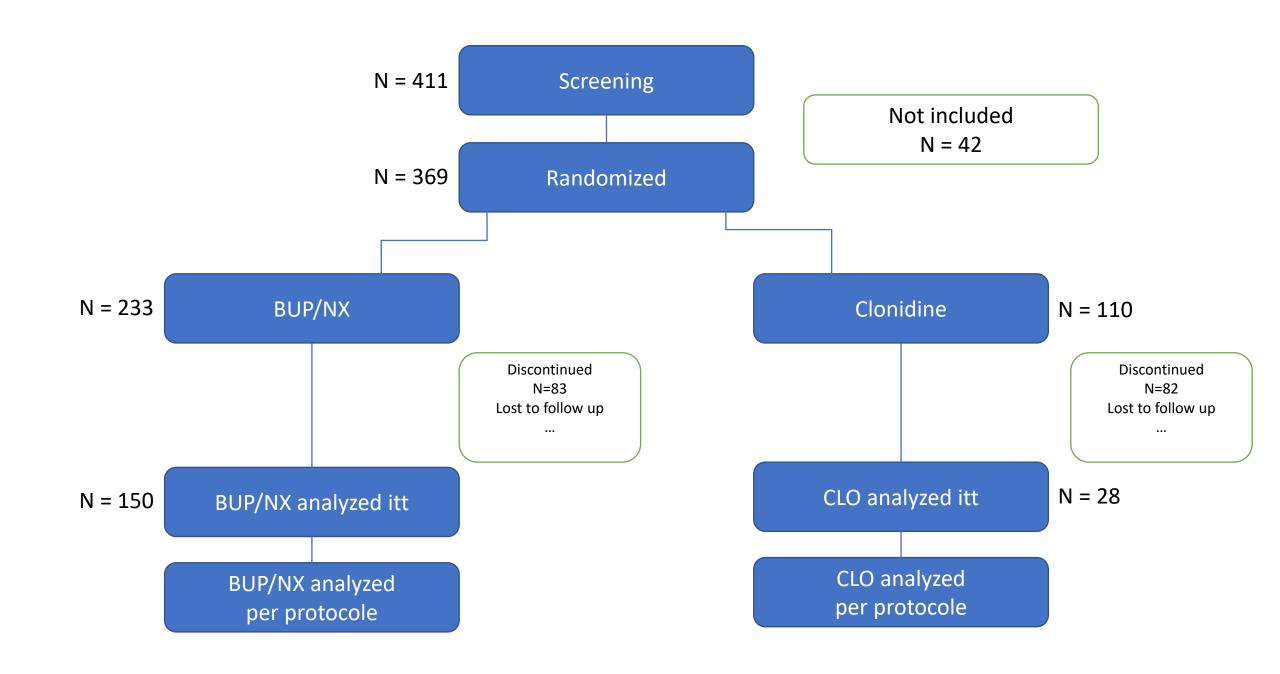
Project tutoré 2 - Murat Simsek et Yuquan Dai

R pour la question 1 et Python pour la question 2

```
# Importer les données nécessaires
dm1 <- read.csv2("dm1.csv", header = TRUE, sep = ",")</pre>
dm2 <- read.csv2("dm2.csv", header = TRUE, sep = ",")</pre>
ie1 <- read.csv2("ie1.csv", header = TRUE, sep = ",")</pre>
ie2 <- read.csv2("ie2.csv", header = TRUE, sep = ",")</pre>
lb1 <- read.csv2("lb1.csv", header = TRUE, sep = ",")</pre>
1b2 <- read.csv2("lb2.csv", header = TRUE, sep = ",")</pre>
# Jointure les données
alldm <- full_join(dm1,dm2)</pre>
## Joining, by = c("STUDYID", "DOMAIN", "USUBJID", "EPOCH", "VISIT", "VISITNUM",
## "RFSTDTC", "RFENDTC", "SITEID", "BRTHDTC", "AGE", "AGEU", "SEX", "RACE",
## "ETHNIC", "ARMCD", "ARM", "COUNTRY", "DMDTC", "DMDY")
allie <- full_join(ie1,ie2)
## Joining, by = c("STUDYID", "DOMAIN", "USUBJID", "EPOCH", "IESEQ", "IETESTCD",
## "IETEST", "IECAT", "IEORRES", "IESTRESC", "VISIT", "VISITNUM", "IEDTC", "IEDY")
alllb <- full_join(lb1,lb2)
## Joining, by = c("STUDYID", "DOMAIN", "USUBJID", "EPOCH", "LBSEQ", "LBTESTCD",
## "LBTEST", "LBCAT", "LBORRES", "LBORRESU", "LBORNRLO", "LBORNRHI", "LBSTRESC",
## "LBSTRESN", "LBSTRESU", "LBSTNRLO", "LBSTNRHI", "LBNRIND", "LBSTAT",
## "LBREASND", "LBSPEC", "LBMETHOD", "LBBLFL", "VISIT", "VISITNUM", "LBDTC",
## "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$IECAT=="EXCLUSION"])]
summary(allusrdm)
##
      Length
                 Class
##
         369 character character
```

```
# Séparer BUPRENORPHINE/NALOXONE et CLONIDINE
allusrBN <- filter(alldm,
                   alldm$ARM=="BUPRENORPHINE/NALOXONE" &
                   alldm$USUBJID %in% allusrdm)
allusrC <- filter(alldm,</pre>
                  alldm$ARM=="CLONIDINE" &
                  alldm$USUBJID %in% allusrdm)
n_distinct(allusrBN$USUBJID)
## [1] 233
n_distinct(allusrC$USUBJID)
## [1] 110
\# On considérera les patients qui ont des résultats au tests urinaires à J13 ou J14
usrBNfin <- filter(alllb,
                   (alllb$VISITNUM==13 | alllb$VISITNUM==14)&
                     (all1b$LBSTAT!="NOT DONE")&
                     (alllb$USUBJID %in% allusrBN$USUBJID))
usrCfin <- filter(all1b,
                  (alllb$VISITNUM==13 | alllb$VISITNUM==14)&
                    (alllb$LBSTAT!="NOT DONE")&
