# Package ‘dalycare’

January 25, 2024

**Title** Danish Lymphoid Cancer Research

**Priority** NA

**Version** 0.2.0

**Date** 2024-1-15

**Depends** R (>= 3.5.0), dplyr,

**Imports** Codes\_NPU

**LazyData** ?

**LazyDataCompression** ?

**ByteCompile** ?

**Description** Contains definitions and grouping of Danish electronic health data from SDS, RKKP, and SP.

**License** ?

**URL** NA

**NeedsCompilation** NA

**Author** Christian Brieghel [aut, cre], Casper Møller Frederiksen [ctb, trl], Mikkel Werling [ctb, trl]

**Maintainer** Christian Brieghel

**Repository** ?

**Date/Publication** ?

## Index

Package “dalycare” is loaded on our NGC cloud as:

source(“/ngc/projects2/dalyca\_r/clean\_r/load\_data.R”)

## Cleaning

##### clear\_ram

Description

Clears Global environment and frees RAM from NGC/dalycare

Usage

clear\_ram()

##### clean\_RKKP\_LYFO

Description

Cleans the dataset RKKP\_LYFO. Works only for LYFO version 20 or higher, please see [rkkp-documentation](https://www.rkkp-dokumentation.dk/Public/Default.aspx?msg=ChooseDB&error=WrongParm)

Note

Notes and specific comments are based on meetings with Peter Brown, who provided  
critical knowledge of what variables indicate.

Usage

RKKP\_LYFO\_CLEAN = RKKP\_LYFO %>% clean\_ RKKP\_LYFO()

##### clean\_RKKP\_LYFO\_SNOMED

Description

Cleans SNOMED codes in RKKP\_LYFO. Works only for LYFO version 20 or higher, please see [rkkp-documentation](https://www.rkkp-dokumentation.dk/Public/Default.aspx?msg=ChooseDB&error=WrongParm)

Usage

RKKP\_LYFO %>%

mutate(icd10 = clean\_ RKKP\_LYFO\_SNOMED(snomed = Reg\_WHOHisto)

##### clean\_RKKP\_CLL

Description

Cleans the dataset RKKP\_CLL. Works only for CLL registry version 15 or higher, please see [rkkp-documentation](https://www.rkkp-dokumentation.dk/Public/Default.aspx?msg=ChooseDB&error=WrongParm)

Usage

RKKP\_CLL\_CLEAN = RKKP\_CLL %>% clean\_ RKKP\_CLL()

##### clean\_RKKP\_DAMYDA

Description

Cleans (or translates) the dataset RKKP\_DAMYDA. Works only for DAMYDA version 18 or higher, please see [rkkp-documentation](https://www.rkkp-dokumentation.dk/Public/Default.aspx?msg=ChooseDB&error=WrongParm)

Usage

RKKP\_DAMYDA\_CLEAN = RKKP\_DAMYDA %>% clean\_ RKKP\_DAMYDA()

##### clean\_RKKP\_DAMYDA\_SNOMED

Description

Cleans SNOMED (or translates) codes in RKKP\_DAMYDA. Works only for DAMYDA version 20 or higher, please see [rkkp-documentation](https://www.rkkp-dokumentation.dk/Public/Default.aspx?msg=ChooseDB&error=WrongParm)

Usage

RKKP\_DAMYDA %>%

mutate(icd10 = clean\_ RKKP\_ DAMYDA\_SNOMED(snomed = Reg\_WHOHisto)

##### clean\_SP\_OS

Description

Cleans the dataset SP\_OS.

Usage

SP\_OS %>% clean\_SP\_OS()

##### clean\_abbreviations

Description

Replaces commonly used Danish abbreviations containing punctuation to allow for better separation of free text into complete sentences.

E.g. “f.eks.” to “f\_eks” pattern.

Caveat: time lapse with large datasets: subset data before use.

