

The MOISCRUST dataset: a spatio-temporal continuous soil moisture dataset from a Mediterranean semiarid dryland from 2006 to 2020

SUPPLEMENTARY MATERIAL

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1 Summary

The **MOISCRUST** database contains volumetric water content (VWC, m³/m³) measures taken by soil moisture sensors EC-5, Decagon Devices Inc., Pullman, USA) every 120 minutes (17th November 2006 to 31th January 2017) and 150 minutes (1st February 2017 to 16th December 2020) from three replicates in five different microsites (*Stipa* tussocks, *Retama* shrubs, and areas with low, medium and high cover of biocrust-forming lichens) located in The Aranjuez Experimental Station (central Iberian Peninsula, 40°02' N, 3°32'W; 590 m.a.s.l.). During the long time-span these sensors have been working, there have been periods when data capture has not possible due to technical issues, and as consequence, 34.63% of the database records are missing entries. This reproducible workflow describes in detail the method used to impute missing data in the **MOISCRUST** database.

The **MOISCRUST** database and this reproducible document are distributed under the license Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International.

2 Reproducing this workflow

This reproducible workflow is available as an interactive Rstudio notebook in the file **moisrust.Rmd** stored in this repository. It is packaged with **renv** to facilitate reproducibility. To run it in your computer, execute the code chunk below to prepare the session. You will need to replace `reval = TRUE` with `eval = TRUE` in the header of the code chunk.

```
install.packages("renv")
library(renv)
renv::restore()
```

3 Data loading and preparation

3.1 Installing and loading the required libraries

The following libraries are required to run this workflow. These are already installed in the local **renv** folder, so there is no need to install them if they are not available in your computer.

```
#automatic install of packages if they are not readily available
required_packages <- c(
  "data.table",
  "tidyverse",
  "kableExtra",
  "foreach",
  "doParallel",
  "readr",
```

```

"writexl",
"RSSQLite",
"zip",
"knitr",
"DBI"
)

#loading packages
invisible(
lapply(
  required_packages,
  library,
  character.only = TRUE
)
)

#knitr options
knitr::opts_chunk$set(echo = TRUE, warning = FALSE, message = FALSE)
knitr::knit_hooks$set(document = function(x) {sub('`\\usepackage{xcolor}`', '`, fixed = TRUE)`)}}

#removing objects
rm(required_packages)

```

3.2 Loading and preparing the raw data

The raw data, stored in the file *moiscrust_raw.csv* was compiled by the members of Maestre Lab from the data provided by the soil moisture sensors.

```
#load, clean names, and rename time columns
moiscrust <- data.table::fread(file = "moiscrust_raw.csv") %>%
  as.data.frame()
```

date	time	retama_1	retama_2	retama_3	stipa_1	stipa_2	stipa_3	bare_soil_1	bare_soil_2	bare_soil_3	biocrust_medium_1	biocrust_medium_2	biocrust_medium_3	biocrust_high_1	biocrust_high_2	biocrust_high_3
17/11/2006	18:00:00	0.197	NA	NA	0.132	NA	NA	0.232	NA	NA	0.205	NA	NA	0.121	NA	NA
17/11/2006	20:00:00	0.195	NA	NA	0.131	NA	NA	0.233	NA	NA	0.203	NA	NA	0.117	NA	NA
17/11/2006	22:00:00	0.194	NA	NA	0.131	NA	NA	0.234	NA	NA	0.203	NA	NA	0.117	NA	NA
18/11/2006	0:00:00	0.194	NA	NA	0.131	NA	NA	0.234	NA	NA	0.203	NA	NA	0.116	NA	NA
18/11/2006	2:00:00	0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.203	NA	NA	0.116	NA	NA
18/11/2006	4:00:00	0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.116	NA	NA
18/11/2006	6:00:00	0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.115	NA	NA
18/11/2006	8:00:00	0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.115	NA	NA
18/11/2006	10:00:00	0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.115	NA	NA
18/11/2006	12:00:00	0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.116	NA	NA
18/11/2006	14:00:00	0.195	NA	NA	0.131	NA	NA	0.234	NA	NA	0.202	NA	NA	0.116	NA	NA
18/11/2006	16:00:00	0.195	NA	NA	0.131	NA	NA	0.233	NA	NA	0.201	NA	NA	0.115	NA	NA
18/11/2006	18:00:00	0.194	NA	NA	0.130	NA	NA	0.233	NA	NA	0.200	NA	NA	0.114	NA	NA
18/11/2006	20:00:00	0.193	NA	NA	0.129	NA	NA	0.233	NA	NA	0.199	NA	NA	0.112	NA	NA
18/11/2006	22:00:00	0.192	NA	NA	0.129	NA	NA	0.234	NA	NA	0.199	NA	NA	0.111	NA	NA
19/11/2006	0:00:00	0.192	NA	NA	0.128	NA	NA	0.234	NA	NA	0.199	NA	NA	0.111	NA	NA
19/11/2006	2:00:00	0.191	NA	NA	0.128	NA	NA	0.234	NA	NA	0.198	NA	NA	0.110	NA	NA
19/11/2006	4:00:00	0.190	NA	NA	0.127	NA	NA	0.234	NA	NA	0.198	NA	NA	0.109	NA	NA
19/11/2006	6:00:00	0.189	NA	NA	0.127	NA	NA	0.234	NA	NA	0.198	NA	NA	0.109	NA	NA
19/11/2006	8:00:00	0.188	NA	NA	0.127	NA	NA	0.234	NA	NA	0.198	NA	NA	0.109	NA	NA

3.3 Formatting dates and times

The raw data contains two fields representing time, namely *date* (year, month, and day), and *time* (hour, minute, and seconds). Below we format these fields according to the POSIX standard, and add new fields adding criteria to subset the data by time:

- *date_time*: Date and time in POSIX format.
- *date_time_id*: Unique identifier for each *date_time*.
- *year*: Year number.
- *year_day*: Day of the year.
- *month*: Month number.
- *month_day*: Day of the month.
- *week*: Week of the year.
- *week_day*: Day of the week.

```
#date to Year-month-day
moisrust$date <- format(  
  as.POSIXct(  
    strptime(  
      moisrust$date,  
      "%d/%m/%Y",  
      tz = ""  
    ),  
    format = "%Y-%m-%d"  
  )  
  
#time to Hour-Minute
moisrust$time <- format(  
  as.POSIXct(  
    strptime(  
      moisrust$time,  
      "%H:%M:%S",  
      tz = ""  
    ),  
    format = "%H:%M"  
  )  
  
#joining date and time
moisrust$date_time <- as.POSIXct(  
  paste(  
    moisrust$date,
```

```

moisrust$time
),
format="%Y-%m-%d %H:%M"
)

#unique id for each observation
moisrust$date_time_id <- 1:nrow(moisrust)

#creating year, month, and day related columns
moisrust$year <- lubridate::year(moisrust$date)
moisrust$year_day <- lubridate::yday(moisrust$date)
moisrust$month <- lubridate::month(moisrust$date)
moisrust$month_day <- lubridate::mdy(moisrust$date)
moisrust$week <- lubridate::week(moisrust$date)
moisrust$week_day <- lubridate::wday(moisrust$date)

```

3.4 Reordering time and data columns and arranging the data into long format

At this point, the *MOISCRUST* data has 15 columns representing soils moisture measures (microsites per three replicates per microsite), and 10 columns representing *time*. The data is also structured in what is known as a “wide format”. Below we reorder these columns to facilitate arranging the data into a “long format”.

```

#names of the sensors
sensors <- c(
  "retama_1",
  "retama_2",
  "retama_3",
  "stipa_1",
  "stipa_2",
  "stipa_3",
  "bare_soil_1",
  "bare_soil_2",
  "bare_soil_3",
  "biocrust_medium_1",
  "biocrust_medium_2",
  "biocrust_medium_3",
  "biocrust_high_1",
  "biocrust_high_2",
  "biocrust_high_3"
)
```

```
)
```

```
#reordering columns of moisrust to have time in the left side
```

```
moisrust <- moisrust[, c(
```

```
  "date_time",
  "date_time_id",
  "date",
  "time",
  "year",
  "year_day",
  "month",
  "month_day",
  "week",
  "week_day",
  sensors
```

```
)]
```

```
#to long format
```

```
moisrust_long <- tidyverse::pivot_longer(
```

```
  moisrust,
  cols = all_of(sensors),
  names_to = "sensor",
  values_to = "soil_moisture"
```

```
)
```

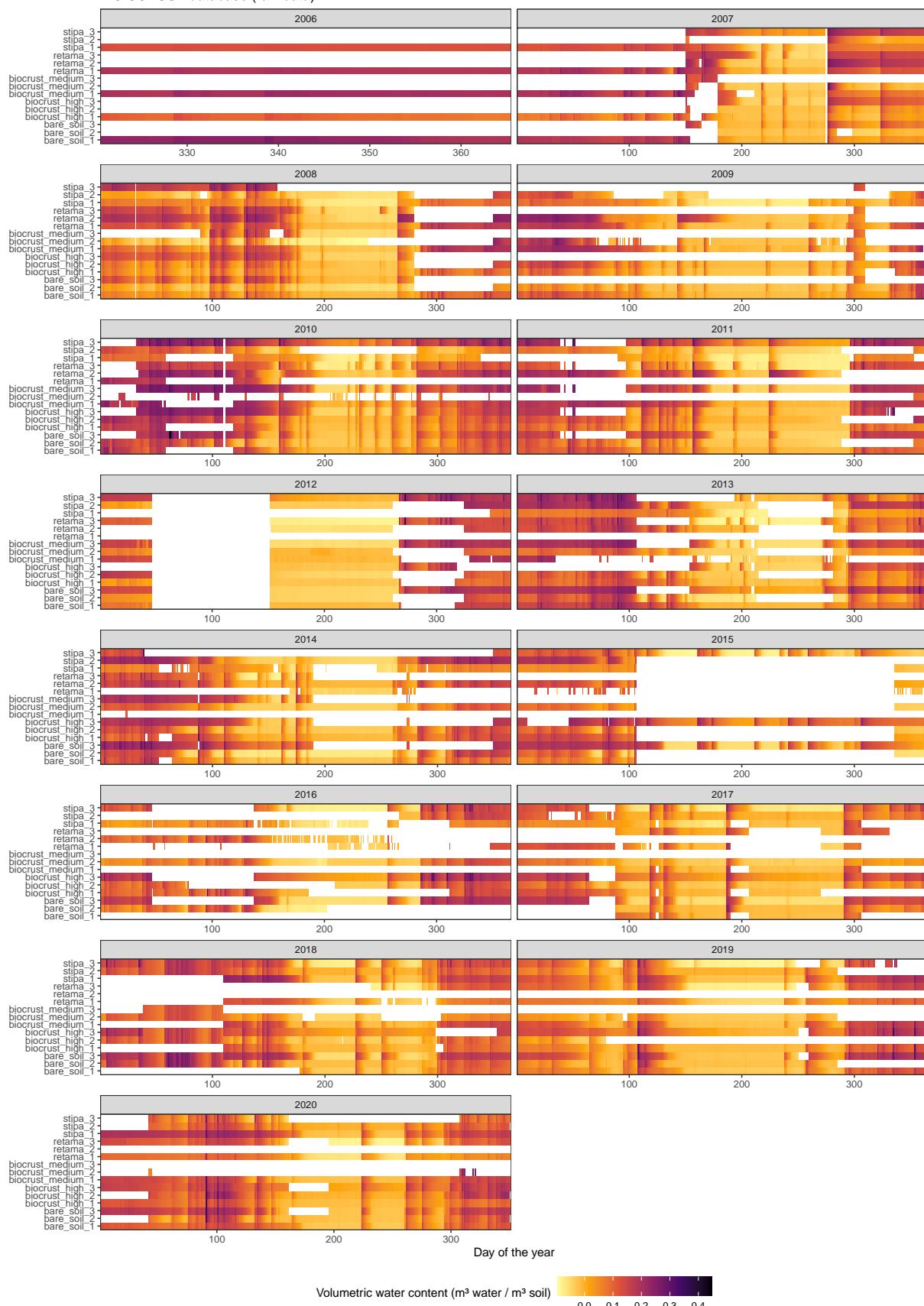
date_time	date_time_id	date	time	year	year_day	month	month_day	week	week_day	sensor	soil_moisture
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	retama_1	0.197
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	retama_2	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	retama_3	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	stipa_1	0.132
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	stipa_2	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	stipa_3	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	bare_soil_1	0.232
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	bare_soil_2	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	bare_soil_3	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	biocrust_medium_1	0.205
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	biocrust_medium_2	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	biocrust_medium_3	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	biocrust_high_1	0.121
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	biocrust_high_2	NA
2006-11-17 18:00:00	1	2006-11-17	18:00	2006	321	11	17	46	6	biocrust_high_3	NA
2006-11-17 20:00:00	2	2006-11-17	20:00	2006	321	11	17	46	6	retama_1	0.195
2006-11-17 20:00:00	2	2006-11-17	20:00	2006	321	11	17	46	6	retama_2	NA
2006-11-17 20:00:00	2	2006-11-17	20:00	2006	321	11	17	46	6	retama_3	NA
2006-11-17 20:00:00	2	2006-11-17	20:00	2006	321	11	17	46	6	stipa_1	0.131
2006-11-17 20:00:00	2	2006-11-17	20:00	2006	321	11	17	46	6	stipa_2	NA

