# HW6

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### HW6

## Question 1

I tried to adapt (http://simpy.readthedocs.io/en/latest/examples/carwash.html) but I couln'd make this good. I don't get how to generate randomness into the model. I tried with CHECKTIME \* expon.rvs(scale = 0.75). But I was lost with that. But I think that is a good try.

Passenger 0 arrives at the BoardingChecks at 0.00. Passenger 1 arrives at the BoardingChecks at 0.00. Passenger 2 arrives at the BoardingChecks at 0.00. Passenger 3 arrives at the BoardingChecks at 0.00. Passenger 0 enters the BoardingChecks at 0.00. Passenger 0 leaves the BoardingChecks at 1.00. Passenger 0 enters the Security Checks at 1.00. Passenger 0 leaves the Security Checks at 2.00. Passenger 1 enters the BoardingChecks at 2.00. Passenger 1 leaves the BoardingChecks at 3.00. Passenger 1 enters the Security Checks at 3.00. Passenger 1 leaves the Security Checks at 4.00. Passenger 2 enters the BoardingChecks at 4.00. Passenger 4 arrives at the BoardingChecks at 5.00. Passenger 2 leaves the BoardingChecks at 5.00. Passenger 2 enters the Security Checks at 5.00. Passenger 2 leaves the Security Checks at 6.00. Passenger 3 enters the BoardingChecks at 6.00. Passenger 3 leaves the BoardingChecks at 7.00. Passenger 3 enters the Security Checks at 7.00. Passenger 3 leaves the Security Checks at 8.00. Passenger 4 enters the BoardingChecks at 8.00. Passenger 4 leaves the BoardingChecks at 9.00. Passenger 4 enters the Security Checks at 9.00. Passenger 5 arrives at the BoardingChecks at 10.00. Passenger 4 leaves the Security Checks at 10.00. Passenger 5 enters the BoardingChecks at 10.00. Passenger 5 leaves the BoardingChecks at 11.00. Passenger 5 enters the Security Checks at 11.00. Passenger 5 leaves the Security Checks at 12.00. Passenger 6 arrives at the BoardingChecks at 17.00. Passenger 6 enters the BoardingChecks at 17.00. Passenger 6 leaves the BoardingChecks at 18.00.

Passenger 6 enters the Security Checks at 18.00. Passenger 6 leaves the Security Checks at 19.00. Passenger 7 arrives at the BoardingChecks at 23.00.

```
Passenger 7 enters the BoardingChecks at 23.00.
```

Passenger 7 leaves the BoardingChecks at 24.00.

Passenger 7 enters the Security Checks at 24.00.

Passenger 7 leaves the Security Checks at 25.00.

Passenger 8 arrives at the BoardingChecks at 29.00.

Passenger 8 enters the BoardingChecks at 29.00.

Passenger 8 leaves the BoardingChecks at 30.00.

Passenger 8 enters the Security Checks at 30.00.

Passenger 8 leaves the Security Checks at 31.00.

Passenger 9 arrives at the BoardingChecks at 35.00.

Passenger 9 enters the BoardingChecks at 35.00.

Passenger 9 leaves the BoardingChecks at 36.00.

Passenger 9 enters the Security Checks at 36.00.

Passenger 9 leaves the Security Checks at 37.00.

Passenger 10 arrives at the BoardingChecks at 40.00.

Passenger 10 enters the BoardingChecks at 40.00.

Passenger 10 leaves the BoardingChecks at 41.00.

Passenger 10 enters the Security Checks at 41.00.

Passenger 10 leaves the Security Checks at 42.00.

Passenger 11 arrives at the BoardingChecks at 49.00.

Passenger 11 enters the BoardingChecks at 49.00.

Passenger 11 leaves the BoardingChecks at 50.00.

Passenger 11 enters the Security Checks at 50.00.

Passenger 11 leaves the Security Checks at 51.00.

Passenger 12 arrives at the BoardingChecks at 54.00.

Passenger 12 enters the BoardingChecks at 54.00.

Passenger 12 leaves the BoardingChecks at 55.00.

Passenger 12 enters the Security Checks at 55.00.

Passenger 12 leaves the Security Checks at 56.00.

Passenger 13 arrives at the BoardingChecks at 63.00.

