

CRATE: User Manual

Version 1.0

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1. Overview

CRATE (*Cancer Registries Aggregation Tool for ECIS*) is the R routine which aggregates record-level data from cancer registries' archives according to the dimensions considered in the ECIS web application. The input file of CRATE is the record-level incidence data extracted from the registry archive according to the requirements of the [ECIS data-call protocol](#). Incidence data for CRATE needs to be cleaned and validated.

2. Installation

Before running CRATE, the R environment needs to be configured according to the following preparatory steps:

1. Install the R software (<https://www.r-project.org/>) on your computer (at least version 4.2.2)
2. Unzip the "*crate-<version>.zip*" package in any directory on your computer
3. Take note of the path where you unzip the ZIP package, since this will be your **working directory**
4. Launch the R console
5. If not already installed before, install the following three packages:
 - a. `install.packages("dplyr");`
 - b. `install.packages("stringr");`
 - c. `install.packages("lifecycle");`
6. **Select the input dataset** that is the record-level incidence file compliant with the [ECIS data-call protocol](#) requirements. This must be a text file using the **semicolon** (i.e. ";") to separate the different variables correctly named and coded.

Once you unzip the "*crate-<version>.zip*" file, the following files will appear in your working directory:

- **crate.R**: the script to be executed
- **config/age_groups_18.csv**: configuration file containing definitions for the age breakdown in 18 age groups
- **config/age_groups_20.csv**: configuration file containing definitions for the age breakdown in 20 age groups
- **config/cancer_entities_2024.csv**: configuration file containing the cancer-entities' definitions
- **docs/CRATE-aggregation-with-R-user-manual.pdf**: user manual (this document)
- **docs/Notice.txt**: policy and information about CRATE usage licence
- **docs/Licence.txt**: the user license for using the CRATE software.

These files should never be edited or modified by the user, since this could trigger unpredictable behaviour or wrong aggregation results.

Optional: to verify that all the required packages have been correctly installed, please execute in the R console the three commands below:

```
system.file(package='dplyr');  
system.file(package='stringr');  
system.file(package='lifecycle');
```

If the results are different from an empty string, then the three packages are correctly installed.

Remark: the maximum number of records that can be handled by CRATE depends on the amount of the internal memory of the user's computer (a minimum of 4GB of RAM is suggested).

3. Usage

To run CRATE, the user can choose two different options:

1. Run CRATE using the default configuration, without performing any setup of the R environment
2. Setup a custom run time environment, in order to have more control over the script execution.

Advanced users can change also other configuration parameters (see section [6. Advanced Configuration](#) for details).

Option 1: default configuration

Using the default configuration, the record-level incidence file to be aggregated MUST be copied to the **working directory**, and the file MUST be renamed as **dataset.csv**. Then, to run CRATE the user must open an R console and copy-paste the following command:

```
source("<absolute path of your working directory>/crate.R")
```

For example:

```
source("C:/Home/Temp/crate/crate.R")
```

Option 2: custom configuration

This option allows running CRATE without renaming the record-level incidence file. To enable this option, the name and extension of the input dataset MUST be setup using the **dataset_meta** variable in the R console, as follow:

```
# General syntax:
dataset_metadata <- c(<dataset file's name>, <dataset file's extension>, <working directory>);
```

Example:

```
# Usage example:
dataset_metadata <- c("my_file_name", "txt", "C:\\Temp\\ENCR\\data");
```

Warning

The custom-configuration approach implies that the output reports will be produced in the new working directory (in the example above: "C:\\Temp\\ENCR\\data"), and the name of ALL output files will be changed accordingly. For instance, in the example above with "my_file_name.txt", the custom-configuration approach would produce the file "my_file_name_aggregated.txt" instead of "dataset_aggregated.txt" (see section [5. Output reports](#) for details).

This approach can be useful when the user wishes to aggregate different datasets with different names, namely data separated by incidence period or other stratifications inside the same registry. By choosing a custom configuration, the user could:

1. Copy all input datasets in the custom working folder
2. Set the *dataset_meta* variable (in the R console) in order to match the name of the first dataset to be processed
3. Run CRATE
4. Go back to step 2, assign to the *dataset_meta* variable the name of the next input dataset to be processed, then repeat the step 3.

4. Aggregation levels

The current version of CRATE aggregates records according to the following variables:

- Sex (SEX): male or female
- Year of incidence (YOI): the whole incidence time period included in the input record-level data file
- Age group (AG) : 5-year age groups, from minimum "0-4 years" to maximum "95+ years"
- Cancer entity (ENTITY_ID): cancer entity definitions as described in **config/cancer_entities_2024.csv**
- Geographical area of residence at diagnosis (GEO_CODE): the geographical codes provided by the cancer registry.

As specified in the **config/cancer_entities_2024.csv**:

- the cancer entities contributing to the definition of "All entities excluding keratinocytic skin cancers" are those where the column "ce_inall" is different from "NO";
- the cancer entities that will be published in the ECIS web application are those where the column "ecis_web" is different from "NO".

5. Output reports

CRATE produces in the working directory a series of **output files**:

- **dataset_checklog.txt**: report documenting the results of the aggregation process
- **dataset_discarded.csv**: dataset containing all records discarded because of missing or invalid values of the main variables (topography, morphology, behaviour, grade, sex, year of incidence, age/year of birth) or because of excluded values (valid values, but excluded from the aggregation)

- **dataset_notinall.csv**: dataset containing records matching the definition of at least one cancer entity, but not matching the definition of "All entities excluding keratinocytic skin cancers"
- **dataset_unmatched.csv**: dataset containing all valid records not matching any cancer entity definitions
- **dataset_selected.csv**: dataset containing a copy of the records actually used for the aggregation (i.e. records not discarded, nor excluded and therefore matching at least one cancer entity definition)
- **dataset_aggregated.csv**: dataset containing the aggregated number of cases by sex, age group, year of incidence and cancer entity.
- **dataset_aggregated_by_area.csv**: similar to "dataset_aggregated.csv", with aggregation also over the GEO_CODE variable

As reported in the section "3.Usage", the names of these output files can change using a custom configuration.

