SimRisk: A simulation-based covid-19 risk estimator

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Abstract

This note and Julia notebook presents a simulation-based method and associated Julia software package for estimating covid-19 infection risks.

Our approach differs from many covid-19 simulations, in that it is *small-scale*: it doesn't try to model an entire population, but only a few individuals (from one to perhaps two dozen). The primary goal is to estimate the probability that each individual is infected, based on a history of their recent contacts and test results (as well as certain assumptions and other information).

A simulation consists of many *simulation runs*; we also call a simulation run a *scenario* or a *world*. Each simulation run is based on the provided history of contacts and test results, but may vary in the pattern of how infection starts and spreads among the individuals. Simulation runs that give results inconsistent with provided test results are discarded. The probability that an individual is infected at the end is estimated as the fraction of remaining simulation runs in which that individual is infected.

A simulation may also take into account: * whether individuals are wearing **masks** (and if so, what type of mask) * the **duration** of contacts (disease transmission is modeled in a **dose-based** manner) * **multi-person contacts** (e.g. for a dinner) * the presence of one or more **anonymous individuals** in a multi-person contact (e.g. bus riders) * given probabilities for the prevalence of the disease in the population, and the likelihood of mask-wearing in the population, both used to model anonymous individuals * different **types of tests** with differing probabilities for detection and false alarms * many infected individuals are **asymptomatic** * infected individuals progress through a series of stages of the disease, * the **infectiousness** of an infected individual may vary over time, * infected individuals typically recover after a certain time (e.g. 14 days) * an infected individual, if symptomatic, has symptom onset around a certain time since infection (e.g. on the 5th day).

1 Approach

Our approach is *agent-based*; each individual is separately modeled in the simulation.

In our agent-based model each individual may have a complex state consisting of a number of attributes. We consider attributes to be of two types: the “disease state’ ’ of the agent (e.g. Susceptible, Infected, or Recovered), and other “observable state” attributes (e.g. whether the individual is masked).

The disease state is not directly observable, but may be measured with a Test (which will give a result of positive – meaning infected – or negative – meaning uninfected).
In our model we further subdivide the Infected state into a sequence of states I1, I2, ..., ILast (e.g. I14) according to the number of days the individual has been infected.

As a pedagogic digression, we note that an interesting class of agent-based models are the “billiard-ball models”, as exemplified in this Washington Post article. Each billiard ball represents a person, and the color of the ball represents the disease state of that person (healthy, sick, recovered). The billiard ball’s position and velocity are also part of the state information for the person modelled. Collisions between balls represent contact events where an infected person may infect an uninfected person.

Each time you reload the Washington Post page, it starts a new simulation run, where the positions, velocities, and initial disease states of the balls are freshly and randomly generated; a new run may thus give somewhat different results. Performing many such simulation runs allows one to estimate statistics such as the fraction of individuals infected after a certain amount of time has elapsed.

We adopt a similarf approach, but restrict the rerandomization to the initial disease states and the test results obtained.

Our approach is not compartmental; a compartmental model keeps only aggregate estimates about the number of individuals in each compartment, and a set of differential equations determines how these estimates evolve over time. An SIR model is a typical example of a compartmental model, wherein the model state consists only of the estimated number of Susceptible (“S”), Infectious (“I”), and Recovered (“R”) individuals.

1.1 Fixed versus stochastic contact schedules

We now elaborate and clarify this distinction between agent-based models with fixed contact schedules and agent-based models with variable or stochastic contact schedules, as this distinction is not often made or adopted in the simulation literature.

We restrict attention to agent-based models where the sequence of contacts made is fixed and independent of the spread of the disease.

If we consider a given simulation run, we see a sequence of *contact events*, such as: * on day 1, person A has a close contact with person B, * on day 2, person A has a close contact with person C, * on day 3, person B has a close contact with person C, then * on day 3, person A, B, and C have a three-way close contact * and so on... (We use the phrases “has a contact with” and “has a close contact with” interchangeably to denote a contact where disease transmission is possible.)

In a "billiard ball" model, the sequence of contacts is determined by the initial positions and velocities of the balls, but *not* by any other information, such as the disease states of the individuals. The schedule of contacts is fixed by the initial position and velocities.

