# APPENDIX 1: Introductory reading for macroecologists interested in learning more about Quaternary pollen analysis

Here we provide a selection of digitally available references that serve as introductory reading for macroecologists and multi-disciplinary readers. They are specifically aimed at sections within the *FOSSILPOL* Workflow related to:

**I. Extraction of sequences and depositional environments**
**II. Age-depth modelling**
**III. Pollen and spore taxonomy**
**IV. Taxonomic harmonisation and resolution**
**V. Quaternary pollen-analytical research in general**

It is not our intention to provide an exhaustive list of topics related to Quaternary palaeoecology, but only to target the key parts within the Workflow where these readings can help the user have the necessary background to start thinking about the criteria to apply. We recommend that users follow up the detailed references within these papers for more in-depth background reading.

## I. Extraction of records and depositional environments

**1) Extraction and processing of fossil pollen records**

a) Chevalier, M., Davis, B.A.S., Heiri, O., Seppä, H., Chase, B.M., Gajewski, K., Lacourse, T., Telford, R.J., Finsinger, W., Guiot, J., Kühl, N., Maezumi, S.Y., Tipton, J.R., Carter, V.A., Brussel, T., Phelps, L.N., Dawson, A., Zanon, M., Vallé, F., Nolan, C., Mauri, A., de Vernal, A., Izumi, K., Holmström, L., Marsicek, J., Goring, S., Sommer, P.S., Chaput, M., Kupriyanov, D., 2020. Pollen-based climate reconstruction techniques for late Quaternary studies. Earth-Science Reviews 210, 103384. https://doi.org/10.1016/j.earscirev.2020.103384

b) Daniau, A.-L., Desprat, S., Aleman, J.C., Bremond, L., Davis, B., Fletcher, W., Marlon, J.R., Marquer, L., Montade, V., Morales-Molino, C., Naughton, F., Rius, D., Urrego, D.H., 2019. Terrestrial plant microfossils in palaeoenvironmental studies, pollen, microcharcoal and phytolith. Towards a comprehensive understanding of vegetation, fire and climate changes over the past one million years. Revue de Micropaléontologie 63, 1–35. https://doi.org/10.1016/j.revmic.2019.02.001

**2) Understanding the relevance of pollen source areas:**

a) Chevalier, M., Davis, B.A.S., Heiri, O., Seppä, H., Chase, B.M., Gajewski, K., Lacourse, T., Telford, R.J., Finsinger, W., Guiot, J., Kühl, N., Maezumi, S.Y., Tipton, J.R., Carter, V.A., Brussel, T., Phelps, L.N., Dawson, A., Zanon, M., Vallé, F., Nolan, C., Mauri, A., de Vernal, A., Izumi, K., Holmström, L., Marsicek, J., Goring, S., Sommer, P.S., Chaput, M., Kupriyanov, D., 2020. Pollen-based climate reconstruction techniques for late Quaternary studies. Earth-Science Reviews 210, 103384. https://doi.org/10.1016/j.earscirev.2020.103384

b) Daniau, A.-L., Desprat, S., Aleman, J.C., Bremond, L., Davis, B., Fletcher, W., Marlon, J.R., Marquer, L., Montade, V., Morales-Molino, C., Naughton, F., Rius, D., Urrego, D.H., 2019. Terrestrial plant microfossils in palaeoenvironmental studies, pollen, microcharcoal and phytolith. Towards a comprehensive understanding of vegetation, fire and climate changes over

the past one million years. Revue de Micropaléontologie 63, 1–35. https://doi.org/10.1016/j.revmic.2019.02.001

c) Jacobson, G.L., Bradshaw, R.H.W., 1981. The selection of sites for paleovegetational studies. Quaternary Research 16, 80–96. https://doi.org/10.1016/0033-5894(81)90129-0

d) Sugita, S., 1994. Pollen representation of vegetation in Quaternary sediments: Theory and method in patchy vegetation. Journal of Ecology 82, 881–897. https://doi.org/10.2307/2261452

