BCODE SOFTWARE TOOLKIT DOCUMENTATION - DISEASE MODEL REFERENCE

CONTENTS

INTRODUCTION

BCoDE disease models are built as collections of outcome trees. Every model must have at least 1 outcome tree. Figure 1 shows outcome tree of the Salmonellosis disease model.
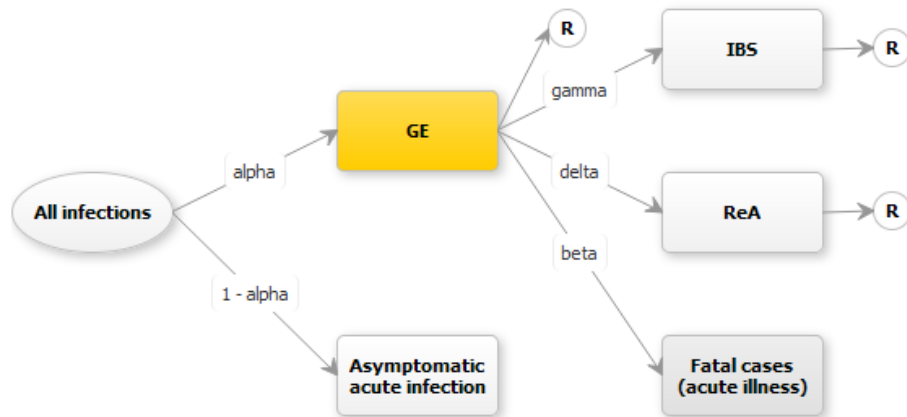
FIGURE 1. EXAMPLE OF A DISEASE MODEL COMPOSED OF 1 OUTCOME TREE (SALMONELLOSIS).

Outcome tree is simply a diagram outlining transitioning through various stages of a disease from infection to recovery or death. Each outcome tree defined for a disease model is mapped to a specific age and sex category. Later when output results are presented in the interface results are gathered from for each category by referencing data in the appropriate outcome tree.

An outcome tree is a collection of **health outcomes** and **transition probabilities**. The computational engine of the toolkit transitions through the health outcomes according to the orientation of the transition probabilities arrows from parent to child.

Health outcome, in turn, is composed of a set of **health states**. Health states distinguish various states of the same health outcome between each other. A health outcome must have at least one health state defined, because all computations are executed in the health state. If a health outcome has only one health state, then it is not explicitly drawn in the outcome tree, just like in Figure 1. However, if more health states are defined, then these are presented (see Figure 2).
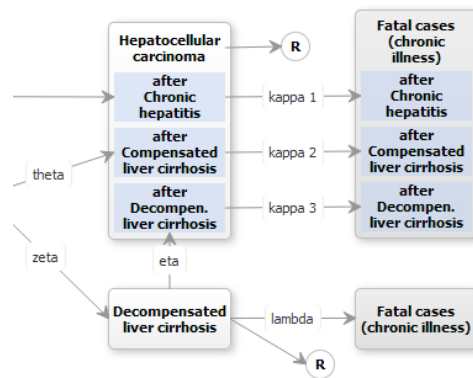
FIGURE 2. HEALTH OUTCOMES WITH MULTIPLE HEALTH STATES (HEPATITIS B).

