

# Build GRASS GIS database

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```
# Load packages
require(dplyr)
require(rgrass7)
require(NinaR)

require(sp)
require(raster)
require(terra)
require(rgdal)
require(sf)
```

## Connect to GRASS GIS

We start by connecting the R session to GRASS GIS, in my local user mapset (u\_bernardo.brandao).

```
# Connect to GRASS
NinaR::grassConnect(location = "ETRS_33N", mapset = "user")

# example of command
# execGRASS("g.mapset", parameters = list(), flags = )
```

## Get read access to the existing mapsets

```
# list all mapsets
sep <- " "
all_mapsets <- execGRASS("g.mapsets", flags = c("l"), intern = T) %>%
  strsplit(sep) %>%
  first()

# list mapsets for "rein"
mapset_patt_rein <- c("Rein", "rein") %>%
  paste(collapse = "|")
mapsets_rein <- all_mapsets %>%
  grep(pattern = mapset_patt_rein, value = T)

# list mapsets for "Prodchange"
mapset_patt_pc <- c("change") %>%
  paste(collapse = "|")
mapsets_pc <- all_mapsets %>%
  grep(pattern = mapset_patt_pc, value = T) %>%
  grep(pattern = paste(mapsets_rein, collapse = "|"), invert = T, value = T)

# list some more mapsets we know we'll use
land_use_mapsets <- c("p_RenRein_norut", "g_LandCover_Norway_NORUT_SAM_TT", "p_prodchange_er")
landscape_mapsets <- c(
  "g_Elevation_Fenoscandia", "g_LandCover_Fenoscndia_PHENOLOGY_SAM_TT",
  "g_Elevation_Fenoscandia_TPI"
)
climate_mapsets <- c(
  "g_BiogeographicalRegions_Norway_PCA_klima", "u_bram.van.moorter",
  "g_EnergyResources_Fenoscandia", "u_torkildtveraa"
)
infrastructure_mapsets <- c(
  "p_prodchange_envpointsTT", "p_prodchange_roadsTT", "p_RenRein_trails2",
  "p_prodchange_trailsTT"
)

all_relevant_mapsets <- c(
  mapsets_rein, mapsets_pc,
  land_use_mapsets, landscape_mapsets,
  climate_mapsets, infrastructure_mapsets
) %>%
  unique()

# access to those mapsets
execGRASS("g.mapsets", parameters = list(mapset = all_relevant_mapsets))
```

---

## Create new mapsets

Let's create the new mapsets here. There are six mapsets:

- climate\_phenology
- landscape
- species
- industr
- transport\_urban
- urban

Describe the idea of each one here.

```
# Create mapsets
mapsets <- c(
  "climate_phenology", "landscape", "species",
  "industry", "transport_urban", "tourism"
)
mapsets <- paste0("p_sam_", mapsets)

for (ms in mapsets) {
  execGRASS("g.mapset", parameters = list(mapset = ms), flags = "c")
}
```

## Load data

Before starting to load data, we define here some paths to the folders where the datasets are located. If it is necessary, one can simply change the path and re-load the data.

```
# Define paths

# root folder Sweden
sw_dir <- "~/Mounts/R/Prosjekter/Rein/oneimpact/"
```

## Load landscape data

### Data from Norway

First we'll copy the datasets from Norway that have already been in use in the previous projects (e.g. Renewable Reindeer, Prodchange).

```
# go into mapset
ms <- "p_sam_landscape"
execGRASS("g.mapset", mapset = ms)

#---
# settings
type_of_info <- "landscape"

#---
# land use
ms_from <- "p_RenRein_norut"
maps <- execGRASS("g.list", type = "raster", mapset = ms_from, intern = T)

# copy
for (i in maps) {
  map_in <- paste0(i, "@", ms_from)
  map_out <- i
  execGRASS("g.region", raster = map_in)
  execGRASS("g.copy", raster = paste0(map_in, ",", map_out), flags = c("overwrite"))
}

