

Math 42 Final Project

2022-06-10

```
data <- read.csv("MCM_NFLIS_Data.csv")
sapply(data, class) |> table()
```

```
##
## character integer
##      3      7
```

```
numeric <- unlist(lapply(data, is.numeric), use.names = FALSE)
char <- unlist(lapply(data, is.character), use.names = FALSE)
summary(data[numeric])
```

```
##      YYYY      FIPS_State  FIPS_Count  FIPS_Combined
## Min.   :2010  Min.   :21.00  Min.    : 1.0  Min.   :21001
## 1st Qu.:2012  1st Qu.:39.00  1st Qu.: 43.0  1st Qu.:39015
## Median :2014  Median :42.00  Median : 87.0  Median :42005
## Mean   :2014  Mean   :39.64  Mean   :114.5  Mean   :39757
## 3rd Qu.:2016  3rd Qu.:51.00  3rd Qu.:141.0  3rd Qu.:51069
## Max.   :2017  Max.   :54.00  Max.   :840.0  Max.   :54109
## DrugReports  TotalDrugReportsCounty TotalDrugReportsState
## Min.    : 1.00  Min.    : 1.0    Min.    : 3672
## 1st Qu.: 1.00  1st Qu.: 136.0    1st Qu.: 28285
## Median : 4.00  Median : 314.0    Median : 41462
## Mean   : 25.37  Mean   : 991.8    Mean   : 56084
## 3rd Qu.: 13.00  3rd Qu.: 737.0    3rd Qu.: 78577
## Max.   :5075.00  Max.   :33513.0    Max.   :119349
```

```
lapply(names(data)[char], function(i) table(data[i], useNA = "always", dnn = i) |> sort() |> tail())
```

```
## [[1]]
## State
## <NA> WV PA KY VA OH
##      0 1699 4362 5429 6218 6354
##
## [[2]]
## COUNTY
```

```
## WASHINGTON JEFFERSON FAYETTE WARREN MONTGOMERY FRANKLIN
## 249 262 282 302 330 357
##
## [[3]]
## SubstanceName
## Methadone Morphine Buprenorphine Heroin Hydrocodone
## 1795 2102 2524 2727 2979
## Oxycodone
## 3124
```

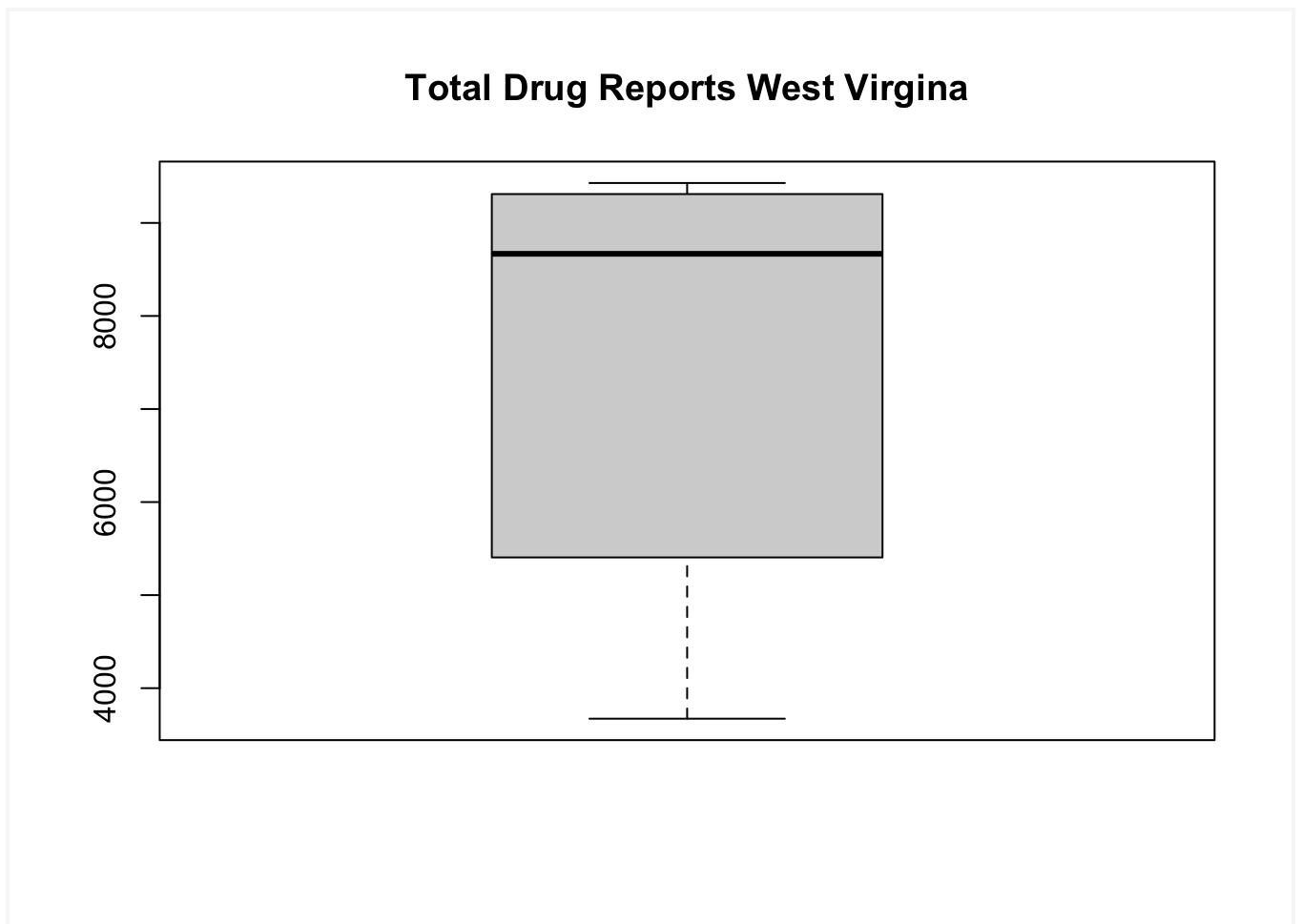
```
typesofdrugs<- sort(tapply(data$DrugReports, data$SubstanceName, length), decreasing = TRUE)
names(typesofdrugs)
```

```
## [1] "Oxycodone" "Hydrocodone"
## [3] "Heroin" "Buprenorphine"
## [5] "Morphine" "Methadone"
## [7] "Fentanyl" "Tramadol"
## [9] "Hydromorphone" "Oxymorphone"
## [11] "Codeine" "Furanyl fentanyl"
## [13] "Propoxyphene" "Acetyl fentanyl"
## [15] "Carfentanil" "U-47700"
## [17] "Methorphan" "4-Fluoroisobutyryl fentanyl"
## [19] "Acryl fentanyl" "3-Methylfentanyl"
## [21] "Cyclopropyl fentanyl" "Meperidine"
## [23] "Butyryl fentanyl" "Mitragnine"
## [25] "Methoxyacetyl fentanyl" "Pentazocine"
## [27] "Dextropropoxyphene" "ANPP"
## [29] "Fluoroisobutyryl fentanyl" "Opiates"
## [31] "Opium" "Phenyl fentanyl"
## [33] "Dihydrocodeine" "Pethidine"
## [35] "Valeryl fentanyl" "Benzylfentanyl"
## [37] "U-48800" "p-Fluorobutyryl fentanyl"
## [39] "Desmethylprodine " "U-49900"
## [41] "Acetylcodeine" "Butorphanol"
## [43] "Crotonyl fentanyl" "o-Fluorofentanyl"
## [45] "Tetrahydrofuran fentanyl" "Thebaine"
## [47] "Furanyl/3-Furanyl fentanyl" "Acetyldihydrocodeine"
## [49] "cis-3-methylfentanyl" "Hydrocodeinone"
## [51] "trans-3-Methylfentanyl" "Cyclopropyl/Crotonyl Fentanyl"
## [53] "Fluorobutyryl fentanyl " "Fluorofentanyl"
## [55] "Isobutyryl fentanyl" "Levorphanol"
```

