Spatial Sampling

Sampling optimization for soil mapping

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Overview

- Digital soil mapping
- Sampling for soil mapping

Hands-on:

- Sampling for model training to create a soil map
- Sampling for map validation
- Do the sampling (virtually) and create a map

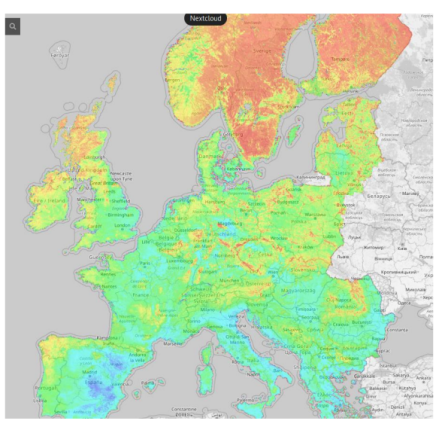
1 Motivation for sampling: Soil mapping

1.1 Need for soil information

Soil data or information: maps, point observations, monitoring networks.

Needed by many actors like governments, companies, farms:

- Local applications: prevent soil compaction, subsidies to prevent erosion
- Spatial planning: save high-quality soils for agriculture and plan nature reserves at locations with high habitat potential
- Monitor soil health on European level



(Der rekultivierte Boden, https://boden-des-jahres.ch / BAFU Magazin / Ecodatacube)

Example: Soil depth determines agricultural use

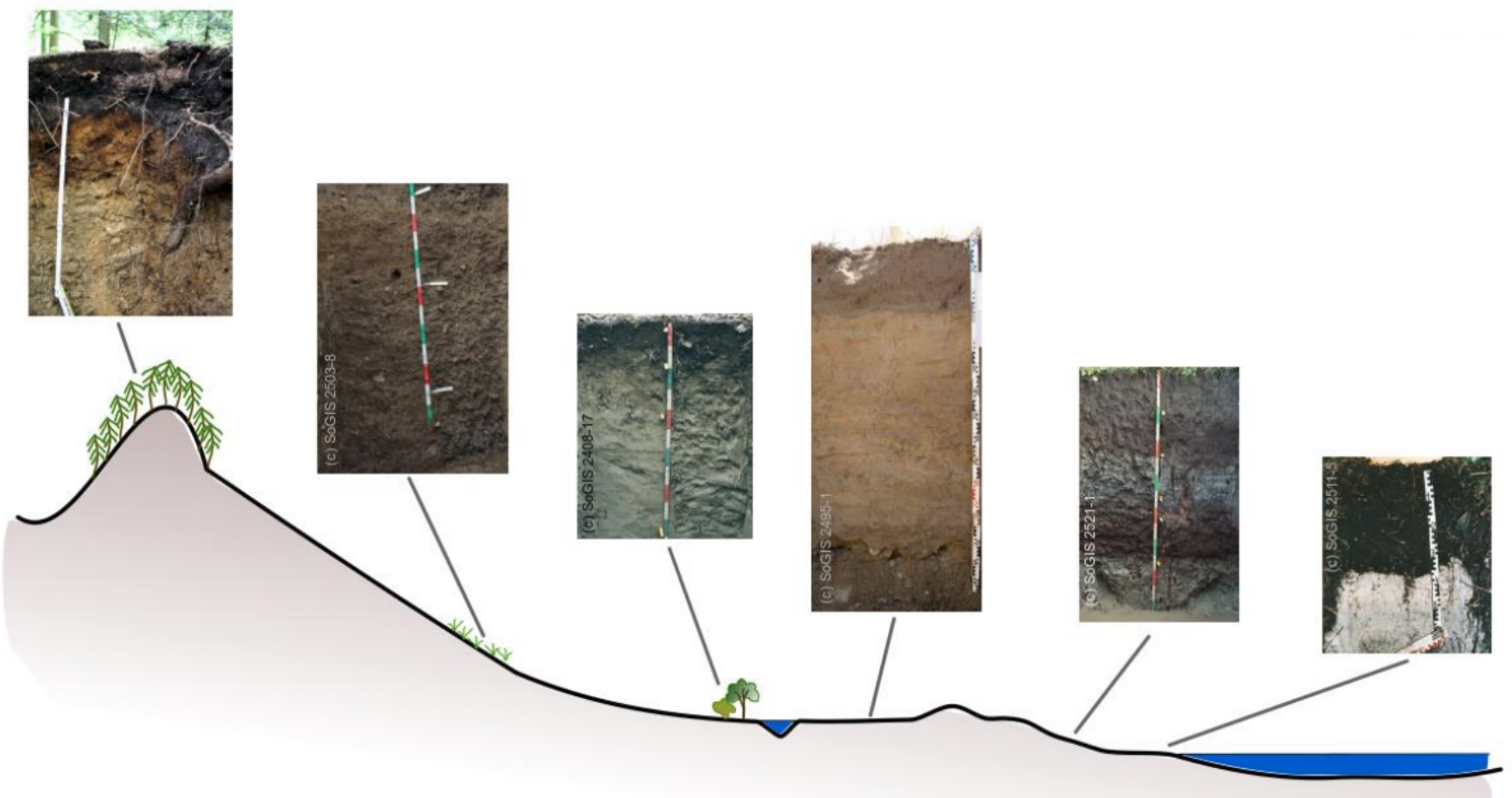
Grasland on shallow soil formed on limestone (Rendzina, https://boden-des-jahres.ch)

Crops on deep soil formed on glacial till (Ackerboden, https://boden-des-jahres.ch)

Soil forming factors

Factors influencing soil formation:

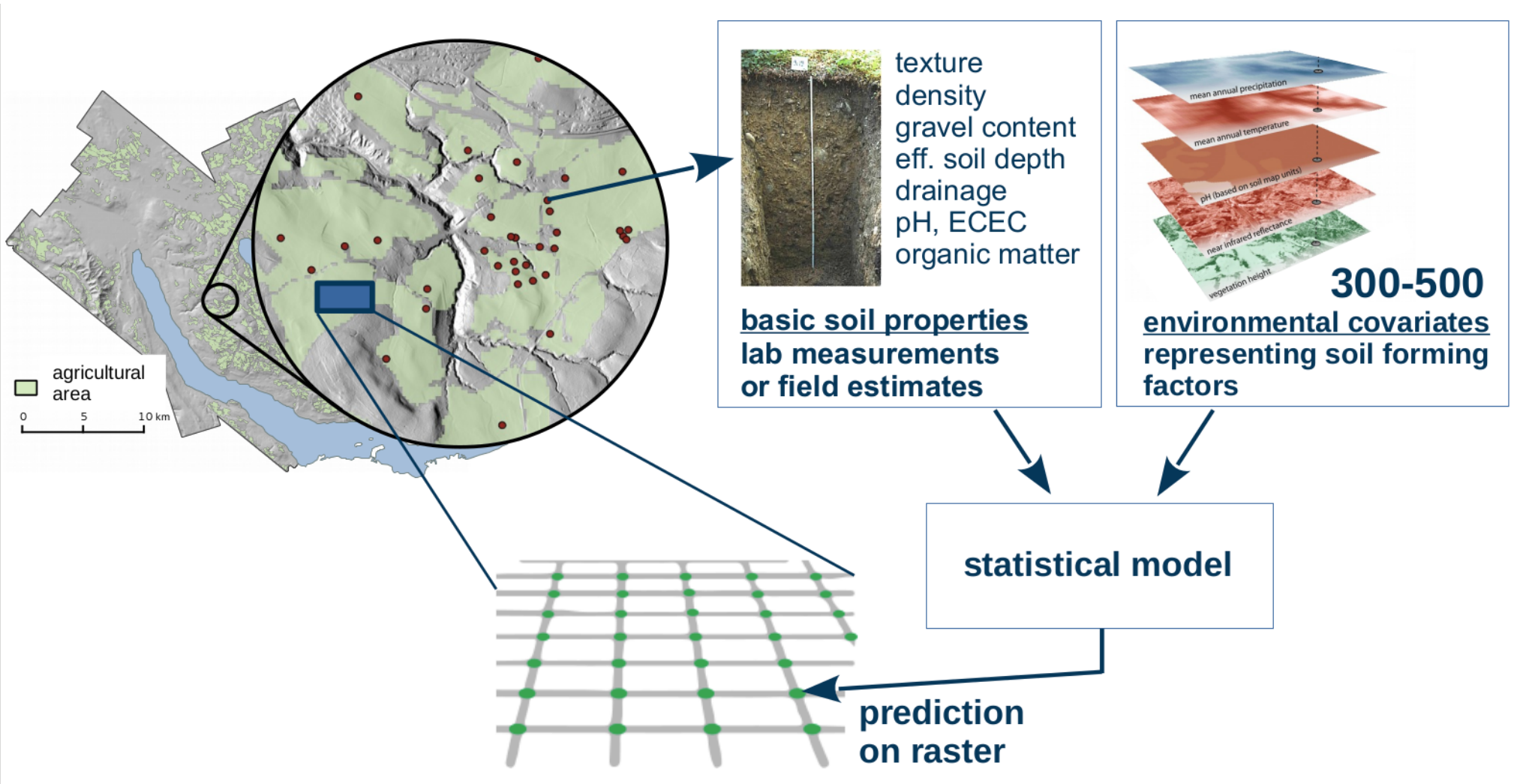
Parent material, terrain, climate, organism including humans, time.



Soil variability along a toposequence.

Digital soil mapping

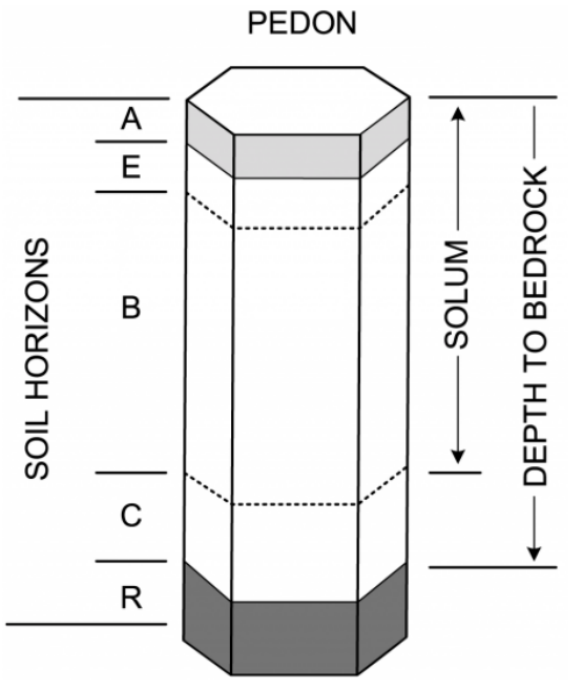
Commonly used approach: geostatistical prediction/interpolation, from point observations to continuous raster.

