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List of Files in the submitted Archive/Bundle in format ZIP / TAR / RAR / $7z$ etc.		
1. Q1.pl		
2.		
3.		
4.		
5.		
6.		
7.		
8.		
9.		
10.		
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Special Assignment

Question 1 Documention is presented here. The prolog implementation is in the zip file with name Q1.pl.

We have a **limited vocabulary** as follows(case sensitive):

- Nouns: ram, shyam, seeta, geeta, apple, banana, lasagna, meat, cat, dog, children.
- **Pronouns** :- he, she, we, they.
- **Articles** :- a, an, the.
- **Verbs** :- eat, eats, cook, cooks, play, plays, jumps.

How to use:

◆ To encode a given grammatically correct message sentence "ram eats an apple", type in the command line exactly as; change([ram, eats, an, apple],[]).

If your sentence is grammatcally incorrect, the promt will display it. Otherwise your sentence will be encoded.

Working:

- **1.** Takes a list of words(the sentence).
- **2.** Checks first if grammatically correct by implementing the grammar coded in prolog file.[**This is the important functionality.**]
- **3.** Displays "Grammar Incorrect" if grammar is incorrect.
- **4.** Displays "False" if a word out of the vocabulary is used.
- **5.** If everything is fine, displays the encoded message with a "True" in the next line.
- **6.** Press Enter to stop and semicolon to see further calls.

Question 2(with all of its parts) is answered in this document. No Prolog implmentation is done for this question.

Epidemic Modelling

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Notes:

- Calculation and derivations are not shown, only the important equations and calculated data is presented to keep it concise.
- This pdf contains total 9 pages.

a). Choosing a model:

Perspective chosen – **Human Perspective (HP).**

The modelling of the epidemic would yield similar results regardless of the perspective chosen if the scope of the model actually captured reality with all uncertain variables.

Hence, we chose a perspective through which we can have more insights and data.

<u>Arguments in support</u>:

- Human world is better known to us than pathogen world. Hence the number of uncertain variables will be less.
- Mechanism of the pathogen is unkown(as in any burgeoning epidemic) to us. Hence prediction with the perspective of the virus becomes difficult.
- The medium of spread of the pathogen is Humans. Expansion of the pathogen solely depends upon Human mobility and contact duration(according to the question). Hence chosing **HP** would be more beneficial to fit in the factors into the model.
- Of both, the **PP** model the **HP** model, the latter would be easily applicable to other Human related areas as the variable mapping would not change much(however the **PP** would also be applicable but the mapping would be tough).

b). A mathematical model:

We try to formulate the task into an equation which accounts for different variables.

Since each zone has different values for different factors, we create an equation with these factors and apply to each zone seprately.

The spread of the virus can be seen as a reaction between two reactants, A and B(Humans and Pathogens). The rate of reaction will give the rate of cumulative poulation infection at time t.

So C(t) is the number of cumulative infectious people and $C'(t) = \mathbf{dC}(t)/\mathbf{dt}$ gives the rate of growth of infection.

The rate C'(t) depends on the number of infectious people present at time t i.e,C(t) and the growth factor \mathbf{r} :

$$C'(t) = dC(t)/dt = r * C(t)^{k}$$
(1)

Where the growth parameter is $\mathbf{k} \in [0,1]$. $\mathbf{k} = 0$ means the rate is linear and equals \mathbf{r} , and $\mathbf{k} = 1$ means the rate is exponential. Considering the given task <u>we chose \mathbf{k} to be 0.95</u> as the infection is epidemic and \mathbf{k} will be uniform for all zones(as given in the task).

The growth factor \mathbf{r} depends upon the average inter-person(radial) space \mathbf{R} , average duration of time between when two person contact $<\mathbf{t}_c>$ and the probability \mathbf{P} of transission of infection, all according to the given zone.

$$\mathbf{r} = \langle \mathbf{t}_{c} \rangle * \mathbf{P} / \mathbf{R} \tag{2}$$

Upon solving eq.(1) we get,

$$C(t) = ((1/m) * r * t + A)^{m}$$
(3)

where m = 1 / (1 - k), and $A = C(0)^{1/m}$ when t = 0 was put in solved equation to get the integration constant.

