

# Prediction Model for Human and Mosquito Populations in Malaria Afflicted Regions

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# Basic Model Assumptions -> System Simplification



Infected mosquitoes always die (ie. no recovery)

No new people/mosquitoes move into a population

The malaria death rate, human death rate, immune rate, recovery rate, etc. are assumed to be the same all year long

Simplifies system by modeling both the number of sick/healthy/immune villagers over time and the number of healthy/infected mosquitoes over time

# Code: Villagers

```
def Healthy_Villagers ( i, hV, sV, brV, drV, rrV, M, iM, brfM, iV ) :  
    hV[i+1] = hV[i] + (((hV[i] + iV[i] + sV[i]) * brV) - (hV[i] * drV) -  
(hV[i] * brfM * (iM[i] / max(M[i],1))))
```

```
def Sick_Villagers ( i, hV, sV, rrV, irV, drV, M, iM, brfM, midrV ,rV):  
    sV[i+1] = sV[i] + ((brfM * hV[i] * (iM[i] / max(M[i],1))) - (sV[i] *  
rrV) - (sV[i] * irV) - (sV[i] * (drV+midrV)) + (rV[i]*.17))
```

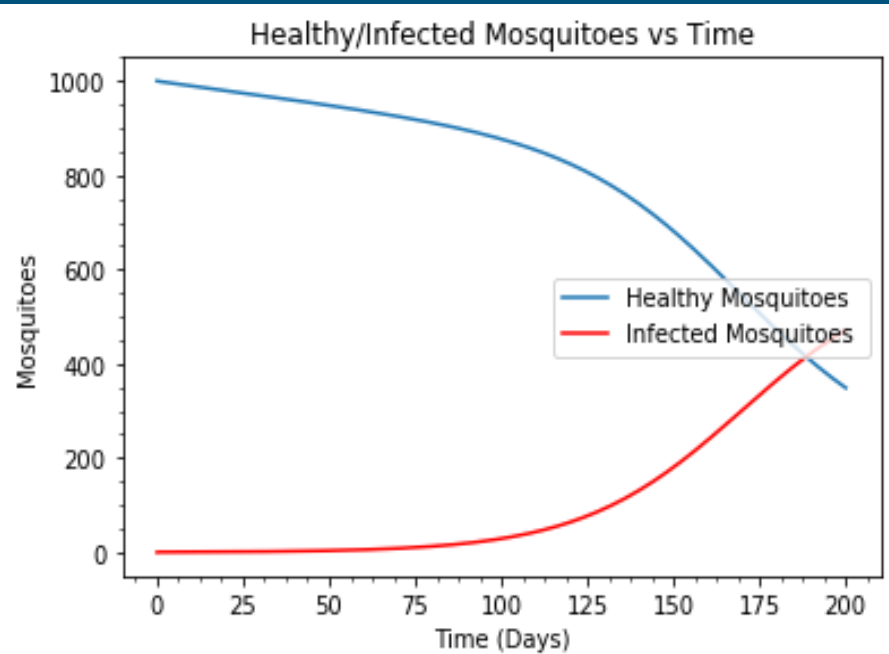
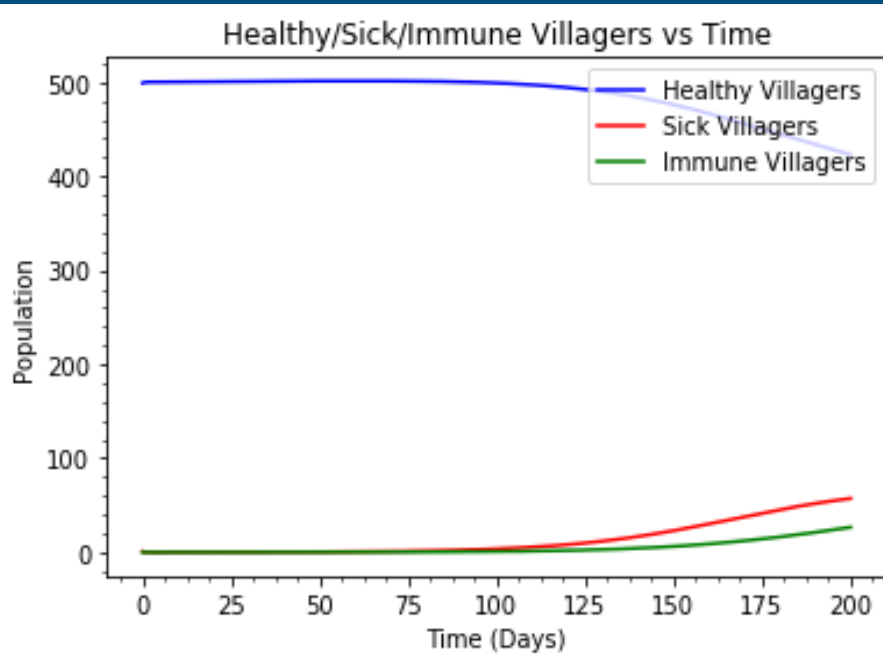
```
def Immune_Villagers (i, iV, sV, irV, drV ):  
    iV[i+1] = iV[i] + ((sV[i] * irV) - (iV[i] * drV))
```