3.5 Visualization of the raw data

Having the data in long format facilitates plotting and manipulation. The figure below shows the raw data, with missing data represented by the white color.

```
ggplot(moiscrust_long) +  
  facet_wrap("year", scales = "free_x", ncol = 2) +  
  aes(x = year_day, y = sensor, fill = soil_moisture) +  
  geom_tile() +  
  coord_cartesian(expand = FALSE) +  
  theme_bw() +  
  scale_fill_viridis_c(direction = -1, na.value = "white", option = "B") +  
  theme(legend.position = "bottom") +  
  ylab("") +  
  xlab("Day of the year") +  
  ggtitle("MOISCRUST database (raw data)") +  
  labs(fill = expression("Volumetric water content (m³ water / m³ soil)")) +  
  theme(legend.key.width = unit(1, "cm"))
```

MOISCRUST database (raw data)



3.6 Number of NA per sensor

Due to technical constraints, there is a large number of missing data in the *MOISCRUST* dataset. To better understand the extent of such missing data, the code below counts the number of missing entries per sensor.

```
#counting NA values per sensor
moisrust_NA <- moisrust_long %>%
  group_by(sensor) %>%
  summarise(na_count = sum(is.na(soil_moisture))) %>%
  mutate(na_count_percent = round((na_count * 100) / nrow(moisrust), 1))

#adding sensor microsite to the moisrust_NA data frame
moisrust_NA$microsite <- c(
  "bare_soil",
  "bare_soil",
  "bare_soil",
  "biocrust_high",
  "biocrust_high",
  "biocrust_high",
  "biocrust_medium",
  "biocrust_medium",
  "biocrust_medium",
  "retama",
  "retama",
  "retama",
  "stipa",
  "stipa",
  "stipa"
)

#reordering columns and arranging by na_count
moisrust_NA <- moisrust_NA[, c(
  "sensor",
  "microsite",
  "na_count",
  "na_count_percent"
)] %>%
  dplyr::arrange(na_count) %>%
  as.data.frame()
```

sensor	microsite	na_count	na_count_percent
biocrust_high_1	biocrust_high	7674	16.5
stipa_1	stipa	10553	22.7
bare_soil_1	bare_soil	10987	23.6
bare_soil_3	bare_soil	11114	23.9
bare_soil_2	bare_soil	11188	24.1
biocrust_high_2	biocrust_high	11776	25.3
biocrust_high_3	biocrust_high	14125	30.4
stipa_2	stipa	15363	33.0
stipa_3	stipa	15604	33.5
biocrust_medium_1	biocrust_medium	16934	36.4
biocrust_medium_2	biocrust_medium	18743	40.3
retama_3	retama	20505	44.1
retama_1	retama	22840	49.1
retama_2	retama	22999	49.4
biocrust_medium_3	biocrust_medium	31225	67.1

4 Imputation of missing data

The imputation of missing data we implement here to impute missing data in *MOISCRUST* works by finding, for a given entry y with missing data at a time t , the sensor x with data for t that is in the same type of microsite (if possible), has the longest extent in common, and the highest correlation with the sensor to which y belongs, and estimates y with the linear model $y \sim x$.

4.1 Developing criteria to find candidates for gap filling

To generate the criteria to find the best possible candidate x to estimate the missing data y , we compute the common length and correlation between all pairs of sensors, and generate a column indicating whether they belong to the same microsite or not. With the values stored in these columns we compute a *selection score* based on the following expression:

$$S_x = \%vc_{x,y} + (R_{x,y}^2 * 100) + \begin{cases} 100, & \text{if } \text{microsite}_x == \text{microsite}_y \\ 0, & \text{otherwise} \end{cases}$$

Where:

- y is the sensor with a missing value to be estimated.
- x is the sensor to be used as candidate predictor to estimate the missing value in y .
- S_x is the selection score of the candidate sensor x , in the range [0, 300].
- $\%vc_{x,y}$ is the percent of common valid cases of the sensors x and y .

- $R^2_{x,y}$ is the Pearson's R² of the common valid cases of the sensors x and y .
- microsite_x and microsite_y are the respective microsites of the sensors x and y .

During data imputation, for each missing value, the sensor with the higher selection score is used to estimate it.

