

State-transition models in R

Decision Modeling for Public Health Workshop

December 7, 2022

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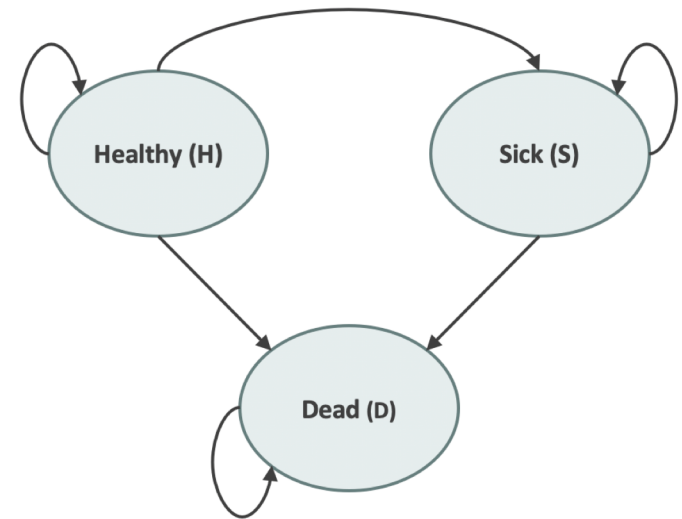
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The aim of this session:

- to give a short recap of the theory of state-transition models
- before we dive into coding in R

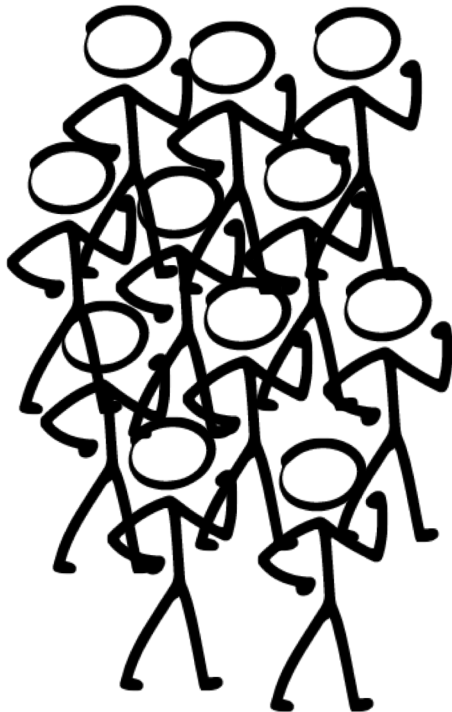
State-Transition Models

- Describes disease progression using a set collectively exhaustive and mutually exclusive health states
- Transitions allowed between health states with some probability
- Transitions occur in discrete time cycles (months, years, etc.)



Cohort and individual based state-transition models

Cohort



Individuals



Cohort State-Transition Models



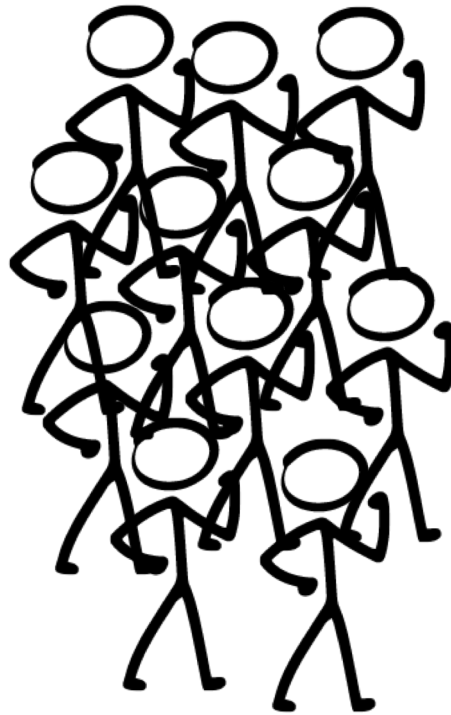
- Dynamic model that reflects disease progression and other events in a **cohort**
- Advantages:
 - Represents dynamic processes
 - Still relatively simple and so computationally efficient
- Best for dynamic processes that
 - Can be represented with a reasonable number of states
 - Don't dependent too much on individual heterogeneity (e.g., homogeneous cohort is a good approximation)
 - Minimal dependence on clinical history or time-in-state
- Deterministic model that generate mean outcomes

Individual based state-transition/ “Microsimulation”



- Stochastic dynamic model that simulates **individuals**, usually as a closed population
- Advantages:
 - Represents ***stochastic*** dynamic processes
 - Most flexible model type
 - Can capture ***complex dependencies*** on individual features, clinical history, time-since-event
- Best when a state-transition model is not sufficient
- Disadvantages
 - Computationally intensive, but can leverage parallel computing
 - Data intensive

