full_join(DS_richness) %>%
  na.exclude() %>%
  mutate(
    HDS_turnover       = DS_richness - mean_HDS_richness,
    HDS_turnover2      = DS_richness - mean_QDS_richness2,
    HDS_turnover_prop  = HDS_turnover/DS_richness,
    HDS_turnover2_prop = HDS_turnover2/DS_richness
  )

m1 <- lm(QDS_richness        ~ PC1, data2$QDS)
m2 <- lm(log(QDS_richness)   ~ PC1, data2$QDS)
m3 <- lm(log10(QDS_richness) ~ PC1, data2$QDS)
AIC(m1, m2, m3)
```

```
##    df       AIC
## m1  3 13255.088
## m2  3  3396.644
## m3  3  1848.680
```

```r
# Choose m3
m4 <- lm(log10(QDS_richness) ~ PC1 + region, data2$QDS)
m5 <- lm(log10(QDS_richness) ~ PC1 * region, data2$QDS)
AIC(m3, m4, m5)
```

```
##    df      AIC
## m3  3 1848.680
## m4  4 1760.522
## m5  5 1746.358
```

```r
# Choose m5
visreg::visreg(m5,
  xvar = "PC1", by = "region", overlay = TRUE,
  gg = TRUE
)
```



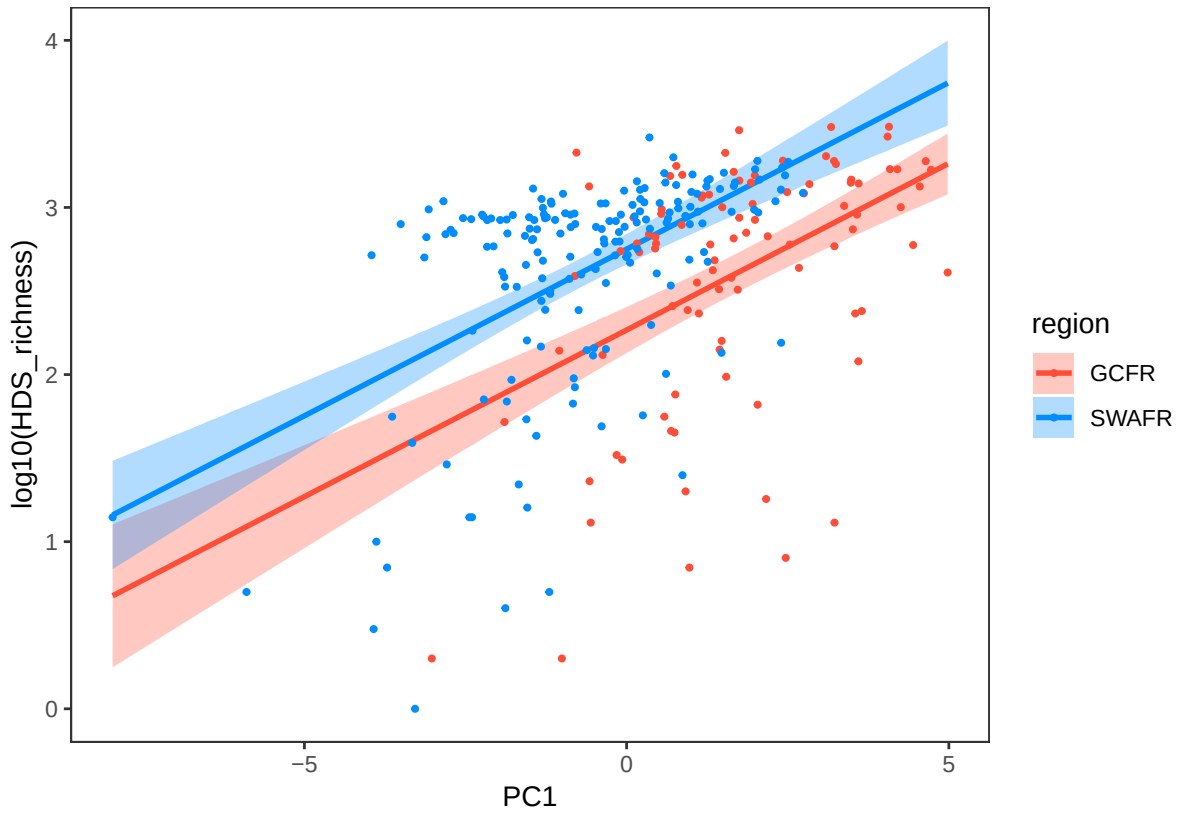

