

METHODOLOGIES FOR DISCRETE-EVENT MODELLING AND SIMULATION

(SYSC-5104)

Assignment 2

Cell-DEVS model

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I. DESCRIPTION

This is a model to simulate a typical process. The proposed model for this assignment is to explore elementary aspects of cellular automata and its application in analyzing contagious disease. In this assignment is focused on modelling the spread of influenza disease. The paper being used is entitled EPIDEMIOLOGY THROUGH CELLULAR AUTOMATA Case of Study: Avian Influenza in Indonesia and is written by *Hokky Situngkir*, Dept. Computational Sociology in Bandung Fe Institute. Avian Influenza is a cell-devs model and is implemented in CD++, and can be viewed in CD++ modeller directly. This disease come in front with the death of many chickens and firstly treated as a common poultry disease but later is found deadly for humans also. This virus will spread among human due to interaction with infected poultry. This virus was mainly found among people who work in poultry areas and live in the surrounding.

In this model each cell is composed of a population of living inhabitants. The boundary of the cell space is null, meaning the boundary is not wrapped. The neighbourhood for the cell is the Moore neighbourhood, which includes North, East, South, West, North-East, South-East, North-West and South-West. Avian influenza is unique activity which spreads from poultry to other poultries. It attacks poultry, and may attack other species of animals and It also attacks human through direct contact with living infected poultry or animals.

This model is based on the concept of Epidemiology explained in Rhodes & Anderson (1998) and also include the death factor caused by the flu infection. This model is focusing in virus diffusion occurs in society.

In this assignment I will work on three kind of Cell-DEVS models

- My first model will show the spreading of virus at different probabilities and I will show the result of spreading with 8 neighbours. I will use 2 state model to show the spread of flu, which is composed by S (susceptible) and I (Infected).
- My second model is same as the first one with the excepection that it will sho the spreading of flu inside the boundary.
- My third model will show the spreading of virus among 24 neighbours. I will use a five-state model to show the spread of worm, which is composed by S (susceptible), Q (questionable), I (Infected), R (Recovered) and D(Dead). This model is an additional work.

II. DEFINITIONS and SIMULATION RESULTS

1. Cell-Model

The following is the formal definition for the my first CELL-DEVS model, which typically shows the spreading of virus at different probabilities.

CD = $\langle X, Y, I, S, \theta, N, d, \delta_{int}, \delta_{ext}, \tau, \lambda, D \rangle$

$X = \emptyset$

$Y = \emptyset$

$S = \{ 0, 2 \}$

$N = \{ (-1, 0), (0, -1), (0, 1), (1, 0), (0,0), (-1, -1), (-1, 1), (1, -1), (1, 1) \}$

$d = 1 \text{ ms}$

where, 0 represent the *Suspected* inhabitant (Colour: Light Cyan) and,
2 represent the *Infected* (Colour: Grey) ones who are responsible for spreading the flu.

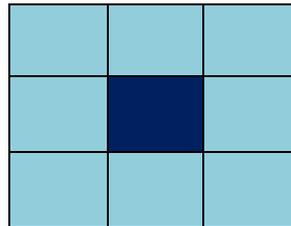


Figure-1 Neighbors.

In this model, I have consider a Area containing 1250 inhabitants and one of them is a root cause of spreading flu.

Rules

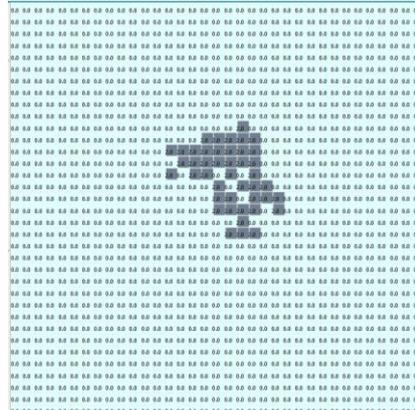
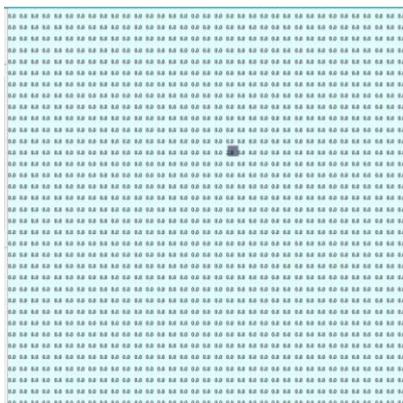
The transition (S to I) indicates that inhabitant is infected by the avian fly and will spread the flu to others. Here, to perform the result I have put one Inhabitant as Infected. The rule in CD++ can be written as below:

```
rule : 2 100 { (0,0)=0 and stateCount(2) > 0 and random <
#macro(Spreading)}
rule : { (0,0) } 100 { t }
```

