Author: Danis Alukaev   Student ID: 19BS551

Assignment 2 – Report

Description of algorithms.

The first algorithm is based on **backtracking** and utilizes two techniques to optimize the search. The idea is to discover all possible solutions to reach the goal from the original position. The solutions are built incrementally and accepted only ones that meet the set of requirements. Then, the path that has the minimal length is determined. However, pure backtracking needs to be optimized to speed up the search for solutions. The first optimization technique allows not to consider the solutions whose approximate length is greater than the length of the current minimal path. At each new step, the program checks if the sum of path length discovered and Chebyshev distance from the current cell to the Home is less than the number of cells in the currently minimal path. The second technique permits first to observe the cells from which the estimated distance to the Home is minimal. Thus, for each current cell in recursive rule, there is found a set of candidate cells. These cells are sorted by priority. In case the agent got the mask or has visited the doctor, the infected cells might appear in the set of candidate cells. Finally, the cell with the highest priority is set to be current. Further, the prioritization allows implementing the different perceptions of Covid by the Actor agent. Apparently, for the second variant of the Backtracking algorithm, there can be added overhead on cost for candidate cells which Moore neighborhood contains infected cells to make the agent beware of the Covid.

The second algorithm is based on the **A-star** algorithm. To describe the algorithm flow, primarily observe the possible representation of all solutions for a given problem. In fact, the set of all paths from the agent to the Home could split up into two subsets. The first set contains sequences of cells from the agent to the Home which do not pass through the Mask or Doctor. The second set consists of paths going through the Mask or Doctor. The solution is the path of minimal length located in one of these subsets. In the proposed implementation each cell has a cost. The initial position has zero cost. Further, each cell has an estimated cost that is the sum of Manhattan distance

from the current cell to the Home and the cost defined earlier. Finally, cells have a parent that is updated when the cost of adjacent cells can be decreased. The priority queue called 'open' is sorted by the estimated cost. Once the cell is processed it is placed in the list 'closed'. When all the possible destinations are covered, i.e., the list 'open' is empty, one can restore the path from any of the points in list 'closed'. Similarly, for the second variant, there can be added overhead on the estimated cost for candidate cells which Moore neighborhood contains infected cells to make the agent beware of the Covid.

Statistical analysis.

Statistical analysis of Backtracking and A-star searching algorithms was performed based on the execution time of these algorithms (and their variants) on the randomly generated maps. Data set consists of 30 entries, each of them having 4 runtimes for different algorithms (see Figure 1).

The t-values were computed in Google Sheet. The sheet is available online.

Map #	Backtracking (variant 1)	A-star (variant 1)	Backtracking (variant 2)	A-star (variant 2)
1	0,012725591659545800	0,20455932617187500	0,00262355804443359	0,16234040260314900
2	0,007003068923950190	0,20556521415710400	0,00626611709594726	0,15913081169128400
3	0,000238180160522460	1,47364187240600000	0,00010704994201660	1,94411396980285000
4	0,010280370712280200	0,20957303047180100	0,00611400604248046	0,16615247726440400
5	0,002037525177001950	0,22657752037048300	0,00247859954833984	0,15299654006958000
6	0,038910627365112300	0,17886185646057100	0,03826069831848140	0,15898227691650300
7	0,023387908935546800	0,21243453025817800	0,02172088623046870	0,20249867439270000
8	0,002342700958251950	0,22226428985595700	0,00386667251586914	0,15474557876586900
9	0,022794723510742100	0,1829404830932610 0	0,01881599426269530	0,15278720855712800
10	0,005944967269897460	0,20769429206848100	0,00252914428710937	0,16354227066040000
11	0,021376371383666900	0,21359133720397900	0,00508618354797363	0,17519474029541000
12	0,011488914489746000	0,21990680694580000	0,00619125366210937	0,16336345672607400
13	0,015450239181518500	0,20809197425842200	0,00201034545898437	0,16666412353515600
14	0,022957801818847600	0,19432258605957000	0,00891160964965820	0,16474461555480900
15	0,002894639968872070	0,23602271080017000	0,00369858741760253	0,15921473503112700
16	0,032063722610473600	0,19220471382141100	0,01604056358337400	0,16992139816284100
17	0,021137237548828100	0,20924210548400800	0,00561714172363281	0,16361260414123500
18	0,001811981201171870	0,23754405975341700	0,00192880630493164	0,16584706306457500
19	0,022084474563598600	0,20140385627746500	0,00577402114868164	0,14956808090209900
20	0,036897182464599600	0,18804907798767000	0,00734043121337890	0,15345907211303700
21	0,000156879425048828	1,27147436141967000	0,00016903877258301	1,59552288055419000
22	0,002849578857421870	0,22322583198547300	0,00364613533020019	0,16475701332092200
23	0,030911922454833900	0,20642876625061000	0,00334692001342773	0,16761469841003400
24	0,024000883102416900	0,1975200176239010 0	0,00781083106994628	0,14415144920349100
25	0,002071142196665270	0,24130725860595700	0,00265216827392578	0,16867136955261200
26	0,007231235504150390	0,23158454895019500	0,00401353836059570	0,16241765022277800
27	0,002237796783447260	0,22978544235229400	0,00268244743347167	0,16065454483032200
28	0,000158786773681640	1,45925736427307000	0,00018167495727539	1,89318585395812000
29	0,004561424255371090	0,21802425384521400	0,00630187988281250	0,17248916625976500
30	0,018676519393920900	0,19054436683654700	0,02820754051208490	0,16229891777038500

