

hidden markov  
models  
19 oct  
2022

CSCI  
373

let's travel back to the  
first days of the  
semester when we  
were reconnecting with  
all our old friends...



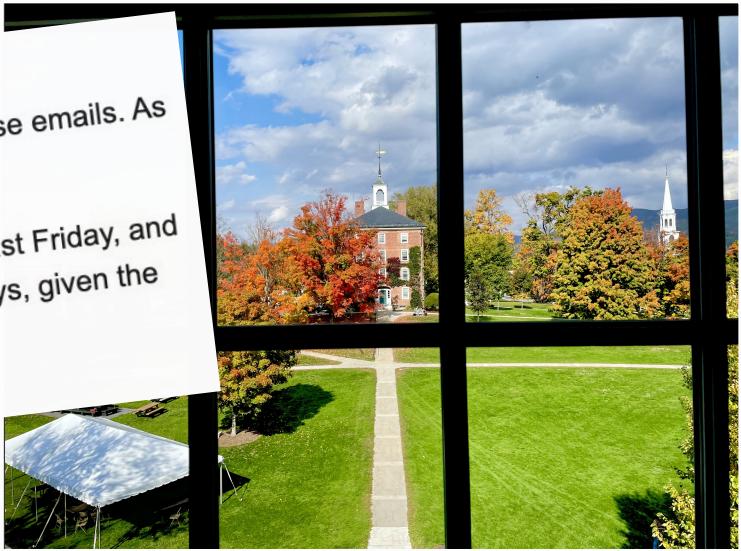
# let's travel back to 11

## Case counts

Starting now, we'll share case counts with you whenever I send these emails. As of today we have:

- **110 current student positives.** This is down from 165 last Friday, and the total is expected to decline further in the next few days, given the number of people almost done with isolation.
- **31 current faculty/staff positives.**

# all our old friends...

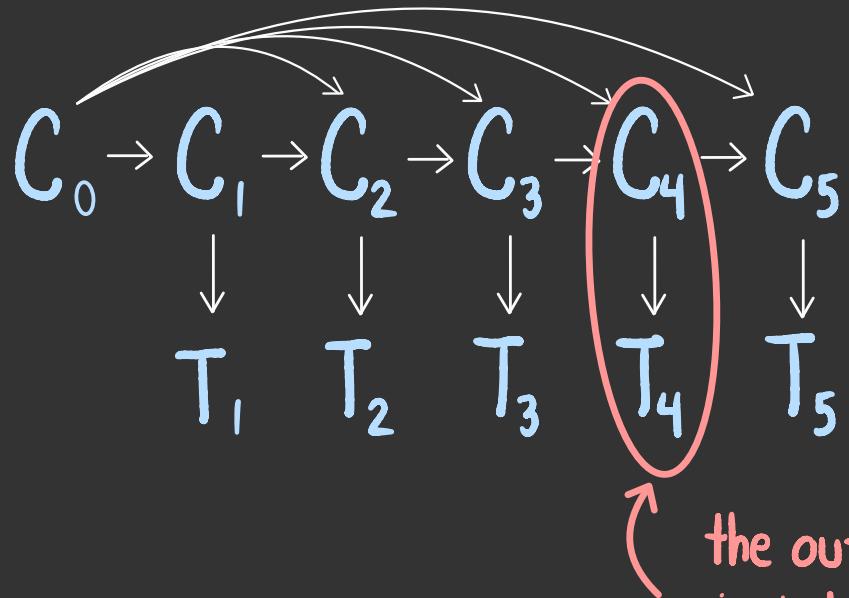


# like covid-19

design a bayesian network  
that allows us to compute  
the probability of having  
covid during your first  
five days on campus

use the following variables:

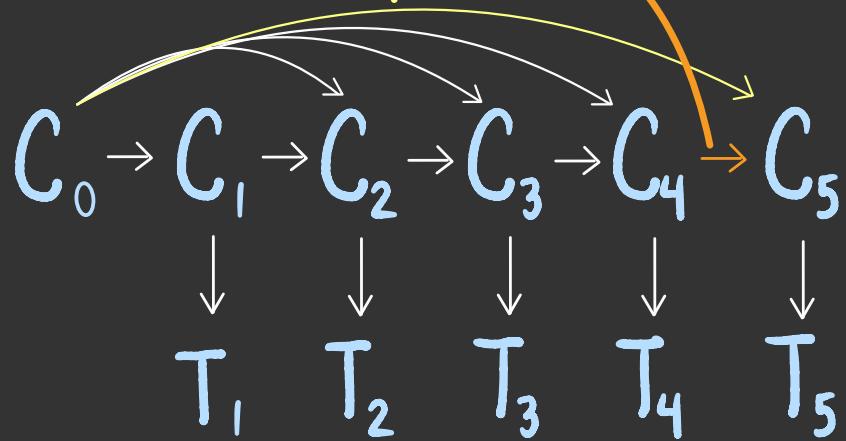
- $C_0 \in \{-, +\}$  is whether you arrived with covid
- $C_d \in \{-, +\}$  is whether you have covid on day  $d$  of being on campus
- $T_d \in \{-, +\}$  is the result of a rapid antigen test taken on day  $d$



the outcome of a test  
is independent of the  
other variables, given  
our current covid status

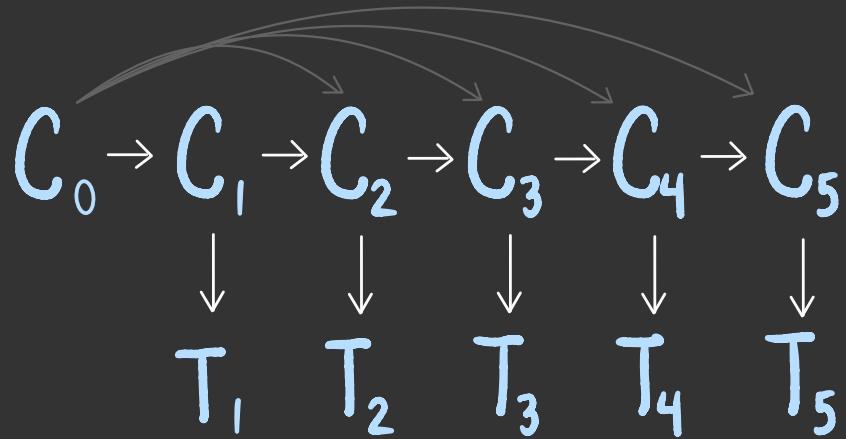
the likelihood of having covid on day d depends on

- whether we already have covid
- how long we've had it

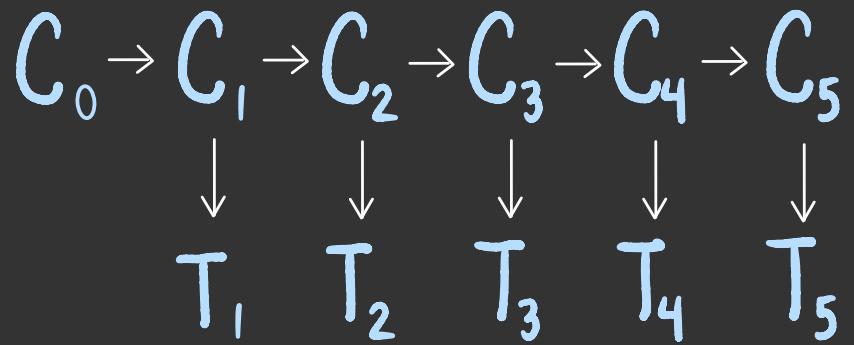


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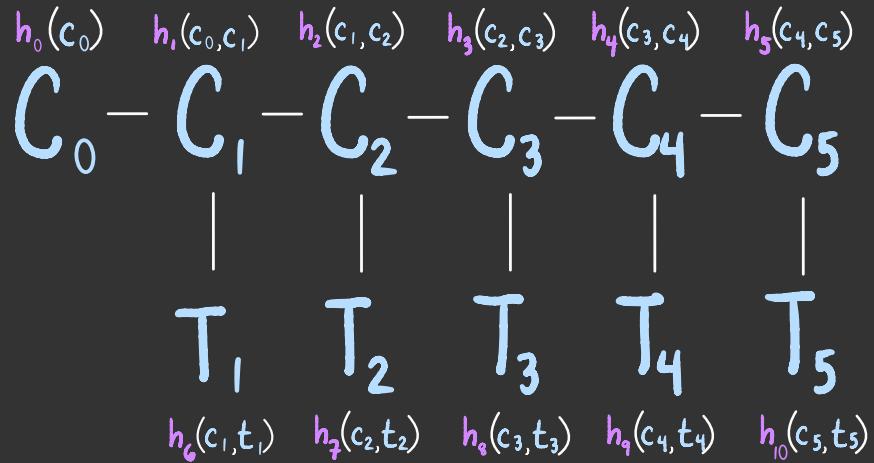
why might we make such a simplification?



