Workshop DSM 2025: Pattern Analysis for Evaluating Soil Maps

D G Rossiter

D G Rossiter (ORCID 0000-0003-4558-1286)

2025-01-30

Table of contents

1. Abstract

This tutorial presents methods to evaluate the spatial patterns of the spatial distribution of soil properties and map units as shown in gridded maps produced by digital soil mapping (DSM). Methods include whole-map statistics, visually identifiable landscape features, level of detail, range and strength of spatial autocorrelation, landscape metrics (Shannon diversity and evenness, shape, aggregation, mean fractal dimension, and co-occurrence vectors), and spatial patterns of property maps classified by histogram equalization or user-defined cutpoints. The tutorial also shows how to aggregate raster maps into "supercells" to find landscape elements..

This workshop uses an examples from SoilGrids v2.0, but the methods are applicable to any gridded DSM product or polygon map of soil classes.

2. Motivation

Digital soil maps are usually evaluated by point-wise "validation statistics" (Piikki et al., 2021). This evaluation is quite limited from both the mapper's and map user's perspectives.

Internally, from the mapper's perspective:

1. The evaluation is based on a necessarily limited number of observations, far fewer than the number of predictions (grid cells, pixels).
2. The evaluation points are very rarely from an independent probability sample (Brus et al., 2011).
3. Cross-validation and data-splitting approaches rely on a biased point set. Note that so-called "spatial cross-validation" does not solve the problem of biased sampling, just cross-validation biases caused by clustered spatial sampling (Mahoney et al., 2023).
4. Evidence has shown that widely different DSM approaches can result in maps with quite similar "validation statistics" but obviously different spatial patterns.

Externally, from the map user's perspective:

1. Soils are managed as units, not point-wise.
2. Land-surface models often rely on 2D or 3D connectivity between grid cells.

3. More than a century of fieldwork has shown that soils occur in more-or-less homogeneous patches of various sizes, not as isolated pedons (Boulaine, 1982; Fridland, 1974; Johnson, 1963).
4. The map user may confuse *artefacts* of the mapping process with real soil patterns.

3. Setup

3.1 Packages

These R packages will be used in the analysis. They must be pre-installed.

First, packages in common use for many applications.

```
options(warn = -1)
# data wrangling
library(dplyr, warn.conflicts=FALSE, quiet = TRUE)
# colour palettes for graphics
library(RColorBrewer, warn.conflicts=FALSE, quiet = TRUE)
# ggplot graphics
library(ggplot2, warn.conflicts=FALSE, quiet = TRUE)
# multiple graphics in one plot
library(gridExtra, warn.conflicts=FALSE, quiet = TRUE)
```

Second, packages in common use for spatial analysis.

```
# Robert Hijmans raster and vector data; also replaces `raster`
library(terra, warn.conflicts=FALSE, quiet = TRUE)
```

```
terra 1.8.7
```

```
# ggplot with terra SpatRaster objects
library(tidyterra, warn.conflicts=FALSE, quiet = TRUE)
# older package still needed to convert to `sp` objects
library(raster, warn.conflicts=FALSE, quiet = TRUE)
# Pebesma et al. spatio-temporal data
# Simple Features
library(sf, warn.conflicts=FALSE, quiet = TRUE)
```

```
Linking to GEOS 3.13.0, GDAL 3.10.0, PROJ 9.5.1; sf_use_s2() is TRUE
```

Third, packages specific to the pattern analysis in this workshop:

```
# variogram modelling
library(gstat, warn.conflicts=FALSE, quiet = TRUE)
# Co-occurrence vectors
library(motif, warn.conflicts=FALSE, quiet = TRUE)
# multivariate distance metrics
library(philentropy, warn.conflicts=FALSE, quiet = TRUE)
# FRAGSTATS-style metrics
# this package is in active development, maybe use the development version
```

```
# install.packages("remotes")
# remotes::install_github("r-spatialecology/landscapemetrics")
library(landscapemetrics, warn.conflicts=FALSE, quiet = TRUE)
# aggregate maps with supercells
# this package is in active development, maybe use the development version
# install.packages("supercells", repos = "https://nowosad.r-universe.dev")
library(supercells, warn.conflicts=FALSE, quiet = TRUE)
# Gray Level Co-occurence Matrices (GLCM)
library(glcm, warn.conflicts=FALSE, quiet = TRUE)
library(GLCMTextures, warn.conflicts=FALSE, quiet = TRUE)
```

3.2 Directories

Task: Set up the base directory.

This is on my system, change to wherever you store your DSM GeoTIFF. Note that in Unix-alike systems the ~ symbol refers to the user's home directory.

```
(file.dir <- path.expand("~/ds_reference/DSM2025/"))
```

```
[1] "/Users/rossiter/ds_reference/DSM2025/"
```

3.3 DSM product to evaluate

The output of a DSM prediction can be saved as a GeoTIFF (Open Geospatial Consortium, 2023).

Here we provide an example: (1°~longitude x 1°~latitude) tiles of the SoilGrids v2.0 product (Poggio et al., 2021), with a set of soil properties at six standard depth slices. The example tile is from Dindigul District, Tamil Nadu State (India). It was selected for this workshop because it has a good contrast of many soil properties within the tile.

You can create a similar files as GeoTIFF raster stack for a tile of your preference; see the scripts `SoilGrids250_WCS_import.Rmd`, `GetTiles.R`, and `SoilGrids250_MakeRasterStack.Rmd`.

Here is a map of the sample study area, obviously yours will be different.

Figure 1: Sample study area: 77-78E, 10-11N

We process the raster stack in R with the `terra` package, which has the advantage that it only loads into computer memory as needed, and can load lower resolution automatically if that's appropriate.

Task: Import the raster stack as `terra::SpatRaster` objects.

```
# the GeoTIFF file name
sg.fn <- "lat1011_lon7778_stack.tif"
(sg <- rast(paste0(file.dir, sg.fn)))
```

```
class       : SpatRaster
dimensions  : 476, 476, 42  (nrow, ncol, nlyr)
resolution  : 0.002100326, 0.002100326  (x, y)
extent      : 77.00086, 78.00062, 10.00124, 11.00099  (xmin, xmax, ymin,
ymax)
```

```
coord. ref. : lon/lat WGS 84 (EPSG:4326)
source      : lat1011_lon7778_stack.tif
names       : bdod_~_mean, bdod_~_mean, bdod_~_mean, bdod_~_mean,
bdod_~_mean, bdod_~_mean, ...
min values  :    83.34045,    103.1984,    90.17023,     94.4779,
88.24824,    100.3863, ...
max values  :   154.86685,    155.7222,   161.71574,    158.0000,
155.93663,    157.8423, ...
```

The properties and depth slices in this raster stack:

```
# layers of the raster stack
layer.names <- names(sg)
tmp <- strsplit(layer.names, "_")
(property.names <- unique(unlist(lapply(tmp, FUN = function(x) x[1]))))
```

```
[1] "bdod"  "cec"   "cfvo"  "clay"  "phh2o" "silt"  "soc"
```

```
(depth.names <- unique(unlist(lapply(tmp, FUN = function(x) x[2]))))
```

```
[1] "0-5cm"     "100-200cm" "15-30cm"   "30-60cm"   "5-15cm"    "60-100cm"
```

The raster stack has 42 layers, this is six depth slices for each of 7

Task: Plot one layers of all the properties.

```
to.plot <- grep(depth.names[1], layer.names, fixed = TRUE)
tmp <- terra::plot(sg[[to.plot]], nr = 2)
```

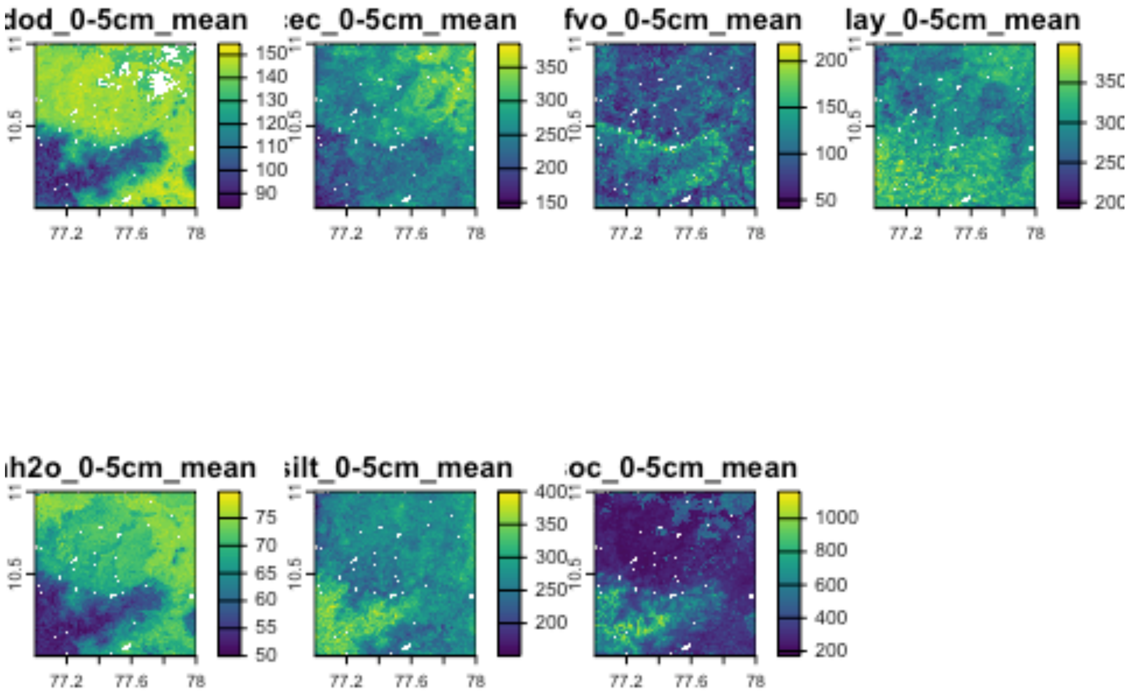


Figure 2: All properties, surface layer

We see a wide range of values and patterns.

Task: Plot all layers of one property.

```
to.plot <- grep(property.names[3], names(sg), fixed = TRUE)
r.max <- ceiling(max(global(sg[[to.plot]], fun = "max", na.rm = TRUE)))
r.min <- floor(min(global(sg[[to.plot]], fun = "min", na.rm = TRUE)))
tmp <- terra::plot(sg[[to.plot]], range = c(r.min, r.max), nr = 2)
```

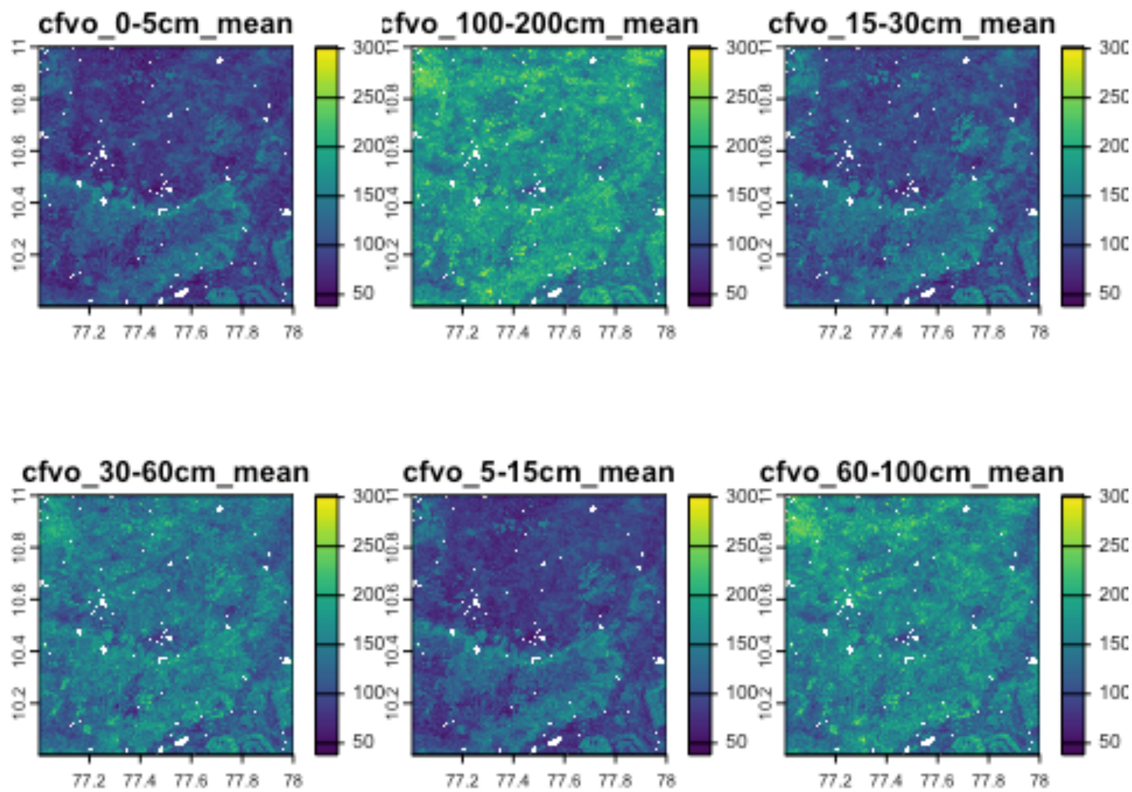


Figure 3: One property, all layers

3.4 Crop to a test area

For quicker computation, we restrict the maps (1° x 1^) to a quarter-map (0.25° x 0.25°), centred to show some interesting patterns.

Task: Crop the raster stack to a quarter-map.

```
test.tile.size <- 0.25  # degrees
test.tile.x.offset <- 0.25 # lrc west from right edge
test.tile.y.offset <- 0.25  # lrc north from bottom edge
ext.crop <- round(as.vector(ext(sg)),2) # line up to .00 decimal degrees
ext.crop["xmax"] <- ext.crop["xmax"] - test.tile.x.offset
ext.crop["xmin"] <- ext.crop["xmax"] - test.tile.size
ext.crop["ymin"] <- ext.crop["ymin"] + test.tile.y.offset
ext.crop["ymax"] <- ext.crop["ymin"] + test.tile.size
ext(ext.crop)
```

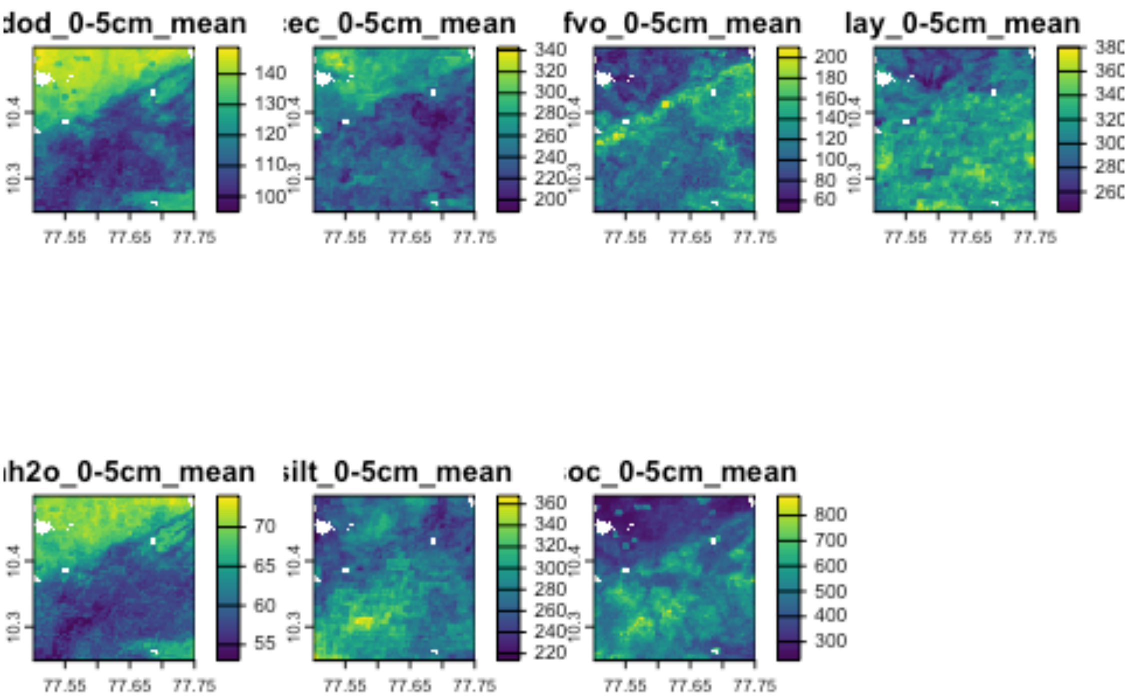
```
SpatExtent : 77.5, 77.75, 10.25, 10.5 (xmin, xmax, ymin, ymax)
```

```
sg4 <- crop(sg, ext(ext.crop))
```

Task: Repeat the plots, but just for the quarter-tile.

Task: Plot one layers of all the properties.

```
to.plot <- grep(depth.names[1], layer.names, fixed = TRUE)
tmp <- terra::plot(sg4[[to.plot]], nr = 2)
```



{#fig-layer1-properties-1/4}

We see a wide range of values and patterns.