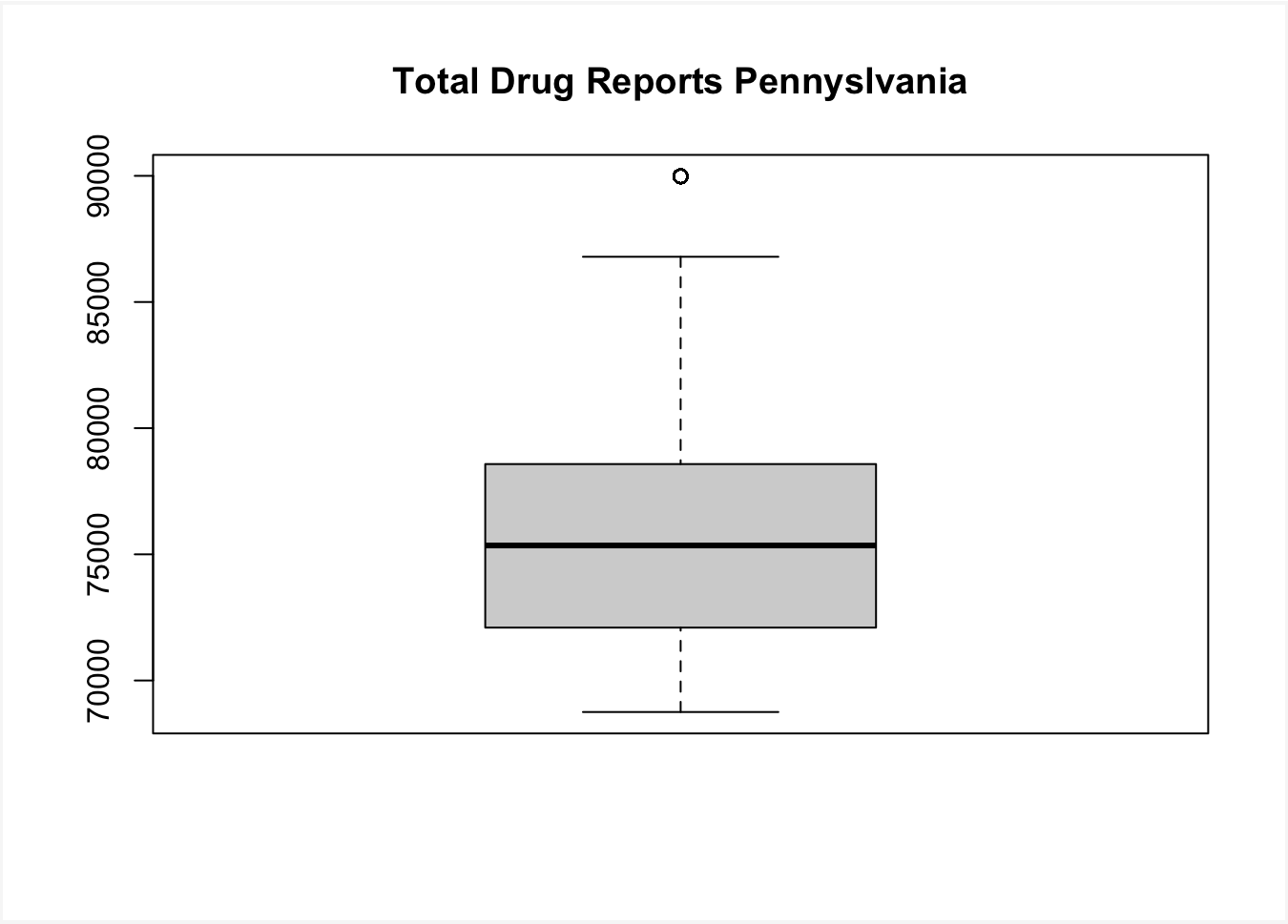
```
## [57] "MT-45"          "p-Fluorofentanyl"
## [59] "3-Fluorofentanyl"  "3,4-Methylenedioxy U-47700"
## [61] "4-Methylfentanyl"  "Alphaprodine"
## [63] "Cyclopentyl fentanyl" "Dihydromorphone"
## [65] "Metazocine"        "Nalbuphine"
## [67] "p-methoxybutyryl fentanyl" "Remifentanyl"
## [69] "U-51754"
```

```
WV <- data[data$State == "WV", ]
PA <- data[data$State == "PA", ]
KY <- data[data$State == "KY", ]
VA <- data[data$State == "VA", ]
OH <- data[data$State == "OH", ]
```