**3) Depositional environments and taphonomy**

a) See Box in: Nieto-Lugilde, D., Blois, J.L., Bonet-García, F.J., Giesecke, T., Gil-Romera, G., Seddon, A., 2021. Time to better integrate paleoecological research infrastructures with neoecology to improve understanding of biodiversity long-term dynamics and to inform future conservation. Environmental Research Letters 16, 095005. https://doi.org/10.1088/1748-9326/ac1b59

b) Cleal, C., Pardoe, H.S., Berry, C.M., Cascales-Miñana, B., Davis, B.A.S., Diez, J.B., Filipova-Marinova, N.V. et al., 2021. Palaeobotanical experiences of plant diversity in deep time. 1: how well can we identify past plant diversity in the fossil record? Palaeogeography, Palaeoclimatology, Palaeoecology 576, 110481. https://doi.org/10.1016/j.palaeo.2021.110481

**4) Dealing with depositional environments in multi-records analyses and databases:**

a) Jacobson, G.L., Bradshaw, R.H.W., 1981. The selection of sites for paleovegetational studies. Quaternary Research 16, 80–96. https://doi.org/10.1016/0033-5894(81)90129-0

b) Goring, S., Lacourse, T., Pellatt, M.G., Walker, I.R., Mathewes, R.W., 2010. Are pollen-based climate models improved by combining surface samples from soil and lacustrine substrates? Review of Palaeobotany and Palynology 162, 203–212. https://doi.org/10.1016/j.revpalbo.2010.06.014

c) Wilmshurst, J.M., McGlone, M.S., 2005. Origin of pollen and spores in surface lake sediments: Comparison of modern palynomorph assemblages in moss cushions, surface soils and surface lake sediments. Review of Palaeobotany and Palynology 136, 1–15. https://doi.org/10.1016/j.revpalbo.2005.03.007

# II. Age-depth modelling

1) Blaauw, M. 2010. (Outdated) manual of Clam but with relevant explanations: https://chrono.qub.ac.uk/blaauw/clam.html

2) Blaauw, M., & Heegaard, E. (2012). Estimation of Age-Depth Relationships. In H. J. B. Birks, A. F. Lotter, S. Juggins, & J. P. Smol (Eds.), *Tracking Environmental Change Using Lake Sediments, Vol. 5: Data Handling and Numerical Techniques* (pp. 379–413). Springer Netherlands. https://doi.org/10.1007/978-94-007-2745-8_12

3) Grimm, E.C., Blaauw, M., Buck, C., Williams, J., 2014. Age models, chronologies, and databases workshop. PAGES Magazine 22, 104–104. https://doi.org/10.22498/pages.22.2.104 and see https://cp.copernicus.org/preprints/cp-2017-31/cp-2017-31-ED1.pdf

4) Trachsel, M., Telford, R.J., 2017. All age–depth models are wrong, but are getting better. The Holocene 27, 860–869. https://doi.org/10.1177/0959683616675939

# III. Pollen and spore taxonomy

**Global online reference material for the identification of pollen:**

a) Hooghiemstra, H., van Geel, B., 1998. World list of Quaternary pollen and spore atlases. Review of Palaeobotany and Palynology 104, 157–182. https://doi.org/10.1016/S0034-6667(98)00053-0
b) Weber, M., Ulrich, S., 2018. PalDat - A useful tool for identifying recent and fossil pollen. Link
c) Global Pollen Project: Link
d) Pollen and spores image database Göttingen: Link
e) See also table 1 in Daniau et al. 2019. Revue de Micropaléontologie for a list of global pollen atlases.

