Project tutoré 2 - Murat Simsek et Yuquan Dai

R pour la question 1

```r
# Importer les données nécessaires
dm1 <- read.csv2("dm1.csv", header = TRUE, sep = ",")
dm2 <- read.csv2("dm2.csv", header = TRUE, sep = ",")
ie1 <- read.csv2("ie1.csv", header = TRUE, sep = ",")
ie2 <- read.csv2("ie2.csv", header = TRUE, sep = ",")
lb1 <- read.csv2("lb1.csv", header = TRUE, sep = ",")
lb2 <- read.csv2("lb2.csv", header = TRUE, sep = ",")

# Jointure les données
alldm <- full_join(dm1,dm2)

## Joining, by = c("STUDYID", "DOMAIN", "USUBJID", "EPOCH", "VISIT", "V
ISITNUM",
## "RFSTDTC", "RFENDTC", "SITEID", "BRTHDTC", "AGE", "AGEU", "SEX", "RA
CE",
## "ETHNIC", "ARMCD", "ARM", "COUNTRY", "DMDTC", "DMDY")

allie <- full_join(ie1,ie2)

## Joining, by = c("STUDYID", "DOMAIN", "USUBJID", "EPOCH", "IESEQ", "I
ETESTCD",
## "IETEST", "IECAT", "IEORRES", "IESTRESC", "VISIT", "VISITNUM", "IEDT
C", "IEDY")

alllb <- full_join(lb1,lb2)

## Joining, by = c("STUDYID", "DOMAIN", "USUBJID", "EPOCH", "LBSEQ", "L
BTESTCD",
## "LBTEST", "LBCAT", "LBORRES", "LBORRESU", "LBORNRLO", "LBORNRHI", "L
BSTRESC",
## "LBSTRESN", "LBSTRESU", "LBSTNRLO", "LBSTNRHI", "LBNRIND", "LBSTAT",
## "LBREASND", "LBSPEC", "LBMETHOD", "LBBLFL", "VISIT", "VISITNUM", "LB
DTC",
## "LBDY")

# On a choisit dm pour travailler
n_distinct(alldm$USUBJID)

## [1] 411

# Faire une exclusion spéciale
allusrdm <- alldm$USUBJID[!(alldm$USUBJID %in% allie$USUBJID[allie$IECA
T=="EXCLUSION"])]
summary(allusrdm)
```

```
##     Length     Class      Mode
##        369 character character
```

```r
# Séparer BUPRENORPHINE/NALOXONE et CLONIDINE
allusrBN <- filter(alldm,
                   alldm$ARM=="BUPRENORPHINE/NALOXONE" &
                   alldm$USUBJID %in% allusrdm)
allusrC <- filter(alldm,
                   alldm$ARM=="CLONIDINE" &
                   alldm$USUBJID %in% allusrdm)
n_distinct(allusrBN$USUBJID)
```

```
## [1] 233
```

```r
n_distinct(allusrC$USUBJID)
```
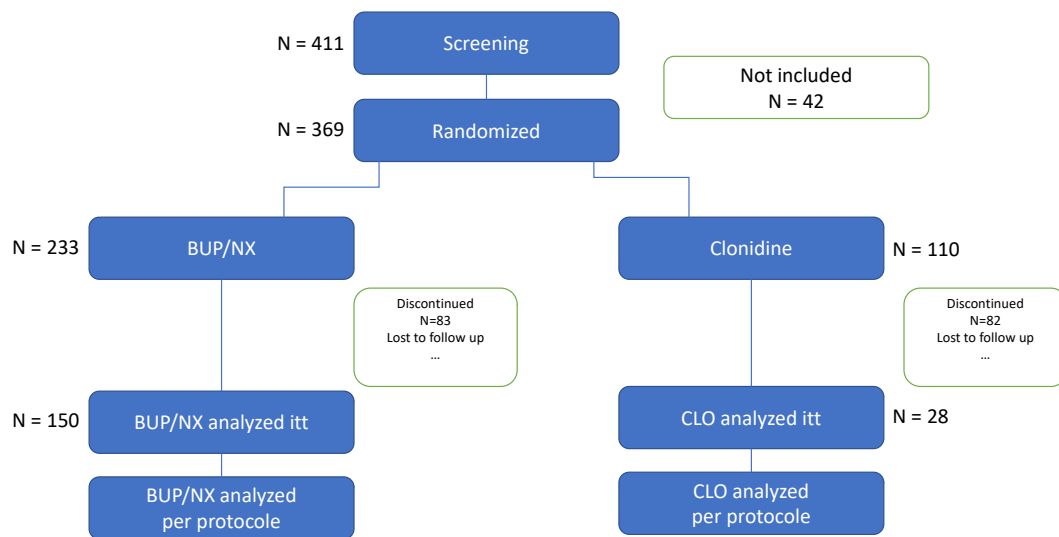
```
## [1] 110
```

```r
# On considérera les patients qui ont des résultats au tests urinaires
à J13 ou J14
usrBNfin <- filter(alllb,
                   (alllb$VISITNUM==13 | alllb$VISITNUM==14)&
                     (alllb$LBSTAT!="NOT DONE")&
                     (alllb$USUBJID %in% allusrBN$USUBJID))
usrCfin <- filter(alllb,
                   (alllb$VISITNUM==13 | alllb$VISITNUM==14)&
                     (alllb$LBSTAT!="NOT DONE")&
                     (alllb$USUBJID %in% allusrC$USUBJID))
n_distinct(usrBNfin$USUBJID)
```

```
## [1] 150
```

```r
n_distinct(usrCfin$USUBJID)
```

```
## [1] 28
```

N = 411	Screening
	Not included N = 42
N = 369	Randomized
N = 233	BUP/NX
	Discontinued N=83 Lost to follow up …
N = 150	BUP/NX analyzed itt
	BUP/NX analyzed per protocole
	Clonidine
	Discontinued N=82 Lost to follow up …
	CLO analyzed itt
	CLO analyzed per protocole

N = 110 (Clonidine)
N = 28 (CLO analyzed itt)

Python pour la question 2