	Backtracking (variant 1)	A-star (variant 1)
Mean:	0,013556146621704100	0,32978812853495200
Standard deviation:	0,01187666626	0,3648886252
Variance:	0,0001410552015	0,1331437088
Number of samples:	30	30
t-value:		4,744343918
p-value:		0,0000140613659

	Backtracking (variant 2)	A-star (variant 2)
Mean:	0,00747979482014973	0,32802145481109500
Standard deviation:	0,008739026117	0,5052810602
Variance:	0,00007637057747	0,2553089498
Number of samples:	30	30
t-value:		3,474138627
p-value:		0,0009762495343

	Backtracking (variant 1)	Backtracking (variant 2)
Mean:	0,013556146621704100	0,00747979482014973
Standard deviation:	0,01187666626	0,008739026117
Variance:	0,0001410552015	0,00007637057747
Number of samples:	30	30
t-value:		2,257085549
p-value:		0,02778468109

	A-star (variant 1)	A-star (variant 2)
Mean:	0,32978812853495200	0,32802145481109500
Standard deviation:	0,3648886252	0,5052810602
Variance:	0,1331437088	0,2553089498
Number of samples:	30	30
t-value:		0,01552558338
p-value:		0,9876661582

Figure 1. Student's t-test

Assume that all samples have normal distribution. Thus, for hypothesis testing there could be used Student's t-test. Recall, the t-value could be found as

$$t-value = \frac{|\bar{X}_1 - \bar{X}_2|}{\sqrt{\frac{S_1^2}{N_1} - \frac{S_2^2}{N_2}}} \qquad \text{(Eq. 1)}$$

where $\bar{X}_1$, $\bar{X}_2$ are sample means, S_1^2, S_2^2 are sample variance of two samples X_1, X_2 of sizes N_1, N_2 accordingly.

For the following section take two-sided significance level $p \le 0.05$ and degrees of freedom $N_1 - 1 = N_2 - 1 = 29$. Consequently, from the t-distribution table the critical level is 2.045.

1. Comparison of Backtracking (variant 1) and A-star (variant 1) algorithms.

The null hypothesis H_0 reflects that there is no significance difference between samples for Backtracking (variant 1) and A-star (variant 1) algorithms, i.e., the algorithms are the same. As an alternative hypothesis H_1 take the opposite to H_0 point that there is significance difference between two samples and algorithms are different.

Using (Eq. 1) compute the t-value for the samples: $t-value = 4.744343$. Obtained $t-value$ is greater than the critical level. The Null hypothesis is rejected and we accept the alternative hypothesis.

Similarly, for the obtained $t-value$ there can be found $p-value = 0.000014$. The $p-value$ is less than chosen significance level, and therefore the H_0 is rejected.

Hence, the Backtracking (variant 1) and A-star (variant 1) algorithms **are different**.

2. Comparison of Backtracking (variant 2) and A-star (variant 2) algorithms.

The null hypothesis H_0 reflects that there is no significance difference between samples for Backtracking (variant 2) and A-star (variant 2) algorithms, i.e., the algorithms are the same. As an alternative hypothesis H_1 take the opposite to H_0 point that there is significance difference between two samples and algorithms are different.

Using (Eq. 1) compute the t-value for the samples: $t-value=3.474139$. Obtained $t-value$ is greater than the critical level. The Null hypothesis is rejected and we accept the alternative hypothesis.

Similarly, for the obtained $t-value$ there can be found $p-value=0.000976$. The $p-value$ is less than chosen significance level, and therefore the H_0 is rejected.

Hence, the Backtracking (variant 2) and A-star (variant 2) algorithms **are different**.