# document
md <- readr::read_csv("../data/spatialdb_metadata_oneimpact_20211122.csv")

# used earlier
used <- grep("100", maps, value = T)
used_names <- c(
  "agricultural lands", "glacier", "grasses", "heather in lowland", "heather in ridges",
  "heathlands", "forest with lichens", "lichens", "meadows", "mires", "ridges", "forest",
  "snow", "snowbed"
)

cont <- 1
for (i in used) {
  which_line <- which(md$layer_name == i)
  md$type_of_information[which_line] <- type_of_info
  md$old_folder[which_line] <- ms_from
  md$folder[which_line] <- ms
}
```

```

md$variable[which_line] <- used_names[cont]
md$institution[which_line] <- NA
md$description[which_line] <- NA
md$unit[which_line] <- NA
md$type_of_spatial_data[which_line] <- "raster"
md$original_raster_range_values[which_line] <- "0-1"
md$year_of_original_data[which_line] <- NA
md$original_pixel_resolution[which_line] <- 30 ##### ?????????
md$final_pixel_resolution[which_line] <- 100
md$extent[which_line] <- "Norway"
md$primary_or_derived[which_line] <- "Primary"
md$derived_from[which_line] <- NA
md$website[which_line] <- NA
md$source[which_line] <- NA
md$obtained_through[which_line] <- "NINA"
md$observations[which_line] <- NA

cont <- cont + 1
}

not_used <- sort(setdiff(maps, used))
not_used_names <- used_names
cont <- 1

n_new <- length(not_used)
tab_new <- md[1:n_new, ]
tab_new[1:n_new] <- NA

cont <- 1
for (i in not_used) {
  which_line <- cont
  tab_new$layer_name[which_line] <- i
  tab_new$type_of_information[which_line] <- type_of_info
  tab_new$old_folder[which_line] <- ms_from
  tab_new$folder[which_line] <- ms
  tab_new$variable[which_line] <- not_used_names[cont]
  tab_new$institution[which_line] <- NA
  tab_new$description[which_line] <- NA
  tab_new$unit[which_line] <- NA
  tab_new$type_of_spatial_data[which_line] <- "raster"
  tab_new$original_raster_range_values[which_line] <- "0-1"
  tab_new$year_of_original_data[which_line] <- NA
  tab_new$original_pixel_resolution[which_line] <- 30 ##### ?????????
  tab_new$final_pixel_resolution[which_line] <- 100
  tab_new$extent[which_line] <- "Norway"

```

```

tab_new$primary_or_derived[which_line] <- "Primary"
tab_new$derived_from[which_line] <- NA
tab_new$website[which_line] <- NA
tab_new$source[which_line] <- NA
tab_new$obtained_through[which_line] <- "NINA"
tab_new$observations[which_line] <- NA

  cont <- cont + 1
}
tab_new

md <- dplyr::bind_rows(md, tab_new)
readr::write_csv(md, file = paste0(
  "../data/spatialdb_metadata_oneimpact_",
  gsub("-", "", lubridate::today()),
  ".csv"
))

#---
# land use density
# This data is present in the mapset "g_LandCover_Norway_NORUT_SAM_TT", but it should be re
# with the data from Sweden
# But we need to compare the land use maps first

mapsets <- c()

```

Now we load the landscape datasets into GRASS GIS.

## Load species data

Now we import species data

```

# go into mapset
execGRASS("g.mapset", parameters = list(mapset = "p_sam_species"))

# folder with raw data
species_dir <- paste0(sw_dir, "03_raster/p_sam_species/")

# list maps in folder
files <- list.files(species_dir, pattern = "tif$", full.names = T)

test <- terra::rast(files[1])

```

```

plot(test)

# load predators data into GRASS
for (i in file) {

  # prepare input name
  name <- strsplit(i, "/", fixed = T)[[1]] %>%
    dplyr::last() %>%
    gsub(pattern = ".tif", replacement = "")
  # execGRASS("r.in.gdal", parameters = list(input = i, output = name), flags = c("overwrite"))

  execGRASS("r.import", parameters = list(input = i, output = name), flags = c("overwrite"))
}

# document

```