These criteria are stored in the data frame **sensors_pairs**. Along with the computation of the selection score, the code below also computes a linear model for each pair x y , and stores it in the object **sensors_pairs_models**. The identifiers of these models are stored in the column *model_id* of the data frame **sensors_pairs**.

```
#combining sensors in pairs x-
sensors_pairs <- combin(
  x = sensors,
  m = 2
) %>%
  t() %>%
  as.data.frame()

#adding combinations y-x so all pairs have both directions
#removing repeated pairs
#joining with moisrust_NA to get sensor groups
#add column same_microsite to check if x and y are or not in the same sensor group
#add empty columns to store % of shared data, model's R squared, and model ID
sensors_pairs <- sensors_pairs %>%
  rbind(
    data.frame(
      V1 = sensors_pairs$V2,
      V2 = sensors_pairs$V1
    )
  ) %>%
  distinct(
    V1,
    V2,
    .keep_all = TRUE
  ) %>%
  left_join(
    moisrust_NA[, c("sensor", "microsite")],
    by = c("V1" = "sensor")
  ) %>%
  left_join(
    moisrust_NA[, c("sensor", "microsite")],
    by = c("V2" = "sensor")
```

```

) %>%
rename(  

  y = V1,  

  x = V2,  

  y_microsite = microsite.x, #not a mistake  

  x_microsite = microsite.y, #not a mistake  

) %>%
mutate(  

  same_microsite = ifelse(  

    x_microsite == y_microsite,  

    TRUE,  

    FALSE  

  ),  

  sensors_shared_valid_percent = NA,  

  sensors_r_squared = NA,  

  model_id = row_number()  

)  
  

#list to store models  

sensors_pairs_models <- list()  
  

#looping through sensors pairs to:  

#fit lm model y ~ x and save it in sensors_pairs_models  

#  

for(i in 1:nrow(sensors_pairs)){  
  

  #names of the sensors y and x  

  y_i <- sensors_pairs[i, "y"]  

  x_i <- sensors_pairs[i, "x"]  
  

  #data of the sensor pair  

  sensor_pair_i <- moisrust[, c(y_i, x_i)]  
  

  #complete cases of the sensor pair  

  sensor_pair_i <- sensor_pair_i[complete.cases(sensor_pair_i), ]  
  

  #common cases  

  sensors_pairs[i, "sensors_shared_valid_percent"] <-  

  nrow(sensor_pair_i) / nrow(moisrust) * 100  
  

  #R squared of the sensor pair

```

```

sensors_pairs[i, "sensors_r_squared"] <- cor(
  sensor_pair_i[, 1],
  sensor_pair_i[, 2]
)

#model formula y ~ x
formula_i <- as.formula(paste(y_i, "~", x_i))

#linear model
sensors_pairs_models[[i]] <- lm(
  formula = formula_i,
  data = sensor_pair_i
)

}

#selection score to find candidates during gap filling
#(sensors_r_squared * 100) +
#sensors_shared_valid_percent +
#same_microsite (TRUE = 100, FALSE = 0)
sensors_pairs <- mutate(
  sensors_pairs,
  selection_score =
    (sensors_r_squared * 100) +
    sensors_shared_valid_percent +
    ifelse(same_microsite == TRUE, 100, 0)
)

#removing objects we don't need
rm(
  sensor_pair_i,
  formula_i,
  i,
  x_i,
  y_i
)

```

The resulting data frame, named **sensors_pairs**, has columns with the names of the sensor *y* (the one with missing data to impute), the sensor *x* (the candidate to be used as predictor to estimate *y*), their respective microsites, a column indicating if they belong to the same microsite, the percent of shared valid data, the R squared of their shared data, a

y	x	y_microsite	x_microsite	same_microsite	sensors_shared_valid_percent	sensors_r_squared	model_id	selection_score
retama_1	retama_2	retama	retama	TRUE	20.503945	0.8825786	1	208.76181
retama_1	retama_3	retama	retama	TRUE	28.736052	0.9065618	2	219.39223
retama_1	stipa_1	retama	stipa	FALSE	49.437792	0.6546707	3	114.90486
retama_1	stipa_2	retama	stipa	FALSE	34.751575	0.6570769	4	100.45926
retama_1	stipa_3	retama	stipa	FALSE	27.985724	0.8494829	5	112.93401
retama_1	bare_soil_1	retama	bare_soil	FALSE	45.825898	0.8610431	6	131.93021
retama_1	bare_soil_2	retama	bare_soil	FALSE	39.137445	0.6276224	7	101.89968
retama_1	bare_soil_3	retama	bare_soil	FALSE	34.364586	0.8118848	8	115.55307
retama_1	biocrust_medium_1	retama	biocrust_medium	FALSE	44.099499	0.8808309	9	132.18258
retama_1	biocrust_medium_2	retama	biocrust_medium	FALSE	31.105282	0.7429876	10	105.40404
retama_1	biocrust_medium_3	retama	biocrust_medium	FALSE	5.892976	0.8384753	11	89.74050
retama_1	biocrust_high_1	retama	biocrust_high	FALSE	48.414422	0.7630192	12	124.71634
retama_1	biocrust_high_2	retama	biocrust_high	FALSE	38.305420	0.7500951	13	113.31493
retama_1	biocrust_high_3	retama	biocrust_high	FALSE	32.943478	0.8490180	14	117.84528
retama_2	retama_3	retama	retama	TRUE	32.057704	0.8394976	15	216.00746
retama_2	stipa_1	retama	stipa	FALSE	42.633242	0.7653060	16	119.16384
retama_2	stipa_2	retama	stipa	FALSE	37.522843	0.5339814	17	90.92099
retama_2	stipa_3	retama	stipa	FALSE	31.636317	0.8561540	18	117.25171
retama_2	bare_soil_1	retama	bare_soil	FALSE	43.684561	0.7455036	19	118.23492
retama_2	bare_soil_2	retama	bare_soil	FALSE	48.896008	0.6940089	20	118.29689

4.2 Generating the x and y matrices to predict imputed values

During data imputation, two data frames are needed. The data frame **x** contains the data of every sensor for every available time, while the data frame **y**, which starts with empty values, is where the imputed values, their confidence intervals, selection criteria, and other quality-related columns are going to be stored.

```
#creating data frame of predictors
x <- moisrust[, sensors]

#creating data frame to store model results
y <- matrix(
  data = NA,
  nrow = nrow(moisrust),
  ncol = 12
) %>%
  as.data.frame()

#new colnames
colnames(y) <- c(
  "interpolated",
  "model_estimate",
  "model_ci_lower",
  "model_ci_upper",
  "model_predictor",
  "same_microsite",
  "sensors_r_squared",
  "sensors_shared_valid_percent",
  "selection_score",
)
```

```

"date_time_id",
"sensor",
"microsite"
)

#transferring time id
y[, "date_time_id"] <- moisrust[, "date_time_id"]
y[, "interpolated"] <- FALSE

