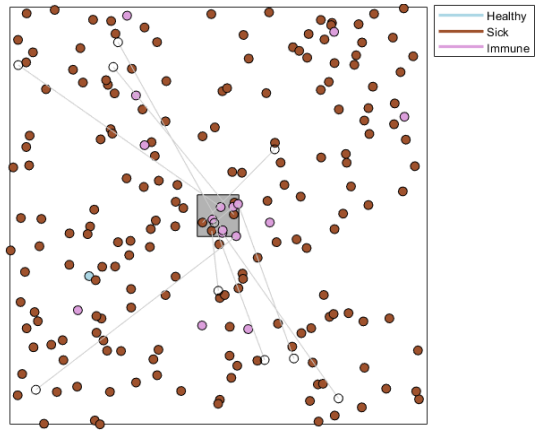
A discrete (stochastical) SIR epidemiological model

Matteo Caldana

16/03/2023

Epidemiological model[1]

Consider a discrete population of agents living in a 2D square domain.



[1] This exercise is inspired by models shown in
`https://www.washingtonpost.com/graphics/2020/world/corona-simulator/` and
`https://github.com/seismotologist/coronaVirusContagion`.

Contagion model

Starting from random initial positions, the population evolves according to the following rules:

1. Each agent can be either Susceptible to a virus, Infected or Recovered;
2. At each timestep agents move randomly of a given step length;
3. A prescribed percentage of agents does **social distancing**, *i.e.* does not move, excepted the following rule;
4. Each agent (*i.e.* including those who do social distancing) goes to a pub placed at the center of the domain once every a fixed number of time steps;
5. A agent is infected when close to another infected agent and recovers after a fixed number of time steps.

Exercise - Part 1

Starting from the given files, start by implementing a C++ program that simulates a simplified model such that

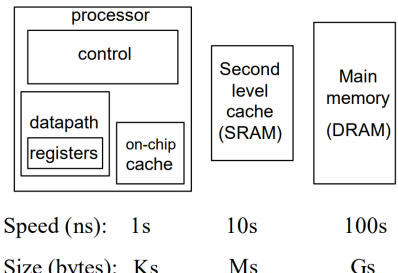
1. Exports the total number of susceptible, infected and recovered agents at each timestep to a `.csv` file (implement `Contagion::output_results`).
2. Exports the positions of each agent at each timestep, use a parameter to set the frequency of the export (implement inside `Contagion::run`).
3. Use an `enum class` to define the possible agents states.
4. Each `Agent` moves at random (implement a `Agent::move` method). Check that the agent stays in the domain, change the direction of the movement otherwise.
5. The simulation is managed by the method `Contagion::run` which at each timestep
   - 5.1 moves each agent
   - 5.2 checks the distance between agents, if one is Infected and the other Susceptible and they are close, than they become Infected
   - 5.3 counts the number of agents in each state

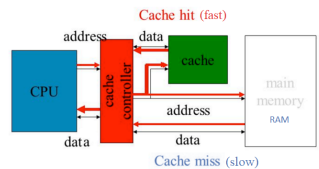
Exercise - Part 2

1. Performs the simulation employing the `<algorithm>` library and parallelize the code using the `<execution>` library where possible;
2. Make the model more accurate by completing the `Agent::move` method following the "Contagion model" slide. Use an `enum class` to define the possible agents actions.

Cache aligment

Modern processors use a variety of techniques for performance. Caches is small amount of fast memory where values are "cached" in hope of reusing recently used or nearby data.





- Taking into account cache aligment is key for linear algebra routines
- Libraries like OpenBLAS (which is among the mk modules) or ATLAS are tuned at compile time to take into account hardware specific parameters (like cache size).
- -03 aggressive compiler optimization option sometimes is able to do this

Exercise - Part 3

Let L1CS be the cache size of a CPU and let v be a large vector of size $K \cdot$L1CS. Consider:

```
// naive
for(size_t i = 0; i < v.size(); ++i)
  // at each iteration i we bring into the cache K different blocks of v
  // since we are accessing to the whole range
  for(size_t j = 0; j < v.size(); ++j)
    // do something with v[i] and v[j]

// partially cache optimized
for(size_t k = 0; k < K; ++k)
  for(size_t i = 0; i < v.size(); ++i)
    // at each iteration i we bring into the cache just one block of v
    // since we access only to the values from L1CS * k to L1CS * (k + 1)
    for(size_t j = L1CS * k; j < L1CS * (k + 1); ++j)
      // do something with v[i] and v[j]
```

- Optimize the cache alignment for the double for loop used for the radius checking step of the (sequential) simulation.
- Use `getconf -a | grep CACHE` to check the cache size of your PC.
- Confront the execution time for different number of agents between the two algorithms.

Possible extensions (homework)

1. Plot the curve of susceptible, infected and recovered using Python, you can read the `.csv` using the pandas module. You may need to install the matplotlib module with `pip install matplotlib`.
2. Create an animation of the positions of the agents at each timestep using Python.
3. Personalize agent-specific parameters, *e.g.*
   - by random generation, or
   - by reading multiple pairs of {agent index, parameter value} for each parameter from file;
4. Take birth and mortality rates into account.
5. Extend the model to 3D domains (possibly using templates).