```
#ggplot(data$QDS, aes(PC1, QDS_richness)) +
#  geom_smooth(method = lm, formula = y ~ x + colour) +
#  geom_point(aes(colour = region)) +
#  scale_y_log10()

m1 <- lm(HDS_richness        ~ PC1, data2$HDS)
m2 <- lm(log(HDS_richness)   ~ PC1, data2$HDS)
m3 <- lm(log10(HDS_richness) ~ PC1, data2$HDS)
AIC(m1, m2, m3)
```

```
##    df       AIC
## m1  3 4149.6462
## m2  3  950.9044
## m3  3  502.1950
```

```
# Choose m3
m4 <- lm(log10(HDS_richness) ~ PC1 + region, data2$HDS)
m5 <- lm(log10(HDS_richness) ~ PC1 * region, data2$HDS)
AIC(m3, m4, m5)
```

```
##    df      AIC
## m3  3 502.1950
## m4  4 476.2938
## m5  5 478.2600
```

```
# Choose m4
visreg::visreg(m4,
  xvar = "PC1", by = "region", overlay = TRUE,
  gg = TRUE
)
```



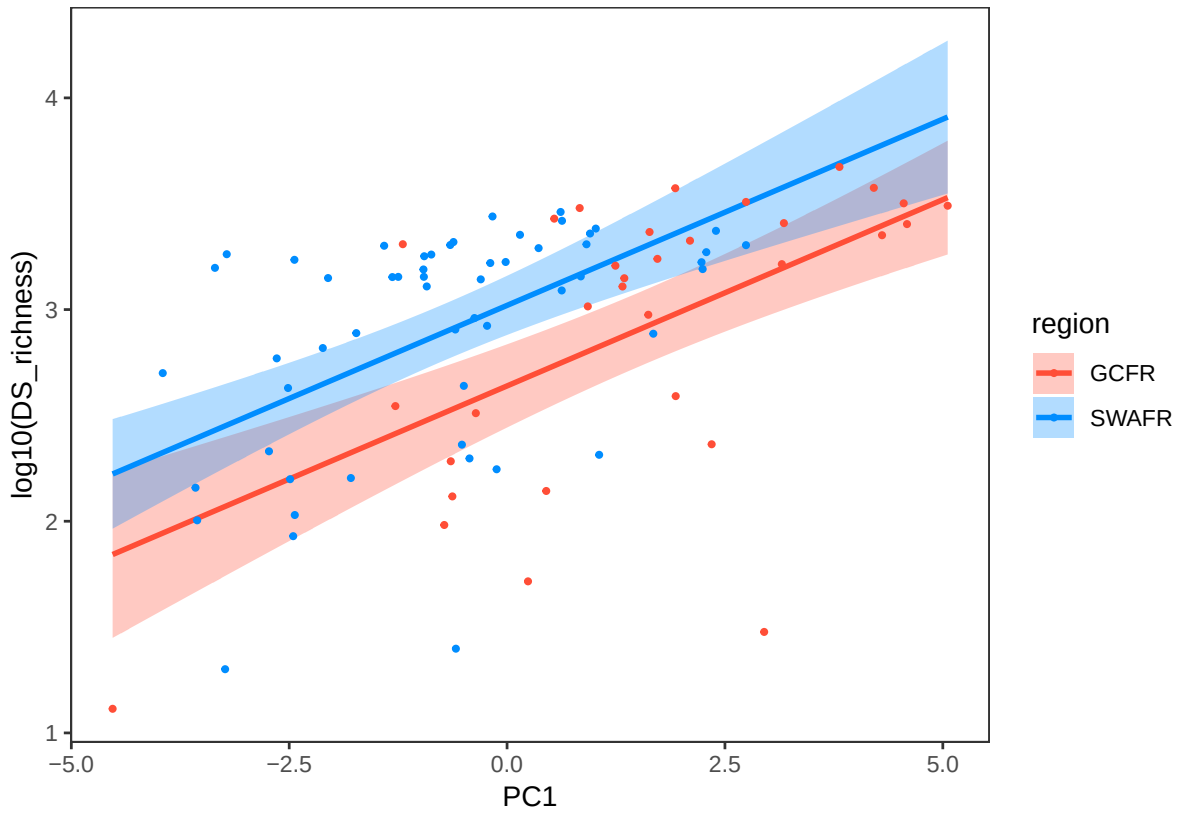