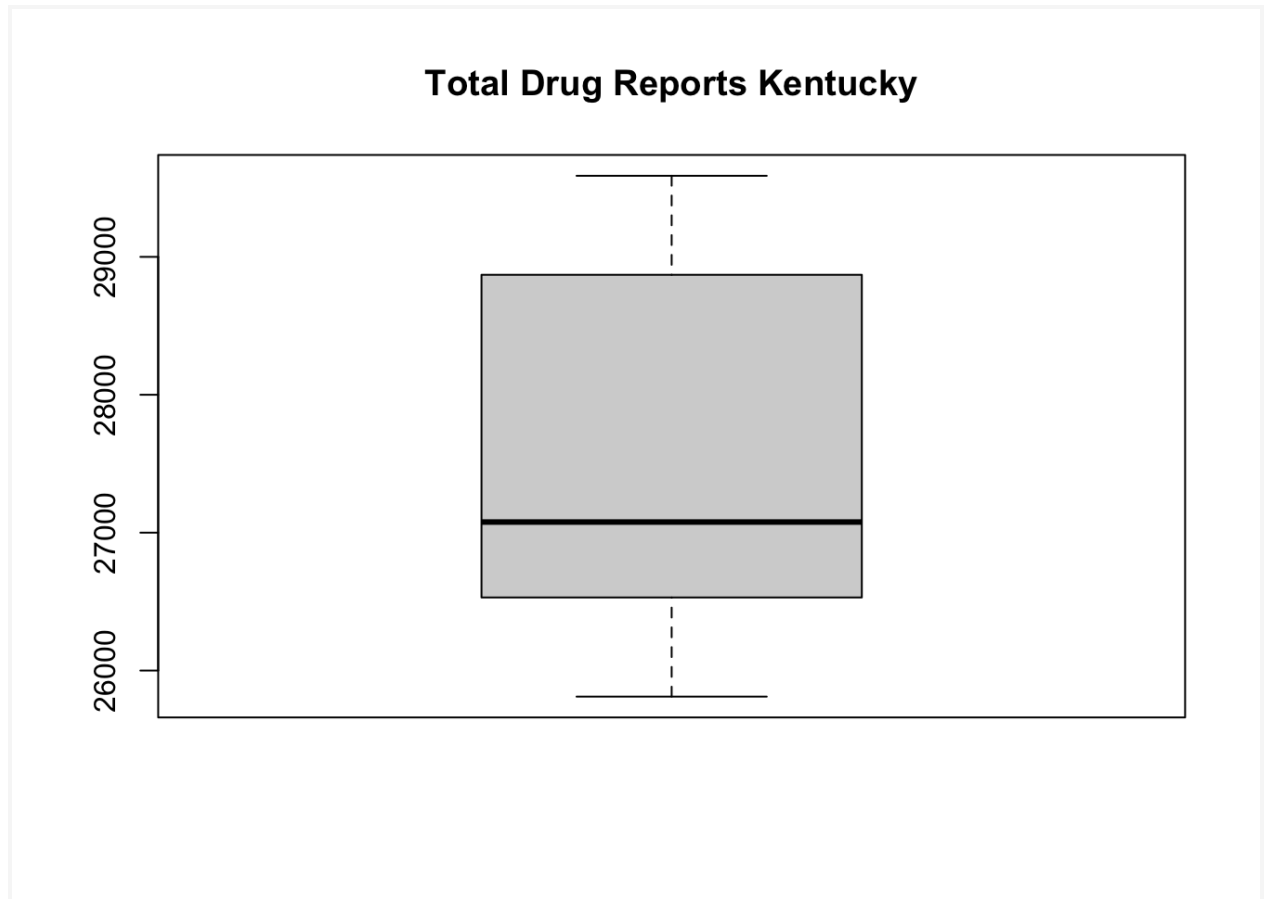
```
boxplot(WV$TotalDrugReportsState, main = "Total Drug Reports West Virginia")
```



boxplot(PA\$TotalDrugReportsState, main = "Total Drug Reports Pennyslvania")

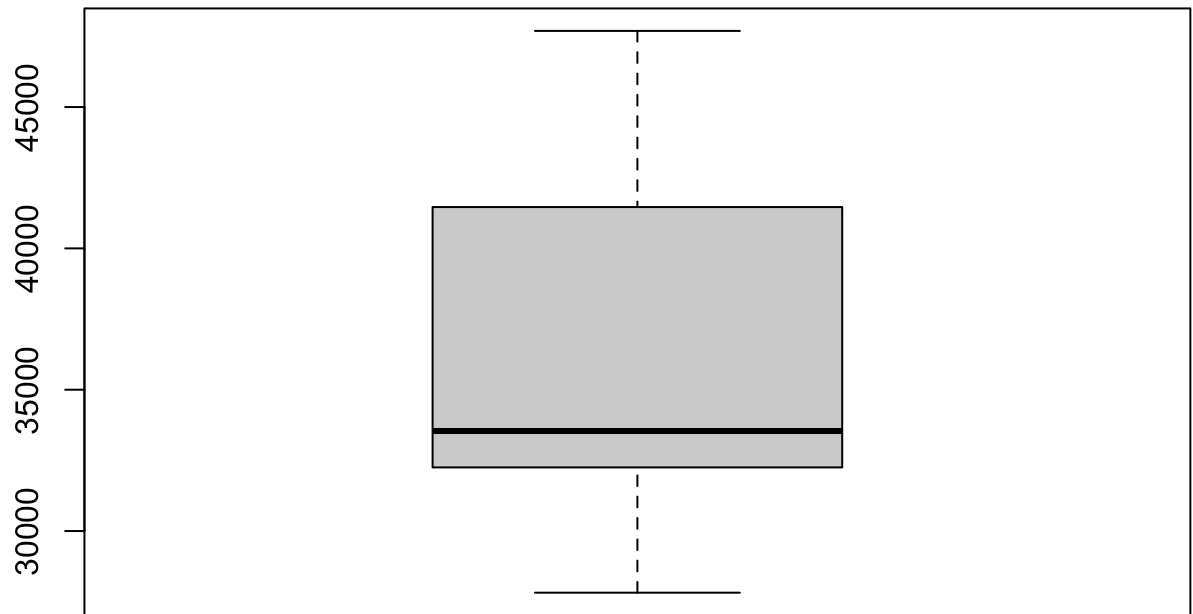


boxplot(KY\$TotalDrugReportsState, main = "Total Drug Reports Kentucky")



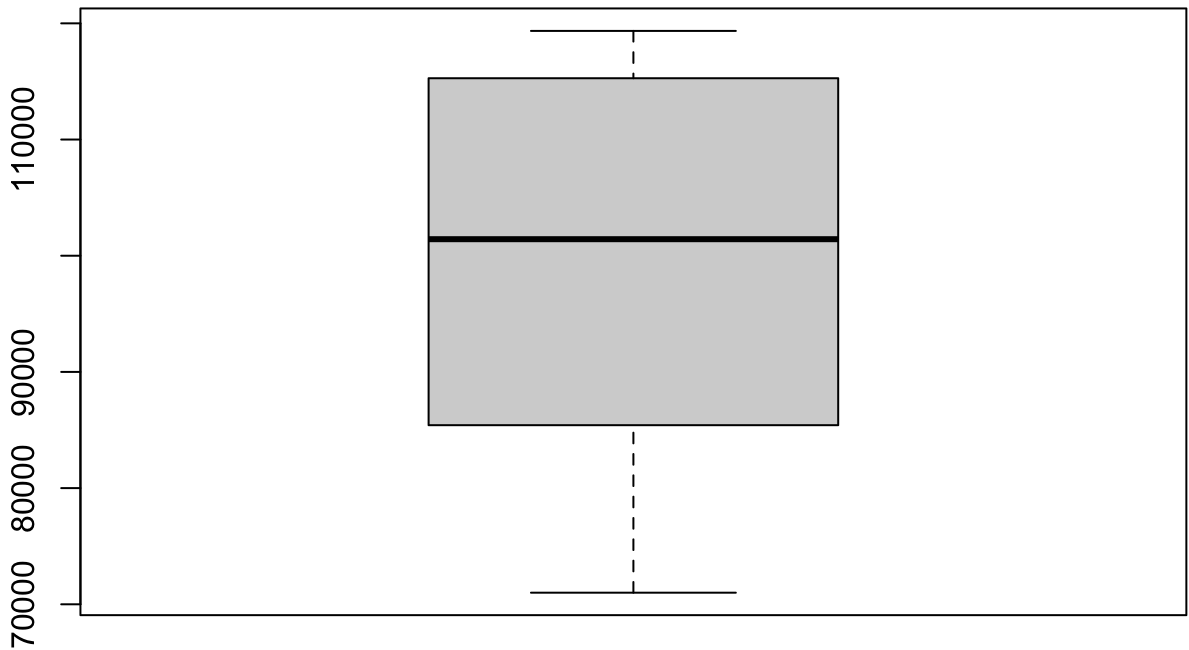
```
boxplot(VA$TotalDrugReportsState, main = "Total Drug Reports Virigina")
```