An individual may become infected during a contact, but he/she thereafter continues life as usual. This is appropriate for a disease that is entirely asymptomatic, and is an interesting and useful restriction to adopt for disease in general.

We therefore adopt the restriction that the model has a **fixed contact schedule**: *the model has a fixed schedule of contacts that is used for any simulation run*.

Even if the model has a fixed contact schedule, the spread of the disease among the simulated individuals in that model may vary stochastically from simulation run to simulation run, since the spread of the disease also depends on other factors, such as: * who is infected at the beginning of the simulation run (the initial conditions) * the stochastic character of disease transmission during a contact (that is, if A and B have a contact, and A is infected but B is not, whether A infects B may happen only randomly with some probability) * whether the simulated individuals are wearing mask (and if so, what sort of mask), which may decrease the disease transmission probability for a contact, and so on...

1.2 Motivation

The reason we are interested in agent-based models having a fixed contact schedule is that *we are interested in real-life situations where the contact history may in fact be known*, and we wish to estimate the probability that an individual is infected in such situations.

For example, the contact history may be known because of smartphone-based (or wearable-token-based) digital contact tracing. It may be known exactly who was in contact with whom for the last two weeks, among the entire population.

(The previous paragraph sets aside the fact that collecting such information may be undesirable for privacy reasons. So, the exercise here is to explore what might be possible if one were to collect such information. But this work should in no way be interpreted as saying that the privacy concerns aren't important, or that they shouldn't prevail if one is considering the possibility of such data collection.)

Of course, it is not required that the contact schedule be known and/or derived from real-life data. It can be pseudorandomly generated, for example. Or, it may be a mix of real-life contact data and pseudorandomly generated data.

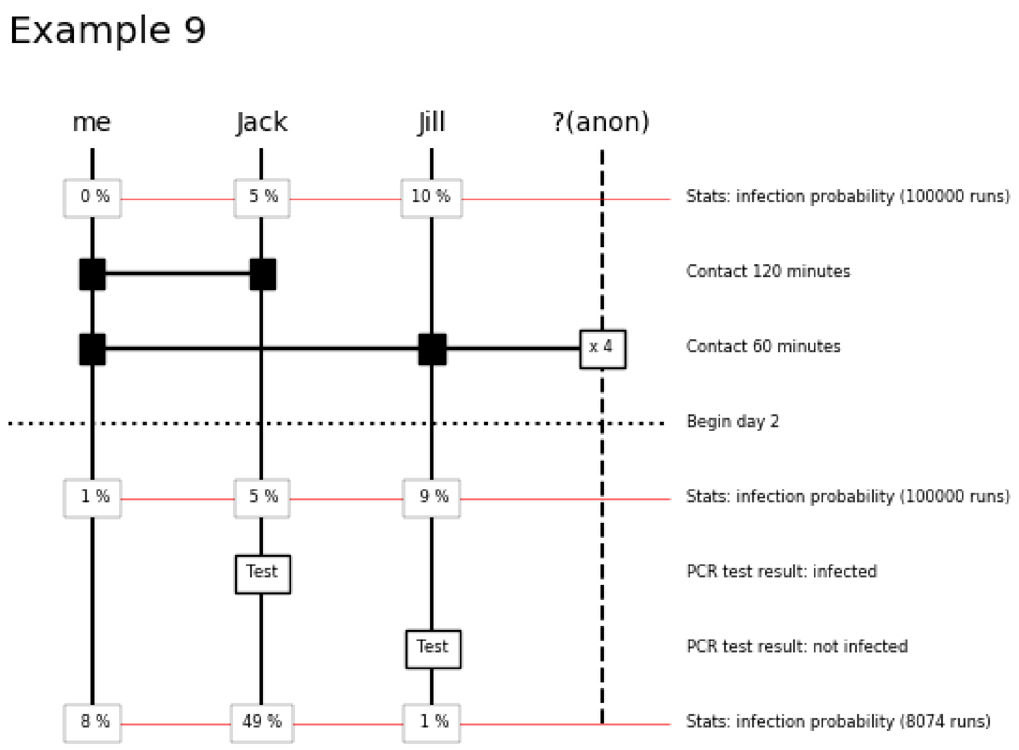
The intent, however, is that the contact schedule be the historical schedule of real people, rather than simulated people. We would like to know how likely it is that a specific real person is infected, so we can advise on a course of action to take (e.g. quarantining).