Task: Plot all layers of one property.

```
to.plot <- grep(property.names[3], layer.names, fixed = TRUE)
r.max <- ceiling(max(global(sg4[[to.plot]], fun = "max", na.rm = TRUE)))
r.min <- floor(min(global(sg4[[to.plot]], fun = "min", na.rm = TRUE)))
tmp <- terra::plot(sg4[[to.plot]], range = c(r.min, r.max), nr = 2)
```

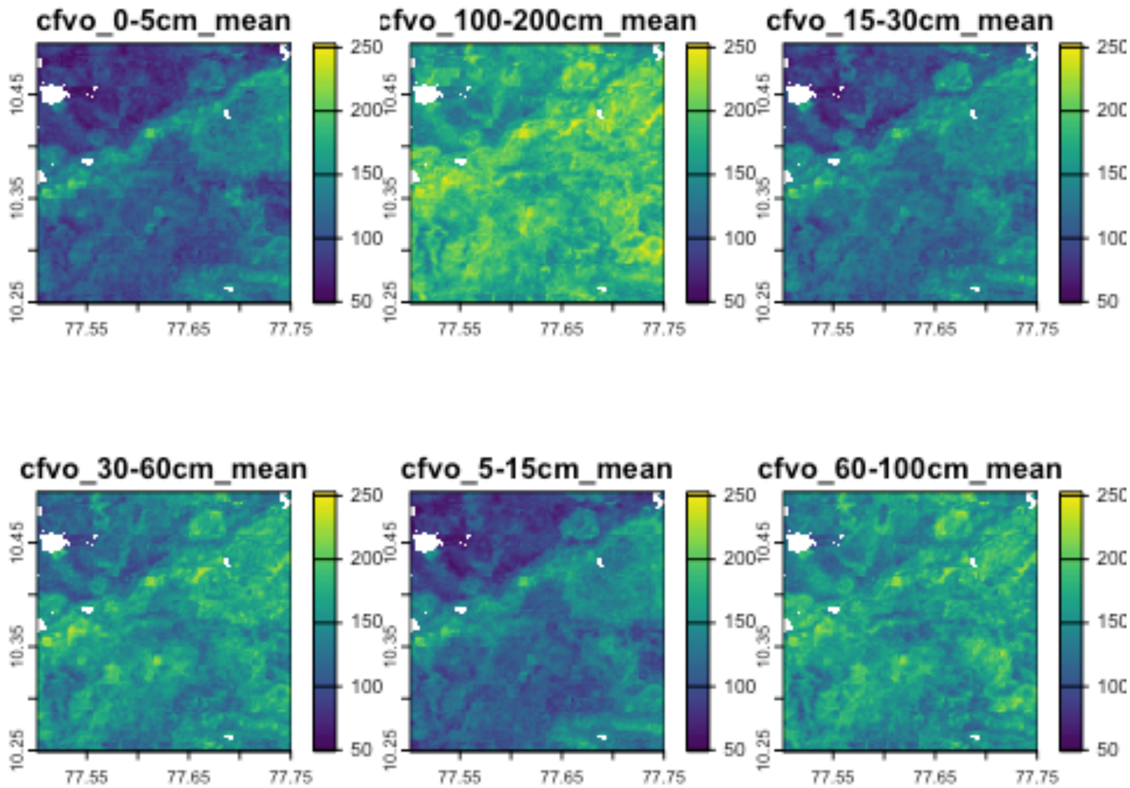


*Figure 4: ?**(caption)***

3.5 Transform to a metric CRS

Landscape metrics require approximately *equal-area* grid cells, so the raster stack, currently in a geographic Coördinate Reference System (CRS), must be projected to a metric system. CRS in R are most easily expressed by their EPSG code.

CRS definitions and EPSG codes can be found at at the EPSG Geodetic Parameter Dataset. A reasonable choice for areas narrower (longitude) than about 6° is the Universal Transmercator (UTM) system, which covers a 6°-wide latitude range with about a 0.5° buffer on each edge. Since our test area is 1°-wide this is a good choice.

Several datums (forms of the Earth, Earth centre origin) can serve as the basis for the UTM CRS. A common choice is the WGS84 datum. This CRS us used by the Global Positioning System (GPS). It is accurate to within 1 m within each 6° UTM slice, of which there are 60.

The EPSG codes for these have the format `326xx`, where xx is the UTM zone number.

Determine the UTM zone from the longitude of the central meridian of the raster stack. Use this to determine the corresponding EPSG code:

```
# a function to find the correct UTM zome
long2UTM <- function(long) { (floor((long + 180)/6) %% 60) + 1 }
# find the zone from the central meridian
utm.zone <- long2UTM(st_bbox(sg)$xmin +
                      0.5*(st_bbox(sg)$xmax - st_bbox(sg)$xmin))
cat(paste("UTM Zone", utm.zone))
```

```
UTM Zone 43
```

```
epsg.utm <- paste0("epsg:326", utm.zone)
cat(paste("CRS code:", epsg.utm))
```

```
CRS code: epsg:32643
```

Task: Resample the maps to the UTM projection, at nominal 250 m grid cell resolution.

Notes:

1. The interpolation method used by `terra::project` is, by default, bilinear. This is appropriate for continuous-valued maps.
2. Specify the grid cell size with the `res` argument to `terra::project`. SoilGrids maps are nominally at this scale, although presented in geographical coördinates and the Homosoline projection.

```
st_bbox(sg4)
```

```
    xmin     ymin     xmax     ymax 
77.50074 10.24908 77.75068 10.49902 
```

```
sg4.utm <- terra::project(sg4, epsg.utm,
                          res = c(250, 250), method = "bilinear")
st_bbox(sg4.utm)
```

```
   xmin    ymin    xmax    ymax 
 773723 1133915  801223 1161915 
```

4. Characterizing patterns

A first step is to characterize maps by statistical measures. This gives objective information about their spatial patterns.

The methods to characterize patterns are different for maps of *continuous* variables (Section 5) and *classified* (categorical) variables (Section 6).

5. Characterizing patterns – Continuous

These are methods that require continuous values on at least an interval scale, and usually a ratio scale (with a true zero). Some properties, e.g., pH, do not have a true zero, so they are an interval scale. Other properties such as coarse fragment volume have a true zero, and one can speak of one location being "twice as stony" than another, for example.

5.1 The global variogram

The variogram (or a correlogram) can be used to characterize the degree of spatial continuity and the "roughness" of a continuous property map, averaged across the entire map. Note that this depends on the grid cell size in two ways:

1. Any pattern at finer resolutions has been removed;
2. The values in grid cells may be produced by punctual or block methods. Block methods smooth values, so that the variogram sill will necessarily be lower than for punctual predictions. Also, the range may be longer.

In this section we compute short-range variograms. These reveal local structure. In DSM maps the variogram is typically unbounded, but we don't care about the long-range structure when we are evaluating patterns. The parameters of the local structure characterize the fine-scale variability.

Note: Variograms are typically produced separately for each mapped soil property. To characterize an inherent landscape scale, a number of properties can be combined by principal component analysis (PCA) and the first component (PC1) can be characterized.

Task: Convert the `terra::SpatRaster` raster stack to an `sf::sf` Simple Features object, in order to compute variograms. The `gstat::variogram` method can not be applied directly to an object of class `terra::SpatRaster`.

```
dim(sg4.utm)
```

```
[1] 112 110  42
```

```
# keep the coordinates in the data frame
sg4.df <- as.data.frame(sg4.utm, xy = TRUE)
# build the SF object, specifying the meaning of the coordinates
sg4.sf <- st_as_sf(sg4.df, coords = c("x", "y"), crs = crs(sg4.utm))
class(sg4.sf)
```

```
[1] "sf"         "data.frame"
```

```
dim(sg4.sf)
```

```
[1] 11948    43
```

```
# examine one property
names(sg4)[[1]]
```

```
[1] "bdod_0-5cm_mean"
```

```
head(sg4.sf[[1]])
```

```
[1] 143.3866 143.1640 144.0793 144.0159 143.0872 141.8891
```

```
summary(sg4.sf[[1]])
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  95.52  106.52  113.98  119.17  132.45  148.71 
```

Each field in the Simple Features points object `sg4.sf` is one property.

Task: Set the initial parameters for empirical variogram as the resolution. Adjust these after seeing the empirical variogram.

If the bin width is the resolution, we get one-grid-cell spatial correlations. We can use this fine resolution because there are so many cell-pairs.

```
range.init <- 8000  # estimated range, m
cutoff.init <- range.init*3  # cutoff for empirical variogram, m
width.init <- 250   # bin width
```

Task: Compute and display the empirical variograms for some properties and layers.

Here is an example with the first layer of the raster stack, accessed by the `[[1]]` syntax. You can substitute any property and layer, according to your interest. You can also use one of the layer names to specify the raster layer to analyse, e.g. `[["cfvo_5-15cm_mean"]]`.

```
print(names(sg4.sf))
```

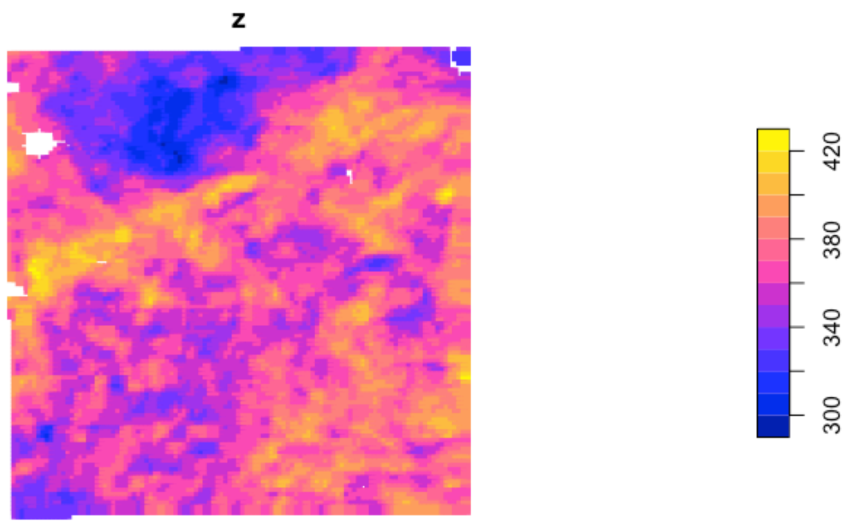
```
 [1] "bdod_0-5cm_mean"      "bdod_100-200cm_mean"  "bdod_15-30cm_mean"   
 [4] "bdod_30-60cm_mean"    "bdod_5-15cm_mean"     "bdod_60-100cm_mean"  
 [7] "cec_0-5cm_mean"       "cec_100-200cm_mean"   "cec_15-30cm_mean"    
[10] "cec_30-60cm_mean"     "cec_5-15cm_mean"      "cec_60-100cm_mean"   
[13] "cfvo_0-5cm_mean"      "cfvo_100-200cm_mean"  "cfvo_15-30cm_mean"   
[16] "cfvo_30-60cm_mean"    "cfvo_5-15cm_mean"     "cfvo_60-100cm_mean"  
[19] "clay_0-5cm_mean"      "clay_100-200cm_mean"  "clay_15-30cm_mean"   
[22] "clay_30-60cm_mean"    "clay_5-15cm_mean"     "clay_60-100cm_mean"  
[25] "phh2o_0-5cm_mean"     "phh2o_100-200cm_mean" "phh2o_15-30cm_mean"  
[28] "phh2o_30-60cm_mean"   "phh2o_5-15cm_mean"    "phh2o_60-100cm_mean" 
[31] "silt_0-5cm_mean"      "silt_100-200cm_mean"  "silt_15-30cm_mean"   
[34] "silt_30-60cm_mean"    "silt_5-15cm_mean"     "silt_60-100cm_mean"  
[37] "soc_0-5cm_mean"       "soc_100-200cm_mean"   "soc_15-30cm_mean"    
[40] "soc_30-60cm_mean"     "soc_5-15cm_mean"      "soc_60-100cm_mean"   
[43] "geometry"            
```

```
# find the column number for a target variable
ix <- which(names(sg4.sf) == "clay_30-60cm_mean")
# give the `sf` object a simple name, also the target variable
var <- sg4.sf[ix]
names(var)[1] <- "z"
summary(var)
```

```
       z                     geometry    
 Min.   :296.5   POINT         :11948  
 1st Qu.:353.6   epsg:32643    :    0  
 Median :367.0   +proj=utm ...:    0  
 Mean   :365.7                          
```

```
 3rd Qu.:380.1
 Max.   :428.7
```

```
plot(var, pch = 15, asp = 1)
```



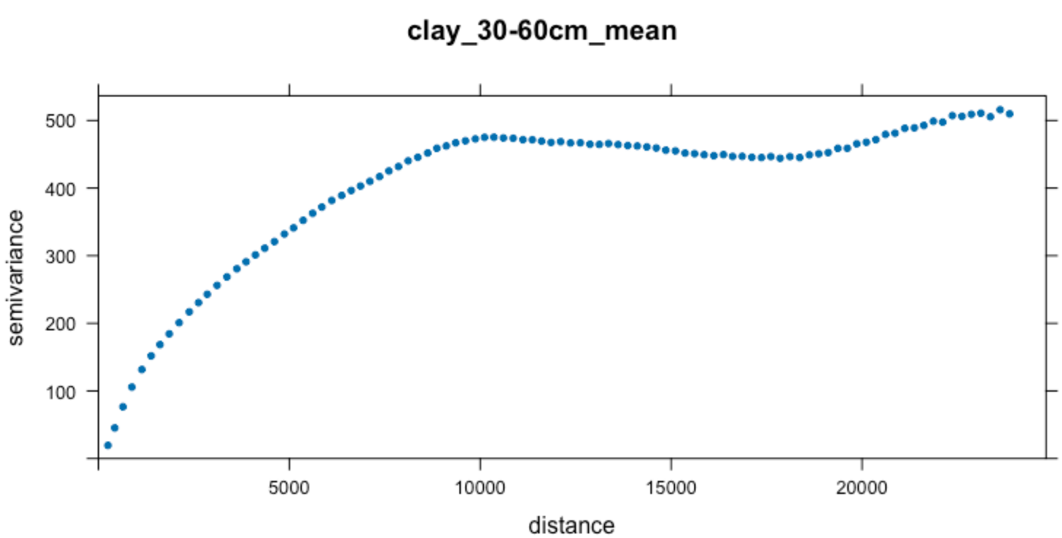

```
v.sg <- variogram(z ~ 1, loc = var,
                  cutoff=cutoff.init, width=width.init)
#
v.sg
```

```
       np      dist     gamma dir.hor dir.ver   id
1   23592  250.0000  19.51567       0       0 var1
2   46671  426.7186  45.21774       0       0 var1
3   92141  643.5849  76.58510       0       0 var1
4  113849  876.6526 105.63105       0       0 var1
5  179584 1138.1362 131.63066       0       0 var1
6  177609 1383.6360 151.84295       0       0 var1
7  197671 1611.9756 168.42234       0       0 var1
8  260131 1854.8928 184.32314       0       0 var1
9  299782 2114.0502 200.95332       0       0 var1
10 337875 2381.1048 216.89514       0       0 var1
11 313626 2622.8507 230.62330       0       0 var1
12 330943 2850.7729 242.89303       0       0 var1
13 448239 3107.6696 256.03602       0       0 var1
14 422759 3367.7018 268.66675       0       0 var1
15 476182 3625.8871 280.64117       0       0 var1
16 432186 3866.5816 291.00205       0       0 var1
17 503549 4111.5294 301.13186       0       0 var1
18 516118 4356.0261 310.99450       0       0 var1
19 566114 4610.5378 320.84946       0       0 var1
20 594373 4871.1562 332.05553       0       0 var1
21 533548 5111.5842 341.16674       0       0 var1
22 651594 5362.7966 352.37520       0       0 var1
23 608027 5612.0492 362.67168       0       0 var1
```

24	618213	5853.1321	371.94865	0	0	var1
25	729588	6111.5345	381.75233	0	0	var1
26	686740	6370.4498	389.12941	0	0	var1
27	709598	6622.3250	396.37078	0	0	var1
28	684348	6864.8841	403.06554	0	0	var1
29	723394	7109.7845	409.99393	0	0	var1
30	776887	7362.0380	417.03529	0	0	var1
31	720304	7607.2496	425.32944	0	0	var1
32	817557	7859.3015	431.87639	0	0	var1
33	776896	8111.3500	440.31775	0	0	var1
34	823572	8365.2608	445.56156	0	0	var1
35	855472	8622.1271	451.94270	0	0	var1
36	743000	8865.5541	458.94297	0	0	var1
37	873750	9111.1540	462.39880	0	0	var1
38	791009	9356.9080	466.97078	0	0	var1
39	929439	9613.3899	469.90697	0	0	var1
40	860191	9871.3751	472.77636	0	0	var1
41	809745	10113.6303	475.08144	0	0	var1
42	885851	10357.1808	475.18106	0	0	var1
43	872826	10607.5063	474.17154	0	0	var1
44	933661	10863.5856	473.70509	0	0	var1
45	905498	11120.5659	471.60949	0	0	var1
46	830073	11364.3047	471.47092	0	0	var1
47	911493	11606.6490	469.51598	0	0	var1
48	885217	11855.5277	467.48149	0	0	var1
49	925923	12106.7747	468.61125	0	0	var1
50	933916	12363.3869	466.84117	0	0	var1
51	939052	12622.2687	467.04065	0	0	var1
52	910039	12874.2917	464.81869	0	0	var1
53	861809	13118.9372	464.68668	0	0	var1
54	908042	13361.9231	465.89350	0	0	var1
55	881681	13608.7347	464.33598	0	0	var1
56	955747	13863.1301	462.88265	0	0	var1
57	877771	14113.7505	462.29447	0	0	var1
58	919554	14364.6596	460.93708	0	0	var1
59	871836	14611.3388	459.26021	0	0	var1
60	901083	14859.8499	455.94462	0	0	var1
61	919755	15114.4241	455.01143	0	0	var1
62	873487	15365.3659	451.78251	0	0	var1
63	880463	15615.1456	450.91728	0	0	var1
64	878562	15863.6776	449.34777	0	0	var1
65	901390	16119.5774	447.95656	0	0	var1
66	839277	16369.5261	449.58486	0	0	var1
67	821443	16610.8120	446.81382	0	0	var1
68	864015	16860.4708	446.99174	0	0	var1
69	867240	17114.1653	445.55173	0	0	var1
70	808601	17365.7805	445.22403	0	0	var1
71	817811	17610.6227	446.63926	0	0	var1
72	777216	17854.2506	444.06259	0	0	var1
73	860133	18109.6785	446.59332	0	0	var1

```
74 797777 18366.6595 445.16425       0        0 var1
75 788390 18620.1439 449.14095       0        0 var1
76 748364 18866.0086 450.82044       0        0 var1
77 758639 19113.0349 452.46233       0        0 var1
78 772398 19367.3367 458.81368       0        0 var1
79 698151 19614.0344 458.82634       0        0 var1
80 728431 19861.3786 465.63401       0        0 var1
81 717410 20112.8429 467.79129       0        0 var1
82 689842 20363.5999 471.63263       0        0 var1
83 694095 20614.7934 479.46241       0        0 var1
84 641539 20861.8242 481.19924       0        0 var1
85 697825 21117.8831 488.36920       0        0 var1
86 612366 21369.5962 489.07227       0        0 var1
87 631539 21618.0282 492.60705       0        0 var1
88 600568 21867.7117 498.95825       0        0 var1
89 565168 22111.5571 497.64409       0        0 var1
90 613854 22365.4128 507.20349       0        0 var1
91 541539 22618.9452 506.06430       0        0 var1
92 535276 22865.0828 509.15176       0        0 var1
93 524221 23112.7904 510.80071       0        0 var1
94 502933 23362.2165 505.56472       0        0 var1
95 509638 23615.9208 515.90609       0        0 var1
96 448479 23864.7565 509.77823       0        0 var1
```

```
plot(v.sg, pch = 20, main = names(sg4.sf)[ix])
```



Here you should go back and adjust the cutoff so only the local part of the variogram is shown and will thus be modelled (next step).