Total Drug Reports Virigina



```
boxplot(OH$TotalDrugReportsState, main = "Total Drug Reports Ohio")
```

Total Drug Reports Ohio



```
AverageDrugCountWV <- mean(WV$TotalDrugReportsState)
```

```
AverageDrugCountPA <- mean(PA$TotalDrugReportsState)
```

```
AverageDrugCountKY <- mean(KY$TotalDrugReportsState)
```

```
AverageDrugCountVA <- mean(VA$TotalDrugReportsState)
```

```
AverageDrugCountOH <- mean(OH$TotalDrugReportsState)
```

```
AverageDrugCountWVPerDay <- mean(WV$TotalDrugReportsState)/365
```

```
AverageDrugCountPAPerDay <- mean(PA$TotalDrugReportsState)/365
```

```
AverageDrugCountKYPerDay <- mean(KY$TotalDrugReportsState)/365
```

```
AverageDrugCountVAPerDay <- mean(VA$TotalDrugReportsState)/365
```

```
AverageDrugCountOHPerDay <- mean(OH$TotalDrugReportsState)/365
```

```
# Ohio and Pennsylvania are the big players here.
```

```
summary(WV$TotalDrugReportsState)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
##   3672   5405   8668   7383   9310   9429
```

```
summary(PA$TotalDrugReportsState)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
##   68751  72096  75351  77122  78577  89981
```

```
summary(KY$TotalDrugReportsState)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
##   25811  26530  27077  27560  28870  29588
```

```
summary(VA$TotalDrugReportsState)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
##   27819  32251  33539  35704  41462  47694
```

```
summary(OH$TotalDrugReportsState)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.   Max.
##   70999  85415 101423  98979 115276 119349
```

```
HighestDrugCountsCountyWV <-sort(tapply(WV$DrugReports, WV$COUNTY, sum), decreasing = TRUE)
head(HighestDrugCountsCountyWV, 10)
```

```
## KANAWHA  MERCER  RALEIGH  CABELL HARRISON BERKELEY NICHOLAS  WOOD
##   3046   2126   1974   1732   1465   1399   1165   1100
##  LOGAN  MARION
##   1036   1005
```

```
HighestDrugCountsCountyPA <-sort(tapply(PA$DrugReports, PA$COUNTY, sum), decreasing = TRUE)
head(HighestDrugCountsCountyPA, 10)
```

```
## PHILADELPHIA  ALLEGHENY  DELAWARE    BUCKS    YORK    LUZERNE
##   50810    33193    10814    7587    6845    6161
##  DAUPHIN  LANCASTER WESTMORELAND  BERKS
##   5057    4632    4349    3734
```

```
HighestDrugCountsCountyKY <-sort(tapply(KY$DrugReports, KY$COUNTY, sum), decreasing = TRUE)
```



```
head(HighestDrugCountsCountyKY, 10)
```

```
## JEFFERSON  FAYETTE  KENTON  CAMPBELL  MADISON  PERRY  HARLAN  BOONE
## 13979  5321  4855  4042  2744  2081  2000  1927
## BELL  BOYD
## 1886  1866
```

```
HighestDrugCountsCountyVA <- sort(tapply(VA$DrugReports, VA$COUNTY, sum), decreasing = TRUE)
head(HighestDrugCountsCountyVA, 10)
```

```
## FAIRFAX  HENRICO  CHESTERFIELD  PRINCE WILLIAM  TAZEWELL
## 4900  4673  4046  3767  2826
## SPOTSYLVANIA  STAFFORD  WISE  WARREN  ROANOKE
## 2539  2254  2136  2000  1769
```

```
HighestDrugCountsCountyOH <- sort(tapply(OH$DrugReports, OH$COUNTY, sum), decreasing = TRUE)
head(HighestDrugCountsCountyOH, 10)
```

```
## HAMILTON  CUYAHOGA  MONTGOMERY  FRANKLIN  LAKE  BUTLER  LUCAS
## 42933  27630  21771  17541  9559  7246  5803
## MAHONING  STARK  SUMMIT
## 5768  4388  4350
```

Estimating Population

```
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
## filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
## intersect, setdiff, setequal, union
```

```
household_data <- read.csv("ACS_11_5YR_DP02_with_ann.csv")
```

```
KentuckyHouseholdData <- household_data %>% filter(grepl('Kentucky',
```

```
household_data$GEO.display.label))
```

```
TotalHouseholdsKentucky <- sum(as.numeric(KentuckyHouseholdData$HC01_VC03))
TotalPopulationKentucky <- TotalHouseholdsKentucky*4
TotalPopulationKentucky
```

```
## [1] 6724340
```

```
WestVirginiaHouseholdData <- household_data %>% filter(grepl('West Virginia',
household_data$GEO.display.label))
```

```
TotalHouseholdsWestVirginia <- sum(as.numeric(WestVirginiaHouseholdData$HC01_VC03))
TotalPopulationWestVirginia <- TotalHouseholdsWestVirginia*4
TotalPopulationWestVirginia
```

```
## [1] 2960320
```

```
PennsylvaniaHouseholdData <- household_data %>% filter(grepl('Pennsylvania',
household_data$GEO.display.label))
```

```
TotalHouseholdsPennsylvania<- sum(as.numeric(PennsylvaniaHouseholdData$HC01_VC03))
TotalPopulationPennsylvania <- TotalHouseholdsPennsylvania*4
TotalPopulationPennsylvania
```

```
## [1] 19810264
```

```
VirginiaHouseholdData <- household_data %>% filter(grepl('Virginia', household_data$GEO.display.label))
```

```
TotalHouseholdsVirginia<- sum(as.numeric(VirginiaHouseholdData$HC01_VC03))
TotalPopulationVirginia <- TotalHouseholdsVirginia*4
TotalPopulationVirginia
```

```
## [1] 14924420
```

```
OhioHouseholdData <- household_data %>% filter(grepl('Ohio', household_data$GEO.display.label))
```

```
TotalHouseholdsOhio<- sum(as.numeric(OhioHouseholdData$HC01_VC03))
TotalPopulationOhio <- TotalHouseholdsOhio*4
TotalPopulationOhio
```

```
## [1] 18325192
```

```
KentuckyInfectionRate <- AverageDrugCountKY/TotalPopulationKentucky
WestVirginiaInfectionRate <- AverageDrugCountWV/TotalPopulationWestVirginia
```

```

PennsylvaniaInfectionRate <- AverageDrugCountPA/TotalPopulationPennsylvania
VirginiaInfectionRate <- AverageDrugCountVA/TotalPopulationVirginia
OhioInfectionRate <- AverageDrugCountOH/TotalPopulationOhio

