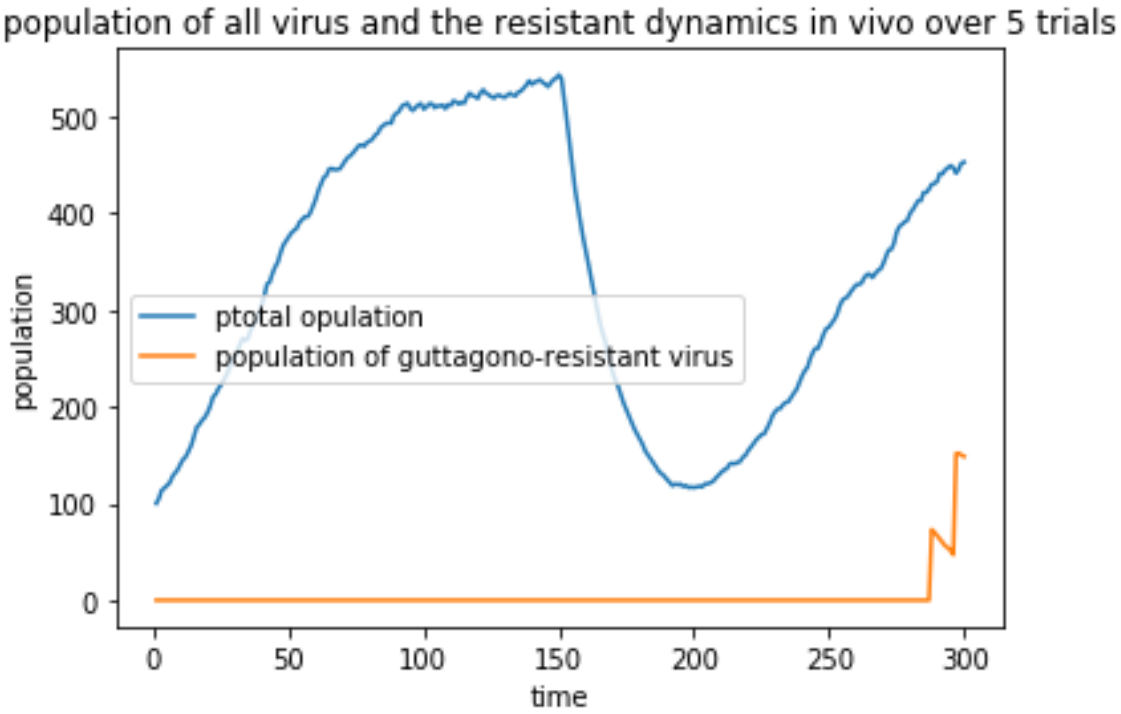
experiment report

Problem 4

First Results: In the first picture, the results for the blue line is roughly consistently with the evidence. Before 150 time step, i.e the point where patient start to take a drug, viruses grow quickly and nearly stop growing In 100 time step. It shows that the population density is one of the effect to the growth of virus.

But the orange line is not consistent with the evidence. The population of resistant viruses keep zero until 280 time step.



Guess: the error will be either in the function that calculates the population or in the reproduce function that administrative the reproduction.

Next: design a repeatable experiment for the simplest version of the same problem

Experiment:

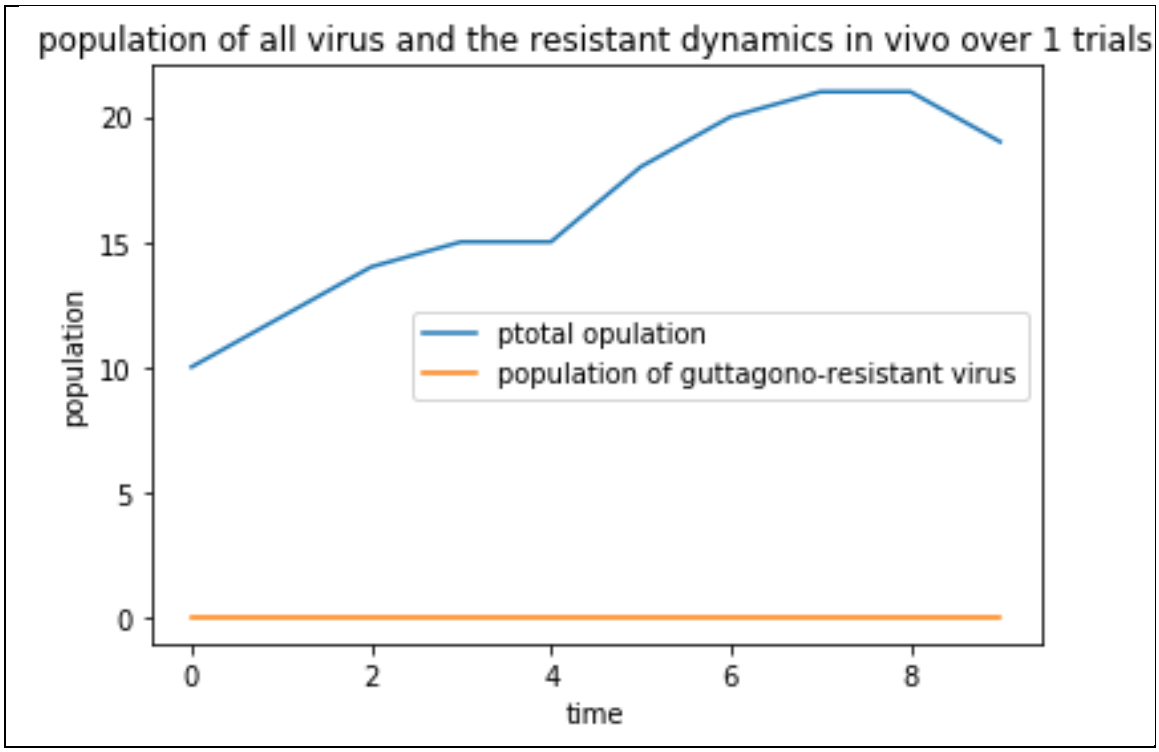
set the parameters as below :1 trial, 10 time steps, 10 initial viruses, 100 max population, 0.5 mutProb

Print: print the population every time step, print the resistance of the offspring reproduced by original viruses every time step. If there 10 viruses in after clearance in a time step, there will be roughly (probability*10) offspring reproduced.

Results: we can see that even though the resistant viruses were created through mutation, but the population didn't grow, So the range of error is narrowed down to the function that calculate the population of the resistant viruses.

In order to check it clearly without 干扰, so we delete the function of clearing the viruses(comment that out), and check the how it run

```
timestep:0,total population after clearance: 10 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:1,total population after clearance: 12 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:2,total population after clearance: 14 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} True
timestep:3,total population after clearance: 15 resistant pop:0
timestep:4,total population after clearance: 15 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:5,total population after clearance: 18 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:6,total population after clearance: 20 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} True
timestep:7,total population after clearance: 21 resistant pop:0
timestep:8,total population after clearance: 19 resistant pop:0
timestep:9,total population after clearance: 18 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} True
```

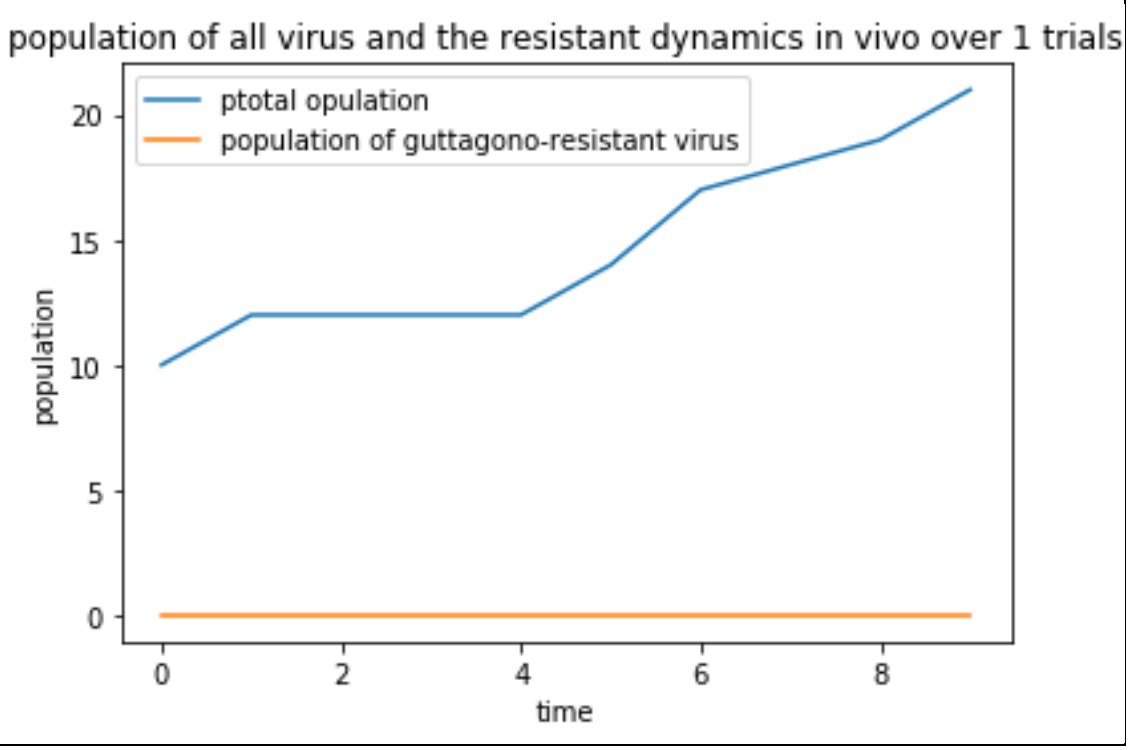


Results(following):

obviously, the number of reproduced offspring is consistent with the total population growth. So far, except the calculation of the population resistant viruses, there are no other error from the given evidence.

```
timestep:0,total population after clearance: 10 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:1,total population after clearance: 12 resistant pop:0
timestep:2,total population after clearance: 12 resistant pop:0
timestep:3,total population after clearance: 12 resistant pop:0
timestep:4,total population after clearance: 12 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:5,total population after clearance: 14 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} True
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:6,total population after clearance: 17 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:7,total population after clearance: 18 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} True
timestep:8,total population after clearance: 19 resistant pop:0
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} False
timestep:9,total population after clearance: 21 resistant pop:0
```

```
the resistance to guttagonol of offspring after reproduce:{0} True
the resistance to guttagonol of offspring after reproduce:{0} False
the resistance to guttagonol of offspring after reproduce:{0} True
```



