1 APPENDIX 1: Introductory reading for macroecologists interested

2 in learning more about Quaternary pollen analysis

- 3 Here we provide a selection of digitally available references that serve as introductory
- 4 reading for macroecologists and multi-disciplinary readers. They are specifically aimed at
- 5 sections within the *FOSSILPOL* Workflow related to:
- 6 I. Extraction of sequences and depositional environments
- 7 II. Age-depth modelling
- 8 III. Pollen and spore taxonomy
- 9 IV. Taxonomic harmonisation and resolution
- 10 V. Quaternary pollen-analytical research in general
- 11 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
- 15 background reading.

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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

- 41 the past one million years. Revue de Micropaléontologie 63, 1–35. 42 <u>https://doi.org/10.1016/j.revmic.2019.02.001</u>
- 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
- 92 c) Global Pollen Project: Link

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- 93 d) Pollen and spores image database Göttingen: Link
- 94 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

97 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

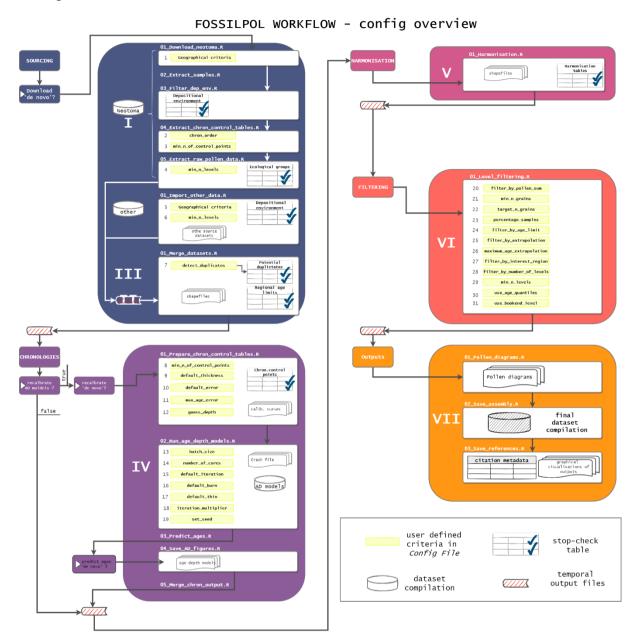
- a) Birks, H.J.B., Berglund, B.E., 2018. One hundred years of Quaternary pollen analysis 1916—2016. Vegetation History and Archaeobotany 27, 271–309. https://doi.org/10.1007/s00334-017-0630-2
- b) Birks, H.J.B., 2019. Contributions of Quaternary botany to modern ecology and biogeography. Plant Ecology & Diversity 12, 189–385. https://doi.org/10.1080/17550874.2019.1646831
- 158 c) Rull, V., 2020. Quaternary ecology, evolution, and biogeography, 1st ed. Elsevier.