```

Kentucky SIR

```

require(deSolve)

## Loading required package: deSolve

SEIR <- function(time, current_state, params){

  with(as.list(c(current_state, params)),{

    N <- S+E+I+R
    dS <- -(beta*S*I)/N
    dE <- (beta*S*I)/N - sigma*E
    dI <- sigma*E - gamma*I - mu*I
    dR <- gamma*I
    dM <- mu*I

    return(list(c(dS,dE,dI,dR,dM)))
  })
}

params <- c(beta= KentuckyInfectionRate, sigma=1/50, gamma=0, mu=0)

initial_state <- c(S=TotalPopulationKentucky, E=0, I=AverageDrugCountKY, R=0, M=0)

times <- 0:3650

Kentuckymodel <- ode(initial_state, times, SEIR, params)

Kentuckynewmodel <- as.data.frame(Kentuckymodel)$I

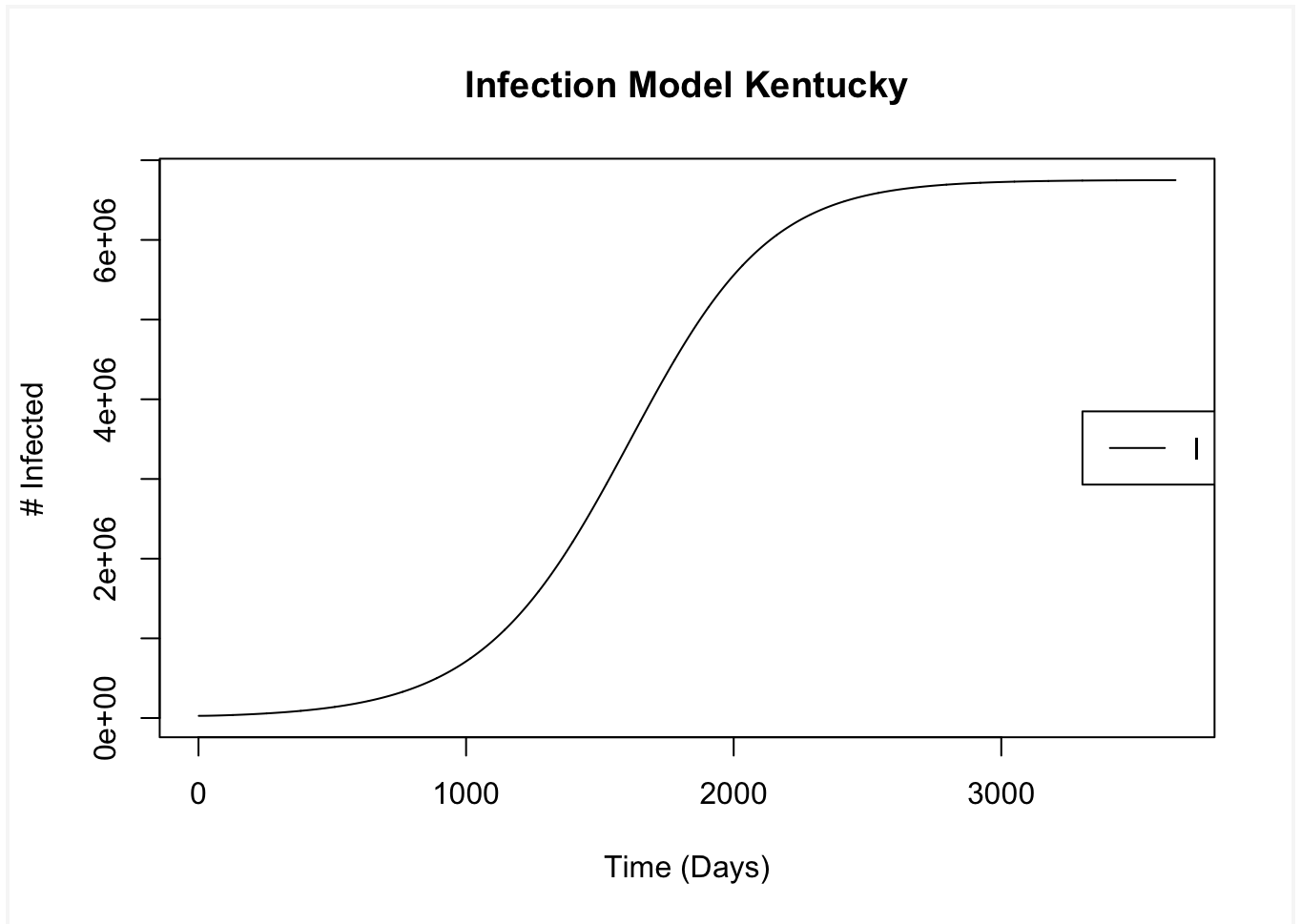
summary(Kentuckynewmodel)

##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 27560 539419 4751863 3823071 6678387 6750129

matplot(Kentuckynewmodel, type="l", lty=1, main="Infection Model Kentucky", xlab="Time (Days)", ylab = "#
Infected")

```

```
legend("right", legend= "I", lty = 1)
```



West Virginia SIR

```
require(deSolve)
```

```
SEIR <- function(time, current_state, params){
```

```
  with(as.list(c(current_state, params)),{
```

```
    N <- S+E+I+R
```

```
    dS <- -(beta*S*I)/N
```

```
    dE <- (beta*S*I)/N - sigma*E
```

```
    dI <- sigma*E - gamma*I - mu*I
```

```
    dR <- gamma*I
```

```
    dM <- mu*I
```

```
    return(list(c(dS,dE,dI,dR,dM)))
```

```
  })
```

```
}
```

```
params <- c(beta= WestVirginiaInfectionRate, sigma=1/50, gamma=0, mu=0)
```

```
initial_state <- c(S=TotalPopulationWestVirginia, E=0, I=AverageDrugCountWV, R=0, M=0)
```

```
times <- 0:3650
```

```
WestVirginiamodel <- ode(initial_state, times, SEIR, params)
```

```
WestVirginianewmodel <- as.data.frame(WestVirginiamodel)$I
```

```
summary(WestVirginianewmodel)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
```