                    (alllb$USUBJID %in% allusrC$USUBJID))
n_distinct(usrBNfin$USUBJID)
## [1] 150
n_distinct(usrCfin$USUBJID)
```

[1] 28



In []: ## PROJET TUTORE TABLEAU DES VARIABLES ## In [115... import mitosheet from mitosheet import * import pandas as pd In [116... # Subject Characteristics Dataset(SC) df sc 1 = pd.read csv('C:/Users/Casper/Desktop/Master1-Cours/Projet tutoré/ascii 1/sc.csv') df sc 2 = pd.read csv('C:/Users/Casper/Desktop/Master1-Cours/Projet tutoré/ascii 2/sc.csv') $df_sc = pd.concat([df_sc_1, df_sc_2])$ # Pivoted df sc unused columns = df sc.columns.difference(set(['USUBJID']).union(set(['SCTEST'])).union(set({'SCORRES'}))) tmp df = df sc.drop(unused columns, axis=1) pivot table = tmp df.pivot table(index=['USUBJID'], columns=['SCTEST'], values=['SCORRES'], aggfunc={'SCORRES': ['sum']} # Flatten the column headers pivot table.columns = [make valid header(col) for col in pivot table.columns.values] # Reset the column name and the indexes df sc = pivot table.rename axis(None, axis=1).reset index() # Exposure Dataset(EX) df_ex_1 = pd.read_csv('C:/Users/Casper/Desktop/Master1-Cours/Projet tutoré/ascii 1/ex.csv') df ex 2 = pd.read csv('C:/Users/Casper/Desktop/Masterl-Cours/Projet tutoré/ascii 2/ex.csv') $df_ex = pd.concat([df_ex_1, df_ex_2])$ df ex = df ex[['USUBJID','EXTRT']] # Selecting Extrt for Clodine and Burp df ex.drop duplicates(subset ="USUBJID", keep = 'first', inplace = True) # Demographics Dataset(DM) df dm 1 = pd.read csv('C:/Users/Casper/Desktop/Master1-Cours/Projet tutoré/ascii 1/dm.csv') df dm 2 = pd.read csv('C:/Users/Casper/Desktop/Master1-Cours/Projet tutoré/ascii 2/dm.csv') df dm = pd.concat([df dm 1,df dm 2]) df dm = df dm[['USUBJID','AGE','SEX','ARM']] df dm.drop duplicates(subset ="USUBJID", keep = 'first', inplace = True) df dm['AGE'] = df dm['AGE'].str[:2] # age change # Vital Signs Dataset (VS) df vs 1 = pd.read csv('C:/Users/Casper/Desktop/Master1-Cours/Projet tutoré/ascii 1/vs.csv') df vs 2 = pd.read csv('C:/Users/Casper/Desktop/Masterl-Cours/Projet tutoré/ascii 2/vs.csv') df vs = pd.concat([df vs 1,df vs 2]) # Filtered VISIT in vs csv df vs = df vs[df vs['VISIT'].str.contains('BASE', na=False)] df_vs = df_vs.reset_index(drop=True) # Pivoted vs csv into df4 unused_columns = df_vs.columns.difference(set(['USUBJID']).union(set(['VSTEST'])).union(set({'VSORRES'}))) tmp