# IV. Taxonomic harmonisation and resolution

**Existing harmonisation tables of fossil pollen data:**

a) Cao, X., Tian, F., Andreev, A., Anderson, P.M., Lozhkin, A.V., Bezrukova, E., Ni, J., Rudaya, N., Stobbe, A., Wieczorek, M., Herzschuh, U., 2020. A taxonomically harmonized and temporally standardized fossil pollen dataset from Siberia covering the last 40 kyr. Earth System Science Data 12, 119–135. https://doi.org/10.5194/essd-12-119-2020
b) Gavin, D.G., Oswald, W.W., Wahl, E.R., Williams, J.W., 2003. A statistical approach to evaluating distance metrics and analog assignments for pollen records. Quaternary Research 60, 356–367. https://doi.org/10.1016/S0033-5894(03)00088-7. Note: Called "P25" and includes 25 pollen taxa. Available in Neotoma package.
c) Giesecke, T., Wolters, S., van Leeuwen, J.F.N., van der Knaap, P.W.O., Leydet, M., Brewer, S., 2019. Postglacial change of the floristic diversity gradient in Europe. Nature Communications 10, 5422. https://doi.org/10.1038/s41467-019-13233-y
d) Herzschuh, U., Li, C., Böhmer, T., Postl, A.K., Heim, B., Andreev, A.A., Cao, X., Wieczorek, M., & Ni, J. 2022. LegacyPollen 1.0: a taxonomically harmonized global late Quaternary pollen dataset of 2831 records with standardized chronologies. Earth System Science Data 14: 3213–3227. https://doi.org/10.5194/essd-14-3213-2022
e) Li, C., Postl, A.K., Böhmer, T., Cao, X., Dolman, A.M., Herzschuh, U., 2022. Harmonized chronologies of a global late Quaternary pollen dataset (LegacyAge 1.0). Earth System Science Data 14, 1331–1343. https://doi.org/10.5194/essd-14-1331-2022
f) Mottl, O., Flantua, S.G.A., Bhatta, K.P., Felde, V.A., Giesecke, T., Goring, S., Grimm, E.C., Haberle, S., Hooghiemstra, H., Ivory, S., Kuneš, P., Wolters, S., Seddon, A.W.R., Williams, J.W., 2021. Global acceleration in rates of vegetation change over the past 18,000 years. Science 372, 860–864. https://doi.org/10.1126/science.abg1685
g) Phelps, L.N., Chevalier, M., Shanahan, T.M., Aleman, J.C., Courtney-Mustaphi, C., Kiahtipes, C.A., Broennimann, O., Marchant, R., Shekeine, J., Quick, L.J., Davis, B.A.S., Guisan, A., Manning, K., 2020. Asymmetric response of forest and grassy biomes to climate variability across the African Humid Period: influenced by anthropogenic disturbance? Ecography 43, 1118–1142. https://doi.org/10.1111/ecog.04990
h) Sánchez Goñi, M.F., Desprat, S., Daniau, A.-L., Bassinot, F.C., Polanco-Martínez, J.M., Harrison, S.P., Allen, J.R.M., et al., 2005. Modern pollen data from North America and Greenland for multi-scale paleoenvironmental applications. Quaternary Science Reviews 24, 1828–1848. https://doi.org/10.1016/j.quascirev.2005.03.005. Note: "WhitmoreFull", full list.

"WhitmoreSmall", As WhitmoreFull but taxa for which both fully resolved and undifferentiated exist these taxa are summed. Both available in Neotoma package.

i) Williams, J.W., Shuman, B., 2008. Obtaining accurate and precise environmental reconstructions from the modern analog technique and North American surface pollen dataset. Quaternary Science Reviews 27, 669–687. https://doi.org/10.1016/j.quascirev.2008.01.004. Note: Called "WS64" and available in Neotoma package.

**The influence of taxonomic resolution and harmonisation levels for different research purposes:**

a) Deza-Araujo, M., Morales-Molino, C., Conedera, M., Pezzatti, G.B., Pasta, S., Tinner, W., 2022. Influence of taxonomic resolution on the value of anthropogenic pollen indicators. Vegetation History and Archaeobotany 31, 67–84. https://doi.org/10.1007/s00334-021-00838-x

b) Mitchell, E.A.D., Lamentowicz, M., Payne, R.J., Mazei, Y., 2014. Effect of taxonomic resolution on ecological and palaeoecological inference – a test using testate amoeba water table depth transfer functions. Quaternary Science Reviews 91, 62–69. https://doi.org/10.1016/j.quascirev.2014.03.006

c) Rull, V. (2012) Palaeobiodiversity and taxonomic resolution: linking past trends with present patterns. Journal of Biogeography 39:1005–1006. https://doi.org/10.1111/j.1365-2699.2012.02735.x

**Difference between plant taxa and pollen types:**

De Klerk, P., Joosten, H., 2007. The difference between pollen types and plant taxa: a plea for clarity and scientific freedom. E & G Quaternary Science Journal 56, 162–171. https://doi.org/10.3285/eg.56.3.02