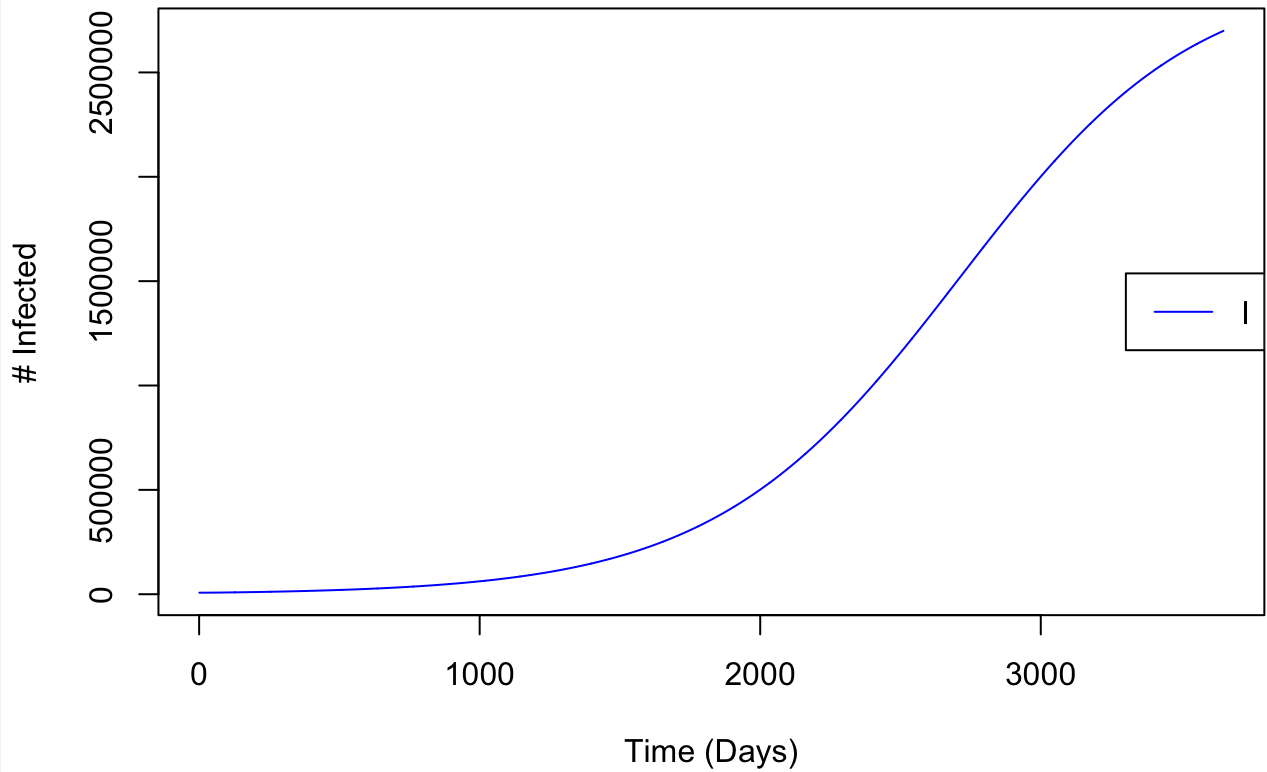
```
##  7383  51188 357515 820973 1564226 2698912
```

```
matplot(WestVirginianewmodel, type="l", lty=1, main="Infection Model West Virginia", xlab="Time (Days)",
```

```
ylab = "# Infected", col = "blue")
```

```
legend("right", legend= "I", lty = 1, col = "blue")
```

Infection Model West Virginia



Pennsylvania SIR

```
require(deSolve)
```

```
SEIR <- function(time, current_state, params){
```

```
  with(as.list(c(current_state, params)),{
```

```
    N <- S+E+I+R
```

```
    dS <- -(beta*S*I)/N
```

```
    dE <- (beta*S*I)/N - sigma*E
```

```
    dI <- sigma*E - gamma*I - mu*I
```

```
    dR <- gamma*I
```

```
    dM <- mu*I
```

```
    return(list(c(dS,dE,dI,dR,dM)))
```

```
  })
```

```
}
```

```
params <- c(beta= PennsylvaniaInfectionRate, sigma=1/50, gamma=0, mu=0)
```

```
initial_state <- c(S=TotalPopulationPennsylvania, E=0, I=AverageDrugCountPA, R=0, M=0)
```

```
times <- 0:3650
```

```
Pennsylvaniamodel <- ode(initial_state, times, SEIR, params)
```