Passenger 13 enters the BoardingChecks at 63.00.

Passenger 13 leaves the BoardingChecks at 64.00.

Passenger 13 enters the Security Checks at 64.00.

Passenger 13 leaves the Security Checks at 65.00.

Passenger 14 arrives at the BoardingChecks at 71.00.

Passenger 14 enters the BoardingChecks at 71.00.

Passenger 14 leaves the BoardingChecks at 72.00.

Passenger 14 enters the Security Checks at 72.00.

Passenger 14 leaves the Security Checks at 73.00.

Passenger 15 arrives at the BoardingChecks at 76.00.

Passenger 15 enters the BoardingChecks at 76.00.

Passenger 15 leaves the BoardingChecks at 77.00.

Passenger 15 enters the Security Checks at 77.00.

Passenger 15 leaves the Security Checks at 78.00.

Passenger 16 arrives at the BoardingChecks at 81.00.

Passenger 16 enters the BoardingChecks at 81.00.

Passenger 16 leaves the BoardingChecks at 82.00.

Passenger 16 enters the Security Checks at 82.00. Passenger 16 leaves the Security Checks at 83.00.

Passenger 17 arrives at the BoardingChecks at 86.00.

Passenger 17 enters the BoardingChecks at 86.00.

Passenger 17 leaves the BoardingChecks at 87.00.

Passenger 17 enters the Security Checks at 87.00.

Passenger 17 leaves the Security Checks at 88.00.

Passenger 18 arrives at the BoardingChecks at 92.00.

Passenger 18 enters the BoardingChecks at 92.00.

```
Passenger 18 leaves the BoardingChecks at 93.00.
Passenger 18 enters the Security Checks at 93.00.
Passenger 18 leaves the Security Checks at 94.00.
Passenger 19 arrives at the BoardingChecks at 98.00.
Passenger 19 enters the BoardingChecks at 98.00.
Passenger 19 leaves the BoardingChecks at 99.00.
Passenger 19 enters the Security Checks at 99.00.
Passenger 19 leaves the Security Checks at 100.00.
Passenger 20 arrives at the BoardingChecks at 107.00.
Passenger 20 enters the BoardingChecks at 107.00.
Passenger 20 leaves the BoardingChecks at 108.00.
Passenger 20 enters the Security Checks at 108.00.
Passenger 20 leaves the Security Checks at 109.00.
Passenger 21 arrives at the BoardingChecks at 116.00.
Passenger 21 enters the BoardingChecks at 116.00.
Passenger 21 leaves the BoardingChecks at 117.00.
Passenger 21 enters the Security Checks at 117.00.
Passenger 21 leaves the Security Checks at 118.00.
Passenger 22 arrives at the BoardingChecks at 121.00.
Passenger 22 enters the BoardingChecks at 121.00.
Passenger 22 leaves the BoardingChecks at 122.00.
Passenger 22 enters the Security Checks at 122.00.
Passenger 22 leaves the Security Checks at 123.00.
Passenger 23 arrives at the BoardingChecks at 130.00.
Passenger 23 enters the BoardingChecks at 130.00.
Passenger 23 leaves the BoardingChecks at 131.00.
Passenger 23 enters the Security Checks at 131.00.
Passenger 23 leaves the Security Checks at 132.00.
Passenger 24 arrives at the BoardingChecks at 136.00.
Passenger 24 enters the BoardingChecks at 136.00.
Passenger 24 leaves the BoardingChecks at 137.00.
Passenger 24 enters the Security Checks at 137.00.
Passenger 24 leaves the Security Checks at 138.00.
Passenger 25 arrives at the BoardingChecks at 145.00.
Passenger 25 enters the BoardingChecks at 145.00.
Passenger 25 leaves the BoardingChecks at 146.00.
Passenger 25 enters the Security Checks at 146.00.
Passenger 25 leaves the Security Checks at 147.00.
import random
```

import random
import scipy
from scipy.stats import expon
import simpy

RANDOM SEED = 42

NUM\_MACHINES = 1 # Number of machines in the BoardingChecks
CHECKTIME = 1 # Minutes it takes to bording check below I adjusted with exponential dist
CHECKTIME2 = 1 # Minutes it takes to security checke below I adjusted with exponential dist
T\_INTER = 1 # Create a passenger every ~n minutes, below I adjusted it to a exponential dist
SIM\_TIME = 150 # Simulation time in minutes