```

The **x** data frame looks as follows:

retama_1	retama_2	retama_3	stipa_1	stipa_2	stipa_3	bare_soil_1	bare_soil_2	bare_soil_3	biocrust_medium_1	biocrust_medium_2	biocrust_medium_3	biocrust_high_1	biocrust_high_2	biocrust_high_3
0.197	NA	NA	0.132	NA	NA	0.232	NA	NA	0.205	NA	NA	0.121	NA	NA
0.195	NA	NA	0.131	NA	NA	0.233	NA	NA	0.203	NA	NA	0.117	NA	NA
0.194	NA	NA	0.131	NA	NA	0.234	NA	NA	0.203	NA	NA	0.117	NA	NA
0.194	NA	NA	0.131	NA	NA	0.234	NA	NA	0.203	NA	NA	0.116	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.203	NA	NA	0.116	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.116	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.115	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.115	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.115	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.115	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.116	NA	NA
0.194	NA	NA	0.130	NA	NA	0.234	NA	NA	0.202	NA	NA	0.116	NA	NA
0.195	NA	NA	0.131	NA	NA	0.234	NA	NA	0.202	NA	NA	0.116	NA	NA
0.195	NA	NA	0.131	NA	NA	0.233	NA	NA	0.201	NA	NA	0.115	NA	NA
0.194	NA	NA	0.130	NA	NA	0.233	NA	NA	0.200	NA	NA	0.114	NA	NA
0.193	NA	NA	0.129	NA	NA	0.233	NA	NA	0.199	NA	NA	0.112	NA	NA
0.192	NA	NA	0.129	NA	NA	0.234	NA	NA	0.199	NA	NA	0.111	NA	NA
0.192	NA	NA	0.128	NA	NA	0.234	NA	NA	0.199	NA	NA	0.111	NA	NA
0.191	NA	NA	0.128	NA	NA	0.234	NA	NA	0.198	NA	NA	0.110	NA	NA
0.190	NA	NA	0.127	NA	NA	0.234	NA	NA	0.198	NA	NA	0.109	NA	NA
0.189	NA	NA	0.127	NA	NA	0.234	NA	NA	0.198	NA	NA	0.109	NA	NA
0.188	NA	NA	0.127	NA	NA	0.234	NA	NA	0.198	NA	NA	0.109	NA	NA

And this is the **y** data frame, that will be filled during data imputation:

interpolated	model_estimate	model_ci_lower	model_ci_upper	model_predictor	same_microsite	sensors_r_squared	sensors_shared_valid_percent	selection_score	date_time_id	sensor	microsite
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	1	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	2	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	3	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	4	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	5	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	6	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	7	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	8	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	9	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	10	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	11	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	12	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	13	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	14	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	15	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	16	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	17	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	18	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	19	NA	NA
FALSE	NA	NA	NA	NA	NA	NA	NA	NA	20	NA	NA

4.3 Data imputation, step by step

The steps to fill the gaps in the **MOISCRUST** database go as follows:

1. A given sensor name is selected: "retama_2"

```
sensor = "retama_2"
```

2. The sensors pairs from the table **sensors_pairs** where the selected sensor is *y* (the sensor which values are to be imputed) are selected.

```
sensors_pair <- sensors_pairs %>%
```

```
dplyr::filter(y == sensor)
```

y	x	y_microsite	x_microsite	same_microsite	sensors_shared_valid_percent	sensors_r_squared	model_id	selection_score
retama_2	retama_3	retama	retama	TRUE	32.05770	0.8394976	15	216.00746
retama_2	stipa_1	retama	stipa	FALSE	42.63324	0.7653060	16	119.16384
retama_2	stipa_2	retama	stipa	FALSE	37.52284	0.5339814	17	90.92099
retama_2	stipa_3	retama	stipa	FALSE	31.63632	0.8561540	18	117.25171
retama_2	bare_soil_1	retama	bare_soil	FALSE	43.68456	0.7455036	19	118.23492
retama_2	bare_soil_2	retama	bare_soil	FALSE	48.89601	0.6940089	20	118.29689
retama_2	bare_soil_3	retama	bare_soil	FALSE	37.40030	0.7494452	21	112.34481
retama_2	biocrust_medium_1	retama	biocrust_medium	FALSE	30.22811	0.7692882	22	107.15692
retama_2	biocrust_medium_2	retama	biocrust_medium	FALSE	37.38525	0.7255941	23	109.94466
retama_2	biocrust_medium_3	retama	biocrust_medium	FALSE	26.50872	0.8334687	24	109.85559
retama_2	biocrust_high_1	retama	biocrust_high	FALSE	47.95649	0.6954543	25	117.50191
retama_2	biocrust_high_2	retama	biocrust_high	FALSE	47.88339	0.8146773	26	129.35112
retama_2	biocrust_high_3	retama	biocrust_high	FALSE	33.64221	0.8001904	27	113.66124
retama_2	retama_1	retama	retama	TRUE	20.50395	0.8825786	106	208.76181

3. The first row of the data frame **x** is selected.

```
x_row <- x[1, ]
```

retama_1	retama_2	retama_3	stipa_1	stipa_2	stipa_3	bare_soil_1	bare_soil_2	bare_soil_3	biocrust_medium_1	biocrust_medium_2	biocrust_medium_3	biocrust_high_1	biocrust_high_2	biocrust_high_3
0.197	NA	NA	0.132	NA	NA	0.232	NA	NA	0.205	NA	NA	0.121	NA	NA

3.1. If there is a valid value of soil moisture for the sensor "stipa5063", the algorithm goes to the next row, until there is a row with a missing value.