 159 https://www.elsevier.com/books/quaternary-ecology-evolution-and-biogeography/rull/978-0-160
 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

```
169
     #----#
170
171
172
                     The FOSSILPOL workflow
173
174
                         Config file
175
176
177
        O. Mottl, S. Flantua, K. Bhatta, V. Felde, A. Seddon
178
179
180
181
182
     # Configuration script with the variables that should be consistent
183
     throughout
184
        the whole repo. It loads packages, defines important variables,
185
        authorises the user, and saves the config file.
186
     # Points that require the user's attention are flagged by "[USER]" - flag,
187
     # meaning that these are criteria that need to be checked by the user
188
189
     # Version of the Workflow
190
     workflow version <-
191
      "0.0.2"
192
193
     # Set the current environment
194
     current env <- environment()</pre>
195
196
     #----#
197
     # 1. Load packages -----
198
     #----#
199
200
201
      isFALSE(
202
         exists("already_synch", envir = current env)
203
204
205
      already synch <- FALSE
206
207
208
209
      isFALSE(already_synch)
210
211
      library(here)
212
      # Synchronise the package versions
213
      renv::restore(
214
        lockfile = here::here("renv/library list.lock")
215
216
      already_synch <- TRUE
217
218
       # Save snapshot of package versions
219
       # renv::snapshot(lockfile = "renv/library list.lock") # do only for
220
     update
221
222
223
     # Define packages
224
     package list <-
225
226
        "RFossilpol",
```

```
227
        "RUtilpol",
228
        "here",
229
        "tidyverse"
230
231
232
     # Attach all packages
233
     sapply(package list, library, character.only = TRUE)
234
235
236
     #----#
237
     # 2. Current date and working directory ----
238
     #----#
239
240
     current date <- Sys.Date()</pre>
241
242
     # Project directory is set up by the {here} package, Adjust if needed
243
     current dir <- here::here()</pre>
244
245
     # Define the directory (external) for storing big data files
246
     # Default is in the current project
247
     data storage path <- current dir # [USER]</pre>
248
249
     # Create all essential folders
250
     RFossilpol::util make datastorage folders(
251
      dir = data storage path # [config_criteria]
252
253
254
     #-----#
255
     # 3. Load functions -----
256
     #_____#
257
258
     # Get a vector of general functions
259
     fun list <-
260
      list.files(
261
        path = "R/Functions/",
262
        pattern = "*.R",
263
        recursive = TRUE
264
      )
265
266
     # Load the function into the global environment
267
268
     paste0("R/Functions/", fun list, sep = ""),
269
      source
270
     )
271
272
273
274
     # 4. Project dataset database -----
275
     #----#
276
277
     # Check the presence of a dataset database and create it if necessary
278
     if (
279
      isFALSE(
280
        "project dataset database.rds" %in%
281
          list.files(
282
            paste0(
283
              data storage path, # [config criteria]
284
              "/Data/Personal database storage"
285
286
          )
287
      )
```

```
288
     ) {
289
       project dataset database <-
290
        RFossilpol:::proj db class()
291
292
       readr::write rds(
293
         project dataset database,
294
         paste0(
295
           data storage path, # [config criteria]
296
           "/Data/Personal database storage",
297
           "/project dataset database.rds"
298
         ),
299
         compress = "qz"
300
       )
301
     }
302
303
304
      #-----#
305
      # 5. Define variables ----
306
307
308
      #----#
309
      # 5.1. Define individual run ----
310
311
312
      # Include/exclude Neotoma download in run
313
     dataset type <- "pollen"</pre>
314
315
      # Selected variable element (proxy)
316
     sel var element <- "pollen"</pre>
317
318
      # Set geographical boundaries
319
     long min <- -180 # [USER]
320
     long max <- 180 # [USER]
321
     lat min \leftarrow -90 # [USER]
322
     lat max <- 90 # [USER]
323
     alt min <- NA # [USER]
324
     alt max <- NA # [USER]
325
326
     neotoma new download <- TRUE</pre>
327
328
      # Define access to datasets from other sources than Neotoma
329
     use other datasource <- FALSE # [USER]</pre>
330
     detect_duplicates <- TRUE # [USER]</pre>
331
332
      # Include/exclude age modelling in run
333
     recalib AD models <- TRUE # [USER]
334
     calc AD models denovo <- FALSE # [USER]</pre>
335
     predict_ages_denovo <- FALSE # [USER]</pre>
336
337
      # Select the final variables
338
     select final variables <- TRUE # [USER]</pre>
339
340
341
      # 5.2. Chronology order ----
342
343
      #----#
344
345
      # Selected and preferred order of age type of existing chronologies in
346
     Neotoma