Task: Fit a variogram model to the empirical variogram.

The differences can be quantified by the parameters of a fitted variogram model. We try an exponential model because (1) it has the simplest theory, and (2) we expect to not reach a sill within the short range investigated.

We use the `fit.variogram` method to adjust an initial estimate by weighted least squares (linear in the number of point-pairs and inverse squared in the separation disatance, i.e., the default `gstat` method 7). The estimated sill is the maximum γ in the empirical variogram.

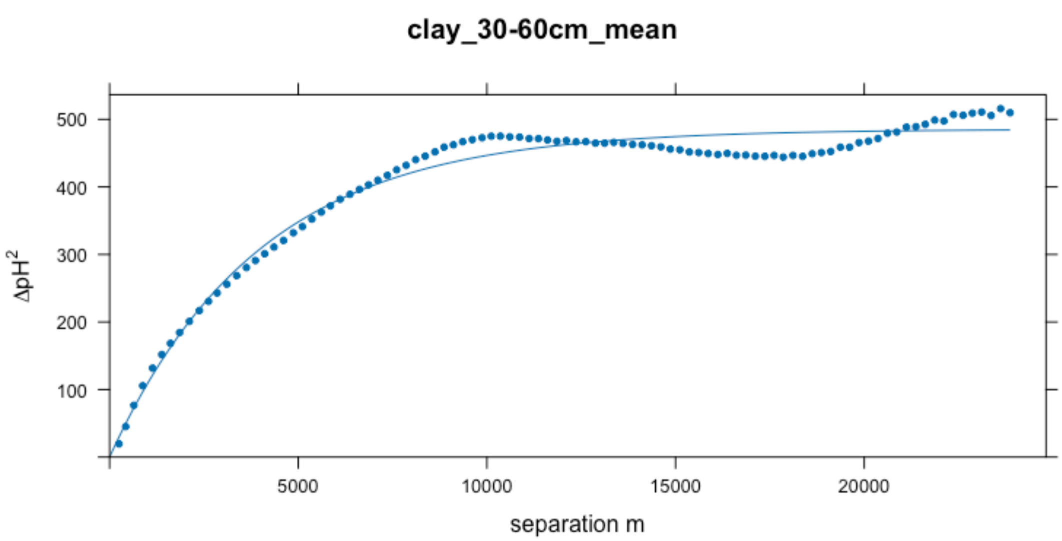
You can experiment with different variogram model forms. Notice that the nugget is likely zero due to the large cell size.

```
# fit with Exponential, a default model for many environmental variables
vm.sg <- vgm(psill = 0.8*max(v.sg$gamma),
             model = "Exp",
             range = range.init,
             nugget = 0)
print(vmf.sg <- fit.variogram(v.sg, model=vm.sg))
```

```
  model    psill    range
1   Nug   0.0000    0.000
2   Exp 485.4503 3959.509
```

Plot the empirical variogram and the fit:

```
plot(v.sg, model=vmf.sg, main = names(sg4.sf)[ix], pch = 20,
     xlab = "separation m", ylab = expression(paste(Delta, plain(pH)^2)))
```



Q: How well does the fitted model match the empirical variogram? If the fit has some problems, what could be a solution? Recall, the variogram represents the average *short range* spatial structure.

5.2 Moving-window local association

The local spatial structure may not be consistent across the mapped area – that is, the assumption of second-order stationarity may be (and often is) false. This means that the average variogram, computed over that area, is misleading.

The gridded maps have so many cells that it's possible to compute **moving-window variograms**, as in the VESPER program (Minasny et al., 2005) developed for precision agriculture applications. This will show if the local spatial association is consistent across the map. This also allows maps to be compared window-by-window. I have not (yet?) implemented this in R, so we must use another method to assess moving-window local spatial association.

A quick way to see the local degree of autocorrelation is with Moran's I applied to a window of appropriate size around each grid cell, using the `terra::autocor` function.

Moran's I is defined as:

$$I = \frac{n}{\sum_i \sum_j w_{ij}} \frac{\sum_i \sum_j w_{ij} (y_i - \bar{y})(y_j - \bar{y})}{\sum_i (y_i - \bar{y})^2}$$

where y_i is the value of the variable in the ith of n neighbouring grid cells, $\bar{y}$ is the global mean of the variable, w_{ij} is the spatial **weight** of the link between the target cell i and its neighbour cell j. The expected value of Moran's I is $-1/(n-1)$ if the pattern of the response variable is random, i.e., no spatial correlation. So for a 5×5 neighbourhood the expected value is $-1/24 = -0.041\bar{6} \approx 0$.

The second term numerator is the weighted covariance. Its denominator normalizes by the variance. The first term normalizes by the sum of all weights, so that the test is comparable among tests with different numbers of neighbours and using different weightings.

Task: Construct a weights matrix for local Moran's I, for a 5×5 grid cell neighbourhood, i.e., up to $\pm\ 500\ m$ in the N/S directions and $\pm\ 500 \times \sqrt{2} \approx 707\ m$ along the diagonals.

We determine the weights matrix for Moran's I from the fitted global variogram of the previous section and the grid cell size. Weights are the one minus the semivariance at each cell distance, so that the centre pixel receives the maximum weight.

Here is a function to make an odd-sized square window (default 5 x 5) with weights taken from the variogram model, scaled to the resolution.

```
make.weights <- function(n = 5, res = 250, vgm) {
  m <- matrix(0, nrow = n, ncol = n)
  center <- ceiling(n / 2)
  for (i in 1:n) {
    for (j in 1:n) {
      # distance in cell units, multipled by the grid resolution
      m[i, j] <- sqrt((i - center)^2 + (j - center)^2)*250
    }
  }
```

```
  w <- 1 - variogramLine(vm.sg, dist_vector = m)
  return(w)
}
```

Figure 5 shows the Euclidean distance weights in a 5 x 5 window.

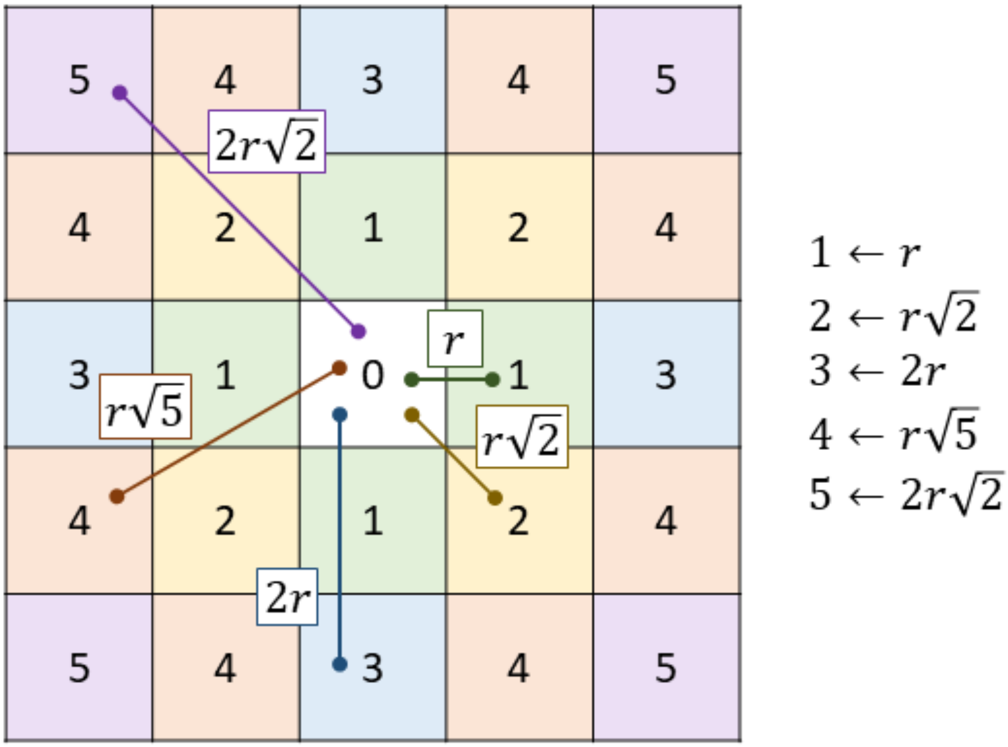


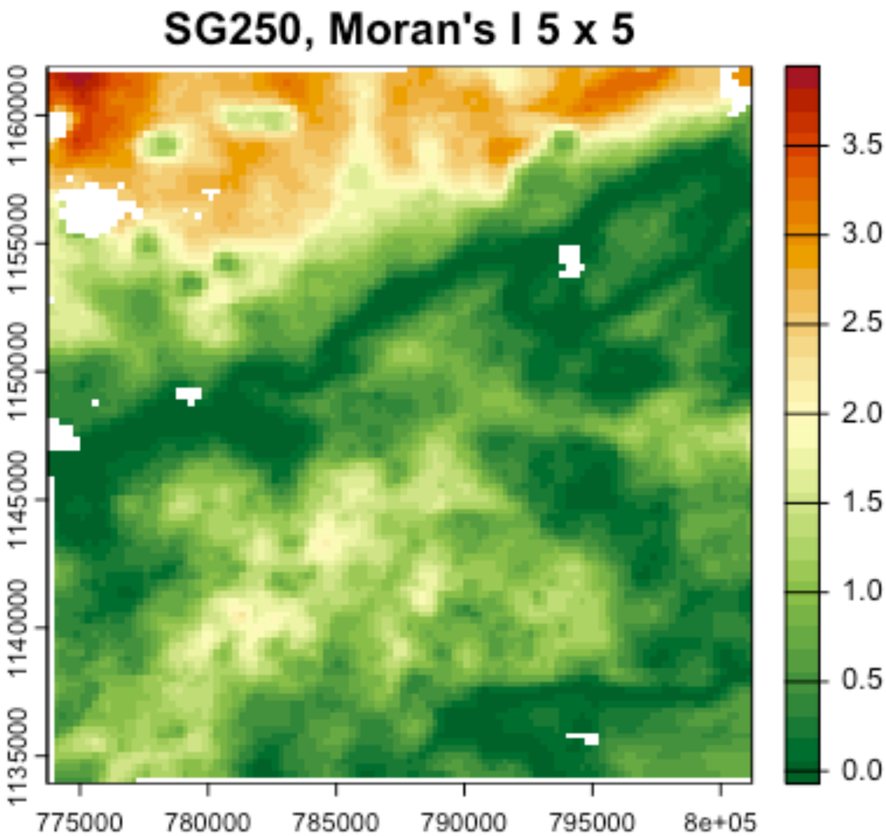
Figure 5: Computation of local Moran's neighbour weights (credit: Diana Collazo, ISRIC)

Here is a function to use this to compute and display the moving-window autocorrelation for any odd window size. This uses the `terra::autocor` method, applied to a weighted window.

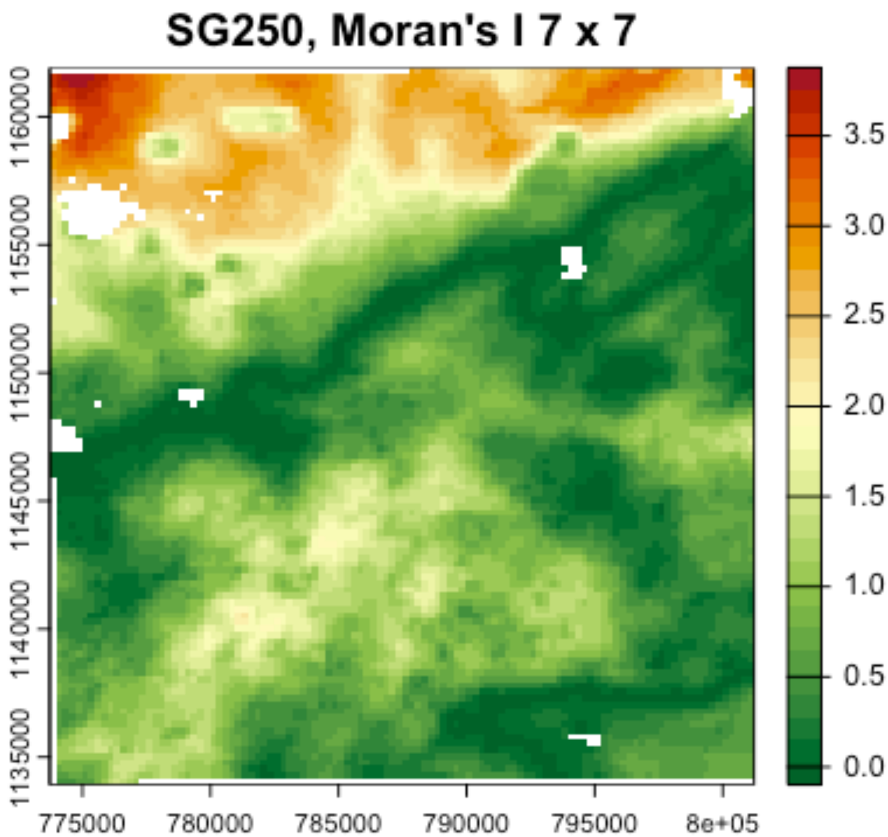
```
show.autocor <- function(n = 5) {
  sg.utm.autocor <- terra::autocor(sg4.utm[[1]],
                                   w=make.weights(n, res(sg4.utm)[1],
vmf.sg),
                                   method="moran", global = FALSE)
  terra::plot(sg.utm.autocor, main = paste("SG250, Moran's I", n, "x", n),
              col = rev(hcl.colors(32, palette = "RdYlGn")))
}
```

Task: Compute and display the moving-window autocorrelation, for a 5 x 5 window, in this case 1250 x 1250 m; a 7 x 7 window (1500 x 1500); and a 9 x 9 window (1750 x 1750).

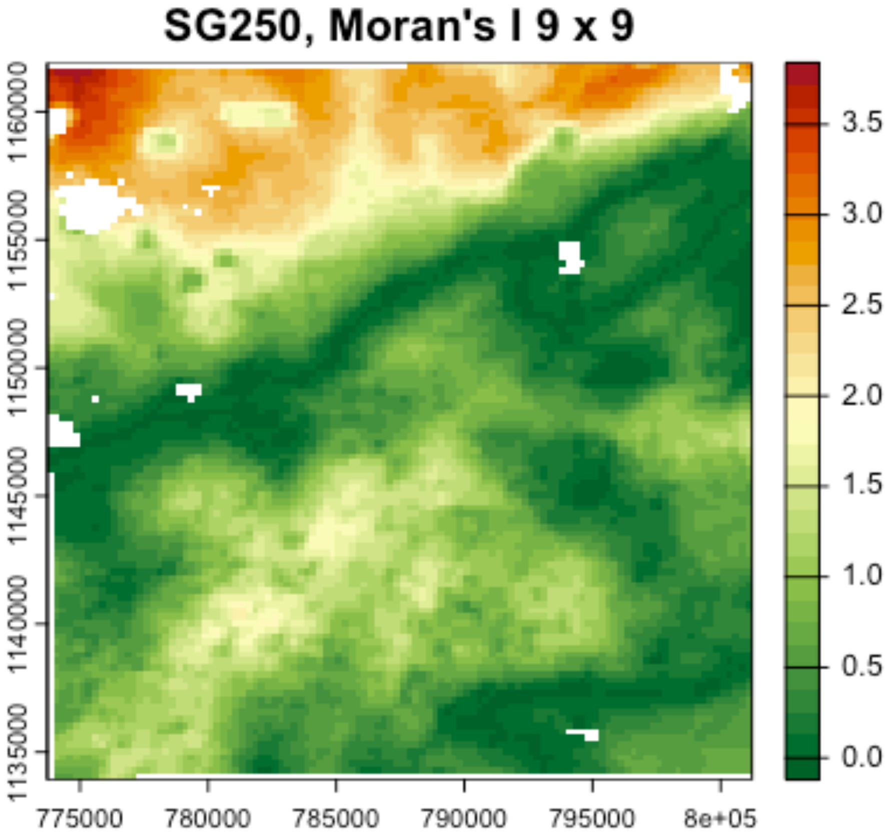
```
show.autocor(5)
```




```
show.autocor(7)
```




```
show.autocor(9)
```



These are all very far from the random value $-0.041\bar{6}$. Both maps show hot spots with much larger local autocorrelation than the map average. Some areas have almost none or even more dispersed than random (negative values).