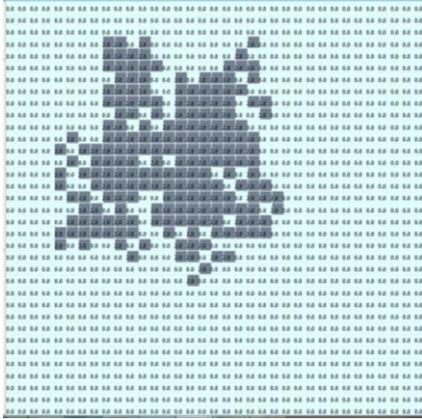
Simulation Result

Avian Influenza with diffusion rate =0.3

Files for this experiment are *Avainflu.ma*, *f_rule.inc* and *Avain.val*

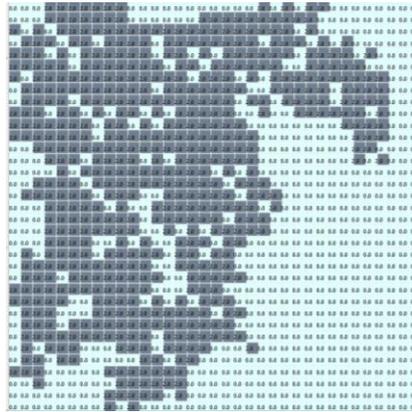


a) t=0



c) t=2000ms

b) t=1000ms



d) t=4000ms

2. Cell-Model

The following is the formal definition for the my fsecond CELL-DEVS model, which typically shows the spreading of virus at different probabilities inside the boundary.

$CD = \langle X, Y, I, S, \theta, N, d, \delta_{int}, \delta_{ext}, \tau, \lambda, D \rangle$

$X = \emptyset$

$Y = \emptyset$

$S = \{ 0, 2, 5 \}$

$N = \{ (-1, 0), (0, -1), (0, 1), (1, 0), (0,0), (-1, -1), (-1, 1), (1, -1), (1, 1) \}$

$d = 1 \text{ ms}$

where, 0 represent the Suspected inhabitant (Colour: Light Cyan) ,

2 represent the Infected (Colour: Grey) ones who are responsible for spreading the flu,

5 represent the boundary (Colour : gold)

This model basically satisfy the conditions of research paper. .

Rules

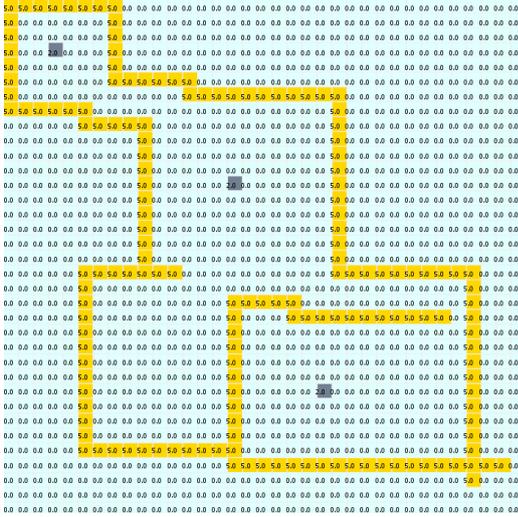
```
[flu]
rule : { (0,0) } 1 { undefCount >=1 }
rule : { (0,0) } 1 { t }
```

```
[flu-rule]
rule : 2 100 { (0,0)=0 and stateCount(2) > 0 and random <
#macro(Spreading) }
rule : { (0,0) } 100 { t }
```