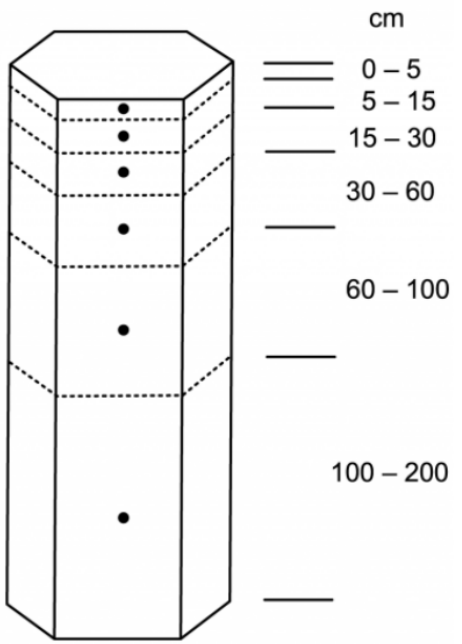


Digital soil mapping

- Response $\boldsymbol{y}$: what is displayed on the map
- Many $\mathbf{X}$, derivaties from elevation model, satellite images, geological maps
- Maps by depth intervals

$$\hat{y}_i \sim f\left(X_i\right) + \epsilon$$

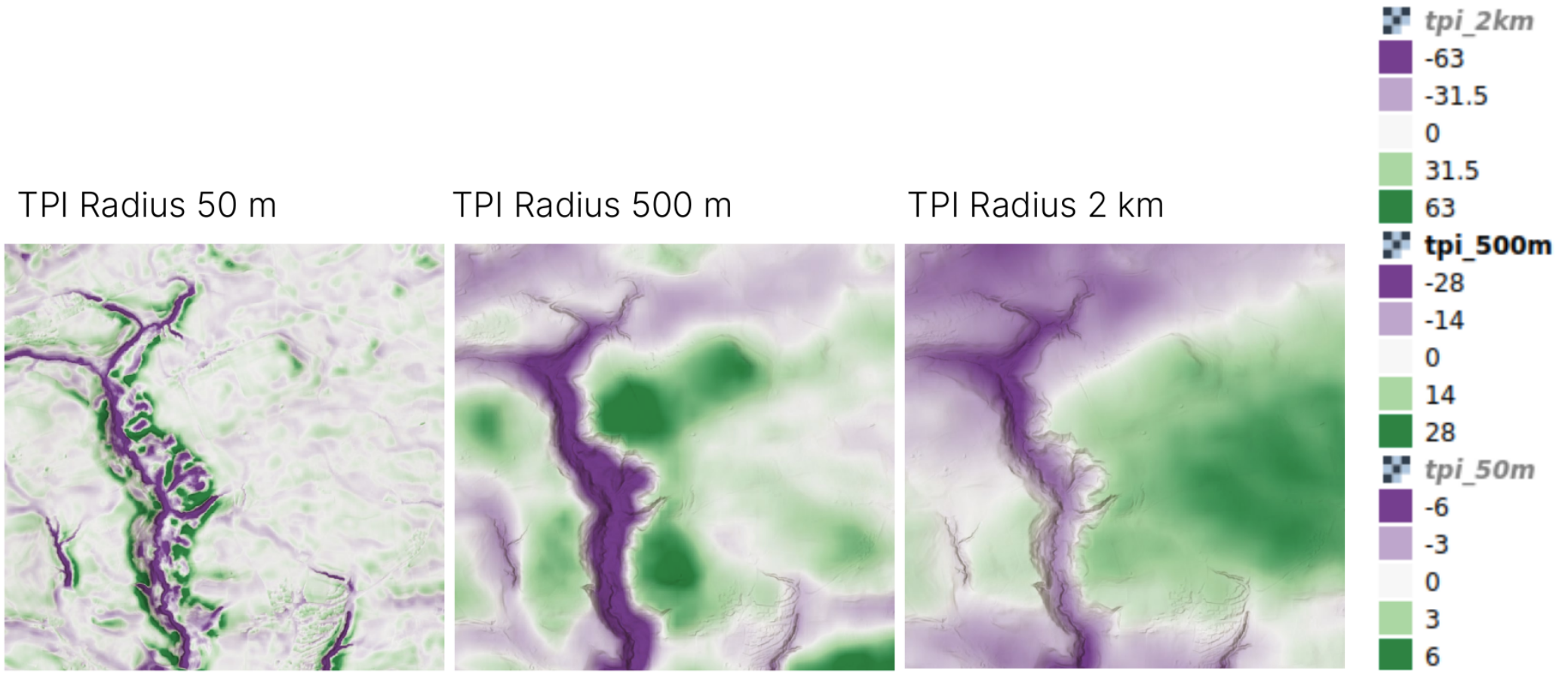




GlobalSoilMap project

Example predictors: Terrain attributes

Topographic position index, identifying valleys and hilltops at multiple scales.



1.2 What samples do we use?

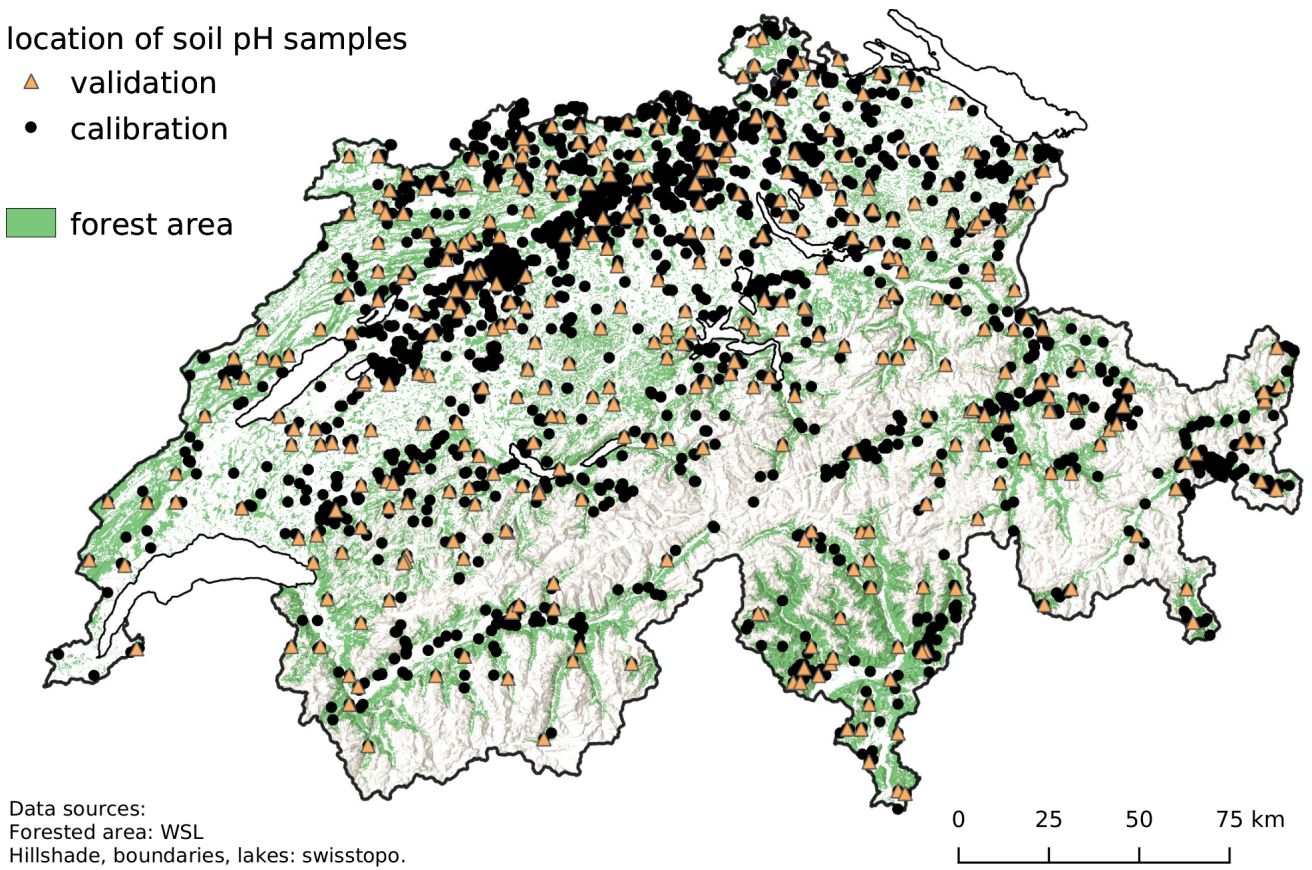
Common situation:

Use what is there and do our best …

Example: maps for forested area of Switzerland

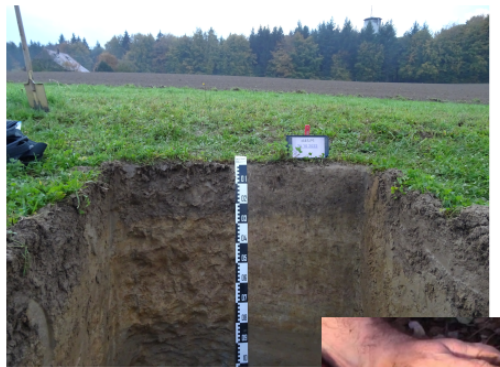
Example: Mapping of soil properties (e.g. pH, soil organic carbon content, clay content) for forested area of Switzerland.

Goal: model scenarios of tree species under climate change.

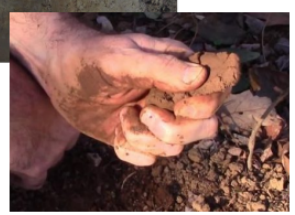


2,700 sites available from several soil data bases (325 for map validation)