#### class BoardingChecks(object):

"""A Boarding Checks has a limited number of machines (``NUM\_MACHINES``) to checks ID passenger in parallel.

```
,,,,,,
  def __init__(self, env, num_machines, CHECKTIME, CHECKTIME2):
    self.env = env
    self.machine = simpy.Resource(env, num machines)
    self.CHECKTIME = CHECKTIME
    self.CHECKTIME2 = CHECKTIME2
  def checkId(self, passenger):
    yield self.env.timeout(CHECKTIME)
  def checkSecurity(self, passenger):
    yield self.env.timeout(CHECKTIME2)
def passenger(env, name, cw):
  """The passenger process (each passenger has a ``name``) arrives at the BoardingChecks
  (``cw``) and requests a check machine and then security check.
  print('%s arrives at the BoardingChecks at %.2f.' % (name, env.now))
  with cw.machine.request() as request:
    yield request
    print('%s enters the BoardingChecks at %.2f.' % (name, env.now))
    yield env.process(cw.checkId(name))
    print('%s leaves the BoardingChecks at %.2f.' % (name, env.now))
    print('%s enters the Security Checks at %.2f.' % (name, env.now))
    yield env.process(cw.checkSecurity(name))
    print('%s leaves the Security Checks at %.2f.' % (name, env.now))
def setup(env, num_machines, CHECKTIME, CHECKTIME2, t_inter):
  boardingChecks = BoardingChecks(env, num_machines, CHECKTIME * expon.rvs(scale = 0.75),
CHECKTIME2 * expon.rvs(scale = 0.5))
  # Create 4 initial passenger
  for i in range(4):
    env.process(passenger(env, 'Passenger %d' % i, boardingChecks))
  # Create more passengers while the simulation is running
  while True:
    yield env.timeout(random.randint(t_inter - 2, t_inter + 2))
    env.process(passenger(env, 'Passenger %d' % i, boardingChecks))
```

```
print('BoardingChecks')
random.seed(RANDOM_SEED) # This helps reproducing the results

# Create an environment and start the setup process
env = simpy.Environment()
env.process(setup(env, NUM_MACHINES, CHECKTIME, CHECKTIME2, T_INTER))

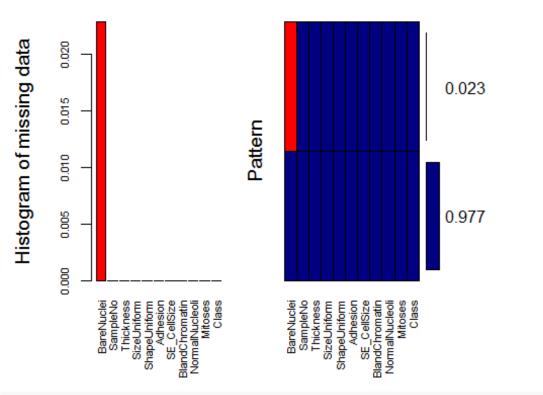
# Execute!
env.run(until=SIM_TIME)
```