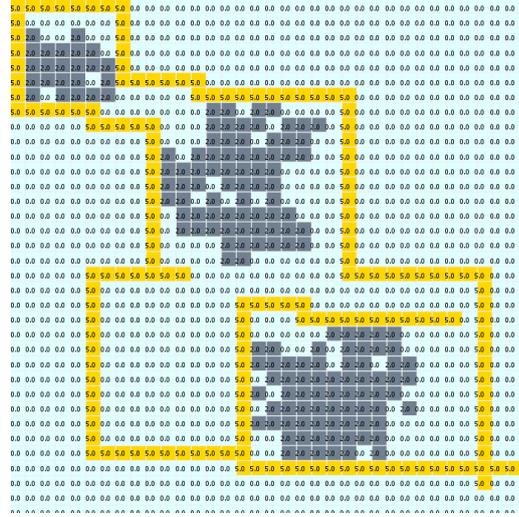
Simulation Result

Avian Influenza with diffusion rate =0.5

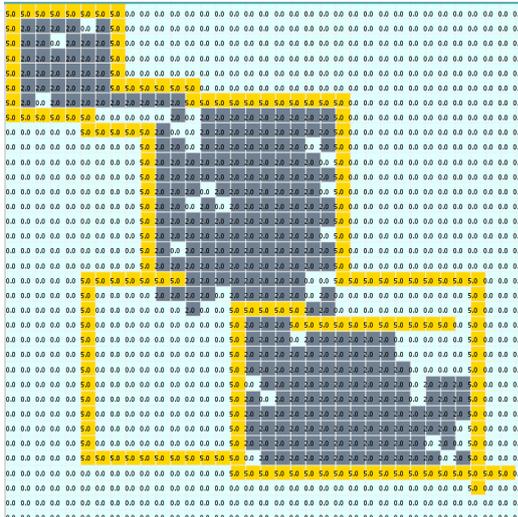
Files for this experiment are *Avainflu(boundary).ma*, *F_rule_1.inc* and *flurule.val*



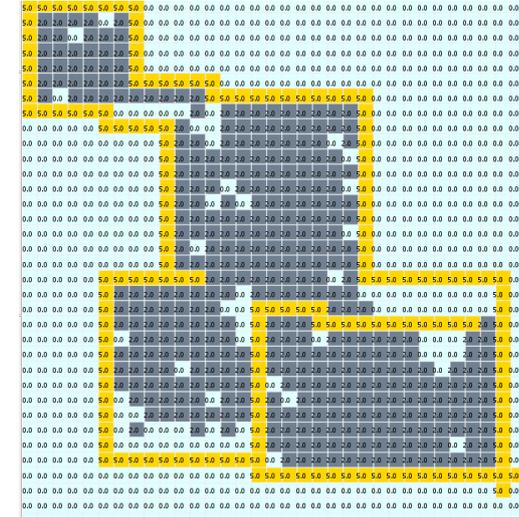
t = 0



t = 500



t = 1000



t = 2000

3. Cell model

The following is the formal definition for the CELL-DEVS model.

$CD = \langle X, Y, I, S, \theta, N, d, \delta_{int}, \delta_{ext}, \tau, \lambda, D \rangle$

$X = \emptyset$

$Y = \emptyset$

$S = \{-1, 0, 1, 2, 3\}$

$N = \{ (-1, 0), (0, -1), (0, 1), (1, 0), (0, 0), (-1, -1), (-1, 1), (1, -1), (1, 1), (-2, -2), (-2, -1), (-2, 0), (-2, 1), (-2, 2), (-1, -2), (-1, 2), (0, -2), (0, 2), (1, -2), (1, 2), (2, -2), (2, -1), (2, 0), (2, 1), (2, 2) \}$

$d = 100 \text{ ms}$

where, **0** represent the *Suspected* (Colour: Light Cyan) inhabitant ,

2 represent the *Infected* (Colour: Grey) ones who are responsible for spreading the flu.

1 represent the *Questionable*(Colour: Orange)

-1 represent Immuned (Colour: Green) after getting in notice

3 represent *Dead*. (Colour: Red)

Here, I introduce two kinds of neighbor. The first sort is called “adjacent_neighbour” which is next to the central cell. Another one called “remote_neighbour” which is a little farther.

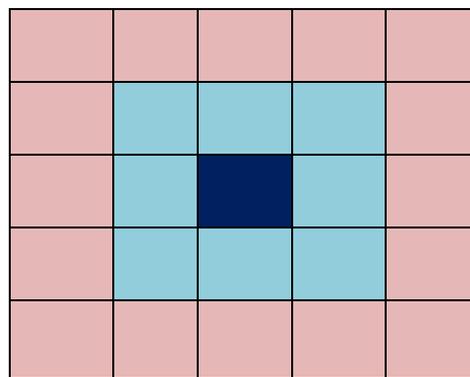


Figure-2 Kinds of neighbours.

Inhabitants have 24 contacts at most, which can be used to spread the flu. 16 of them are in “remote_neighbour”, while 8 are in “adjacent_neighbour”. Cells in “adjacent_neighbour” have more chances of infection as compared to the remote_neighbour.

Rules.

(1) Susceptible to Infected : In this Transition Inhabitants are infected by the flu which is spread by animals. The possibility of transition relate to number of infected inhabitants in the neighbourhood along with the diffusion rate.