Dig

Eventually, 定位出错误（记得还有一个单词）located the error

the line of code marked in red is the source of error

isResist=True # this should be reset in every check of the virus

```
def getResistPop(self, drugResist):
    """
    Get the population of virus particles resistant to the drugs listed in
    drugResist.

    drugResist: Which drug resistances to include in the population (a list
    of strings - e.g. ['guttagonol'] or ['guttagonol', 'grimpex'])

    returns: the population of viruses (an integer) with resistances to all
    drugs in the drugResist list.
    """
    # TODO
    popResisV=0
    isResist=True # this should be reset in every check of the virus
```

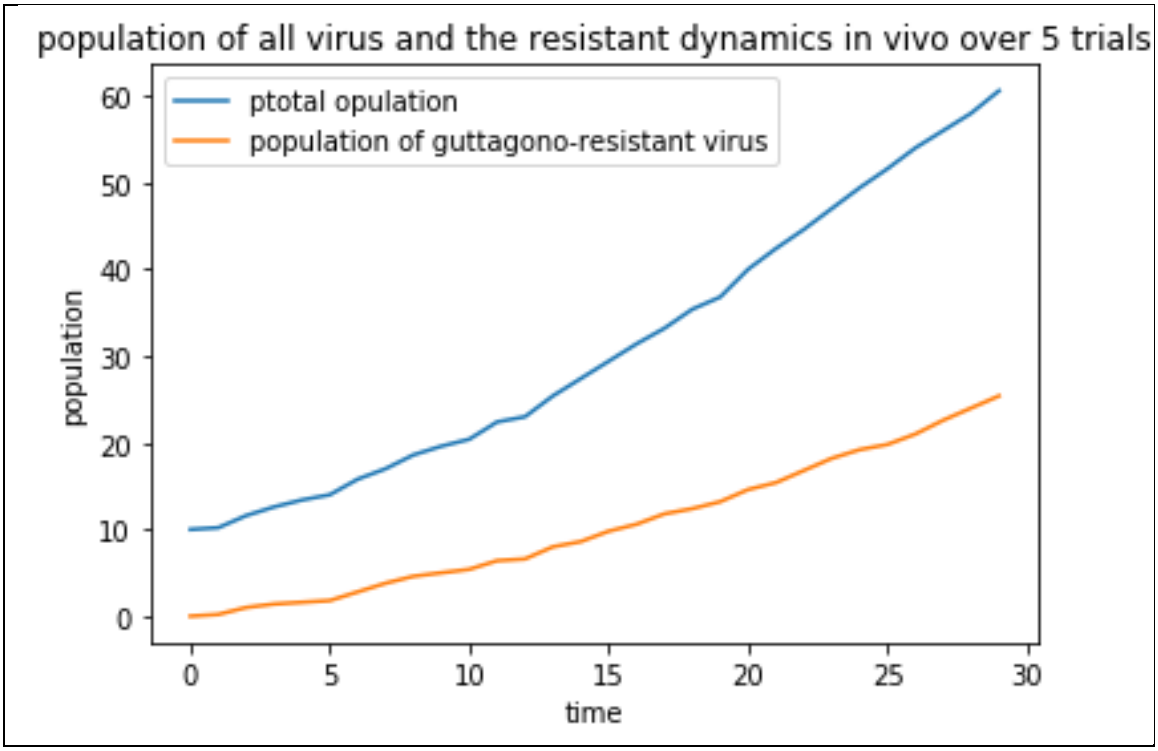
```
        for virus in self.viruses:
#           if type(virus)==ResistantVirus:
              # ??? is it right
              # the instance of superclass would not have the attribute of
              # its subclass, but vice-versa, i.e. if a statement is  instance.attribute,
              # then it will directly override that of superclass, no matter how many
arguments of the method
            for drug in drugResist:
                isResist=isResist and virus.getResistance(drug)
            if isResist: popResisV+=1
#             print(isResist,popResisV)
        return popResisV
```

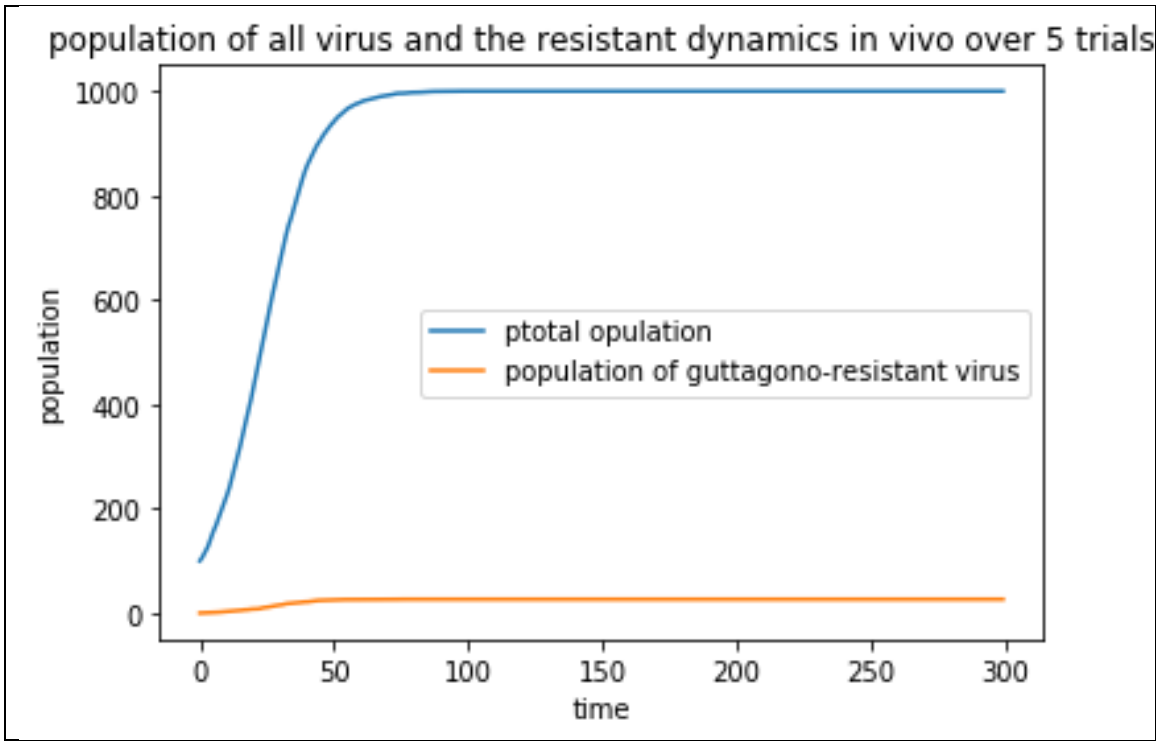
Then:

Modify the code, then run It again, results is shown below, one is smaller version, one is bigger version.

what the hell

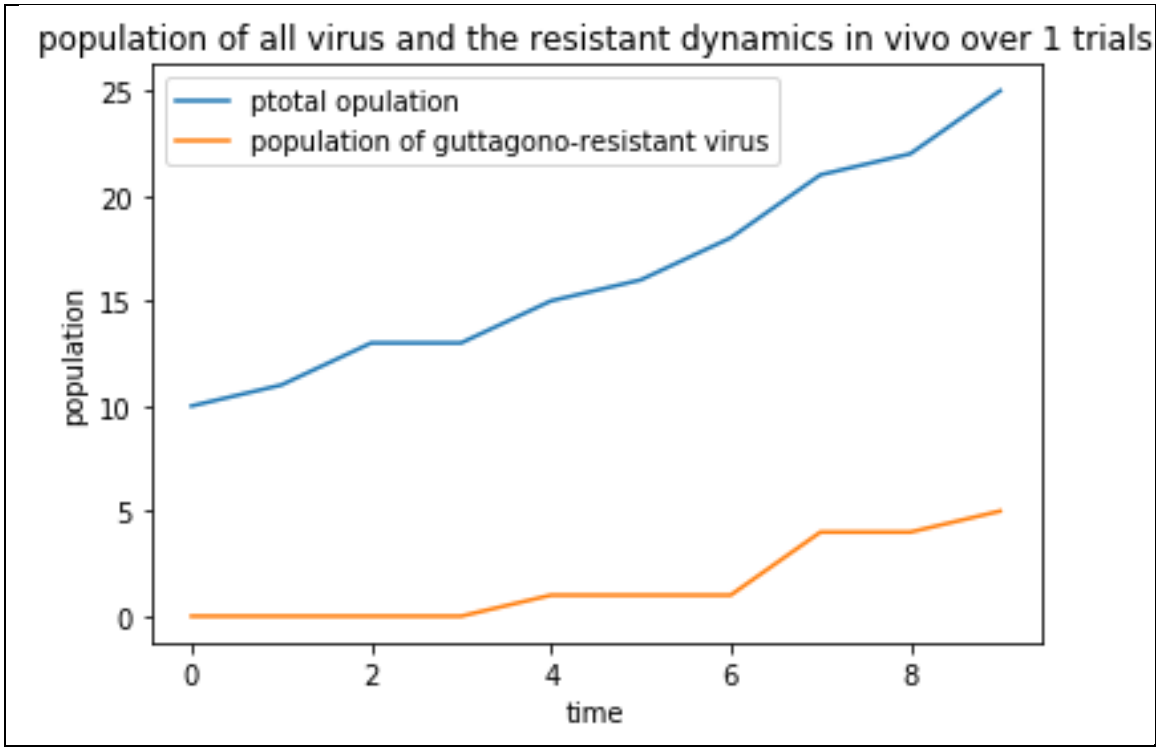
We won't panic, think, whoops, forget to uncomment out the codes that execute clearance function for the viruses.