compute the width of elimination order

$C_0, T_1, C_1, T_2, C_2, T_3, C_3, T_4, C_4, T_5, C_5$

I. create an undirected graph where two variables are adjacent if they appear in a **common factor**



compute the width of elimination order

$C_0, T_1, C_1, T_2, C_2, T_3, C_3, T_4, C_4, T_5, C_5$

2. eliminate each variable by connecting all its neighbors

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max clique  
2

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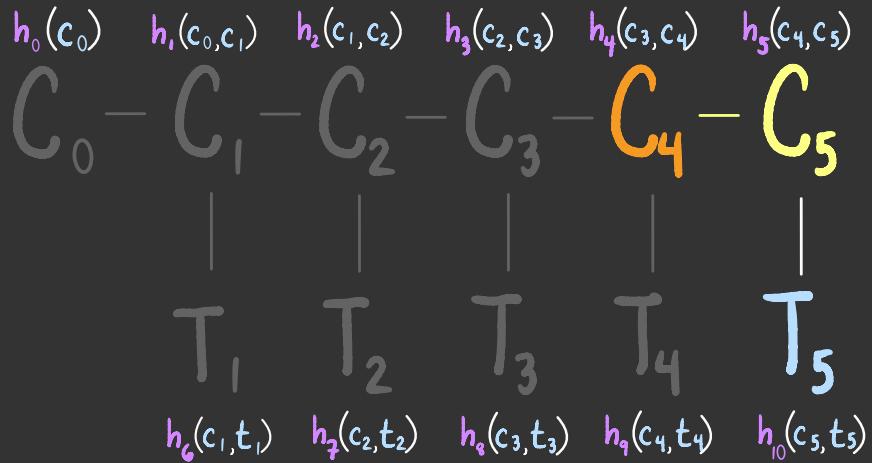
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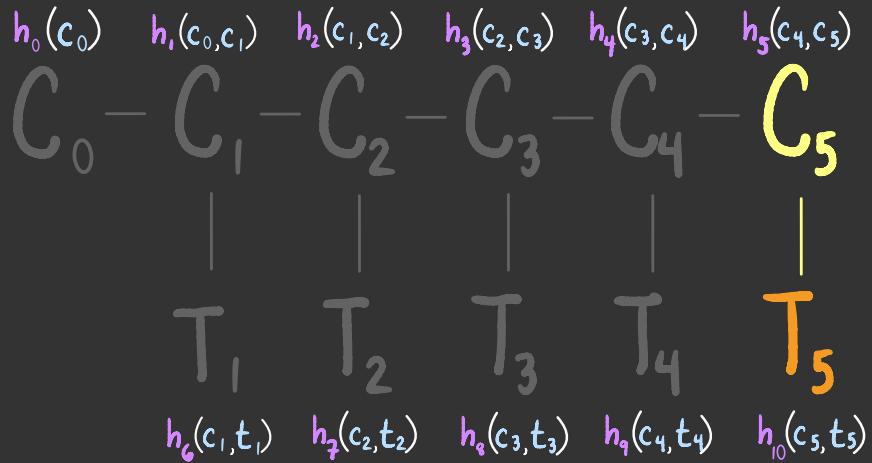


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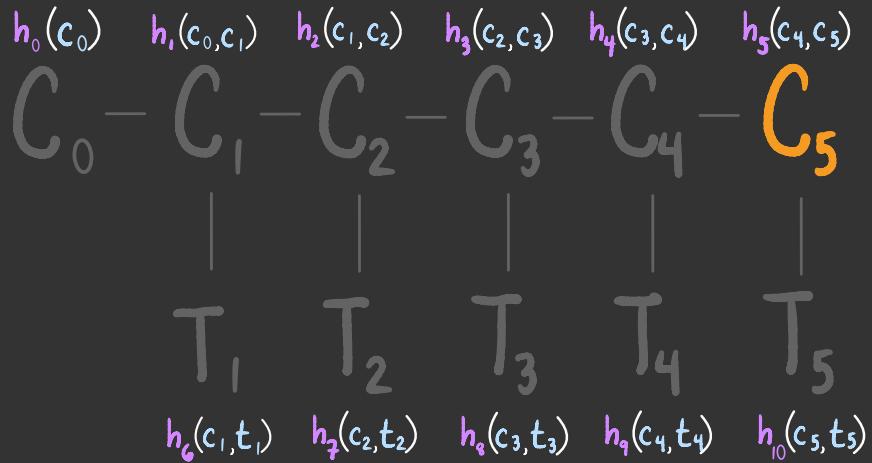