The rule in CD++ can be written as below:

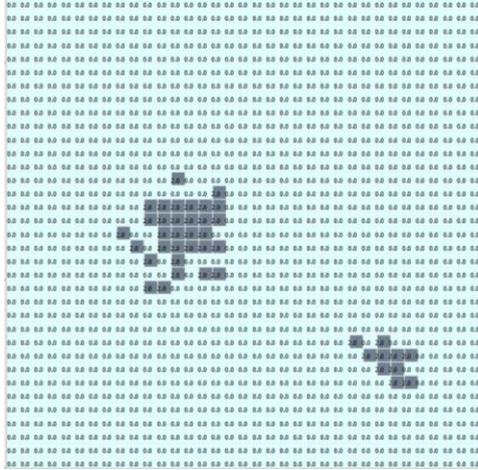
```
rule : 2 100 { (0,0)=0 and stateCount(2) > 0 and random < #macro(Spreading)
* ( #macro(Inner) * #macro(inner_2)/8 + #macro(Outer) * #macro(outer_2)/16 )
}
```

Where Inner and Outer indicate influences of “adjacent neighbour” and “remote neighbour” and (inner_2) and (outer_2) indicate the number of infected inhabitant in “adjacent neighbour” and “remote neighbour”.

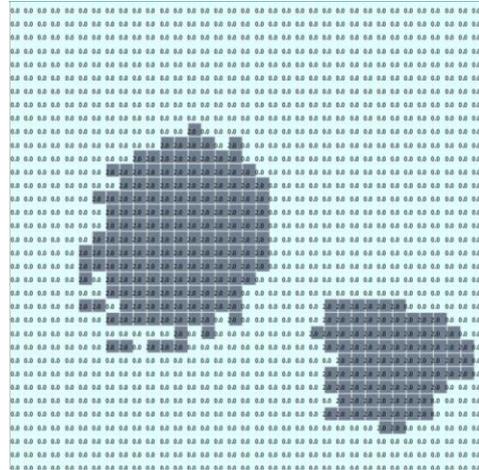
Result

Avian Influenza with diffusion rate =0.8

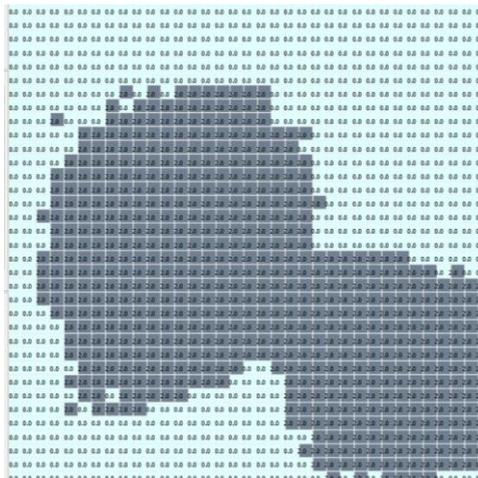
Files for this experiment are A_spreading.ma, A_rule.inc and Avain.val



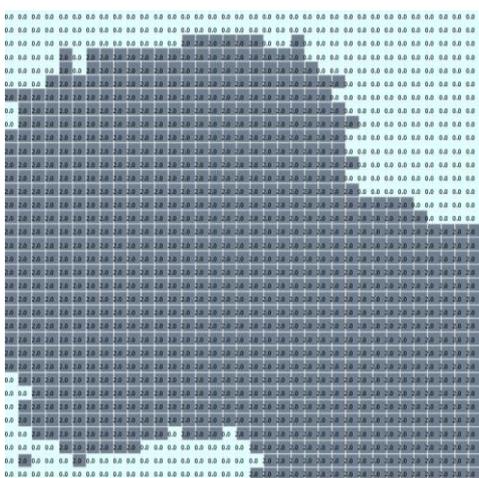
1) t=200



2) t=400



3)t=600



4) t=800

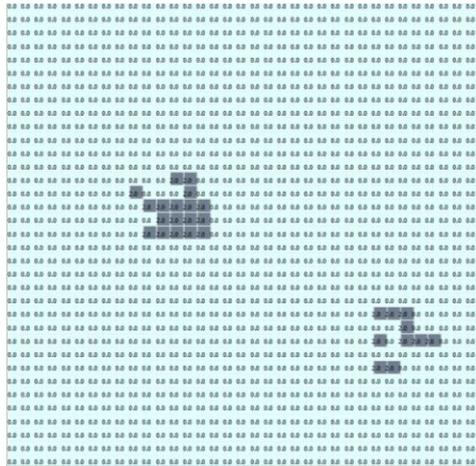
(2) Susceptible to Questionable : In this transition danger/flu has been noticed. Here, possible steps may be taken to immune the inhabitants. Vigilance of user is also relate to transition.