Cohort state-transition model implementation in R



Transition Matrix Calculations

- Summarize transition probabilities as a matrix

		To				
		Healthy	Sick	Dead		
From:	Healthy	0.75	0.20	0.05	=	A
	Sick	0	0.85	0.15		
	Dead	0	0	1.0		

- Cohort distribution at next time step calculated through matrix multiplication

$$\begin{bmatrix} \text{Healthy} & x_{t+1} & \text{Sick} & \text{Dead} \end{bmatrix} = \begin{bmatrix} \text{Healthy} & x_t & \text{Sick} & \text{Dead} \end{bmatrix} \begin{bmatrix} A \end{bmatrix}$$

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Transition Matrix Calculations

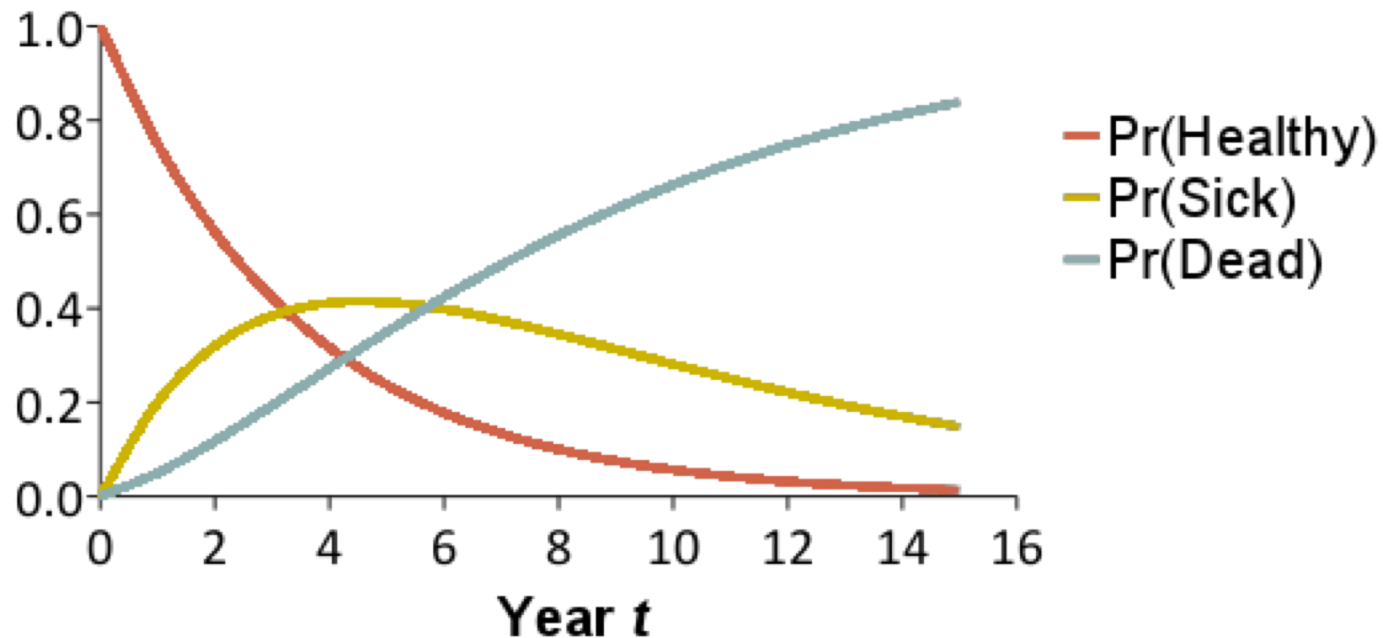
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- Cohort distribution at next time step calculated through matrix multiplication

$$\begin{array}{c} x_1 \\ \left[\begin{array}{ccc} 0.75 & 0.20 & 0.05 \end{array} \right] \end{array} = \begin{array}{c} x_0 \\ \left[\begin{array}{ccc} 1.0 & 0.0 & 0.0 \end{array} \right] \end{array} \begin{array}{c} A \\ \left[\begin{array}{ccc} 0.75 & 0.20 & 0.05 \\ 0 & 0.85 & 0.15 \\ 0 & 0 & 1.0 \end{array} \right] \end{array}$$

Results in a Markov trace



Calculate the model Outcomes

- At each cycle, multiply state-specific outcomes (utilities & costs) by proportion of cohort in each state
- In CEA, outcomes are discounted to reflect time preferences
 - Prefer benefits now, costs later
 - Typical discount rate of 3% per year in US