New sampling: what does that mean



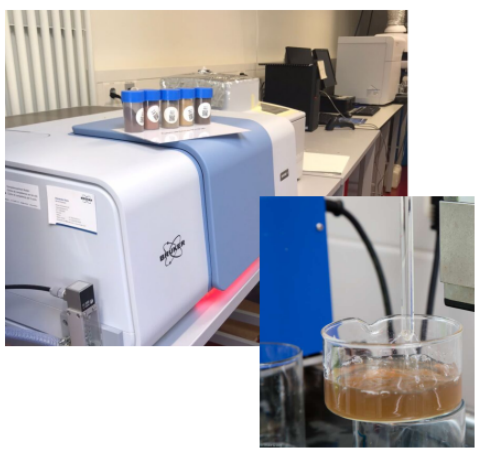
Profile pits



Field estimates

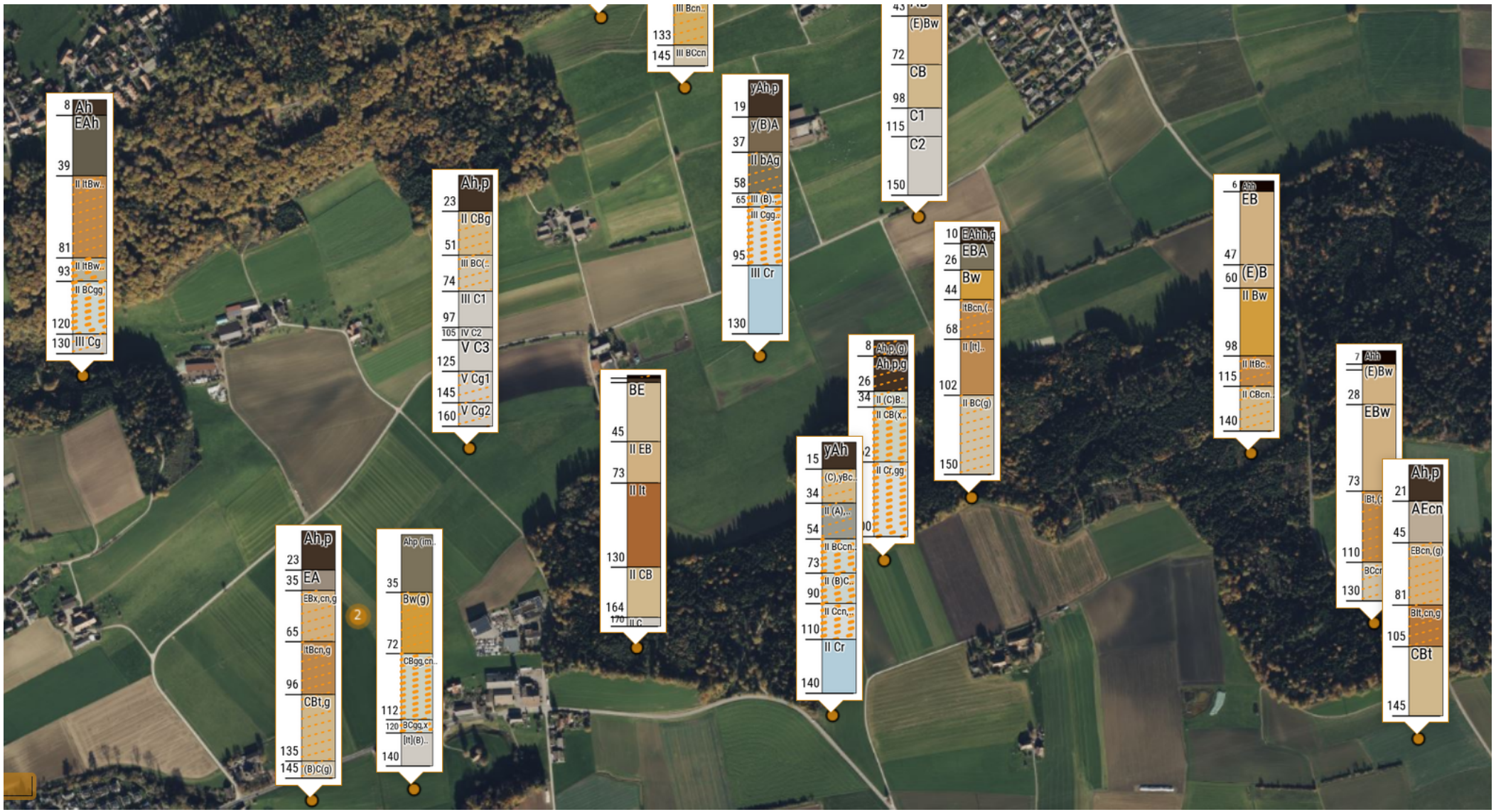
Drill core systems

Laboratory analysis



Agronomy students taking hand-auger samples

New sampling: where to go?



Bern study area, subsection Meikirch, only sites with laboratory samples (https://maps.soil.bfh.science)

Result based on new survey

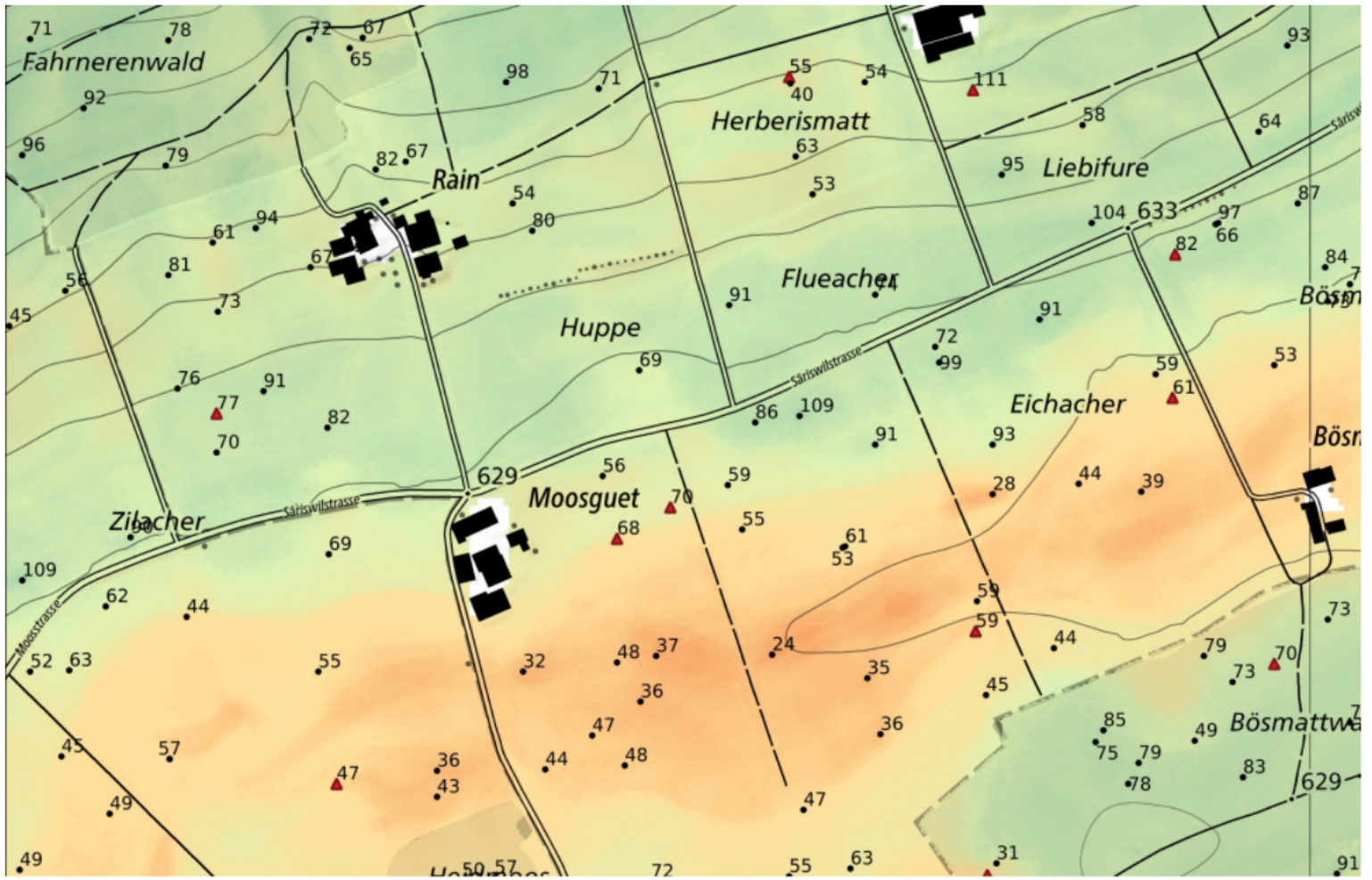
Rootable soil depth (RSD)
soil available to plant roots, without rocks or soil in groundwater

observed RSD [cm]

- calibration
- validation

Predicted rootable soil depth RSD [cm]

- 10
- 30
- 50
- 70
- 100
- 150



2 Manual determination of sampling locations

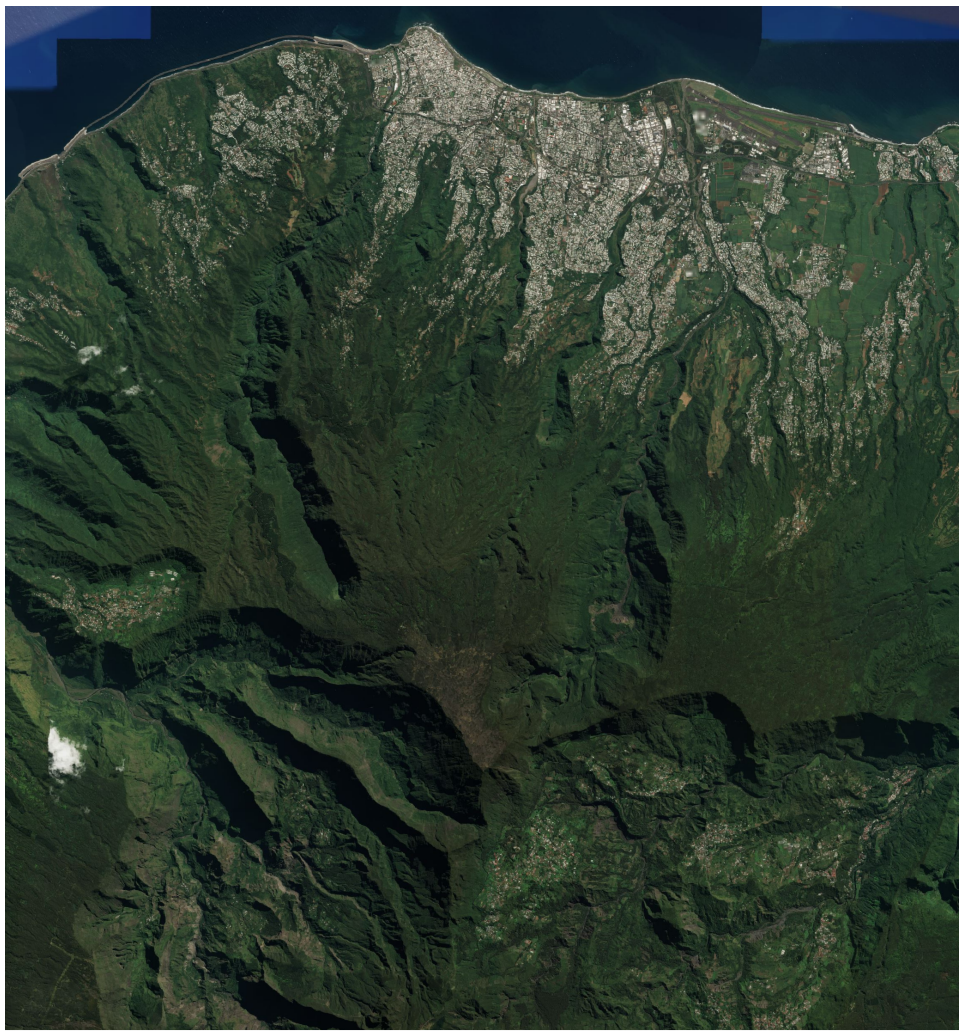
2.1 How would you place samples?

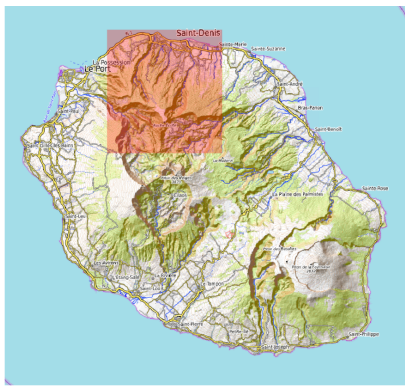
Example study area:
La Réunion

Goal: Create a topsoil organic carbon map.

Task: Draw locations where you would sample.

- 10 locations for model training (cross)
- 5 locations for model validation (triangle)





0 1 2 3 4 5 km

2.2 Sampling for land use classification

-> overview of your surveys from the last lab

3 Spatial sampling: some theory

3.1 Large number of sampling approaches

Sampling: always regarding a specific goal.