# **Question 2**

```
require(dplyr)
## Loading required package: 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
##
require(mice)
## Loading required package: mice
require(knitr)
## Loading required package: knitr
library(VIM)
## Loading required package: colorspace
## Loading required package: grid
## Loading required package: data.table
##
## Attaching package: 'data.table'
## The following objects are masked from 'package:dplyr':
##
       between, first, last
##
## VIM is ready to use.
    Since version 4.0.0 the GUI is in its own package VIMGUI.
##
##
##
             Please use the package to use the new (and old) GUI.
```

```
## Suggestions and bug-reports can be submitted at:
https://github.com/alexkowa/VIM/issues
##
## Attaching package: 'VIM'
## The following object is masked from 'package:datasets':
##
##
       sleep
breast.data <- read.csv("http://archive.ics.uci.edu/ml/machine-learning-</pre>
databases/breast-cancer-wisconsin/breast-cancer-wisconsin.data",
                      header = F, na.strings = "?")
colnames(breast.data) <- c("SampleNo",</pre>
                          "Thickness",
                          "SizeUniform",
                          "ShapeUniform",
                          "Adhesion",
                          "SE CellSize",
                          "BareNuclei",
                          "BlandChromatin",
                          "NormalNucleoli".
                          "Mitoses",
                          "Class")
summary(breast.data)
                                        SizeUniform
##
       SampleNo
                        Thickness
                                                         ShapeUniform
## Min.
         :
              61634
                      Min. : 1.000
                                       Min. : 1.000
                                                        Min.
                                                               : 1.000
   1st Qu.: 870688
                      1st Qu.: 2.000
                                       1st Qu.: 1.000
                                                        1st Qu.: 1.000
   Median : 1171710
                      Median : 4.000
                                       Median : 1.000
##
                                                        Median : 1.000
          : 1071704
                             : 4.418
                                              : 3.134
                                                        Mean
                                                               : 3.207
##
   Mean
                      Mean
                                       Mean
   3rd Qu.: 1238298
                      3rd Qu.: 6.000
                                       3rd Qu.: 5.000
                                                        3rd Qu.: 5.000
   Max. :13454352
                      Max. :10.000
##
                                       Max.
                                              :10.000
                                                        Max.
                                                               :10.000
##
##
      Adhesion
                      SE_CellSize
                                       BareNuclei
                                                      BlandChromatin
   Min. : 1.000
                    Min. : 1.000
                                     Min. : 1.000
                                                      Min. : 1.000
##
##
   1st Qu.: 1.000
                     1st Qu.: 2.000
                                     1st Qu.: 1.000
                                                      1st Qu.: 2.000
                     Median : 2.000
##
   Median : 1.000
                                     Median : 1.000
                                                      Median : 3.000
   Mean : 2.807
                                            : 3.545
                                                      Mean : 3.438
##
                     Mean : 3.216
                                     Mean
   3rd Qu.: 4.000
##
                     3rd Qu.: 4.000
                                     3rd Qu.: 6.000
                                                      3rd Qu.: 5.000
   Max. :10.000
                           :10.000
##
                    Max.
                                     Max.
                                            :10.000
                                                      Max. :10.000
##
                                     NA's
                                            :16
##
   NormalNucleoli
                       Mitoses
                                         Class
##
   Min.
          : 1.000
                    Min. : 1.000
                                     Min.
                                            :2.00
   1st Qu.: 1.000
                     1st Qu.: 1.000
                                     1st Qu.:2.00
##
## Median : 1.000
                    Median : 1.000
                                     Median :2.00
   Mean : 2.867
                    Mean : 1.589
                                     Mean :2.69
##
## 3rd Qu.: 4.000
                     3rd Qu.: 1.000
                                     3rd Qu.:4.00
```