```
#ggplot(data$HDS, aes(PC1, HDS_richness, colour = region)) +
#  geom_smooth(method = lm, formula = y ~ x) +
#  geom_point() +
#  scale_y_log10()

m1 <- lm(DS_richness         ~ PC1, data2$DS)
m2 <- lm(log(DS_richness)    ~ PC1, data2$DS)
m3 <- lm(log10(DS_richness) ~ PC1, data2$DS)
AIC(m1, m2, m3)
```

```
##    df       AIC
## m1  3 1429.2997
## m2  3  282.1689
## m3  3  137.0472
```

```
# Choose m3
m4 <- lm(log10(DS_richness) ~ PC1 + region, data2$DS)
m5 <- lm(log10(DS_richness) ~ PC1 * region, data2$DS)
AIC(m3, m4, m5)
```

```
##    df      AIC
## m3  3 137.0472
## m4  4 130.4597
## m5  5 131.4508
```

```
# Choose m4
visreg::visreg(m4,
  xvar = "PC1", by = "region", overlay = TRUE,
  gg = TRUE
)
```




```
models_non_region <- map(predictor_names,
  ~lm(paste("QDS_richness ~", .x), data2$QDS)
)
names(models_non_region) <- predictor_names
models_add_region <- map(predictor_names,
  ~lm(paste("QDS_richness ~", .x, "+ region"), data2$QDS)
)
names(models_add_region) <- predictor_names
models_int_region <- map(predictor_names,
  ~lm(paste("QDS_richness ~", .x, "* region"), data2$QDS)
)
names(models_int_region) <- predictor_names
knitr::kable(pmap_dfr(
  .l  = list(models_non_region, models_add_region, models_int_region),
  .id = "variable",
  .f  = ~ AIC(..1, ..2, ..3) %>%
    mutate(
      model_rank = 1:3,
      model_type = c(" ", "+", "x")[model_rank],
      delta_AIC  = AIC - min(AIC),
      best_model = (model_rank == min(model_rank[delta_AIC < 2]))
    ) %>%
    filter(best_model) %>%
    dplyr::select(-df, -AIC, -model_rank, -best_model)
))
```

variable	model_type	delta_AIC
Elevation	x	0.000000
MAP	x	0.000000
PDQ	x	0.000000
Surface_T	+	1.527141

variable	model_type	delta_AIC
NDVI	x	0.000000
CEC	x	0.000000
Clay		0.000000
Soil_C	x	0.000000
pH		0.000000
PC1	x	0.000000