1.3 Graphical representation

We now introduce the graphical representation of a schedule. This consists of the following components and semantics: * a two-dimensional canvas to hold the graphical elements * the vertical axis represents time, with time increasing from top to bottom (measured in days). * the canvas is divided into blocks representing days by horizontal dotted lines * each named person in the schedule is represented by a solid vertical line (or *wire*) * each wire carries information from top to bottom about the state of the individual, such as whether they are infected or not, or whether they are masked * there are several kinds of events possible in the schedule: - ***NewPerson*** events, which introduces a new **named** person, and representing that for each simulation run the individual's disease state may be simulated via a random draw from a specified distribution. Typically, just the overall prevalence is specified, and the distribution is uniform over I1..ILast. - ***Contact*** events representing the possibility of transmission of disease between individuals. Each contact event represents a close contact when an uninfected party may become infected, if another party is infected. The transmission probability of the disease depends on the duration of the contact and on whether the parties are wearing masks. Transmission may go either way between two parties. If the number n of parties is greater than two, than the event is equivalent to having choose(n, 2) pairwise contacts (that is, having a contact between each pair of people at the event). A person infected at an event can not infect another person at the same event (but can infect someone else at a later event that day). A number of parties to the contact event may be *anonymous*. - ***Test*** events, representing the person getting a test, represented by a square containing "Test" (with the result given in the rightmost column). Simulation runs are counted only if they are *consistent* with the specified test results. We assume that the test result is available immediately. - ***Mask-setting*** events: the individual takes off or puts on a mask, represented by a square with either "MaskOn" or "MaskOff". - ***NewDay*** events representing the start of a new day. Some of the participants will recover in this transition. - ***Stats*** event representing the gathering of statistics – the fraction of consistent runs wherein each named person is infected.

1.4 Example schedule

Consider the following example schedule


Example 9
me
Jack
Jill
?(anon)
0 %
5 %
10 %
Stats: infection probability (100000 runs)
Contact 120 minutes
x 4
Contact 60 minutes
Begin day 2
1 %
5 %
9 %
Stats: infection probability (100000 runs)
Test
PCR test result: infected
Test
PCR test result: not infected
8 %
49 %
1 %
Stats: infection probability (8074 runs)

This example shows a contact schedule for three named individuals (me, Jack and Jill) over a period of two days. There are eleven events.

The following code specifies the model to be simulated:

```
function example9()::Model
    m = Model("Example 9")
    # day 1
    notePerson!(m, "me", infectedProbability=0.00, maskedProbability=0.500)
    notePerson!(m, "Jack", infectedProbability=0.05, maskedProbability=0.000)
    notePerson!(m, "Jill", infectedProbability=0.10, maskedProbability=1.00)
    noteStats!(m)
    noteContact!(m, ["me", "Jack"], minutes=120)
    noteContact!(m, ["me", "Jill"], anonymousNumber=4, minutes=60)
    # day 2
    noteNewDay!(m)
    noteStats!(m)
    noteTest!(m, "Jack", PCRTest, true)
    noteTest!(m, "Jill", PCRTest, false)
    noteStats!(m)
    return m
end
```