No sampling design is optimal for all cases, but we can combine different goals (e.g. in model-assisted sampling)

Some possible approaches:

- Random sampling: Simple or stratified random sampling
- Systematic sampling: Regular grid sampling
- Nested sampling: Main locations with sublocations
- Targeted sampling: e.g. for finding pollution or rare species
- Sampling for monitoring: repeated measures
- Geostatistical sampling: optimal for variogram estimation
- Model based sampling for model training

Design-based vs. Model-based Sampling

Design-based Sampling

- **Definition**: Randomness ensures unbiased estimation
- **Key Idea**: Each unit has a known, non-zero probability of being sampled.
- **Assumptions**: No model assumptions; inference is based on probability theory.
- **Example**: Simple Random Sampling (SRS), Stratified Sampling.

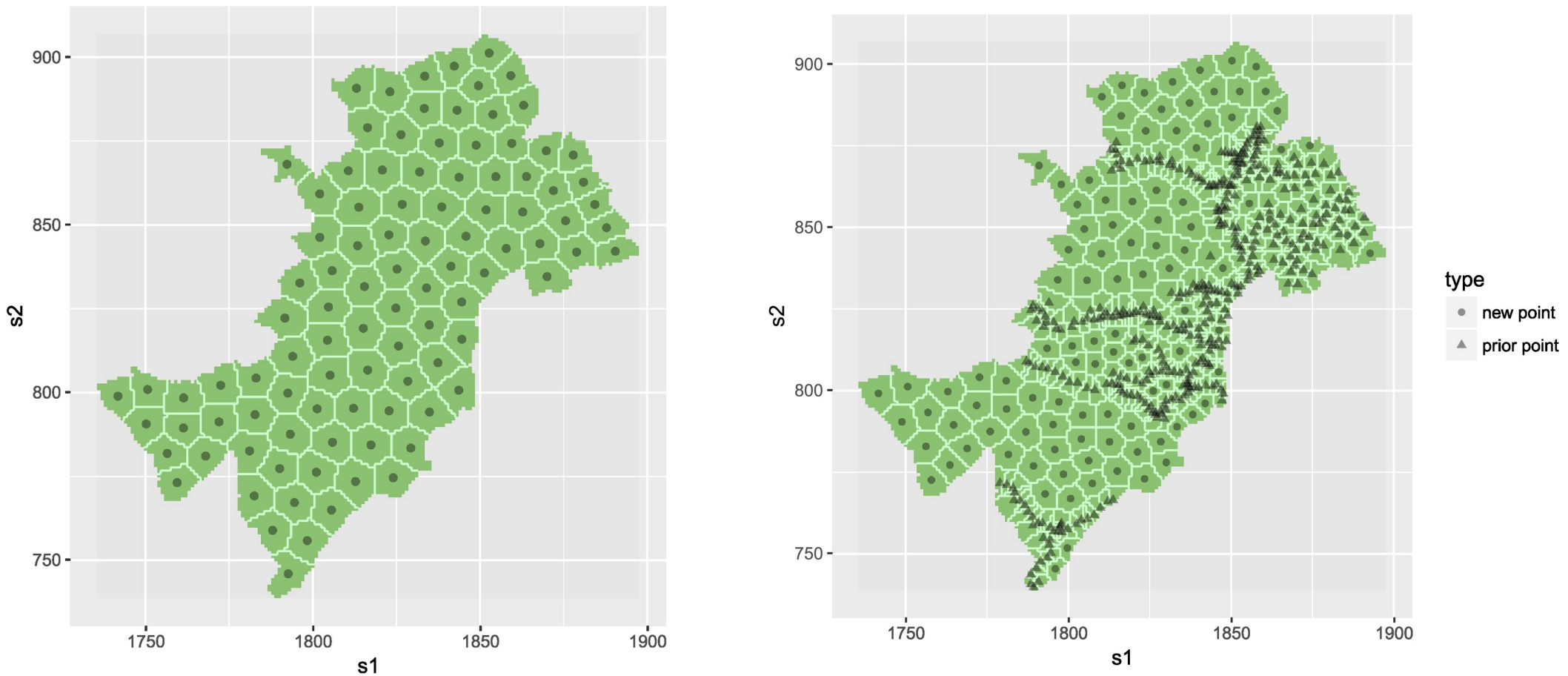
Model-based Sampling

- **Definition**: Assumes an underlying model for the population.
- **Key Idea**: The inference is based on the assumed model rather than sampling probabilities.
- **Assumptions**: Requires a correctly specified model.
- **Example**: Sampling based on variogram (kriging), regression-based estimation or prediction.

3.2 Coverage sampling for model training

Spatial coverage sampling

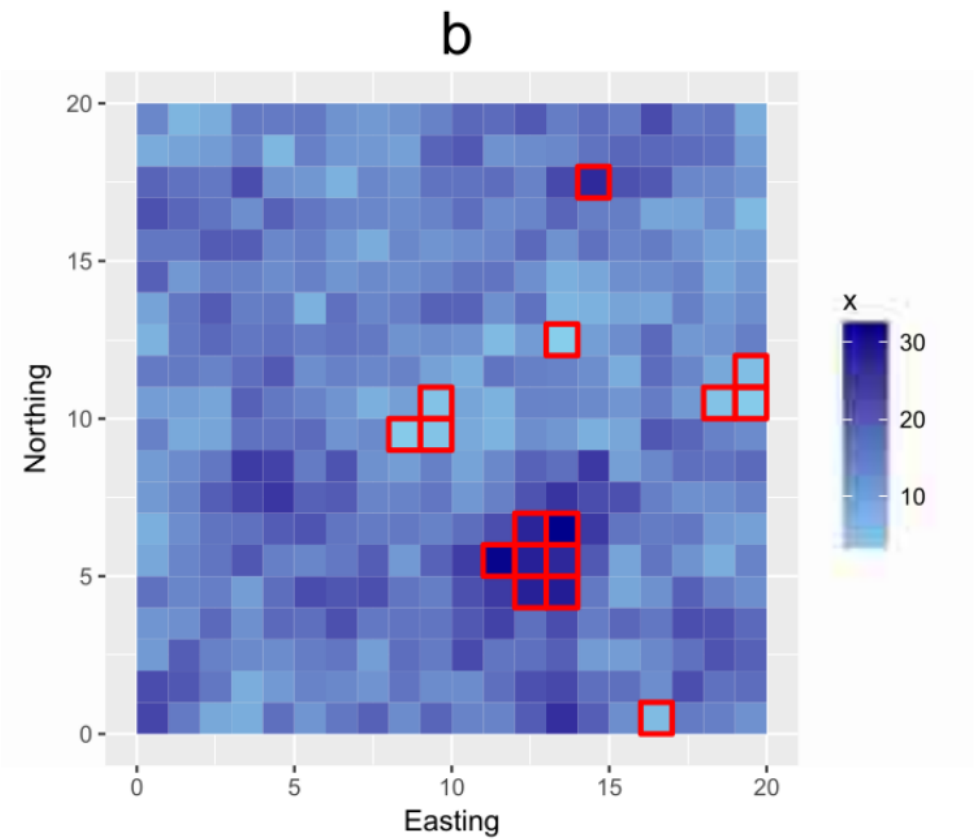
Apply k-means clustering to spatial coordinates.



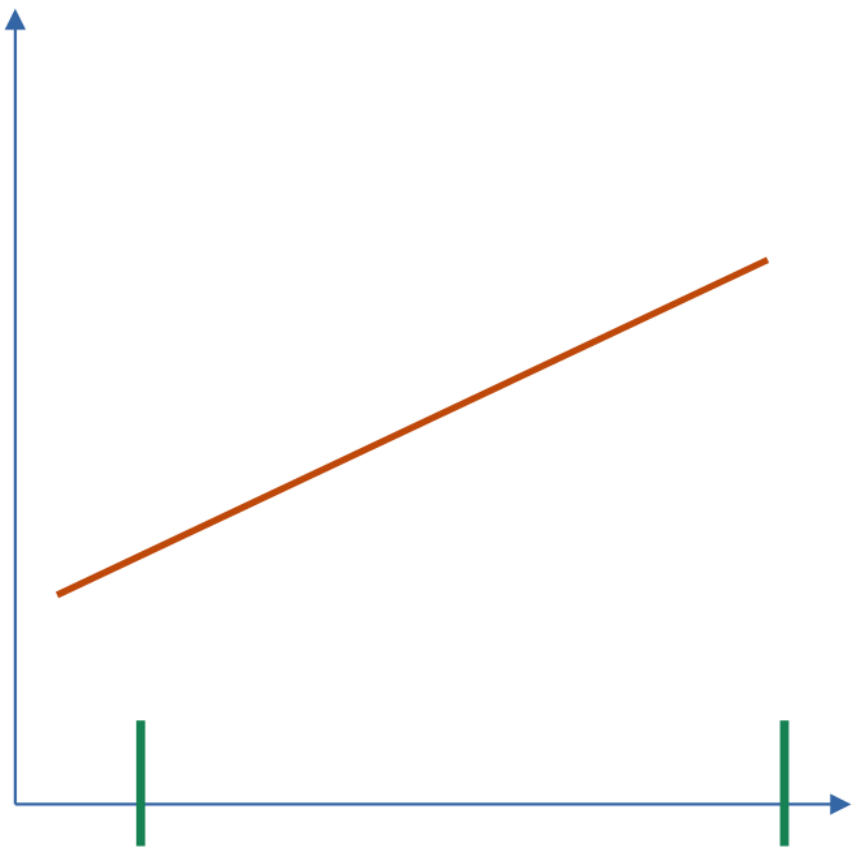
Spatial coverage design (left), spatial in-fill design (right) (Brus, 2019)

Sampling for calibration of linear regression

Ideal case: univariate linear dependence with known minimum and maximum.