Finally, v1.0

uncomment that out and run it

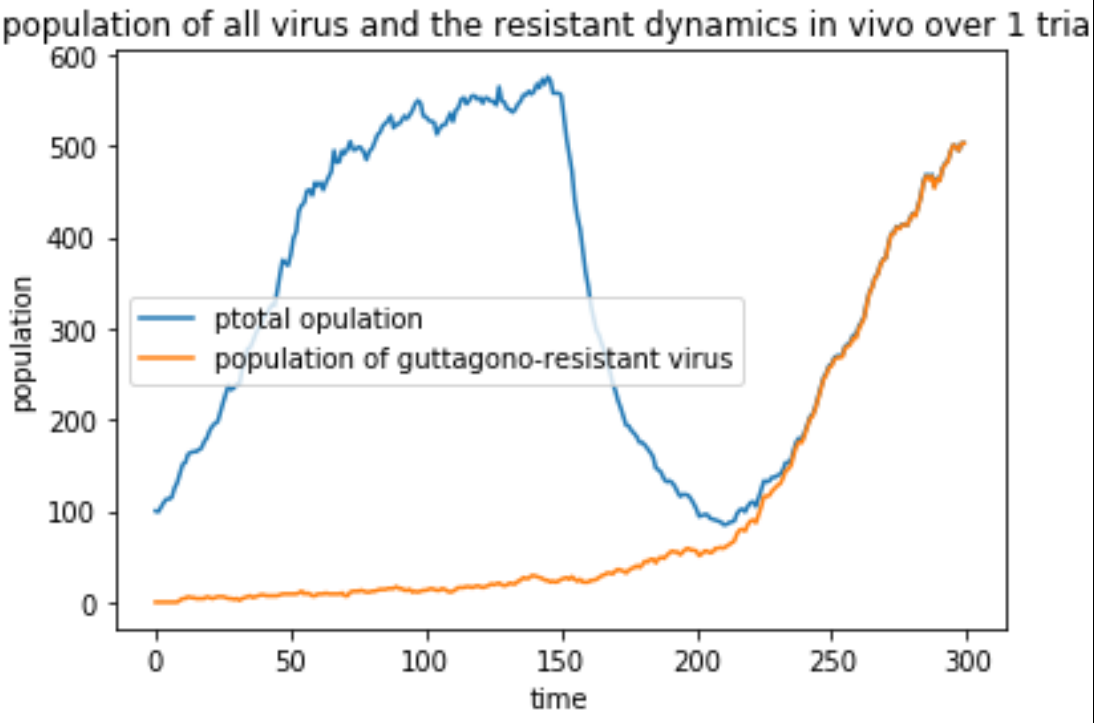


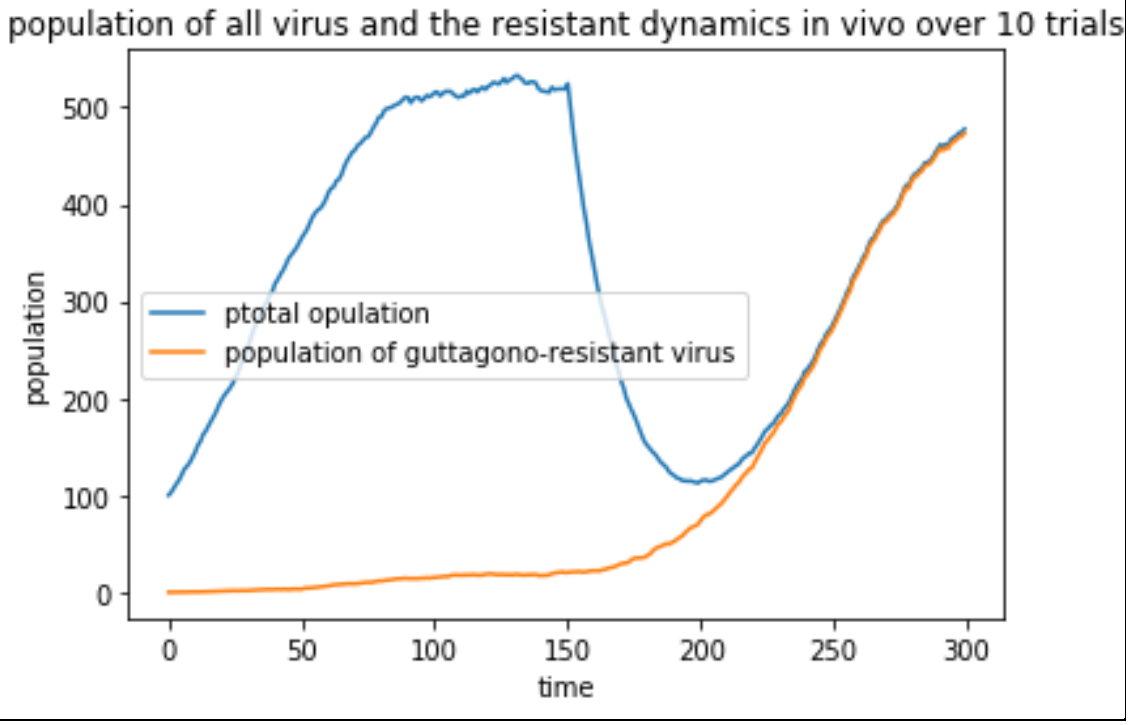
Finally v1.1

Reset all the parameters to the original bigger version and run it

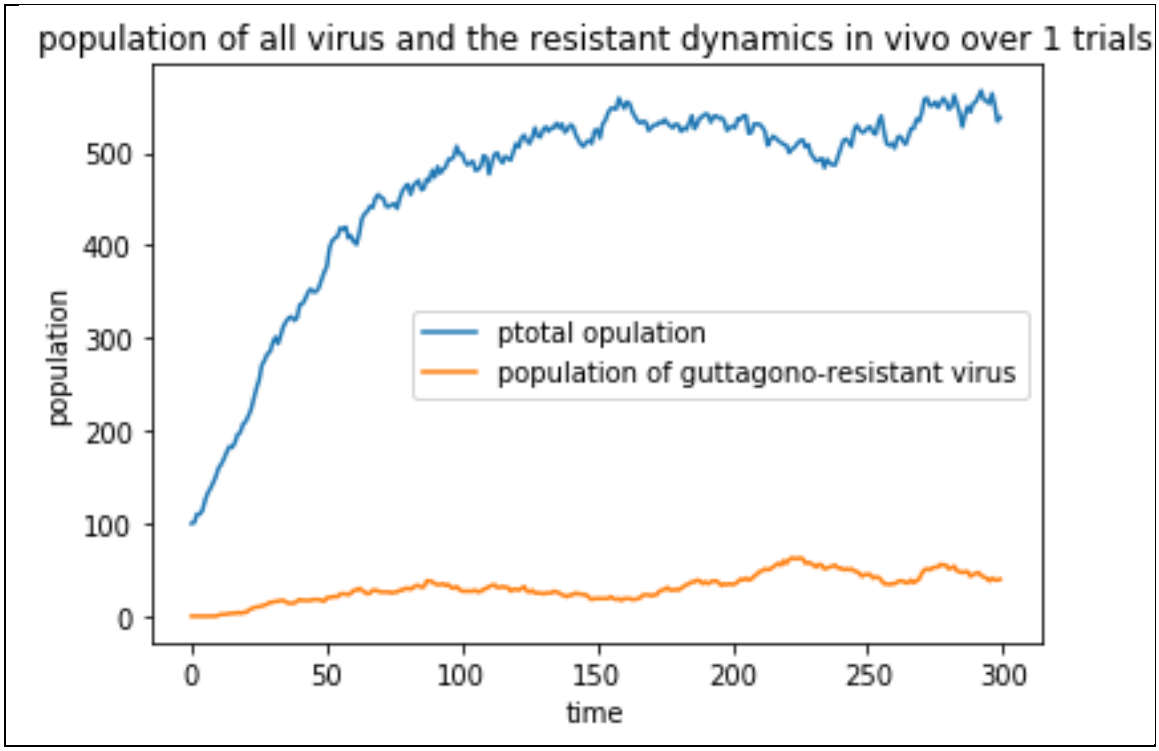
maxBirthProb,clearProb,resistances,muProb=0.1,0.05,{'guttagonol':False},0.005
timesteps,numViruses,maxPop=300,100,1000

the first one only run 1 times, which is sort of jaggy, the second one smoother over 10 trials