The main output file of CRATE is the **dataset_aggregated.csv** output report containing the results of the aggregation process on all valid records that did match a valid cancer entity as defined in the **config/cancer_entities_2024.csv**. If opened using a text editor, this file should look like the following:

SEX;YOI;AG;ENTITY_ID;NUMBERS
1;2006;14;68;1
1;2006;15;21;2
1;2006;15;88;1
1;2006;16;21;1
1;2006;16;60;1
1;2006;17;21;3
1;2006;17;22;1
1;2006;17;25;1
1;2006;17;30;1
1;2006;17;65;2
1;2006;17;69;1

Figure 1: example of results in the "dataset_aggregated.csv" output file

- The ENTITY_ID column refers to the ID of the ECIS cancer entities, as defined in the **ECIS_ID** column of the **config/cancer_entities_2024.csv** configuration file
- The NUMBERS column reports the number of incident cases corresponding to the same combination of SEX, YOI, AG and ENTITY_ID

The **dataset_aggregated_by_area.csv** is optional, because it is produced only if the GEO_CODE variable contains at least **2** different values: if all GEO_CODE values are missing (or set to the same identical NUTS code), this report is **not** produced.

6. Advanced configuration

CRATE can be run using the default configuration, as explained in section "3. Usage". However, advanced users can exploit the flexibility of the R script by tweaking some parameters to match specific needs.

If no parameter is set in the R console, the script will perform the aggregation using the **default** configuration producing output files with the name convention as described in the section "4. Output reports". Moreover, the aggregation is executed under the following assumptions:

- Any missing numeric value (**NA** in R) is replaced with an empty string
- Aggregation is performed using **20 Age Groups** (0-4, 5-9, ... 90-94, 95+)

Advanced users can run the R script overriding this configuration from the R console, as explained below. It's also possible to change some parameters directly in the R script by searching the "CUSTOM_SELECTION" keyword in the source file. However this is **NOT** suggested when preparing the dataset for the ECIS submission since tampering with the source code could lead to unpredictable results.

6.1. Metadata of input file

Name and extension of the input dataset can be changed setting the **dataset_meta** variable (in the R console). For details, see *Option 2* in the "3. Usage" section.

6.2. Execution flags

The execution of CRATE can be changed by setting the **flags** variable (in the R console) *before* running the script.

```
# General syntax:
flags <- c(<use_20_age_groups>,<fill_missing_with_empty_string>,<clean_all_resources>);
```

```
# Usage example:
flags <- c(TRUE, TRUE, TRUE);
```

The code in the example above enables all the *flags-related* features, which are (in the same order as the command above):

- *use_20_age_groups*: if set to FALSE, the definition of 18 Age Groups is used (instead of 20 Age Groups)
- *fill_missing_with_empty_string*: if set to FALSE, all produced output datasets contain the value "NA" where the input dataset has missing value (i.e. empty string)
- *clean_all_resources*: if set to FALSE, all final objects (intermediate data frames) are kept in the current workspace.

6.3. Output reports

The **number of output files** produced during the aggregation process can be changed by setting the **output_reports** variable (in the R console) *before* running the script.

```
# General syntax:
output_reports <- c(<discarded_report>, <unmatched_report>);

# Usage example:
output_reports <- c(FALSE, FALSE);
```

The code in the example above disables the production of the following output reports:

- If the *discarded_report* flag is set to FALSE: the report named like "*dataset_discarded.csv*" will NOT be produced
- If the *unmatched_report* flag is set to FALSE: the report named like "*dataset_unmatched.csv*" will NOT be produced

7. Insights

CRATE applies few selected checks and replacements on missing and unknown values of aggregation variables before processing the input dataset:

- **MOI (Month Of Incidence)** and **MOB (Month Of Birth)**: missing (i.e. empty) and *unknown* ("99") values are replaced with value **6** (June)
- **AGE**: if missing or unknown, AGE is calculated as the difference between the incidence date (MOI, YOI) and the birthdate (MOB, YOB) - if available for the calculation
- **GRADE**: if missing (i.e. empty), GRADE is replaced with the value **9** (Grade *unknown*)
- **BEH (behaviour)**: if BEH is **6** or **9**, BEH is replaced with value **3** (Malignant neoplasms stated or presumed to be primary)

8. Known issues

CRATE is currently in the **beta testing** stage. For this reason, the user experience could be not straightforward, since some manual tasks must be performed when installing and/or running the software.

The following improvements will be considered in the future:

1. Replace step 4 of the installation procedure with a task such as: "install the CRATE package using the R **install package** feature from local files menu option and the ZIP file provided by the JRC". This should allow users to install the script using something like "*library/crate*" and then running a command like "*df_aggregated <- crate.R(path, fromYear=1980, toYear=2022)*"
2. It is currently not possible to **run CRATE from a operating system (OS) console** (using the target OS's "RScript" executable)
3. If more R installations are available (for instance: both R base and RStudio), then some local settings could be shared by these installations. In case of issues, try to run the tool **twice**: in the second run the settings (proper values in the *input_path* and *output_path* variables) from previous runs are no longer used.

For **support** please contact JRC-ENCR@ec.europa.eu.