Brus, 2019



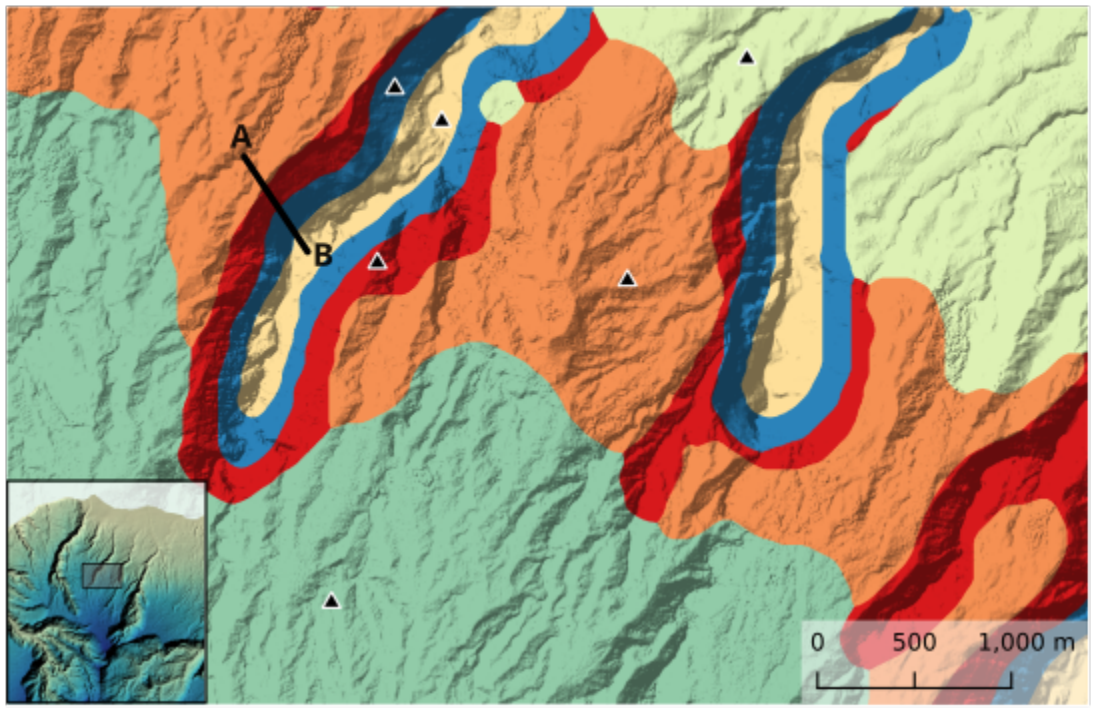
Coverage over predictors

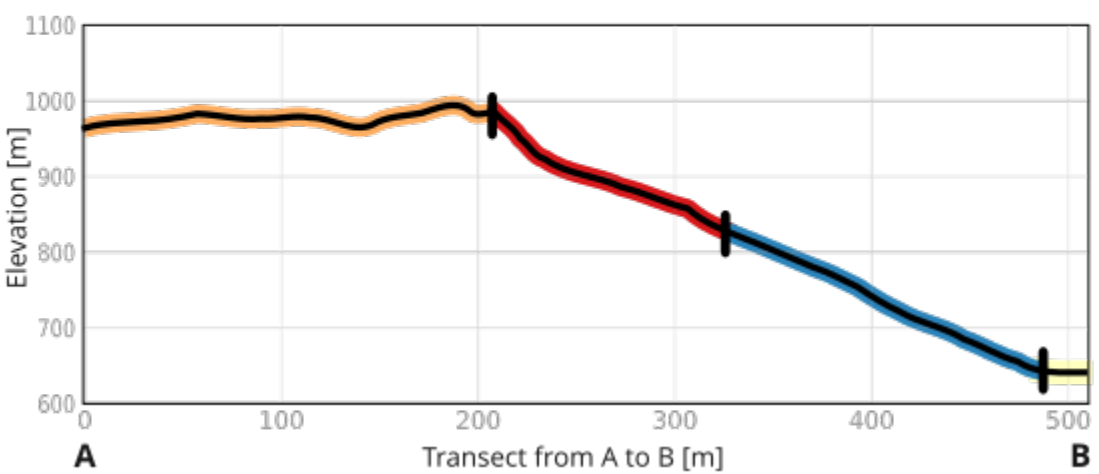
Feature space coverage sampling design

Apply clustering method to all candidate sampling locations.

Variables for clustering: most important predictors (here elevation, slope, TPI 1500 m).

Replacement: move within same cluster.





3.3 Probability sampling for map validation

- **Goal**: estimation of average map error = estimation of a population parameter
- Recommended approach: **Stratified random sampling**.
- **Strata**: sub-units with more homogenouous distribution of errors
- Compared to simple random sampling: more accurate estimates with the same number of samples.
- **Replacement samples**: if a location is not accessible, another random location needs to be sampled (even if it is faraway).

Horvitz-Thompson Estimator

Purpose: Unbiased estimator for population parameters when inclusion probabilities are not the same for every point (number of samples not proportional to area).

Formula for stratified random sampling over all strata (see p. 51, Brus, 2022)

$$\hat{\bar{z}} = \frac{1}{N} \sum_{h=1}^{H} \sum_{k \in S} \frac{1}{\pi_k} z_k$$

where:

- $\hat{\bar{z}}$ unbiased mean parameter estimate.
- z_k is the observed value for sample k.
- π_k is the inclusion probability of sample k, for each stratum are $\pi_k = \frac{n_h}{N_h}$ for all k in stratum h with n the sample size of stratum h and N_h the size of the stratum.
- S is the sample for stratum h.

Note: With equal sample sizes per stratum the formula can be simplified to a weighted mean of the stratum means, with weights $w_k = N_h / N$.

Example

Suppose we sample 2 samples from three areas (strata) with size **200, 500 and 400 km^2**. To compute inclusion probability we consider each 1 x 1 km grid node as finite sample candidates (total $N = 1100$).

For our example $\pi_1 = 0.01$, $\pi_2 = 0.004$, and $\pi_3 = 0.005$. Their corresponding observed values are (2,3), (4,5) and (6,7).

The estimator correcting for unequal stratum size is:

$$\hat{\bar{z}} = \frac{1}{1100}\left(\frac{2}{0.01} + \frac{3}{0.01} + \frac{4}{0.004} + \frac{5}{0.004} + \frac{6}{0.005} + \frac{7}{0.005}\right) = 4.863.$$

As opposed to the unweighted mean = 4.5

4 Hands-on: Create sampling design for model training

4.1 Installation and data download

Install required R packages

```
1 l.p <- c("terra", "sf", "fields", "ranger", "ggplot2") # optional: "mapview"
2 install.packages(l.p)
```

Download dataset

Download link

This zip contains a folder **terrain** with derivaties from the elevation model and folder **soil** with a map of soil organic carbon stocks extracted from the global overview soil map SoilGrids.

4.2 Prepare data

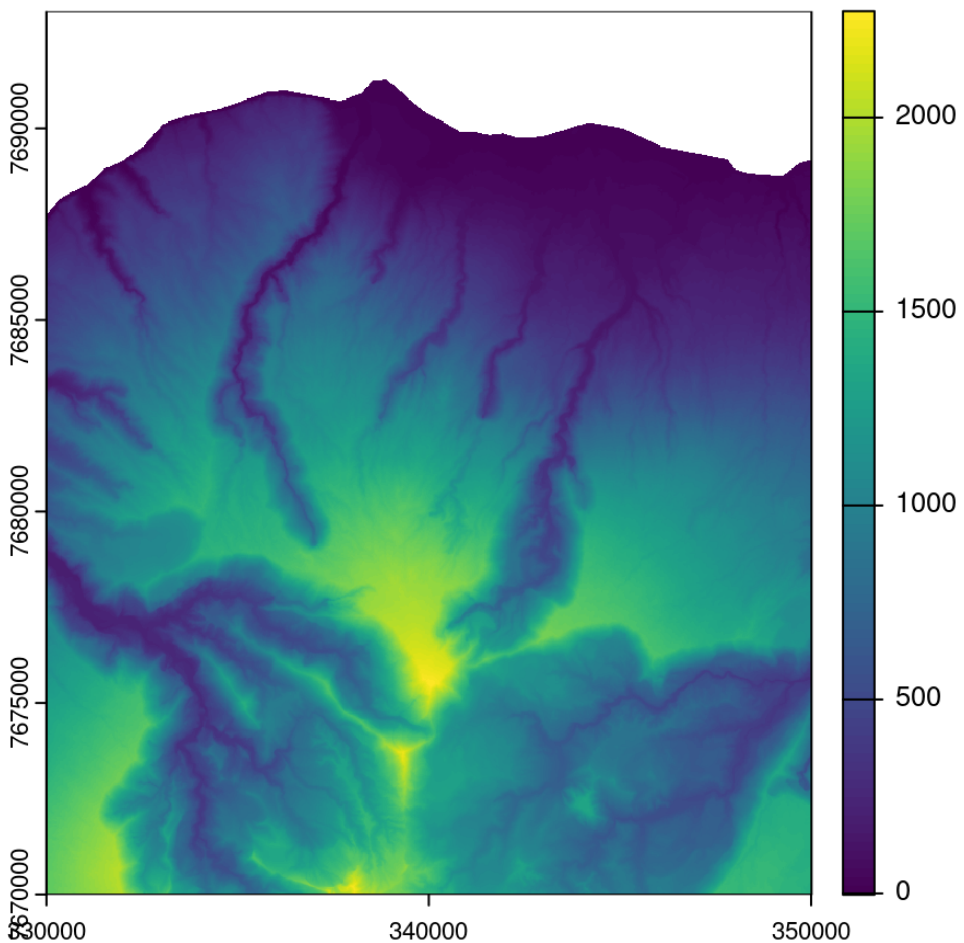
Read in data and check content

```r
library(terra)
library(sf)
library(fields)

# set working directory to folder above "data"
r.dem <- rast("data/terrain/reunion_30m.tif")
r.dem
```

```
class       : SpatRaster
dimensions  : 769, 667, 1  (nrow, ncol, nlyr)
resolution  : 30, 30  (x, y)
extent      : 330000, 350010, 7669992, 7693062  (xmin, xmax, ymin, ymax)
coord. ref. : WGS 84 / UTM zone 40S (EPSG:32740)
source      : reunion_30m.tif
name        : reunion_30m
min value   :   -3.551687
max value   : 2274.301270
```

Create first display

```
1  plot(r.dem)
```



Select variables for sampling design and transform into data.frame

For now we decided to use elevation (reunion_30m.tif), slope computed on 100 by 100 m pixels (slope100m-perc.tif) and a topographic position index calculated at 900 m diameter (tpi_900m.tif).

```
1  # create a list of file names
2  l.rast <- paste0("data/terrain/", c("reunion_30m.tif", "slope100m-perc.tif", "tpi_900m.tif"))
3
4  # create a raster stack
5  r.stack <- rast(l.rast)
6
7  # create a data frame, each row corresponds to a pixel
8  d.pixels <- as.data.frame(r.stack, xy = T, na.rm = F)
9  str(d.pixels)
```

```
'data.frame':   512923 obs. of  5 variables:
 $ x             : num  330015 330045 330075 330105 330135 ...
 $ y             : num  7693047 7693047 7693047 7693047 7693047 ...
 $ reunion_30m   : num  NA NA NA NA NA NA NA NA NA NA ...
 $ slope100m-perc: num  NA NA NA NA NA NA NA NA NA NA ...
 $ tpi_900m      : num  NA NA NA NA NA NA NA NA NA NA ...
```

Select relevant pixels

To reduce computational load and ensure a minimal distance between sampling points we use every second pixel (60 m distance).

```
# only use every second pixel, ensures 60 m distance between sampling points
t.sel.x <- d.pixels$x %in% seq(min(d.pixels$x), max(d.pixels$x), by = res(r.stack)[1]*2)
t.sel.y <- d.pixels$y %in% seq(min(d.pixels$y), max(d.pixels$y), by = res(r.stack)[1]*2)

# remove NA, and remove every second pixel
d.pixels <- d.pixels[ complete.cases(d.pixels) & t.sel.x & t.sel.y, ]

str(d.pixels)
```

```
'data.frame':   102777 obs. of  5 variables:
 $ x             : num  338655 338715 338775 338835 338655 ...
 $ y             : num  7690707 7690707 7690707 7690707 7690647 ...
 $ reunion_30m   : num  19.7 18.8 18.3 17.4 21.9 ...
 $ slope100m-perc: num  0.0443 0.0448 0.0439 0.041 0.0477 ...
 $ tpi_900m      : num  2.81 2.02 1.76 2.21 2.9 ...
```