Individuals



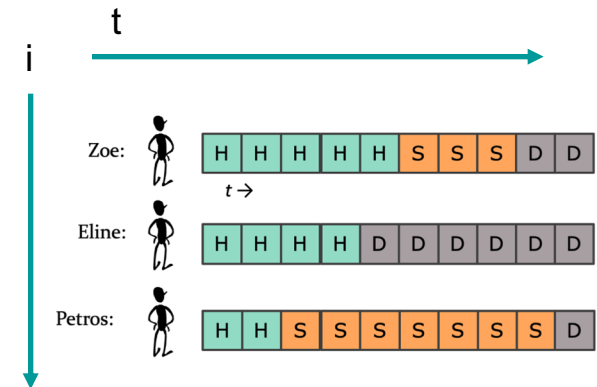
Implementation

- Simulating one individual at a time is an intuitive approach...

```
for(i in 1:n_i) { # open individual loop
  for (t in 1:n_t) { # open time loop

    # simulation code here #

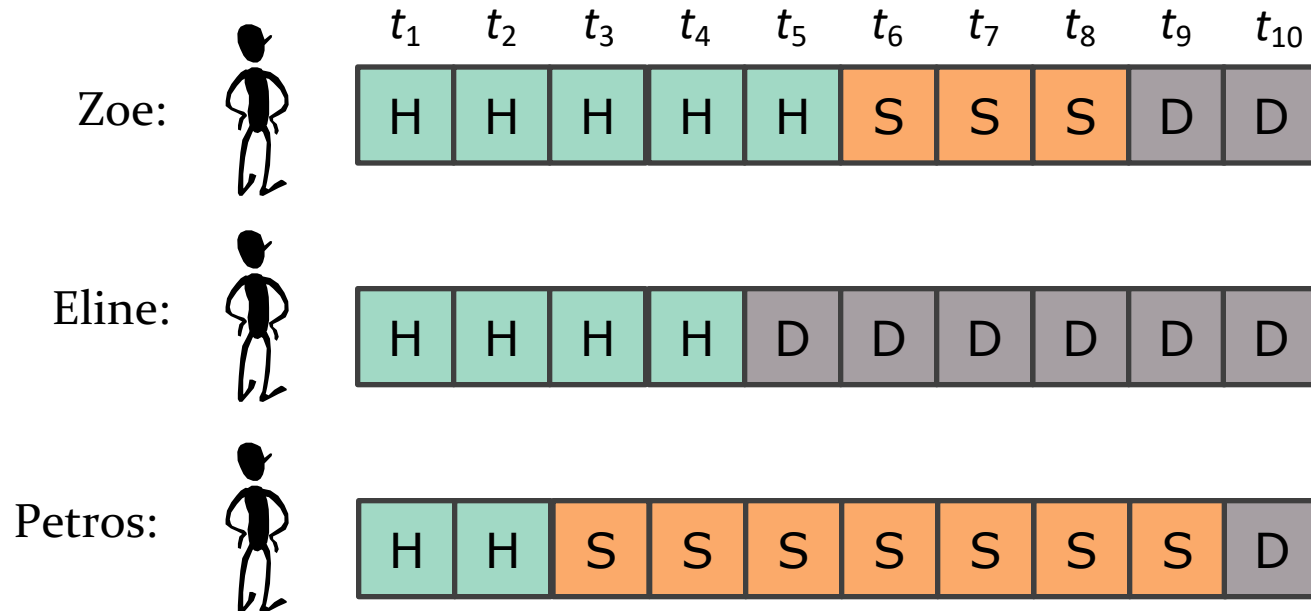
  } # close time loop
} # close individual loop
```



.... however, inefficient and can make a microsimulation computationally intensive

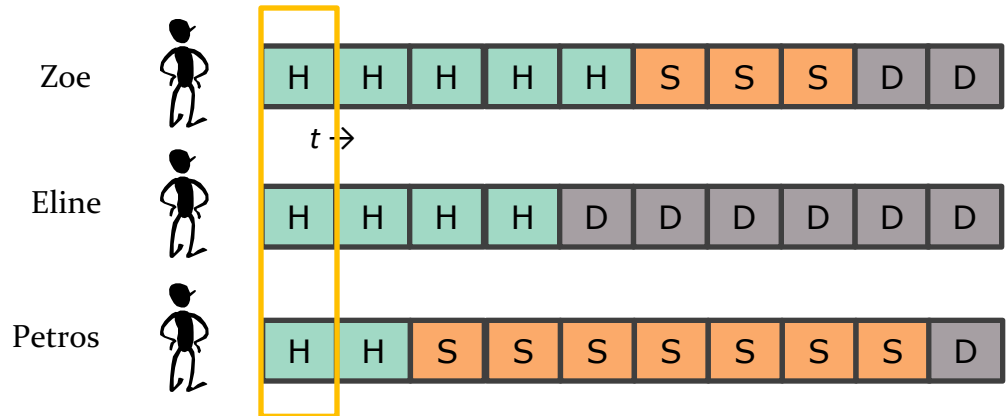
Efficiency in Microsimulation

- **"Batch process"** individual at each time step (one for-loops, function samplev)