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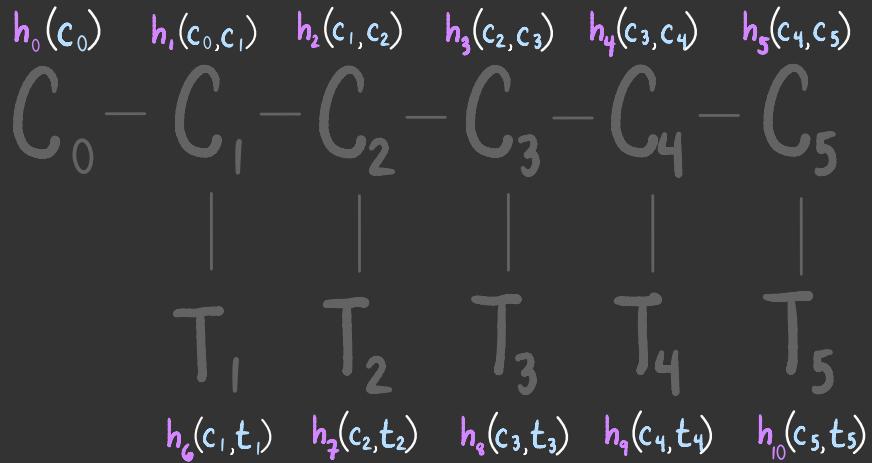


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width  
2

compute the width of elimination order

$C_0, T_1, C_1, T_2, C_2, T_3, C_3, T_4, C_4, T_5, C_5$

recall:

the worst-case runtime of variable elimination is  $O(nd^\omega)$ , where

- $n$  is the number of bayesian network variables
- $d$  is the size of the largest variable domain
- $\omega$  is the width of the elimination order

for:

$$C_0 \rightarrow C_1 \rightarrow C_2 \rightarrow C_3 \rightarrow C_4 \rightarrow C_5$$
$$\downarrow \quad \downarrow \quad \downarrow \quad \downarrow \quad \downarrow$$
$$T_1 \quad T_2 \quad T_3 \quad T_4 \quad T_5$$

$$n = \boxed{?}$$

$$d = \boxed{?}$$

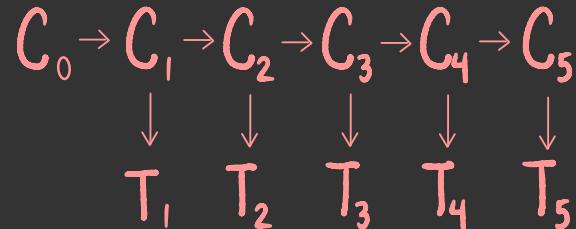
$$\omega = \boxed{?}$$

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- $n$  is the number of bayesian network variables
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for:



$$n = 1 + 2 \cdot \frac{\text{number of days}}{m}$$

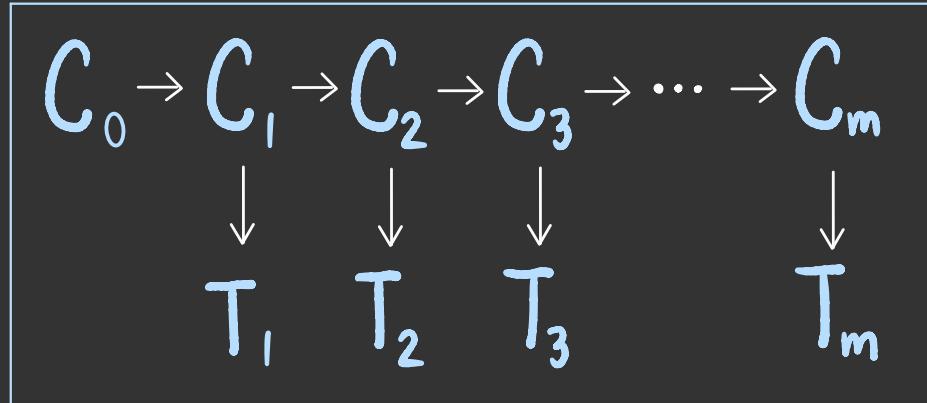
call this

$$d = 2$$

$$\omega = 2$$

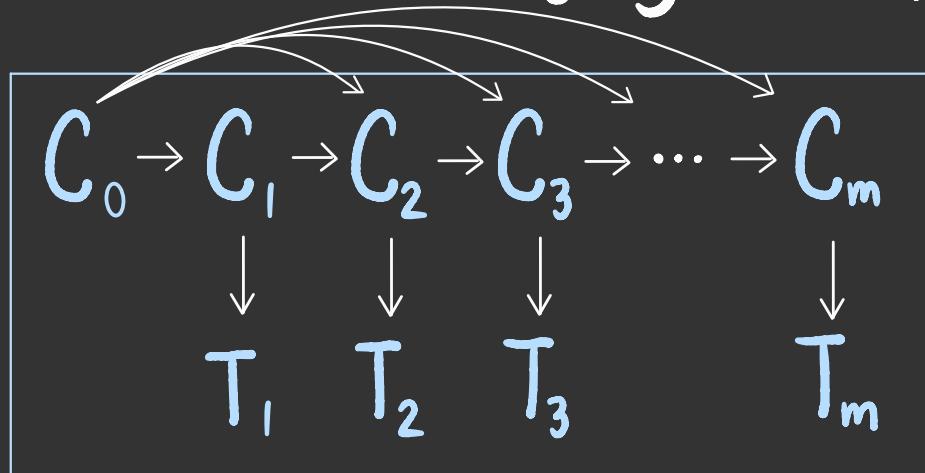
so the worst-case runtime is  $O((1+2m)2^2) = O(4+8m) = O(m)$

so we can run variable elimination on any bayesian network with this graph structure

