

# Absorbing Markov Chains

MATH 107: Finite Mathematics

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## Inescapable states

Regular Markov chains are those where every state is, eventually, reachable from every other.

However, many real-world situations have states which, once reached, don't change.

### Examples of inescapable states

- ▶ In an epidemic model: vaccinated and dead
- ▶ In an mouse maze: a chamber with food
- ▶ In a consumer preference system: a long-term contract

Regular Markov chains will *not* model these, because those states are never left!

## Absorbing chains and absorbing states

A state of a Markov chain is called *absorbing* if it is one which never transitions to another state.

A Markov chain where it is possible (perhaps in several steps) to get from every state to an absorbing state is called a *absorbing Markov chain*.

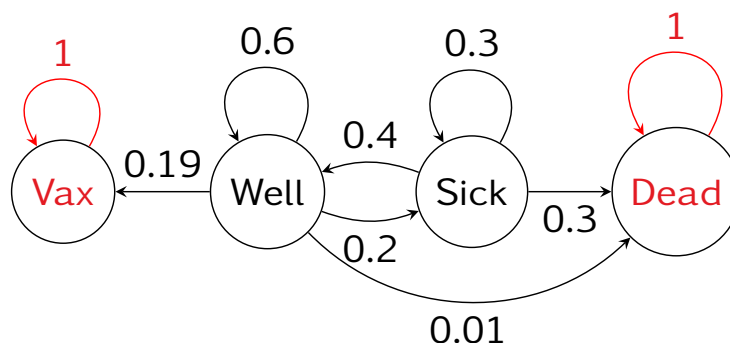
The situations described on the last slide are well modeled by absorbing Markov chains.

## An epidemic-modeling Markov chain

### Disease spreading

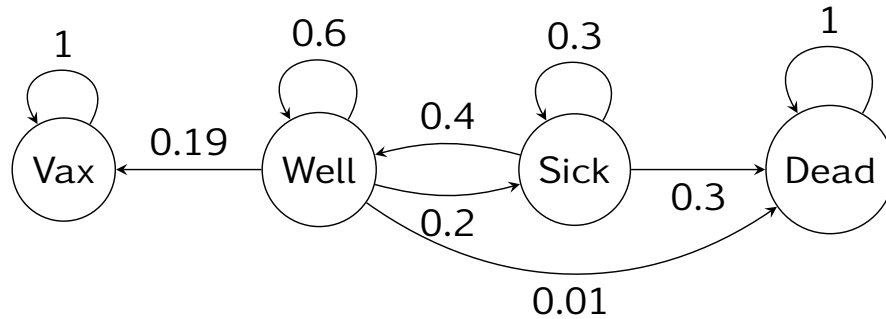
A virulent and deadly but vaccinatable disease is raging in a population. Every day, 40% of the sick recover and 30% of the sick die, while from the healthy, 1% die, 19% are vaccinated, and 20% get sick. What happens over the long term?

We might begin with a state diagram.



Note that the absorbing states have characteristic outflows!

## Epidemic-modeling with matrices



We could put this same state data into a matrix:

$$P = \begin{array}{cccc|l} & \text{Dead} & \text{Sick} & \text{Well} & \text{Vax} & \\ \text{Dead} & 1.00 & 0.00 & 0.00 & 0.00 & \text{Dead} \\ \text{Sick} & 0.30 & 0.30 & 0.40 & 0.00 & \text{Sick} \\ \text{Well} & 0.01 & 0.20 & 0.60 & 0.19 & \text{Well} \\ \text{Vax} & 0.00 & 0.00 & 0.00 & 1.00 & \text{Vax} \end{array}$$

Note that absorbing states have characteristic associated rows!

## Identifying absorbing states

We thus have three ways of identifying absorbing states.

- ▶ In a description, look for “naturally inescapable” states.
- ▶ In a state diagram, look for states with a self-directed arrow of weight 1.
- ▶ In a matrix, look for rows with a “1” on the diagonal entry.

Once we have identified absorbing states, we can be certain that long-term, repeated application of the matrix will put everything into one of these states.

## Application of an absorbing Markov chain

$$P = \begin{array}{cccc|l} & \text{Dead} & \text{Sick} & \text{Well} & \text{Vax} & \\ \left[ \begin{array}{cccc} 1.00 & 0.00 & 0.00 & 0.00 \\ 0.30 & 0.30 & 0.40 & 0.00 \\ 0.01 & 0.20 & 0.60 & 0.19 \\ 0.00 & 0.00 & 0.00 & 1.00 \end{array} \right] & \text{Dead} \\ & & & & & \text{Sick} \\ & & & & & \text{Well} \\ & & & & & \text{Vax} \end{array}$$

Let us consider the effect of this chain on a population where 10% were originally sick and 90% well.

$$\begin{aligned} S_0 &= [0 \quad 0.1 \quad 0.9 \quad 0] \\ S_1 &= S_0 P = [0.039 \quad 0.21 \quad 0.58 \quad 0.171] \\ S_5 &= S_0 P^5 \approx [0.246 \quad 0.083 \quad 0.199 \quad 0.474] \\ S_{20} &= S_0 P^{20} \approx [0.361 \quad 0.002 \quad 0.004 \quad 0.633] \\ S_{99} &= S_0 P^{99} \approx [0.3635 \quad 0.000 \quad 0.000 \quad 0.6365] \end{aligned}$$

so, long-term, this epidemic ends with 36.35% of the population dead and 63.65% vaccinated.

