Pre Lab 8- Aniket Bhatia

Ans 1:

What we can do is we can take the genetic sequence of a healthy individual, a person who is infected with hepatitis A, and another person who is infected with hepatitis C. We can then use BLAST, to align and compare these DNA sequences and look for where the sequences are different. This would potentially give us the changes caused by the hepatitis's and then we can start to understand what those changes mean.

Ans 2:

The first sub-goal is to obtain the three sequences- Data Acquisition. Here, I described the need for only three sequences but in actual research one should consider a lot many, hence data acquisition an important step.

The next sub-goal would be to do Sequence Alignment. We can start to point out differences and similarities only after we have the sequences aligned, which makes this step important.

The next sub-goal would be look for differences. This would help us come up with hypothesis statements for what could be the possible reason for the phenomenon that we see.

The next sub-goal would be to verify the hypothesis. This might have to be done by wet lab experiments depending on the problem statement.

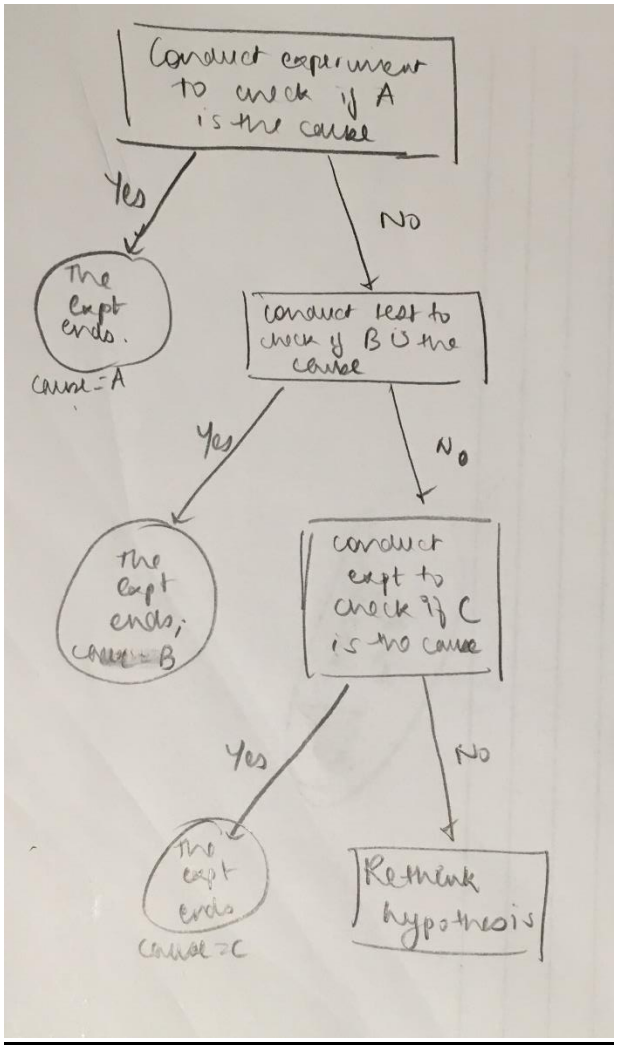
Ans 3:

The necessary information would be the availability of the locations of the change of the nucleotides and what changes are present (like what is the difference and where is the difference). This would help us to make hypothesis of various molecular interactions, pathways, etc. to explain the phenomenon at hand.

Ans 4:

Let's assume if we have identified changes at 3 places (call them A, B, and C), and we have established that the probability of the cause of those changes being the actual cause is in the order: A>B>C.

The decision tree is attached below:


Conduct experiment to check if A is the cause
Yes
No
The expt ends.
cause = A
conduct test to check if B is the cause
Yes
No
The expt ends;
conduct expt to check if C is the cause
Yes
No
The expt ends
cause = C
Rethink hypothesis