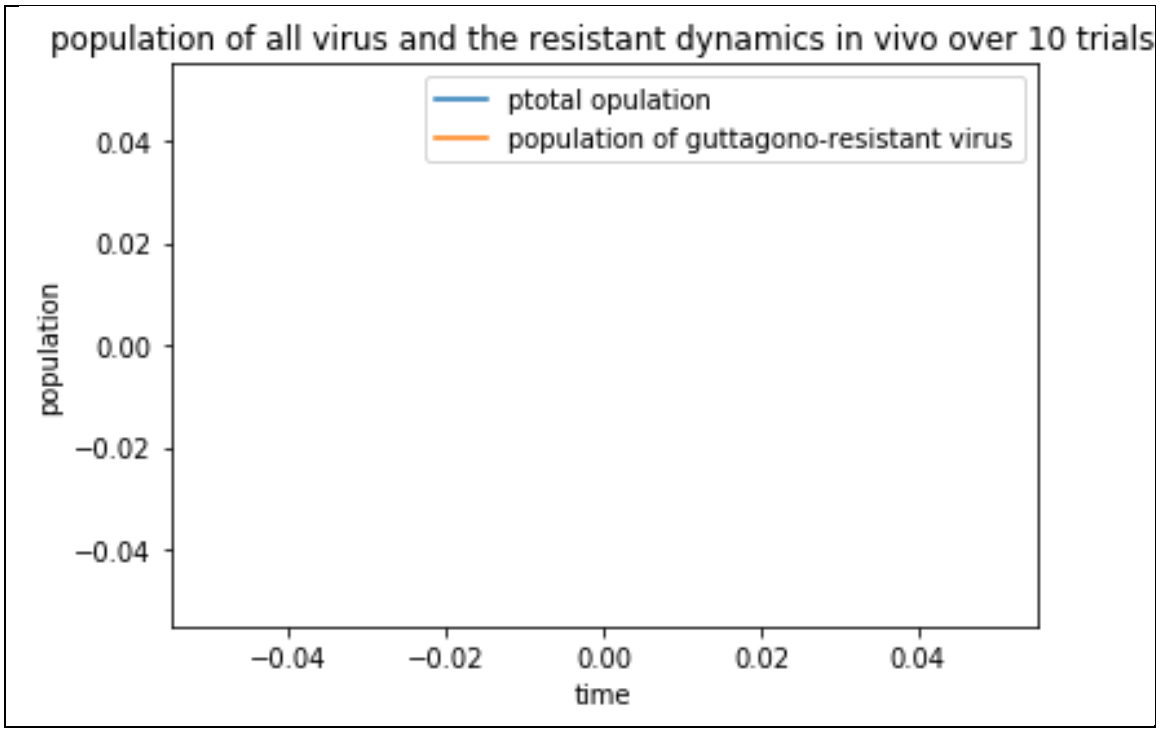


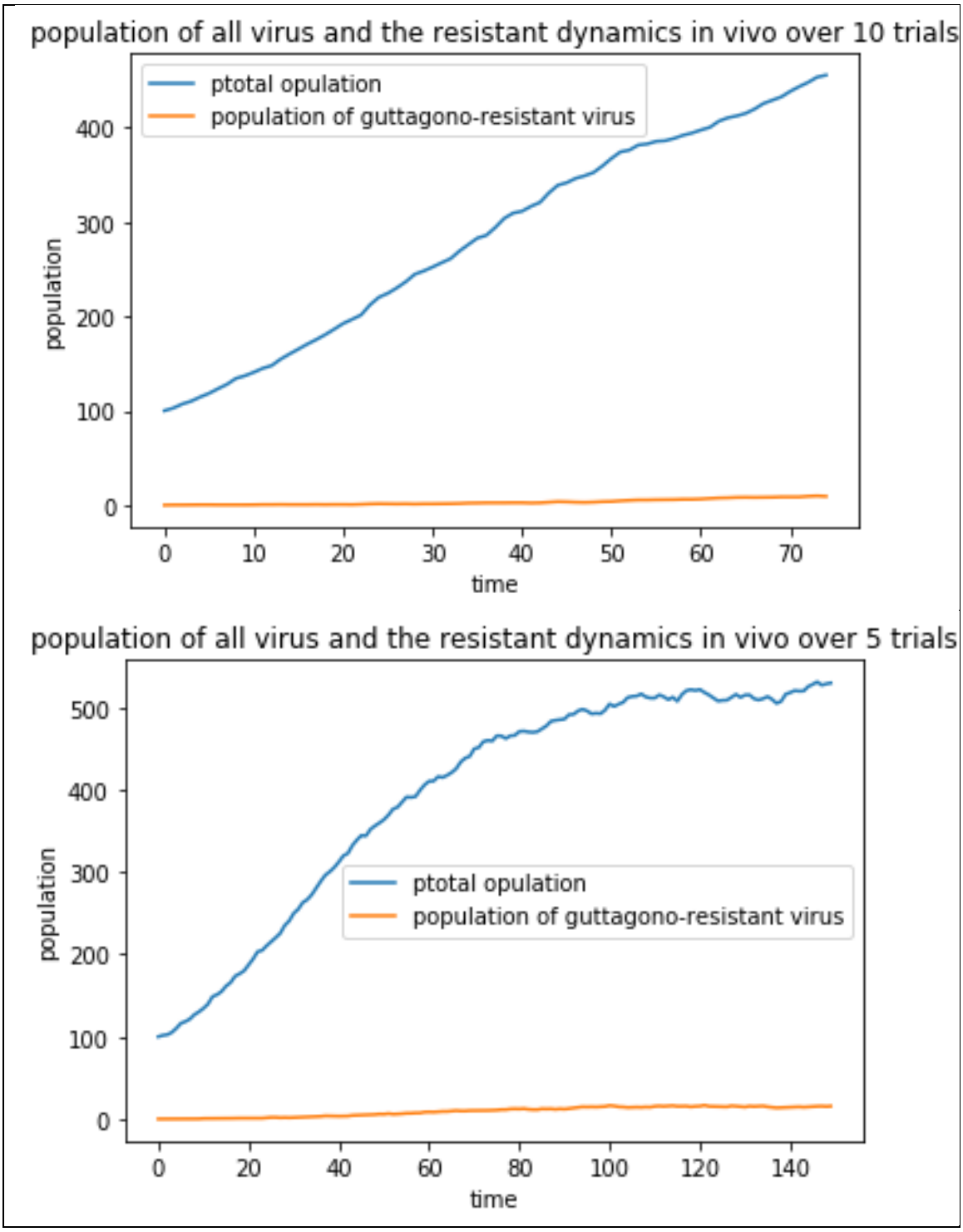
For fun , we run it without administering guttagonol to the patient