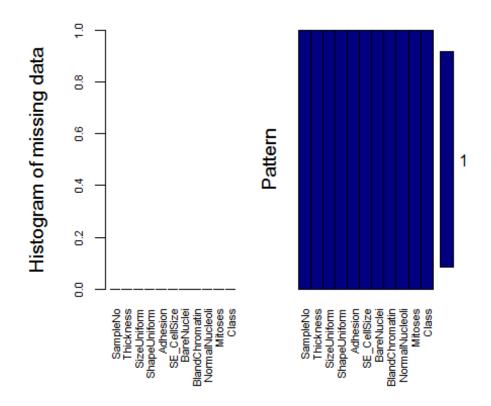
```
##
    Max.
           :10.000
                      Max.
                             :10.000
                                       Max.
                                               :4.00
##
str(breast.data)
## 'data.frame':
                     699 obs. of 11 variables:
                            1000025 1002945 1015425 1016277 1017023
    $ SampleNo
                     : int
1017122 1018099 1018561 1033078 1033078 ...
                     : int
##
    $ Thickness
                            5 5 3 6 4 8 1 2 2 4 ...
##
    $ SizeUniform
                     : int
                            1 4 1 8 1 10 1 1 1 2 ...
                            1 4 1 8 1 10 1 2 1 1 ...
##
    $ ShapeUniform
                     : int
##
    $ Adhesion
                     : int
                            1511381111...
    $ SE CellSize
                     : int
                            2 7 2 3 2 7 2 2 2 2
##
                            1 10 2 4 1 10 10 1 1 1 ...
##
    $ BareNuclei
                     : int
    $ BlandChromatin: int
##
                            3 3 3 3 3 9 3 3 1 2 ...
                            1 2 1 7 1 7 1 1 1 1
##
    $ NormalNucleoli: int
##
                            1 1 1 1 1 1 1 1 5 1 ...
    $ Mitoses
                     : int
##
    $ Class
                     : int
                            2 2 2 2 2 4 2 2 2 2 ...
#Checking % of NAs
aggr_plot <- aggr(breast.data, col=c('navyblue','red'), numbers=TRUE,</pre>
sortVars=TRUE, labels=names(breast.data), cex.axis=.7, gap=3,
ylab=c("Histogram of missing data", "Pattern"))
```



```
##
## Variables sorted by number of missings:
## Variable Count
## BareNuclei 0.02288984
```

```
SampleNo 0.00000000
##
##
         Thickness 0.00000000
##
       SizeUniform 0.00000000
##
      ShapeUniform 0.00000000
##
           Adhesion 0.00000000
##
       SE CellSize 0.00000000
##
    BlandChromatin 0.00000000
##
    NormalNucleoli 0.00000000
##
           Mitoses 0.00000000
##
              Class 0.00000000
# Setting seed.
set.seed(123)
# mean values
mean.imputation <- mice(breast.data, method = "pmm", maxit = 10)</pre>
##
##
    iter imp variable
##
     1
             BareNuclei
             BareNuclei
##
     1
##
     1
             BareNuclei
##
     1
         4
             BareNuclei
##
     1
             BareNuclei
##
     2
             BareNuclei
     2
             BareNuclei
##
##
     2
             BareNuclei
     2
##
         4
             BareNuclei
##
     2
             BareNuclei
     3
##
             BareNuclei
     3
##
             BareNuclei
     3
         3
             BareNuclei
##
##
     3
         4
             BareNuclei
##
     3
             BareNuclei
##
     4
             BareNuclei
##
     4
             BareNuclei
         3
##
     4
             BareNuclei
##
     4
             BareNuclei
##
     4
             BareNuclei
     5
##
             BareNuclei
##
     5
         2
             BareNuclei
##
     5
         3
             BareNuclei
##
     5
             BareNuclei
##
     5
             BareNuclei
##
     6
             BareNuclei
##
     6
             BareNuclei
##
     6
             BareNuclei
##
     6
             BareNuclei
##
         5
     6
             BareNuclei
##
     7
         1
             BareNuclei
##
     7
         2
             BareNuclei
```

```
##
     7
          3
             BareNuclei
##
     7
          4
             BareNuclei
##
     7
             BareNuclei
##
     8
          1
             BareNuclei
     8
##
             BareNuclei
##
     8
          3
             BareNuclei
     8
##
          4
             BareNuclei
##
     8
          5
             BareNuclei
##
     9
          1
             BareNuclei
##
     9
          2
             BareNuclei
##
     9
          3
             BareNuclei
##
     9
             BareNuclei
     9
##
             BareNuclei
##
     10
              BareNuclei
##
     10
           2
              BareNuclei
##
           3
              BareNuclei
     10
##
           4
              BareNuclei
     10
##
     10
           5
              BareNuclei
complete.data.mean <- complete(mean.imputation,1)</pre>
#Checking % of NAs with mean imputation
aggr_plot <- aggr(complete.data.mean, col=c('navyblue','red'),</pre>
numbers=TRUE, sortVars=TRUE, labels=names(breast.data), cex.axis=.7,
gap=3, ylab=c("Histogram of missing data", "Pattern"))
```



```
##
##
    Variables sorted by number of missings:
##
          Variable Count
##
          SampleNo
##
                        0
         Thickness
##
       SizeUniform
                        0
##
                        0
      ShapeUniform
##
          Adhesion