```
models_non_region <- map(predictor_names,
  ~lm(paste("HDS_richness ~", .x), data2$HDS)
)
names(models_non_region) <- predictor_names
models_add_region <- map(predictor_names,
  ~lm(paste("HDS_richness ~", .x, "+ region"), data2$HDS)
)
names(models_add_region) <- predictor_names
models_int_region <- map(predictor_names,
  ~lm(paste("HDS_richness ~", .x, "* region"), data2$HDS)
)
names(models_int_region) <- predictor_names
pmap_dfr(
  .l  = list(models_non_region, models_add_region, models_int_region),
  .id = "variable",
  .f  = ~ AIC(..1, ..2, ..3) %>%
    mutate(
      model_rank = 1:3,
      model_type = c(" ", "+", "x")[model_rank],
      delta_AIC  = AIC - min(AIC),
      best_model = (model_rank == min(model_rank[delta_AIC < 2]))
    ) %>%
    filter(best_model) %>%
    dplyr::select(-df, -AIC, -model_rank, -best_model)
)
```

```
##     variable model_type delta_AIC
## 1  Elevation          + 0.0000000
## 2        MAP          x 0.0000000
## 3        PDQ          x 0.0000000
## 4  Surface_T            0.2090424
## 5       NDVI            0.0000000
## 6        CEC            0.8032547
## 7       Clay            0.0000000
## 8     Soil_C            1.7063035
## 9         pH            0.5914092
## 10       PC1          + 0.0000000
```

```
models_non_region <- map(predictor_names,
  ~lm(glue("DS_richness ~", .x), data2$DS)
)
names(models_non_region) <- predictor_names
models_add_region <- map(predictor_names,
  ~lm(paste("DS_richness ~", .x, "+ region"), data2$DS)
)
names(models_add_region) <- predictor_names
models_int_region <- map(predictor_names,
  ~lm(paste("DS_richness ~", .x, "* region"), data2$DS)
)
```

```r
names(models_int_region) <- predictor_names
pmap_dfr(
  .l  = list(models_non_region, models_add_region, models_int_region),
  .id = "variable",
  .f  = ~ AIC(..1, ..2, ..3) %>%
    mutate(
      model_rank = 1:3,
      model_type = c(" ", "+", "x")[model_rank],
      delta_AIC  = AIC - min(AIC),
      best_model = (model_rank == min(model_rank[delta_AIC < 2]))
    ) %>%
    filter(best_model) %>%
    dplyr::select(-df, -AIC, -model_rank, -best_model)
)
```

```
##     variable model_type delta_AIC
## 1  Elevation          + 0.0000000
## 2        MAP            1.6628310
## 3        PDQ            0.2455868
## 4  Surface_T            0.0000000
## 5       NDVI            0.4523170
## 6        CEC            0.0000000
## 7       Clay            0.0000000
## 8     Soil_C          x 0.0000000
## 9         pH            0.9403592
## 10       PC1            0.1841860
```

```r
m_QDS_richness <- lm(glue("QDS_richness ~ {full_formula}"), data2$QDS)
m_HDS_richness <- lm(glue("HDS_richness ~ {full_formula}"), data2$HDS)
m_DS_richness  <- lm(glue("DS_richness ~ {full_formula}"),  data2$DS)

m_QDS_richness %<>% step(direction = "backward", trace = 0)
m_HDS_richness %<>% step(direction = "backward", trace = 0)
m_DS_richness  %<>% step(direction = "backward", trace = 0)

m_QDS_richness %<>% reparameterise()
m_HDS_richness %<>% reparameterise()
m_DS_richness  %<>% reparameterise()

models <- list(
  QDS_richness = m_QDS_richness,
  HDS_richness = m_HDS_richness,
  DS_richness  = m_DS_richness
)
models_summary <- models %>%
  map_df(.id = "response", tidy, conf.int = TRUE) %>%
  dplyr::select(-std.error, -statistic) %>%
  filter(term != "(Intercept)")

models_R2 <- models %>%
  map_df(.id = "response", glance) %>%
  dplyr::select(response, adj.r.squared)

models_summary %<>% full_join(models_R2)

glance(m_QDS_richness)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value    df logLik    AIC
```