# Code: Mosquitoes

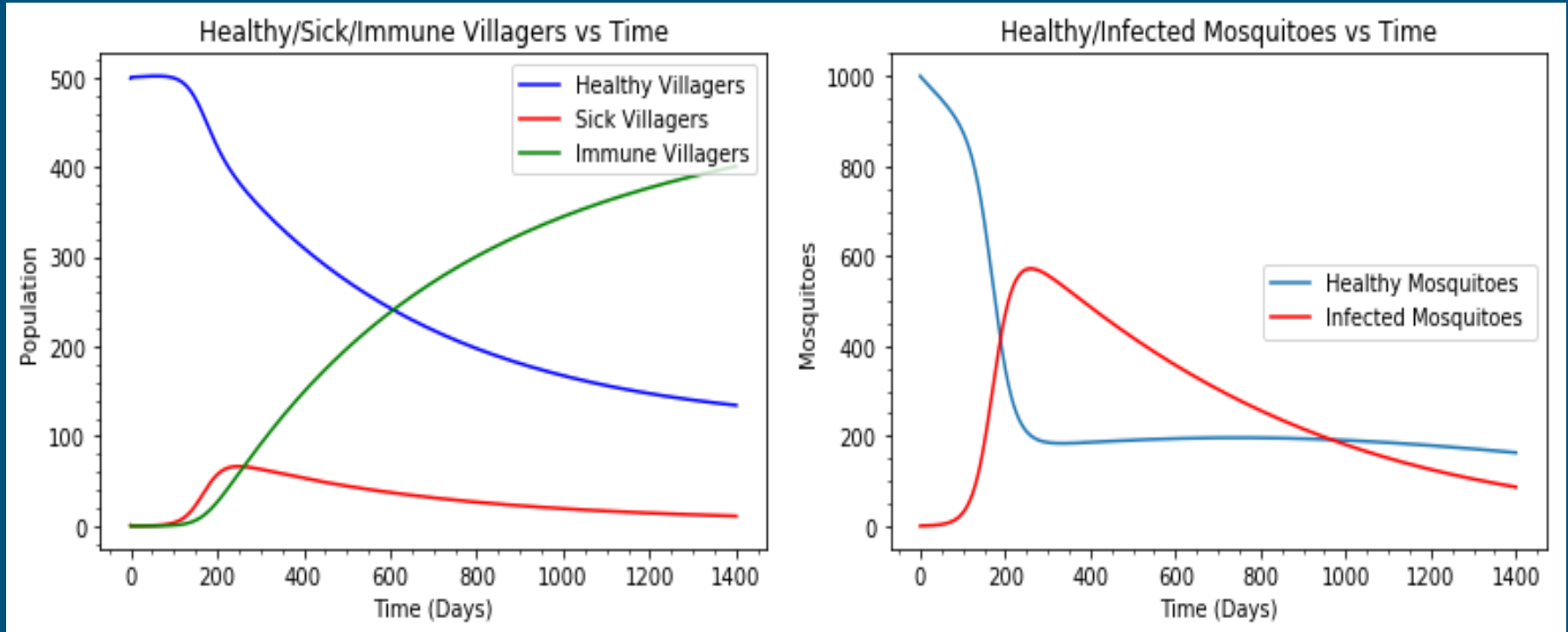
```
def Healthy_Mosquitoes (i, V, sV, M, hM, brM, drM, brfM ):
    hM[i+1] = hM[i] + ((M[i] * brM) - (hM[i] * drM) - ((sV[i] /
max((V[i]+1),1)) * hM[i] * brfM))

def Infected_Mosquitoes (i, V, sV, hM, iM, drM, brfM ):
    iM[i+1] = iM[i] + (((sV[i] / max((V[i]+1),1)) * hM[i] * brfM) - (iM[i]
* drM))
```