# V. Quaternary pollen-analytical research in general

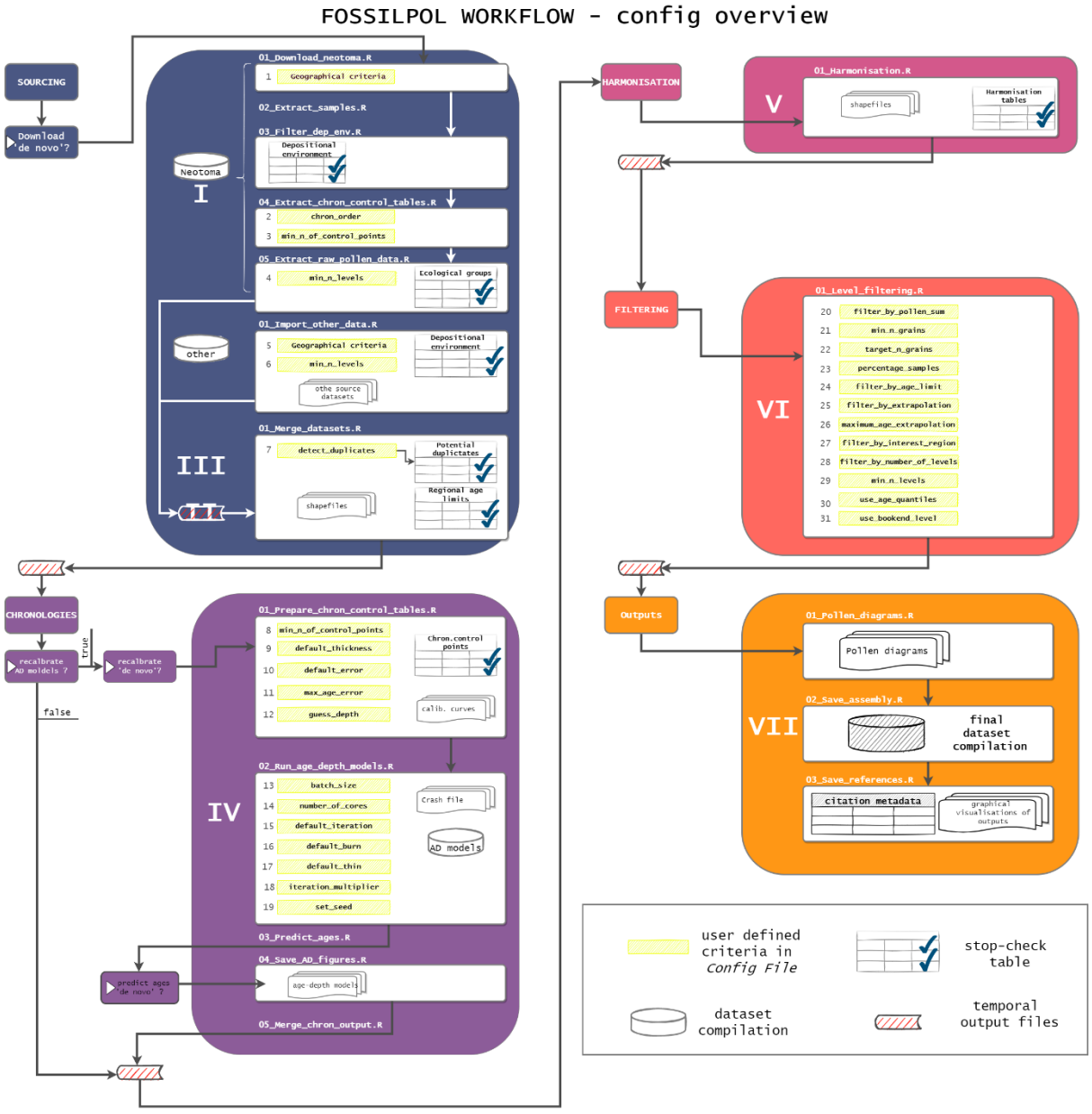
a) Birks, H.J.B., Berglund, B.E., 2018. One hundred years of Quaternary pollen analysis 1916–2016. Vegetation History and Archaeobotany 27, 271–309. https://doi.org/10.1007/s00334-017-0630-2

b) Birks, H.J.B., 2019. Contributions of Quaternary botany to modern ecology and biogeography. Plant Ecology & Diversity 12, 189–385. https://doi.org/10.1080/17550874.2019.1646831

c) Rull, V., 2020. Quaternary ecology, evolution, and biogeography, 1st ed. Elsevier. https://www.elsevier.com/books/quaternary-ecology-evolution-and-biogeography/rull/978-0-12-820473-3

d) Dillon, E., Dunne, E., Womack, T., Kouvari, M., Larina, E., Claytor, J., . . . Zill, M. (2023). Challenges and directions in analytical paleobiology. Paleobiology, 1-17. https://doi.org/10.1017/pab.2023.3

APPENDIX 2: Detailed figure of the FOSSILPOL workflow with all steps included in the Config file.