347
     chron order <-
348
       tibble::tibble(
```

```
349
         order = seq(1, 6),
350
         type = c(
351
           "Varve years BP",
352
           "Calibrated radiocarbon years BP",
353
           "Calendar years BP",
354
           "Radiocarbon years BP",
355
           "Calendar years AD/BC",
356
357
358
       )
359
360
361
     #----#
362
     # 5.5. Age depth models ----
363
     #----#
364
365
     # Chronology needs to have at least X control points [example: X=2]
366
     min n of control points <- 2 # [USER]</pre>
367
368
     # If the thickness of a control point is missing, assign X cm [example:
369
     X=11
370
     default thickness <- 1 # [USER]</pre>
371
372
     # If the age error of a control point is missing, assign X yr [example:
373
     X=1001
374
     default error <- 100 # [USER]</pre>
375
376
     # Maximum accepted age error of chron.control point [example: X=3000]
377
     max age error <- 3000 # [USER]</pre>
378
379
     # Depth at which "Guess" is accepted as a chronology control
380
     # point [example: X=10]
381
     guess depth <- 10 # [USER]
382
383
     # Bchron settings
384
     number of cores <- parallel::detectCores() - 1</pre>
385
     batch size <- number of cores * 3
386
     set seed <- 1234
387
388
     default iteration <- 10e3
389
     default burn <- 2000
390
     default thin <- 8 # [USER]
391
     iteration multiplier <- 5 # [USER]</pre>
392
393
394
395
     # 5.6. Filtering criteria ----
396
     #----#
397
398
     # Criteria to filter out stratigraphic levels and pollen records
399
400
     #----#
401
402
     # Pollen sums
403
     filter by pollen sum <- TRUE # [USER]
404
405
     # Each stratigraphic level of at least X individual pollen gains [example:
406
     X = 0
407
     min n grains <- 0 # [USER]
408
     # Ideal number of counts
409
     target n grains <- 100 # [USER]
```

```
410
     # Threshold of number of samples with ideal counts
411
     percentage samples <- 0 # [USER]</pre>
412
413
     #----#
414
415
     # Age limits
416
     # Note that the actual ages have to be specified per region, defined
417
     during
418
     # the process of Workflow
419
     filter by age limit <- TRUE # [USER]
420
421
     #----#
422
423
     # Maximum extrapolation
424
     filter by extrapolation <- TRUE # [USER]
425
426
     # How much age can be extrapolated beyond the oldest chronology control
427
     point?
428
     maximum age extrapolation <- Inf # [USER]</pre>
429
430
     #----#
431
432
     # Beyond the period of interest
433
     # Note that the actual ages have to be specified per region, defined
434
     during
435
     # the process of Workflow
436
     filter by interest region <- TRUE # [USER]
437
438
     #----#
439
440
     # Number of stratigraphic levels
441
     filter by number of levels <- TRUE # [USER]
442
443
     # At least X number stratigraphic levels within the period
444
     # of interest [example: X=3]
445
     min n levels <- 3
446
447
     #----#
448
449
     # Additional setting
450
451
     # Should the 95th age quantile be used for data filtration?
452
     # If FALSE (default), the estimated age will be used for all checks about
453
     t.he
454
        age of a stratigraphic level. However, if TRUE, then the 95th age
455
     quantile
456
        will be used.
457
     # This will result in more stable data assembly between different results
458
       of age-depth modelling BUT require additional data preparation before
459
       the analytical part.
460
     use age quantiles <- FALSE # [USER]</pre>
461
462
     # Should all data filtration omit one additional stratigraphic level in
463
     # the old period?
464
     # If TRUE, all filtering will proceed normally but one additional "bookend"
465
     # stratigraphic level will be always kept.
466
     # A "bookend" stratigraphic level is a subsequential stratigraphic level
467
     # older than the oldest stratigraphic level that passed the filtration.
468
     # A "bookend" can help provide anchor information older than the period of
469
     #
          interest.
470
     use bookend level <- FALSE # [USER]</pre>
```

```
471
472
473
    #-----#
474
    # 6. Set graphical options ----
475
    #----#
476
477
    # Set ggplot output
478
    ggplot2::theme set(
479
     ggplot2::theme classic()
480
481
482
    # Define general
483
    text size <- 16 # [USER]
484
    line size <- 0.1 # [USER]
485
    point size <- 3 # [USER]
486
487
    # Define output sizes
488
    image width <- 30 # [USER]</pre>
489
    image_height <- 15 # [USER]</pre>
490
    image_units <- "cm" # [USER]</pre>
491
    image dpi <- 300 # [USER]
492
493
    # Define pallets
494
495
    # Define common colours
496
497
498
    #----#
499
    # 7. Save current config setting ----
500
    #----#
501
502
    current setting <-
503
      RFossilpol::util extract config data()
504
```