Usage

SP\_Journalnotater\_del1 %>%

mutate(notat\_text = clean\_abbreviations(notat\_text))

##### clean\_lab\_values

Description

Cleans and converts common laboratory values with correct units based on NPU codes.

E.g. B2M nmol/l converts to mg/l.

Usage

LAB\_data = load\_common\_biochemistry(labs = “INFECTION”, combine = TRUE)

LAB\_clean = clean\_lab\_values(LAB\_data)

##### clean\_Date

Description

Cleans dates annotated as seconds from 1970-01-01 found in SP dates.

Usage

SP\_VitaleVaerdier %>% clean\_Date(recoded\_time)

## Load data

##### load\_dataset

Description

Loads data directly from the DALYCARE database when specifying dataset(s).

*Dataset* may be specified as a vector of datasets.

Returns a complete list of dataset options when *dataset* is NULL (default).

Imports subset of dataset(s) when specifying *sample* as a vector of *patientid(s).*

Also imports subset of dataset on other existing variables specifying *filter* argument.

Usage

load\_dataset() #Returns a list of available *datasets*

load\_dataset(c(“PATIENT”, “RKKP\_CLL\_CLEAN”)) # loads both

load\_dataset(“RKKP\_DAMYDA”, value = sample(PATIENT$patientid, 100)) #only sample

load\_dataset(“SP\_OrdineretMedicin”, value = c(“J06BA02”, “J01CE01”), column = “atc”)

##### load\_dalycare\_dx

Description

Loads all diagnoses defined in DALY CARE:

C81.x-C90.x, C91.1-C91.9, C95.1, C95.7, C59.9, D47.2, D47.9B, and E85.8A.

RKKP > ICD10 > SP > SNOMED. See Table1.R

Usage

dalycare = load\_dalycare\_dx()

##### load\_bmi\_SP

Description

Loads body mass index and body surface area data as defined by BMI()

Usage

bmi = load\_bmi\_SP()

##### load\_blood\_culture\_SP

Description

Loads blood cultures from SP\_AlleProevesvar

Usage

BC = load\_blood\_culture\_SP()

##### load\_common\_biochemistry

Description

Loads a list of datasets containing common biochemistry from Lab\_forsker.

NB! Remember to save data as suggested in usage.

`labs` = NULL returns options



You may also specify sets of biochemistry by specifying `labs` as:



Usage

LAB\_LIST = load\_common\_biochemistry(labs = c(“B2M”, “LDH”))

LAB\_DF = load\_common\_biochemistry(labs = c(“B2M”, “LDH”), combine = TRUE)

##### load\_npu\_common

Description

Loads a list of vectors containing common NPU codes to your Global Environment.

You may also specify individual codes such as NPU.LYM (ie. lymphocytes) or groups of NPU codes such as GROUP.NPU.CBC (i.e. complete blood count) or NPU.GROUP.MYELOMA (i.e. standard myeloma blood test set).

Usage

load\_npu\_common()

NPU.HGB # returns NPU02319

# Use NPUs to load\_data() subset

load\_data(“SDS\_lab\_forsker”, c(NPU.B2M, NPU.LYM), ”analysiscode”)

View(SDS\_lab\_forsker\_subset)

##### go\_live

Description

Loads SP (EPIC) go live dates for the three hospitals HGH, Herlev; Rigshopitalet; and SUH, Roskilde.

Usage

go\_live()

## Definitions

##### scr\_low\_48h

Description

Defines lowest serum creatinine (scr) within 48 hours using lab\_forsker data.

SDS\_lab\_forsker data should be filtered to contain creatinine only (NPU.KREA) to avoid time-lapse. Used to define acute kidney injury (AKI).

