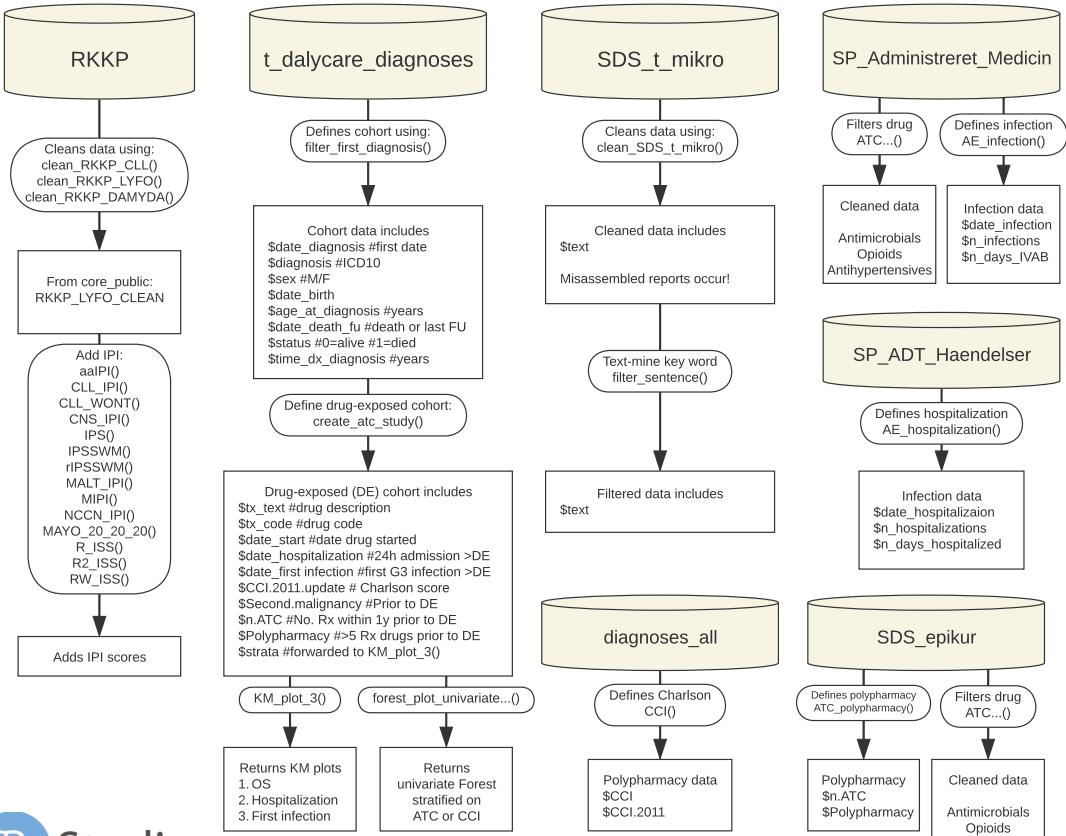




# dalyCare :: CHEAT SHEET

dalyCare functions work with pipes (%>%) similar to dplyr



## Examples

```

source('~/ngc/projects2/dalyca_r/clean_r/load_dalyCare_package.R') #load dalyCare package
help_info() # Examples of how to load dataset(s)

#RKKP (CLL, LYFO, DaMyDa)
load_dataset(RKKP_LYFO) #load dataspecifically or
load_dataset(RKKP_DATASETS) # generally to load all three

LYFO_clean = RKKP_LYFO %>% clean_RKKP_LYFO() #clean LYFO
KM_plot(survfit(Surv(time_to_death/365, dead) ~ sex, LYFO_clean %>% filter(subtype == "DLBL1")) )#OS
MCL = RKKP_LYFO %>% clean_RKKP_LYFO() %>% MIPI() #calculate MIPI risk
KM_plot(survfit(Surv(time_to_death/365, dead) ~ MIPI, MCL)) #OS

#t_dalycare_diagnoses
load_dataset(c('patient', 't_dalycare_diagnoses')) #Loads base tables
load_ATC_icd10() # Loads ICD10 diagnoses as a set of vectors with prefix "ICD10."
CLL = t_dalycare_diagnoses %>% filter_first_diagnosis(ICD10.CL1)
FL = t_dalycare_diagnoses %>%
  filter(tablename == "t_pato") %>% #filter biopsy-verified
  filter_first_diagnosis(ICD10.FL)
KM_plot(survfit(Surv(time_dx_death, status) ~ sex, CLL)) #OS

#create_antineoplastic_study
MM = t_dalycare_diagnoses %>%
  filter_first_diagnosis(ICD10.MM) %>%
  filter(age_at_diagnosis < 50) %>%
  create_antineoplastic_study() #from date_diagnosis
MM %>%
  mutate(strata = sex) %>%
  KM_plot(3) # creates OS, hospitalization, and first infection plots
load_ATC_antineoplastics() # Loads ATC codes as a set of vectors with prefix "ATC."
CLL = t_dalycare_diagnoses %>%
  filter_first_diagnosis(ICD10.CLL) %>%
  create_antineoplastic_study(ATC.venetoclax, ATC.ibritinib) #Calculations/baseline from drug-exposure
CLL %>% forest_plot_univariate_infection() #Plots univariate Forest plot default ATC 3rd level
CLL %>% forest_plot_univariate_infection(CCI) #Plots univariate Forest plot stratified on CCI category

CLL = t_dalycare_diagnoses %>%
  filter_first_diagnosis(ICD10.CLL) %>%
  create_antineoplastic_study(ATC.venetoclax, ATC.ibritinib) #Double drug-exposure, whichever came last
CLL %>% forest_plot_univariate_OS()

#SDS_t_mikro
load_dataset(SDS_t_mikro)
SDS_t_mikro %>%
  clean_SDS_t_mikro() %>%
  sample_frac(0.001) %>% #For training purposes
  filter_sentence(text, c('amyloid', 'congo')) #pattern1 or pattern2 #expect latency

# Evaluate bias
LYFO_clean %>% nrow_npatients() #Evaluate no. row and no. patients
LYFO_clean$subtype %>% table() # Evaluate diagnosis
LYFO_clean$time_to_death %>% summary() # Evaluate negative follow-up time
CLL$diagnosis %>% table() # Evaluate diagnosis
LYFO_clean %>% ggplot() + geom_histogram(aes(date_diagnosis)) #Evaluate time bias
  
```