                        0
##
       SE CellSize
                        0
##
        BareNuclei
                        0
##
    BlandChromatin
                        0
## NormalNucleoli
                        0
##
           Mitoses
                        0
##
             Class
                        0
# regressed values
regressed.imputation <- mice(breast.data, method = "norm.predict", maxit
= 10)
##
##
    iter imp variable
            BareNuclei
##
     1
##
     1
            BareNuclei
##
         3 BareNuclei
     1
            BareNuclei
##
     1
##
         5 BareNuclei
     1
##
     2
            BareNuclei
##
     2
         2 BareNuclei
         3 BareNuclei
##
     2
##
     2
         4 BareNuclei
##
     2
         5 BareNuclei
##
     3
         1 BareNuclei
##
     3
         2 BareNuclei
##
     3
         3 BareNuclei
##
     3
         4 BareNuclei
##
     3
            BareNuclei
##
     4
            BareNuclei
##
     4
            BareNuclei
##
     4
         3 BareNuclei
##
     4
         4 BareNuclei
##
     4
         5 BareNuclei
##
     5
            BareNuclei
##
     5
            BareNuclei
##
     5
         3 BareNuclei
     5
         4 BareNuclei
##
     5
         5 BareNuclei
##
##
     6
            BareNuclei
##
         2 BareNuclei
     6
##
     6
            BareNuclei
##
     6
         4 BareNuclei
```

```
##
     6
         5
            BareNuclei
            BareNuclei
##
     7
         1
##
     7
         2 BareNuclei
##
     7
            BareNuclei
     7
##
         4 BareNuclei
         5
##
     7
            BareNuclei
##
     8
         1 BareNuclei
         2 BareNuclei
##
     8
##
     8
         3 BareNuclei
##
     8
         4 BareNuclei
     8
         5 BareNuclei
##
##
     9
       1 BareNuclei
##
     9
            BareNuclei
     9
##
         3 BareNuclei
         4 BareNuclei
##
     9
##
     9
         5 BareNuclei
        1 BareNuclei
##
     10
##
     10
          2 BareNuclei
##
     10
        3 BareNuclei
##
          4
             BareNuclei
     10
##
     10
          5 BareNuclei
complete.data.imputation <- complete(mean.imputation,1)</pre>
#Checking % of NAs with regressed values
aggr_plot <- aggr(complete.data.imputation, col=c('navyblue','red'),</pre>
numbers=TRUE, sortVars=TRUE, labels=names(breast.data), cex.axis=.7,
gap=3, ylab=c("Histogram of missing data", "Pattern"))
##
   Variables sorted by number of missings:
##
##
          Variable Count
##
          SampleNo
##
         Thickness
                        0
       SizeUniform
                        0
##
##
      ShapeUniform
                        0
##
          Adhesion
                        0
       SE CellSize
                        0
##
##
        BareNuclei
                        0
    BlandChromatin
                        0
##
##
  NormalNucleoli
                        0
                        0
##
           Mitoses
##
             Class
                        0
# Impute using pertubation
ind <- is.na(breast.data[,7])</pre>
data.nona <- breast.data[!ind, ]</pre>
complete.data.perturbation = breast.data
perturbation = rnorm(nrow(data.nona ))*0.1
model <- lm(BareNuclei + perturbation ~ ., data = data.nona )</pre>
complete.data.perturbation[, 7] = round(predict(model, breast.data),
```

```
digits = 0)
#Checking % of NAs with regressed+perturbation values
aggr_plot <- aggr(complete.data.perturbation, col=c('navyblue','red'),</pre>
numbers=TRUE, sortVars=TRUE, labels=names(breast.data), cex.axis=.7,
gap=3, ylab=c("Histogram of missing data", "Pattern"))
##
   Variables sorted by number of missings:
##
##
          Variable Count
##
          SampleNo
##
         Thickness
                        0
##
       SizeUniform
                        0
##
      ShapeUniform
                        0
##
                       0
          Adhesion
       SE CellSize
                       0
##
##
                       0
        BareNuclei
                       0
## BlandChromatin
## NormalNucleoli
                       0
##
           Mitoses
                       0
##
             Class
```

# **Question 3**

A linear optimization problem for could be *Portfolio Asset Allocation*. I work in investment strategy for voluntary pension fund. We need to rebalance the portfolios periodically and we need to allocate resources wisely. For that I implemented an investment portfolio optimizer.

### **As Target:**

Weight for n Assets for allocate money

### As input:

Daily % Price Change for n Assets Expected 12 months returns

**As Constrains:** Asset Max Weight

Asset Min Weight
Sector Max Weight
Sector Min Weight
Max volatility allowed
Min Volatility Allowed
All weight of asset sum = 1