APPENDIX 4: FOSSILPOL Config file used for the Northern

Europe example

```
507
      The important changes in comparison to the default template are highlighted blue.
508
509
510
511
                  Fossil pollen data from Scandinavia
512
513
                            Config file
514
515
516
         O. Mottl, S. Flantua, K. Bhatta, V. Felde, A. Seddon
517
                                2023
518
519
520
521
522
523
524
      # 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.
525
      # Points that require the user's attention are flagged by "[USER]" - flag,
526
      # meaning that these are criteria that need to be checked by the user
527
528
      # Version of the Workflow
529
      workflow version <-
530
        "0.0.2"
531
532
      # Set the current environment
533
      current env <- environment()</pre>
534
535
      #----#
536
      # 1. Load packages -----
537
538
539
      if (
540
      isFALSE(
541
          exists("already synch", envir = current env)
542
543
      ) {
544
      already_synch <- FALSE
545
546
547
      if (
548
      isFALSE(already synch)
549
550
       library(here)
551
        # Synchronise the package versions
552
       renv::restore(
553
          lockfile = here::here("renv/library list.lock")
554
555
        already synch <- TRUE
556
557
        # Save snapshot of package versions
558
        # renv::snapshot(lockfile = "renv/library list.lock") # do only for
559
      update
560
561
```

```
562
     # Define packages
563
     package list <-
564
      С (
565
        "RFossilpol",
566
        "RUtilpol",
567
        "here",
568
        "tidyverse"
569
570
571
     # Attach all packages
572
     sapply(package list, library, character.only = TRUE)
573
574
575
     #----#
576
     # 2. Current date and working directory -----
577
     #----#
578
579
     current date <- Sys.Date()</pre>
580
581
     # Project directory is set up by the {here} package, Adjust if needed
582
     current dir <- here::here()</pre>
583
584
     # Define the directory (external) for storing big data files
585
     # Default is in the current project
586
     data storage path <- current dir # [USER]</pre>
587
588
     # Create all essential folders
589
     RFossilpol::util make datastorage folders(
590
      dir = data storage path # [config criteria]
591
592
593
     #-----#
594
     # 3. Load functions -----
595
     #----#
596
597
     # Get a vector of general functions
598
     fun list <-
599
      list.files(
600
        path = "R/Functions/",
601
        pattern = "*.R",
602
        recursive = TRUE
603
      )
604
605
     # Load the function into the global environment
606
607
     paste0("R/Functions/", fun list, sep = ""),
608
      source
609
     )
610
611
612
613
     # 4. Project dataset database -----
614
     #----#
615
616
     # Check the presence of a dataset database and create it if necessary
617
     if (
618
      isFALSE(
619
        "project dataset database.rds" %in%
620
          list.files(
621
            paste0(
622
              data storage path, # [config criteria]
```

```
623
               "/Data/Personal database storage"
624
625
           )
626
       )
627
     ) {
628
       project dataset database <-
629
        RFossilpol:::proj db class()
630
631
       readr::write rds(
632
         project_dataset_database,
633
         paste0(
634
           data_storage_path, # [config criteria]
635
           "/Data/Personal_database_storage",
636
           "/project dataset database.rds"
637
638
         compress = "qz"
639
       )
640
     }
641
642
643
     #----#
644
     # 5. Define variables -----
645
646
647
     #----#
648
     # 5.1. Define individual run ----
649
650
651
     # Include/exclude Neotoma download in run
652
     dataset type <- "pollen"</pre>
653
654
     # Selected variable element (proxy)
655
     sel var element <- "pollen"</pre>
656
657
     # Set geographical boundaries
658
     long min <- 5 # [USER]</pre>
     long max <- 30 # [USER]
659
660
     lat min <- 55 # [USER]
661
     lat max <- 73 # [USER]
662
     alt min <- NA # [USER]
663
     alt max <- NA # [USER]
664
665
     neotoma new download <- TRUE
666
667
     # Define access to datasets from other sources than Neotoma
668
     use other datasource <- FALSE # [USER]</pre>
     detect_duplicates <- TRUE # [USER]</pre>
669
670
671
     # Include/exclude age modelling in run
672
     recalib AD models <- TRUE # [USER]</pre>
673
     calc AD models denovo <- FALSE # [USER]</pre>
674
     predict_ages_denovo <- FALSE # [USER]</pre>
675
676
     # Select the final variables
677
     select final variables <- TRUE # [USER]</pre>
678
679
680
681
     # 5.2. Chronology order ----
682
     #-----#
683
```

```
684
     # Selected and preferred order of age type of existing chronologies in
685
     Neotoma
686
     chron order <-
687
      tibble::tibble(
688
         order = seq(1, 6),
689
         type = c(
690
          "Varve years BP",
691
          "Calibrated radiocarbon years BP",
692
          "Calendar years BP",
693
          "Radiocarbon years BP",
694
          "Calendar years AD/BC",
695
696
        )
697
       )
698
