Microsimulation modeling in R - Theory -

DARTH workgroup

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Introduction to discrete time microsimulation

The aim of this session:

- to give a short introduction to the theory of discrete time microsimulation models
- define the terminology we use

What is discrete time microsimulation?

- Micro = individual-level
- Simulation = imitation of a situation or process
- **Discrete time** = fixed time intervals

- Reflects events experienced by an individual
- Stochastic implementation of a dynamic process

Microsimulation terminology

 Sometimes called "Markov Monte Carlo" or "First-Order Monte Carlo" or "Individual statetransition model"

 Need not explicitly follow a state-transition model structure

 In our courses we refer to discrete time individual state-transition models when we talk about a microsimulation model

Simple example

- Simulates *individual* disease progression through a state-transition model
 - Track individual's health state over time (can only be in one state at any given time)



General Microsimulation

- Track current state of individual as well as relevant history/characteristics
 - Need not be discrete categories; continuous measures possible
- Probabilities of simulated events can depend on
 - Individual characteristics (age, gender, etc.)
 - Full clinical history, time since clinical events

Pros and Cons

Advantages

- Flexible model structure
- Easy to include:
 - Individual heterogeneity
 - Complex historydependencies
 - Continuous health measures
 - Relation among individuals (network)

Disadvantages

- Complex to implement
- Computationally intensive
- Requires more data to inform model parameter values



http://darthworkgroup.com/



https://github.com/organizations/DARTH-git



https://www.linkedin.com/groups/8635339

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Microsimulation modeling in R - Efficiency -

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The aim of this session is:

- to discuss the fundamental concept of microsimulation implementation
- to discuss batch-processing to improve efficiency

Microsimulation Basics

- Simulate disease progression and health outcomes in **an individual**
- Simulate many individuals to estimate expected value and standard deviation of health outcomes over a large population



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, inefficent and can make a microsimulation computationally intensive

Efficiency in Microsimulation

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



Microsimulation Tutorial

Tutorial

Microsimulation Modeling for Health Decision Sciences Using R: A Tutorial

Eline M. Krijkamp, Fernando Alarid-Escudero, Eva A. Enns, Hawre J. Jalal, M. G. Myriam Hunink, and Petros Pechlivanoglou

Abstract

Microsimulation models are becoming increasingly common in the field of decision modeling for health. Because microsimulation models are computationally more demanding than traditional Markov cohort models, the use of computer programming languages in their development has become more common. R is a programming language that has gained recognition within the field of decision modeling. It has the capacity to perform microsimulation models more efficiently than software commonly used for decision modeling, incorporate statistical analyses within decision models, and produce more transparent models and reproducible results. However, no clear guidance for the implementation of microsimulation models in R exists. In this tutorial, we provide a step-by-step guide to build microsimulation models in R and illustrate the use of this guide on a simple, but transferable, hypothetical decision problem. We guide the reader through the necessary steps and provide generic R code that is flexible and can be adapted for other models. We also show how this code can be extended to address more complex model structures and provide an efficient microsimulation approach that relies on vectorization solutions.



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iterative vs vectorized ("batch proces")

Sample size	Time to run (in seconds)	
	sample()	samplev()
1,000	5.42	0.16
10,000	38.41	1.21
100,000	378.76	11.71
1,000,000	4538.80	128.79



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Microsimulation modeling in R - The implementation concept -

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The aim of this session:

- to discuss the structures and steps that are needed for the implementation of a microsimulation in R
- Example with time constant probabilities
- Discuss time dependent probabilities

3-state example

- Three-state model of disease: Healthy, Sick, Dead
- Time horizon: 10 annual cycles
- Probability of transitioning from healthy to dead is sex-dependent

Female	0.0382
Male	0.0463



Individual characteristics

 Sex – assume equal proportion of women and men

Microsimulation in R

- Generate a representative, virtual population (df_X)
 - Sample characteristics from demographic data
 - Male: Female ratio, age distribution, etc.
- Simulate the occurrence of events
 - Write functions that calculate individual-specific probabilities of different events
 - $p_{HD} = f(sex)$
 - $p_{event1} = f(age, sex, health status, time since event, ...)$
 - Simulate events (and their consequences) over time using random numbers
- Calculate population-level outcomes by averaging individual outcomes

Structure with Individuals Characteristics (df_X)







Update individuals Characteristics

















Time dependency

- Time constant probabilities in previous example
- Most models need time dependent probabilities
- The concept of indexing values based on personal characteristics works similar
 - age is updated in the df_X structure
 - update the age specific probability of dying
 - recalculate other parameters related to age



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Microsimulation modeling in R - State-residence -

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The aim of this session:

 is to discuss state-residence in the context of implementation of a microsimulation in R

Time dependency

• Since start of the model

- Transition probability often depend on age
 - Background mortality
 - Risk of developing disease or experiencing an event

• Depending on state residency

- Some transition probabilities depend on time since an event, not age
 - e.g., The risk of developing recurrence among newly diagnosed cancer patients declines with time

• **Probability** might be dependent on how long someone is in a state

Example:

 The probability to die depends on the duration of being sick



Duration of being sick (step)	p_SD
1	0.1
2	0.2
3	0.3
4	0.4
5	0.5
6+	0.7

























Example (2)

The **probability to die** still depends on the duration of being sick

3 state model where **recovery is possible**



New Trajectories



Track duration of Sick



With reset: remove history after recovery

- e.g.: stop taking drugs with possible severe side effects

Without reset: history stays

- e.g.: number of surgeries, with max











Without removing history













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