## Non-regularity of absorbing Markov chains

$$P = \begin{array}{cccc|l} & \text{Dead} & \text{Sick} & \text{Well} & \text{Vax} & \\ \left[ \begin{array}{cccc} 1.00 & 0.00 & 0.00 & 0.00 \\ 0.30 & 0.30 & 0.40 & 0.00 \\ 0.01 & 0.20 & 0.60 & 0.19 \\ 0.00 & 0.00 & 0.00 & 1.00 \end{array} \right] & \text{Dead} \\ & & & & & \text{Sick} \\ & & & & & \text{Well} \\ & & & & & \text{Vax} \end{array}$$

Recall, these chains are not regular—a different start scenario has a different outcome. Suppose 50% were originally sick and 50% well.

$$\begin{aligned} S_0 &= [0 \quad 0.5 \quad 0.5 \quad 0] \\ S_1 &= S_0 P = [0.155 \quad 0.25 \quad 0.5 \quad 0.095] \\ S_5 &= S_0 P^5 \approx [0.367 \quad 0.078 \quad 0.184 \quad 0.370] \\ S_{20} &= S_0 P^{20} \approx [0.475 \quad 0.001 \quad 0.004 \quad 0.519] \\ S_{99} &= S_0 P^{99} \approx [0.4775 \quad 0.000 \quad 0.000 \quad 0.5225] \end{aligned}$$

so in this scenario, 47.75% die and 52.25% are vaccinated.

## Characterizing long-term behavior

To discover the long-term behavior of this non-regular chain, we end up needing to find the *limiting matrix*.

### Definition

The *limiting matrix*  $\bar{P}$  of a transition matrix  $P$  is the matrix which  $P^n$  tends towards as  $n$  gets very large.

One important property of the limiting matrix is that  $\bar{P}P = \bar{P}$ ; much like the stationary vector, it is unaffected by multiplication by  $P$ .

We could calculate  $\bar{P}$  by brute force, finding a very large power of  $P$ , but there are better ways!

## Reordering states and standard form

The order of states in a matrix is arbitrary, but we will describe a matrix as being in *standard form* if absorbing states precede the other states.

$$\begin{array}{cccc}
 \text{Dead} & \text{Sick} & \text{Well} & \text{Vax} \\
 \left[ \begin{array}{cccc}
 1.00 & 0.00 & 0.00 & 0.00 \\
 0.30 & 0.30 & 0.40 & 0.00 \\
 0.01 & 0.20 & 0.60 & 0.19 \\
 0.00 & 0.00 & 0.00 & 1.00
 \end{array} \right] & \begin{array}{l} \text{Dead} \\ \text{Sick} \\ \text{Well} \\ \text{Vax} \end{array} & \Rightarrow & \begin{array}{cccc}
 \text{Dead} & \text{Vax} & \text{Well} & \text{Sick} \\
 \left[ \begin{array}{cccc}
 1.00 & 0.00 & 0.00 & 0.00 \\
 0.00 & 1.00 & 0.00 & 0.00 \\
 0.01 & 0.19 & 0.60 & 0.20 \\
 0.30 & 0.00 & 0.40 & 0.30
 \end{array} \right] & \begin{array}{l} \text{Dead} \\ \text{Vax} \\ \text{Well} \\ \text{Sick} \end{array}
 \end{array}$$

For instance, in our epidemic model, we'd like to reorder the entries to get vaccinated and dead at the beginning (in some order)

## Standard form structure

$$P = \left[ \begin{array}{cc|cc} 1.00 & 0.00 & 0.00 & 0.00 \\ 0.00 & 1.00 & 0.00 & 0.00 \\ \hline 0.01 & 0.19 & 0.60 & 0.20 \\ 0.30 & 0.00 & 0.40 & 0.30 \end{array} \right]$$

Standard form matrices always have a particular structure:

$$P = \left[ \begin{array}{c|c} I & 0 \\ \hline Q & R \end{array} \right]$$

Here, for instance,  $Q = \begin{bmatrix} 0.01 & 0.19 \\ 0.30 & 0.00 \end{bmatrix}$  and  $R = \begin{bmatrix} 0.6 & 0.2 \\ 0.4 & 0.3 \end{bmatrix}$ .

In addition, we would expect  $\bar{P} = \left[ \begin{array}{c|c} I & 0 \\ \hline S & 0 \end{array} \right]$ . All we need is  $S$ !