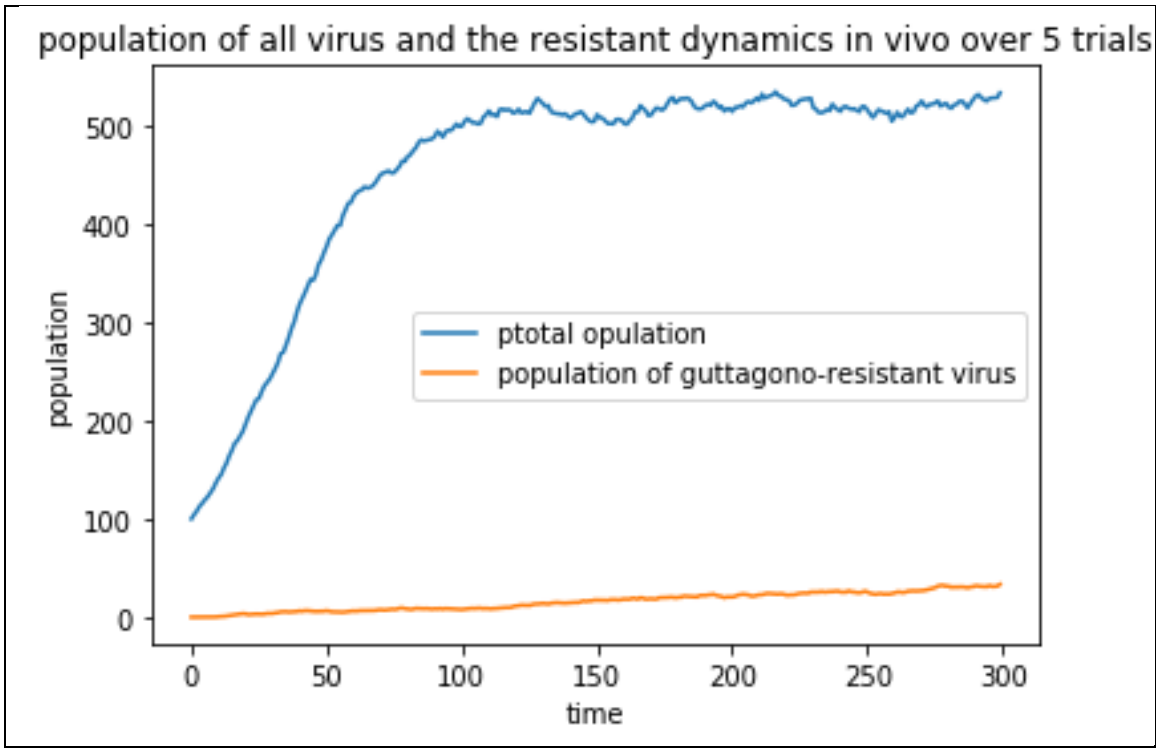


problem 5

0,75,150,300 time steps before administering guttagonol to the patient

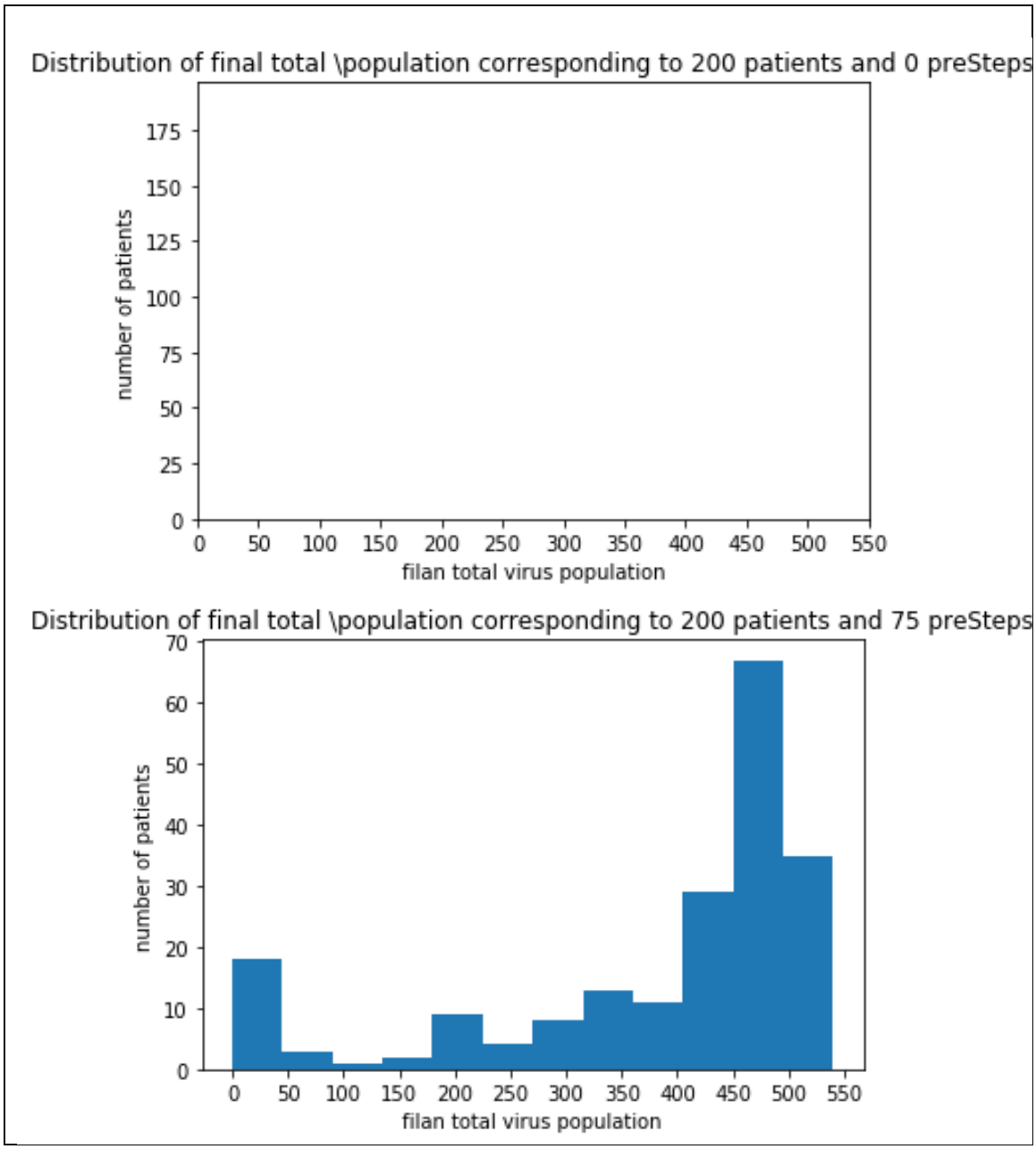

population of all virus and the resistant dynamics in vivo over 10 trials
ptotal opulation
population of guttagono-resistant virus
0.04
0.02
0.00
−0.02
−0.04
population
−0.04
−0.02
0.00
0.02
0.04
time

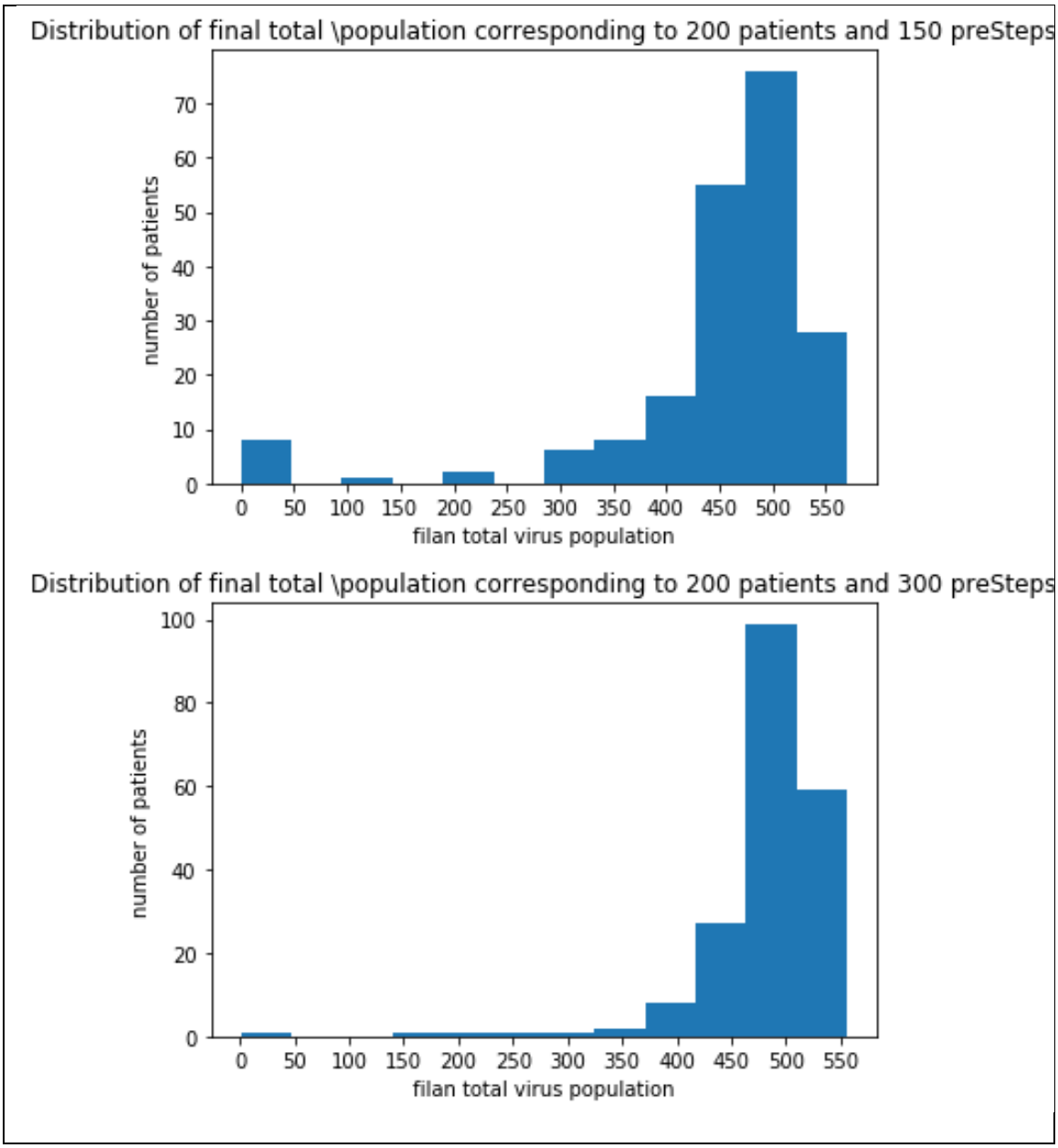

population of all virus and the resistant dynamics in vivo over 10 trials
ptotal opulation
population of guttagono-resistant virus
population
time
0
100
200
300
400
0
10
20
30
40
50
60
70
population of all virus and the resistant dynamics in vivo over 5 trials
ptotal opulation
population of guttagono-resistant virus
population
time
0
100
200
300
400
500
0
20
40
60
80
100
120
140