df = df vs.drop(unused columns, axis=1) pivot_table = tmp_df.pivot_table(index=['USUBJID'], columns=['VSTEST'], values=['VSORRES'], aggfunc={'VSORRES': ['sum']}) # Flatten the column headers pivot table.columns = [make valid header(col) for col in pivot table.columns.values] # Reset the column name and the indexes df vs = pivot table.rename axis(None, axis=1).reset index() #Laboratory Tests Dataset (LB) df lb 1 = pd.read csv(r'C:\Users\Casper\Desktop\Masterl-Cours\Projet tutoré\ascii 1\lb.csv') df lb 2 = pd.read csv(r'C:\Users\Casper\Desktop\Master1-Cours\Projet tutoré\ascii 2\lb.csv') $df_lb = pd.concat([df_lb_1, df_lb_2])$ # Filtered VISIT in lb csv df lb = df lb[df lb['VISIT'].str.contains('BASELINE', na=False)] df lb = df lb.reset index(drop=True) # Pivoted lb csv into df7 unused columns = df lb.columns.difference(set(['USUBJID']).union(set(['LBTEST'])).union(set({'LBORRES'}))) tmp df = df lb.drop(unused columns, axis=1) pivot_table = tmp_df.pivot table(index=['USUBJID'], columns=['LBTEST'], values=['LBORRES'], aggfunc={'LBORRES': ['sum']} # Flatten the column headers pivot_table.columns = [make_valid_header(col) for col in pivot_table.columns.values] # Reset the column name and the indexes df lb = pivot table.rename axis(None, axis=1).reset index() In [53]: df lb.columns Index(['USUBJID', 'LBORRES sum AMPHETAMINES', 'LBORRES sum BARBITURATES', Out[53]: 'LBORRES_sum_BENZODIAZEPINES', 'LBORRES_sum_COCAINE', 'LBORRES_sum_CREATININE', 'LBORRES_sum_METHADONE', 'LBORRES_sum_METHAMPHETAMINE', 'LBORRES_sum_MORPHINE', 'LBORRES_sum_NONE', 'LBORRES_sum_OPIATE', 'LBORRES_sum_PCP', 'LBORRES_sum_TCA', 'LBORRES_sum_THC'], dtype='object') In [54]: df_lb.drop(['LBORRES_sum_AMPHETAMINES', 'LBORRES_sum_BARBITURATES', 'LBORRES_sum_BENZODIAZEPINES', 'LBORRES sum COCAINE', 'LBORRES_sum_CREATININE', 'LBORRES_sum_METHAMPHETAMINE', 'LBORRES_sum_NONE', 'LBORRES sum PCP', 'LBORRES_sum_TCA', 'LBORRES_sum_THC'], axis = 1,inplace=True) In [55]: # Merge Data df = df sc.merge(df ex,on= 'USUBJID', how= 'right') df = df.merge(df dm,on= 'USUBJID') df = df.merge(df vs,on= 'USUBJID',how= 'left') df = df.merge(df lb,on= 'USUBJID',how= 'left') USUBJID SCORRES_sum_EDUCATION_COMPLETED SCORRES_sum_MARITAL_STATUS SCORRES_sum_MET_ALL_INCLUSION_NO_EXCLUSION_CR Out[55]: 0 01_000579 