The rule in CD++ is below:

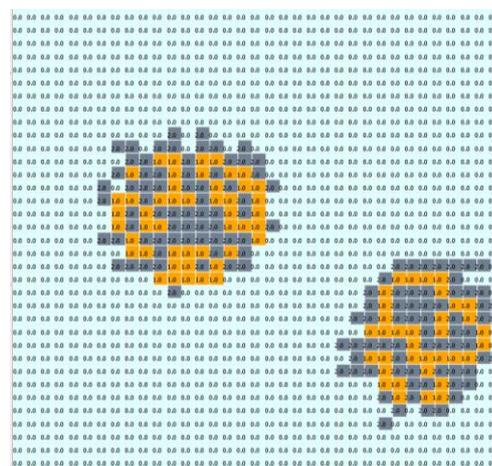
```
rule : 1 100 { (0,0)=0 and ( #macro(Inner) * #macro(inner_2) +  
#macro(Outer) * #macro(outer_2) > 2) and random < ( #macro(Vigilance) * (  
#macro(Inner) * #macro(inner_2)/8 + #macro(Outer) * #macro(outer_2)/16 ) ) }  
  
rule : 1 100 { (0,0)=0 and ( #macro(Inner) * #macro(inner_1) +  
#macro(Outer) * #macro(outer_1) > 0) and random < ( #macro(Vigilance) * (  
#macro(Inner) * #macro(inner_1)/8 + #macro(Outer) * #macro(outer_1)/16 ) ) }
```

Result

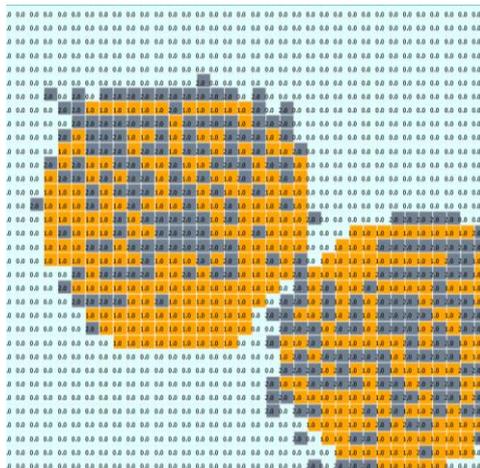
Files for this experiment are Avain2(questionable)ma, A_rule.inc and Avain.val