4. If there is a missing value (NA), the potential candidate predictors are selected from the row by removing the data of other sensors with NA, and the data of the target sensor.

```
predictor_candidates <- as.vector(x[1, ])  
predictor_candidates <- predictor_candidates[which(  
  !is.na(predictor_candidates) &  
  names(predictor_candidates) != sensor  
)]
```

retama_1	stipa_1	bare_soil_1	biocrust_medium_1	biocrust_high_1
0.197	0.132	0.232	0.205	0.121

5. From these predictors, the one with the highest selection score is selected from the data frame **sensors_pair** generated in the step 2..

```
best_predictor <- sensors_pair %>%  
dplyr::filter(x %in% names(predictor_candidates)) %>%  
dplyr::arrange(desc(selection_score)) %>%  
dplyr::slice(1)
```

y	x	y_microsite	x_microsite	same_microsite	sensors_shared_valid_percent	sensors_r_squared	model_id	selection_score
retama_2	retama_1	retama	retama	TRUE	20.50395	0.8825786	106	208.7618

6. The model to use, stored in the list **sensors_pairs_model**, is selected from *model_id* column of the **best_predictor** data frame , and used to predict a value for the empty cell.

```
predict(  
  object = sensors_pairs_models[[best_predictor$model_id]],  
  newdata = x_row,  
  se.fit = TRUE,  
  type = "response",  
  interval = "confidence"  
)$fit
```

```
##     fit    lwr    upr  
## 1 0.2442059 0.2422496 0.2461622
```

7. The imputed value, its confidence intervals, and other values about the imputation quality available in **best_predictor** are transferred to the same row in the data frame **y**.

8. Once all the sensors and rows have been processed this way, the matrix **y** is joined with **moisrust_long**, and its interpolated values are transferred to the *soil_moisture* column, along with other columns indicating the quality of the interpolation.

4.4 Applying the algorithm to the complete dataset

The code below applies the algorithm to every sensor and row with missing data. Sensors are processed in parallel to speed up the data imputation operation.

```
#setup for parallel execution  
if(.Platform$OS.type == "windows"){  
  temp_cluster <- parallel::makeCluster(  
    parallel::detectCores() - 1,  
    type = "PSOCK"  
  )  
} else {  
  temp_cluster <- parallel::makeCluster(  
    parallel::detectCores() - 1,  
    type = "FORK"  
  )  
}  
doParallel::registerDoParallel(cl = temp_cluster)  
  
#parallelized loop (each sensor is processed in one separated thread)  
moisrust_interpolation <- foreach::foreach(  
  sensor_i = sensors,  
  .packages = "tidyverse"  
) %dopar% {
```

```

#subset sensors_pairs
sensors_pair_i <- sensors_pairs %>%
  dplyr::filter(y == sensor_i)

#fill microsite
y[ "microsite"] <-sensors_pair_i$y_microsite[1]

#scanning the rows of x one by one
for(row_i in 1:nrow(x)) {

  #if is not NA, next iteration
  if(!is.na(x[row_i, sensor_i])){next}

  #getting target row row
  x_row_i <- x[row_i, ]

  #getting predictor candidates available in x_row_i
  predictor_candidates_i <- as.vector(x_row_i)
  predictor_candidates_i <- predictor_candidates_i[which(
    !is.na(predictor_candidates_i) &
    names(predictor_candidates_i) != sensor_i
  )]

  #selecting the predictor candidate with the best selection_score score
  best_predictor_i <- sensors_pair_i %>%
    dplyr::filter(x %in% names(predictor_candidates_i)) %>%
    dplyr::arrange(desc(selection_score)) %>%
    dplyr::slice(1)

  #if there is no best candidate available, next iteration
  if(nrow(best_predictor_i) == 0){next}

  #compute estimates with the model of the best predictor
  y[row_i, c(
    "model_estimate",
    "model_ci_lower",
    "model_ci_upper"
  )] <- predict(
    object = sensors_pairs_models[[best_predictor_i$model_id]],
    newdata = x_row_i,
    se.fit = TRUE,

```

```

    type = "response",
    interval = "confidence"
  )$fit

#adding interpolation flag
y[row_i, "interpolated"] <- TRUE
y[row_i, "model_predictor"] <- best_predictor_i$x
y[row_i, "sensors_r_squared"] <- best_predictor_i$sensors_r_squared
y[row_i, "selection_score"] <- best_predictor_i$selection_score
y[row_i, "sensors_shared_valid_percent"] <- best_predictor_i$sensors_shared_valid_percent
y[row_i, "same_microsite"] <- best_predictor_i$same_microsite

}

#adding sensor_i name
y[, "sensor"] <- sensor_i

return(y)

}

#stop cluster
parallel::stopCluster(temp_cluster)

#removing loop objects
rm(
  x,
  y,
  temp_cluster
)

```

The imputation algorithm produces an object (a list) named **moisrust_interpolation**, with one slot per sensor, each one with one **y** data frame containing the imputation results. Below we transform this object into the data frame **moisrust_interpolation_long** and join it with **moisrust_long**, to start preparing the database format.

```

#naming the output
names(moisrust_interpolation) <- sensors

#to data frame
moisrust_interpolation_long <- do.call(
  "rbind",

```

```

moisrust_interpolation
)

#joining with moisrust_long
moisrust_long <- dplyr::left_join(
  moisrust_long,
  moisrust_interpolation_long,
  by = c("date_time_id", "sensor")
)

#transferring estimates to the soil_moisture column
moisrust_long$soil_moisture <- ifelse(
  is.na(moisrust_long$soil_moisture),
  moisrust_long$model_estimate,
  moisrust_long$soil_moisture
)

#adding a interpolation_quality flag following the criteria in the paper
moisrust_long$interpolation_quality <- ifelse(
  moisrust_long$sensors_r_squared > 0.85 &
  moisrust_long$sensors_shared_valid_percent > 20,
  "acceptable",
  "poor"
)

#filling NA with "observation"
moisrust_long[
  is.na(moisrust_long$interpolation_quality), "interpolation_quality"
] <- "observation"

#adding NA where there are no values
moisrust_long[is.na(moisrust_long$soil_moisture), "interpolation_quality"] <- NA

#computing number of NA cases again
moisrust_NA <- moisrust_long %>%
  group_by(sensor) %>%
  summarise(na_count_after = sum(is.na(soil_moisture))) %>%
  mutate(na_count_percent_after = round((na_count_after * 100) / nrow(moisrust), 1)) %>%
  left_join(
    y = moisrust_NA,
    by = "sensor"
)

```

```

) %>%
transmute(
  sensor,
  na_count_before = na_count,
  na_count_after,
  na_count_percent_before = na_count_percent,
  na_count_percent_after
)

#removing moisrust_interpolation
rm(moisrust_interpolation)

