



System Specification

A specific disease can progress as described by the above HnMM.

The probabilities for the specific test results in each stage are given by the matrices below:

(Fever F or not nF ; Blood test result Ba , Bb or Bc ; Urine test Ua , Ub , Uc)

	nF	F		Ba	Bb	Bc		Ua	Ub	Uc
S1	0.9	0.1	S1	0.7	0.2	0.1	S1	0.8	0.1	0.1
S2	0.5	0.5	S2	0.5	0.3	0.2	S2	0.6	0.3	0.1
S3	0.2	0.8	S3	0.2	0.3	0.5	S3	0.5	0.3	0.2

Implementation

Extend your hard coded Proxel program with symbol outputs and path tracking

Tasks and Questions

Construct the state space and RG of the above model, including symbol emissions.

Write down the formal description of the above HnMM.

Use your program to answer the following questions:

- What is the probability of the given sequence of symptoms (patient1.seq)?
- What are the 5 most likely generating paths of that sequence?
- What are the actual portions of time spent in each disease stage for each of these paths?

We are not sure, what disease the patient is suffering from. We have the description of the progress of another possible disease below. The general 3-stage structure of Disease 2 is the same as in Disease 1 (above). The difference lies in the duration of the phases and the symptom probabilities:

Lehrstuhl für Simulation

$$T_{\text{Heal}} \sim \text{Normal}(10,2)$$

$$T_{\text{Incubation}} \sim \text{Normal}(3,0.5)$$

$$T_{\text{GetWorse}} \sim \text{Exp}(0.3)$$

	nF	F		Ba	Bb	Bc		Ua	Ub	Uc
$S1$	$\begin{bmatrix} 0.7 & 0.3 \end{bmatrix}$		$S1$	$\begin{bmatrix} 0.7 & 0.2 & 0.1 \end{bmatrix}$			$S1$	$\begin{bmatrix} 0.8 & 0.2 & 0.0 \end{bmatrix}$		
$S2$	$\begin{bmatrix} 0.3 & 0.7 \end{bmatrix}$		$S2$	$\begin{bmatrix} 0.5 & 0.3 & 0.2 \end{bmatrix}$			$S2$	$\begin{bmatrix} 0.7 & 0.2 & 0.1 \end{bmatrix}$		
$S3$	$\begin{bmatrix} 0.1 & 0.9 \end{bmatrix}$		$S3$	$\begin{bmatrix} 0.2 & 0.3 & 0.5 \end{bmatrix}$			$S3$	$\begin{bmatrix} 0.7 & 0.2 & 0.1 \end{bmatrix}$		

- Compute the probability of each disease.
- Which disease is the patient most likely suffering from?
- We have further measurements from patients (2-5) that were infected by our original subject, so they must be suffering from the same disease. What does your program say to that claim?

Hint: You can compute the answers for different time step sizes, or pick one time step size and state reasons for your decision.