# APPENDIX 3: General template for FOSSILPOL Config file

```
#------------------------------------------------------------#
#
#
#                 The FOSSILPOL workflow
#
#                     Config file
#
#
#   O. Mottl, S. Flantua, K. Bhatta, V. Felde, A. Seddon
#                         2023
#
#------------------------------------------------------------#

# Configuration script with the variables that should be consistent
throughout
#   the whole repo. It loads packages, defines important variables,
#   authorises the user, and saves the config file.
# Points that require the user's attention are flagged by "[USER]" - flag,
#  meaning that these are criteria that need to be checked by the user

# Version of the Workflow
workflow_version <-
  "0.0.2"

# Set the current environment
current_env <- environment()

#------------------------------------------------------------#
# 1. Load packages -----
#------------------------------------------------------------#

if (
  isFALSE(
    exists("already_synch", envir = current_env)
  )
) {
  already_synch <- FALSE
}

if (
  isFALSE(already_synch)
) {
  library(here)
  # Synchronise the package versions
  renv::restore(
    lockfile = here::here("renv/library_list.lock")
  )
  already_synch <- TRUE

  # Save snapshot of package versions
  # renv::snapshot(lockfile =  "renv/library_list.lock")  # do only for
update
}

# Define packages
package_list <-
  c(
    "RFossilpol",
```

```
    "RUtilpol",
    "here",
    "tidyverse"
  )

# Attach all packages
sapply(package_list, library, character.only = TRUE)


#------------------------------------------------------------#
# 2. Current date and working directory -----
#------------------------------------------------------------#

current_date <- Sys.Date()

# Project directory is set up by the {here} package, Adjust if needed
current_dir <- here::here()

# Define the directory (external) for storing big data files
#   Default is in the current project
data_storage_path <- current_dir # [USER]

# Create all essential folders
RFossilpol::util_make_datastorage_folders(
  dir = data_storage_path # [config_criteria]
)

#------------------------------------------------------------#
# 3. Load functions -----
#------------------------------------------------------------#

# Get a vector of general functions
fun_list <-
  list.files(
    path = "R/Functions/",
    pattern = "*.R",
    recursive = TRUE
  )

# Load the function into the global environment
sapply(
  paste0("R/Functions/", fun_list, sep = ""),
  source
)


#------------------------------------------------------#
# 4. Project dataset database -----
#------------------------------------------------------#

# Check the presence of a dataset database and create it if necessary
if (
  isFALSE(
    "project_dataset_database.rds" %in%
      list.files(
        paste0(
          data_storage_path, # [config_criteria]
          "/Data/Personal_database_storage"
        )
      )
  )
```

```
) {
  project_dataset_database <-
    RFossilpol:::proj_db_class()

  readr::write_rds(
    project_dataset_database,
    paste0(
      data_storage_path, # [config_criteria]
      "/Data/Personal_database_storage",
      "/project_dataset_database.rds"
    ),
    compress = "gz"
  )
}


#------------------------------------------------------------#
# 5. Define variables -----
#------------------------------------------------------------#

#-------------------------------------------------#
# 5.1. Define individual run -----
#-------------------------------------------------#

# Include/exclude Neotoma download in run
dataset_type <- "pollen"

# Selected variable element (proxy)
sel_var_element <- "pollen"

# Set geographical boundaries
long_min <- -180 # [USER]
long_max <- 180 # [USER]
lat_min <- -90 # [USER]
lat_max <- 90 # [USER]
alt_min <- NA # [USER]
alt_max <- NA # [USER]

neotoma_new_download <- TRUE

# Define access to datasets from other sources than Neotoma
use_other_datasource <- FALSE # [USER]
detect_duplicates <- TRUE # [USER]

# Include/exclude age modelling in run
recalib_AD_models <- TRUE # [USER]
calc_AD_models_denovo <- FALSE # [USER]
predict_ages_denovo <- FALSE # [USER]

# Select the final variables
select_final_variables <- TRUE # [USER]


#-------------------------------------------------#
# 5.2. Chronology order  -----
#-------------------------------------------------#