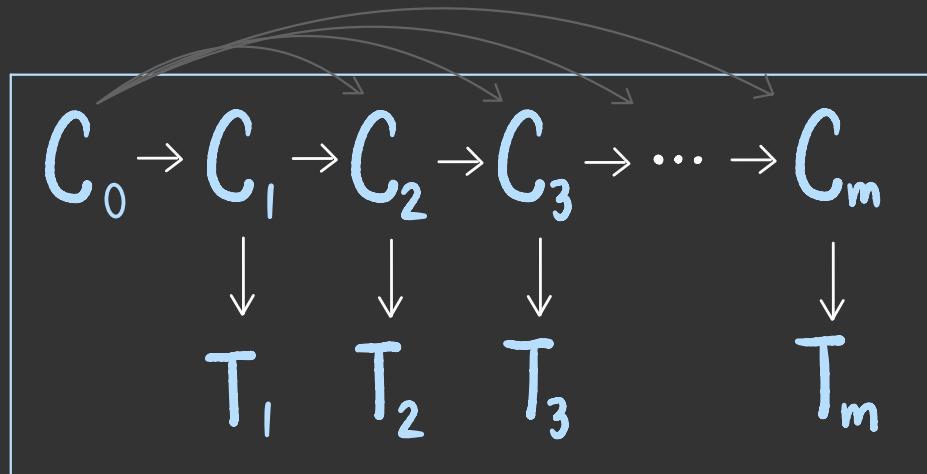


in time  $O(m)$

this would not have been the case without  
our earlier simplifying assumption

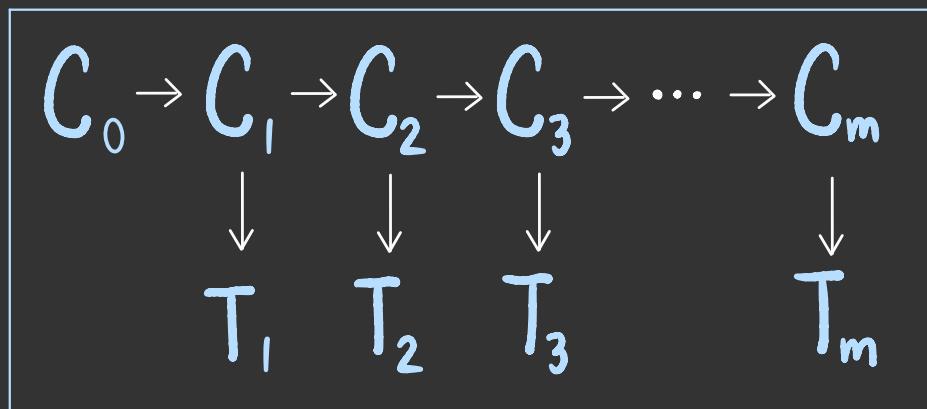


this assumption is called a markov assumption



namely, the probability of our current state depends only on the previous state

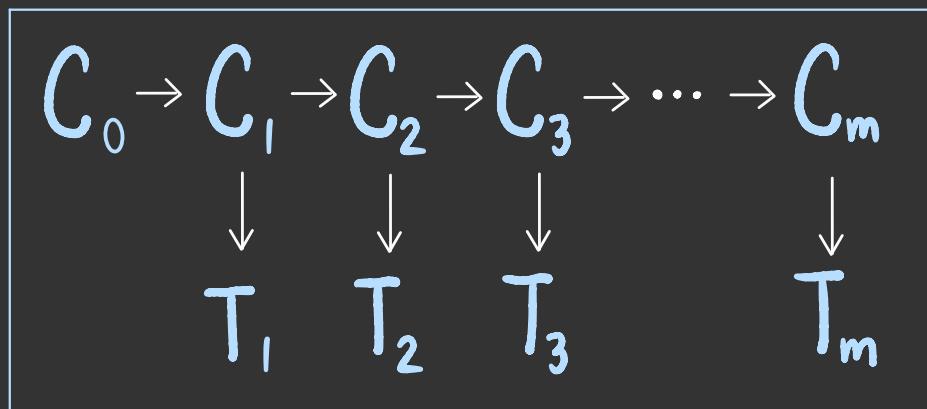
markov assumption : the probability of our current state depends only on the previous state



how would this be expressed as a conditional independence statement?

