ageR: Supervised Age Modelling

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What data do you need?

- **Core:** `labID`, `age`, `error`, `depth`, and `cc`
- **Sampling:** `ID` and `depth`
- **(Optional) Hiatuses:** `ID` and `depth`

How do you get the data?

- A comma-separated values (CSV) file
- A query to a database

Installation

Current version can be installed from the GitHub repository:

```
install.packages("remotes")
remotes::install_github("special-uor/ageR")
```

To verify you are running the latest version, run the following command:

```
?ageR
```

Demo

Example (Toy data)

File structure

```
ageR::file_structure(entity = "X", am = "bacon")
```

```
##                          levelName
## 1 X
## 2  ¦--Bacon_runs
## 3  ¦    °--X
## 4  ¦        ¦--X_depths.txt
## 5  ¦        ¦--X_sample_ids.csv
## 6  ¦        °--X.csv
## 7  ¦--hiatus.csv
## 8  °--not_used_dates.csv
```

Input data

Core data

```r
core <- data.frame(labID = paste0("X", sprintf("%03d", 1:5)),
                   age = c(50, 200, 1150, 2060, 4050),
                   error = c(10, 15, 5, 1, 70),
                   depth = c(5, 100, 230, 300, 450),
                   cc = 1)
knitr::kable(core)
```

labID	age	error	depth	cc
X001	50	10	5	1
X002	200	15	100	1
X003	1150	5	230	1
X004	2060	1	300	1
X005	4050	70	450	1

Input data (2)

Sampling depths

```r
sample_depths <- data.frame(id = 1:100,
                            depth = seq(0, 500, length.out = 100))
knitr::kable(head(sample_depths))
```

id	depth
1	0.000000
2	5.050505
3	10.101010
4	15.151515
5	20.202020
6	25.252525

Input data (3)

(Optional) Hiatuses

```r
hiatus <- data.frame(id = c(1, 2),
                     depth = c(50, 150))
knitr::kable(hiatus)
```

id	depth
1	50
2	150

Input data (4)

```
ageR::create_input(data = list(sample_depths = sample_depths,
                               core = core,
                               # Optional
                               hiatus = hiatus),
                   wdir = "./",
                   entity = "X",
                   am = "bacon")
```

```
## [1] "sample_depths" "core"            "hiatus"
```

Databases: RPD

```
conn <- dabr::open_conn_mysql("RPD-latest")
query <- paste0(
"SELECT entity_name,
       entity.ID_ENTITY as entity_id,
         lab_number AS labID,
       age_C14 AS age,
       error,
       avg_depth*100 AS depth,
       date_type,
       thickness
FROM date_info INNER JOIN entity
    ON date_info.ID_ENTITY = entity.ID_ENTITY
WHERE latitude >= 45")

rpd <- dabr::select(conn, query, quiet = TRUE)
nrow(rpd)
```

```
## [1] 5226
```

Databases: RPD (2)

```r
`%>%` <- dplyr::`%>%`
rpd <- rpd %>%
  dplyr::filter(!is.na(age)) %>%
  dplyr::filter(!is.na(error)) %>%
  dplyr::filter(!is.na(depth)) %>%
  dplyr::mutate(error =  ifelse(error <= 0, 1, error)) %>%
  dplyr::arrange(depth) %>%
  dplyr::mutate(cc = ifelse(grepl("*carbon", date_type), 1, 0))

entities <- sort(unique(rpd$entity_name))
head(entities)
```

```
## [1] "7-M core 1"        "Abbeyknockmoy Bog core 1"
## [3] "Abeille-5"         "Aero-1"
## [5] "Aero-5"            "Air-1"
```

Databases: RPD (3)

```r
test_entity <- "Burnt Knob core 1"
test_entity_id <- unique(rpd$entity_id[rpd$entity_name == test_entity])

# Extract sampling depths
query <- paste0("SELECT ID_SAMPLE AS id, sample_depth*100 AS depth
                FROM sample
                WHERE ID_ENTITY = ", test_entity_id)
sample_tb <- dabr::select(conn, query, quiet = TRUE)
sample_tb <- sample_tb %>%
  dplyr::filter(depth != -9999)

# Extract core data
my_core <- rpd[rpd$entity_name == test_entity,
               c("labID", "age", "error", "depth", "cc")]

# Create input
ageR::create_input(data = list(core = my_core,
                               sample_depths = sample_tb),
                   wdir = "./",
                   entity = test_entity)
```

```
## [1] "core"          "sample_depths"
```

Run Bacon

```r
ageR::Bacon(wdir = "./",
            entity = "X",
            # Optional parameters
            cpus = 1,
            postbomb = 0,
            cc = 0,
            seed = NA,
            alt_depths = NULL,
            quiet = FALSE,
            acc_step = 5,
            acc_lower = NULL,
            acc_upper = NULL,
            thick_step = 5,
            thick_lower = NULL,
            thick_upper = NULL,
            dry_run = FALSE,
            ...)
```

More details: https://special-uor.github.io/ageR/reference/Bacon

Run Bacon: Dry-run

```
out <- ageR::Bacon(wdir = "./", entity = "X", dry_run = TRUE, quiet = TF
```

```
## The following scenarios will be executed:

##
##
## | Accumulation rate| Thickness|
## |-----------------:|---------:|
## |                 5|        10|
## |                10|        10|
## |                20|        10|
## |                 5|        15|
## |                10|        15|
## |                20|        15|
## |                 5|        20|
## |                10|        20|
## |                20|        20|
## |                 5|        30|
## |                10|        30|
## |                20|        30|
## |                 5|        40|
## |                10|        40|
```

Run Bacon: *Mixed calibration curves*

```r
ccdir <- "./ccurves"
ageR::mix_curves(proportion = 0.5,
                 cc1 = 1,
                 cc = 3,
                 name = "neotropics.14C",
                 dirname = ccdir)
```

```
## ---------------------------------------------------------------------
## |                     Mixed curved: 50/50 created.
## ---------------------------------------------------------------------
```

```r
out <- ageR::Bacon(wdir = "./",
                   entity = "X",
                   cc4 = "neotropics.14C",
                   ccdir = ccdir)
```

Wishlist (aka GitHub issues)

Create new "Issues" to request new features, report an error, etc.

https://github.com/special-uor/ageR/issues

Thanks!

Slides created using the R package **xaringan**.