3. Comparison of Backtracking (variant 1) and Backtracking (variant 2) algorithms.

The null hypothesis H_0 reflects that there is no significance difference between samples for Backtracking (variant 1) and Backtracking (variant 2) algorithms, i.e., the algorithms are the same. As an alternative hypothesis H_1 take the opposite to H_0 point that there is significance difference between two samples and algorithms are different.

Using (Eq. 1) compute the t-value for the samples: $t-value=2.257086$. Obtained $t-value$ is greater than the critical level. The Null hypothesis is rejected and we accept the alternative hypothesis.

Similarly, for the obtained $t-value$ there can be found $p-value=0.027786$. The $p-value$ is less than chosen significance level, and therefore the H_0 is rejected.

Hence, Backtracking (variant 1) and Backtracking (variant 2) algorithms **are different**.

4. Comparison of A-star (variant 1) and A-star (variant 2) algorithms.

The null hypothesis H_0 reflects that there is no significance difference between samples for A-star (variant 1) and A-star (variant 2)algorithms, i.e., the algorithms are the same. As an alternative hypothesis H_1 take the opposite to H_0 point that there is significance difference between two samples and algorithms are different.

Using (Eq. 1) compute the t-value for the samples: $t-value = 0.015526$. Obtained $t-value$ is less than the critical level. The Null hypothesis is failed to reject, so the H_0 is accepted.

Similarly, for the obtained $t-value$ there can be found $p-value = 0.987666$. The $p-value$ is greater than chosen significance level, and therefore the H_0 is failed to reject.

Hence, the A-star (variant 1) and A-star (variant 2) algorithms **are same**.

Description in terms of PEAS.

By the problem statement, the Actor agent can be categorized using the Performance measure, Environment, Actuator, Sensor (PEAS) model. Primarily, the Performance measure might be expressed in terms of the run outcome: either win or lose. Further, the number of steps reflects the effectiveness of the agent in finding the shortest path. The fewer moves in the found way from the initial position to the Home, the better the performance. Besides, the time spent on finding the solution indicates how fast the system searches for the optimal path. During the runtime, the agent prioritizes the candidates to improve the performance. For instance, the Manhattan and Chebyshev distances allow approximating the residual path. Using this path agent can estimate how a move to a candidate cell affects the performance. Besides, the agent could assess the surroundings of the candidate position. For example, it either explores the neighborhood of infected cells first (variant 1) or beware of infected cells and does not go near them (variant 2).

The environment is a lattice of fixed size with one Actor and two Covid agents. The Moore neighborhood of cells with Covid agent is infected. Mask and Doctor cells allow passing through the infected cells. However, the agent does not know the location of the Mask and Doctor. Therefore, the described environment is partially observable: the agent might lose relevant information. By the problem statement, the environment has multiple agents: Actor and Covid agents. The agent cannot foresee whether the cell is the Doctor or Mask. Hence, the environment is stochastic. Any move is dependent on the previous sequence of moves, and therefore, the

environment is sequential. As the agent searches for the optimal move, the environment does not change: Covid agents remain in defined positions, Mask and Doctor do not move around the lattice. So, the environment is static. Yet another property of this environment is discreteness. There can be defined the state through the accumulated path and presence of the Mask or Doctor. The environment evolves by going from one state to another. The designer of the agent in advance does know all rules in the environment. There were provided constraints on the location of Covid agents, Mask, and Doctor cells. The agent can move only within the lattice and go at any of the adjacent cells. It makes the environment known.

The Actor agent can be represented as a robot driven by wheels equipped with Covid perceiver and camera. As the actuators, the Actor agent has wheels. Consequently, the Actor agent can move from one cell to another while searching for the Home. As sensors, the agent has the camera and Covid perceiver. The camera is used to move around the lattice and determine whether the Mask, Doctor, or Home cells were reached. Covid perceiver allows the Actor agent to determine the location of the Covid within a neighborhood of one cell (variant 1) and two cells (variant 2).

Graphical representation of maps that were impossible to solve.

In the source file *map.pl* there were prepared two maps that are impossible to solve. They are located in rules *impossible_map1_9x9* and *impossible_map2_9x9* (see Figures 2, 3).