```
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl> <int>  <dbl>  <dbl>
## 1     0.231         0.219  282.      18.6 4.34e-41    15 -6227. 12486.
## # ... with 3 more variables: BIC <dbl>, deviance <dbl>, df.residual <int>
```

```
glance(m_HDS_richness)
```

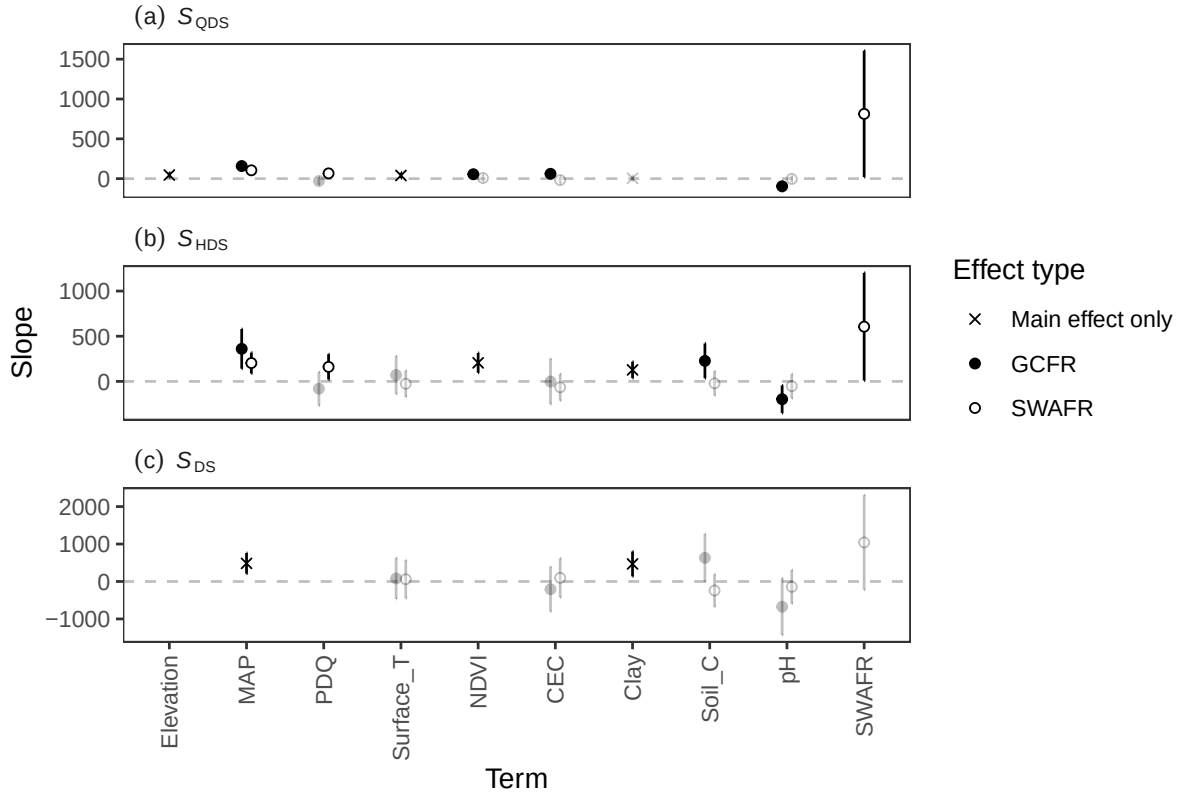
```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic  p.value    df logLik   AIC   BIC
##       <dbl>         <dbl> <dbl>     <dbl>    <dbl> <int>  <dbl> <dbl> <dbl>
## 1     0.361         0.320  491.      8.88 3.29e-16    16 -1911. 3856. 3916.
## # ... with 2 more variables: deviance <dbl>, df.residual <int>
```