# Selected and preferred order of age type of existing chronologies in
Neotoma
chron_order <-
  tibble::tibble(
```

```
    order = seq(1, 6),
    type = c(
      "Varve years BP",
      "Calibrated radiocarbon years BP",
      "Calendar years BP",
      "Radiocarbon years BP",
      "Calendar years AD/BC",
      NA
    )
  )


#------------------------------------------------#
# 5.5. Age depth models  -----
#------------------------------------------------#

# Chronology needs to have at least X control points [example: X=2]
min_n_of_control_points <- 2 # [USER]

# If the thickness of a control point is missing, assign X cm [example:
X=1]
default_thickness <- 1 # [USER]

# If the age error of a control point is missing, assign X yr [example:
X=100]
default_error <- 100 # [USER]

# Maximum accepted age error of chron.control point [example: X=3000]
max_age_error <- 3000 # [USER]

# Depth at which "Guess" is accepted as a chronology control
#   point [example: X=10]
guess_depth <- 10 # [USER]

# Bchron settings
number_of_cores <- parallel::detectCores() - 1
batch_size <- number_of_cores * 3
set_seed <- 1234

default_iteration <- 10e3
default_burn <- 2000
default_thin <- 8 # [USER]
iteration_multiplier <- 5 # [USER]


#------------------------------------------------#
# 5.6. Filtering criteria -----
#------------------------------------------------#

# Criteria to filter out stratigraphic levels and pollen records

#----------------------------------------#

# Pollen sums
filter_by_pollen_sum <- TRUE # [USER]

# Each stratigraphic level of at least X individual pollen gains [example:
X=0]
min_n_grains <- 0 # [USER]
# Ideal number of counts
target_n_grains <- 100 # [USER]
```

```
# Threshold of number of samples with ideal counts
percentage_samples <- 0 # [USER]

#---------------------------------------#

# Age limits
#   Note that the actual ages have to be specified per region, defined
during
# the process of Workflow
filter_by_age_limit <- TRUE # [USER]

#---------------------------------------#

# Maximum extrapolation
filter_by_extrapolation <- TRUE # [USER]

# How much age can be extrapolated beyond the oldest chronology control
point?
maximum_age_extrapolation <- Inf # [USER]

#---------------------------------------#

# Beyond the period of interest
#   Note that the actual ages have to be specified per region, defined
during
# the process of Workflow
filter_by_interest_region <- TRUE # [USER]

#---------------------------------------#

# Number of stratigraphic levels
filter_by_number_of_levels <- TRUE # [USER]

# At least X number stratigraphic levels within the period
#   of interest [example: X=3]
min_n_levels <- 3

#---------------------------------------#

# Additional setting

# Should the 95th age quantile be used for data filtration?
# If FALSE (default), the estimated age will be used for all checks about
the
#   age of a stratigraphic level. However, if TRUE, then the 95th age
quantile
#   will be used.
# This will result in more stable data assembly between different results
#   of age-depth modelling BUT require additional data preparation before
#   the analytical part.
use_age_quantiles <- FALSE # [USER]

# Should all data filtration omit one additional stratigraphic level in
#   the old period?
# If TRUE, all filtering will proceed normally but one additional "bookend"
#   stratigraphic level will be always kept.
# A "bookend" stratigraphic level is a subsequential stratigraphic level
#   older than the oldest stratigraphic level that passed the filtration.
# A "bookend" can help provide anchor information older than the period of
#     interest.
use_bookend_level <- FALSE # [USER]
```

```
#-------------------------------------------------------------#
# 6. Set graphical options -----
#-------------------------------------------------------------#

# Set ggplot output
ggplot2::theme_set(
  ggplot2::theme_classic()
)

# Define general
text_size <- 16 # [USER]
line_size <- 0.1 # [USER]
point_size <- 3 # [USER]

# Define output sizes
image_width <- 30 # [USER]
image_height <- 15 # [USER]
image_units <- "cm" # [USER]
image_dpi <- 300 # [USER]

# Define pallets

# Define common colours


#-------------------------------------------------------------#
# 7. Save current config setting -----
#-------------------------------------------------------------#

current_setting <-
  RFossilpol::util_extract_config_data()
```