- The first three `notePerson!` events specify the three named individuals in the model.
  - The first named person, `me`, starts every simulation run uninfected. I wear a mask half of the time. (This means that I start off masked in half of the simulation runs.)
  - The second named person, `Jack`, starts off each simulation run with a 5% chance of being infected. Jack never wears a mask.
  - The third named person, `Jill`, starts off each simulation run with a 10% chance of being infected. Jill always wears an N95 mask with 95% filtration ability when Jill is the "sender" or when Jill is the "receiver".
- The first `Stats` event gathers statistics, showing the initial 0% / 5% / 10% infection rates for me, Jack, and Jill. These are computed using 100000 simulation runs, and show the number of such runs wherein each party is infected.
- The next two events on day 1 are contact events:
  - Jack and I have a two-hour meeting.
  - Jill and I, together with four anonymous other individuals, have a one-hour lunch.
- The next event is the beginning of day two. In some simulation runs, some individuals recover in this transition (about 1/14 of them will do so).
- The next event is a `Stats` event, showing that me, Jack, and Jill have infection probabilities of 1% / 5% / 9%. (Remember that Jill always wears a mask!) These percentages are percentages of the 100000 simulation runs wherein each party is infected.
- The next two events are `Test` events:
  - a PCR `Test` event for Jack; it shows him to be infected. This PCR test has a 5% false-positive and a 5% false-negative rate.
  - a similar PCR `Test` event for Jill, it shows her to be uninfected.
- The final event is a `Stats` showing me, Jack, and Jill to be infected with respective probabilities 8%, 49%, and 1%. Note that only 8074 simulation runs showed Jack testing positive and Jill testing negative; the other simulation runs are discarded at this point. The percentages given are the percentages of the 8074 simulation runs that gave results for the two Test events that were consistent with the observed Test results, that showed each of the three named individuals being infected.

In general, events may have stochastic effects, which is why simulation is needed to determine the probability that a named individual is infected at the end of the schedule. A random number seed and appropriate cryptographic for the simulation allow the use of pseudorandomness here, for reproducibility.

Note that the infection probabilities of anonymous individuals are not estimated; each contact including anonymous individuals is assumed to include freshly-minted anonymous individuals with infection probability equal to the overall prevalence rate of infection.

This is clearly a simplistic model that could be made more realistic in a number of ways.

2 Disease States

[1]:
```julia
# We represent the following disease states:
#     Susceptible  I1 I2 ... ILast  Recovered
# We use ILast = I14 here.  Later versions may make "14" variable.
# These are "daily" states, giving the disease state at the end of the day.
# States I1 ... I14 are "infected" states; these states are not necessarily␣
 ↪"infectious".
# An infected person progresses from state I1 to state Recovered, one state at a␣
 ↪time per day.
# Moving from state Susceptible to state I1 is the initial infection.
# Moving from state I14 to state Recovered is "recovery".
# We represent these states as integers as follows:
# a state Id (where d is an integer) is the disease state at the end of the d-th␣
 ↪day of infection.
# So, I1 is the end of the first day of infection, etc.
# We use the encoding of disease states as integers:
#    Susceptible = 0
#    I1 ... I14 = 1 ... 14
#    Recovered = 15

struct DiseaseState <: Integer
    ds::Int64
end
Int64(x::DiseaseState) = x.ds
import Base.<
<(x::DiseaseState, y::DiseaseState) = (x.ds < y.ds)

# Although Julia uses 1-indexing, we start DiseaseState at 0 (= Susceptible);
# so arrays that are indexed by DiseaseState are 0-indexed
const Susceptible = DiseaseState(0)
const I1 = DiseaseState(1)           # when person is infected, they move to␣
 ↪state I1
const ILast = DiseaseState(14)       # last infected disease state
const Recovered = DiseaseState(15)

DiseaseState() = Susceptible         # default starting disease state

infected(x::DiseaseState) = (Susceptible < x < Recovered)

SymptomOnset = DiseaseState(5)  # if symptomatic, symptoms start on day 5

# if state ds on day d, give state on next day
function nextDiseaseState(ds::DiseaseState)
    (ds == Susceptible) && return ds
    (ds == Recovered) && return ds
    return DiseaseState(Int(ds.ds)+1)
end
```

```
[1]: nextDiseaseState (generic function with 1 method)
```

```
[2]: # infectiousness as a function of DiseaseState
     # average of infected states is 1.000
     # using Pkg ;
     # Pkg.add("OffsetArrays") ;
     using OffsetArrays ;

     defaultInfectiousness =       # improve this list?
         OffsetArray([0,
                      0, 1, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1,  # note 0 for I1
                      0],
                     0:15) * (14.0 / 18.0);
```