To appreciate the local Moran's I values, here is the global Moran's I with the same weights matrix. These are the averages of all the local (window) Moran's I.

```
global.moran <- function(n) {
  print(paste("SG:", round(terra::autocor(sg4.utm[[1]],
                                   w=make.weights(n, res(sg4.utm)[1],
vmf.sg),
                                   method="moran", global = TRUE), 3)))
}
global.moran(5)

[1] "SG: 0.968"

global.moran(7)

[1] "SG: 0.952"

global.moran(9)

[1] "SG: 0.937"
```

Q: Is the pattern of local autocorrelation the same across the map?

Q: How does this change as the window size increases?

5.3 Grey Level Co-occurrence Matrix (GLCM)

The idea of characterizing the “texture” of an image has a long history in image processing Haralick et al. (1973). One method for this is the **Grey Level Co-occurrence Matrix**. Here the “grey levels” (GL) refer to pixel values – in our context, the values of the soil property, typically quantized (sliced) to some precision. The “co-occurrence” (C) refers to the statistical properties within some window, either isotropic or weighted in some direction. The GLCM shows how often different combinations of values (“grey levels”) occur over local windows within the map. These local textures can be related to landscape ecology, in our case the local spatial structure of the values of a soil property. Many statistics can then be computed to characterize this matrix.

GLCM statistics, in the context of DSM, show the **local** statistical properties of a window as it moves across the map. These can be interpreted as, for example, homogeneity or contrast within a window, thereby revealing areas of the map with different spatial structure.

See Hall-Beyer (2017a) for a tutorial introduction to the construction, use, and interpretation of GLCM-based textures, and Hall-Beyer (2017b) for guidelines on choosing appropriate GLCM-based textures in the context of land cover classification.

5.3.1 Quantization

The GLCM is constructed from a moving-window analysis of the map, with the (odd-sized) window considered as a matrix of grid cells.

Before analysis the original map is quantized into a fixed number of levels, by analogy with remote sensing image processing, typically from 16 to 64 levels. Quantization is computed by slicing the value range into equal intervals and replacing the original values with the integer level number.

The GLCM approximates the joint probability distribution of the levels of two pixels separated by the specified shift(s), that is, how likely it is that these two levels occur together in the window. We would like to avoid zero probabilities. If there are too many levels, many pairs of will not occur. So we should pick a number of levels for quantization which avoids this.

The following code shows how to quantize the SoilGrids map into 16 levels. This will be done automatically by the `glcm` function, see below, here we show how this process works. In the actual computation of statistics we will use more levels.

```
range(values(sg4.utm[[1]], na.rm = TRUE))
```

```
[1]  95.51815 148.71246
```

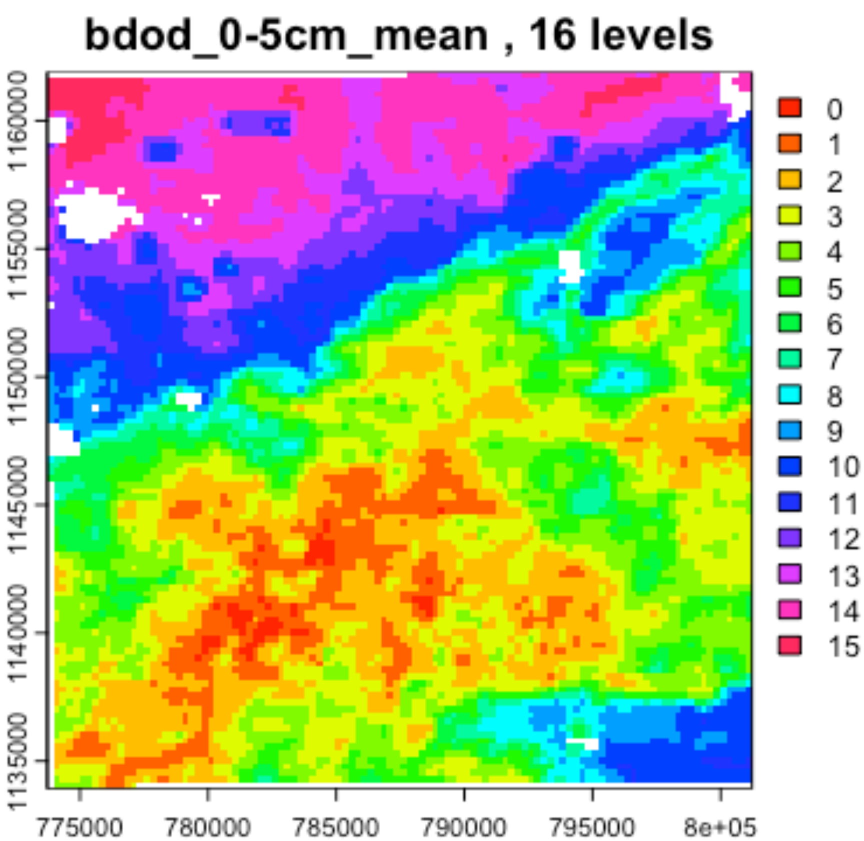
```
sg4.quant <- cut(values(sg4.utm[[1]]), breaks = 16, labels = 0:15,
include.lowest = TRUE)
table(sg4.quant)

sg4.quant
   0    1    2    3    4    5    6    7    8    9   10   11   12   13   14
15
  75  707 1645 1739 1336  772  600  469  397  459  693  519  588  713 1068
168

# show the breakpoints
levels(cut(values(sg4.utm[[1]]), breaks = 16, include.lowest = TRUE))

 [1] "[95.5,98.8]" "(98.8,102]"  "(102,105]"   "(105,109]"   "(109,112]"
 [6] "(112,115]"   "(115,119]"   "(119,122]"   "(122,125]"   "(125,129]"
[11] "(129,132]"   "(132,135]"   "(135,139]"   "(139,142]"   "(142,145]"
[16] "(145,149]"

sg4.utm.quant <- sg4.utm[[1]]
values(sg4.utm.quant) <- sg4.quant
plot(sg4.utm.quant, col = rainbow(16), main = paste(layer.names[1], ", 16
levels"))
```



It is difficult to see just from this map if the GLCM will have too many zeroes, or if a finer quantization could be supported.

5.3.2 Constructing a GLCM

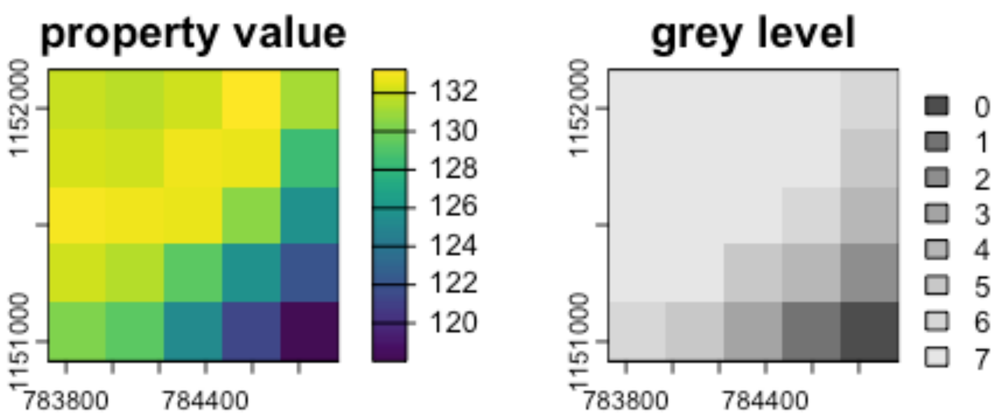
This section shows how a GLCM is constructed. We take a simple example of an 8-class quantization and a 5x5 window near the middle of the map, and a one-cell rightward shift.

The `make_glcm` method is provided by a different GLCM package: `GLCMTextures`.

```
# obtain the bounding box of the test area from cell numbers
xy <- xyFromCell(sg4.utm[[1]], cellFromRowCol(sg4.utm[[1]], 40:45, 40:45))
# crop to this box
w.sg <- crop(sg4.utm[[1]], xy)
test.quant <- cut(values(w.sg), breaks = 8,
                  labels = 0:7, include.lowest = TRUE)
# the classes of the cut
(l.8 <- levels(cut(values(w.sg), breaks = 8, include.lowest = TRUE)))
```

```
[1] "[118,120]" "(120,122]" "(122,124]" "(124,126]" "(126,128]" "(128,129]"
[7] "(129,131]" "(131,133]"
```

```
# add the class labels to the test map
w.sg.8 <- w.sg; values(w.sg.8) <- test.quant
# show the property and the derived grey levels together
par(mfrow = c(1,2))
plot(w.sg, main = "property value")
plot(w.sg.8, main = "grey level", col = grey.colors(8))
```




```r
par(mfrow = c(1,1))
# set up the matrix on which to compute the GLCM
(test.matrix <- as.matrix(w.sg.8, wide = TRUE))
```

```
     [,1] [,2] [,3] [,4] [,5]
[1,]    8    8    8    8    7
[2,]    8    8    8    8    6
[3,]    8    8    8    7    5
[4,]    8    8    6    5    3
[5,]    7    6    4    2    1
```

```r
glcm <- GLCMTextures::make_glcm(test.matrix,
          n_levels = 9, shift = c(1, 0), # shift one cell to the right
          normalize = FALSE )
print(glcm)
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
 [1,]    0    0    0    0    0    0    0    0    0
 [2,]    0    0    1    0    0    0    0    0    0
 [3,]    0    1    0    0    1    0    0    0    0
 [4,]    0    0    0    0    0    1    0    0    0
 [5,]    0    0    1    0    0    0    1    0    0
 [6,]    0    0    0    1    0    0    1    1    0
 [7,]    0    0    0    0    1    1    0    1    2
```

```
 [8,]    0    0    0    0    0    1    1    0    2
 [9,]    0    0    0    0    0    0    2    2   18
```

```
sum(diag(glcm))/sum(glcm)
```

```
[1] 0.45
```

The original matrix is 5 x 5 cells; the GLCM is 9 x 9 levels.

In this example 0.45 of the adjacenies are on the GLCM diagonal, i.e., with no change in level based on the 8-level GLCM. The off-diagonals show how many shifts in class, the large the more abrupt the difference.

5.3.3 Computation of GLCM texture measures

From the quantized matrix, the GLCM can be constructed for one or more specified offsets, called a **shift**. These can be either along the row, column, or diagonal, as specified by the analyst. Each element at position (i, j) in the GLCM counts how many times a pixel with value i and a value j occur together with the specified offset. So for example a map quantized with 32 levels will have a 32 x 32 GLCM.

If multiple shifts are specified, the texture statistics are computed for all the specified shifts, with the result for a pixel being the mean of these statistics for each pixel.

The GLCM describes the spatial relationships of (quantized) values in the map; this can be considered "texture". Many statistics can be computed on the GLCM. Among the relevant statistics for pattern analysis are the mean, variance, homogeneity, contrast, entropy, dissimilarity, second moment, and correlation of the GLCM.

The R `glcm` package computes these metrics. It requires an object in the older `raster` package format.

```
# convert to the older `raster` format
sg4.utm.raster <- raster(sg4.utm)
```

We choose to compute the mean statistics for four shifts: one pixel by row, column, and both diagonals. If there is orientation (anisotropy) evident in the map, just one shift could be used to characterize the shifts in that orientation.

We choose to compute on a 5 x 5 window (both dimensions must be odd). Since the resolution is already coarse (250 m) this will characterize the texture in 1.5625 km^2 squares

```
stat.list <- c("mean","variance","homogeneity","contrast",
               "entropy","dissimilarity","second_moment",
               "correlation")
glcm.sg <- rast(glcm(sg4.utm.raster,
                   window = c(5, 5),
                   n_grey = 32, # number of levels in the GLCM
                   shift=list(c(0,1), c(1,1), c(1,0), c(1,-1)), # all
directions
```

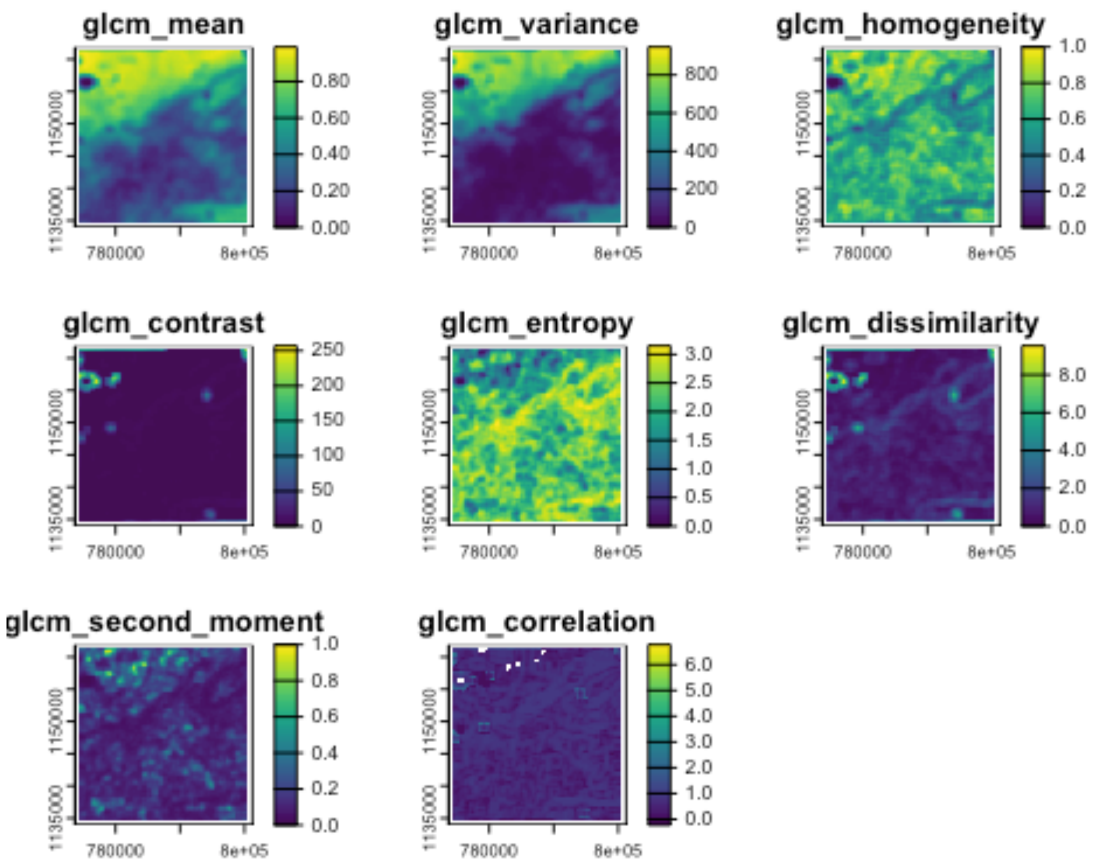
```
                   na_opt = "ignore",
                   statistics = stat.list))
class(glcm.sg)
```

```
[1] "SpatRaster"
attr(,"package")
[1] "terra"
```

```
summary(glcm.sg)
```

```
   glcm_mean       glcm_variance    glcm_homogeneity glcm_contrast
 Min.   :0.0000   Min.   :  0.00   Min.   :0.0000   Min.   :  0.000
 1st Qu.:0.2219   1st Qu.: 49.14   1st Qu.:0.5431   1st Qu.:  0.760
 Median :0.3468   Median :123.28   Median :0.6372   Median :  1.370
 Mean   :0.4461   Mean   :266.69   Mean   :0.6297   Mean   :  6.156
 3rd Qu.:0.6918   3rd Qu.:474.09   3rd Qu.:0.7240   3rd Qu.:  2.620
 Max.   :0.9891   Max.   :947.12   Max.   :1.0000   Max.   :257.050
 NA's   :1192     NA's   :1192     NA's   :1192     NA's   :1192
  glcm_entropy   glcm_dissimilarity glcm_second_moment glcm_correlation
 Min.   :0.000   Min.   :0.000      Min.   :0.0000     Min.   :  -Inf
 1st Qu.:1.879   1st Qu.:0.600      1st Qu.:0.0856     1st Qu.:0.4877
 Median :2.263   Median :0.840      Median :0.1232     Median :0.6575
 Mean   :2.191   Mean   :1.049      Mean   :0.1521     Mean   :  -Inf
 3rd Qu.:2.572   3rd Qu.:1.190      3rd Qu.:0.1848     3rd Qu.:0.8043
 Max.   :3.150   Max.   :9.530      Max.   :1.0000     Max.   :6.7768
 NA's   :1192    NA's   :1192       NA's   :1192       NA's   :1243
```

```
plot(glcm.sg)
```



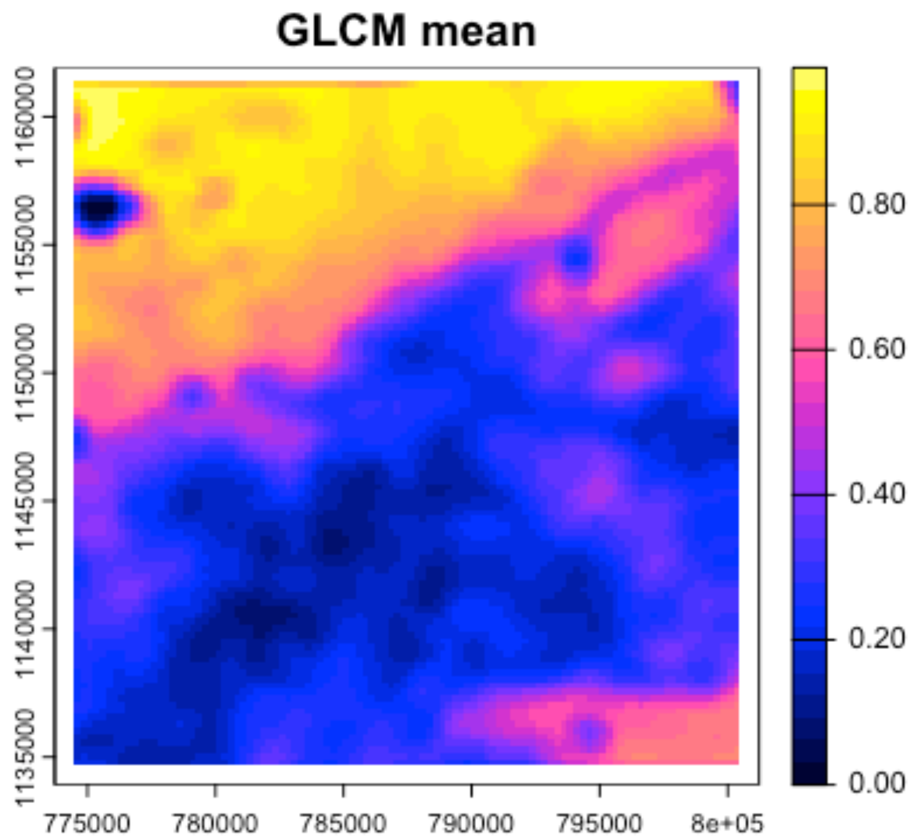
5.3.4 Interpretation

Each of the texture metrics quantifies some aspect of the texture. For a thorough explanation see Hall-Beyer (2017a) and Hall-Beyer (2017b). Here we examine a few of them.