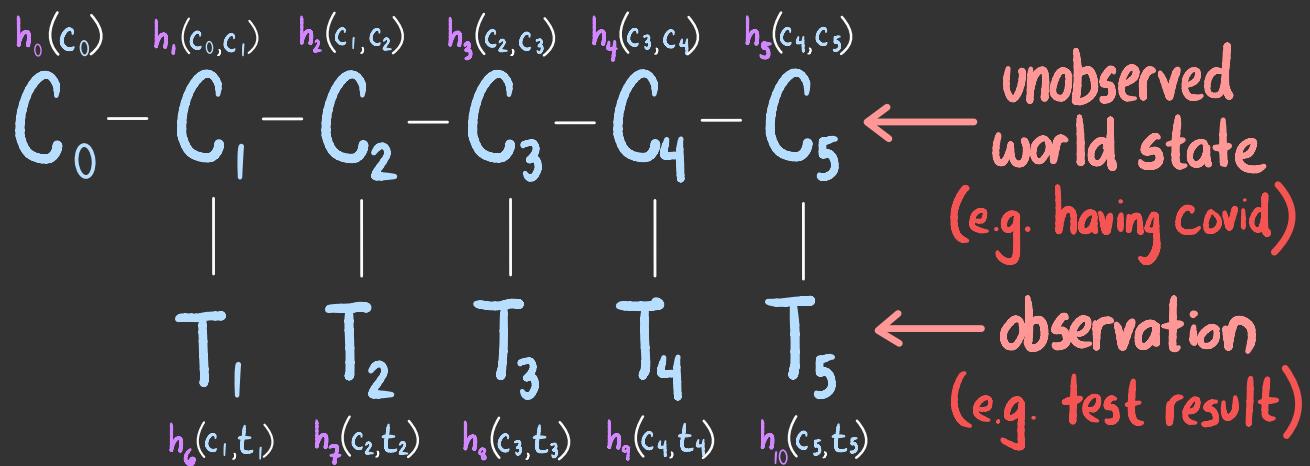


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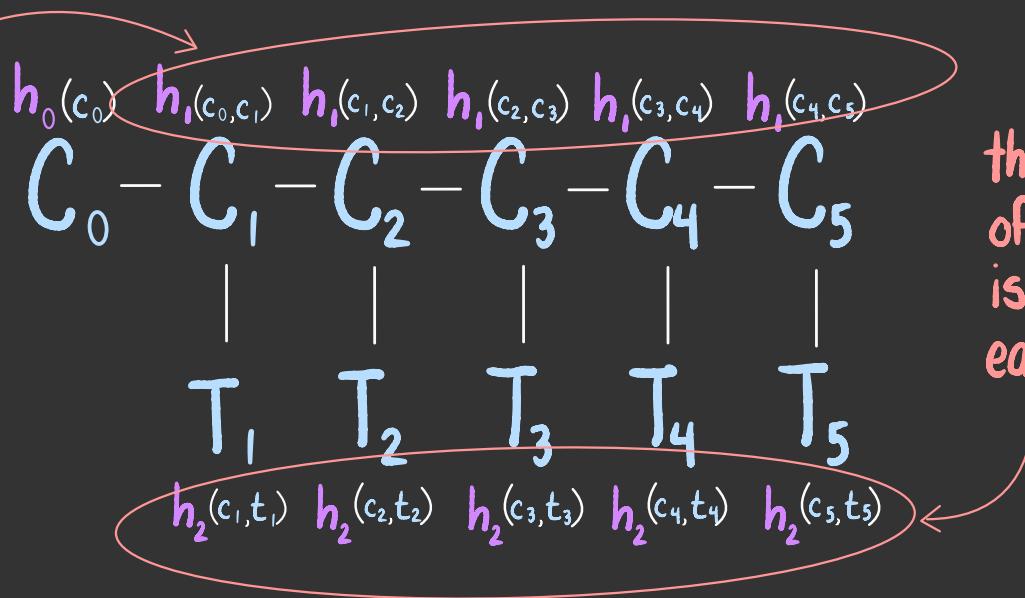
how would this be expressed as a conditional independence statement?

$C_i \perp\!\!\!\perp \{C_0, \dots, C_{i-2}\} \mid C_{i-1}$



this kind of bayesian network is popular  
for temporal reasoning when we have  
noisy observations about the world

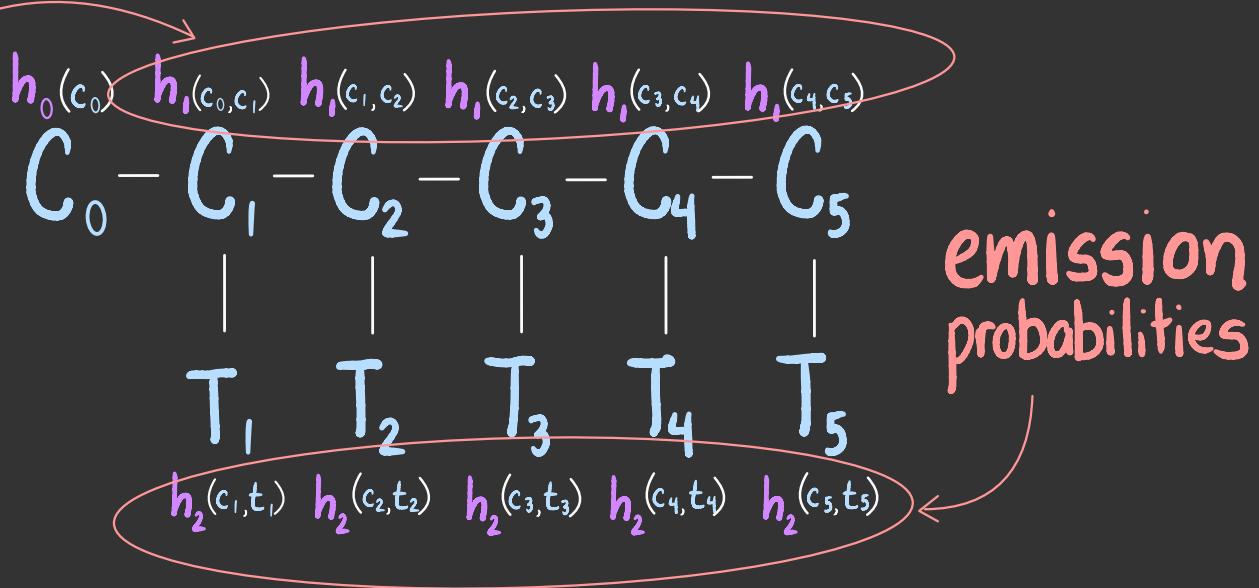
the probability  
of contracting  
covid is the  
same at each  
time step



the accuracy  
of the test  
is the same at  
each time step

for such models, typically we make  
the additional assumption of  
time-invariance

transition  
probabilities



such bayesian networks are called  
hidden markov models