QRDF \_ Changes that should be done:

EASY:

* Add a filters called LINE OF TREATMENT with levels bionaive (line=1), second line (line=2), other lines (line>=3)
* Modify the comparisons in patients and visits to filters
* Add filters (region, line, gender and age) to the biologics graph
* Modify age: instead of having the list of categories, we have a slider (see VAP) (but we keep 5 categories for the big table)
* Add number of patients in the survival table
* Visualize months instead of days in the KM

NOT- EASY:

* When region is selected, we cannot show n<5:
  + Esempio: plot\_sum\_ter$N<-ifelse(unit$N<5,NA,unit$N) fatto solo per patients, da fare per tutti gli altri (besokasdata, bio)
* Group by molecules (CI DEVO PENSARE…)
* BIG TABLES: group by diagnosis, line, gender and age (5 categories)
* Add the 5 months visit (defined in the interval 90-240 days)
* Add concomitant treatments (solo su disease characteristics):

MTX=**0**;

nonMTX=**0**;

/\* MTX and other DMARD use \*/

array dmard dmard1-dmard4;

do over dmard;

if dmard ^= '' then do;

if dmard = 'Methotrexate' then MTX=**1**;

else nonMTX = **1**;

end;

end;

/\* Any csDMARD, will be used to split cohorts \*/

Conc\_DMARD = (sum(MTX, nonMTX)>**0**);

nsaid2=**1**;

if nsaid ='' then nsaid2=**0**;

rename nsaid2 = nsaid;

/\* Oral steroids \*/

steroids=**0**;

if kortison ^='' then steroids=**1**;

* Add zoom in the survival table

MUST BE WRITTEN

Biologics (bDMARDs) and small-molecules (tsDMARDs) are included in this work as the same group, and called biologics.