C(0) is the infectious population at start time, which is

$$C(0) = \mathbf{N} / \mathbf{q} \tag{4}$$

N is the total population of the zone and q defines **no. of carriers per q person** (in the task q is represented by r, here r is used for growth rate).

Time required for x% population to be infected(in a particular zone):

We can get the time **t** (in days) from eq. (3).

Choosing variable values,

 $\mathbf{R} = 2.5$ to $\mathbf{1.5}$ meters (Zone MSZ(2.5m-2m) and MICZ(2m-1.5m) as the variable values will be nearly similar for these two zones). Average is $\mathbf{2}$ meters.

 \mathbf{n} (total population = 20 million) $\mathbf{or} \ \mathbf{N} = 7\% (\mathrm{MSZ}) + 10\% (\mathrm{MICZ})$ of 20 million = 3.4 million.

<**t**_c>(average contact duration b/w two people) = 5 seconds.

P(the probability of transission of infection) = 0.7(given in task).

We get from eq.(2),

$$r = \langle t_c \rangle * P / R$$

 $r = 5 * 0.7 / 2$
 $r = 1.75$.

k = 0.95 (epidemic hence near to exponential growth)

$$m = 1 / (1 - k) = 1 / (1 - 0.95) = 20.$$

From eq.(4)

$$\mathbf{A} = \mathbf{C(0)}^{1/m} = (\text{Initial infectious population})^{1/m} = \mathbf{N} / \mathbf{q}.$$

Let $\mathbf{q} = \mathbf{1}$ million (i.e, $\mathbf{1}$ carrier in a million people),

$$A = (3.4 / 1)^{1/20} = (3.4 / 1)^{0.05} = 1.06.$$

Now, for x = 25, we have to find the time required for 25% population to get infected.

$$C(t) = 25\%$$
 of 3.4 million = 850k.

Put all calculated values of \mathbf{A} , \mathbf{r} , $\mathbf{C}(t)$ and \mathbf{m} in eq.(3),

$$\mathbf{t} = [C(t)^{1/m} - \mathbf{A}] * m / r$$

= $[(850,000)^{0.05} - 1.06] * 20 / 1.75$
= $\mathbf{10.50}$ days.

Hence, time required for zones MSZ and MICZ to get **25%** of their total population to get infected under given circumstances is **10.5 days.**

(ii).

MOP conditions on answer of (i).

a). MOP is S, i.e, everyone stays at home.

Effect on variable ${\bf r}$,

<tc> average contact time increases, say 100 seconds,

P remains same as average time increased had the effect = 0.7,

R should decrease as everyone is as home say 1 meter.

$$r = 70.$$

Effect on growth parameter \mathbf{k} ,

Since groups do not interact with each other k decreases to 0.4.

$$m = 1.6$$

Hence,

$$t = [C(t)^{1/m} - A] * m / r$$

 $t = 116.09$ days.

Hence staying at home increases infection spread time.

b). $\underline{\text{MOP is D}}$, i.e, normal movement, which is the one we calculated in (i) as $10.5 \ days$.

c). MOP is SN, i.e, only sick stay at home.

Effect on **r,**

only **P** will decrease as less infectious persons are contacting, say 0.5.

Also **k** will decrease, say 0.6.

So,

$$\mathbf{r} = \mathbf{5} * \mathbf{0.5} / 2 = \mathbf{1.25}.$$

 $\mathbf{m} = 1 / (1 - 0.6) = \mathbf{2.4}.$
 $\mathbf{t} = [C(t)^{1/m} - \mathbf{A}] * \mathbf{m} / \mathbf{r}$
 $\mathbf{t} = [(850,000)^{0.41} - 1.06] * 2.4 / 1.25$
 $\mathbf{t} = \mathbf{516.00 \ days}.$

Hence applying this MOP would be the best to longer the time of spread of virus.

(iii).

The most important change as we could see in (ii) was to control the mobility by having only sick/infectious people stay at home.

It reduces the carrier contact power(k), infection probability (**P**) which account for most of the effect in our equation.

However, the major and most sensitive contributor is \mathbf{k} . Even a slight change in it will affect the outcome by great extent.