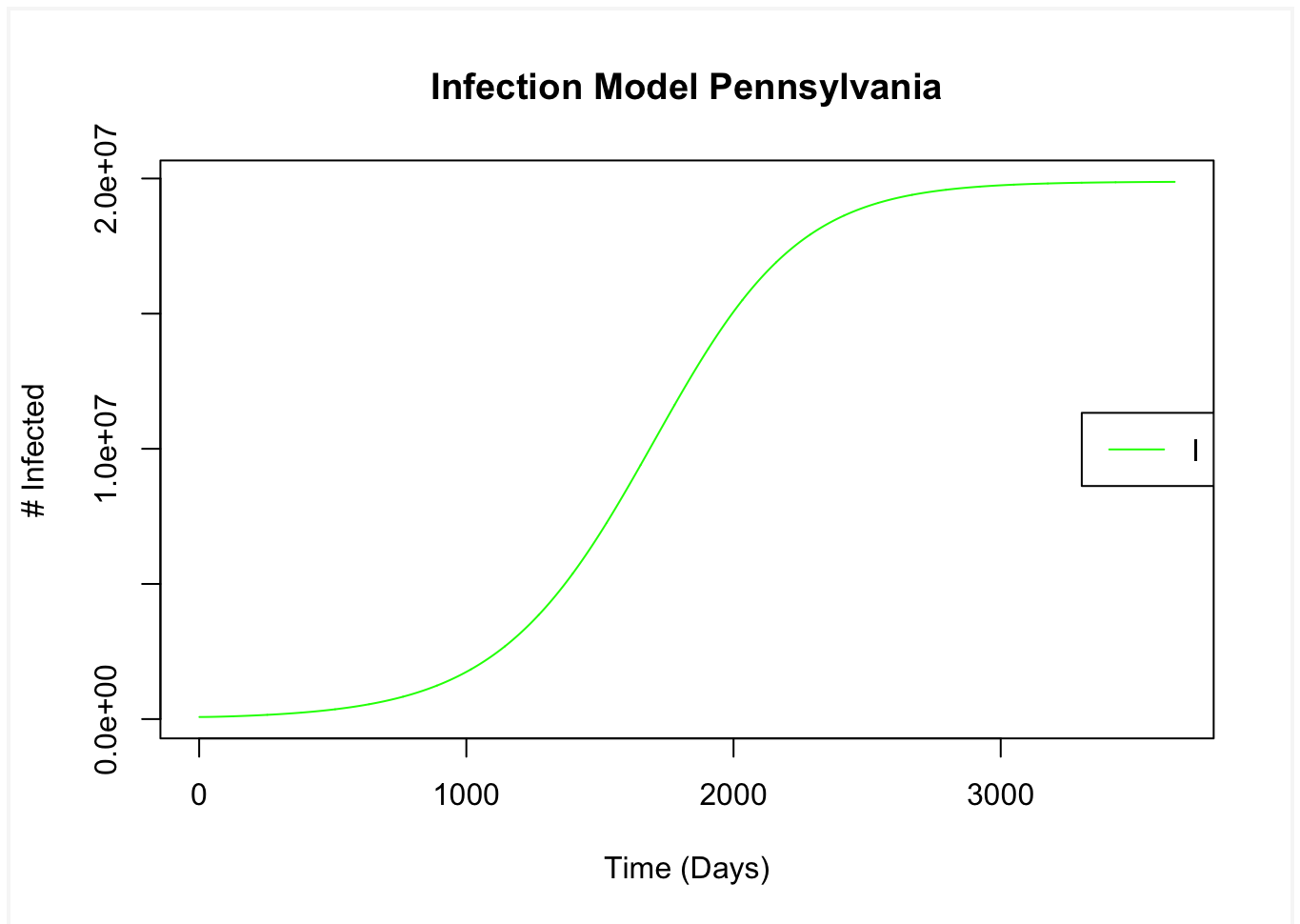
```
Pennsylvanianewmodel <- as.data.frame(Pennsylvaniamodel)$I
```

```
summary(Pennsylvanianewmodel)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  77122 1334981 12417454 10784268 19510210 19876310
```

```
matplot(Pennsylvanianewmodel, type="l", lty=1, main="Infection Model Pennsylvania", xlab="Time (Days)",
ylab = "# Infected", col = "green")
```

```
legend("right", legend= "I", lty = 1, col = "green")
```



Virginia SIR

```
require(deSolve)
```

```
SEIR <- function(time, current_state, params){
```

```
  with(as.list(c(current_state, params)),{
```

```
    N <- S+E+I+R
```

```
    dS <- -(beta*S*I)/N
```

```
    dE <- (beta*S*I)/N - sigma*E
```

```
    dI <- sigma*E - gamma*I - mu*I
```

```
    dR <- gamma*I
```

```
    dM <- mu*I
```

```
    return(list(c(dS,dE,dI,dR,dM)))
```

```
  })
```

```
}
```



```
params <- c(beta= VirginialInfectionRate, sigma=1/50, gamma=0, mu=0)
```

```
initial_state <- c(S=TotalPopulationVirginia, E=0, I=AverageDrugCountVA, R=0, M=0)
```

```
times <- 0:3650
```

```
Virginiamodel <- ode(initial_state, times, SEIR, params)
```

```
Virginianewmodel <- as.data.frame(Virginiamodel)$I
```

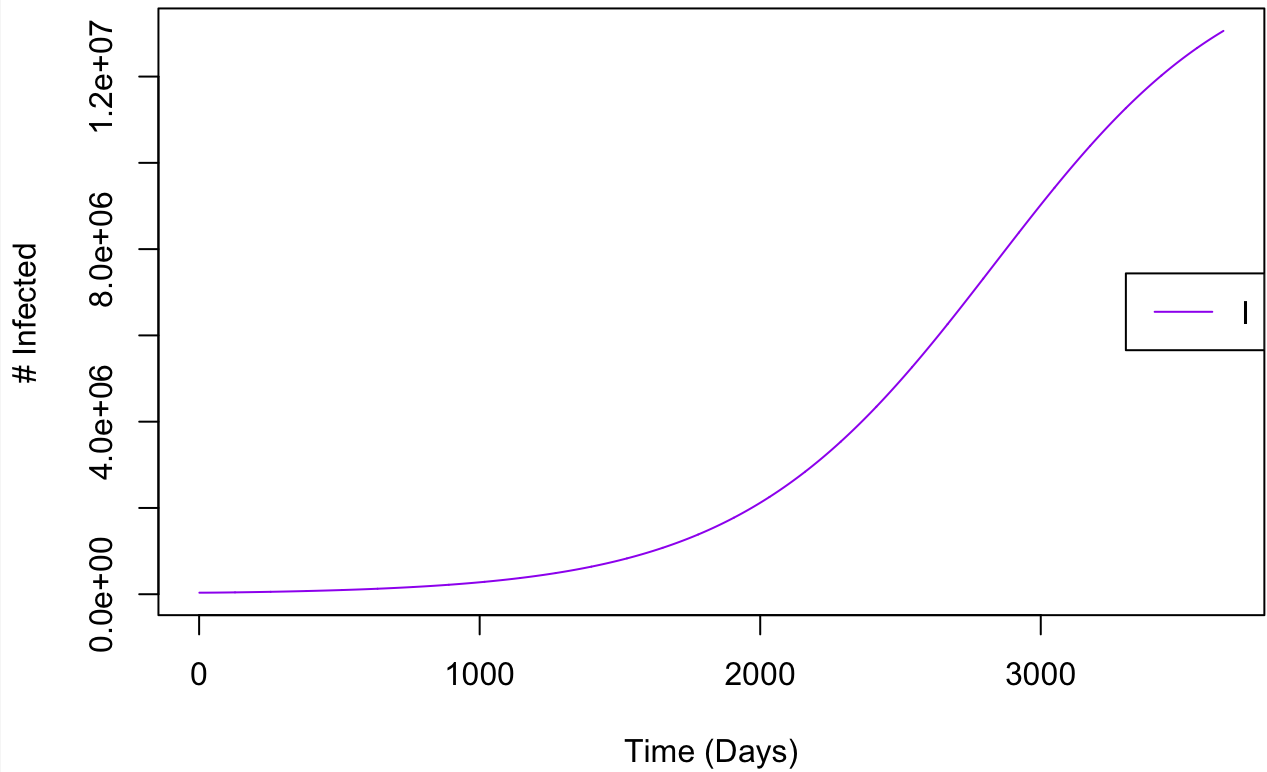
```
summary(Virginianewmodel)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  35704  230524 1519053 3715894 6843209 13058537
```

```
matplot(Virginianewmodel, type="l", lty=1, main="Infection Model Virginia", xlab="Time (Days)", ylab = "#
Infected", col = "purple")
```

```
legend("right", legend= "I", lty = 1, col = "purple")
```