Mean and **Variance** represent the overall inhomogeneity of the window. The mean is the mean change in the selected shift(s) and the variance is how variable are the changes.

$$\mu = \sum_{i,j=0}^{N-1} i \cdot P_{i,j}$$

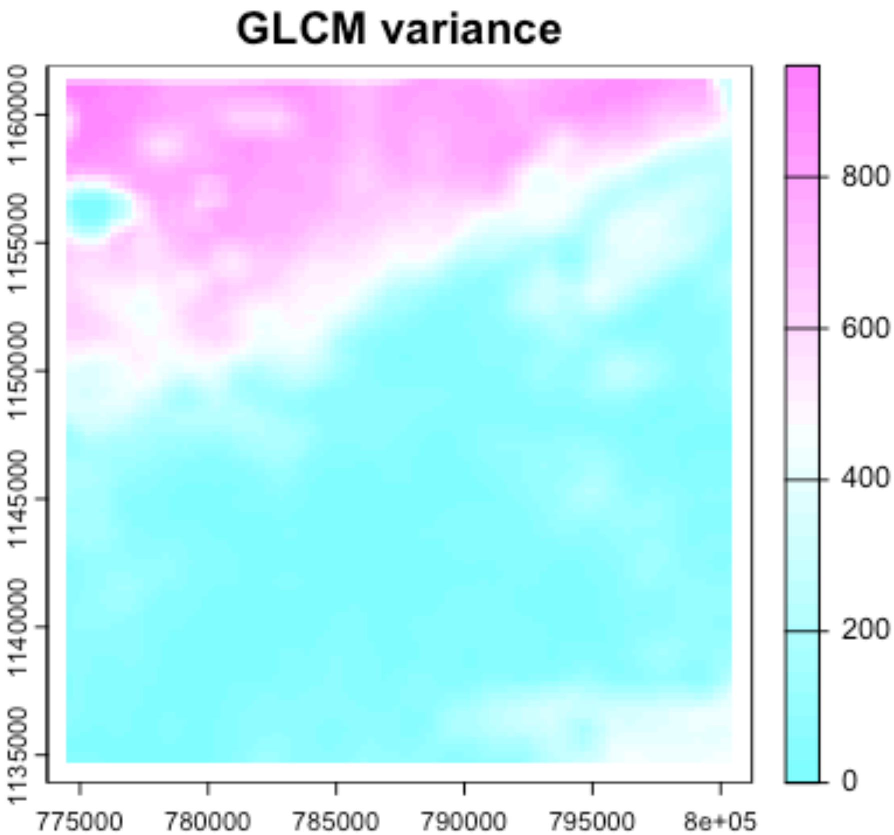
```
plot(glcm.sg[["glcm_mean"]], main = "GLCM mean",
     col=(sp::bpy.colors(32)))
```



Areas with the higher values have more and/or larger differences between neighbours.

$$\sigma^2 = \sum_{i,j=0}^{N-1} P_{i,j} \cdot (i - \mu)^2$$

```
plot(glcm.sg[["glcm_variance"]], main = "GLCM variance",
      col=(cm.colors(32)))
```

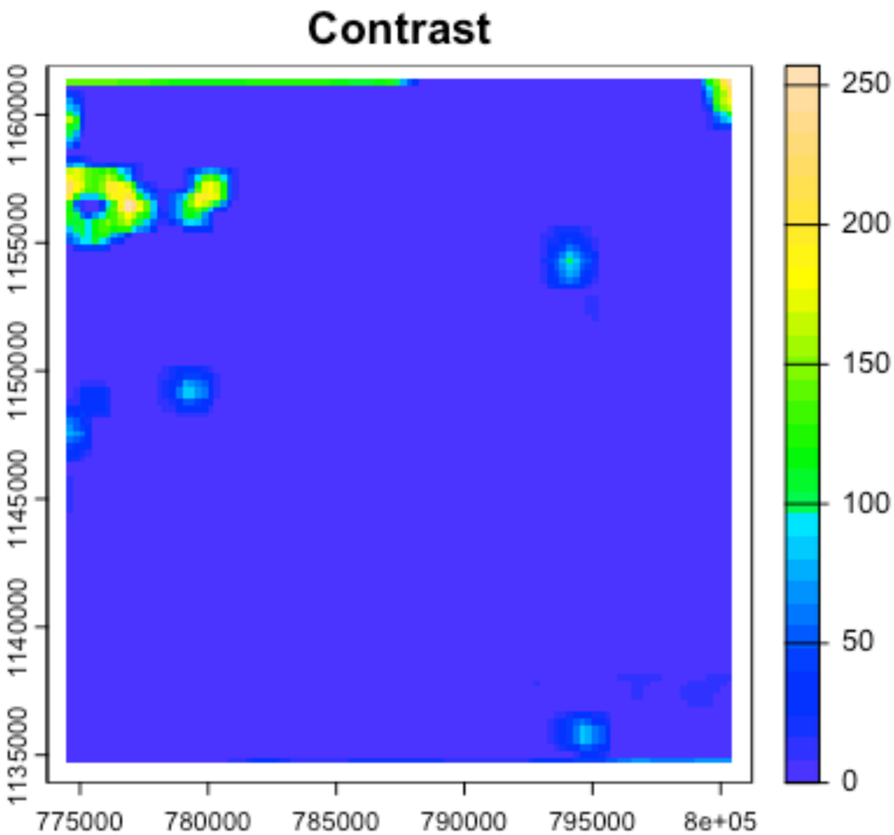


Contrast is the amount of local variation in a window, with emphasis (squared distance) on the off-diagonals of the GLCM, i.e., larger changes in the quanta level.

$$\sum_{i,j=0}^{N-1} P_{i,j} \cdot (i-j)^2$$

where $P_{i,j}$ is the proportion of the class i and j co-occurrence in the window.

```
plot(glcm.sg[["glcm_contrast"]], main = "Contrast",
     col=(topo.colors(32)))
```

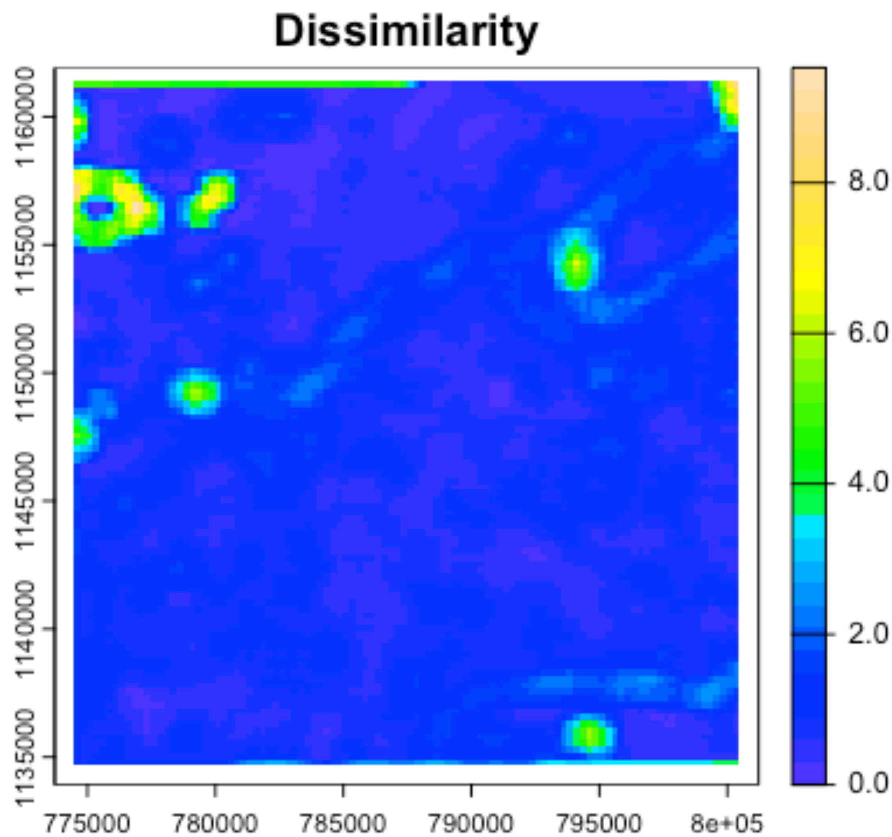


There are “hot spots” of high contrast, i.e., areas in the map with a relatively wide range of propertu values. Note that this shows that the assumption of second-order stationarity used in the variogram analysis Section 5.1 is definitely not correct.

A variant is the **dissimilarity**, where the weights are linear away from the diagonal, rather than quadratic:

$$\sum_{i,j=0}^{N-1} P_{i,j} \cdot |i-j|$$

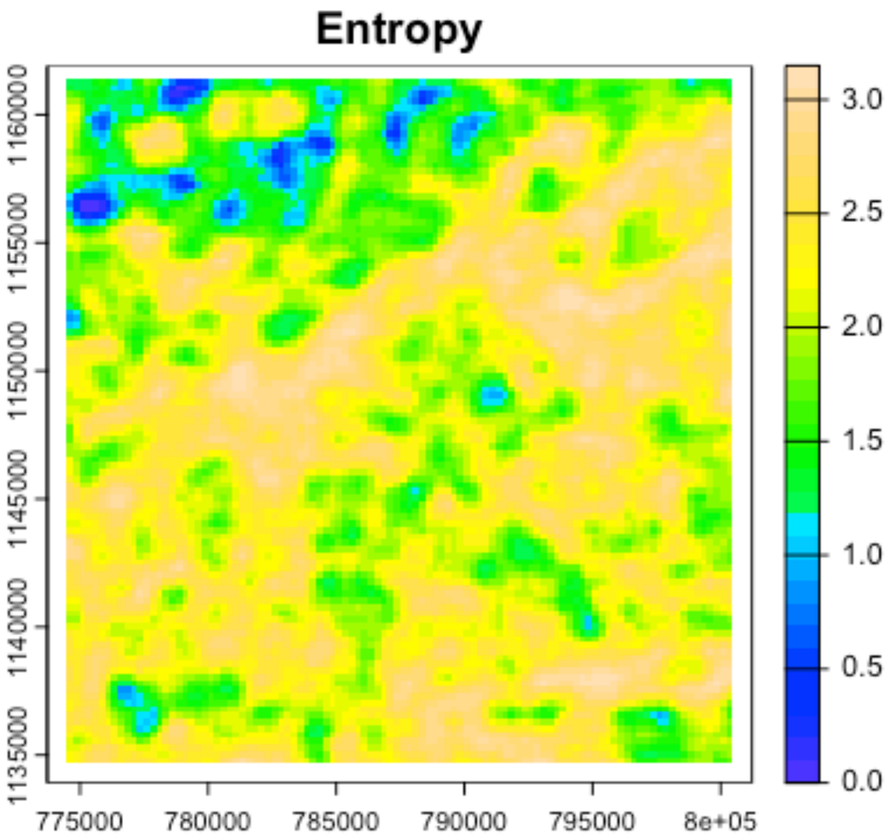
```
plot(glcm.sg[["glcm_dissimilarity"]], main = "Dissimilarity",
     col=(topo.colors(32)))
```



Entropy is a measure of information within a window. It accounts for the number of different levels in the window (the others will have "probability" zero) and their relative frequencies. More classes and more even distribution of classes results in increased entropy. This can be thought of as "lack of information".

$$\sum_{i,j=0}^{N-1} P_{i,j} \cdot -\ln(P_{i,j})$$

```
plot(glcm.sg[["glcm_entropy"]], main = "Entropy",
     col=(topo.colors(32)))
```



Challenge: compute the GLCM statistics for different window sizes.

6. Characterizing patterns – Classified

The spatial unit of conventional (legacy) maps is the polygon, not the grid cell. These maps show a discrete number of legend entries (classes), each with one to many polygons. In the soil survey context these are called **mapping units**, and generally are soil classes, possibly with some landscape features (e.g., erosion class, slope class) as part of the definition. Some mapping units may represent water bodies and various other kinds of non-soil.

Here we continue with the continuous property maps of a single property. To use these techniques on continuous property maps, the maps must be **sliced** (discretized) into classes. There are several choices:

- meaningful limits, matching some thresholds known to be important for a soil function;
- equal intervals;
- histogram equalization.

For equal intervals or histogram equalization, the cutpoints should be the same for all maps, and therefore derived from their combined distribution of values. We illustrate the process here, but do not use it for the landscape metrics examples later on in the tutorial.

6.1 Classifying by histogram equalization

This section shows how to classify by histogram equalization; the results will not be used later in the tutorial. Instead, we will use meaningful limits (see Section 6.2) to slice the map.

Task: Slice the map by histogram equalization

First, compute the histogram equalization and display the limits on a histogram plot:

```
n.class <- 8
# combined values
values.sort <- sort(values(sg4.utm[[1]]))
range(values.sort)
```

```
[1]  95.51815 148.71246
```

```
# number of pixels not NA
n.nna <- length(values.sort) - sum(is.na(values.sort))
# how many pixels in each bin
(cut.positions <- round(n.nna/n.class))
```

```
[1] 1494
```

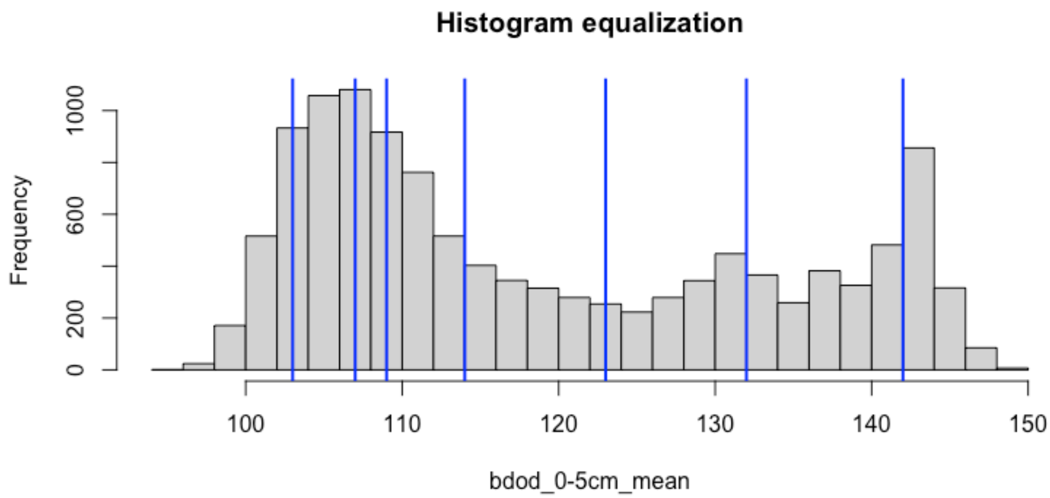
```
# the cut positions
(cuts <- values.sort[cut.positions * 1:(n.class-1)])
```

```
[1] 103.6808 106.5202 109.4846 113.9927 123.1471 132.4583 141.3245
```

```
# integer values for the cuts
cuts[1] <- floor(cuts[1]); cuts[n.class-1] <- ceiling(cuts[n.class-1])
cuts[2:n.class-2] <- round(cuts[2:n.class-2])
print(cuts)
```

```
[1] 103 107 109 114 123 132 142
```

```
hist(values.sort, breaks=36, main="Histogram equalization",
     xlab = layer.names[1])
abline(v=cuts, col="blue", lwd=2)
```



In this plot each slice has the same number of pixels.

Task: slice the map with histogram equalizatioj and display the result.