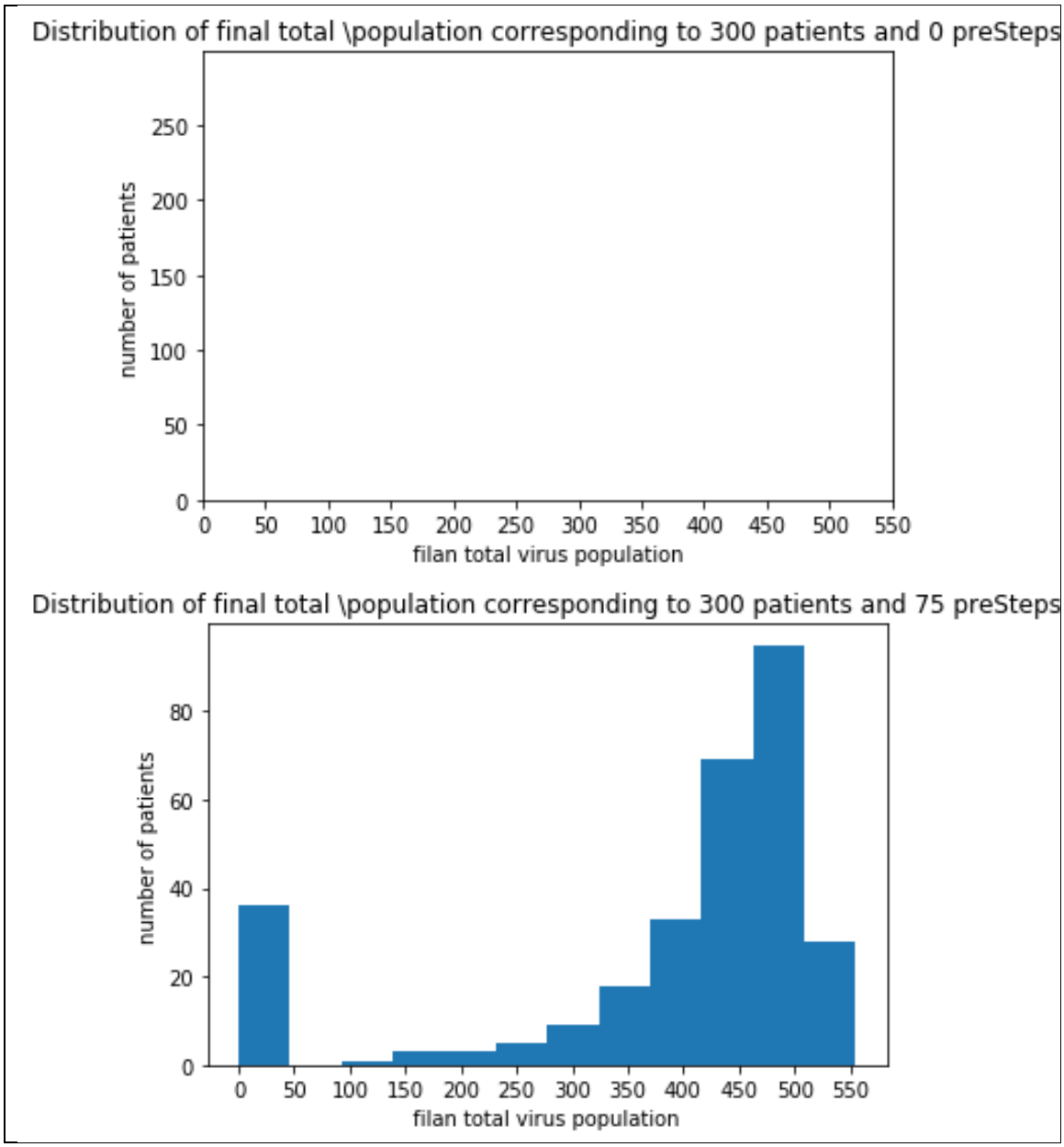
problem5

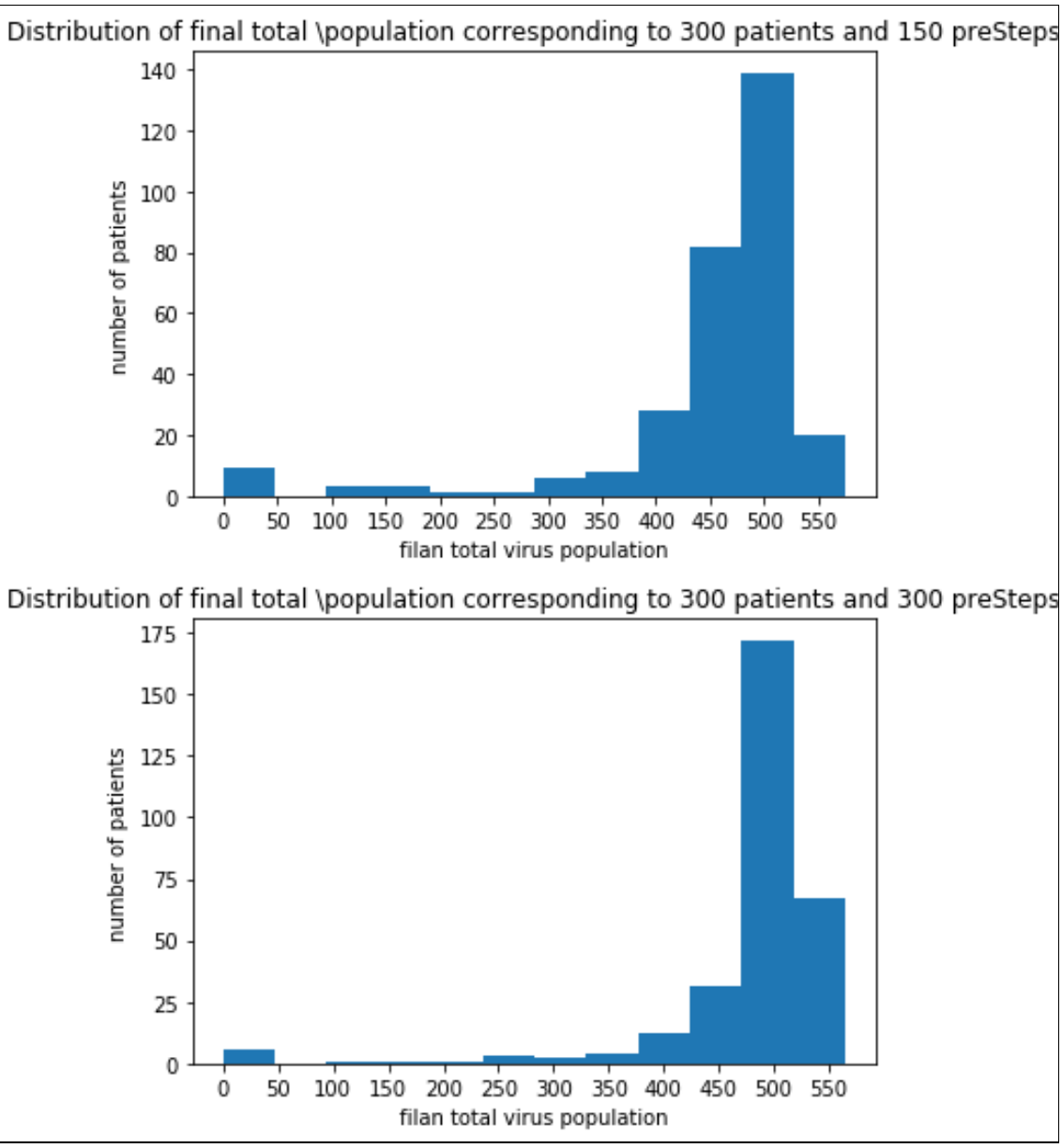
```
Histogram plotting for preSteps 0
Histogram plotting done for preSteps 0
Histogram plotting for preSteps 75
Histogram plotting done for preSteps 75
Histogram plotting for preSteps 150
Histogram plotting done for preSteps 150
Histogram plotting for preSteps 300
Histogram plotting done for preSteps 300
time using:  112.20539927482605
```


Distribution of final total \population corresponding to 200 patients and 0 preSteps
number of patients
filan total virus population
0
25
50
75
100
125
150
175
0
50
100
150
200
250
300
350
400
450
500
550
Distribution of final total \population corresponding to 200 patients and 75 preSteps
number of patients
filan total virus population
0
10
20
30
40
50
60
70
0
50
100
150
200
250
300
350
400
450
500
550



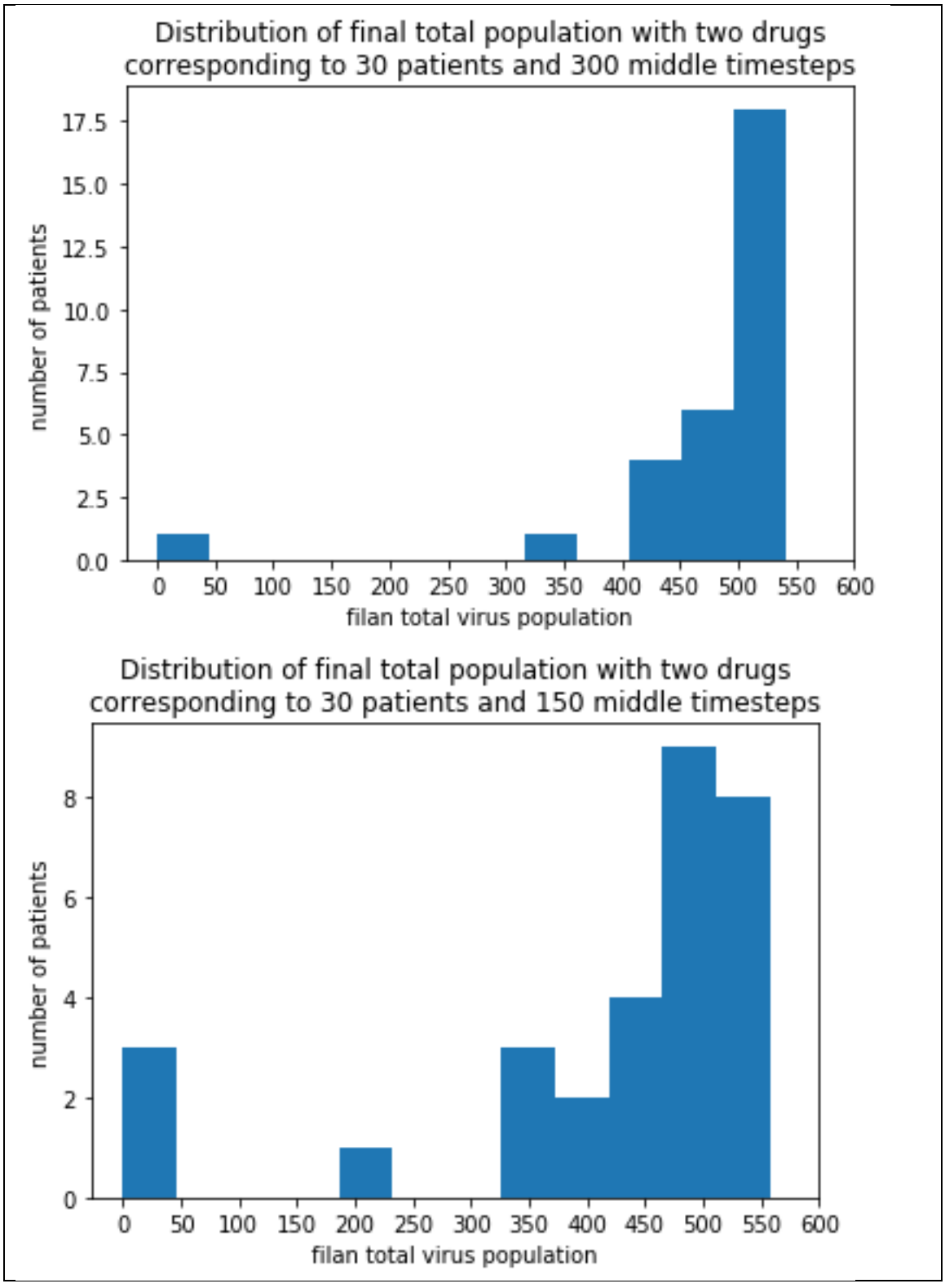

```
Histogram plotting for preSteps 0
Histogram plotting done for preSteps 0
Histogram plotting for preSteps 75
Histogram plotting done for preSteps 75
Histogram plotting for preSteps 150
Histogram plotting done for preSteps 150
Histogram plotting for preSteps 300
Histogram plotting done for preSteps 300
time using:  167.0388786792755
```

