Package ‘dalycare’

October 17, 2023

Title Danish Lymphoid Cancer Research
Priority NA
Version 1.0.0
Date 2024-4-22
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
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Repository ?
Date/Publication: 2024-04-22

DALY CARE
NGC CLOUD

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

Feltkode ændret

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

Feltkode ændret

Usage

```
RKKP_LYFO %>%
  mutate(clean_RKKP_LYFO_snomed(snomed = Reg_WHOHistologikode1))
```

clean_RKKP_CLL

Description

Cleans the dataset RKKP_CLL. Works only for CLL registry version 15 or higher, please see rkkp-documentation

Feltkode ændret

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

Feltkode ændret

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

Feltkode ændret

Usage

```
RKKP_DAMYDA %>%
mutate(clean_ RKKP_ DAMYDA_SNOMED(snomed = Reg_WHOHistologikode1)
```

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

```
load_npu_common()
LAB_clean = load_biochemistry(NPU.GROUP.INFECTION) %>%
  clean_lab_values()
```

Load data

load_dataset

Description

Loads data directly from the DALY-CARE 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_all_variables

Description

Loads all variables of all DALY-CARE datasets: Please see Table S2 and Appendix3

Usage

```
load_all_variables() %>% print_data()
```

load_dalycare_icd10

Description

Loads definitions of DALY-CARE entities based on ICD10 diagnoses into vectors located in your Global Environment in R: Please see Table S7

Usage

```
load_dalycare_icd()
FL = t_dalycare_diagnoses %>%
  filter(diagnosis %in% ICD10.FL)
```

load_blood_culture_SP

Description

Loads blood cultures from SP_AlleProvesvar

Usage

```
BC = load_blood_culture_SP()
```

load_npu_common

Description

Loads a list of vectors containing common NPU codes to 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_dataset('SDS_lab_forsker', c(NPU.B2M, NPU.LYM), 'analysiscode')
SDS_lab_forsker_subset$analysiscode %>% table()
```

load_biochemistry

Description

Loads dataset containing biochemistry from SDS_lab_forsker.
'labs' must contain NPU codes, e.g. from lists from load_npu_common()

Usage

```
LAB_df = load_biochemistry(c(NPU.B2M, NPU.LDH))
BSI_df = load_biochemistry(NPU.BSI) #Blood cultures

#assign data as SDS_lab_forsker_subset into Global Environment
load_biochemistry(labs = NPU.GROUP.MSPIKE, assign = TRUE)
```

go_live

Description

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

Usage

```
go_live()
```

Definitions

filter_first_diagnosis

Description

Defines first DALY-CARE diagnosis from 't_dalycare_diagnoses' as the earliest occurrence, and calculates KM years from table 'patient'.

Usage

```
load_data('t_dalycare_diagnoses', 'patient') #loads all DALY-CARE diagnoses
```

```
PCD = t_dalycare_diagnoses %>%
  filter_first_diagnosis(c('DC90')) #includes any DC90.x

MZL = t_dalycare_diagnoses %>%
 filter_first_diagnosis(c('DC830C', 'DC830D', 'DC884', 'DC884A', 'DC884B', 'DC884C'))

SLL = t_dalycare_diagnoses %>%
 filter_first_diagnosis('DC830', str_contains = FALSE) #matches 'DC830'

RICHTER = t_dalycare_diagnoses %>%
 filter_first_diagnosis(c('DC833', 'DC911'), multiple = 'both') #matches both
```

first_diagnosis

Description

Defines first DALY-CARE diagnosis from view_dalycare_diagnoses as the earliest occurrence, regardless of source/tablename.

Usage

```
load_data('t_dalycare_diagnoses') #loads all DALY-CARE diagnoses
CLL = t_dalycare_diagnoses %>%
  first_diagnosis('DC911')


MZL = t_dalycare_diagnoses %>%
  first_diagnosis(c('DC830C', 'DC830D', 'DC884' , 'DC884A', 'DC884B', 'DC884C'))
```

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

```
load_npu_common()
HGB = load_biochemistry(NPU.HGB) %>% clean_lab_values()
ANEMIA_AE = HGB %>%
  CTCAE_lab() %>%
  select(patientid, ANEMIA.GRADE, everything())

HEMOLYSIS = load_biochemistry(NPU.GROUP.HEMOLYSIS) %>%
  clean_lab_values()
# expect time-lapse for large samples, consider down sampling
HEMOLYSIS_AE = HEMOLYSIS %>%
  CTCAE_lab() %>%
  select(patientid, HEM.GRADE, everything())
```

TX_group

Description

Groups treatment protocols into meaningful groups as class characters.

Usage

```
SP_Behandlingsplaner_del1 %>% TX_group() %>% pull(TX_group)
```

filter_virus

Description

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

Usage

```
SP_Bloddyrkning_del1 %>% filter_virus() %>% select(patientid, type, result)
```

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; please 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) %>% pull(Polypharmacy)
```

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.
exclude_CLL_score = FALSE (default) includes the DC911 score, if present.
include_LC_score = FALSE (default) calculates the LC score only if present.

Usage

```
SDS_t_adm %>% CCI(icd10 = c_adiag) %>% select(patientid, CCI.score, CCI.2011.update)
view_diagnoses_all %>% CCI() %>% select(patientid, CCI.score, CCI.2011.update)
```

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 (A) replaces GCS < 15.

Usage

```
SP_VitaleVaerdier %>% qSOFA() %>% pull(qSOFA)
```

BMI

Description

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

Usage

```
SP_VitaleVaerdier %>% BMI() %>%
  select(patientid, BMI, BSA_DuBois, BSA_Mosteller)
```

BSA

Description

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

Usage

```
SP_VitaleVaerdier %>% BSA() %>%
  select(patientid, BMI, BSA_DuBois, BSA_Mosteller)
```

CLL_IPI

Description

Calculates CLL-IPI risk as class factor.

Usage

```
RKKP_CLL_CLEAN %>% CLL_IPI() %>% pull(CLL.IPI) %>% table()
```

Citation

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

CLL_WONT

Description

Calculates CLL-WONT risk as class factor. Needs ALC (NPU02636) and LDH (NPU19658; NPU19978; NPU19975) from e.g. SDS_lab_forsker. Consider skipping data preparation.

Usage

```
# Data preparation
load_npu_common()
LAB = load_biochemistry (labs = c(NPU.LYM, NPU.LDH)) %>%
  clean_lab_values()
ALC = LAB %>%
  filter(NPU %in% NPU.LYM) %>%
  transmute(patientid, date_ALC = samplingdate, ALC = value2)
LDH = LAB %>%
  filter(NPU %in% NPU.LDH) %>%
  transmute(patientid, date_LDH = samplingdate, LDH = value2)

# Data preparation continued…
RKKP_CLL_WITH_ALC_AND_LDH = RKKP_CLL_CLEAN %>%
  left_join(ALC, by = 'patientid') %>%
  left_join(LDH, by = 'patientid') %>%
  mutate(time_ALC = diff_days(Date_diagnosis, date_ALC),
          time_LDH = diff_days(Date_diagnosis, date_LDH)) %>%
  filter(time_ALC <= 0, time_ALC >= -90,
        time_LDH <= 0, time_LDH >= -90) %>%
  group_by(patientid) %>%
  arrange(patientid, desc(time_ALC), desc(time_LDH)) %>%
  slice(1) %>%
  ungroup()

# CLLWONT calculation
RKKP_CLL_WITH_ALC_AND_LDH %>%  CLL_WONT() %>%
  pull(CLLWONT) %>% table()
```

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 not generalizable.

Usage

```
RKKP_LYFO %>% clean_RKKP_LYFO() %>%
  NCCN_IPI() %>% pull(NCCN_IPI) %>% table()
```

Citation

Zhou et al. *Blood*. Feb 6 2014;123(6):837-42.
Jelicic et al. BJC. 2023;13(1):157.

MIPI

Description

Calculates MIPI risk for Mantle cell lymphoma as class factor

Usage

```
RKKP_LYFO %>% clean_RKKP_LYFO() %>%
  MIPI() %>% pull(MIPI) %>% table()
```

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_RKKP_LYFO() %>%
  IPS() %>% pull(IPS) %>% table()
```

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_RKKP_LYFO() %>%
  rIPSSWM() %>% pull(rIPSSWM) %>% table()
```

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() %>%
  pull(MAYO_20_20_20) %>%
  table()
```

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() %>% pull(R_ISS) %>% table()

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() %>% pull(R2_ISS) %>% table()

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() %>% pull(RW_ISS) %>% table()

House keeping

is_odd

Description

Logical output from numeric values .

Usage

sample(1:10, 5) %>% is_odd()

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

```
CLL = t_dalycare_diagnoses %>%
  filter_first_diagnosis('DC911')
load_dataset('SP_Behandlingsplaner_del1', CLL$patientid, 500)

SP_Behandlingsplaner_del1_subset %>%
  filter_str_detect(protocol_navn, c('OBI', 'VEN'))
```

str_between

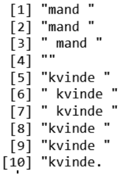
Description

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

Usage

```
load_dataset('SP_Journalnotater_del1', patient$patientid, 500)

SP_Journalnotater_del1_subset %>%
  filter(notat_type=='AOP') %>%
  mutate(sex = str_between(notat_text, 'årig', c('henvist|møder|kendt|indlægges')))%>%
  pull(sex)
```



```
 [1] "mand "
 [2] "mand "
 [3] " mand "
 [4] ""
 [5] "kvinde "
 [6] " kvinde "
 [7] " kvinde "
 [8] "kvinde "
 [9] "kvinde "
[10] "kvinde.
```

censor_med_keep_first

Description

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

Usage

```
censor_med_keep_first(date, 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 %>% censor_med_keep_first(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

```
patient %>% n_patients()
```

nrow_npatients

Description

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

Usage

```
patient %>% nrow_npatients()
```

slice_closest_value

Description

Slices the absolute closest value to a baseline date (date_baseline) within time interval (interval_days, c(-90, 0) default). Useful when adding lab values to wide format data.

Usage

```
load_dataset('SP_AlleProvesvar',  NPU.HGB, 'component')
load_dataset('patient')

patient %>%
  left_join(SP_AlleProvesvar_subset %>%
  transmute(  patientid,
              date_lab = as_date(specimn_taken_time),
              HGB =  as.numeric(ord_value))) %>%
  slice_closest_value(date_baseline = date_diagnosis, date_value = date_lab)
```

ggplots

KM_plot

Description

Depends on library('ggplot') and library('survminer').
Plots survminer::ggsurvplot with really nice aesthetics.

Usage

```
CLL = t_dalycare_diagnoses %>%
filter_first_diagnosis('DC911’)

fit = survfit(Surv(time_dx_death, status) ~ sex, data = CLL)
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

```
CLL = t_dalycare_diagnoses %>%
filter_first_diagnosis('DC911') %>%
left_join(RKKP_CLL_CLEAN, by = 'patientid')

pairwise_survdiff(Surv(time_dx_death, status) ~ CLL.IPI, data = CLL, p.adjust.method =
'none') %>% tile_pairwise_survdiff(position = 'LL',  palette = c(1,2,3,4), labs = FALSE)
```