Slice the map:

```
# `rcl` is a vector with the lowest limit 0, the cuts, and the maximum valie
#       so that all values are classified
sg4.class <- terra::classify(sg4.utm[[1]],
                             rcl= c(0, cuts, ceiling(max(values.sort))))
table(values(sg4.class))
```

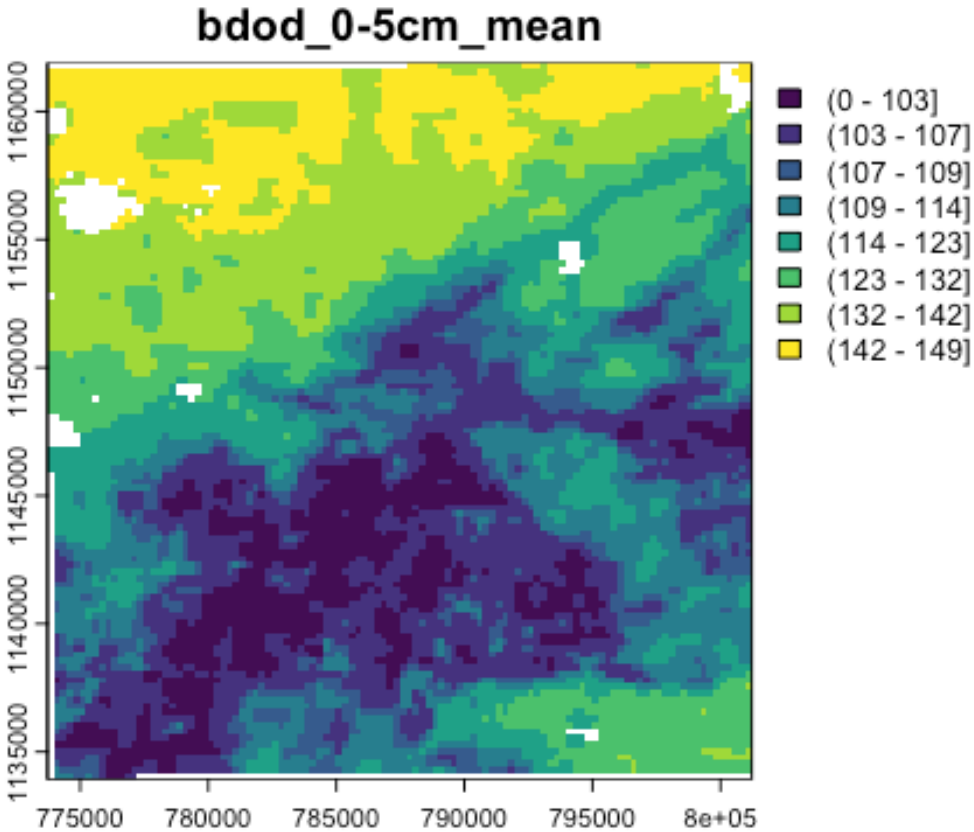
```

   0    1    2    3    4    5    6    7 
1156 2095 1014 1714 1470 1420 1815 1264 
```

```
names(sg4.class) <- "class"
```

Display the classified map:

```
terra::plot(sg4.class,
            type="classes",
            main=layer.names[1])
```



Q: Describe the patterns of the map.

Q: How would these change with different class numbers or limits?

6.2 Classifying by meaningful limits

For soil properties we usually have limits that correspond to approximate thresholds in land use. For example, in the case of pH, we can refer to extension or crop consultant publications, or environmental models. Unlike in histogram equalization, the number of classes depends on the user requirements.

For example, the Cornell pH test kit has a "Wide Range Kit" measuring the soil pH over the range of 4.0–8.6, in increments of 0.2 for an experienced user. Here we will be somewhat less precise, and slice the map in increments of 0.4 pH.

Task: slice the map of surface soil pH and display with a common colour ramp.

Find the combined range and divide into classes of 0.4 pH, starting and ending on even units of 0.4. For SoilGrids, the units are x10, so the limits are every 4.

Set up the cut points.

```
# find the layer number for this property
# note: SoilGrids is pH x 10
(ix.ph05 <- which(layer.names == "phh2o_0-5cm_mean"))
```

```
[1] 25
```

```
(cuts <- seq(floor(min(values(sg4.utm[[ix.ph05]], na.rm = TRUE))),
             ceiling(max(values(sg4.utm[[ix.ph05]], na.rm = TRUE))),
             by = 4))
```

```
[1] 53 57 61 65 69 73
```

Slice the map of surface soil pH:

```
sg.ph.class <- terra::classify(sg4.utm[[ix.ph05]], rcl= cuts)
table(values(sg.ph.class))
```

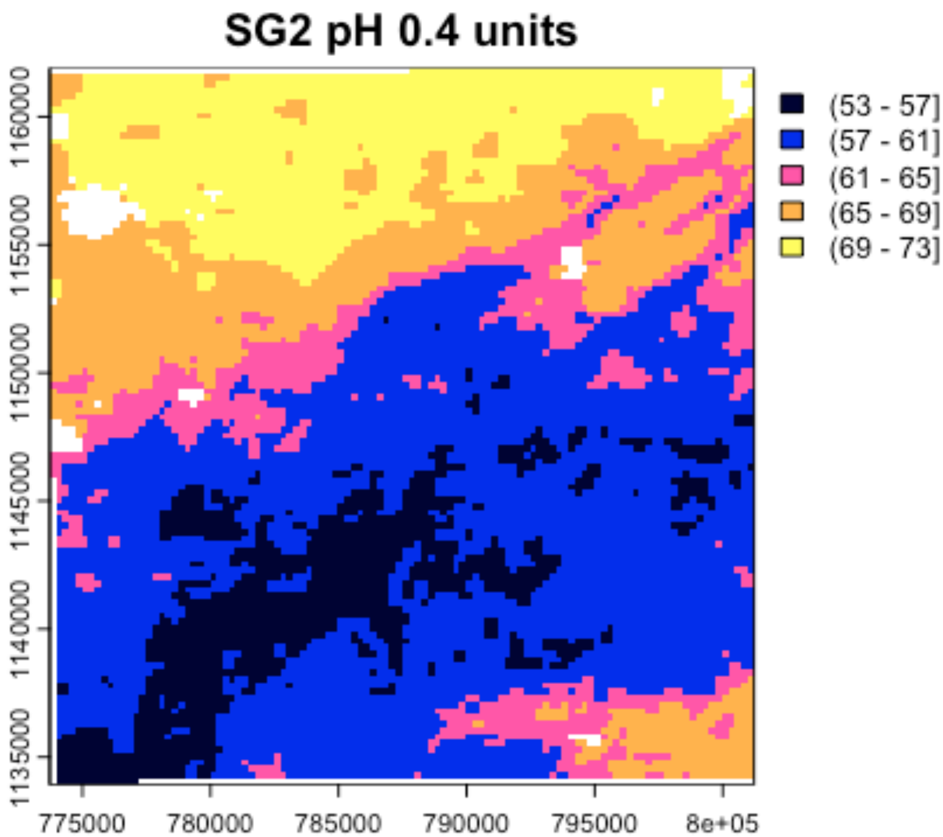
```

   0    1    2    3    4 
1485 5047 1374 2061 1972 
```

```
names(sg.ph.class) <- "class"
```

Display it:

```
terra::plot(sg.ph.class,
            col=sp::bpy.colors(length(cuts)), type="classes",
            main="SG2 pH 0.4 units")
```



Q: Describe the pattern of the map.

Q: How would the maps change with wider or narrower class intervals? You are welcome to experiment!

6.3 Co-occurrence matrices

One question for a classified map is which classes tend to be adjacent to each other. In the case of the pH map, we might expect adjacent classes to be in the pH sequence, but maybe not – there may be abrupt transitions of parent materials, for example.

A co-occurrence *matrix* counts all the pairs of adjacent cells for each category in a local landscape, as a cross-classification matrix.

Task: Compute the co-occurrence *matrices*, using Queen's Case neighbours (i.e., diagonal links are considered).

Co-occurrence vectors are computed with the `lsp_signature` function of the `motif` package, specifyin `coma` = co-occurrence matrix as the signature.

```
coma.ph <- lsp_signature(sg.ph.class, type="coma", neighbourhood = 8)
head(coma.ph.matrix <- as.matrix(coma.ph$signature)[[1]])
```

```
     1     2    3     4     5
1 9308  2470    0     0     0
2 2470 35808 1705     6     0
3    0  1705 7628  1405     0
4    0     6 1405 13714   904
5    0     0    0   904 14368
```

```
# proportion with adjacent of the same class
sum(diag(coma.ph.matrix))/sum(coma.ph.matrix)
```

```
[1] 0.8616293
```

The proportion of neighbour pixels with the same class as the corresponding centre pixel is 0.86.

Q: Describe the co-occurrence structure. What does this imply for the spatial pattern?

6.4 Co-occurrence vectors

The **Co-occurrence vector** "COVE" proposed by Nowosad & Stepinski (2018) summarizes the *entire adjacency structure* of a map and can be used to compare map structures. This is a normalized form of the co-occurrence matrix (see the previous section). Normalization means the matrix sums to 1, and so is independent of the number of grid cells in the map. Therefore this vector can be considered as a probability vector for the co-occurrence of different classes.

Task: Compute the co-occurrence *vectors*, using Queen's Case neighbours.

Co-occurrence vectors are computed with the `lsp_signature` function of the `motif` package, specifying `cove` (normalized co-occurrence vector) as the signature.

```
# normalized co-occurence vector 8 x 8
print(cove.ph <- lsp_signature(sg.ph.class, type="cove", neighbourhood = 8))
```

```
# A tibble: 1 × 3
     id na_prop signature
* <int>   <dbl> <list>
1     1  0.0309 <dbl [1 × 15]>
```

6.5 Integrated co-occurrence vector

An *integrated* co-occurrence vector considers *several input layers*, for example representing different soil properties of the same area.

To examine this we need another soil property map. Let's use silt of the 0–5~cm layer. We process this as we did for the pH map. Here the "meaningful limits" for silt content are 5% intervals. Since the SG2 map is expressed in g kg^{-1}, these are intervals of 50 g kg^{-1}.

```
(ix.silt05 <- which(layer.names == "silt_0-5cm_mean"))
```

```
[1] 31
```

```r
summary(sg4.utm[[ix.silt05]])
```

```
 silt_0.5cm_mean
 Min.   :213.7
 1st Qu.:261.6
 Median :276.7
 Mean   :278.9
 3rd Qu.:295.4
 Max.   :366.6
 NA's   :372
```

```r
(cuts <- seq(floor(min(values(sg4.utm[[ix.silt05]]-50, na.rm = TRUE))),
             ceiling(max(values(sg4.utm[[ix.silt05]]+50, na.rm = TRUE))),
             by = 50))
```

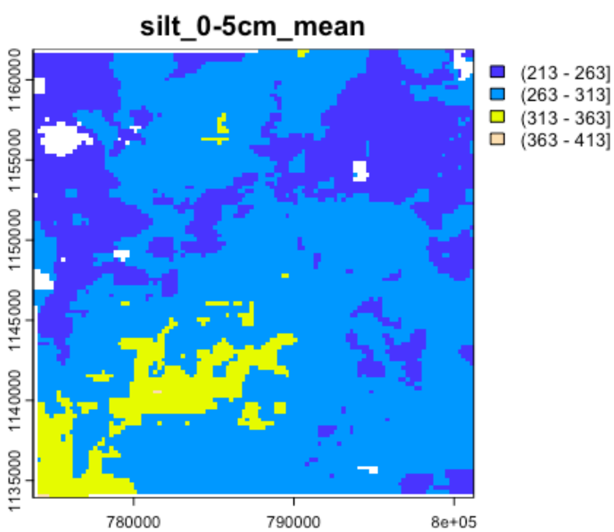
```
[1] 163 213 263 313 363 413
```

```r
sg.silt.class <- terra::classify(sg4.utm[[ix.silt05]], rcl= cuts)
table(values(sg.silt.class))
```

```

   1    2    3    4
3261 7743  939    5
```

```r
names(sg.silt.class) <- "class"
plot(sg.silt.class, col = topo.colors(11),
     main = layer.names[ix.silt05])
```



This map has much larger homogeneous areas than the pH map.

Examine this single map's co-occurrence matrix and vector:

```r
#|.label: coma-cove
coma.silt <- lsp_signature(sg.silt.class, type="coma", neighbourhood = 8)
print(coma.silt.matrix <- as.matrix(coma.silt$signature)[[1]])
```

```
      2     3    4   5
2 21978  3406    0   0
3  3406 56252 1451   0
4     0  1451 5896  23
5     0     0   23   6
```

```
sum(diag(coma.silt.matrix))/sum(coma.silt.matrix)
```

```
[1] 0.8960508
```

```
# the co-occurrence vector
(cove.silt <- lsp_signature(sg.silt.class, type="cove", neighbourhood = 8))
```

```
# A tibble: 1 × 3
     id na_prop signature
* <int>   <dbl> <list>
1     1  0.0302 <dbl [1 × 10]>
```

Most of the adjacencies are to the same class, or the adjacent class.

Task: Compute the distance between the co-occurrence vectors for pH and silt:

```
cove.df <- data.frame(cove.ph)$signature[[1]][1,]
cove.df <- rbind(cove.df, cove.silt$signature[[1]][1,])
cove.dists <- round(
  philentropy::distance(cove.df, method = "jensen-shannon",
                        use.row.names =TRUE,
                        as.dist.obj = FALSE,
                        diag = FALSE) ,4)
```

```
Metric: 'jensen-shannon' using unit: 'log'; comparing: 2 vectors.
```

```
print(cove.dists)
```

```
jensen-shannon
        0.4302
```

6.6 Clustering pattern differences

Once a pattern metric is shown across a map, a natural question is whether different areas of the map have different patterns. We illustrate this with the pattern of the integrated co-occurrence vectors.

Any size window can be used. If too small the result is erratic, if too large, local differences may be missed.

Task: Identify which parts of the SG2 map have similar *integrated co-occurrence* pattern differences, considering both properties. For this we use 4 x 4 km windows, i.e., 16 x 16 grid cells.

Again we use `lsp_signature`, type `"incove"`, but now specifying a `window` size within which to compute the pattern.

```
sg.ph.silt.class <- c(sg.ph.class, sg.silt.class)
incove.sg <- lsp_signature(sg.ph.silt.class,
                            type = "incove",
                            neighbourhood = 8,
                            ordered = TRUE,  # the pH classes are ordered
                            window = 16,
                            normalization = "pdf")  #sum to one
summary(incove.sg.dist <- lsp_to_dist(incove.sg,
                            dist_fun = "jensen-shannon"))
```

```
Metric: 'jensen-shannon' using unit: 'log2'; comparing: 49 vectors.
```

```
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
0.003583 0.246388 0.559705 0.509044 0.729169 0.996896
```

```
dim(incove.sg.dist)
```

```
[1] 49 49
```

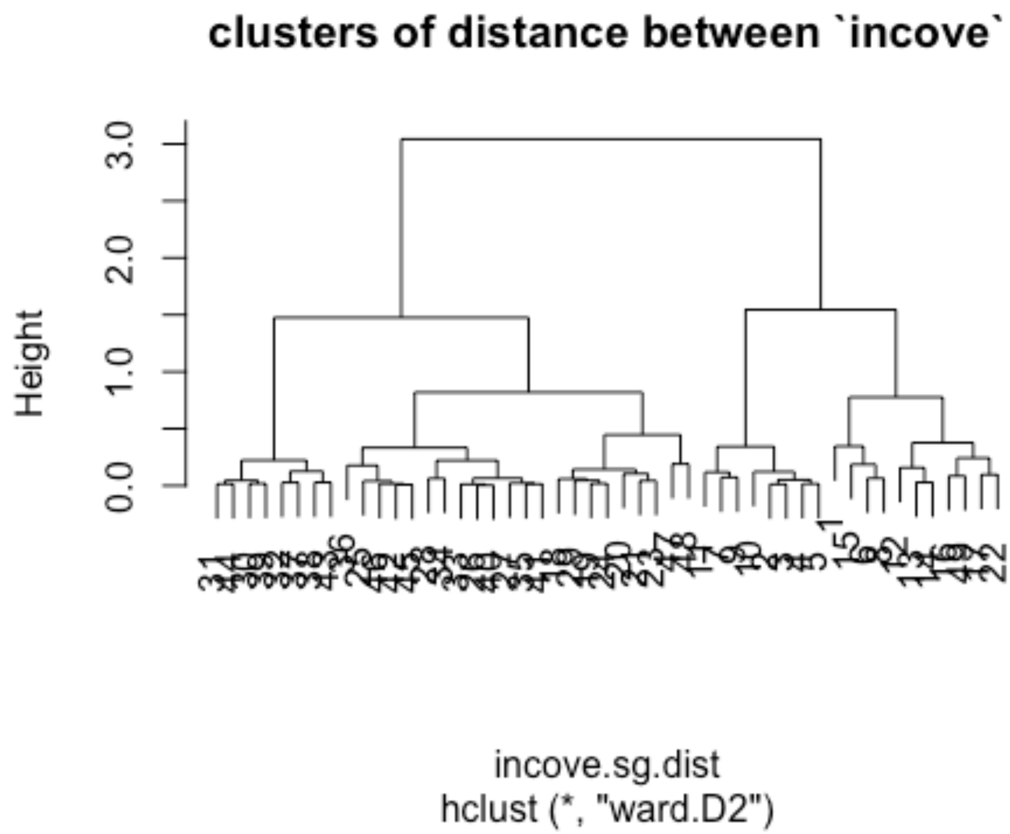
Here we have defined 49 x 49 distances, i.e., paired distances between each of the windows' signatures.

Are any of these distances similar? Let's see with a *cluster analysis*.

Task: Make a hierarchical clustering of the distances between the integrated co-occurrence vectors of the windows.