```

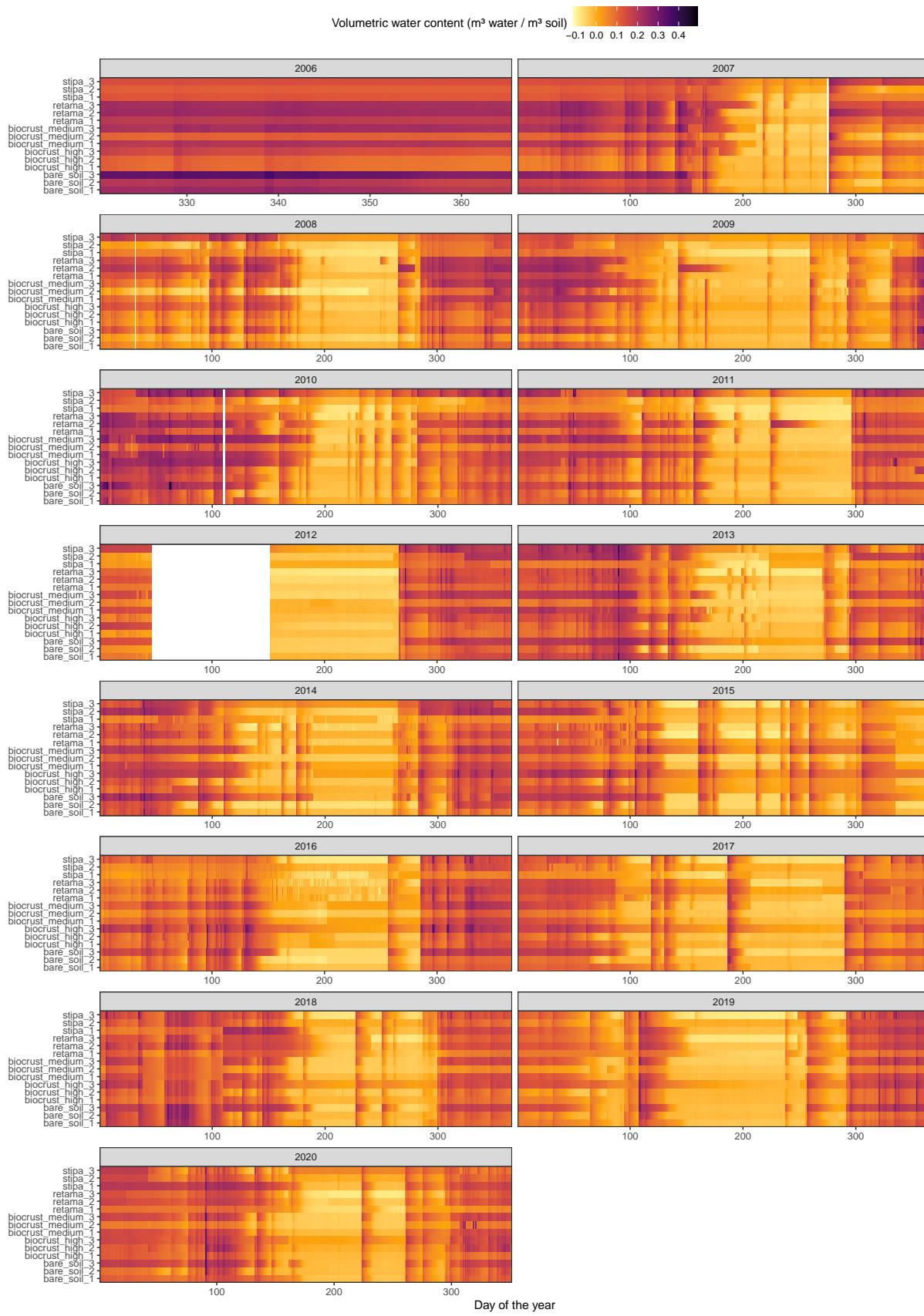
The interpolation has removed all gaps where there was a value to interpolate from, as shown in the table below.

Sensor	NA before interpolation	NA after interpolation	NA % before interpolation	NA % after interpolation
bare_soil_1	10987	989	23.6	2.1
bare_soil_2	11188	989	24.1	2.1
bare_soil_3	11114	989	23.9	2.1
biocrust_high_1	7674	989	16.5	2.1
biocrust_high_2	11776	989	25.3	2.1
biocrust_high_3	14125	989	30.4	2.1
biocrust_medium_1	16934	989	36.4	2.1
biocrust_medium_2	18743	989	40.3	2.1
biocrust_medium_3	31225	989	67.1	2.1
retama_1	22840	989	49.1	2.1
retama_2	22999	989	49.4	2.1
retama_3	20505	989	44.1	2.1
stipa_1	10553	989	22.7	2.1
stipa_2	15363	989	33.0	2.1
stipa_3	15604	989	33.5	2.1