DIVORCED 14 γ **1** 01_001362 13 **NEVER MARRIED** 2 01_001490 **NEVER MARRIED** 14 **3** 01_002199 13 **NEVER MARRIED** 4 01_002844 **NEVER MARRIED** 11 **338** 02_098074 12 DIVORCED **339** 02_098425 12 DIVORCED **340** 02_099053 11 **NEVER MARRIED 341** 02_099368 **NEVER MARRIED** 11 **342** 02_099926 13 **NEVER MARRIED** 343 rows × 20 columns In [56]: df.columns = ['ID', 'EDUCATION COMPLETED', 'MARITAL STATUS', 'MET ALL INCLUSION NO EXCLUSION CRIT ', 'EMPLOYMENT PATTERN PAST 3 YEARS', 'EMPLOYMENT PATTERN PAST 30 DAYS', 'EXTRT', 'AGE', 'SEX', 'ARM', 'DIASTOLIC BLOOD PRESSURE', 'HEIGHT', 'PULSE', 'RESPIRATIONS', 'SYSTOLIC BLOOD PRESSURE', 'TEMPERATURE', 'WEIGHT', 'METHADONE', 'MORPHINE', 'OPIATE'] In [57]: Out[57]: ID EDUCATION_COMPLETED MARITAL_STATUS MET_ALL_INCLUSION_NO_EXCLUSION_CRIT_ EMPLOYMENT_PATTERN_PAST_3_YEARS 0 01 000579 DIVORCED YES FULL TIME (35+ HRS/WK) 14 **1** 01_001362 13 **NEVER MARRIED** YES UNEMPLOYED 2 01_001490 **NEVER MARRIED** YES PART TIME (IRREGULAR DAYWORK) 14 **3** 01_002199 **NEVER MARRIED** YES PART TIME (REGULAR HOURS) 13 **STUDENT** 4 01_002844 11 **NEVER MARRIED** YES **338** 02_098074 12 DIVORCED YES UNEMPLOYED **339** 02_098425 DIVORCED YES FULL TIME (35+ HRS/WK) **NEVER MARRIED 340** 02_099053 11 YES PART TIME (IRREGULAR DAYWORK) **341** 02_099368 11 **NEVER MARRIED** YES PART TIME (IRREGULAR DAYWORK) **342** 02_099926 13 **NEVER MARRIED** YES FULL TIME (35+ HRS/WK) 343 rows × 20 columns In [59]: df.info() <class 'pandas.core.frame.DataFrame'> Int64Index: 343 entries, 0 to 342 Data columns (total 20 columns): # Column Non-Null Count Dtype _____ ID 343 non-null object
EDUCATION_COMPLETED 343 non-null object
MARITAL_STATUS 343 non-null object
MET_ALL_INCLUSION_NO_EXCLUSION_CRIT 341 non-null object
EMPLOYMENT PATTERN PAST 3 YEARS 342 non-null object 0 ID EMPLOYMENT PATTERN_PAST_3_YEARS 342 non-null object object EMPLOYMENT PATTERN PAST 30 DAYS 343 non-null object EXTRT 343 non-null object AGE 343 non-null object SEX 343 non-null object ARM 343 non-null 10 DIASTOLIC BLOOD PRESSURE 340 non-null float64 11 HEIGHT 337 non-null float64 12 PULSE 342 non-null float64 RESPIRATIONS 335 non-null float64 float64 14 SYSTOLIC BLOOD PRESSURE 340 non-null 15 TEMPERATURE 335 non-null float64 16 WEIGHT 338 non-null float64 object 17 METHADONE 343 non-null 