

Medicare dental

Sanjay Basu

8/31/2021

Download MEPS data

```

# restrict to medicare
df = df %>%
  filter(INSURCY2==4 | INSURCY2==5 | INSURCY2==6) %>% # https://www.meps.ahrq.gov/
  mepsweb/data_stats/download_data_files_codebook.jsp?PUFId=H172&varName=INSURCY2
  mutate(total_mcare = T)

# how many people had new dental insurance during MEPS
df$nodental = (df$DENTIN1==2 | df$DENTIN2==2 | df$DENTIN3==2 | df$DENTIN4==2 | d
f$DENTIN5==2)

# by race/ethnicity
df <- df %>%
  mutate(
    hisp    = (RACETHX == 1),
    white   = (RACETHX == 2),
    black   = (RACETHX == 3),
    native  = (RACETHX > 3 & RACEV1X %in% c(3,6)),
    asian   = (RACETHX > 3 & RACEV1X %in% c(4,5)),

    race = 1*hisp + 2*white + 3*black + 4*native + 5*asian,
    race = recode_factor(race,
      "1" = "Hispanic",
      "2" = "White",
      "3" = "Black",
      "4" = "Amer. Indian, AK Native, or mult. races",
      "5" = "Asian, Hawaiian, or Pacific Islander"))

# by income subgroup
df <- df %>%
  mutate(
    poor     = (POVCATY1 == 1),
    nearpoor = (POVCATY1 == 2),
    lowinc   = (POVCATY1 == 3),
    midinc   = (POVCATY1 == 4),
    hiinc    = (POVCATY1 == 5),

    income = 1*poor + 2*nearpoor + 3*lowinc + 4*midinc + 5*hiinc,
    income = recode_factor(income,
      "1" = "<= 100% poverty line",
      "2" = "101-125% poverty line",
      "3" = "126-200% poverty line",
      "4" = "201-400% poverty line",
      "5" = ">= 400% poverty line"))

```

```
## Warning: Unreplaced values treated as NA as .x is not compatible. Please specify
## replacements exhaustively or supply .default
```

```
# by region
df <- df %>%
  mutate(
    northeast = (REGIONY1 == 1),
    midwest = (REGIONY1 == 2),
    south = (REGIONY1 == 3),
    west = (REGIONY1 == 4),

    region = 1*northeast + 2*midwest + 3*south + 4*west,
    region = recode_factor(income,
                          "1" = "Northeast",
                          "2" = "Midwest",
                          "3" = "South",
                          "4" = "West"))

# who had no annual visits at baseline
df$noannvisit_baseline = (df$DVTOTY1==0 | df$DVTOTY2==0)

# edentulous at baseline
df$edentulous_baseline = (df$LSTETH5==1)

# apply survey sample weights
options(survey.lonely.psu='adjust')
mepsdsgn <- svydesign(
  id = ~VARPSU,
  strata = ~VARSTR,
  weights = ~newwt,
  data = df,
  nest = TRUE)

tab0 <- svyCreateTableOne(vars = c("total_mcare", "race", "income", "region", "noannv
isit_baseline", "edentulous_baseline"),
  data = mepsdsgn,
  strata = "nodental",
  factorVars = c("nodental", "race", "income", "region"))

tab0
```

```

##                                     Stratified by nodental
##                                     FALSE
##      n                               7609564.5
##      total_mcare = TRUE (%)          7609564.5 (100.0)
##      race (%)
##          Hispanic                    312767.5 ( 4.1)
##          White                       6056264.2 ( 79.6)
##          Black                       650503.4 (  8.5)
##          Amer. Indian, AK Native, or mult. races 154139.6 (  2.0)
##          Asian, Hawaiian, or Pacific Islander  435889.8 (  5.7)
##      income (%)
##          </= 100% poverty line        329077.5 (  4.3)
##          101-125% poverty line         91388.8 (  1.2)
##          126-200% poverty line        574006.2 (  7.5)
##          201-400% poverty line       1825242.5 ( 24.0)
##          >/= 400% poverty line       4789849.5 ( 62.9)
##      region (%)
##          </= 100% poverty line        329077.5 (  4.3)
##          101-125% poverty line         91388.8 (  1.2)
##          126-200% poverty line        574006.2 (  7.5)
##          201-400% poverty line       1825242.5 ( 24.0)
##          >/= 400% poverty line       4789849.5 ( 62.9)
##      noannvisit_baseline = TRUE (%)    3202518.5 ( 42.1)
##      edentulous_baseline = TRUE (%)    633582.3 (  8.3)
##                                     Stratified by nodental
##                                     TRUE           p           test
##      n                               42851468.6
##      total_mcare = TRUE (%)          42851468.6 (100.0)           NA
##      race (%)                                0.007
##          Hispanic                    3713435.8 (  8.7)
##          White                       32537139.8 ( 75.9)
##          Black                       3899016.2 (  9.1)
##          Amer. Indian, AK Native, or mult. races 817573.4 (  1.9)
##          Asian, Hawaiian, or Pacific Islander 1884303.4 (  4.4)
##      income (%)                                <0.001
##          </= 100% poverty line        5350226.3 ( 12.5)
##          101-125% poverty line        2431573.9 (  5.7)
##          126-200% poverty line        7348468.3 ( 17.2)
##          201-400% poverty line       12470576.3 ( 29.1)
##          >/= 400% poverty line       15239278.8 ( 35.6)
##      region (%)                                <0.001
##          </= 100% poverty line        5350226.3 ( 12.5)
##          101-125% poverty line        2431573.9 (  5.7)
##          126-200% poverty line        7348468.3 ( 17.2)
##          201-400% poverty line       12470576.3 ( 29.1)
##          >/= 400% poverty line       15239278.8 ( 35.6)
##      noannvisit_baseline = TRUE (%)    28170973.1 ( 65.7) <0.001
##      edentulous_baseline = TRUE (%)    8436649.1 ( 19.7) <0.001

```

Outcome 1

```
# restrict to those without other dental insurance at any point in survey
df = df %>%
  filter(nodental==1) # https://www.meps.ahrq.gov/mepsweb/data_stats/download_data_files_codebook.jsp?PUFId=H210&varName=DENTIN1

df$newcover_nomeans = T
df$newcover_means = (df$POVCATY1==1 | df$POVCATY1==2 | df$POVCATY1==3 | df$POVCATY2==1 | df$POVCATY2==2 | df$POVCATY2==3) # https://www.meps.ahrq.gov/mepsweb/data_stats/download_data_files_codebook.jsp?PUFId=H210&varName=POVCATY1
# see poverty status categories at: https://www.meps.ahrq.gov/survey_comp/hc_technical_notes.shtml

# apply survey sample weights
options(survey.lonely.psu='adjust')
mepsdsgn <- svydesign(
  id = ~VARPSU,
  strata = ~VARSTR,
  weights = ~newwt,
  data = df,
  nest = TRUE)

# OUTCOME 1: overall coverage number
# if means tested, coverage just for those <200% FPL
svytotal(~newcover_means, design = mepsdsgn)
```

```
##                total      SE
## newcover_meansFALSE 23371730 656187
## newcover_meansTRUE  19479739 558072
```

```
# if not means tested
svytotal(~newcover_nomeans, design = mepsdsgn)
```

```
##                total      SE
## newcover_nomeansFALSE      0      0
## newcover_nomeansTRUE 42851469 957044
```

Outcome 2

```

# OUTCOME 2: how many people have an annual visit
# if means tested, we increase the probability of an annual visit by 7.2 percentag
e points among those who didn't have a annual visit before
set.seed(123)
df$newvisit_means = (df$noannvisit_baseline==1)*(df$newcover_means==1)*rbinom(dim
(df)[1],1,0.072) # https://www.healthaffairs.org/doi/10.1377/hlthaff.2020.00386
# if not means tested, we increase the probability to match that of insured peopl
e, which is 58.8%
set.seed(123)
df$newvisit_nomeans = (df$noannvisit_baseline==1)*rbinom(dim(df)[1],1,0.588) # 58.
8% calculated from MEPS if changing line 33 to those with continuous coverage

mepsdsgn <- svydesign(
  id = ~VARPSU,
  strata = ~VARSTR,
  weights = ~newwt,
  data = df,
  nest = TRUE)
svytotal(~noannvisit_baseline, design = mepsdsgn) # currently having no annual vis
it

```

```

##                total      SE
## noannvisit_baselineFALSE 14680496 507809
## noannvisit_baselineTRUE  28170973 663330

```

```

svytotal(~newvisit_means, design = mepsdsgn) # newly having annual visit, if means
tested

```

```

##                total      SE
## newvisit_means 1063899 87540

```

```

svytotal(~newvisit_nomeans, design = mepsdsgn) # newly having annual visit, if not
means tested

```

```

##                total      SE
## newvisit_nomeans 16659886 468329

```

Outcome 3

```
# OUTCOME 3: resulting difference in edentulism

#reduced risk of edentulism at baseline = 0.223 x previous risk
df$edentulous_means = (df$LSTETH5==1)*(df$newvisit_means==1)*(rbinom(dim(df)[1],1,
1-0.230))
df$edentulous_nomeans = (df$LSTETH5==1)*(df$newvisit_nomeans==1)*(rbinom(dim(d
f)[1],1,1-0.230))

mepsdsgn <- svydesign(
  id = ~VARPSU,
  strata = ~VARSTR,
  weights = ~newwt,
  data = df,
  nest = TRUE)
svytotal(~edentulous_baseline, design = mepsdsgn) # currently expected to become e
dentulous annually
```

```
##
##
## edentulous_baselineFALSE 34414820 812950
## edentulous_baselineTRUE 8436649 293541
```

```
svytotal(~edentulous_means, design = mepsdsgn) # if means tested, expected to beco
me edentulous annually
```

```
##
##
## edentulous_means 241640 35920
```

```
svytotal(~edentulous_nomeans, design = mepsdsgn) # if not means tested, expected t
o become edentulous annually
```

```
##
##
## edentulous_nomeans 3641455 175151
```

formatted table

```
# output weighted/formatted table
tab1 <- svyCreateTableOne(vars = c("total_mcare", "newcover_means", "newcover_nomean
s", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_baselin
e", "edentulous_means", "edentulous_nomeans"),
  data = mepsdsgn,
  factorVars = c("total_mcare", "newcover_means", "newcover
_nomeans", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_b
aseline", "edentulous_means", "edentulous_nomeans"))
tab1
```

```
##
##                                Overall
##      n                        42851468.6
##      total_mcare = TRUE (%)    42851468.6 (100.0)
##      newcover_means = TRUE (%) 19479738.8 ( 45.5)
##      newcover_nomeans = TRUE (%) 42851468.6 (100.0)
##      noannvisit_baseline = TRUE (%) 28170973.1 ( 65.7)
##      newvisit_means = 1 (%)    1063899.3 (  2.5)
##      newvisit_nomeans = 1 (%)  16659885.9 ( 38.9)
##      edentulous_baseline = TRUE (%) 8436649.1 ( 19.7)
##      edentulous_means = 1 (%)   241639.6 (  0.6)
##      edentulous_nomeans = 1 (%) 3641455.2 (  8.5)
```

Subgroup analysis 1: by race/ethnicity

```
mepsdsgn <- svydesign(
  id = ~VARPSU,
  strata = ~VARSTR,
  weights = ~newwt,
  data = df,
  nest = TRUE)

# output weighted/formatted table with race/ethnic subgroups
tab2 <- svyCreateTableOne(vars = c("total_mcare", "newcover_means", "newcover_nomean
s", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_baselin
e", "edentulous_means", "edentulous_nomeans"),
  data = mepsdsgn,
  strata = "race",
  factorVars = c("total_mcare", "newcover_means", "newcover
_nomeans", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_b
aseline", "edentulous_means", "edentulous_nomeans"))
tab2
```



```

##                                     Stratified by race
##                                     Hispanic           White
##      n                               3713435.8       32537139.8
##      total_mcare = TRUE (%)         3713435.8 (100.0) 32537139.8 (100.0)
##      newcover_means = TRUE (%)      2382787.8 ( 64.2) 13158965.7 ( 40.4)
##      newcover_nomeans = TRUE (%)    3713435.8 (100.0) 32537139.8 (100.0)
##      noannvisit_baseline = TRUE (%) 3106447.0 ( 83.7) 19569555.7 ( 60.1)
##      newvisit_means = 1 (%)         121503.9 (  3.3)  720354.5 (  2.2)
##      newvisit_nomeans = 1 (%)       1896906.8 ( 51.1) 11361958.8 ( 34.9)
##      edentulous_baseline = TRUE (%)  739702.7 ( 19.9)  6110648.9 ( 18.8)
##      edentulous_means = 1 (%)       27676.0 (  0.7)  170527.5 (  0.5)
##      edentulous_nomeans = 1 (%)     336816.6 (  9.1) 2643444.6 (  8.1)
##                                     Stratified by race
##                                     Black
##      n                               3899016.2
##      total_mcare = TRUE (%)         3899016.2 (100.0)
##      newcover_means = TRUE (%)      2475085.0 ( 63.5)
##      newcover_nomeans = TRUE (%)    3899016.2 (100.0)
##      noannvisit_baseline = TRUE (%) 3350604.8 ( 85.9)
##      newvisit_means = 1 (%)         129567.4 (  3.3)
##      newvisit_nomeans = 1 (%)       2098120.1 ( 53.8)
##      edentulous_baseline = TRUE (%) 1020077.2 ( 26.2)
##      edentulous_means = 1 (%)       23528.8 (  0.6)
##      edentulous_nomeans = 1 (%)     409828.4 ( 10.5)
##                                     Stratified by race
##                                     Amer. Indian, AK Native, or mult. races
##      n                               817573.4
##      total_mcare = TRUE (%)         817573.4 (100.0)
##      newcover_means = TRUE (%)      516407.5 ( 63.2)
##      newcover_nomeans = TRUE (%)    817573.4 (100.0)
##      noannvisit_baseline = TRUE (%) 665937.4 ( 81.5)
##      newvisit_means = 1 (%)         34565.5 (  4.2)
##      newvisit_nomeans = 1 (%)       433911.0 ( 53.1)
##      edentulous_baseline = TRUE (%) 254655.0 ( 31.1)
##      edentulous_means = 1 (%)       11399.8 (  1.4)
##      edentulous_nomeans = 1 (%)     119909.8 ( 14.7)
##                                     Stratified by race
##                                     Asian, Hawaiian, or Pacific Islander p
##      n                               1884303.4
##      total_mcare = TRUE (%)         1884303.4 (100.0)          NA
##      newcover_means = TRUE (%)      946492.9 ( 50.2)          <0.001
##      newcover_nomeans = TRUE (%)    1884303.4 (100.0)          NA
##      noannvisit_baseline = TRUE (%) 1478428.3 ( 78.5)          <0.001
##      newvisit_means = 1 (%)         57908.0 (  3.1)          0.055
##      newvisit_nomeans = 1 (%)       868989.3 ( 46.1)          <0.001
##      edentulous_baseline = TRUE (%) 311565.2 ( 16.5)          <0.001
##      edentulous_means = 1 (%)       8507.6 (  0.5)          0.500
##      edentulous_nomeans = 1 (%)     131455.9 (  7.0)          0.010
##                                     Stratified by race

```

```
##                                test
##      n
##      total_mcare = TRUE (%)
##      newcover_means = TRUE (%)
##      newcover_nomeans = TRUE (%)
##      noannvisit_baseline = TRUE (%)
##      newvisit_means = 1 (%)
##      newvisit_nomeans = 1 (%)
##      edentulous_baseline = TRUE (%)
##      edentulous_means = 1 (%)
##      edentulous_nomeans = 1 (%)
```

Subgroup analysis 2: by income

```
mepsdsgn <- svydesign(
  id = ~VARPSU,
  strata = ~VARSTR,
  weights = ~newwt,
  data = df,
  nest = TRUE)

# output weighted/formatted table with income subgroups
tab3 <- svyCreateTableOne(vars = c("total_mcare", "newcover_means", "newcover_nomean
s", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_baselin
e", "edentulous_means", "edentulous_nomeans"),
  data = mepsdsgn,
  strata = "income",
  factorVars = c("total_mcare", "newcover_means", "newcover
_nomeans", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_b
aseline", "edentulous_means", "edentulous_nomeans"))
tab3
```

```

##                                     Stratified by income
##                                     </= 100% poverty line 101-125% poverty line
##      n                               5350226.3                2431573.9
##      total_mcare = TRUE (%)          5350226.3 (100.0)        2431573.9 (100.0)
##      newcover_means = TRUE (%)       5350226.3 (100.0)        2431573.9 (100.0)
##      newcover_nomeans = TRUE (%)     5350226.3 (100.0)        2431573.9 (100.0)
##      noannvisit_baseline = TRUE (%)  4451446.2 ( 83.2)        1954363.4 ( 80.4)
##      newvisit_means = 1 (%)          320501.6 (  6.0)         147564.3 (  6.1)
##      newvisit_nomeans = 1 (%)        2624118.4 ( 49.0)        1179909.5 ( 48.5)
##      edentulous_baseline = TRUE (%)  1553029.5 ( 29.0)         643804.5 ( 26.5)
##      edentulous_means = 1 (%)         94163.2 (  1.8)          26282.9 (  1.1)
##      edentulous_nomeans = 1 (%)      696467.2 ( 13.0)         287755.6 ( 11.8)
##                                     Stratified by income
##                                     126-200% poverty line 201-400% poverty line
##      n                               7348468.3                12470576.3
##      total_mcare = TRUE (%)          7348468.3 (100.0)        12470576.3 (100.0)
##      newcover_means = TRUE (%)       7348468.3 (100.0)         3166289.6 ( 25.4)
##      newcover_nomeans = TRUE (%)     7348468.3 (100.0)        12470576.3 (100.0)
##      noannvisit_baseline = TRUE (%)  5609481.0 ( 76.3)         8636499.0 ( 69.3)
##      newvisit_means = 1 (%)          382358.0 (  5.2)         166100.0 (  1.3)
##      newvisit_nomeans = 1 (%)        3174840.7 ( 43.2)         5346503.0 ( 42.9)
##      edentulous_baseline = TRUE (%)  1897382.7 ( 25.8)         2638690.9 ( 21.2)
##      edentulous_means = 1 (%)         83921.9 (  1.1)          30447.4 (  0.2)
##      edentulous_nomeans = 1 (%)      845799.9 ( 11.5)         1158238.2 (  9.3)
##                                     Stratified by income
##                                     >/= 400% poverty line p      test
##      n                               15239278.8
##      total_mcare = TRUE (%)          15239278.8 (100.0)        NA
##      newcover_means = TRUE (%)       1178838.5 (  7.7)        <0.001
##      newcover_nomeans = TRUE (%)     15239278.8 (100.0)        NA
##      noannvisit_baseline = TRUE (%)  7507838.5 ( 49.3)        <0.001
##      newvisit_means = 1 (%)          47375.5 (  0.3)        <0.001
##      newvisit_nomeans = 1 (%)        4329457.0 ( 28.4)        <0.001
##      edentulous_baseline = TRUE (%)  1698777.7 ( 11.1)        <0.001
##      edentulous_means = 1 (%)         6824.3 (  0.0)        <0.001
##      edentulous_nomeans = 1 (%)      653194.3 (  4.3)        <0.001