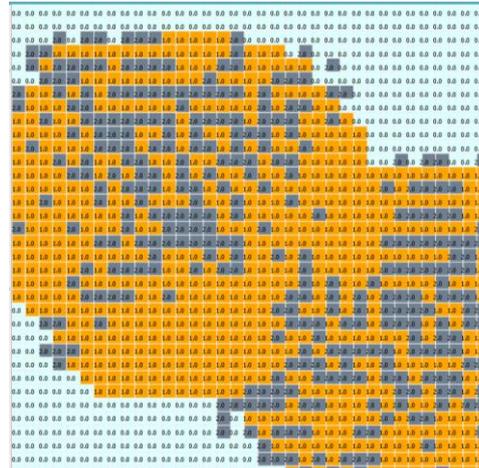
t = 200



t = 400



t = 600



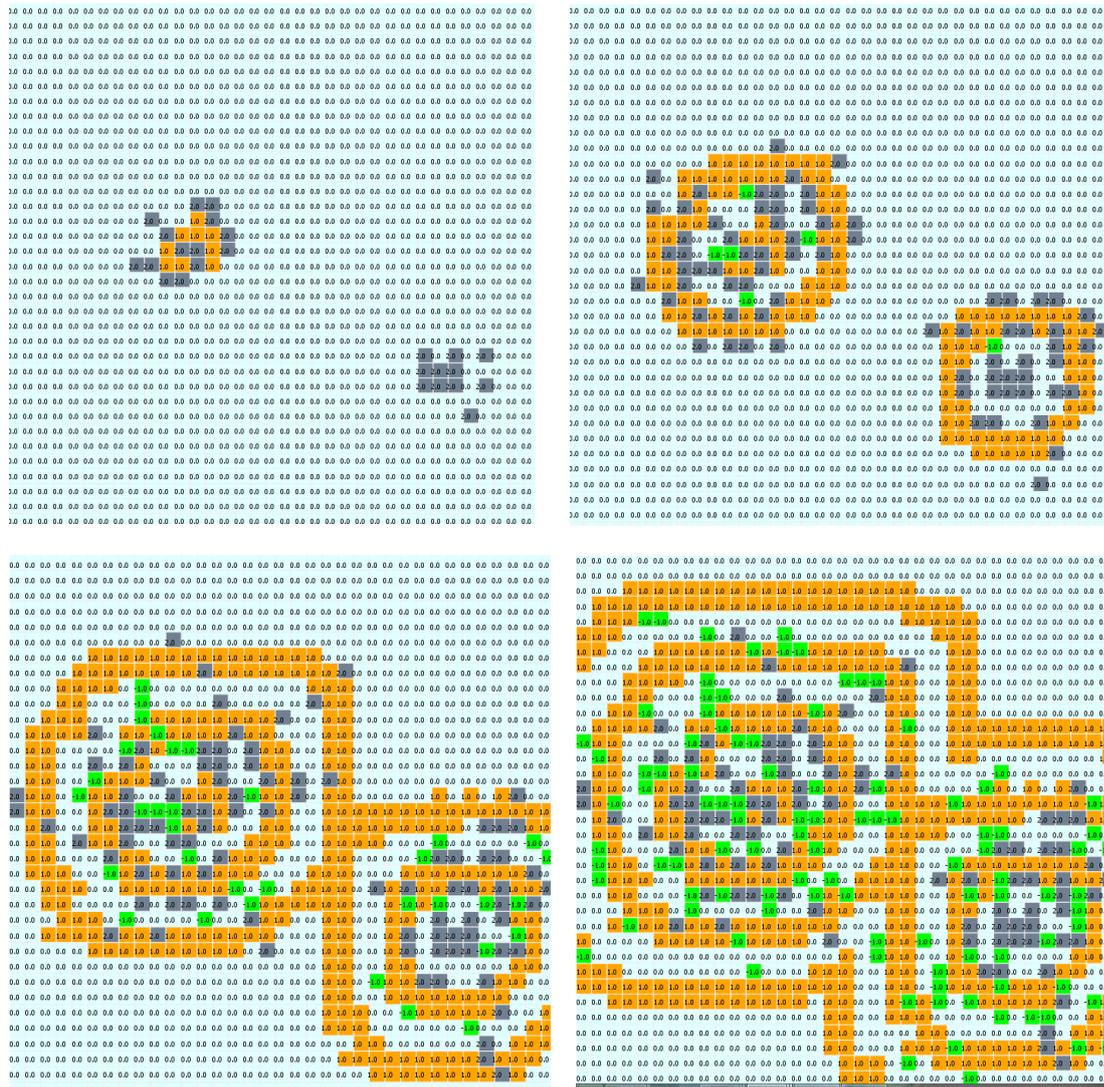
t = 800

(3) Questionable to Immune: In this transition inhabitants will try to get immune after flu symptoms has been noticed. This means they may spread no or less flu virus.

The rule in CD++ is below:

```
rule : { if ( random < #macro(Immune), -1, 0) } 100 { (0,0)=1 }
```

Files for this experiment are Avain3(immune).ma, A_rule.inc and Avain.val



(4) Infected to Dead: In this transition inhabitant who do not get the treatment are dead because of dangerous flu.

```
rule : { if ( random < #macro(dead), 3, 0 ) } 100 { (0,0)=2 }
```

Test Result

After setting parameters, I now plant infected cells among the population

As it is described below:

Light Cyan cell is in the state of susceptible

Gray one is in state of infectede

Orange cel is in state of questionable

Green ones shows Immuned

Red cell define the state of death

Test 1

1. Files for this experiment are A_dead).ma, A_rule.inc and Avain.val

#BeginMacro(Immune)

0.1

#EndMacro

#BeginMacro(dead)

0.9

#EndMacro

#BeginMacro(Outer)

uniform(0, 0.05)

#EndMacro

#BeginMacro(Inner)

uniform(0, 0.75)

#EndMacro

#BeginMacro(Spreading)