The `hclust` function can cluster using many methods to build the dendrogram. Here we use Ward's D2 method, which aims at finding compact, spherical clusters.

```
sg.hclust <- hclust(incove.sg.dist, method = "ward.D2")
plot(sg.hclust, main = "clusters of distance between `incove`")
```



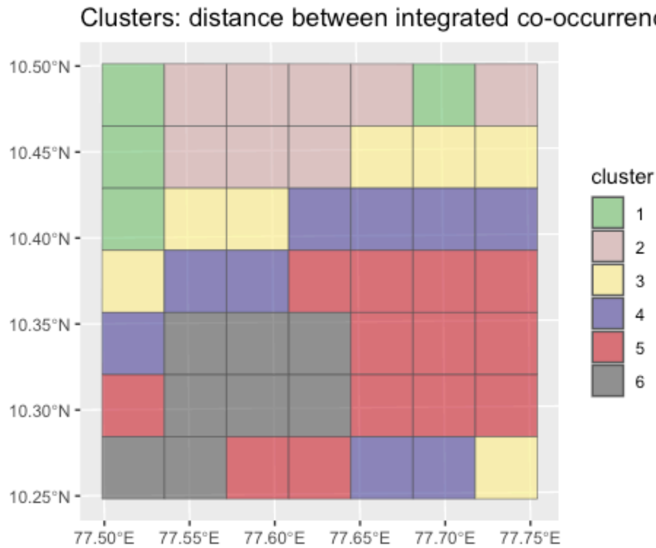
Task: Define classes of similar distances by cutting the dendrogram.

Examining the dendrogram, it seems that height `h = 0.5` is a good cutting point, which captures the main differences. Alternatively, a set number of clusters can be requested with the `k` argument.

```
sg.clusters <- as.factor(cutree(sg.hclust, h = 0.5))  # cutpoint by visual inspection
levels(sg.clusters)
```

```
[1] "1" "2" "3" "4" "5" "6"
```

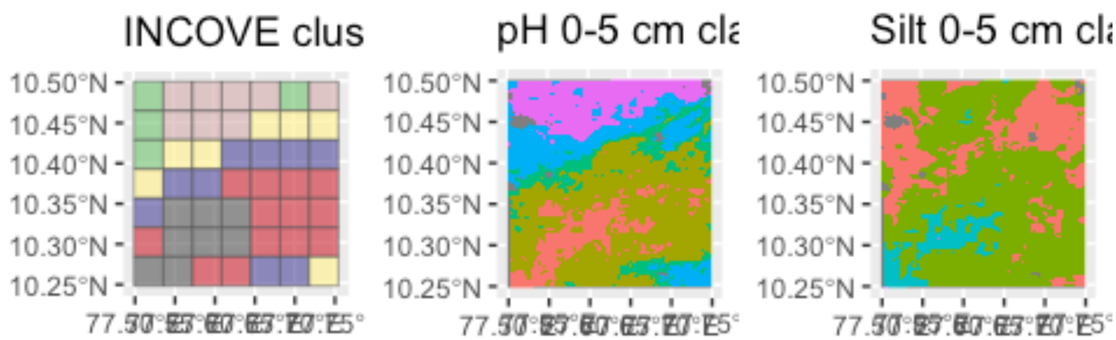
```
sg.grid.sf = lsp_add_clusters(incove.sg, sg.clusters)
sg.grid.sf$clust <- as.factor(sg.grid.sf$clust)
my.pal <- colorRampPalette(brewer.pal(8, "Accent"))(length(levels(sg.grid.sf$clust)))
ggplot(data = sg.grid.sf) +
  geom_sf(aes(fill = clust), alpha = 0.7) +
  scale_fill_discrete(type = my.pal) +
  labs(title = "Clusters: distance between integrated co-occurrence vectors",
       fill = "cluster")
```



This shows which areas of the map have similar integrated co-occurrence patterns. These can be interpreted as similar soils, in the sense that the sum of propertied defines a soil type.

Compare this to a visual inspection of the patterns, next to the 7 x 6 cluster grid.

```
p1 <- ggplot(data = sg.grid.sf) +
  geom_sf(aes(fill = clust), alpha = 0.7) +
  scale_fill_discrete(type = my.pal) +
  labs(fill = "cluster", title = "INCOVE clusters")  +
  theme(legend.position="none")
p2 <- ggplot() +
  tidyterra::geom_spatraster(data = sg.ph.class, aes(fill = class)) +
   theme(legend.position="none") +
   labs(title = "pH 0-5 cm classes")
p3 <- ggplot() +
  tidyterra::geom_spatraster(data = sg.silt.class, aes(fill = class)) +
   theme(legend.position="none") +
   labs(title = "Silt 0-5 cm classes")
gridExtra::grid.arrange(p1, p2, p3, nrow=1)
```



Careful examination reveals that the cluster in the NW corner corresponds to an intricate pattern of pH and mostly one class of silt concentration.

6.7 Landscape metrics

Landscape metrics have a long history of use in landscape ecology (Uuemaa et al., 2013). A wide variety have been collected in the well-known FRAGSTATS computer program (McGarigal et al., 2012). These have been implemented in the R context by the `landscapemetrics` package[1] (Hesselbarth et al., 2019; Hesselbarth, 2021). Although the ecological relevance of FRAGSTATS metrics have been criticized (Kupfer, 2012), here we use them to *characterize spatial patterns of soil properties* or *classes*, not as inputs to landscape ecology models.

These were used to compare soil maps of the same area by Rossiter et al. (2022).

The patterns of soil classes or properties are not expected to have the same characteristics as those for land cover or vegetation types. Land cover is largely controlled by humans, and where it is not, vegetation is mostly placed on the landscape by different mechanisms than are soils. There is a link, however: if the soil property is largely controlled by the o

[1] https://r-spatialecology.github.io/landscapemetrics/

(organism) or h (human) factor, then the patterns on the landscape could be similar to those under it.

There are many metrics, of three levels of detail. We list them here for reference; each has its own help text.

First, the *patch-level metrics*. These describe every patch, i.e., contiguous cells belonging to the same class.

```
landscapemetrics::list_lsm(level="patch") %>% print(n = 12)
```

```
# A tibble: 12 × 5
   metric name                               type           level
function_name
   <chr>  <chr>                              <chr>          <chr> <chr>
 1 area   patch area                         area and edge… patch lsm_p_area
 2 cai    core area index                    core area met… patch lsm_p_cai
 3 circle related circumscribing circle      shape metric   patch
lsm_p_circle
 4 contig contiguity index                   shape metric   patch
lsm_p_contig
 5 core   core area                          core area met… patch lsm_p_core
 6 enn    euclidean nearest neighbor distance aggregation m… patch lsm_p_enn
 7 frac   fractal dimension index            shape metric   patch lsm_p_frac
 8 gyrate radius of gyration                 area and edge… patch
lsm_p_gyrate
 9 ncore  number of core areas               core area met… patch
lsm_p_ncore
10 para   perimeter-area ratio               shape metric   patch lsm_p_para
11 perim  patch perimeter                    area and edge… patch
lsm_p_perim
12 shape  shape index                        shape metric   patch
lsm_p_shape
```

Second, the *class-level* metrics. These describe all patches belonging to a specified class.

```
landscapemetrics::list_lsm(level="class") %>% print(n = 12)
```

```
# A tibble: 55 × 5
   metric    name                         type                 level
function_name
   <chr>     <chr>                        <chr>                <chr> <chr>
 1 ai        aggregation index            aggregation metr… class lsm_c_ai
 2 area_cv   patch area                   area and edge me… class
lsm_c_area_cv
 3 area_mn   patch area                   area and edge me… class
lsm_c_area_mn
 4 area_sd   patch area                   area and edge me… class
lsm_c_area_sd
 5 ca        total (class) area           area and edge me… class lsm_c_ca
 6 cai_cv    core area index              core area metric  class
```

```
lsm_c_cai_cv
 7 cai_mn     core area index                core area metric  class
lsm_c_cai_mn
 8 cai_sd     core area index                core area metric  class
lsm_c_cai_sd
 9 circle_cv related circumscribing circle shape metric      class
lsm_c_circle…
10 circle_mn related circumscribing circle shape metric      class
lsm_c_circle…
11 circle_sd related circumscribing circle shape metric      class
lsm_c_circle…
12 clumpy     clumpiness index               aggregation metr… class
lsm_c_clumpy
# ℹ 43 more rows
```

Finally, the *landscape-level* metrics. These describe the characteristics of the entire landscape, i.e., the assemblage of classes and patches.

```
landscapemetrics::list_lsm(level="landscape") %>% print(n = 12)
```

```
# A tibble: 66 × 5
   metric    name                           type              level
function_name
   <chr>     <chr>                          <chr>             <chr> <chr>
 1 ai        aggregation index              aggregation metr… land… lsm_l_ai
 2 area_cv   patch area                     area and edge me… land…
lsm_l_area_cv
 3 area_mn   patch area                     area and edge me… land…
lsm_l_area_mn
 4 area_sd   patch area                     area and edge me… land…
lsm_l_area_sd
 5 cai_cv    core area index                core area metric  land…
lsm_l_cai_cv
 6 cai_mn    core area index                core area metric  land…
lsm_l_cai_mn
 7 cai_sd    core area index                core area metric  land…
lsm_l_cai_sd
 8 circle_cv related circumscribing circle shape metric      land…
lsm_l_circle…
 9 circle_mn related circumscribing circle shape metric      land…
lsm_l_circle…
10 circle_sd related circumscribing circle shape metric      land…
lsm_l_circle…
11 cohesion  patch cohesion index           aggregation metr… land…
lsm_l_cohesi…
12 condent   conditional entropy            complexity metric land…
lsm_l_condent
# ℹ 54 more rows
```

6.7.1 Landscape-level metrics

These measures summarize the pattern of the entire map. The following five seem to be most useful for characterizing soil maps.

- **ai**: The **landscape aggregation index** LAI is an 'Aggregation metric'. This shows how much the classes occur as large units, vs. as scattered patches. It is independent of the number of classes.

It equals the number of like adjacencies divided by the theoretical maximum possible number of like adjacencies for that class summed over each class for the entire landscape. The metric is based on the adjacency matrix. It equals 0 for maximally disaggregated and 100 for maximally aggregated classes. More info

$$\mathrm{LAI} = \left[\sum_{i=1}^{m} \left(\frac{g_{ii}}{max - g_{ii}}\right) P_i\right] (100)$$

where g_{ii} is the number of like adjacencies, $(\max - g_{ii})$ is the class-wise maximum possible number of like adjacencies of class i (i.e., if all pixels in the class were in one cluster), and P_i is the proportion of landscape comprised of class i, to weight the index by class prevalence.

- **frac_mn**: The **mean fractal dimension** FRAC_MN is a 'Shape metric'. It summarises the landscape as the mean of the fractal dimension index of all patches in the landscape, i.e., the complexity of the map.

The fractal dimension index is based on the patch perimeter and the patch area and describes the patch complexity. The Coefficient of variation is scaled to the mean and thus is comparable among different landscapes. More info

$$\mathrm{FRAC} = \frac{2 * \ln * (0.25 * p_{ij})}{\ln a_{ij}}$$

where the patch perimeters are p_{ij} in linear units and the areas are a_{ij} in square units.

- **lsi**: **landscape shape index** LSI is an 'Aggregation metric'. It is the ratio between the actual edge length of class i and the hypothetical minimum edge length of class i. It measures how compact are the classes. For example, long thin classes will have low LSI.

The minimum edge length equals the edge length if class i would be maximally aggregated. LSI = 1 when only one square patch is present or all patches are maximally aggregated. Increases, without limit, as the length of the actual edges increases, i.e. the patches become less compact. More info

$$\mathrm{LSI} = \frac{0.25E'}{\sqrt{A}}$$

where A is the total area of the landscape and E' is the total length of edges, including the boundary.

- **shdi**: The **Shannon diversity index** SHDI is a 'Diversity metric'. It is a widely used metric in biodiversity and ecology and takes both the number of classes and the abundance of each class into account. It is related to the concept of entropy: how much "information" is in the landscape pattern. More classes and more even distribution of their areas implies high information.

SHDI = 0 when only one patch is present and increases, without limit, as the number of classes increases while the proportions are equally distributed. More info

$$D = -\sum_{i=1}^{N} p_i \ln p_i$$

where p_i is the proportion of pixels of class $i = (1 \ldots N)$,

- **shei**: The **Shannon evenness index** SHEI is a 'Diversity metric'. It is the ratio between the Shannon's diversity index D (see previous) and and the theoretical maximum Shannon diversity index $\ln N$. It can be understood as a measure of dominance.

SHEI = 0 when only one patch present; SHEI = 1 when the proportion of classes is equally distributed. More info

$$E = \frac{D}{\ln N}$$

These methods must be applied to classified maps. Continuous soil property maps must first be classified into ranges before analysis, see (Section 6.1) and (Section 6.2), above. Different choices of class limits and widths will result in different values of these measures.

6.7.2 Computing landscape-level metrics

The `landscapemetrics` package implements a set of metrics as used in ecology and derived from the FRAGSTATS computer program; the metrics are explained in the previous section. Here we compute them for the two maps we are comparing.

To compute landscape metrics:

- Input is raster map (here, a `terra::SpatRaster`) with integer values, each of which represents a category, i.e., landscape class.
- The map must be in a projected CRS, with distance units in meters;
- Results are in meters, square meters or hectares, depending on the function;

Task: Check that the maps have the proper structure for the landscape metrics.

This is done with the `landscapemetrics::check_landscape` function.

```
check_landscape(sg.ph.class)
```

```
  layer       crs units   class n_classes OK
1     1 projected     m integer         5  ✓
```

```
check_landscape(sg.silt.class)
```

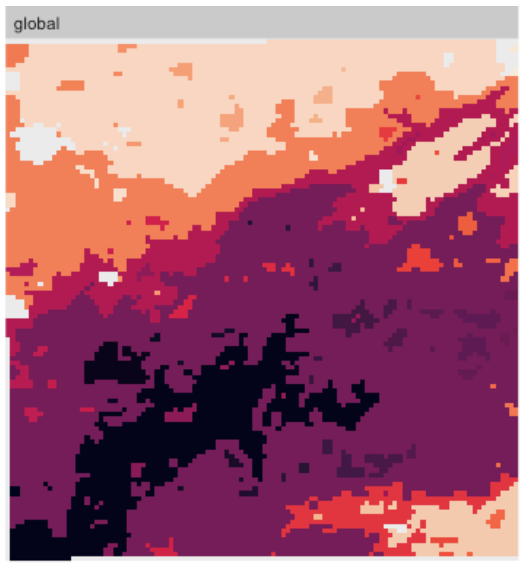
```
  layer       crs units   class n_classes OK
1     1 projected     m integer         4  ✓
```

Task: Show the landscapes of each layer, first with all classes on one map, then with the classes separate:

global:

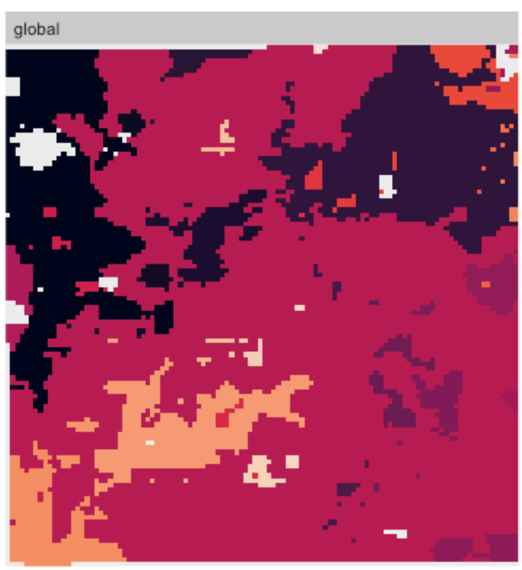
```
show_patches(sg.ph.class, class = "global")
```

```
$layer_1
```




```
show_patches(sg.silt.class, class = "global")
```

```
$layer_1
```



per-class:

```
show_patches(sg.ph.class, class = "all", nrow = 3)
```

```
$layer_1
```


```
show_patches(sg.silt.class, class = "all", nrow = 3)
```

```
$layer_1
```

Q: Describe the main differences between the patterns. Which map seems more aggregated? More diverse?

Task: compute the metrics and tabulate them:

```
lst <- paste0("lsm_l_", c("shdi", "shei", "lsi", "ai",  "frac_mn"))
ls.metrics.ph <- calculate_lsm(sg.ph.class, what=lst)
ls.metrics.silt <- calculate_lsm(sg.silt.class, what=lst)
metrics.table <- data.frame(product=c("pH", "silt"),
                            rbind(round(ls.metrics.ph$value, 3),
                                  round(ls.metrics.silt$value, 3)))
names(metrics.table)[2:6] <- ls.metrics.ph$metric
metrics.table
```

```
  product     ai frac_mn   lsi  shdi  shei
1      pH 88.716   1.033 7.806 1.473 0.915
2    silt 91.379   1.033 6.132 0.839 0.605
```

Q: Referring to the descriptions of these metrics (above), what are the differences between these maps' landscape patterns? Where do the maps most differ?

- Aggregation Index

- Mean Fractal Dimension
- Landscape Shape Index
- Shannon Diversity
- Shannon Evenness

Question: Which maps in the DSM stack do you expect to have similar landscape metrics?