## A spoiler and some justification

### Theorem

$$\text{If } P = \left[ \begin{array}{c|c} I & 0 \\ \hline Q & R \end{array} \right], \text{ then } \bar{P} = \left[ \begin{array}{c|c} I & 0 \\ \hline (I-R)^{-1}Q & 0 \end{array} \right].$$

$$\left[ \begin{array}{c|c} I & 0 \\ \hline S & 0 \end{array} \right] = \bar{P} = P\bar{P} = \left[ \begin{array}{c|c} I & 0 \\ \hline Q & R \end{array} \right] \left[ \begin{array}{c|c} I & 0 \\ \hline S & 0 \end{array} \right] = \left[ \begin{array}{c|c} I & 0 \\ \hline Q+RS & 0 \end{array} \right]$$

so we want  $S = Q + RS$ . Thus  $(I-R)S = Q$  and  $S = (I-R)^{-1}Q$ .

## Long-term behavior in our epidemic model

$$P = \left[ \begin{array}{cc|cc} 1.00 & 0.00 & 0.00 & 0.00 \\ 0.00 & 1.00 & 0.00 & 0.00 \\ \hline 0.01 & 0.19 & 0.60 & 0.20 \\ 0.30 & 0.00 & 0.40 & 0.30 \end{array} \right]$$

The relevant corner of  $\bar{P}$  is going to be

$$\left( \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} - \begin{bmatrix} 0.6 & 0.2 \\ 0.4 & 0.3 \end{bmatrix} \right)^{-1} \begin{bmatrix} 0.01 & 0.19 \\ 0.30 & 0.00 \end{bmatrix}$$

so as our first step we'd calculate the inverse of

$$\begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix} - \begin{bmatrix} 0.6 & 0.2 \\ 0.4 & 0.3 \end{bmatrix} = \begin{bmatrix} 0.4 & -0.2 \\ -0.4 & 0.7 \end{bmatrix}$$

## Bet you hoped we were done with inverses!

We can find  $\begin{bmatrix} 0.4 & -0.2 \\ -0.4 & 0.7 \end{bmatrix}^{-1}$  using the known  $2 \times 2$  inverse formula or Gauss-Jordan elimination:

$$\begin{aligned} \left[ \begin{array}{cc|cc} 0.4 & -0.2 & 1 & 0 \\ -0.4 & 0.7 & 0 & 1 \end{array} \right] &\rightarrow \left[ \begin{array}{cc|cc} 1 & -0.5 & 2.5 & 0 \\ -0.4 & 0.7 & 0 & 1 \end{array} \right] \\ &\rightarrow \left[ \begin{array}{cc|cc} 1 & -0.5 & 2.5 & 0 \\ 0 & 0.5 & 1 & 1 \end{array} \right] \\ &\rightarrow \left[ \begin{array}{cc|cc} 1 & -0.5 & 2.5 & 0 \\ 0 & 1 & 2 & 2 \end{array} \right] \\ &\rightarrow \left[ \begin{array}{cc|cc} 1 & 0 & 3.5 & 1 \\ 0 & 1 & 2 & 2 \end{array} \right] \end{aligned}$$

$$\text{so } \begin{bmatrix} 0.4 & -0.2 \\ -0.4 & 0.7 \end{bmatrix}^{-1} = \begin{bmatrix} 3.5 & 1 \\ 2 & 2 \end{bmatrix}.$$

## The limiting matrix, at last

Since we have  $(I - R)^{-1}$ , we only need a multiplication to find  $(I - R)^{-1}Q$ . So

$$S = \begin{bmatrix} 3.5 & 1 \\ 2 & 2 \end{bmatrix} \begin{bmatrix} 0.01 & 0.19 \\ 0.30 & 0.00 \end{bmatrix} = \begin{bmatrix} 0.335 & 0.665 \\ 0.620 & 0.380 \end{bmatrix}$$

and thus

$$\bar{P} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0.335 & 0.665 & 0 & 0 \\ 0.620 & 0.380 & 0 & 0 \end{bmatrix}$$

## From our original question

Recall our computational results:

### Mortality rates

10% initially sick: 36.35% dead at end

50% initially sick: 47.75% dead at end

Does our limiting matrix  $\bar{P} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0.335 & 0.665 & 0 & 0 \\ 0.620 & 0.380 & 0 & 0 \end{bmatrix}$  bear this out?

$$\begin{bmatrix} 0 & 0 & 0.9 & 0.1 \end{bmatrix} \bar{P} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0.335 & 0.665 & 0 & 0 \\ 0.620 & 0.380 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 0.3635 & 0.6365 & 0 & 0 \end{bmatrix}$$

$$\begin{bmatrix} 0 & 0 & 0.5 & 0.5 \end{bmatrix} \bar{P} = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0.335 & 0.665 & 0 & 0 \\ 0.620 & 0.380 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 0.4775 & 0.5225 & 0 & 0 \end{bmatrix}$$