2.1 Tests

When using a fixed contact schedule, we assume that testing affects the *transmission probability* but not the *contact schedule* or other observable attributes such as whether a person is wearing a mask.

```
[3]: struct TestType
         name::String          # name of test type
         P_det::Float64        # Probability of detecting infection
                               #     = P(pos test result | infected)
                               #     = sensitivity
         P_FA::Float64            # Probability of a false alarm
                               #     = P(pos test result | uninfected)
                               #     = 1 - specificity
     end

     PerfectTest = TestType("Perfect", 1.0, 0.0)       # this test is always right
     PCRTest = TestType("PCR", 0.95, 0.05)             # check (if adjust here, also␣
      ↪adjust examples)
     OtherTest = TestType("Other", 0.90, 0.10)         # for comparison purposes, not␣
      ↪a real test
```

```
[3]: TestType("Other", 0.9, 0.1)
```

2.2 Masks

Same for masks; being masked affects transmission probability but not the event schedule.

A MaskType is defined by is filtration efficiencies (separately as source and as recipient).

```
[4]: struct MaskType
         sourceMaskTransmission::Float64    # 1 - filtrationEfficiency for source, if␣
      ↪source wearing this mask type
         recipientMaskTransmission::Float64 # 1 - filtrationEfficiency for recipient,␣
      ↪if recipient wearing this mask type
     end

     N95 = MaskType(0.05, 0.05)           # Check numbers
     Surgical = MaskType(0.30, 0.20)      # Check numbers
     NoMask = MaskType(1.00, 1.00)
```

```
[4]: MaskType(1.0, 1.0)
```

2.3 Quarantine

We do not explicitly model quarantining; we assume that the given events already incorporate any effects that quarantining might have had.

3 People

Each person is represented in the simulation by a Person object. We might also call this a *node* or a *vertex*, using graph-theoretic terminology.

The node contains a number of attributes, which may change value as the simulation progresses; the Person object is a *mutable* data structure.

[5]:
```
struct VisibleState
    # represents state elements that are visible and may affect disease␣
 ↪transmission
    mask::MaskType
end
# Default VisibleState is unmasked
VisibleState() = VisibleState(NoMask)
```

[5]:
```
VisibleState
```

[6]:
```
mutable struct Person # aka Agent

    # static attributes of person
    personID::String

    # per-run attributes of person
    asymptomatic::Bool                   # whether asymptomatic on this run

    # per-run dynamic attributes of person (changes over time)
    diseaseState::DiseaseState
    visibleState::VisibleState
end
```

4 Key Additional Concepts

4.1 Global parameters

One struct gives a list of global parameters, such as prevalence rate, in a timeless manner.

[7]:
```
mutable struct GlobalParameters
    # parameters for random named people
    infectedProbability::Float64        # probability that a random person is␣
 ↪infected
    maskedProbability::Float64          # probability that a random person is␣
 ↪masked
    asymptomaticProbability::Float64    # probability that a random person is␣
 ↪asymptomatic

    # same parameters for random anonymous people
    anonymousInfectedProbability::Float64
    anonymousMaskedProbability::Float64
    anonymousAsymptomaticProbability::Float64

    # ContactEvent parameters

    # A contact with a give dose (arbitrary units) between two maskless␣
 ↪individuals
    # has a probability of transmission of 1 - exp(-dose*transmissionConstant)
    transmissionConstant::Float64
    asymptomaticFactor::Float64   # reduce dose by this factor if source is␣
 ↪asymptomatic

    # infectiousness as a function of DiseaseState (indices will be -1:
 ↪infectionDurationDays)
    infectiousness::OffsetArray{Float64,1,Array{Float64,1}}
end

# default parameters for named people
defaultInfectedProbability = 0.02      # prevalence in community
defaultMaskedProbability = 0.000
defaultAsymptomaticProbability = 0.40  # https://www.cdc.gov/coronavirus/
 ↪2019-ncov/hcp/planning-scenarios.html

# same parameters for anonymous people
defaultAnonymousInfectedProbability = defaultInfectedProbability
defaultAnonymousMaskedProbability = defaultMaskedProbability
defaultAnonymousAsymptomaticProbability = defaultAsymptomaticProbability

# We choose the transmission constant so that
# a fifteen-minute contact has a 5% chance of transmission.
defaultContactDuration = 15.0                    # 15 minutes in close contact
defaultContactTransmissionProbability = 0.05   # yields 5% chance of transmission
defaultTransmissionConstant = log(1-defaultContactTransmissionProbability)/␣
 ↪(-defaultContactDuration)
# following value is from
#   https://www.cdc.gov/coronavirus/2019-ncov/hcp/planning-scenarios.html
defaultAsymptomaticFactor = 0.75

defaultGlobalParameters =
    GlobalParameters( defaultInfectedProbability,
                      defaultMaskedProbability,
                      defaultAsymptomaticProbability,
                      defaultAnonymousInfectedProbability,
                      defaultAnonymousMaskedProbability,
                      defaultAnonymousAsymptomaticProbability,
                      defaultTransmissionConstant,
                      defaultAsymptomaticFactor,
                      defaultInfectiousness
                    )
```