```
glance(m_DS_richness)
```

```
## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic p.value    df logLik   AIC   BIC
##       <dbl>         <dbl> <dbl>     <dbl>   <dbl> <int>  <dbl> <dbl> <dbl>
## 1     0.371         0.269  889.      3.64 4.39e-4    12  -650. 1327. 1357.
## # ... with 2 more variables: deviance <dbl>, df.residual <int>
```

```
models_summary_for_plot <- models_summary %>%
  mutate(
    response = case_when(
      response == "QDS_richness" ~ "(a)~~italic(S)[QDS]",
      response == "HDS_richness" ~ "(b)~~italic(S)[HDS]",
      response == "DS_richness"  ~ "(c)~~italic(S)[DS]"
    ),
    region =
      case_when(
        str_detect(term, "regionSWAFR") ~ "SWAFR",
        str_detect(term, "regionGCFR")  ~ "GCFR",
        TRUE                            ~ "Main effect only"
      ) %>%
      factor(levels = c("Main effect only", "GCFR", "SWAFR")),
    term = term %>%
      str_replace_all("\\.", " ") %>%
      str_remove_all("regionSWAFR:") %>%
      str_remove_all("regionGCFR:") %>%
      str_replace_all("regionSWAFR", "SWAFR") %>%
      factor(levels = c(str_replace_all(var_names, " ", "_"), "SWAFR")),
    sig = (p.value < 0.05)
  )
ggplot(models_summary_for_plot) +
  aes(
    term, estimate,
    fill = region, group = region, shape = region,
    alpha = sig
  ) +
  geom_hline(yintercept = 0, linetype = "dashed", colour = "grey75") +
  geom_errorbar(
    aes(ymin = conf.low, ymax = conf.high),
    position = position_dodge(width = 0.25),
    width = 0
  ) +
  geom_point(position = position_dodge(width = 0.25)) +
  labs(x = "Term", y = "Slope") +
  scale_fill_manual(values = c(NA, "black", "white")) +
  scale_shape_manual(values = c(4, 21, 21)) +
  scale_alpha_manual(values = c(0.25, 1)) +
  facet_wrap(~response, nrow = 3, scales = "free_y", labeller = label_parsed) +
```

```
  guides(
    fill = FALSE,
    shape = guide_legend(
      title = "Effect type",
      override.aes = list(fill = c(NA, "black", "white"))
    ),
    alpha = FALSE
  ) +
  theme(
    axis.text.x  = element_text(angle = 90, hjust = 1, vjust = 0.5),
    strip.text.x = element_text(angle =  0, hjust = 0)
  )
```




```
ggplot(models_summary_for_plot[models_summary_for_plot$term != "SWAFR", ]) +
  aes(
    term, estimate,
    fill = region, group = region, shape = region,
    alpha = sig
  ) +
  geom_hline(yintercept = 0, linetype = "dashed", colour = "grey75") +
  geom_errorbar(
    aes(ymin = conf.low, ymax = conf.high),
    position = position_dodge(width = 0.25),
    width = 0
  ) +
  geom_point(position = position_dodge(width = 0.25)) +
  labs(x = "Term", y = "Slope") +
  scale_fill_manual(values = c(NA, "black", "white")) +
  scale_shape_manual(values = c(4, 21, 21)) +
  scale_alpha_manual(values = c(0.25, 1)) +
  facet_wrap(~response, nrow = 3, scales = "free_y", labeller = label_parsed) +
```

```
guides(
  fill = FALSE,
  shape = guide_legend(
    title = "Effect type",
    override.aes = list(fill = c(NA, "black", "white"))
  ),
  alpha = FALSE
) +
theme(
  axis.text.x  = element_text(angle = 90, hjust = 1, vjust = 0.5),
  strip.text.x = element_text(angle =  0, hjust = 0)
)
```