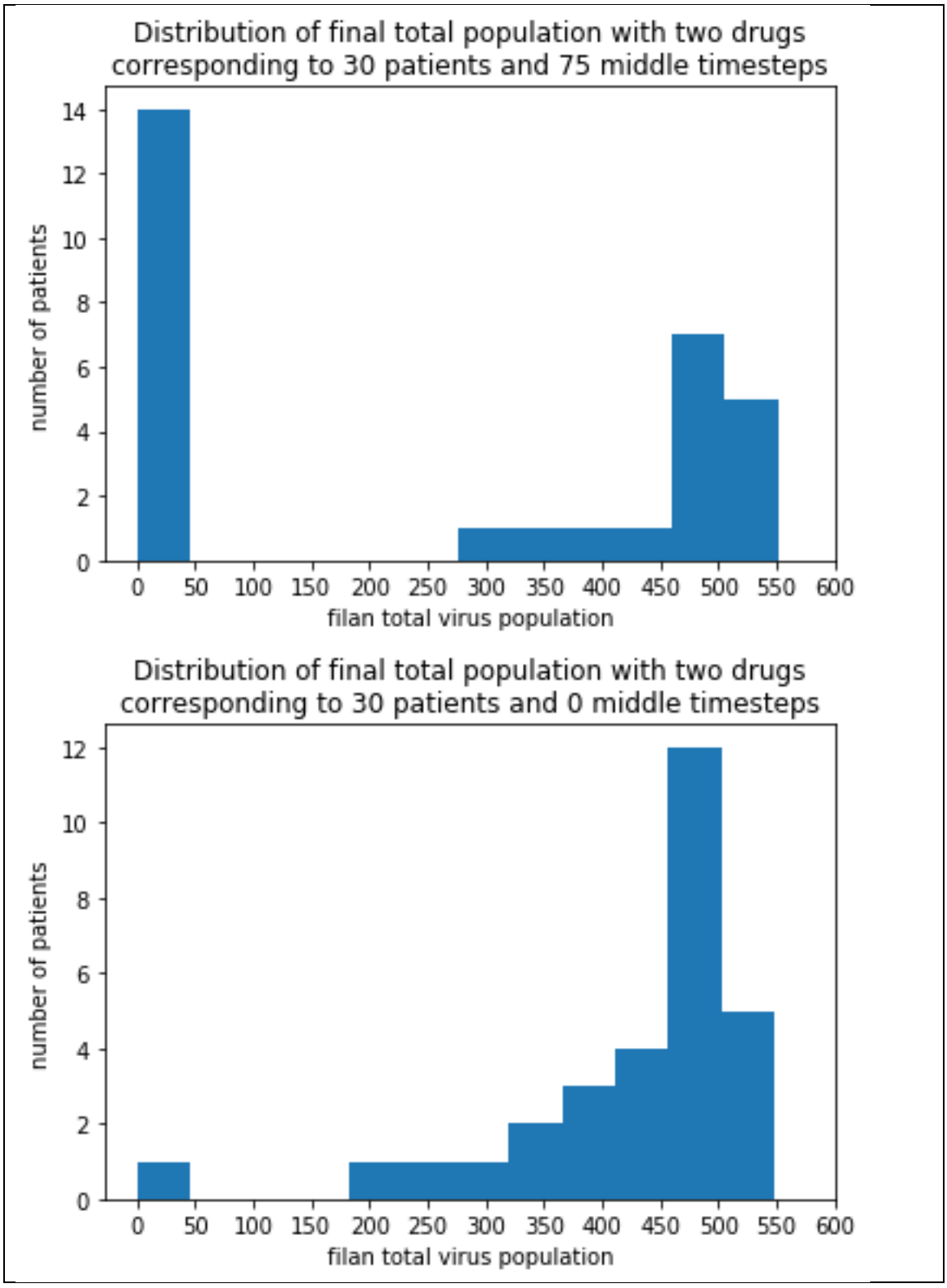

Distribution of final total \population corresponding to 300 patients and 0 preSteps
number of patients
0
50
100
150
200
250
0
50
100
150
200
250
300
350
400
450
500
550
filan total virus population
Distribution of final total \population corresponding to 300 patients and 75 preSteps
number of patients
0
20
40
60
80
0
50
100
150
200
250
300
350
400
450
500
550
filan total virus population



problem6(75 middle time steps is the best)

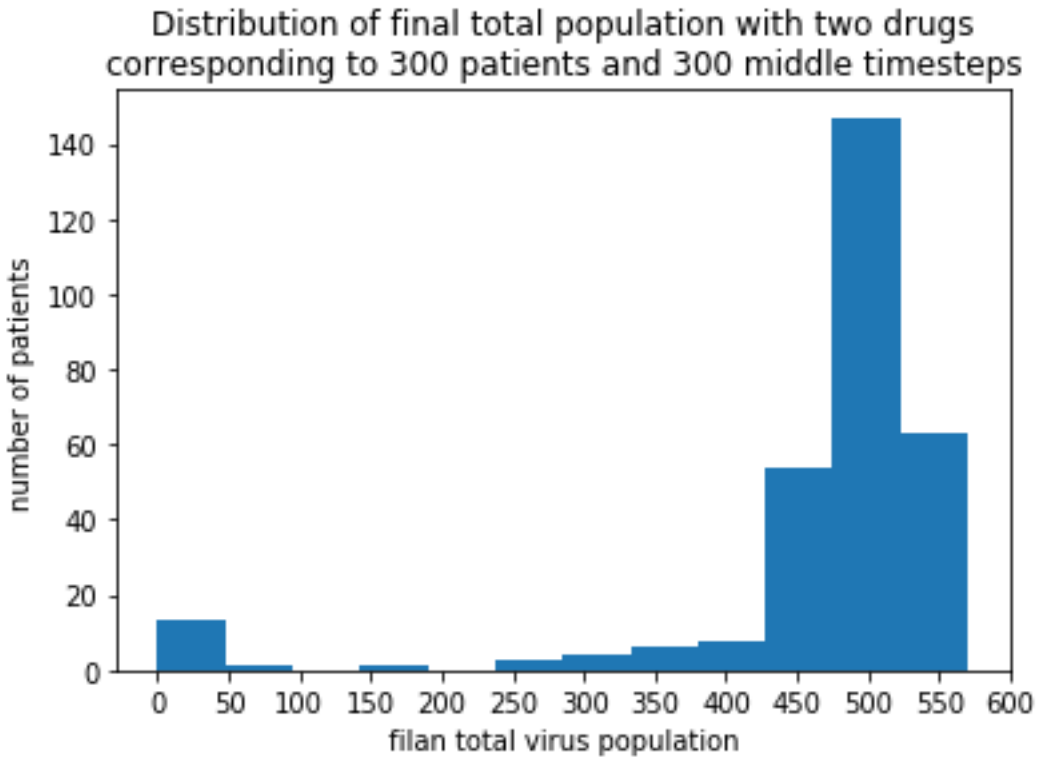
```
for 30 patients
Histogram plotting for middle timesteps 300
Histogram plotting done for middle timesteps 300
Histogram plotting for middle timesteps 150
Histogram plotting done for middle timesteps 150
Histogram plotting for middle timesteps 75
Histogram plotting done for middle timesteps 75
Histogram plotting for middle timesteps 0
Histogram plotting done for middle timesteps 0
time using:  30.40410017967224
```

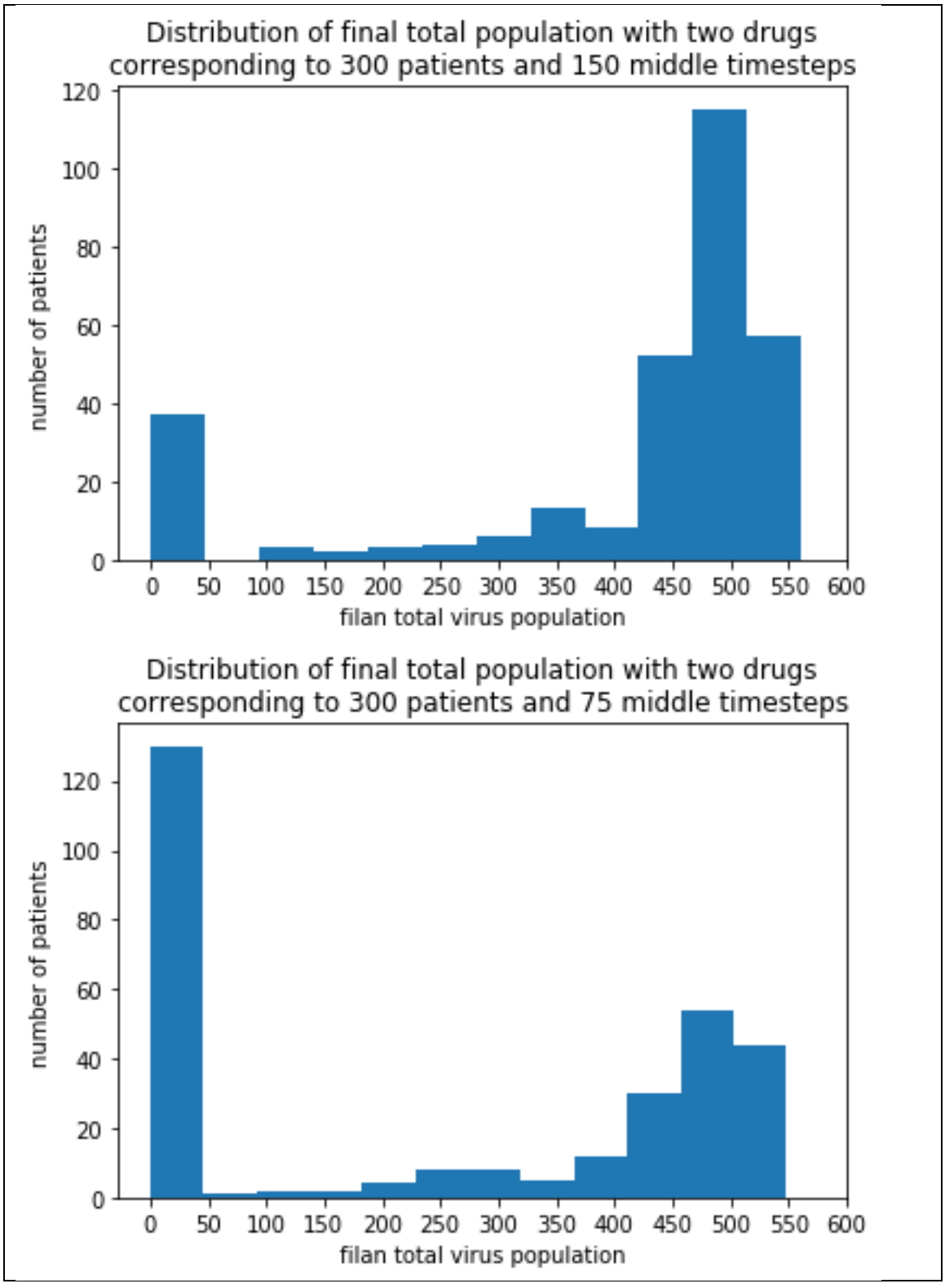

Distribution of final total population with two drugs
corresponding to 30 patients and 300 middle timesteps
number of patients
filan total virus population
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
0
50
100
150
200
250
300
350
400
450
500
550
600
Distribution of final total population with two drugs
corresponding to 30 patients and 150 middle timesteps
number of patients
filan total virus population
0
2
4
6
8
0
50
100
150
200
250
300
350
400
450
500
550
600