4.3 k-means clustering

Form as many clusters as we like to have samples. For the clusering we use the 3 variables defined above, but also the spatial coordinates to ensure equal spatial coverage.

```
 1  # scale variables and round to 5 digits to make clustering more stable
 2  d.pixels.sc <- round(scale(d.pixels), 5)
 3
 4  # set seed for reproducibility
 5  set.seed(11)
 6  # k-means clustering, with centers = numbers of samples to plan
 7  m.kmeans <- kmeans(d.pixels.sc, centers = 150, iter.max = 50)
 8
 9  # number of pixels per cluster
10  m.kmeans$size
```

```
  [1]  334  634  385  971  406  249  444  483  479  601  451 1090  893  578  952
 [16]  517  769  197  624  704 1001  590  510  682  673  949  652  933  308  668
 [31]  461  796  431  742  849  809  509  473  678 1172  506 1132 1032 1409  739
 [46]  439  652  467  831  534  545  415  808  276  420  882  191  851  778 1579
 [61]  709  634  717  931 1625  333  411  815  436  579  622  821 1033  399  973
 [76]  788  511  445  358  661  521 1150  467  513 1142  620  900  397  770  706
 [91]  629  408  694  296  499  737 1006  904  427  603  573 1284  702  544 1179
[106]  913  437 1015  764  835  532  658  826  620 1409 1036  883  797  314  512
[121]  520  799  363 1001  694 1222  605  471  605  825 1026  202  362  567  463
[136]  898  447  955  435 1195  719  367  705  593  991  892  293  875  385  146
```

Select sampling point

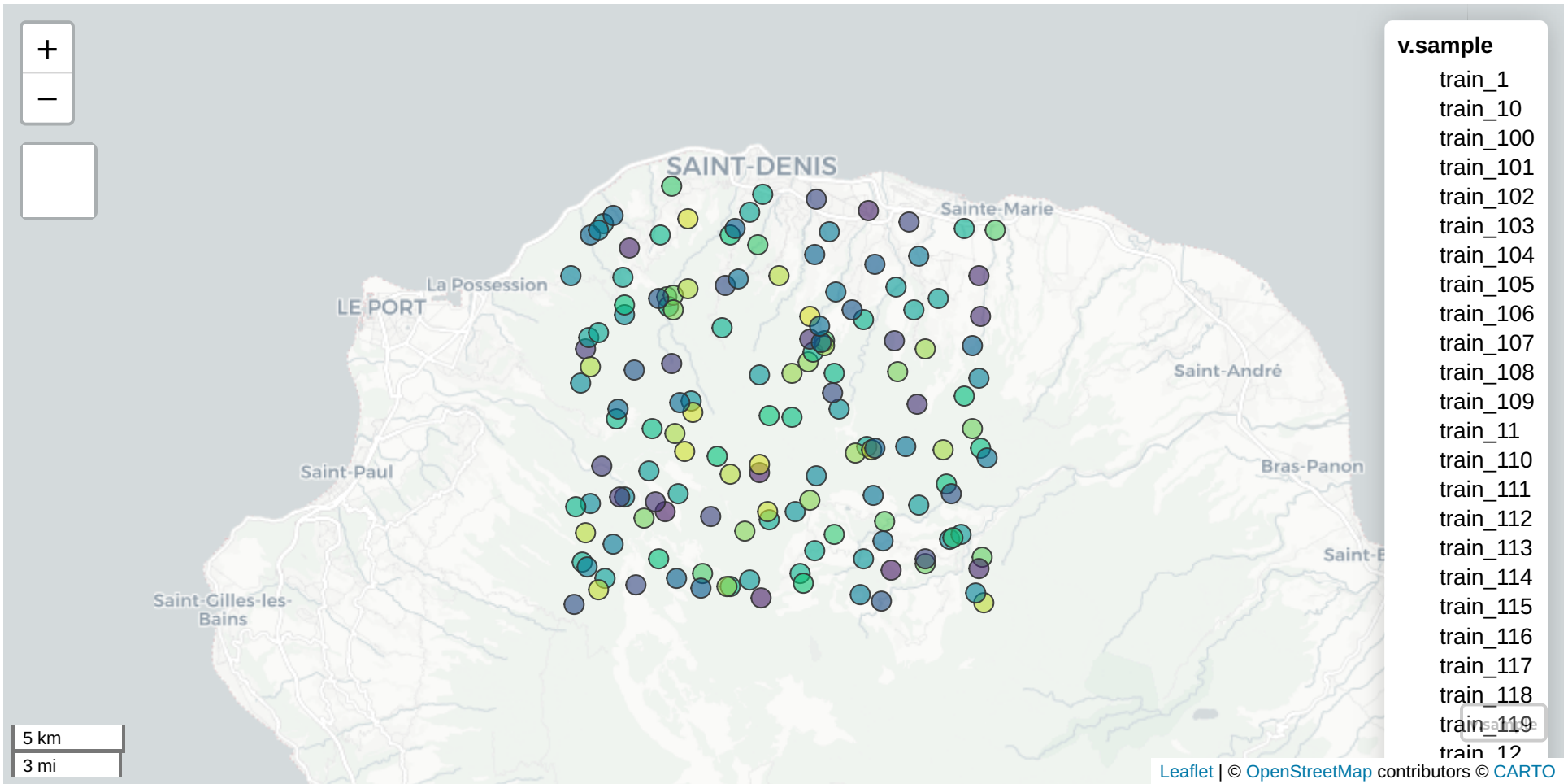
Select pixel that is closest to cluster center (cluster center is a calculated mean).

```r
# extract real points closest to cluster center
m.dist <- rdist(d.pixels.sc, m.kmeans$centers)
# select row indices
idx <- apply(m.dist, 2, which.min)

d.sample <- d.pixels[idx, 1:2]

# create sample IDs
d.sample$id <- paste0("train_", 1:nrow(d.sample))

# create a spatial points object and save to Geopackage
v.sample <- st_as_sf(d.sample, coords = c("x", "y"), crs = 32740)
write_sf(v.sample, "results/fsc_design_150.gpkg")

v.sample
```

```
Simple feature collection with 150 features and 1 field
Geometry type: POINT
Dimension:     XY
Bounding box:  xmin: 330675 ymin: 7671147 xmax: 349335 ymax: 7689387
Projected CRS: WGS 84 / UTM zone 40S
First 10 features:
             id                geometry
357815  train_1 POINT (339075 7676967)
273509  train_2 POINT (331155 7680747)
177921  train_3 POINT (344955 7685067)
404519  train_4 POINT (339495 7674867)
261875  train_5 POINT (342315 7681287)
```

Display created sampling points

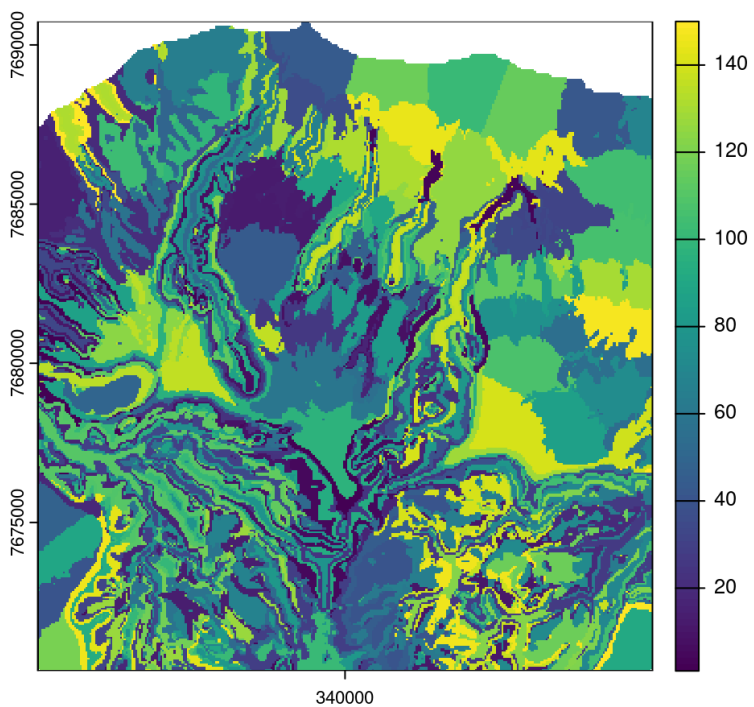
```
1  library(mapview)
2  mapview(v.sample)
```



4.4 Create a map of cluster zones

Create predictions of clustered areas.

```
# extract cluster for each pixel
d.pixels$clusters <- fitted(m.kmeans, "classes")
# create a raster object
r.clusters <- rast(d.pixels[, c("x", "y", "clusters")], type="xyz", crs= "epsg:32740")
writeRaster(r.clusters, filename = "results/fsc_design_150_clusters.tif", overwrite = T)
plot(r.clusters)
```



4.5 Additional Tasks

Additional Task 1

Display the created sampling points and cluster zones in QGis. Also add background map. Verify your result. Would you pass it to the surveyors? Or what would you improve?

Additional Task 2

Remove the spatial coordinates from the clustering. Do you see a difference and why?

Additional Task 3

Change other criteria such as the number of sampling points or chose other variables for the clustering. Observe the changes and compare with how you would manually place sampling points on a map.

5 Hands-on: Create sampling for map validation

5.1 Form strata

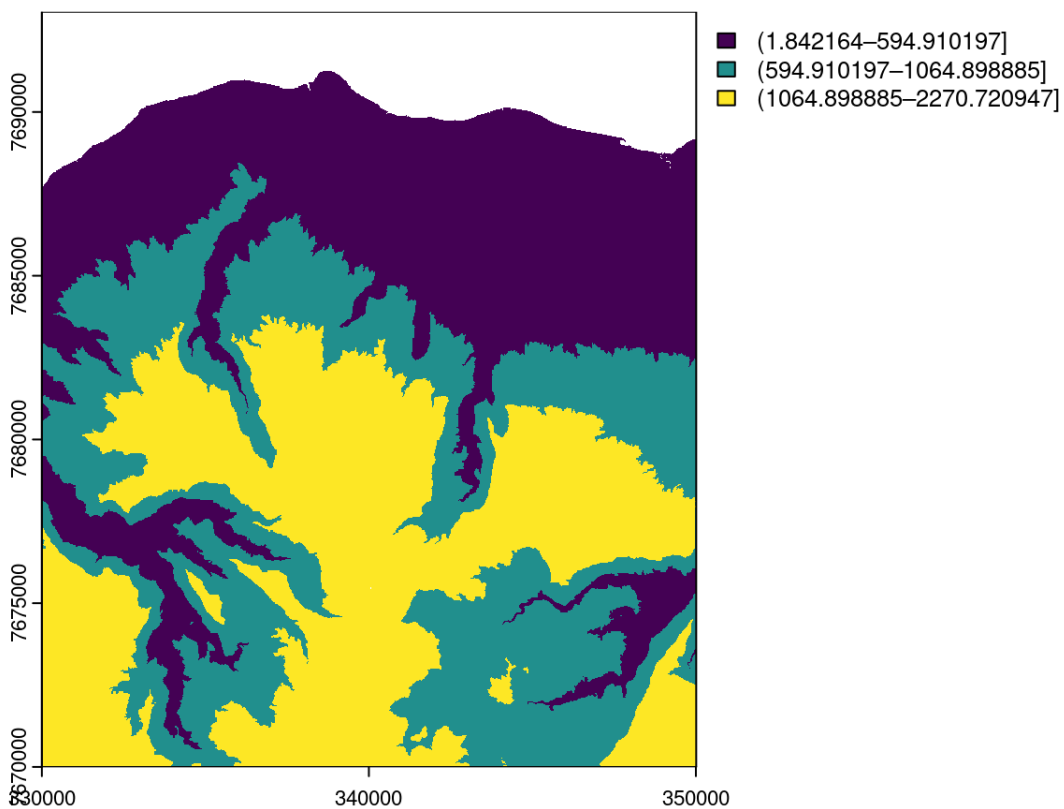
As we have no further information on the distribution of the map errors we assume elevation is a relevant factor. We plan 30 sampling points and from 3 strata, thus 10 random points per stratum.

```
# use elevation as strata, from 3 strata
t.breaks <- quantile(d.pixels$reunion_30m, probs = seq(0,1,1/3))
d.pixels$strata <- cut(d.pixels$reunion_30m, breaks = t.breaks, labels = 1:3)

# check if it worked
table(d.pixels$strata)
```

```
    1     2     3
34258 34259 34259
```