7. Supercells

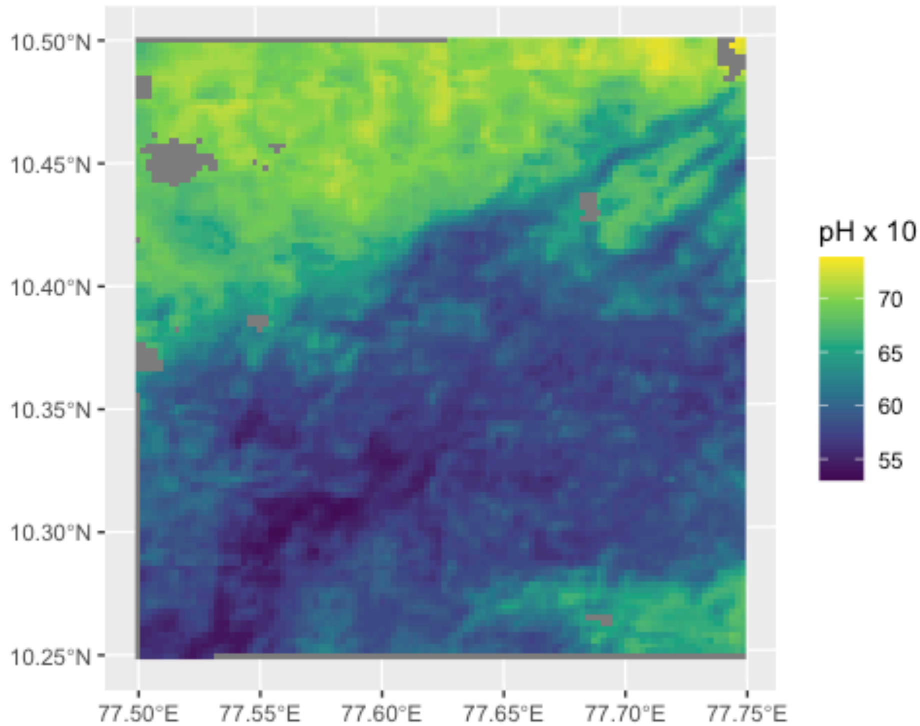
"Superpixels" is a generic name for grouping pixels with similar characteristics into larger assemblages. In the soil map context, the aim is to regionalize into areas with similar values of one or more raster layers.

The `supercells::supercells` function controls the segmentation: the user can specify the `k` argument for the number of supercells, and the `compactness` argument to control shape: larger values lead to more square, less long/twisted shapes. It is also possible to specify a set of initial supercell centres (with an `sf` POINTS geometry) or a separation between initial centres with the `step` argument.

This function implements the SLIC algorithm (Achanta et al., 2012).

As an example with the pH map, we divide into about 50 supercells, with low compactness since we don't expect near-square natural units. Here is the source map:

```
ggplot() +
  geom_spatraster(data=sg4.utm[[ix.ph05]]) +
  scale_fill_viridis_c() +
  labs(fill = "pH x 10")
```

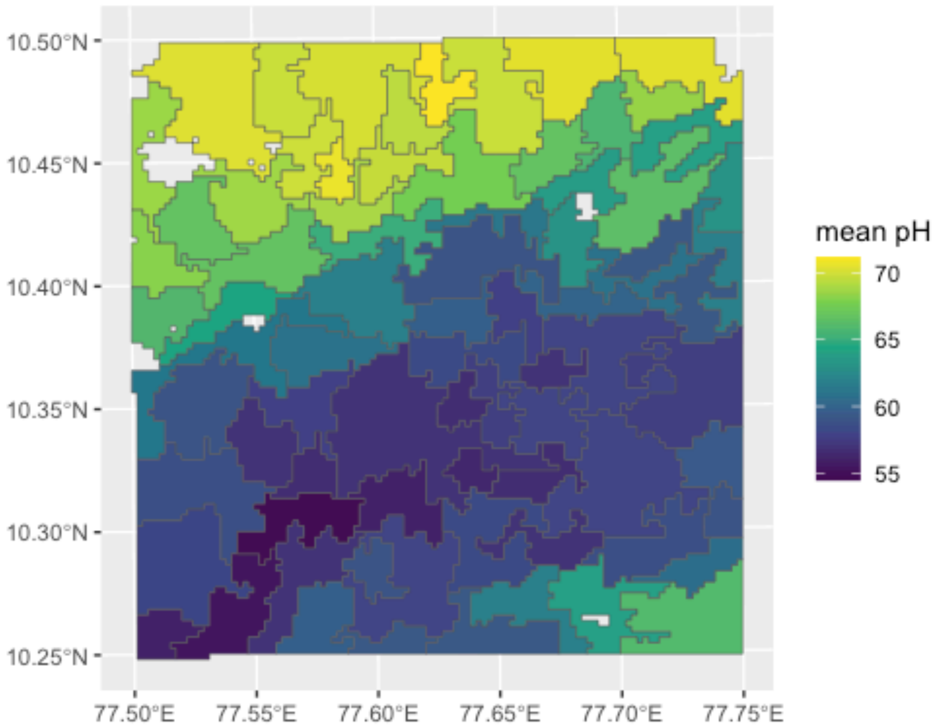


And here are the 50 supercells, with very low compactness, i.e., allowing for irregular and elongated shapes:

```
sg4.ph.50 = supercells(sg4.utm[[ix.ph05]], k = 100, compactness = 0.05)
names(sg4.ph.50)
```

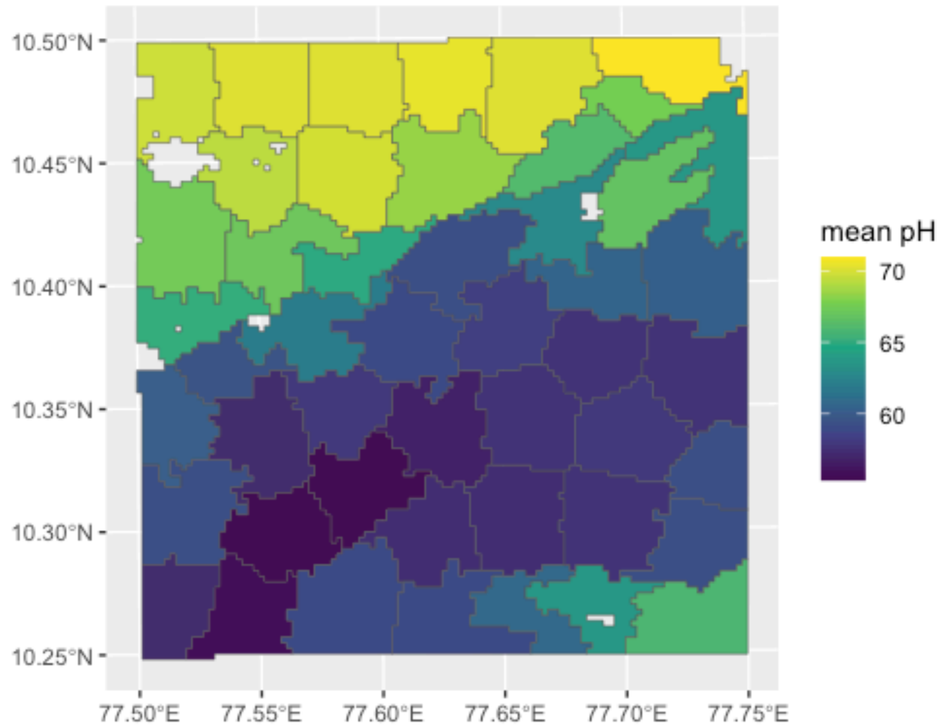
```
[1] "supercells"        "x"                   "y"
"phh2o_0.5cm_mean"
[5] "geometry"
```

```
names(sg4.ph.50)[4] <- "pH_05cm" # `supercells` changes the name -- a bug?
ggplot(data=sg4.ph.50) +
  geom_sf(aes(fill = pH_05cm)) +
  scale_fill_viridis_c() +
  labs(fill = "mean pH")
```



Try to form more compact supercells:

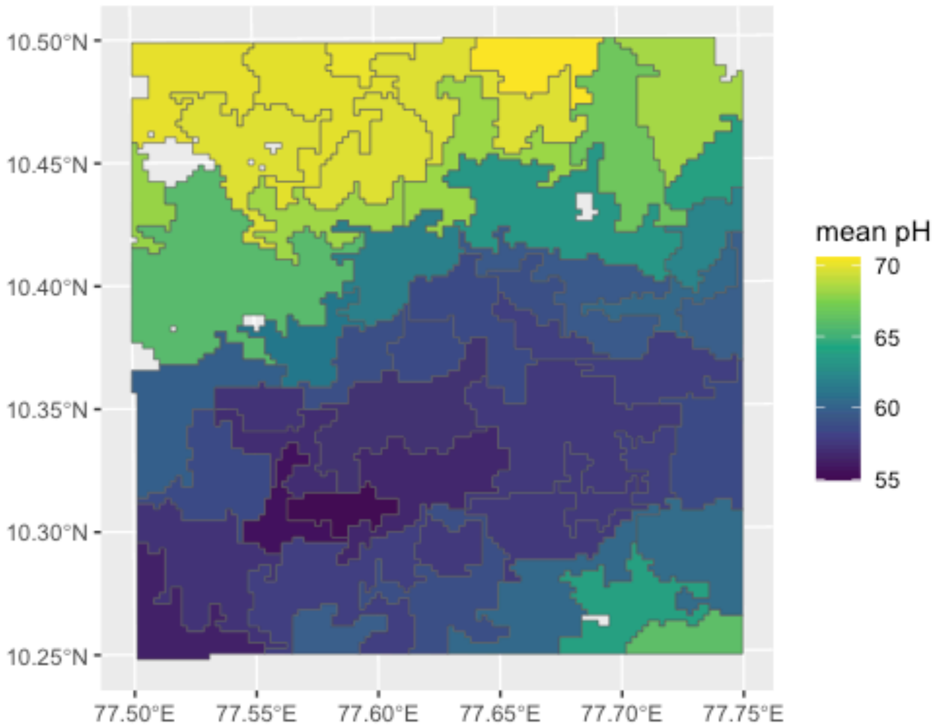
```
sg4.ph.50 = supercells(sg4.utm[[ix.ph05]], k = 50, compactness = 3)
names(sg4.ph.50)[4] <- "pH_05cm" # `supercells` changes the name -- a bug?
ggplot(data=sg4.ph.50) +
  geom_sf(aes(fill = pH_05cm)) +
  scale_fill_viridis_c() +
  labs(fill = "mean pH")
```



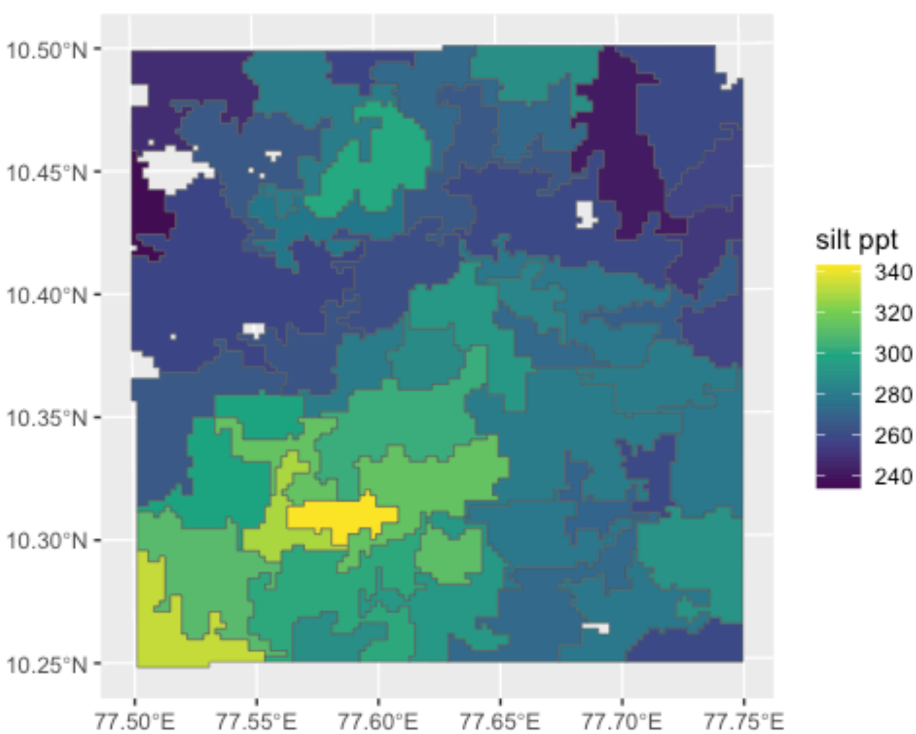
These do not look realistic.

Try with multiple rasters, here pH and silt concentrations:

```
r <- c(sg4.utm[[ix.ph05]], sg4.utm[[ix.silt05]])
r.50 = supercells(r, k = 50, compactness = 0.1)
ggplot(data=r.50) +
  geom_sf(aes(fill = phh2o_0.5cm_mean)) +
  labs(fill = "mean pH") +
  scale_fill_continuous(type = "viridis")
```




```
ggplot(data=r.50) +
  geom_sf(aes(fill = silt_0.5cm_mean)) +
  labs(fill = "silt ppt") +
  scale_fill_continuous(type = "viridis")
```



The segments are the same in the two visualizations.

Challenge: Experiment with different `compactness` and `k` parameters. Which seem to give a more "realistic" landscape pattern?

8. References

Achanta, R., Shaji, A., Smith, K., Lucchi, A., Fua, P., & Süsstrunk, S. (2012). SLIC Superpixels compared to state-of-the-art superpixel methods. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, *34*(11), 2274–2282. IEEE Transactions on Pattern Analysis and Machine Intelligence. https://doi.org/10.1109/TPAMI.2012.120

Boulaine, J. (1982). Remarques sur quelques notions élémentaires de la pédologie". *Cahiers O.R.S.T.O.M., Série Pédologie*, *19*(1), 29–41.

Brus, D. J., Kempen, B., & Heuvelink, G. B. M. (2011). Sampling for validation of digital soil maps. *European Journal of Soil Science*, *62*, 394–407. https://doi.org/10.1111/j.1365-2389.2011.01364.x

Fridland, V. M. (1974). Structure of the soil mantle. *Geoderma*, *12*, 35–42. https://doi.org/10.1016/0016-7061(74)90036-6

Hall-Beyer, M. (2017a). *GLCM Texture: A Tutorial v. 3.0 March 2017*. http://hdl.handle.net/1880/51900

Hall-Beyer, M. (2017b). Practical guidelines for choosing GLCM textures to use in landscape classification tasks over a range of moderate spatial scales. *International Journal of Remote Sensing*, *38*(5), 1312–1338. https://doi.org/10.1080/01431161.2016.1278314

Haralick, R. M., Shanmugam, K., & Dinstein, I. (1973). Textural features for image classification. *IEEE Transactions on Systems, Man, and Cybernetics*, *SMC-3*(6), 610–621. IEEE Transactions on Systems, Man, and Cybernetics. https://doi.org/10.1109/TSMC.1973.4309314

Hesselbarth, M. H. K. (2021). *R-Spatialecology/Landscapemetrics*. r-spatialecology. https://github.com/r-spatialecology/landscapemetrics

Hesselbarth, M. H. K., Sciaini, M., With, K. A., Wiegand, K., & Nowosad, J. (2019). Landscapemetrics: An open-source R tool to calculate landscape metrics. *Ecography*, *42*, 1648–1657. https://doi.org/10.1111/ecog.04617

Johnson, W. M. (1963). The Pedon and the Polypedon. *Soil Science Society of America Journal*, *27*(2), 212–215. https://doi.org/10.2136/sssaj1963.03615995002700020034x

Kupfer, J. A. (2012). Landscape ecology and biogeography: Rethinking landscape metrics in a post-FRAGSTATS landscape. *Progress in Physical Geography-Earth and Environment*, *36*(3), 400–420. https://doi.org/10.1177/0309133312439594

Mahoney, M. J., Johnson, L. K., Silge, J., Frick, H., Kuhn, M., & Beier, C. M. (2023). *Assessing the performance of spatial cross-validation approaches for models of spatially structured data* (arXiv:2303.07334). arXiv. https://doi.org/10.48550/arXiv.2303.07334

McGarigal, K., Cushman, S. A., & Ene, E. (2012). *FRAGSTATS v4: Spatial pattern analysis program for categorical and continuous maps*. University of Massachusetts. http://www.umass.edu/landeco/research/fragstats/fragstats.html

Minasny, B., McBratney, A. B., & Whelan, B. M. (2005). *VESPER: Variogram Estimation and Spatial Prediction plus ERror - Australian Centre for Precision Agriculture*. https://precision-agriculture.sydney.edu.au/resources/software/download-vesper/.

Nowosad, J., & Stepinski, T. F. (2018). Spatial association between regionalizations using the information-theoretical V-measure. *International Journal of Geographical Information Science*, *32*(12), 2386–2401. https://doi.org/10.1080/13658816.2018.1511794

Open Geospatial Consortium. (2023). OGC GeoTIFF Standard. In *OGC GeoTIFF Standard*. https://www.ogc.org/standard/geotiff/.

Piikki, K., Wetterlind, J., Söderström, M., & Stenberg, B. (2021). Perspectives on validation in digital soil mapping of continuous attributes a review. *Soil Use and Management*, *37*(1), 7–21. https://doi.org/10.1111/sum.12694

Poggio, L., de Sousa, L. M., Batjes, N. H., Heuvelink, G. B. M., Kempen, B., Ribeiro, E., & Rossiter, D. (2021). SoilGrids 2.0: Producing soil information for the globe with quantified spatial uncertainty. *SOIL*, *7*(1), 217–240. https://doi.org/10.5194/soil-7-217-2021

Rossiter, D. G., Poggio, L., Beaudette, D., & Libohova, Z. (2022). How well does digital soil mapping represent soil geography? An investigation from the USA. *SOIL*, *8*(2), 559–586. https://doi.org/10.5194/soil-8-559-2022

Uuemaa, E., Mander, U., & Marja, R. (2013). Trends in the use of landscape spatial metrics as landscape indicators: A review. *Ecological Indicators*, *28*, 100–106. https://doi.org/10.1016/j.ecolind.2012.07.018