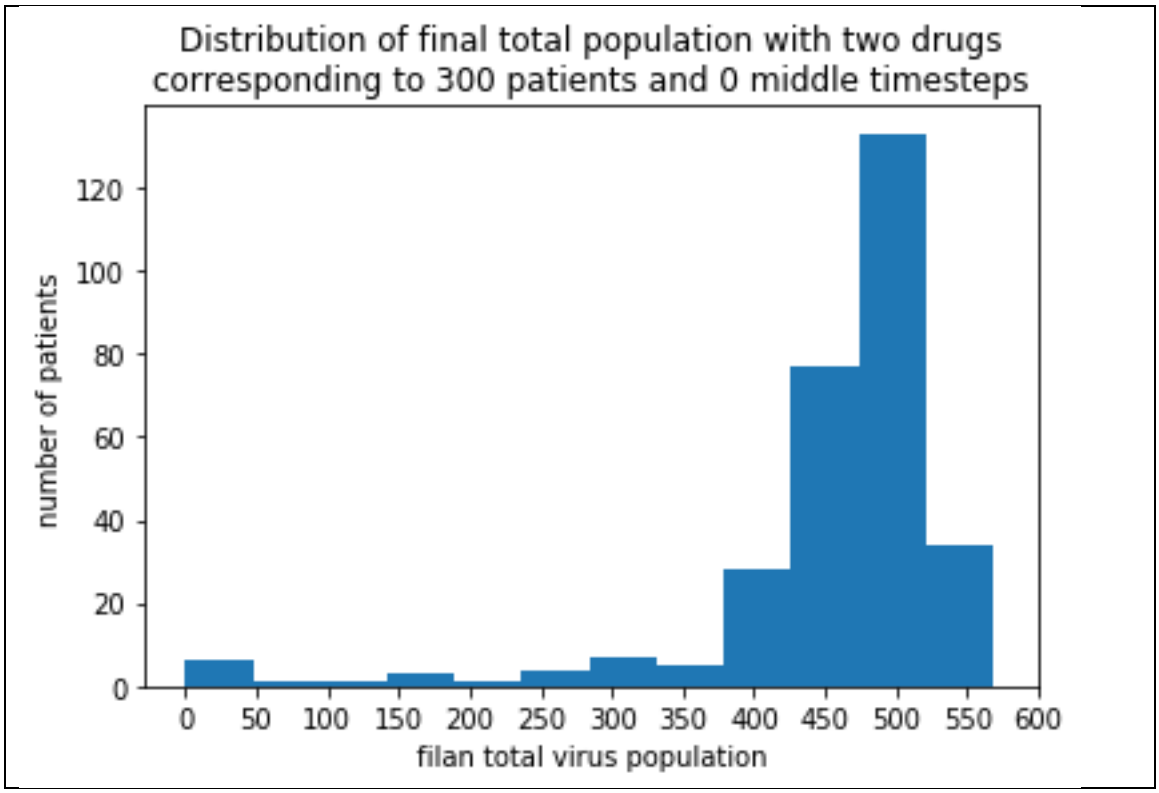


for 300 patients
Histogram plotting for middle timesteps 300
Histogram plotting done for middle timesteps 300

Histogram plotting for middle timesteps 150
Histogram plotting done for middle timesteps 150
Histogram plotting for middle timesteps 75
Histogram plotting done for middle timesteps 75
Histogram plotting for middle timesteps 0
Histogram plotting done for middle timesteps 0
time using: 315.30966567993164

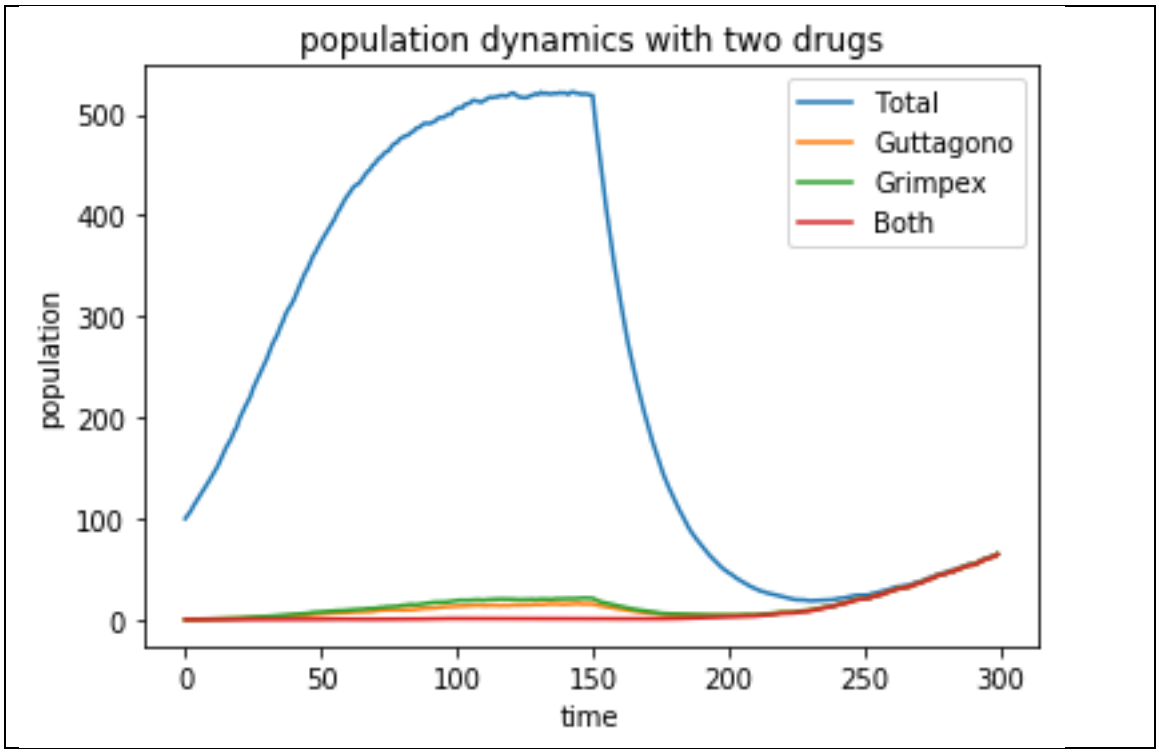



Distribution of final total population with two drugs
corresponding to 300 patients and 150 middle timesteps
number of patients
filan total virus population
0
20
40
60
80
100
120
0
50
100
150
200
250
300
350
400
450
500
550
600
Distribution of final total population with two drugs
corresponding to 300 patients and 75 middle timesteps
number of patients
filan total virus population
0
20
40
60
80
100
120
0
50
100
150
200
250
300
350
400
450
500
550
600

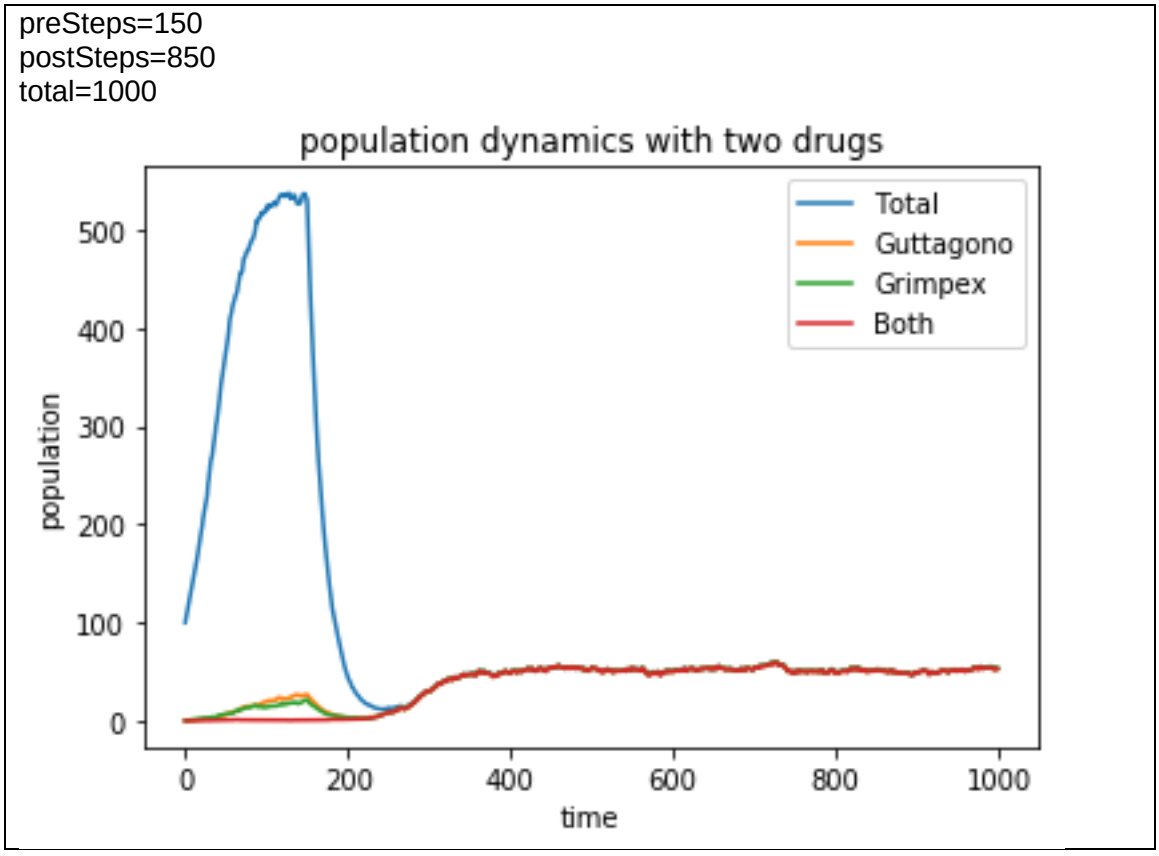


problem7

preSteps=150
postSteps=850
total=1000



preSteps=150
postSteps=850
total=1000



problem8

forget to take drugs

add some code using random and probability to override the effect of prescription in method ResistantVirus.reproduce()