18 MORPHINE 342 non-null object 19 OPIATE 286 non-null object dtypes: float64(7), object(13) memory usage: 56.3+ KB In [60]: import matplotlib.pyplot as plt import seaborn as sns ax = sns.countplot(data = df, x = 'ARM')ax.set xticklabels(ax.get xticklabels(), rotation=40, ha="right") ax.bar label(ax.containers[0]) sns.set(rc={'figure.figsize':(12,9)}) plt.tight_layout() plt.show() 233 200 150 ∞unt 100 50 BUPPENORPHINEMALOXONE 0 SCREENFAILURE CLONIDINE ARM In [61]: df.columns Index(['ID', 'EDUCATION COMPLETED', 'MARITAL STATUS', Out[61]: 'MET ALL INCLUSION NO EXCLUSION CRIT ', 'EMPLOYMENT PATTERN PAST 3 YEARS', 'EMPLOYMENT PATTERN PAST 30 DAYS', 'EXTRT', 'AGE', 'SEX', 'ARM', 'DIASTOLIC BLOOD PRESSURE', 'HEIGHT', 'PULSE', 'RESPIRATIONS', 'SYSTOLIC BLOOD PRESSURE', 'TEMPERATURE', 'WEIGHT', 'METHADONE', 'MORPHINE', 'OPIATE'], dtype='object') In [90]: df['AGE'].replace(' ','Nan',inplace=True) # adjust age to be float and change ' ' to na In [92]: df['AGE'] = df['AGE'].astype(float) In [97]: # Change Weight and Height to BMI # Formula BMI = weight (lb) / [height (in)] 2×703 df2 = df[df['HEIGHT'].notna()] df2 = df[df['WEIGHT'].notna()] df2.drop(308,inplace = True) df['BMI'] = df2['WEIGHT'].astype(int) / (df2['HEIGHT'].astype(int)**2) * 703C:\Users\Casper\anaconda3\lib\site-packages\pandas\core\frame.py:4906: SettingWithCopyWarning: A value is trying to be set on a copy of a slice from a DataFrame See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#ret urning-a-view-versus-a-copy In [98]: df Out[98]: ID EDUCATION_COMPLETED MARITAL_STATUS MET_ALL_INCLUSION_NO_EXCLUSION_CRIT_ EMPLOYMENT_PATTERN_PAST_3_YEARS 0 01_000579 14 DIVORCED YES FULL TIME (35+ HRS/WK) 1 01_001362 **NEVER MARRIED** YES UNEMPLOYED 13 2 01_001490 PART TIME (IRREGULAR DAYWORK) **NEVER MARRIED** YES 14 **3** 01_002199 13 **NEVER MARRIED** YES PART TIME (REGULAR HOURS) 4 01_002844 **NEVER MARRIED** 11 YES **STUDENT 338** 02_098074 12 DIVORCED YES UNEMPLOYED **339** 02_098425 DIVORCED 12 YES FULL TIME (35+ HRS/WK) **340** 02_099053 **NEVER MARRIED** YES PART TIME (IRREGULAR DAYWORK) 11 **NEVER MARRIED** PART TIME (IRREGULAR DAYWORK) **341** 02_099368 11 YES **342** 02_099926 **NEVER MARRIED** YES FULL TIME (35+ HRS/WK) 13 343 rows × 21 columns In [99]: df.describe() PULSE RESPIRATIONS SYSTOLIC_BLOOD_PRESSURE TEMPERATURE