Infection Model Virginia



Ohio SIR

```
require(deSolve)
```

```
SEIR <- function(time, current_state, params){
```

```
  with(as.list(c(current_state, params)),{
```

```
    N <- S+E+I+R
```

```
    dS <- -(beta*S*I)/N
```

```
    dE <- (beta*S*I)/N - sigma*E
```

```
    dI <- sigma*E - gamma*I - mu*I
```

```
    dR <- gamma*I
```

```
    dM <- mu*I
```

```
    return(list(c(dS,dE,dI,dR,dM)))
```

```
  })
```

```
}
```

```
params <- c(beta= OhioInfectionRate, sigma=1/50, gamma=0, mu=0)
```

```
initial_state <- c(S=TotalPopulationOhio, E=0, I=AverageDrugCountOH, R=0, M=0)
```

```
times <- 0:3650
```

```
Ohiomodel <- ode(initial_state, times, SEIR, params)
```

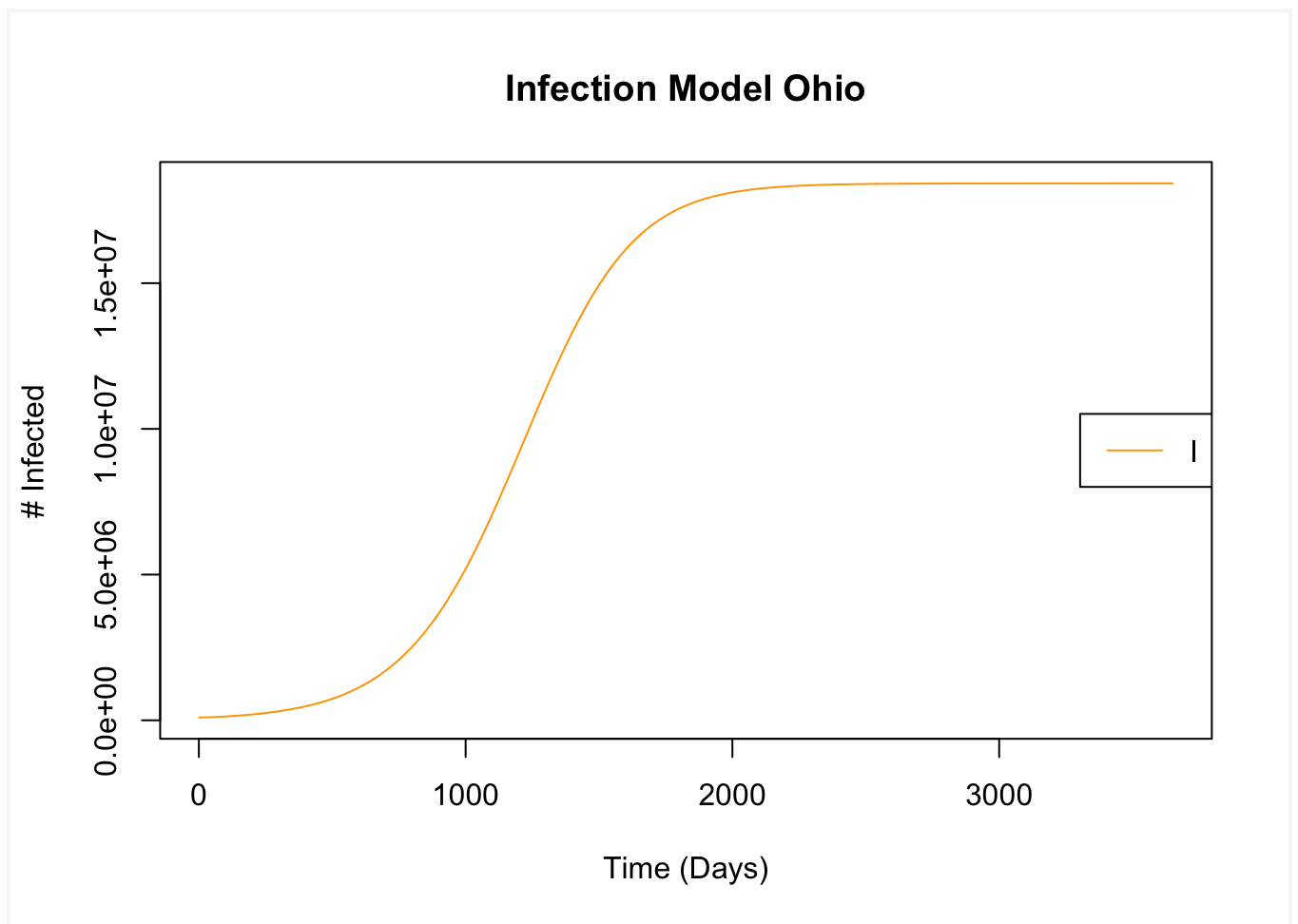
```
Ohionewmodel <- as.data.frame(Ohiomodel)$I
```

```
summary(Ohionewmodel)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  98979 3862516 17662462 12417018 18418291 18424128
```

```
matplot(Ohionewmodel, type="l", lty=1, main="Infection Model Ohio", xlab="Time (Days)", ylab = "#
Infected", col = "orange")
```

```
legend("right", legend= "I", lty = 1, col = "orange")
```



Between States

```
require(deSolve)
```

```
SEIR <- function(time, current_state, params){
```

```
  with(as.list(c(current_state, params)),{
```

```
    N <- S+E+I+R
```

```
    dS <- -(beta*S*I)/N
```

```
    dE <- (beta*S*I)/N - sigma*E
```

```
    dI <- sigma*E - gamma*I - mu*I
```

```
    dR <- gamma*I
```

```
    dM <- mu*I
```

```
    return(list(c(dS,dE,dI,dR,dM)))
```

```
  })
```

```
}
```

```
params <- c(beta= (VirginiaInfectionRate + OhioInfectionRate + PennsylvaniaInfectionRate +  
WestVirginiaInfectionRate + KentuckyInfectionRate), sigma=1/50, gamma=0, mu=0)
```

```
initial_state <- c(S=(TotalPopulationVirginia + TotalPopulationKentucky + TotalPopulationOhio +  
TotalPopulationPennsylvania + TotalPopulationWestVirginia), E=0, I=(AverageDrugCountVA +  
AverageDrugCountKY + AverageDrugCountOH + AverageDrugCountPA + AverageDrugCountWV), R=0,  
M=0)
```

```
times <- 0:3650
```

```
BetweenStatesmodel <- ode(initial_state, times, SEIR, params)
```

```
BetweenStatesnewmodel <- as.data.frame(BetweenStatesmodel)$I
```

```
summary(BetweenStatesnewmodel)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   
## 246748 62828335 62991284 54456518 62991284 62991284
```

```
matplot(Virginianewmodel, type="l", lty=1, main="Infection Model Between States", xlab="Time (Days)", ylab  
= "# Infected", col = "black")  
legend("right", legend= "I", lty = 1, col = "black")
```

Infection Model Between States