Plot maps of strata

```
1  # save strata map
2  r.strata <- classify(r.stack[[1]], rcl = t.breaks)
3  writeRaster(r.strata, filename = "results/strs_design_3_strata.tif", overwrite = T)
4
5  plot(r.strata)
```



5.2 Select random samples per stratum

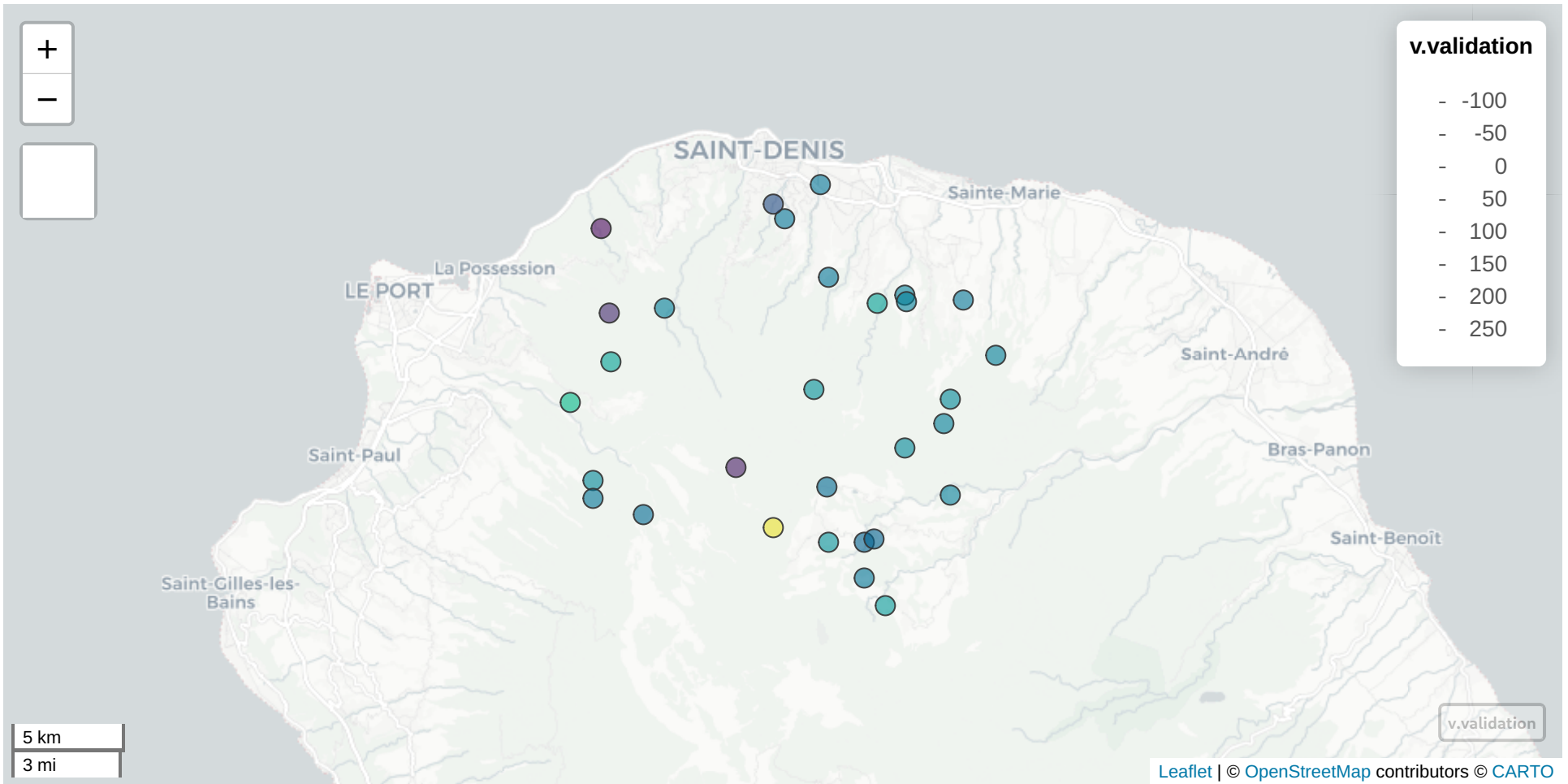
```r
set.seed(1)

# apply random selection of 10 points for each strata
l.sample.rows <- lapply(c("1", "2", "3"), function(stratum){
  # select relevant row names
  l.row <- rownames(d.pixels[ d.pixels$strata == stratum, ])
  # randomly select 10 of the row names
  l.rs <- sample(l.row, 10)
  return(l.rs)
})

# select corresponding pixel
d.sample <- d.pixels[ unlist(l.sample.rows), ]

# check if number per strata are ok
table(d.sample$strata)
```

```
 1  2  3
10 10 10
```

```r
# create sample IDs
d.sample$id <- paste0("val_", 1:nrow(d.sample))

v.validation <- st_as_sf(d.sample[, c(1:2,5)], coords = c("x", "y"), crs = 32740)
write_sf(v.validation, "results/strs_design_30.gpkg")
```

Display results

```
1  mapview(v.validation)
```



5.3 Additional Tasks

Additional Task 1

Is the distribution of point locations as you would expect it? Change the seed. What happens?

Additional Task 2

The Horvitz-Thompson estimator has not been used in this section. Does it apply to this case? Where does it need to be applied?

Additional Task 3

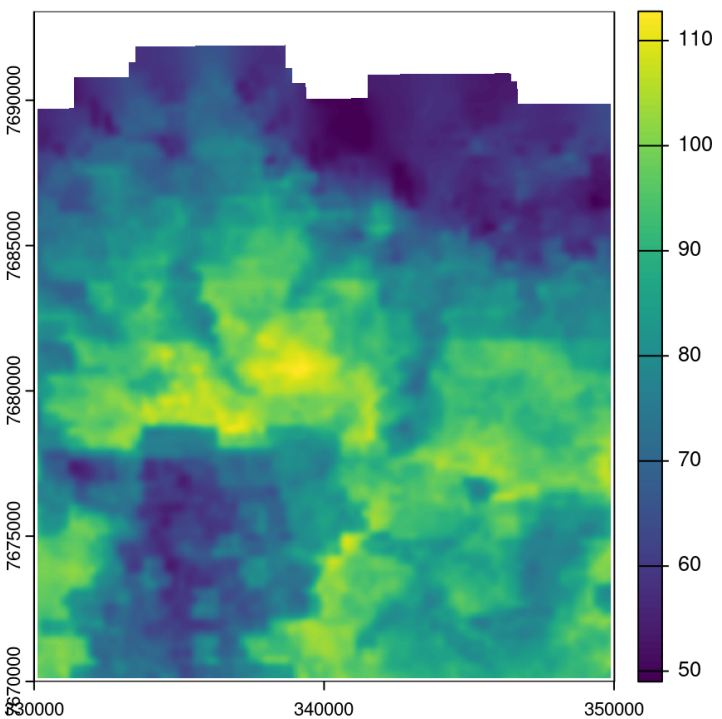
Create strata that have equal area coverage. For this create a k-means clustering (with e.g. k = 3) just using the coordinates. For each clustered zone again take a random sample.

6 Hands-on: Use sampling designs for mapping

6.1 Soil map (instead of real sampling)

In this section we use the created sampling desings to create a map of soil organic stocks and to validate map accuracy. We imitate real sampling by reading out values from the global overview soil map SoilGrids.

```
r.soc <- rast("data/soil/soilgrids_SOCstock_0-30_mean30mSmooth.tif")
plot(r.soc)
```



6.2 Prepare response data

```r
library(ranger)
library(ggplot2)

l.rast <- list.files("data/terrain/", pattern = ".tif$", full.names = T)
r.stack <- rast(l.rast)

v.samples <- st_read("results/fsc_design_150.gpkg")
```

```
Reading layer `fsc_design_150' from data source
  `/home/madlene/cloud-uu/5_teaching/1_1_INFOMSSSL/slides/results/fsc_design_150.gpkg'
  using driver `GPKG'
Simple feature collection with 150 features and 1 field
Geometry type: POINT
Dimension:     XY
Bounding box:  xmin: 330675 ymin: 7671147 xmax: 349335 ymax: 7689387
Projected CRS: WGS 84 / UTM zone 40S
```

```r
# read response value
# (in a real project, we would read the values from the lab measured on soil samples)
d.SOCstock <- extract(r.soc, v.samples)

str(d.SOCstock)
```

```
'data.frame':   150 obs. of  2 variables:
 $ ID                                  : num  1 2 3 4 5 6 7 8 9 10 ...
 $ soilgrids_SOCstock_0-30_mean30mSmooth: num  76.2 79.4 68.7 80.6 88.2 ...
```

Prepare predictor data

```r
# read predictor values at sampling locations
d.predictors <- extract(r.stack, v.samples)

str(d.predictors)
```

```
'data.frame':   150 obs. of  35 variables:
 $ ID              : num  1 2 3 4 5 6 7 8 9 10 ...
 $ asp_eness30m    : num  -0.948 0.167 -0.273 -0.988 0.372 ...
 $ asp_nness30m    : num  -0.2546 0.982 0.953 0.0444 0.9281 ...
 $ curv100m        : num  0.00702 0.00803 -0.00431 -0.00452 0.00263 ...
 $ curv30m         : num  0.009431 0.019959 -0.022337 -0.029317 0.000387 ...
 $ curvplan100m    : num  0.000514 0.003546 -0.026976 -0.001553 0.005157 ...
 $ curvplan30m     : num  -0.01869 0.02169 0.008 -0.00652 -0.00581 ...
 $ curvprof100m    : num  0.002752 0.000615 -0.000834 -0.000241 -0.000348 ...
 $ curvprof30m     : num  0.007082 -0.001764 -0.011551 -0.000702 0.001665 ...
 $ heignor100m     : num  0.939 0.695 0.112 0.407 0.918 ...
 $ heignor30m      : num  0.9834 0.8409 0.0765 0.2528 0.8918 ...
 $ heigslope100m   : num  724.8 161.9 26.6 267.7 403.3 ...
 $ heigslope30m    : num  812.9 174.1 13.6 139.7 346.3 ...
 $ heigstand100m   : num  1887.2 612.9 15.2 625.9 987.7 ...
 $ heigstand30m    : num  1991.43 744.34 6.94 378.71 960.64 ...
 $ heigval100m     : num  46.1 69.4 212.7 389.6 35 ...
 $ heigval30m      : num  13.7 32.9 164 412.8 42 ...
 $ mpi100m_150     : num  0.0669 0.1218 0.1837 0.3102 0.0799 ...
 $ mpi30m_150      : num  0.0173 0.144 0.2481 0.528 0.1072 ...
 $ mrrtf100m       : num  8.22e-02 3.26e-10 2.58e-07 4.70e-14 4.74e-06 ...
 $ mrrtf30m        : num  1.92e-03 2.46e-10 6.74e-09 2.22e-16 6.11e-05 ...
 $ mrvbf100m       : num  3.01e-04 1.14e-11 4.12e-03 1.12e-12 5.24e-08 ...
 $ mrvbf30m        : num  3.09e-05 2.17e-11 1.62e-06 2.91e-14 6.56e-05 ...
 $ reunion_30m     : num  2025 886 134 1508 1078 ...
```