AGE DIASTOLIC_BLOOD_PRESSURE WFIGH Out[99]: HEIGHT **count** 340.000000 340.000000 337.000000 342.000000 340.000000 335.000000 338.00000 335.000000 103.068955 166.66568 mean 37.438235 83.720588 70.041543 155.254386 17.131343 126.485294 40.081571 32.364079 10.149284 35.497963 32.514346 51.138584 std 3.619732 35.71953 18.000000 64.000000 1.000000 94.000000 95.000000 100.00000 min 50.000000 53.000000 25% 29.000000 66.000000 136.000000 16.000000 110.000000 98.000000 140.00000 70.000000 50% 39.000000 68.000000 152.000000 16.000000 120.000000 98.400000 162.00000 79.000000 45.000000 98.900000 188.00000 **75**% 88.000000 71.000000 169.500000 18.000000 132.000000 65.000000 701.000000 715.000000 337.000000 36.000000 430.000000 999.900000 299.00000 max In [102... from tableone import TableOne, load dataset In [103... df.columns index(['ID', 'EDUCATION COMPLETED', 'MARITAL STATUS', Out[103... 'MET_ALL_INCLUSION__NO_EXCLUSION_CRIT_', 'EMPLOYMENT PATTERN PAST 3 YEARS', 'EMPLOYMENT PATTERN PAST 30 DAYS', 'EXTRT', 'AGE', 'SEX', 'ARM', 'DIASTOLIC_BLOOD_PRESSURE', 'HEIGHT', 'PULSE', 'RESPIRATIONS', 'SYSTOLIC_BLOOD_PRESSURE', 'TEMPERATURE', 'WEIGHT', 'METHADONE', 'MORPHINE', 'OPIATE', 'BMI'], dtype='object') In [114.. columns = ['EDUCATION COMPLETED', 'MARITAL STATUS', 'EMPLOYMENT_PATTERN_PAST_3_YEARS', 'EMPLOYMENT_PATTERN_PAST_30_DAYS','AGE', 'ARM', 'DIASTOLIC_BLOOD_PRES 'PULSE', 'RESPIRATIONS', 'SYSTOLIC_BLOOD_PRESSURE', 'TEMPERATURE','BMI','METHADONE', 'MORPHINE', 'OPIATE categorical = ['EDUCATION_COMPLETED', 'MARITAL_STATUS', 'EMPLOYMENT_PATTERN_PAST_3_YEARS', 'EMPLOYMENT_PATTERN_F groupby = 'ARM' mytable = TableOne(df, columns=columns, categorical = categorical, groupby=groupby) mytable Out[114... **Grouped by ARM** SCREEN Missing Overall BUPRENORPHINE/NALOXONE CLONIDINE **FAILURE** n 343 233 107 3 **EDUCATION_COMPLETED, n (%)** 10 0 21 (6.1) 14 (6.0) 6 (5.6) 1 (33.3) 37 11 28 (12.0) 9 (8.4) (10.8)132 12 91 (39.1) 39 (36.4) 2 (66.7) (38.5)13 34 (9.9) 27 (11.6) 7 (6.5) 50 14 28 (12.0) 22 (20.6) (14.6)15 19 (5.5) 16 (6.9) 3 (2.8) 21 (6.1) 13 (5.6) 8 (7.5) 16 17 3 (0.9) 3 (1.3) 18 5 (1.5) 2 (0.9) 3 (2.8) 19 1 (0.3) 1 (0.4) 20 3 (0.9) 1 (0.4) 2 (1.9) 7 2 (0.6) 2 (0.9) 8 6 (1.7) 3 (1.3) 3 (2.8) 9 9 (2.6) 4 (1.7) 5 (4.7) MARITAL_STATUS, n (%) **DIVORCED** 55 0 38 (16.3) 17 (15.9) (16.0)61 **LEGALLY MARRIED** 47 (20.2) 14 (13.1) (17.8)**LIVING WITH** 33 (9.6) 20 (8.6) 12 (11.2) 1 (33.3) PARTNER/COHABITATING 160 **NEVER MARRIED** 109 (46.8) 49 (45.8) 2 (66.7) (46.6)**SEPARATED** 26 (7.6) 14 (6.0) 12 (11.2) **WIDOWED** 8 (2.3) 5 (2.1) 3 (2.8) EMPLOYMENT_PATTERN_PAST_3_YEARS, **FULL TIME (35+ HRS/WK)** 189 127 (54.5) 61 (57.5) 1 (33.3) (55.3)n (%) **HOMEMAKER** 9 (2.6) 5 (2.1) 4 (3.8) IN CONTROLLED 2 (0.6) 2 (0.9) **ENVIRONMENT** PART TIME (IRREGULAR 47 33 (14.2) 14 (13.2) **DAYWORK)** (13.7)**PART TIME (REGULAR** 19 (5.6) 16 (6.9) 3 (2.8) **HOURS**) **RETIRED/DISABILITY** 7 (2.0) 3 (1.3) 4 (3.8) **STUDENT** 11 (3.2) 9 (3.9) 2 (1.9) 58 **UNEMPLOYED** 38 (16.3) 18 (17.0) 2 (66.7) (17.0)EMPLOYMENT_PATTERN_PAST_30_DAYS, **FULL TIME (35+ HRS/WK)** 118 0 73 (31.3) 44 (41.1) 1 (33.3) n (%) (34.4)**HOMEMAKER** 12 (3.5) 8 (3.4) 4 (3.7) IN CONTROLLED 1 (0.3) 1 (0.4) **ENVIRONMENT** PART TIME (IRREGULAR 36 28 (12.0) 8 (7.5) DAYWORK) (10.5)**PART TIME (REGULAR** 15 (4.4) 11 (4.7) 4 (3.7) **HOURS**) **RETIRED/DISABILITY** 9 (2.6) 3 (1.3) 6 (5.6) **STUDENT** 6 (1.7) 4 (1.7) 2 (1.9) 146 **UNEMPLOYED** 105 (45.1) 39 (36.4) 2 (66.7) (42.6)AGE, mean (SD) 37.4 nan 3 36.9 (10.5) 38.6 (9.3) (10.1)(nan) DIASTOLIC_BLOOD_PRESSURE, mean 83.7 80.0 3 82.6 (44.3) 86.2 (29.9) (40.1)(9.5)PULSE, mean (SD) 155.3 150.7 1 153.7 (28.7) 158.7 (39.0) (32.4)(42.4)**RESPIRATIONS, mean (SD)** 17.1 16.0 8 17.1 (3.1) 17.3 (4.5) (3.6)(0.0)SYSTOLIC_BLOOD_PRESSURE, mean (SD) 126.5 118.7 3 123.1 (24.8) 134.0 (44.3) (32.5)(15.9)**TEMPERATURE**, mean (SD) 103.1 98.5 8 103.2 (60.5) 103.0 (21.1) (51.1)(1.4)BMI, mean (SD) 25.1 26.5 6 24.8 (5.1) 25.7 (4.6) (4.9)(5.6)METHADONE, n (%) **NEGATIVE** 56 0 38 (16.3) 18 (16.8) (16.3)253 **NEGATIVENEGATIVE** 172 (73.8) 78 (72.9) 3 (100.0) (73.8)**NEGATIVEPOSITIVE** 3 (0.9) 2 (0.9) 1 (0.9) **POSITIVE** 2 (0.6) 2 (0.9) **POSITIVENEGATIVE** 24 (7.0) 16 (6.9) 8 (7.5) **POSITIVE POSITIVE** 5 (1.5) 3 (1.3) 2 (1.9) MORPHINE, n (%) **NEGATIVE** 96 67 (28.9) 29 (27.1) (28.1)246 **POSITIVE** 165 (71.1) 78 (72.9) 3 (100.0) (71.9)OPIATE, n (%) **NEGATIVE** 48 57 12 (13.3) 36 (18.7) (16.8)238 **POSITIVE** 157 (81.3) 78 (86.7) 3 (100.0) (83.2)**SEX**, n (%) 111 38 (35.5) 72 (30.9) 1 (33.3) (32.4)231 161 (69.1) 69 (64.5) 1 (33.3) (67.3)U 1 (0.3) 1 (33.3) # Murat Simsek et Yuquan Dai In []: