In [2]:
```
# https://data.cdc.gov/Vaccinations/COVID-19-Vaccinations-in-the-United-States-County/8xkx-amqh gives date-wise data
# (and plots) on vaccination (equity) status per county (identified by FIPS Code) of the country (USA).
# https://www.nrcs.usda.gov/wps/portal/nrcs/detail/national/home/?cid=nrcs143_013697 gives (USA) county FIPS Codes
# mapped to states.
# https://www.nber.org/research/data/county-distance-database gives (USA) inter-county distances (in miles).
# Consider a scenario as on a chosen date. (Specifying a date drastically reduces the quantum of relevant data.)
# Imagine the country administration seeks an optimal allocation (to counties)
# of limited vaccine production. "Optimal" could be versus Objectives of:
# - maximizing allocation to counties with most-incompletely-vaccinated population (using `Completeness_pct` and
#   `Census2019`, and maybe as a more-advanced consideration, where severity `SVI-CTGY` is higher).
# - minimizing "cost" through a surrogate variable: county's distance from (states of) vaccine manufacture.
# Now, generate that optimization and an optimal output.
c.chosenDate <- "2022/05/14" # Was: == "05/14/2022"
getwd(); myDir <- file.path("."); myDir # , "optVaccine/"
warning("Beware: following code attempts reading in over 350MB data, maybe over a network. Comment this once ready.")
```

```
'C:/Users/SONY/Downloads/optVaccine'
```

```
'.'
```

```
Warning message in eval(expr, envir, enclos):
"Beware: following code attempts reading in over 350MB data, maybe over a network. Comment this once ready."
```

In [20]:
```
c.mustDebug <- TRUE
myDebug <- function(obj, arg.mustDebug=c.mustDebug){
    if(arg.mustDebug){ print(obj) } # else continue.
    return()
}
transportVaccineMi <- function(fips, county2distRepo=dat.distance, stateFIPSrepo=dat.FIPS,
                               vaccineStateOrig=c("MI", "WI", "KY", "TN"), aggFUN=median){
    if(is.na(fips)){
        fips.aggDist <- NA
    } else {
        # Michigan, Wisconsin, Kentucky, and Tennessee are the assumed vaccine-manufacturing states.
        vso.counties <- stateFIPSrepo[stateFIPSrepo$State %in% vaccineStateOrig, "FIPS5"]
        c2dr.fips <- county2distRepo[(county2distRepo$county1 == fips),]
        c2dr.fips.vsoc <- c2dr.fips[(c2dr.fips$county2 %in% vso.counties),]
            # WHERE (county1==fips) AND (county2 IN vso.counties)
            # Beware: https://stackoverflow.com/questions/6558921/boolean-operators-and
        myDebug(str(c2dr.fips.vsoc))
        # fips.tree <- county2distRepo[c2dr.relevant,]
        if(nrow(c2dr.fips.vsoc) > 0){
            myDebug(c2dr.fips.vsoc)
            fips.aggDist <- aggFUN(c2dr.fips.vsoc$mi_to_county, na.rm=TRUE)
                # do.call(what=aggFUN, args=list(c2dr.fips.vsoc$mi_to_county))
            } else { # did not get any county-specific distances to aggregate
            fips.aggDist <- NA
        }
    }
    return(fips.aggDist)
}
```

In [4]:
```
dat.FIPS <- read.csv(file=file.path(myDir, "UScountyFIPScodes-nrcsUsdaGov.csv"),
                     colClasses=c("integer", rep("factor", times=3))) # stringsAsFactors=FALSE)
str(dat.FIPS)
```

```
'data.frame':   3232 obs. of  4 variables:
 $ FIPS : int  1001 1003 1005 1007 1009 1011 1013 1015 1017 1019 ...
 $ Name : Factor w/ 1933 levels "Abbeville","Acadia",..: 91 98 109 162 177 237 247 260 313 335 ...
 $ State: Factor w/ 56 levels "AK","AL","AR",..: 2 2 2 2 2 2 2 2 2 2 ...
 $ FIPS5: Factor w/ 3228 levels "01001","01003",..: 1 2 3 4 5 6 7 8 9 10 ...
```

In [5]:
```
warning("Beware: following distance data being read in is over 330MB.")
dat.distance <- read.csv(file=file.path(myDir, "sf12010countydistancemiles.csv"),
                         colClasses=c("character", "numeric", "character"))
    # coz reading in as factor causes level mismatches upon comparison later.
    # Was: c("factor", "numeric", "factor")) # stringsAsFactors=FALSE)
# https://stackoverflow.com/questions/24594981/getting-the-error-level-sets-of-factors-are-different-when-running-a-fo
dat.distance$county1 <- factor(dat.distance$county1, levels=levels(dat.FIPS$FIPS5))
dat.distance$county2 <- factor(dat.distance$county2, levels=levels(dat.FIPS$FIPS5))
str(dat.distance); summary(dat.distance)
```

```
Warning message in eval(expr, envir, enclos):
"Beware: following distance data being read in is over 330MB."
```

```
'data.frame':   10371620 obs. of  3 variables:
 $ county1     : Factor w/ 3228 levels "01001","01003",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ mi_to_county: num  22.5 26.8 29.5 30.8 34.5 ...
 $ county2     : Factor w/ 3228 levels "01001","01003",..: 11 43 26 24 51 19 53 4 59 66 ...
```

```
    county1          mi_to_county         county2     
 01001  :    3220   Min.   :   1.408   01001  :    3220  
 01003  :    3220   1st Qu.: 494.739   01003  :    3220  
 01005  :    3220   Median : 806.898   01005  :    3220  
 01007  :    3220   Mean   : 952.651   01007  :    3220  
 01009  :    3220   3rd Qu.:1235.713   01009  :    3220  
 (Other):10326540   Max.   :6273.088   (Other):10326540  
 NA's   :   28980                      NA's   :   28980  
```

In [17]:
```
dat.distance <- na.omit(dat.distance) # Alt: na.exclude() which retains exclusion info used by some functions.
str(dat.distance); summary(dat.distance)
```

```
'data.frame':   10313732 obs. of  3 variables:
 $ county1     : Factor w/ 3228 levels "01001","01003",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ mi_to_county: num  22.5 26.8 29.5 30.8 34.5 ...
 $ county2     : Factor w/ 3228 levels "01001","01003",..: 11 43 26 24 51 19 53 4 59 66 ...
 - attr(*, "na.action")= 'omit' Named int [1:57888] 2651 2929 2985 3188 3189 3190 3193 3195 3217 5807 ...
  ..- attr(*, "names")= chr [1:57888] "2651" "2929" "2985" "3188" ...
```

```
    county1          mi_to_county         county2     
 01001  :    3211   Min.   :   1.408   01001  :    3211  
 01003  :    3211   1st Qu.: 493.162   01003  :    3211  
 01005  :    3211   Median : 803.584   01005  :    3211  
 01007  :    3211   Mean   : 944.892   01007  :    3211  
 01009  :    3211   3rd Qu.:1226.756   01009  :    3211  
 01011  :    3211   Max.   :6273.088   01011  :    3211  
 (Other):10294466                      (Other):10294466  
```

In [6]:
```
warning("Beware: following distance data being read in is over 350MB.")
dat.8xkx.amqh <- read.csv(file=file.path(myDir, "COVID-19_Vaccinations_in_the_United_States_County.csv"),
                          stringsAsFactors=TRUE)
  # https://data.cdc.gov/resource/8xkx-amqh.json is the Socrates Open Data API (SODA) endpoint.
  # That could be accessed programmatically at runtime using R package `RSocrates` or equivalent.
  # It's about 350MB and is updated daily. So, downloaded into CSV for alternative access.
```

```
Warning message in eval(expr, envir, enclos):
"Beware: following distance data being read in is over 350MB."
```

In [7]:
```
dat.8xkx.amqh$Date <- as.Date(dat.8xkx.amqh$Date, format="%m/%d/%Y") # convert factor type to date.
dat.8xkx.amqh$FIPS <- factor(dat.8xkx.amqh$FIPS, levels=levels(dat.FIPS$FIPS5))
str(dat.8xkx.amqh)
```

```
'data.frame':   1700101 obs. of  66 variables:
 $ Date                                  : Date, format: "2022-05-14" "2022-05-14" ...
 $ FIPS                                  : Factor w/ 3228 levels "01001","01003",..: 3093 18 158 163 185 212 250
361 400 537 ...
 $ MMWR_week                             : int  19 19 19 19 19 19 19 19 19 19 ...
 $ Recip_County                          : Factor w/ 1960 levels "Abbeville County",..: 1329 416 1192 1374 17 122
4 315 1187 236 1887 ...
 $ Recip_State                           : Factor w/ 61 levels "","AK","AL","AR",..: 59 3 4 4 7 7 8 12 14 14 ...
 $ Completeness_pct                      : num  96.8 92.5 90.5 90.5 97.6 97.6 97.1 98.7 89.4 89.4 ...
 $ Administered_Dose1_Recip              : int  69678 6882 3869 10536 1514677 120184 14166 70330 31430 2348 ...
 $ Administered_Dose1_Pop_Pct            : num  78.1 57 43.1 59.3 90.6 87.3 69.6 94.7 39.5 29.9 ...
 $ Administered_Dose1_Recip_5Plus        : int  69662 6882 3867 10529 1511943 120031 14159 70308 31428 2347 ...
 $ Administered_Dose1_Recip_5PlusPop_Pct : num  82.4 60.2 45.4 64.1 95 91.5 72.2 95 41.9 31.3 ...
 $ Administered_Dose1_Recip_12Plus       : int  66396 6801 3836 10179 1415356 114250 13716 69384 30686 2314 ...
 $ Administered_Dose1_Recip_12PlusPop_Pct: num  86 65.1 48.4 69.2 95 94.9 74.6 95 44.4 33.1 ...
 $ Administered_Dose1_Recip_18Plus       : int  61371 6476 3695 9420 1300793 104937 13159 66923 28725 2172 ...
 $ Administered_Dose1_Recip_18PlusPop_Pct: num  87.3 67.5 50.5 71.3 95 95 76.1 95 45 33.3 ...
 $ Administered_Dose1_Recip_65Plus       : int  19072 2370 1671 2965 243810 27244 5048 21633 7939 739 ...
 $ Administered_Dose1_Recip_65PlusPop_Pct: num  95 83.7 68.9 85.5 95 95 95 95 85.7 63.8 ...
 $ Series_Complete_Yes                   : int  64375 5383 3274 8008 1277204 107035 12080 58433 27456 2002
```

In [8]:
```
# plot(Completeness_pct ~ Date, data=dat.8xkx.amqh[dat.8xkx.amqh$FIPS == "01001",]) # explore for a county.
myData <- dat.8xkx.amqh[(dat.8xkx.amqh$Date == c.chosenDate),
                        c("Date", "FIPS", "Completeness_pct", "SVI_CTGY", "Census2019")]
str(myData); summary(myData)
```

```
'data.frame':   3284 obs. of  5 variables:
 $ Date            : Date, format: "2022-05-14" "2022-05-14" ...
 $ FIPS            : Factor w/ 3228 levels "01001","01003",..: 3093 18 158 163 185 212 250 361 400 537 ...
 $ Completeness_pct: num  96.8 92.5 90.5 90.5 97.6 97.6 97.1 98.7 89.4 89.4 ...
 $ SVI_CTGY        : Factor w/ 5 levels "","A","B","C",..: 2 5 4 5 3 4 2 3 5 5 ...
 $ Census2019      : int  89221 12067 8986 17782 1671329 137744 20356 74228 79608 7855 ...

      Date                FIPS      Completeness_pct SVI_CTGY
 Min.   :2022-05-14   01001  :   1   Min.   :73.50     : 65
 1st Qu.:2022-05-14   01003  :   1   1st Qu.:93.60    A:806
 Median :2022-05-14   01005  :   1   Median :96.80    B:804
 Mean   :2022-05-14   01007  :   1   Mean   :94.86    C:804
 3rd Qu.:2022-05-14   01009  :   1   3rd Qu.:97.80    D:805
 Max.   :2022-05-14   (Other):3208   Max.   :98.90
                      NA's   :  71   NA's   :23
   Census2019
 Min.   :      86
 1st Qu.:   11131
 Median :   26108
 Mean   :  102950
 3rd Qu.:   67215
 Max.   :10039107
 NA's   :63
```

In [18]:
```
testFIPS <- factor(c("01001", "01003"), levels=levels(dat.FIPS$FIPS5)); myDebug(testFIPS)
duh <- sapply(testFIPS, FUN=transportVaccineMi); myDebug(duh)
```

```
5040   01003     812.8417   26115
5049   01003     814.5249   26025
5069   01003     821.5978   26075
5071   01003     823.8166   55059
5087   01003     827.0140   26005
5092   01003     829.5716   26161
5093   01003     830.8938   55127
5099   01003     833.0908   55105
5105   01003     834.6969   26015
5108   01003     835.8734   55101
5111   01003     836.7070   55045
5117   01003     839.2354   55065
5118   01003     839.6958   26045
5121   01003     840.6504   26163
5136   01003     845.9878   26065
5148   01003     850.8027   26139
5150   01003     851.8911   26093
5157   01003     854.0094   55079
5161   01003     854.5563   55133
```

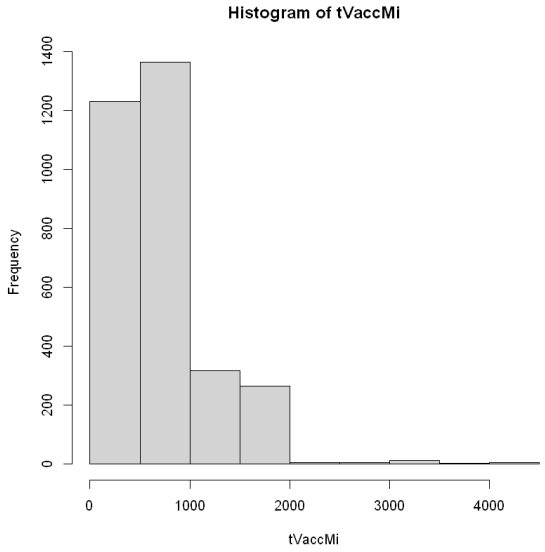
In [ ]:
```
# g.tVaccMi.computed <- 0 # init global variable to tr
```

In [21]:
```
c.mustDebug <- FALSE # coz about to apply on large dataset
tVaccMi <- sapply(myData$FIPS, FUN=transportVaccineMi)
```

In [22]:
```
str(tVaccMi); summary(tVaccMi) # just explore whether ok
hist(tVaccMi)
```

```
 num [1:3284] 396 492 602 469 1958 ...
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  172.6   403.1   580.9   729.5   877.7  4433.4      75 
```



In [23]:
```
myData.tVaccMi <- cbind(myData, tVaccMi=tVaccMi)
```

In [25]:
```
write.csv(myData.tVaccMi, file=file.path(myDir, "myData.tVaccMi.csv"), row.names=FALSE)
```

In [ ]:
```

```