Transition probabilities "link" health states with each other. A transition probability can also link a source health state with target health outcome. In such situation it is the health outcome taking care of splitting transitioning cases to appropriate internal health states.
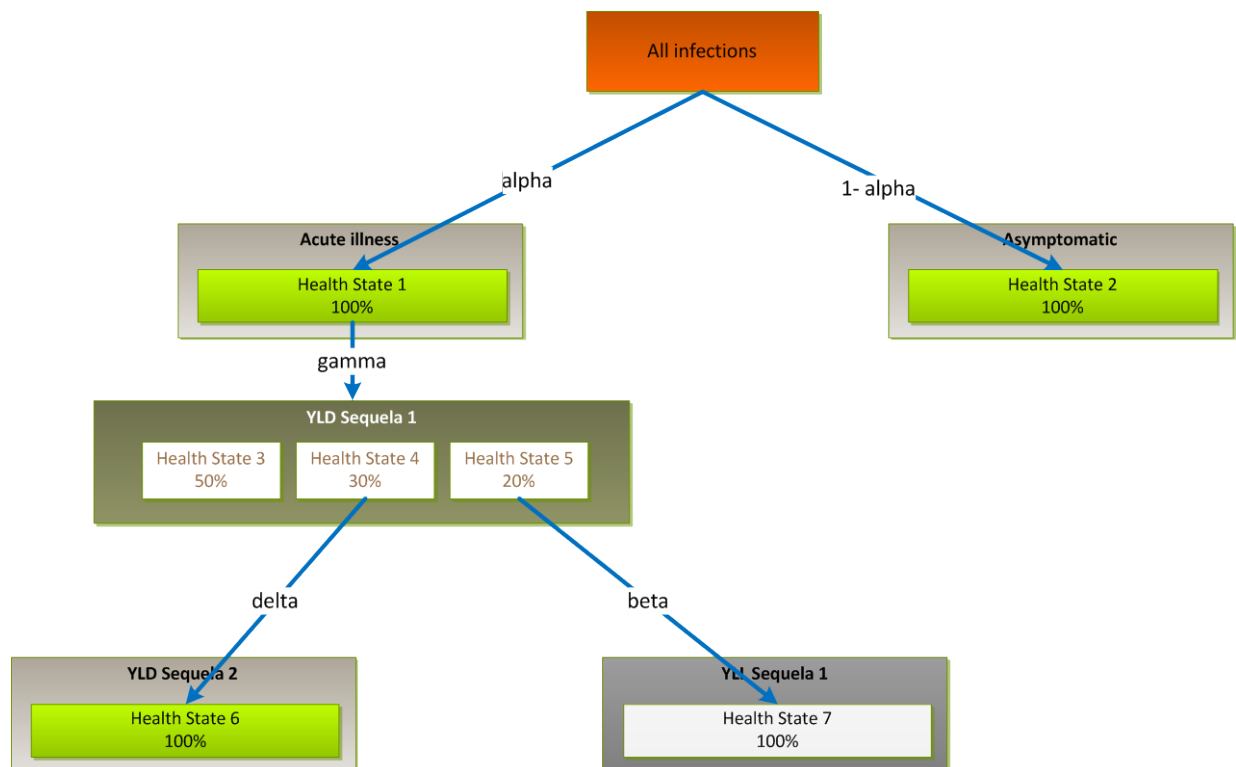

**FIGURE 3. EXAMPLE OF AN OUTCOME TREE WITH FULL VISUALIZATION OF INTERNAL HEALTH STATES.**

NOTES:

- Health state can have a maximum of 1 transition probability entering (see scenario **a** below),
- Health state can have many transition probabilities leaving,
- If health state has no parent health state, then its containing health outcome should have parent health state (see scenario **b** below).

a) Health state to health state
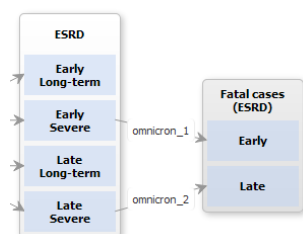
b) Health state to health outcome
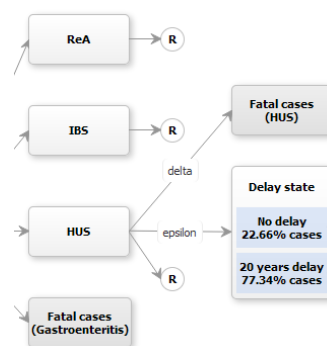
For instance Shigellosis model makes use of both types of transition probabilities. Health state **HUS** is linked to health outcome **Delay state**. This one contains two health states, **No delays**, and **20 years delay**. Each of these states is linked later to separate health states of health outcome **ESRD**.

QUESTION: Why a health state/outcome cannot have more than one transition probabilities entering it?

