Build a DES with R Simmer

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1 Introduction

Here is the text of your introduction.

2 Start from scratch

Here is the background of the case.

Figure 1: Model Diagram

2.1 Blueprint

We have a model structure in mind. Now think about inputs, events, interactions btw inputs and events, measures, strategies.

1. INPUTS

   Gene type: no finding, high (path, unknown,non-path), mod, low;

   Behavioral: modify behavior or not

   Risk: beneficial or harmful change

2. EVENTS (with cost and QALY implication)

   Test

   Behavioral

   Adverse events

3. INTERACTIONS

   Chance of behavioral change differ by gene type

   Risks of adverse events differ by gene type, behavioral change

   Outcomes of adverse events differ by

2.2 Code

Start coding. Some handy functions and tricks.

1. SET ATTRIBUTES

   Each simulation subject can be assigned a set of preset attribute values that carry and can be modified throughout the simulation.

   For example, we can set gene type as an attribute named "gene" in the "initialize_patient" function and draw values 1–6 based on a distribution with probabilites from the inputs list.

   One important status attribute in this model is whether a person is tested or not, so we can create an attribute called "aTest". Please note that all attributes need to be defined before they can be called in the middle.