[7]:
```
GlobalParameters(0.02, 0.0, 0.4, 0.02, 0.0, 0.4, 0.0034195529591700387, 0.75,
[0.0, 0.0, 0.777778, 1.55556, 1.55556, 1.55556, 1.55556, 1.55556, 0.777778,
0.777778, 0.777778, 0.777778, 0.777778, 0.777778, 0.777778, 0.0])
```

5 Events

Each event specifies how the model state is to be updated during a simulation run. The update may be probabilistic.

For example, an event might say that if Bob is infected but Alice is not, then Alice becomes infected with probability 15%.

The effects of an event may depend on the attributes of the input nodes. For example, in our example transmission probability may be smaller if either Alice and Bob are wearing masks, and smaller still if both are wearing masks.

Each event in effect runs some program, that takes as input a person or a set of people, and updates the state of that person or those people.

[8]:
```
struct DefaultParametersEvent      # set model default global parameters to␣
 ↪these values
    infected::Float64
    masked::Float64
end
```

[9]:
```
struct NewPersonEvent
    person::Person                   # person created first, then NewPersonEvent
    infectedProbability::Float64     # e.g. prevalance of infection in the␣
 ↪population individual is drawn from
                                     # assume equally likely to be any of I1...
 ↪ILast
                                     # Todo: update for other distributions.
    maskedProbability::Float64       # probability that new individual is masked
    asymptomaticProbability::Float64 # probability that new individual is␣
 ↪asymptomatic

end
```

[10]:
```
struct NewDayEvent
end
```

[11]:
```
# A Test Event is a measurement of the disease state of a person,
# together with a required (reported) value for that test result.
struct TestEvent
    person::Person
    testType::TestType
    reportedTestResult::Bool         # simulated test result must match this␣
 ↪reportedTestRestult
                                     # or else simulation run doesn't count
end
```

[12]:
```
struct SymptomOnsetEvent
    person::Person
    reportedSymptomOnsetResult::Bool  # true if symptoms start on this day
end
```

[13]:
```
struct ContactEvent  # Close Contact Event between two or more people
                     # An Int means that many people with default parameter␣
 ↪settings
                     # (Vertical line segment joining two or more horizontal␣
 ↪Person lines)
    minutes::Int
    people::Vector{Person}
    anonymousNumber::Int64
    anonymousInfectedProbability::Float64
    anonymousMaskedProbability::Float64
    anonymousAsymptomaticProbability::Float64
end
```

[14]:
```
struct MaskEvent           # cause individual to become masked (with given␣
 ↪MaskType)
    person::Person
    mask::MaskType
end
```

[15]:
```
struct StatsEvent           # collect statistics: is each named person infected?
end
```

[16]:
```
Event = Union{DefaultParametersEvent, NewPersonEvent, NewDayEvent,
              TestEvent, SymptomOnsetEvent, ContactEvent, MaskEvent, StatsEvent}
```

[16]:
```
Union{NewDayEvent, StatsEvent, DefaultParametersEvent, ContactEvent, MaskEvent,
NewPersonEvent, SymptomOnsetEvent, TestEvent}
```

6 Models

The model contains * global parameters, * a list of all named people in the model, * an (ordered) *event list* of *events* (The event list is a *schedule* of events to be run by the scheduler; the events happen in the specified order), and * the number of StatsEvent entries in the event list

[17]:
```
mutable struct Model
    params::GlobalParameters
    people::Vector{Person}    # all people in model
    events::Vector{Event}     # all events in model, ordered by time of␣
 ↪occurrence
    name::String              # name of the model
    nStats::Int64             # number of stats events in event list
    stats::Dict               # statistics gathered
end
Model() = Model(defaultGlobalParameters, [], [], "", 1, Dict())
Model(name::String) = Model(defaultGlobalParameters, [], [], name, 1, Dict())
```

[17]:
```
Model
```

6.1 Model initialization and specification

This section gives the tools for specifying a model.