ANSWER: One of the variables used in the calculations in all health states is remaining life expectancy. Each path in the outcome tree may yield different remaining life expectancy for cases transitioning through this path. Current BCoDE modeling methodology has not developed means of dealing with such cases, other than introducing health states dealing with cases transitioning through different path separately. The best example of this is **Hepatitis A** model: health outcome **Hepatocellular carcinoma** has three health states for each path (directly from **Chronic hepatitis**, through **Compensated liver cirrhosis**, through **Compensated liver cirrhosis** and **Decompensated liver cirrhosis**). Of course, once a split like this is introduced, it must be preserved when transitioning downstream the outcome tree. That's why **Fatal (chronic illness)** has three health states defined as well.
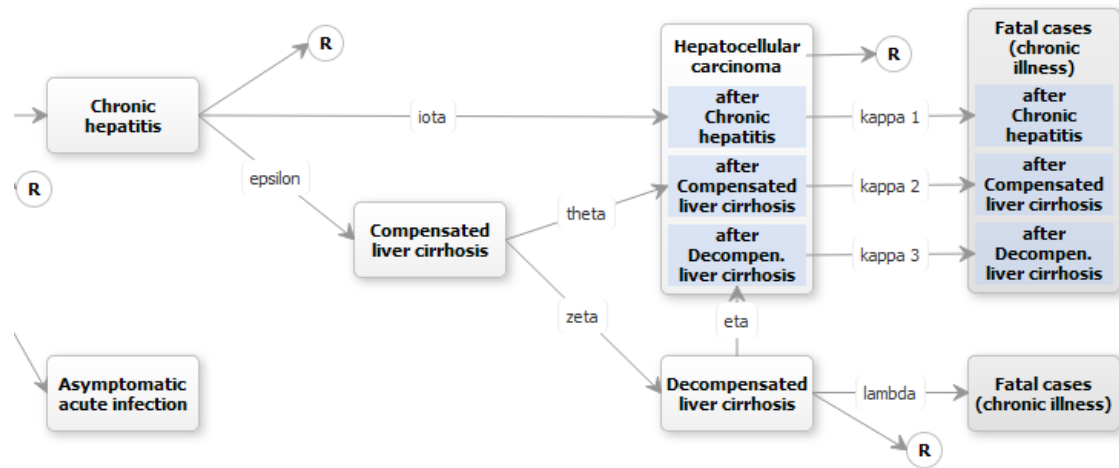
INPUT DATA

The model requires passing a number of parameters to the computational engine:

- General parameters
  1. Life expectancy at birth (constant per age and sex category).
  2. Age distribution (constant per age and sex category).
  3. Underestimation parameter (random variable, currently **NOT** age and sex dependent).
  4. Uncorrected case count (constant per age and sex category).
- Health state parameters
  1. Proportion of cases this health state covers among all health states of its containing health outcome (constant).
  2. Severity of disease (constant per age and sex category).
  3. Duration of disease (constant per age and sex category).
- Transition probability
  1. Source health state
  2. Target health state or health outcome
  3. Transition probability: this is product of a table of age and sex dependent constants and a random variable (not age and sex dependent).

This data is kept in reference data files which basically define disease models and store parameters for the simulation.

FLOW OF COMPUTATIONS

Elements of the outcome tree include their own parameters and containers for output data:

1. All infections
   a. Uncorrected number of cases **UC** – initialized to the uncorrected case count model parameter.
   b. Corrected number of cases **CC** – computed from **UC**.
   c. Remaining life expectancy **RLE** – initialized to the life expectancy at birth model parameter.
   d. List of transition probabilities to children elements (health states or health outcomes).
2. Health outcomes
   a. Parameter - List of health states.
3. Health states
   a. Output cases count **CC**,
   b. Remaining life expectancy **RLE**,
   c. Severity **S**,
   d. Duration **D**,
   e. Burden (**YLD** or **YLL**).
   f. List of transition probabilities to children elements (health states or health outcomes).
4. Transition probability
   a. Transition probability **TP**,
   b. Output cases count **CC**.

Model simulation is executed by traversing through these elements of the outcome trees, as follows:

For each outcome tree
   a. Go to **All infections**
      Compute corrected number of cases **CC**. Transition probability **alpha** and underestimation parameters are read and used to process the uncorrected number of cases **UC**. The outcome of this calculation is the number of all infected cases. It is assumed that transition probability **alpha** is the first defined transition probability!
   b. Go through all transition probabilities of **All infections** and run calculations there.
      Take the input number of cases **UC** from **All infections** and compute output number of cases transitioning through this transition probability to the next health state/outcome. Transition probability can be direct (age dependent or not), or cumulative.
   c. For each health outcome ordered as defined in the reference data go through the list of internal health states and run calculations there.
      i. Take the input remaining life expectancy from the parent health state.
      ii. Compute the output remaining life expectancy as the input remaining life expectancy minus the health state duration. This number is checked against 0 to make sure it is not negative.
      iii. Take the input number of cases UC from the parent transition probability.
      iv. If the health state has type YLD than compute burden as a product of the input number of cases, severity and duration.
      v. If the health state has type YLL than compute burden as a product of the input number of cases and the computed remaining life expectancy.

vi. Go through all the transition probabilities leaving from this health state and run calculations there.

Results at each step are saved and computations are repeated a number of times. Once the last iteration is executed, all saved results are postprocessed to compute various statistics (mean, quantiles) to be outputted in the results view of the toolkit.

NOTE: Transition probability **alpha** receives special treatment in the current BCoDE methodology. It is used to compute the corrected number of all infected cases. It must be defined as the transition probability from **All infections** to **Acute illness** health outcome and it must be the first transition probability defined in the reference data.