Usage

load\_npu\_common()

load\_data(“SDS\_lab\_forsker”, c(NPU.KREA), ”analysiscode”) #loads creatinine

DATA\_scr\_low\_48h = SDS\_labforsker\_subset %>%

mutate(

cpr\_enc = patientid,

date\_time = as.numeric(seconds(as.POSIXct(paste(samplingdate, samplingtime)))),

i.scr\_inhos = 0

) %>%

scr\_low\_48h()

##### scr\_low\_7d

Description

Defines lowest serum creatinine (scr) within 7 days using lab\_forsker data.

SDS\_lab\_forsker data should be filtered to contain creatinine only (NPU.KREA) to avoid time-lapse.

Usage

load\_npu\_common()

load\_data(“SDS\_lab\_forsker”, c(NPU.KREA), ”analysiscode”) #loads creatinine

DATA\_scr\_low\_48h = SDS\_labforsker\_subset %>%

mutate(

cpr\_enc = patientid,

date\_time = as.numeric(seconds(as.POSIXct(paste(samplingdate, samplingtime)))),

i.scr\_inhos = 0

) %>%

scr\_low\_7d()

##### scr\_base\_median

Description

Defines baseline serum creatinine (BL scr) a rolling median using lab\_forsker data.

SDS\_lab\_forsker data should be filtered to contain creatinine only (NPU.KREA) to avoid time-lapse.

Usage

load\_npu\_common()

load\_data(“SDS\_lab\_forsker”, c(NPU.KREA), ”analysiscode”) #loads creatinine

DATA\_scr\_low\_48h = SDS\_labforsker\_subset %>%

mutate(

cpr\_enc = patientid,

date\_time = as.numeric(seconds(as.POSIXct(paste(samplingdate, samplingtime)))),

i.scr\_inhos = 0

) %>%

scr\_base\_median()

##### AE\_AKI

Description

Defines acute kidney injury based on a 1.5x increase from the baseline serum creatinine (scr\_base\_median) within 7 days (scr\_low\_7d) or an absolute scr increase of 26.5 µmol/L within 48 hours (scr\_low\_48h) using lab\_forsker data.

SDS\_lab\_forsker data should be filtered to contain creatinine only (NPU.KREA) to avoid time-lapse.

Usage

load\_data(“SDS\_lab\_forsker”, c(NPU.KREA), ”analysiscode”) #loads creatinine

CREATININE\_clean = SDS\_labforsker\_subset %>% clean\_lab\_values()

AKI = CREATININE\_clean %>% AE\_AKI(value = value2)

Citation

Carrero JJ et al. Kidney Int. 2023 Jan;103(1):53-69.

##### CTCAE\_lab

Description

Defines CTC adverse events (AE) from biochemistry. Works only with lab\_forsker data.

SDS\_lab\_forsker data should be filtered to contain NPU of interest to avoid time-lapse.

E.g. May calculate ‘ANEMIA’, ‘THROMBOCYTOPENIA’, ‘DIC’, and ‘HEMOLYSIS’.

Usage

SDS\_lab\_AE = SDS\_lab\_forsker %>% CTCAE\_lab()

##### TX\_group

Description

Groups treatment protocols into meaningful groups as class characters.

Usage

SP\_Behandlingsplaner\_del1 %>% TX\_group(protocol)

##### filter\_virus

Description

Subsets RSV, SARS-CoV-2 (SARS) and seasonal influenza (FLU) into class character.

Usage

SP\_Bloddyrkning\_del1 %>% filter\_virus()

Citation

Niemann et al. *Blood*. Aug 4 2022;140(5):445-450.

##### filter\_sentence

Description

Subsets all free-text sentences (i.e. from \\. to \\.) containing pattern.

Caveat: Free text often contains punctuation such as abbreviation causing separation; also see clean\_abbreviations()

Usage

SP\_Journalnotater\_del1 %>% filter\_sentence(notat\_text, “SAGM”)

SDS\_t\_mikro\_ny %>% filter\_sentence(v\_fritekst, ’EBER’)

##### ATC\_polypharmacy

Description

Calculates number of 1st to 5th level ATC codes per patient and defines polypharmacy as ≥5 drug classes.