```

Subgroup analysis 3: by income

```
mepsdsgn <- svydesign(  
  id = ~VARPSU,  
  strata = ~VARSTR,  
  weights = ~newwt,  
  data = df,  
  nest = TRUE)  
  
# output weighted/formatted table with region subgroups  
tab4 <- svyCreateTableOne(vars = c("total_mcare", "newcover_means", "newcover_nomean  
s", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_baselin  
e", "edentulous_means", "edentulous_nomeans"),  
  data = mepsdsgn,  
  strata = "region",  
  factorVars = c("total_mcare", "newcover_means", "newcover  
_nomeans", "noannvisit_baseline", "newvisit_means", "newvisit_nomeans", "edentulous_b  
aseline", "edentulous_means", "edentulous_nomeans"))  
tab4
```

```

##                                     Stratified by region
##                                     </= 100% poverty line 101-125% poverty line
##      n                               5350226.3                2431573.9
##      total_mcare = TRUE (%)          5350226.3 (100.0)        2431573.9 (100.0)
##      newcover_means = TRUE (%)        5350226.3 (100.0)        2431573.9 (100.0)
##      newcover_nomeans = TRUE (%)      5350226.3 (100.0)        2431573.9 (100.0)
##      noannvisit_baseline = TRUE (%)   4451446.2 ( 83.2)        1954363.4 ( 80.4)
##      newvisit_means = 1 (%)           320501.6 (  6.0)         147564.3 (  6.1)
##      newvisit_nomeans = 1 (%)         2624118.4 ( 49.0)        1179909.5 ( 48.5)
##      edentulous_baseline = TRUE (%)   1553029.5 ( 29.0)         643804.5 ( 26.5)
##      edentulous_means = 1 (%)         94163.2 (  1.8)          26282.9 (  1.1)
##      edentulous_nomeans = 1 (%)       696467.2 ( 13.0)         287755.6 ( 11.8)
##                                     Stratified by region
##                                     126-200% poverty line 201-400% poverty line
##      n                               7348468.3                12470576.3
##      total_mcare = TRUE (%)          7348468.3 (100.0)        12470576.3 (100.0)
##      newcover_means = TRUE (%)        7348468.3 (100.0)         3166289.6 ( 25.4)
##      newcover_nomeans = TRUE (%)      7348468.3 (100.0)        12470576.3 (100.0)
##      noannvisit_baseline = TRUE (%)   5609481.0 ( 76.3)         8636499.0 ( 69.3)
##      newvisit_means = 1 (%)           382358.0 (  5.2)         166100.0 (  1.3)
##      newvisit_nomeans = 1 (%)         3174840.7 ( 43.2)        5346503.0 ( 42.9)
##      edentulous_baseline = TRUE (%)   1897382.7 ( 25.8)         2638690.9 ( 21.2)
##      edentulous_means = 1 (%)         83921.9 (  1.1)          30447.4 (  0.2)
##      edentulous_nomeans = 1 (%)       845799.9 ( 11.5)        1158238.2 (  9.3)
##                                     Stratified by region
##                                     >/= 400% poverty line p      test
##      n                               15239278.8
##      total_mcare = TRUE (%)          15239278.8 (100.0)        NA
##      newcover_means = TRUE (%)        1178838.5 (  7.7)        <0.001
##      newcover_nomeans = TRUE (%)      15239278.8 (100.0)        NA
##      noannvisit_baseline = TRUE (%)   7507838.5 ( 49.3)        <0.001
##      newvisit_means = 1 (%)           47375.5 (  0.3)        <0.001
##      newvisit_nomeans = 1 (%)         4329457.0 ( 28.4)        <0.001
##      edentulous_baseline = TRUE (%)   1698777.7 ( 11.1)        <0.001
##      edentulous_means = 1 (%)         6824.3 (  0.0)        <0.001
##      edentulous_nomeans = 1 (%)       653194.3 (  4.3)        <0.001

```