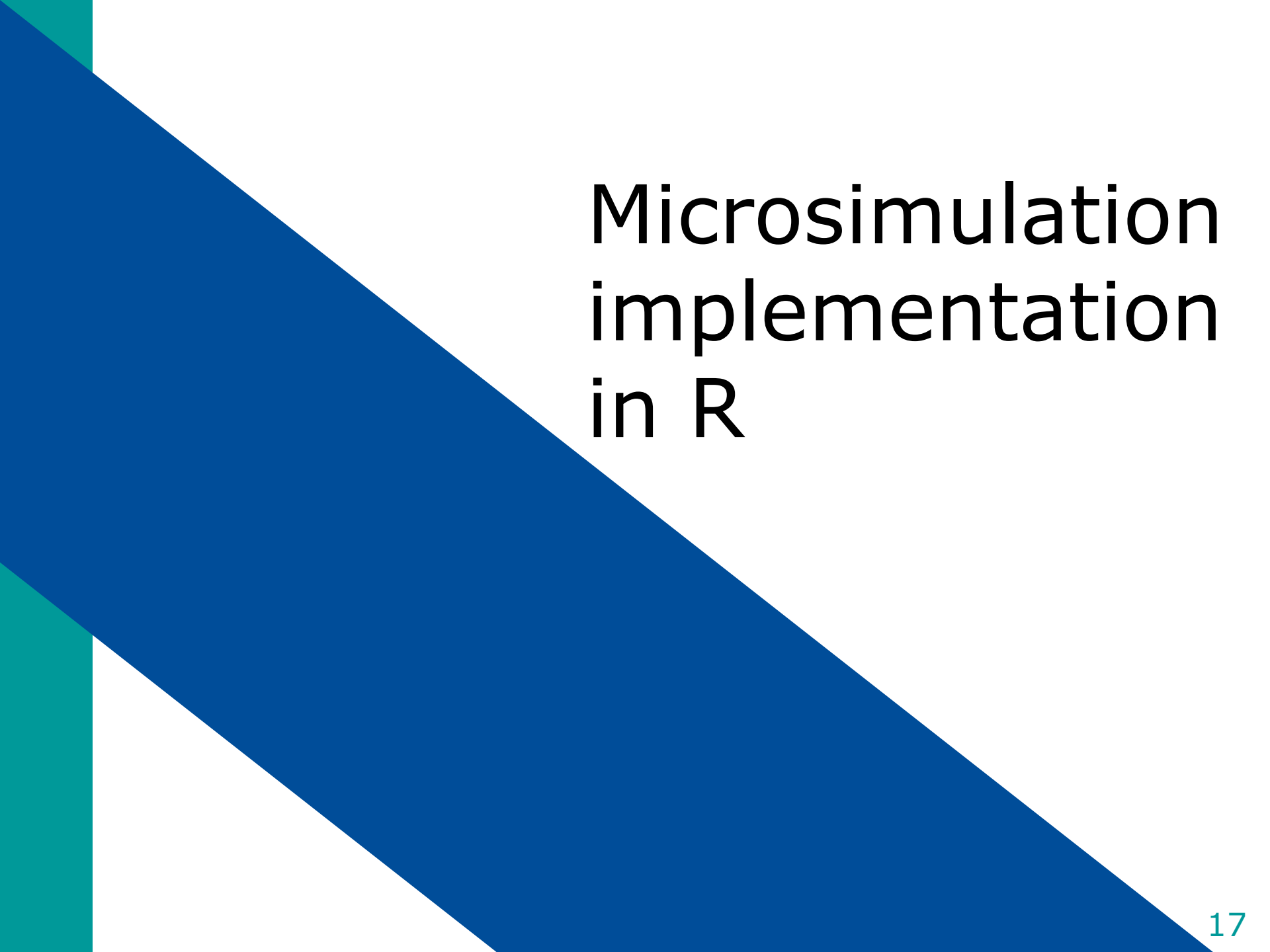


Individual characteristics

$t = 1$



	age	sex	height	Country of birth	time Sick	p_SD
Zoe	35	Female	1.55	Taiwan	0	--
Eline	28	Female	1.68	NL	0	--
Petros	36	Male	1.89	Greece	0	--



Microsimulation implementation in R

Functions

```
calculateMean <- function (x){  
  mean <- sum(x)/length(x)  
}
```

Structure of our code

Specify all the input parameters

- transition probabilities, cycle length etc