The model must be completely specified before simulation can begin.

The model-specification API consists of number of functions, each of whose name begins with `note`, and take as their first argument the model being specified.

Some of the main model-specification functions are:

- `notePerson!` introduces a new named person into the model.

  ```
  notePerson!(m,
              personID,
              infectedProbability,
              maskedProbability,
              asymptomaticProbability)
  ```

- `noteContact!` specifies a contact between two or more people. At least one of them should be named. A number of anonymous individuals may be included in the contact.

  ```
  noteContact!(m,
               personIDs;
               minutes,
               anonymousNumber,
               anonymousInfectedProbability,
               anonymousMaskedProbability,
               anonymousAsymptomaticProbability)
  ```

- `noteTest!` specifies a test given to a named person, and the result.

  ```
  noteTest!(m,
            personID,
            testType,
            reportedTestResult::Bool)
  ```

- `noteStats!` requests a printout or display of the infection probabilities of all named people.

  ```
  noteStats!(m)
  ```

- Others include
  - `noteNewDay!`
  - `noteSymptomOnset!`
  - `noteMaskEvent!`

[18]:
```
function noteDefaultParameters!(m::Model, infectedProbability::Real,␣
↪maskedProbabilty::Real)
    e = DefaultParametersEvent(infectedProbability, maskedProbability)
    push!(m.events, e)
end
```

[18]:
```
noteDefaultParameters! (generic function with 1 method)
```

[19]:
```
function findPersonByID(m, personID)::Person
    for p in m.people
        if p.personID == personID
            return p
        end
    end
    error("No person is known having ID: " * personID)
end
```

[19]:
```
findPersonByID (generic function with 1 method)
```

[20]:
```
function notePerson!(m::Model,
                     personID;
                     infectedProbability::Float64 = m.params.infectedProbability,
                     maskedProbability::Float64 = m.params.maskedProbability,
                     asymptomaticProbability::Float64 = m.params.
↪asymptomaticProbability)
    p = Person(personID, false, DiseaseState(), VisibleState())
    e = NewPersonEvent(p, infectedProbability, maskedProbability,␣
↪asymptomaticProbability)
    push!(m.people, p)
    push!(m.events, e)
end
```

[20]:
```
notePerson! (generic function with 1 method)
```

[21]:
```
function noteNewDay!(m::Model)
    push!(m.events, NewDayEvent())
end
```

[21]:
```
noteNewDay! (generic function with 1 method)
```

[22]:
```
function noteTest!(m::Model,
                   personID::String,
                   testType::TestType,
                   reportedTestResult::Bool)
    person = findPersonByID(m, personID)
    push!(m.events, TestEvent(person, testType, reportedTestResult))
end
```

[22]:
```
noteTest! (generic function with 1 method)
```

[23]:
```
function noteSymptomOnset!(m::Model,
                           personID::String,
                           reportedSymptomOnsetResult)
    person = findPersonByID(m, personID)
    push!(m.events, SymptomOnsetEvent(person, reportedSymptomOnsetResult))
end
```

[23]:
```
noteSymptomOnset! (generic function with 1 method)
```

[24]:
```
function noteContact!(m::Model,
                      personIDs;
                      minutes::Int64 = 15,
                      anonymousNumber::Int64 = 0,
                      anonymousInfectedProbability::Float64 = m.params.
 ↪anonymousInfectedProbability,
                      anonymousMaskedProbability::Float64 = m.params.
 ↪anonymousMaskedProbability,
                      anonymousAsymptomaticProbability::Float64 = m.params.
 ↪anonymousAsymptomaticProbability)
    # here a "personID" should be a String
    # Strings are looked up (converted to existing people);
    people = []
    for personID in personIDs
        push!(people, findPersonByID(m, personID))
    end
    e = ContactEvent(minutes,
                     people,
                     anonymousNumber,
                     anonymousInfectedProbability,
                     anonymousMaskedProbability,
                     anonymousAsymptomaticProbability)
    push!(m.events, e)
end
```