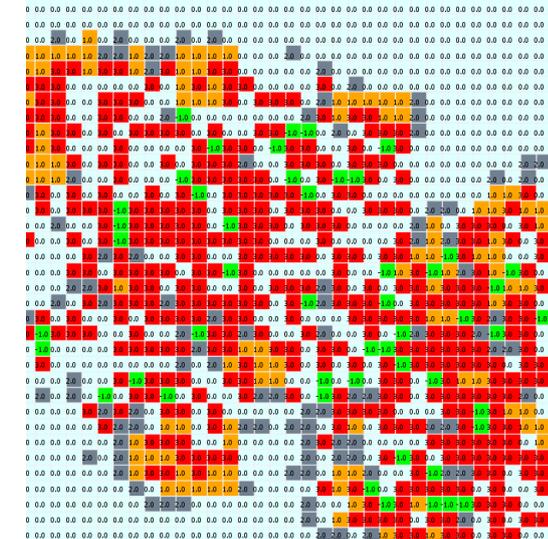
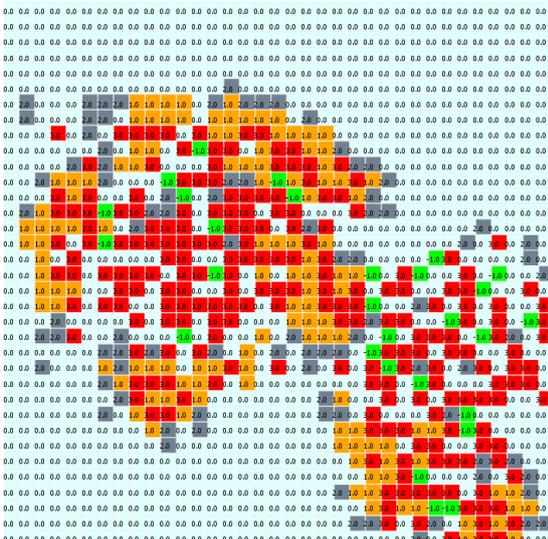
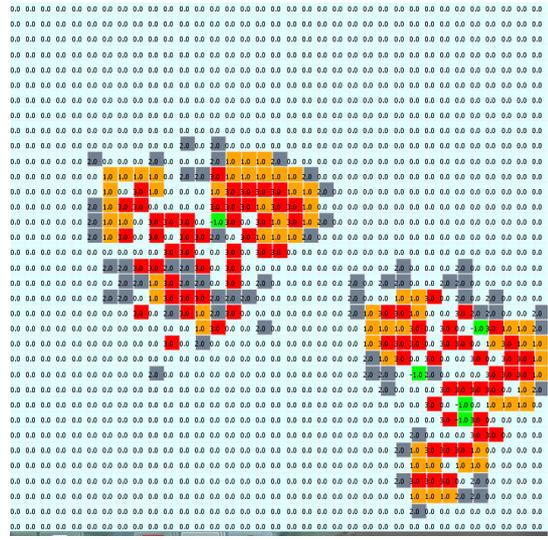
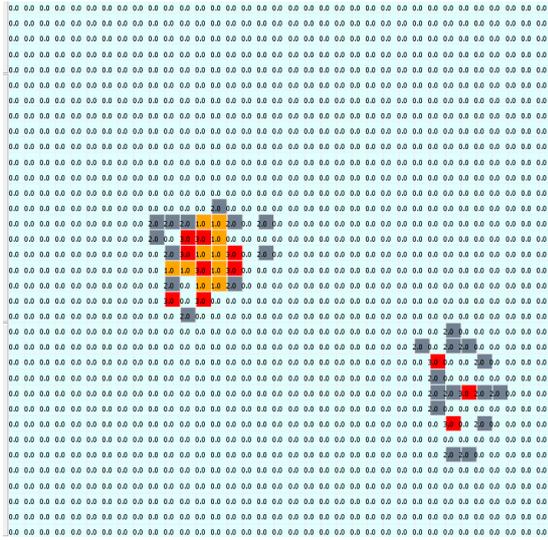
0.2

#EndMacro

#BeginMacro(Vigilance)

0.6

#EndMacro



Test 2

2. Files for this experiment are AvainInfluenza2.ma, A2_rule.inc and Avain.val

```
#BeginMacro(Immune)
```

```
0.3
```

```
#EndMacro
```

```
#BeginMacro(dead)
```

```
0.6
```

```
#EndMacro
```

```
#BeginMacro(Outer)
```

```
uniform(0, 0.05)
```

```
#EndMacro
```

```
#BeginMacro(Inner)
```

```
1
```

#EndMacro

#BeginMacro(Spreading)

0.8

#EndMacro

#BeginMacro(Vigilance)

0.4

#EndMacro

After setting parameters, I now plant infected cells among the population
As it is shown below:

-0.1	0.9	Light Cyan
1.9	2.89	Gray
0.91	1.89	Orange
-1.1	-0.9	Green
2.9	3.9	Red

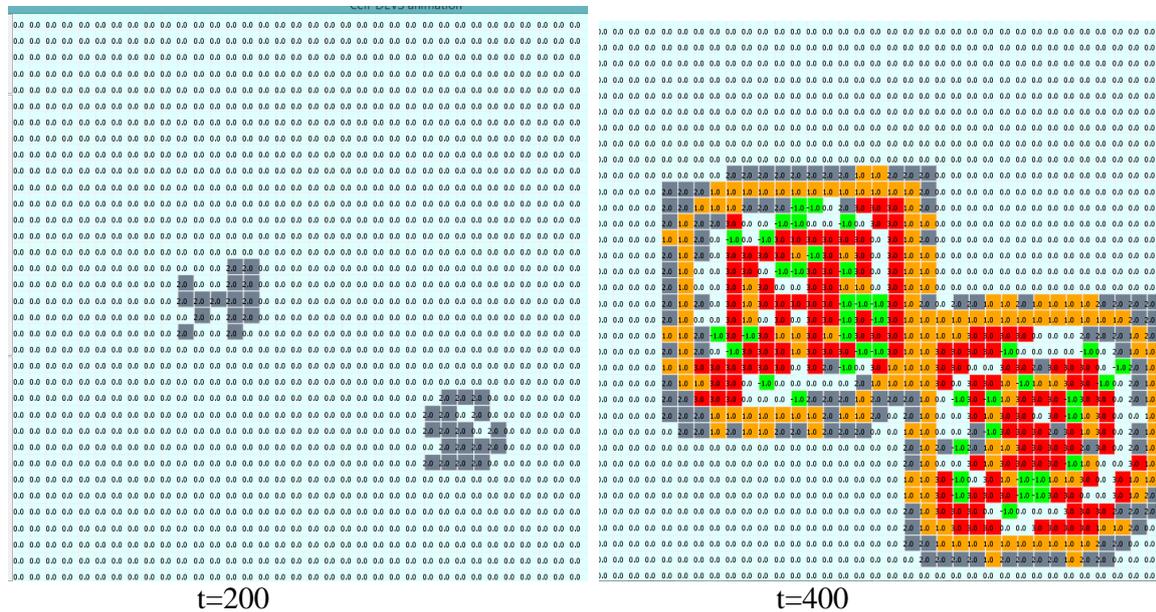
Light Cyan cell is in the state of susceptible

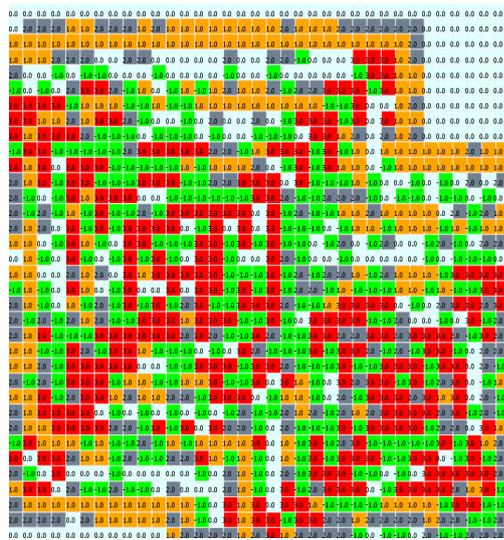
Gray one is in state of infectede

Orange cel is in state of questionable

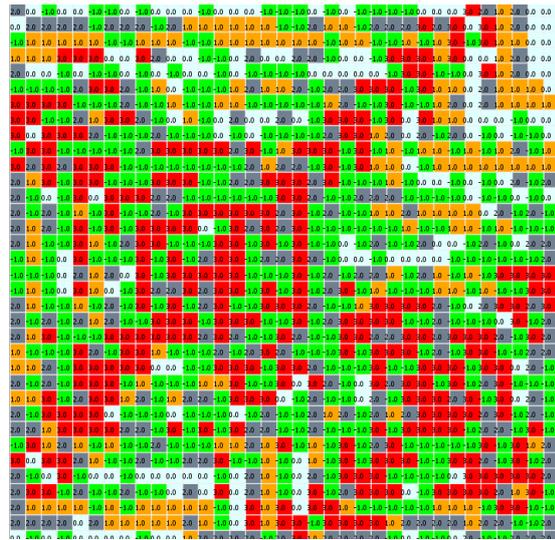
Green ones shows Immuned

Red cell define the state of death





t=800



t=1000

Conclusion

The simulations presented before prove that this model can be used to simulate the process of spread of flu.. Anyonewho wants to reuse this framework only needs to adjust the parameters to specific values.