# APPENDIX 4: FOSSILPOL Config file used for the Northern Europe example

The important changes in comparison to the default template are highlighted blue.

```
#-------------------------------------------------------------#
#
#
#           Fossil pollen data from Scandinavia
#
#                     Config file
#
#
#   O. Mottl, S. Flantua, K. Bhatta, V. Felde, A. Seddon
#                         2023
#
#-------------------------------------------------------------#

# Configuration script with the variables that should be consistent
throughout
#   the whole repo. It loads packages, defines important variables,
#   authorises the user, and saves the config file.
# Points that require the user's attention are flagged by "[USER]" - flag,
#  meaning that these are criteria that need to be checked by the user

# Version of the Workflow
workflow_version <-
  "0.0.2"

# Set the current environment
current_env <- environment()

#-------------------------------------------------------------#
# 1. Load packages -----
#-------------------------------------------------------------#

if (
  isFALSE(
    exists("already_synch", envir = current_env)
  )
) {
  already_synch <- FALSE
}

if (
  isFALSE(already_synch)
) {
  library(here)
  # Synchronise the package versions
  renv::restore(
    lockfile = here::here("renv/library_list.lock")
  )
  already_synch <- TRUE

  # Save snapshot of package versions
  # renv::snapshot(lockfile =  "renv/library_list.lock")  # do only for
update
}
```

```r
# Define packages
package_list <-
  c(
    "RFossilpol",
    "RUtilpol",
    "here",
    "tidyverse"
  )

# Attach all packages
sapply(package_list, library, character.only = TRUE)


#------------------------------------------------------------#
# 2. Current date and working directory -----
#------------------------------------------------------------#

current_date <- Sys.Date()

# Project directory is set up by the {here} package, Adjust if needed
current_dir <- here::here()

# Define the directory (external) for storing big data files
#   Default is in the current project
data_storage_path <- current_dir # [USER]

# Create all essential folders
RFossilpol::util_make_datastorage_folders(
  dir = data_storage_path # [config_criteria]
)

#------------------------------------------------------------#
# 3. Load functions -----
#------------------------------------------------------------#

# Get a vector of general functions
fun_list <-
  list.files(
    path = "R/Functions/",
    pattern = "*.R",
    recursive = TRUE
  )

# Load the function into the global environment
sapply(
  paste0("R/Functions/", fun_list, sep = ""),
  source
)


#------------------------------------------------#
# 4. Project dataset database -----
#------------------------------------------------#

# Check the presence of a dataset database and create it if necessary
if (
  isFALSE(
    "project_dataset_database.rds" %in%
      list.files(
        paste0(
          data_storage_path, # [config_criteria]
```

```
            "/Data/Personal_database_storage"
          )
        )
    )
  ) {
    project_dataset_database <-
      RFossilpol:::proj_db_class()

    readr::write_rds(
      project_dataset_database,
      paste0(
        data_storage_path, # [config_criteria]
        "/Data/Personal_database_storage",
        "/project_dataset_database.rds"
      ),
      compress = "gz"
    )
  }


  #------------------------------------------------------------#
  # 5. Define variables -----
  #------------------------------------------------------------#

  #-----------------------------------------------#
  # 5.1. Define individual run -----
  #-----------------------------------------------#

  # Include/exclude Neotoma download in run
  dataset_type <- "pollen"

  # Selected variable element (proxy)
  sel_var_element <- "pollen"

  # Set geographical boundaries
  long_min <- 5 # [USER]
  long_max <- 30 # [USER]
  lat_min <- 55 # [USER]
  lat_max <- 73 # [USER]
  alt_min <- NA # [USER]
  alt_max <- NA # [USER]

  neotoma_new_download <- TRUE

  # Define access to datasets from other sources than Neotoma
  use_other_datasource <- FALSE # [USER]
  detect_duplicates <- TRUE # [USER]

  # Include/exclude age modelling in run
  recalib_AD_models <- TRUE # [USER]
  calc_AD_models_denovo <- FALSE # [USER]
  predict_ages_denovo <- FALSE # [USER]

  # Select the final variables
  select_final_variables <- TRUE # [USER]


  #-----------------------------------------------#
  # 5.2. Chronology order  -----
  #-----------------------------------------------#
```

```
# Selected and preferred order of age type of existing chronologies in
Neotoma
chron_order <-
  tibble::tibble(
    order = seq(1, 6),
    type = c(
      "Varve years BP",
      "Calibrated radiocarbon years BP",