4.5 Visualizing the interpolated time series

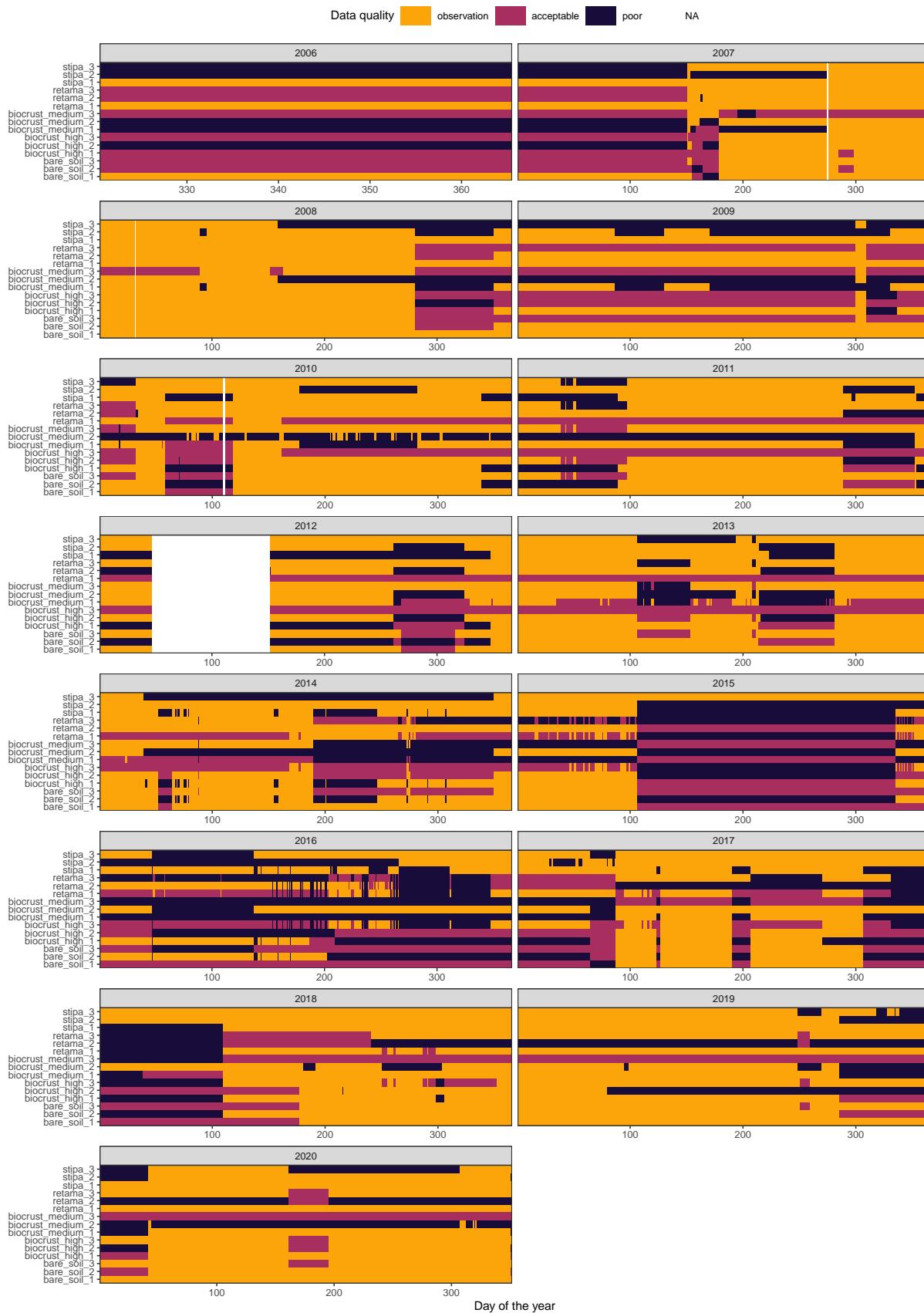
The **MOISCRUST** database looks as follows after applying the imputation algorithm.

MOISCRUST database (observed and interpolated records)



The plot above represents both observed and interpolated values, without a clear differentiation between each type. To provide an indicator of imputation quality, the imputation algorithm also generated a new column named *interpolation_quality*, where the observations are marked with the flag “observation”, the imputed data where x and y shared more than 20% of valid cases and had an R^2 higher than 0.85 are marked with the flag “acceptable”, and the imputed data below these thresholds are marked with the flag “poor”. The plot below shows the values of these flags for each sensor and time, year per year.

MOISCRUST database (data quality)



5 Data base format

The dataset **moiscrust_long** is the database in long format already. Now we can rename it to **moiscrust**.

```
moiscrust <- moiscrust_long
```

The database columns are:

- *date_time*: date and time in POSIX format.
- *date_time_id*: integer, unique ID for each value of *date_time*.
- *date*: date in format year-month-day.
- *time*: time in format hour-minute.
- *year*: integer, year.
- *year_day*: integer, day of the year.
- *month*: integer, month number.
- *week*: integer, week of the year.
- *week_day*: integer, day of the week.
- *sensor*: character, sensor name.
- *soil_moisture*: numeric, soil moisture value in $m^3\text{water}/m^3\text{soil}$.
- *interpolated*: boolean, *TRUE* for interpolated records and *FALSE* for observations.
- *model_estimate*: numeric, prediction of the linear model.
- *model_ci_lower*: numeric, lower bound of the confidence interval of the estimate.
- *model_ci_upper*: numeric, upper bound of the confidence interval of the estimate.
- *model_predictor*: character, name of the sensor used as predictor in the linear model.
- *same_microsite*: boolean, *TRUE* if the sensor and its predictor are in the same group ("stipa", "retama", "biocrust_low", "biocrust_medium", "biocrust_high").
- *sensors_r_squared*: numeric, R squared between *sensor* and *model_predictor*.
- *sensors_shared_valid_percent*: numeric, percentage of shared valid cases between *sensor* and *model_predictor*, taking the total number of values in *date_time_id* as reference.
- *selection_score*: numeric, value used to select the *model_predictor*, based on the sum of *same_microsite* (100 if *TRUE* and 0 if *FALSE*), *sensors_r_squared* multiplied by 100, and *sensors_shared_valid_percent*.
- *interpolation_quality*: character, with the values "observation" for observations, "acceptable" for interpolated values where *sensors_r_squared* is higher than 0.85 and *sensors_shared_valid_percent* is higher than 20, and "poor" for interpolated values below at least one of these thresholds.

5.1 Saving the data base in different formats

To expand its usability as much as possible, we provide the data in four different formats: .RData, .csv, .xlsx, and SQLite.

```

#if the zip file does not exists, creates database directory and populates it
if(!file.exists("database.zip")){
  dir.create("database")

  #save as RData
  save(
    moisrust,
    file = "database/moisrust.RData"
  )

  #save as csv
  readr::write_excel_csv(
    x = moisrust,
    file = "database/moisrust.csv"
  )

  #save as excel file
  writexl::write_xlsx(
    x = moisrust,
    path = "database/moisrust.xlsx"
  )

  #save as SQLite
  db.driver <- DBI::dbDriver("SQLite")
  db.connection <- DBI::dbConnect(
    db.driver,
    dbname = "database/moisrust.db"
  )
  DBI::dbWriteTable(
    db.connection,
    "moisrust",
    moisrust,
    overwrite = TRUE
  )
  DBI::dbDisconnect(db.connection)

  #compressing the file
  zip::zip(
    zipfile = "database.zip",
    files = "database"
}

```

```
)  
  
#removing the database folder  
unlink(  
  "database",  
  recursive = TRUE  
)  
  
#clean the R environment  
rm(  
  db.connection,  
  db.driver,  
  moisrust  
)  
  
}
```