

Opioids

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```
{r setup, include=FALSE} knitr::opts_chunk$set(echo = TRUE)
```

all the forms we use

```
{r cars} #demographics dem<-read.csv("T_FRDEM.csv") #Study Termination (TERM) term<-read.csv("T_FRTERM.csv")
sum(term$TER001==1) #Randomization (RAN)--Treatment group ran <- read.csv("T_FRRAN.csv")
#checklist summary dsm <- read.csv("T_FRDSM.csv") #alchole/urine udsab<-read.csv("T_FRUDSAB.csv")
```

all the subjects that actually completed the study

```
#pick them out
patdeid<-term[term$TER001==1, "patdeid"]
patdeid<-data.frame(patdeid)
dim(patdeid)
#gender
patdeid$gender <- dem[patdeid$patdeid, "DEM002"]
table(patdeid$gender)#1-male, 2-female
#treatment group
n<-nrow(patdeid)
n
patdeid$group <- rep(NA, n)
for(i in 1:n){
  patdeid$group[i]<-ran[ran$patdeid==patdeid$patdeid[i], "INF004"]
}
table(patdeid$group)#1-Buprenorphine/Naloxone, 2-Methadone
```

Dependence checklist

```
patdeid$Opiates <- rep(NA, n)
patdeid$Alcohol <- rep(NA, n)
patdeid$Amphetamines <- rep(NA, n)
patdeid$Cannabis <- rep(NA, n)
patdeid$Cocaine <- rep(NA, n)
patdeid$Sedatives <- rep(NA, n)
for(i in 1:n){
  patdeid$Opiates[i]<-dsm[dsm$patdeid==patdeid$patdeid[i], "DSMOPI"]
  patdeid$Alcohol[i]<-dsm[dsm$patdeid==patdeid$patdeid[i], "DSMAL"]
  patdeid$Amphetamines[i]<-dsm[dsm$patdeid==patdeid$patdeid[i], "DSMAM"]
  patdeid$Cannabis[i]<-dsm[dsm$patdeid==patdeid$patdeid[i], "DSMCA"]
  patdeid$Cocaine[i]<-dsm[dsm$patdeid==patdeid$patdeid[i], "DSMCO"]
  patdeid$Sedatives[i]<-dsm[dsm$patdeid==patdeid$patdeid[i], "DSMSE"]
}#1-Dependence, 2-Abuse 3-No diagnosis
table(patdeid$Amphetamines)
table(patdeid$Opiates)
```

```

table(patdeid$Alcohol)
table(patdeid$Cannabis)
table(patdeid$Cocaine)
table(patdeid$Sedatives)

```

Medical history

```

mdh <- read.csv("T_FRMDH.csv")
dim(mdh)
mdh <- data.frame(mdh$patdeid, mdh$MDH001, mdh$MDH002, mdh$MDH003, mdh$MDH004, mdh$MDH005,
                  mdh$MDH006, mdh$MDH007, mdh$MDH008,mdh$MDH009,mdh$MDH010,
                  mdh$MDH011A,mdh$MDH011B, mdh$MDH012, mdh$MDH013,mdh$MDH014,
                  mdh$MDH015, mdh$MDH016, mdh$MDH017)
dim(mdh)
mdh2<-mdh[1,]
for(i in 2:n){
  mdh2[i,]<-mdh[mdh$mdh.patdeid==patdeid$patdeid[i],]
}
dim(mdh2)
mdh2<-mdh2[,-1]
patdeid<-cbind(patdeid,mdh2)
table(patdeid$mdh.MDH001)
table(patdeid$mdh.MDH002)
table(patdeid$mdh.MDH003)
table(patdeid$mdh.MDH004)
table(patdeid$mdh.MDH005)
table(patdeid$mdh.MDH006)
table(patdeid$mdh.MDH007)
table(patdeid$mdh.MDH008)
table(patdeid$mdh.MDH009)
table(patdeid$mdh.MDH010)
table(patdeid$mdh.MDH011A)
table(patdeid$mdh.MDH011B)
table(patdeid$mdh.MDH012)
table(patdeid$mdh.MDH013)
table(patdeid$mdh.MDH014)
table(patdeid$mdh.MDH015)
table(patdeid$mdh.MDH016)
table(patdeid$mdh.MDH017)
dim(patdeid)

```