# 200 days, 500 villagers, 1 sick, 1000 healthy mosquitoes



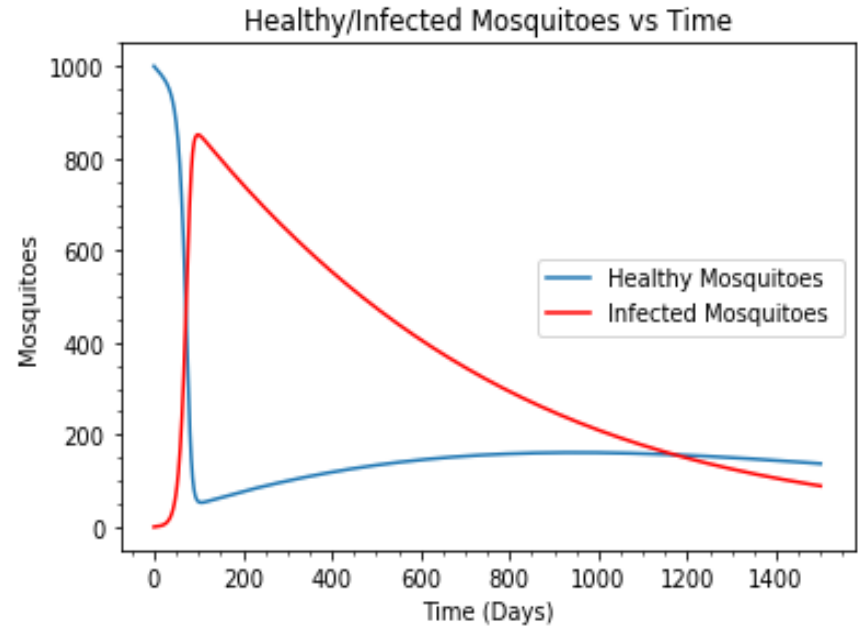
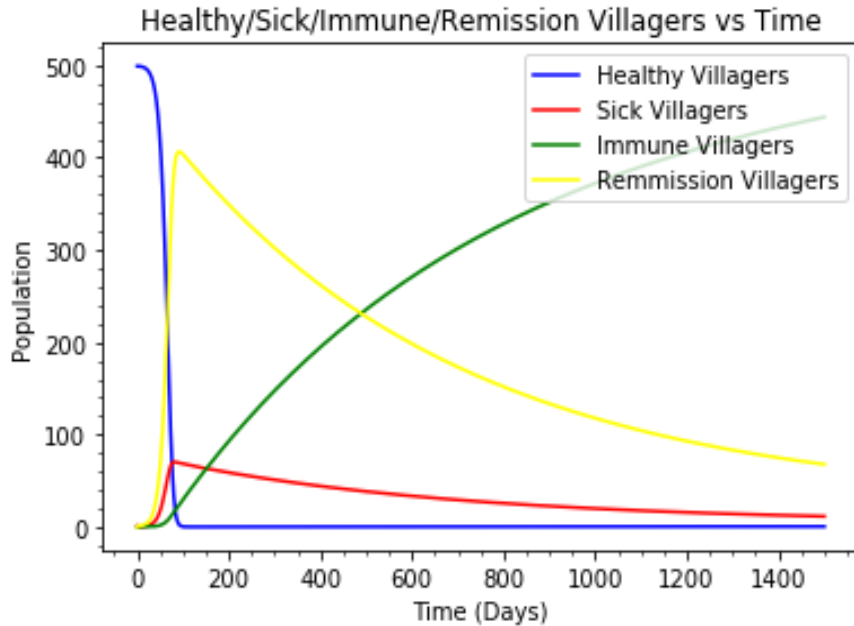
# 1400 days, 500 villagers, 1 sick, 1000 healthy mosquitoes



# Extra Model Additions: Relapse (Code)

```
89 def Healthy_Villagers ( i, hV, sV, brV, drV, rrV, M, iM, brfM, iv ) :
90     hV[i+1] = hV[i] + (((hV[i] + iv[i] + sV[i]) * brV) - (hV[i] * drV) - (hV[i] * brfM * (iM[i] / max(M[i],1))))
91     |
92 def Rem_Villagers (i, sV, rrV, drV, rerV):
93     rV[i+1] = rV[i] + ((sV[i] * rrV) - (rV[i]*rerV) - (rV[i] * drV))
94
95 def Sick_Villagers ( i, hV, sV, rrV, irV, drV, M, iM, brfM, midrV ,rV):
96     sV[i+1] = sV[i] + ((brfM * hV[i] * (iM[i] / max(M[i],1))) - (sV[i] * rrV) - (sV[i] * irV) - (sV[i] * (drV+midrV)) + (rV[i]*.17))
97
```

# Extra Model Additions: Relapse (Graphs)





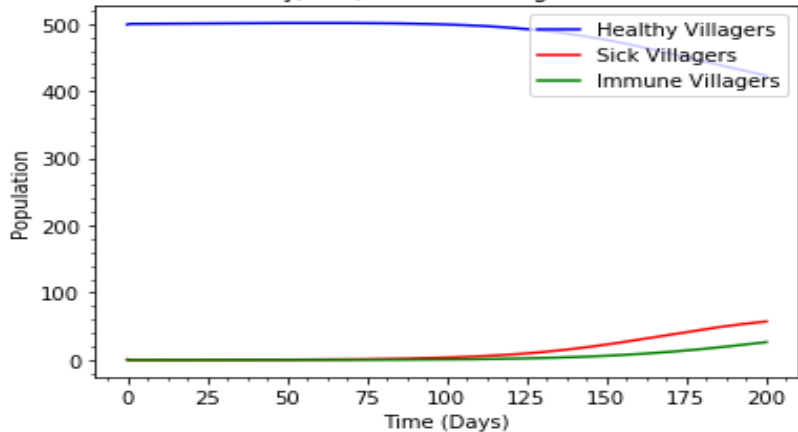
# Extra Model Additions: Seasonal Effect(Code)

