

## The model description

At the start of each time step, the model counter is updated, and the demographic and spatial data of the study area are assigned to the environment (cell agents). Then, human agents are assigned to the population blocks based on demographic information. In other words, to allocate the real population to each population block in the study area, demographic information based on 16 age groups was assigned to each of the 1911 corresponding population blocks in the study area. Accordingly, at the beginning of the modeling, each of the 1911 population blocks has a specific number of human agents in each of the 16 age groups. The characteristics of human agents are determined randomly, such as the infection period (TI), which is calculated randomly based on the normal probability density function ( $N(26,5)$  days, as explained in Table 1) [29]. Human agents can experience different epidemic states such as susceptible, asymptomatic infected, symptomatic infected, etc. (as described in Section SASOARD Model). They can perform various activities according to their age groups at certain times of the day by moving toward different land use during the day. For example, people in the age group of 12 to 14 years attend middle schools (educational land use) at 8 am and return to their population blocks at 2 pm (Section Social Gatherings). Human agents can have varying reactions to different events based on their conditions. For instance, an individual with an aggravated infection who is not treated will have an increased probability of death.

In contrast, cell agents do not move and can be any of the land uses in the studied area. Since Gorgan occupies an almost rectangular area of 10,590 meters in length and 6,690 meters in width, and each cell agent is 30 meters by 30 meters, there are 78,719 cell agents ( $223 \times 353$ ) in the model. To model the spatial spread of COVID-19, a susceptibility value is assigned for each cell agent. If a susceptible human is in close proximity to an infected human, based on a certain probability and the distance from the infected human, the susceptible human can contract the disease and enter the asymptomatic stage. Then, the cell agent in which the susceptible human is located will increase its susceptibility by one unit in response. In each time step, the number of cases and deaths and the basic reproductive number ( $R_0$ ) are updated. Based on the UML sequence diagram, all agents repeat their activities in each time step. Also, each process in the model is activated under certain conditions. For example, if an infected human enters the acute stage of the disease and is unable to recover, the death process will be activated for that agent.