The graphical representation of map *impossible_map1_9x9* is presented below. Apparently, there are two Covids that block the agent and do not allow to it move. Since both mask and doctor are unreachable from initial position, there is no solution for this map.
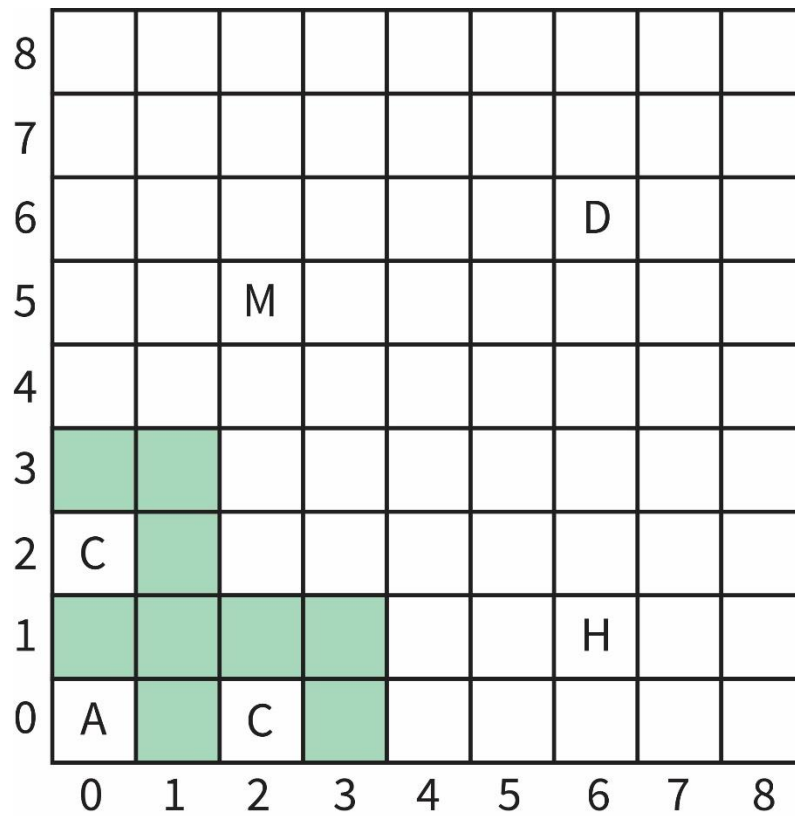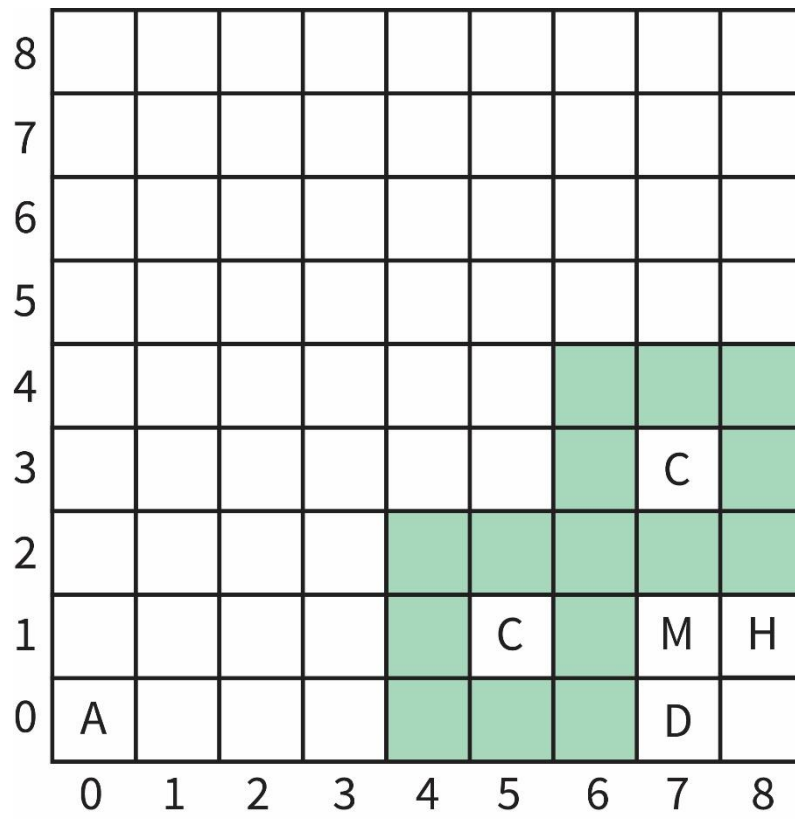
Figure 2. Visualized *impossible_map1_9x9*

The graphical representation of map *impossible_map2_9x9* is presented below. Similarly, there are two Covids that make the mask and doctor unreachable from initial position. Consequently, there is no way to overcome the barrier and solution for this map cannot be found.

Figure 3. Visualized *impossible_map2_9x9*