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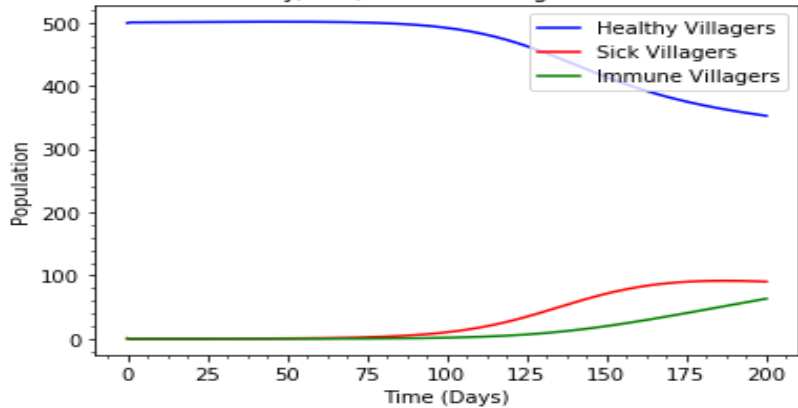
```
for i in range(N):  
    brM = (math.cos( (t[i]*(2*math.pi))/(365)+1))*(.02/2)  
    drM = (math.cos( (t[i]*(2*math.pi))/(365)+1))*(.022/2)  
    t[i+1] = t[i] + time_step
```

# Extra Model Additions: Seasonal Effect

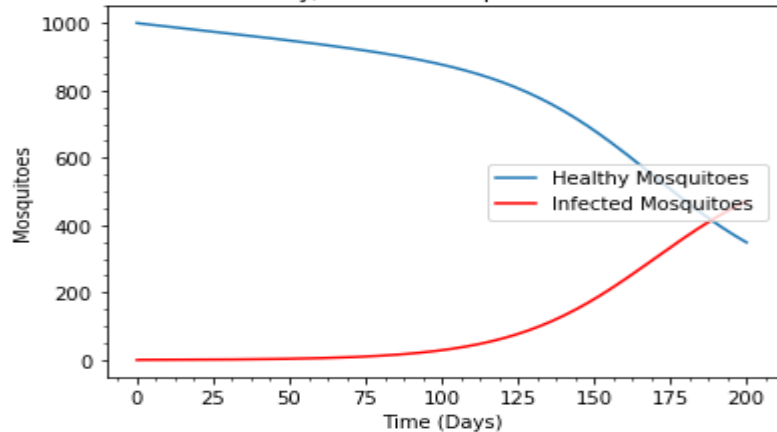
Healthy/Sick/Immune Villagers vs Time



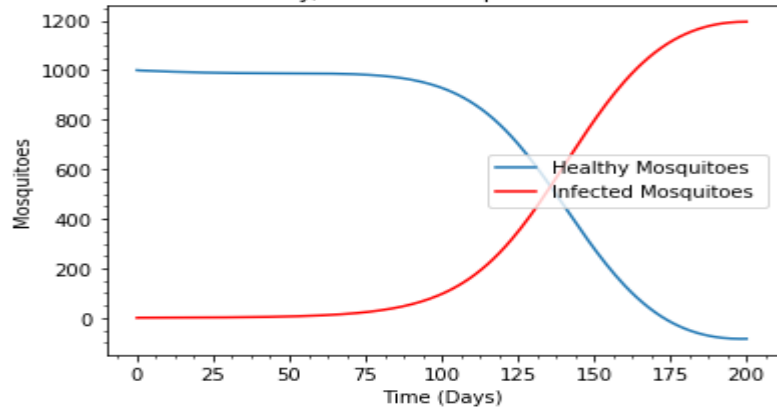
Healthy/Sick/Immune Villagers vs Time



Healthy/Infected Mosquitoes vs Time



Healthy/Infected Mosquitoes vs Time



Without effect

With effect

# Future Steps

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Using a differential equation changes runtime from  $O(n)$  to  $O(1)$

Test with larger populations -> Using HPC to accelerate the calculations of using larger datasets

Zika: would have to consider birth rate in infected patients, as Zika can be spread through pregnancy.

Can also be sexually transmitted

<http://www.who.int/mediacentre/factsheets/zika/en/>