      "Calendar years BP",
      "Radiocarbon years BP",
      "Calendar years AD/BC",
      NA
    )
  )


#------------------------------------------------#
# 5.5. Age depth models  -----
#------------------------------------------------#

# Chronology needs to have at least X control points [example: X=2]
min_n_of_control_points <- 5 # [USER]

# If the thickness of a control point is missing, assign X cm [example:
X=1]
default_thickness <- 1 # [USER]

# If the age error of a control point is missing, assign X yr [example:
X=100]
default_error <- 100 # [USER]

# Maximum accepted age error of chron.control point [example: X=3000]
max_age_error <- 3000 # [USER]

# Depth at which "Guess" is accepted as a chronology control
#   point [example: X=10]
guess_depth <- 10 # [USER]

# Bchron settings
number_of_cores <- parallel::detectCores() - 1
batch_size <- number_of_cores * 3
set_seed <- 1234

default_iteration <- 10e3
default_burn <- 2000
default_thin <- 8 # [USER]
iteration_multiplier <- 5 # [USER]


#------------------------------------------------#
# 5.6. Filtering criteria -----
#------------------------------------------------#

# Criteria to filter out stratigraphic levels and pollen records

#----------------------------------------#

# Pollen sums
filter_by_pollen_sum <- TRUE # [USER]
```

```
# Each stratigraphic level of at least X individual pollen gains [example:
X=0]
min_n_grains <- 100 # [USER]
# Ideal number of counts
target_n_grains <- 150 # [USER]
# Threshold of number of samples with ideal counts
percentage_samples <- 75 # [USER]

#---------------------------------------#

# Age limits
#   Note that the actual ages have to be specified per region, defined
during
# the process of Workflow
filter_by_age_limit <- TRUE # [USER]

#---------------------------------------#

# Maximum extrapolation
filter_by_extrapolation <- TRUE # [USER]

# How much age can be extrapolated beyond the oldest chronology control
point?
maximum_age_extrapolation <- 3000 # [USER]

#---------------------------------------#

# Beyond the period of interest
#   Note that the actual ages have to be specified per region, defined
during
# the process of Workflow
filter_by_interest_region <- TRUE # [USER]

#---------------------------------------#

# Number of stratigraphic levels
filter_by_number_of_levels <- TRUE # [USER]

# At least X number of stratigraphic levels within the period
#   of interest [example: X=3]
min_n_levels <- 5

#---------------------------------------#

# Additional setting

# Should the 95th age quantile be used for data filtration?
# If FALSE (default), the estimated age will be used for all checks about
the
#   age of a stratigraphic level. However, if TRUE, then the 95th age
quantile
#   will be used.
# This will result in more stable data assembly between different results
#   of age-depth modelling BUT require additional data preparation before
#   the analytical part.
use_age_quantiles <- FALSE # [USER]

# Should all data filtration omit one additional stratigraphic level in
#   the old period?
# If TRUE, all filtering will proceed normally but one additional "bookend"
#   stratigraphic level will be always kept.
```

```
# A "bookend" stratigraphic level is a subsequential stratigraphic level
#   older than the oldest stratigraphic level that passed the filtration.
# A "bookend" can help provide anchor information older than the period of
#     interest.
use_bookend_level <- FALSE # [USER]


#------------------------------------------------------------#
# 6. Set graphical options -----
#------------------------------------------------------------#

# Set ggplot output
ggplot2::theme_set(
  ggplot2::theme_classic()
)

# Define general
text_size <- 16 # [USER]
line_size <- 0.1 # [USER]
point_size <- 3 # [USER]

# Define output sizes
image_width <- 30 # [USER]
image_height <- 15 # [USER]
image_units <- "cm" # [USER]
image_dpi <- 300 # [USER]


# Define common colours
col_gray_dark <- "gray30"
col_gray_middle <- "gray50"
col_gray_light <- "gray90"

## Main colour
col_orange_dark <- "#E17D00"
col_orange_light <- "#ff9715"

## Complementary
col_compl_blue <- "#00507B"

## Analogous
col_ana_red <- "#FF2215"

# Define pallets
palette_generic <-
  c(
    "#FF9715",
    "#FF685F",
    "#D3588B",
    "#8C5C99",
    "#4A5783"
  )

palette_matching <-
  c(
    "#00987E",
    "#00D1B2",
    "#B9A89B",
    "#524439",
    "#FF9715"
  )
```

```
866
867 palette_shades <-
868   c(
869     "#570200",
870     "#7B2B00",
871     "#A54E00",
872     "#D17200",
873     "#FF9715"
874   )
875
876
877 #-------------------------------------------------------------#
878 # 7. Save current config setting -----
879 #-------------------------------------------------------------#
880
881 current_setting <-
882   RFossilpol::util_extract_config_data()
883
```