6.3 Fit random forest

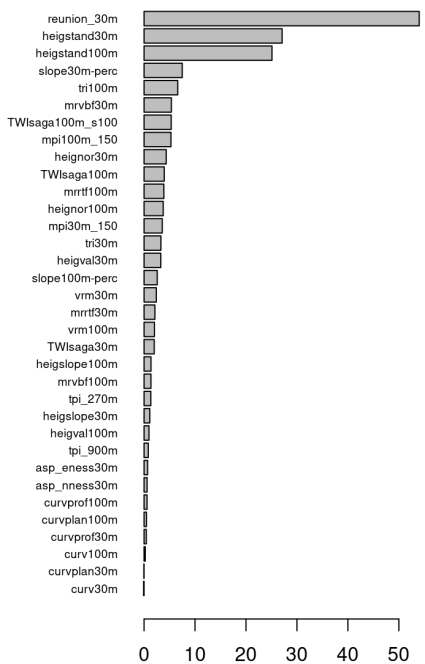
Quick and dirty random forest model fit.

```
## fit RF model
m.rf <- ranger(y = d.SOCstock$`soilgrids_SOCstock_0-30_mean30mSmooth`,
               x = d.predictors[,-c(1)], # do not use ID
               importance ="permutation")
m.rf
```

```
Ranger result

Call:
 ranger(y = d.SOCstock$`soilgrids_SOCstock_0-30_mean30mSmooth`,      x = d.predictors[, -c(1)],
importance = "permutation")

Type:                             Regression
Number of trees:                  500
Sample size:                      150
Number of independent variables:  34
Mtry:                             5
Target node size:                 5
Variable importance mode:         permutation
Splitrule:                        variance
OOB prediction error (MSE):       77.93772
R squared (OOB):                  0.5437146
```

Predictor importance

```
1  t.importance <- importance(m.rf)
2
3  par(oma = c(2,10,2,2))
4  barplot(t.importance[order(t.importance)], horiz= T, las = 1, cex.names = 0.6)
```



6.4 Evaluate map accuracy

Predict on validation sample

```
## Compute validation stats
v.validation <- st_read("results/strs_design_30.gpkg")
```

```
Reading layer `strs_design_30' from data source
  `/home/madlene/cloud-uu/5_teaching/1_1_INFOMSSSL/slides/results/strs_design_30.gpkg'
  using driver `GPKG'
Simple feature collection with 30 features and 1 field
Geometry type: POINT
Dimension:     XY
Bounding box:  xmin: 330375 ymin: 7670487 xmax: 349095 ymax: 7688847
Projected CRS: WGS 84 / UTM zone 40S
```

```
d.predictors.val <- extract(r.stack, v.validation)
d.SOCstock.val <- extract(r.soc, v.validation)

d.SOCstock.val$predictions <- predict(m.rf, d.predictors.val)$prediction
summary(d.SOCstock.val$predictions)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  55.82   74.61   80.41   80.40   88.60   91.93
```

Validation statistics

```
# compute marginal bias (positive values: overestimation, negative values: underestimation)
error <- d.SOCstock.val$`soilgrids_SOCstock_0-30_mean30mSmooth` - d.SOCstock.val$predictions
mean(-error)
```

```
[1] -1.942238
```

```
# RMSE
sqrt(mean(error^2))
```

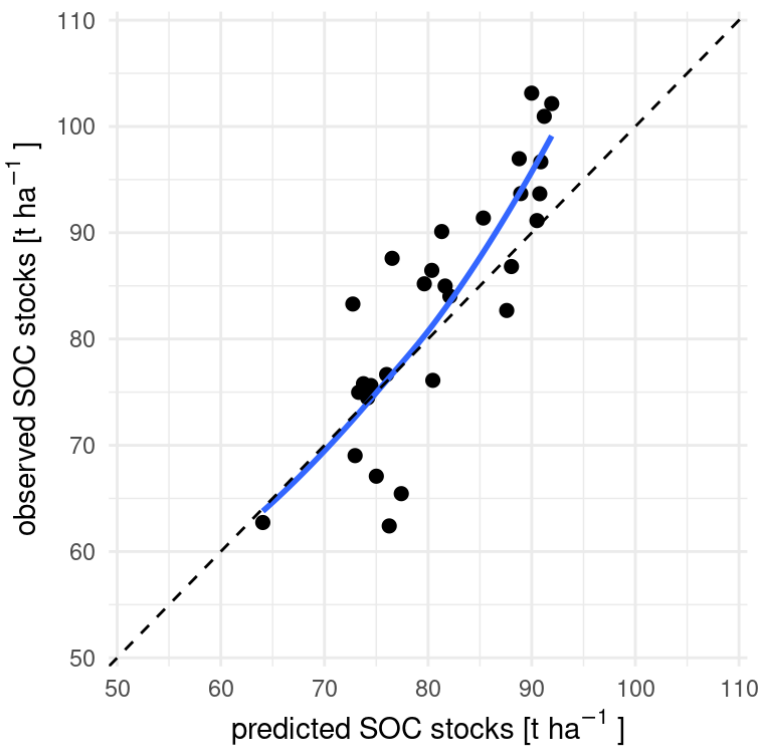
```
[1] 6.949492
```

```
# R2, computed as skill score / model efficiency coefficient
obs <- d.SOCstock.val$`soilgrids_SOCstock_0-30_mean30mSmooth`
1 - ( sum( error^2 ) / sum( (obs - mean(obs))^2 ) )
```

```
[1] 0.711062
```

Validation scatterplot

```
library(ggplot2)
ggplot(d.SOCstock.val, aes(predictions, `soilgrids_SOCstock_0-30_mean30mSmooth`)) +
  geom_point(size = 2) + ylim(52,108) + xlim(52,108) +
  xlab(expression("predicted SOC stocks [t" ~ha^-1~"]")) +
  ylab(expression("observed SOC stocks [t" ~ha^-1~"]")) +
  stat_smooth(se = FALSE, span = 1.5) +
  geom_abline (slope=1, linetype = "dashed", color="black") +
  theme_minimal()
```



6.5 Create spatial predictions

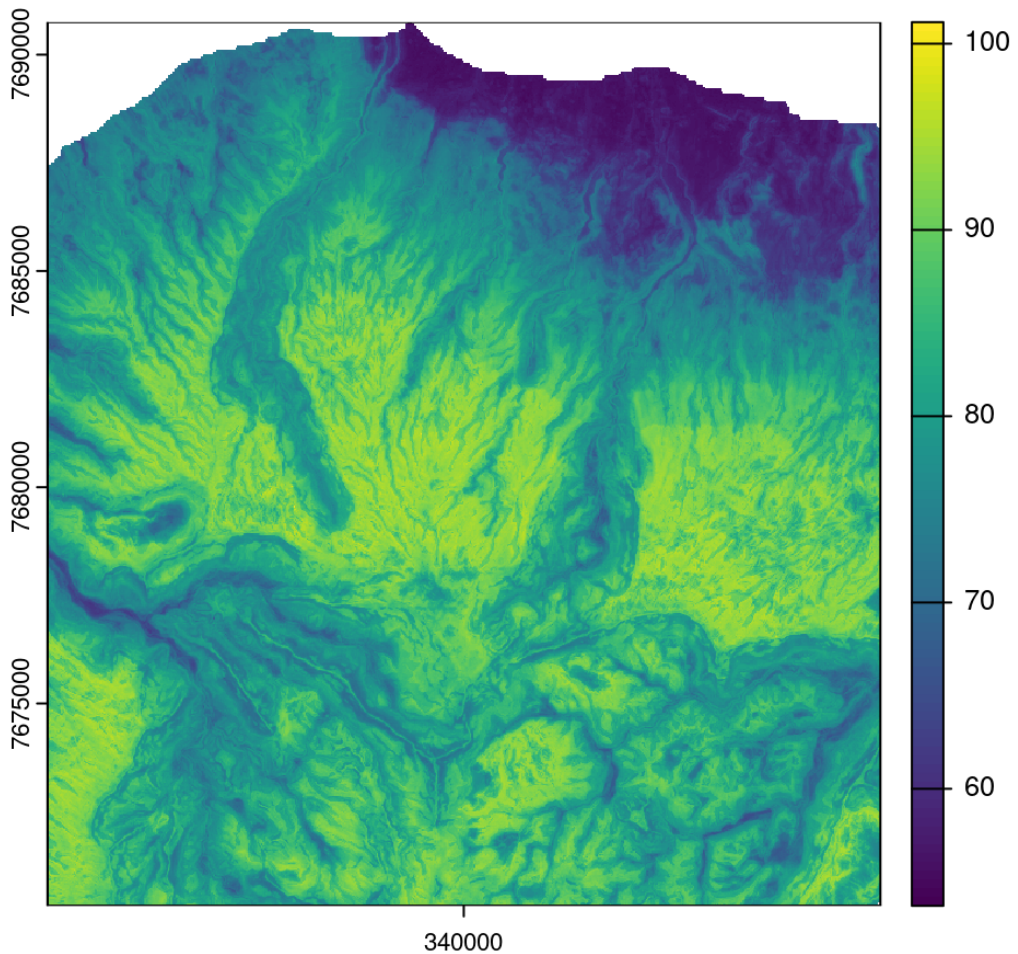
```
# create a data frame, each row corresponds to a pixel
d.pixels <- as.data.frame(r.stack, xy = T, na.rm = F)

# remove NA
d.pixels <- d.pixels[ complete.cases(d.pixels), ]

# check if we have all predictors, list missing columns
names(importance(m.rf))[ !names(importance(m.rf)) %in% names(d.pixels) ]
```

```
character(0)
```

```
# predict using ranger object
d.pixels$SOCstock_predictions <- predict(m.rf, d.pixels)$predictions

# create a raster object and save
r.pred <- rast(d.pixels[, c("x", "y", "SOCstock_predictions")], type="xyz", crs= "epsg:32740")
writeRaster(r.pred, filename = "results/predicted_SOC_stocks.tif", overwrite = T)
```

Display results

```
1  plot(r.pred)
```



6.6 Additional Task

Additional Task

Compare the created map to the soil organic carbon stock map from SoilGrids. How well do they align? Where are major differences? And which map would you trust more as an end-user?