Usage

SDS\_epikur %>% ATC\_polypharmacy(level = 3)

Citation

Brieghel et al. ASH annual meeting 2023. P5133

##### COD2

Description

Groups cause of death (COD) ICD10 codes into meaningful groups. Prioritizes infections.

Usage

SDS\_t\_dodsaarsag\_2 %>%  COD2()

Citation

Rotbain et al. *Leukemia*. 2021;35(9):2570-2580.

##### CCI

Description

Calculates Charlson comorbidity index (CCI) scores from ICD10 codes.

Specifying CLL\_include = FALSE omits the DC911 score.

Usage

SDS\_t\_adm %>% CCI()

diagnosis\_all %>% CCI(patientid = patientid, icd10 = diagnosis)

Citation

Quan et al. Med Care. 2005;45:1130-9 as CCI.score

Quan et al. Am J Epidemiol. 2011;173:676-82 for CCI.2011.update

##### ATC\_AB

Description

Subsets and groups all antimicrobials.

Usage

SDS\_epikur %>% ATC\_AB()

SP\_Administreret\_Medicin %>% ATC\_AB()

##### ATC\_hypertensives

Description

Subsets and groups all antihypertensive drugs.

Usage

SDS\_epikur %>% ATC\_hypertensives()

SP\_Administreret\_Medicin %>% ATC\_hypertensives ()

##### ATC\_opioids

Description

Subsets and groups all opioids.

Usage

SDS\_epikur %>%  ATC\_opioids()

SP\_Administreret\_Medicin %>% ATC\_opioids()

##### qSOFA

Description

Calculates qSOFA scores from vital values assuming that AVPU less than alert replaces GCS < 15.

Usage

SP\_VitaleVaerdier %>% qSOFA()

##### BMI

Description

Calculates body mass index (BMI) and body surface area (BSA) from vital values.

Usage

SP\_VitaleVaerdier %>% BMI()

##### BSA

Description

Calculates body mass index (BMI) and body surface area (BSA) from vital values.

Usage

SP\_VitaleVaerdier %>% BSA()

##### CLL\_IPI

Description

Calculates CLL-IPI risk as class factor

Usage

RKKP\_CLL\_CLEAN %>%  CLL\_IPI()

Citation

da Cunha-Bang et al. *Blood*. Oct 27 2016;128(17):2181-2183.

##### CLL\_WONT

Description

Calculates CLL-WONT risk as class factor

Usage

RKKP\_CLL\_CLEAN %>%  CLL\_WONT()

Citation

Brieghel et al. *Eur J Haematol*. May 2022;108(5):369-378.

##### NCCN\_IPI

Description

Calculates NCCN-IPI risk for DLBCL as class factor.

NB! Input is complex and generalizable. Use RKKP\_LYFO\_CLEAN only.

Usage

RKKP\_LYFO\_CLEAN %>% NCCN\_IPI()

Citation

Zhou et al. *Blood*. Feb 6 2014;123(6):837-42.

##### MIPI

Description

Calculates MIPI risk for Mantle cell lymphoma as class factor

Usage

RKKP\_LYFO\_CLEAN %>% MIPI()

Citation

Hoster et al. *Blood*. Jan 15 2008;111(2):558-65.

##### IPS

Description

Calculates IPS risk for Hodgkin lymphoma as class factor

Usage

RKKP\_LYFO\_CLEAN %>% IPS()

Citation

Hasenclever et al. *NEJM*. 1998;339:1506-14.

##### rIPSSWM

Description

Calculates rIPSSWM risk for Waldenström macroglobulinemia (WM) and LPL as class factor.

Usage

RKKP\_LYFO\_CLEAN %>% rIPSSWM()

Citation

Kastritis et al. *Leukemia*. Nov 2019;33(11):2654-2661.

##### MAYO\_20\_20\_20

Description

Calculates Mayo Institute 20-20-20 risk for progression of smoldering myeloma as class factor.

Usage

RKKP\_DAMYDA\_CLEAN %>%  MAYO\_20\_20\_20()

Citation

Mateos et al. *Blood cancer journal*. Oct 16 2020;10(10):102

##### R\_ISS

Description

Calculates revised ISS (R-ISS) risk for multiple myeloma as class factor.

Usage

RKKP\_DAMYDA\_CLEAN %>%  R\_ISS()

Citation

Palumbo et al. *J Clin Oncol*. Sep 10 2015;33(26):2863-9.

##### R2\_ISS

Description

Calculates second revised ISS (R2-ISS) risk for multiple myeloma as class factor.

Usage

RKKP\_DAMYDA\_CLEAN %>% R2\_ISS()

Citation

D'Agostino et al. *J Clin Oncol*. Oct 10 2022;40(29):3406-3418.

RW\_ISS

Description

Calculates revised-world ISS (RW-ISS) risk for multiple myeloma as class factor.

Usage

RKKP\_DAMYDA\_CLEAN %>% RW\_ISS()

## House keeping

##### is\_odd

Description

Logical output from numeric values .

Usage

sample(1:10, 5) %>% is\_odd()

##### as\_Date

Description

Date output from characters expecting format “%Y-%m-%d”.

Usage

“2023-10-17” %>% as\_Date()

##### diff\_days

Description

Calculates numeric date intervals in days.

Usage

diff\_days(date\_start, date\_end)

##### diff\_years

Description

Calculates numeric date intervals in years.

Usage

diff\_years(date\_start, date\_end)

##### filter\_str\_detect

Description

Subsets data with strings containing vector of patterns.

Usage

SP\_Behandlingsplaner\_del1 %>% filter\_str\_detect(protocol, c(’’Bendamustin”, ”Fludara”))

##### str\_between

Description

Subsets string character between two patterns for text-mining purposes.

Usage

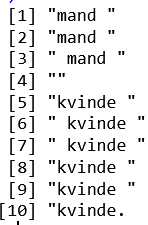
SP\_Journalnotater\_del1 %>%

filter(notat\_type==”AOP”) %>%

mutate(sex = str\_between(notat\_text, ’’årig ”, c(”henvist|møder|kendt”))) %>%

head(10) %>%

pull(text)



##### censor\_med\_keep\_first

Description

Subsets dates x days apart. Useful for censoring medication in grace period.

Usage

censor\_med\_keep\_first(Date\_med, days\_karens = 14)

Citation

Packness et al. EHA annual meeting 2022. P1596

##### cut\_year

Description

Cuts year-time into monthly intervals (e.g. 3-month intervals, by = 0.25) and outputs class factor.

Usage

Data %>% (year\_cut = cut\_year(time = Time, by = 0.25))

##### n\_patients

Description

Counts distinct patients in a dataset assuming that patients are found in `patientid`.

Usage

Data %>% n\_patients()

##### nrow\_npatients

Description

Counts distinct patients and number of rows in a dataset assuming that patients are found in `patientid`.

Usage

Data %>% nrow\_npatients()

## ggplots

##### KM\_plot

Description

Depends on library(“ggplot”) and library(“survminer”).

Plots survminer::ggsurvplot with really nice aesthetics.

Usage

fit = survfit(Surv(time, status) ~ CLL\_IPI, data)

KM\_plot(fit)

##### tile\_pairwise\_survdiff

Description

Depends on library(“ggplot”) and library(“survminer”).

Tiles pairwise log-rank tests from survminer::pairwise\_survdiff for visual purposes.

Usage

pairwise\_survdiff(Surv(time, status) ~ CLL\_IPI, data, p.adjust.method = 'none') %>% tile\_pairwise\_survdiff(position = 'LL', palette = c(1,2,3,4), labs = FALSE)