The next code corresponds to the dynamics of influenza virus, on this script we invoke each function corresponding to each phase of dynamics.

**INITIAL PARAMETERS**

- **parametros_ini()** function load model parameters, a change in the parameters can change some inputs in the simulation. This is an overload function described later.
- **dist()** returns:
  - pGauss: values of the normal distribution
  - t: time vector associated.
- **In par01** we load:
  - b: infection related parameter
  - d: fraction of each day.
  - r: fraction latent rate become infectious
  - g: recovery rate
  - n: birth rate and natural death rate
  - d: death rate by illness
- **In par02** we load:
  - F: number of rows in the grid
  - C: number of columns in the grid
  - Ns: Number of initial susceptible population
  - Ne: Number of initial latent population
  - Ni: Number of initial infectious population
  - Nr: Number of initial recovered population
- **In par03** we load parameters for visualization:
  - S: Susceptible
  - E: Latent
  - A: Asymptomatic
  - I: Infectious
  - R: Recovered
  - D: Death
  - Vacio: Empty
  - obs: Obstacle

**FUNCTION DESCRIPTION:**

**parametros_ini**(escala,vacin): This function sets the initial and general values of the simulator variables, the user can set two of them:
- **parametros_ini**(N) the simulation scale in a range from 1 to N;
- **parametros_ini**(N,1/N) can set a proportion of vaccinated population in a range from 0 to 1/N.

\[
[pGauss \ t1]=\text{dist}()
\]

This function calculates the probabilistic distribution for infected individuals, corresponding to a normal distribution.

- **pGauss**: return the values of the probabilistic distribution.
- **t1** return the value of the temporal associated vector.
This function set the initial state of the grid.

- Outputs:
  - `grilla`: returns the initial spatial individuals distribution in the grid.
  - `grillaI`: returns the initial map of infective individuals.
- Inputs
  - `dist`: probabilistic distribution of infectious individuals.
  - `t`: time vector associated with `dist`.
  - `grilla`: empty grid.
  - `grillaI`: empty density grid.
  - `sec`: the section in the grid where will be distributed the infectious and asymptomatic individuals: 1- all the grid; 2-half of the grid; N-1/N of the grid.

This function describes epidemic dynamics, result are given in the returned grids.

- Outputs:
  - `grilla`: returns the spatial individuals distribution in the grid in the instant `t`.
  - `grillaI`: returns a map of infective individuals in the instant `t`.
- Inputs:
  - `grilla`: spatial individuals distribution in the grid in the instant `t-1`.
  - `grillaI`: a map of infective individuals in the instant `t-1`.
  - `dist`: probabilistic distribution of infectious individuals.
  - `x1`: time vector associated with `dist`.

This function is divided in 5 phases:
- Infective process.
- Latent infective phase.
- Infectious phase.
- Recovery phase.
- Births

This function corresponds to the movement phase, the results are given back in the two grids (`grilla` and `grillaI`), the parameter `mov` corresponds to the movement option 0- Random movement and 1- directed to the center of the grid. The parameters `t` and `tc` model an quarantine state; `t` is the actual time step and `tc` is the begin of quarantine

- Outputs:
  - `grilla`: returns the spatial individuals distribution in the grid in the instant `t`.
  - `grillaI`: returns a map of infective individuals in the instant `t`.
- Inputs:
  - `grilla`: spatial individuals distribution in the grid in the instant `t-1`.
  - `grillaI`: a map of infective individuals in the instant `t-1`.
  - `mov`: 0 for random movement; 1 center directed movement.
  - `t`: the actual time step.
  - `tc`: the time when quarantine begins.
This function keeps track of different population size in each time step.

- **Output:**
  - **St**: total susceptible individuals at time t.
  - **Et**: total latent individuals at time t.
  - **Rt**: total recovered individuals at time t.
  - **At**: total asymptomatic individuals at time t.
  - **It**: total infected individuals at time t.

- **Input:**
  - **grilla**: population grid at time t.
  - **St**: total susceptible individuals at time t-1.
  - **Et**: total latent individuals at time t-1.
  - **Rt**: total recovered individuals at time t-1.
  - **At**: total asymptomatic individuals at time t-1.
  - **It**: total infected individuals at time t-1.
  - **t**: actual time step.

**IMPORTANT NOTES:**

The maps are pre-charged, if you want to charge another map you must uncomment the code. For example:

```matlab
%grilla=load('Maps/grill0101.txt');
%grilla=load('Maps/map.txt');
%grilla=load('Maps/ciudad.txt');
%grilla=load('Maps/plano.txt');
```

in this case, the map grill01 is charged, to charge map:

```matlab
%grilla=load('Maps/grill0101.txt');
grilla=load('Maps/map.txt');
%grilla=load('Maps/ciudad.txt');
%grilla=load('Maps/plano.txt');
```

For try different population densities

```matlab
parametros_ini(0)
```

so, to set a density of 1/3 of the original size the you must set:

```matlab
parametros_ini(3)
```

and for 1/10 of the original one you must set:

```matlab
parametros_ini(10)
```

For try different initial distributions in the grid for infective individuals then you must set the function inicializar()

```matlab
inicializar(pGauss,t,grilla,grillaI,1);
inicializar(pGauss,t,grilla,grillaI,2);
inicializar(pGauss,t,grilla,grillaI,4);
```

and so.

For quarantine you must set the las two parameters of the movimiento function, to stop movement in day 10 then:

```matlab
[grilla,grillaI]=movimiento(grilla,grillaI,mov,t,10).
```