699
700
     #----#
701
     # 5.5. Age depth models -----
702
     #----#
703
704
     # Chronology needs to have at least X control points [example: X=2]
705
     min n of control points <- 5 # [USER]</pre>
706
707
     # If the thickness of a control point is missing, assign X cm [example:
708
     X=1
709
     default thickness <- 1 # [USER]</pre>
710
711
     # If the age error of a control point is missing, assign X yr [example:
712
     X=100]
713
     default error <- 100 # [USER]</pre>
714
715
     # Maximum accepted age error of chron.control point [example: X=3000]
716
     max age error <- 3000 # [USER]</pre>
717
718
     # Depth at which "Guess" is accepted as a chronology control
719
     # point [example: X=10]
720
     guess depth <- 10 # [USER]
721
722
     # Bchron settings
723
     number of cores <- parallel::detectCores() - 1</pre>
724
     batch size <- number of cores * 3
725
     set seed <- 1234
726
727
     default iteration <- 10e3
728
     default burn <- 2000
729
     default thin <- 8 # [USER]
730
     iteration multiplier <- 5 # [USER]
731
732
733
     #----#
734
     # 5.6. Filtering criteria ----
735
     #----#
736
737
     # Criteria to filter out stratigraphic levels and pollen records
738
739
     #----#
740
741
     # Pollen sums
742
     filter by pollen sum <- TRUE # [USER]
743
```

```
744
     # Each stratigraphic level of at least X individual pollen gains [example:
745
746
     min n grains <- 100 # [USER]
747
      # Ideal number of counts
748
     target n grains <- 150 # [USER]
749
      # Threshold of number of samples with ideal counts
750
     percentage samples <- 75 # [USER]</pre>
751
752
753
754
     # Age limits
755
        Note that the actual ages have to be specified per region, defined
756
     during
757
     # the process of Workflow
758
     filter by age limit <- TRUE # [USER]
759
760
     #----#
761
762
     # Maximum extrapolation
763
     filter by extrapolation <- TRUE # [USER]</pre>
764
765
     # How much age can be extrapolated beyond the oldest chronology control
766
767
     maximum age extrapolation <- 3000 # [USER]</pre>
768
769
     #----#
770
771
     # Beyond the period of interest
772
     # Note that the actual ages have to be specified per region, defined
773
     during
774
     # the process of Workflow
775
     filter by interest region <- TRUE # [USER]
776
777
     #----#
778
779
     # Number of stratigraphic levels
780
     filter by number of levels <- TRUE # [USER]
781
782
     # At least X number of stratigraphic levels within the period
783
     # of interest [example: X=3]
784
     min n levels <- 5
785
786
     #----#
787
788
     # Additional setting
789
790
     # Should the 95th age quantile be used for data filtration?
791
     # If FALSE (default), the estimated age will be used for all checks about
792
     the
793
     # age of a stratigraphic level. However, if TRUE, then the 95th age
794
     quantile
795
        will be used.
796
     # This will result in more stable data assembly between different results
797
         of age-depth modelling BUT require additional data preparation before
798
         the analytical part.
799
     use_age_quantiles <- FALSE # [USER]</pre>
800
801
     # Should all data filtration omit one additional stratigraphic level in
802
     # the old period?
803
     # If TRUE, all filtering will proceed normally but one additional "bookend"
804
     # stratigraphic level will be always kept.
```

```
805
      # A "bookend" stratigraphic level is a subsequential stratigraphic level
806
      # older than the oldest stratigraphic level that passed the filtration.
807
      # A "bookend" can help provide anchor information older than the period of
808
           interest.
809
      use bookend level <- FALSE # [USER]
810
811
812
813
      # 6. Set graphical options -----
814
      #----#
815
816
      # Set ggplot output
817
      ggplot2::theme set(
818
       ggplot2::theme classic()
819
820
821
      # Define general
822
      text size <- 16 # [USER]
823
      line size <- 0.1 # [USER]
824
     point size <- 3 # [USER]
825
826
      # Define output sizes
827
     image width <- 30 # [USER]</pre>
828
      image height <- 15 # [USER]</pre>
829
      image_units <- "cm" # [USER]</pre>
830
      image dpi <- 300 # [USER]</pre>
831
832
833
      # Define common colours
834
      col gray dark <- "gray30"</pre>
835
      col gray middle <- "gray50"</pre>
836
      col_gray_light <- "gray90"
837
838
      ## Main colour
839
      col orange dark <- "#E17D00"
840
      col orange light <- "#ff9715"</pre>
841
842
      ## Complementary
843
      col compl blue <- "#00507B"
844
845
      ## Analogous
846
      col ana red <- "#FF2215"
847
848
      # Define pallets
849
      palette generic <-
850
       C (
          "#FF9715",
851
852
         "#FF685F",
853
         "#D3588B",
854
          "#8C5C99",
855
          "#4A5783"
856
       )
857
858
      palette matching <-
859
860
          "#00987E",
861
          "#00D1B2",
          "#B9A89B",
862
          "#524439",
863
864
          "#FF9715"
865
```

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