[24]: noteContact! (generic function with 1 method)

[25]:
```
function noteMaskEvent(m::Model, personID::String, mask::MaskType)
    p = findPersonByID(m, personID)
    push!(m.events, MaskEvent(m, p, mask))
end
```

[25]: noteMaskEvent (generic function with 1 method)

[26]:
```
function noteStats!(m::Model)
    push!(m.events, StatsEvent())
end
```

[26]: noteStats! (generic function with 1 method)

7 Simulation

7.1 Random number generation

```
[27]: using NBInclude   # Use custom routines for generating random numbers, for␣
       ↪reproducibility.
      @nbinclude("SimRiskRandom.ipynb")

      function withProbability(seed::UInt, index::Int, probability::Real)::Bool
          return (SimRiskRandom.myRand(seed, index) < probability)
      end

      function fromRange(seed::UInt, index::Int, range::UnitRange)
          return SimRiskRandom.myRand(seed, index, range)
      end

      function subSeed(seed::UInt, index::Int)::UInt
          return SimRiskRandom.myKDF(seed, index)
      end
```

```
[27]: subSeed (generic function with 1 method)
```

7.2 Statistics

```
[28]: using Formatting

      function initStats!(m::Model)
          return m.stats = Dict()     # mapping from (person, day) pairs to run counts
      end

      function gatherStats!(m::Model, t::Int)
          stats = m.stats
          for p in m.people
              stats[(p,t,"infected runs")] = get(stats, (p,t,"infected runs"), 0.0) +
                                             infected(p.diseaseState)
              stats[(p,t,"total runs")] = get(stats, (p,t,"total runs"), 0.0) + 1
          end
      end

      function printStats(m::Model, runs)
          for t in 1:m.nStats
              printfmtln("  Stats number {}", t)
              for p in m.people
                  infectedRuns = get(m.stats, (p, t, "infected runs"), 0)
                  totalRuns = get(m.stats, (p, t, "total runs"), 0)
```

```
            printfmt("        {:s}:  {:d}/{:d} âĽĹ {:.3f}\n",
                     p.personID,
                     infectedRuns,
                     totalRuns,
                     infectedRuns/totalRuns)
        end
    end
    flush(stdout)
end
```

[28]:
```
printStats (generic function with 1 method)
```

7.3 Event simulation

A function for each event type, to simulate an event of that type. Function returns `true` if simulation is consistent with any relevant reported test results.

[29]:
```
function infectPersonWithProbability(p::Person, t::Int, infectedProbability::
 ↪Real, eventSeed::UInt)
    if withProbability(eventSeed, 1, infectedProbability)
        # following gives uniform distribution over infected states
        p.diseaseState =
         DiseaseState(fromRange(eventSeed, 2, (Int(I1.ds)):(Int(ILast.ds))))
    else
        p.diseaseState = Susceptible
    end
end

function maskPersonWithProbability(p::Person, t::Int, maskProbability::Real,␣
 ↪eventSeed::UInt)
    if withProbability(eventSeed, 3, maskProbability)
        p.visibleState = VisibleState(N95)            # make flexible?
    else
        p.visibleState = VisibleState(NoMask)
    end
end

function makePersonAsymptomaticWithProbability(p::Person,
                                               t::Int,
                                               asymptomaticProbability::Real,
                                               eventSeed::UInt)
    p.asymptomatic = withProbability(eventSeed, 4, asymptomaticProbability)
end

function simulateNewPersonEvent(m::Model, e::Event, t::Int, eventSeed::UInt)::
 ↪Bool
```

```
    p = e.person
    infectPersonWithProbability(p, t, e.infectedProbability, eventSeed)
    maskPersonWithProbability(p, t, e.maskedProbability, eventSeed)
    makePersonAsymptomaticWithProbability(p, t, e.asymptomaticProbability,␣
↪eventSeed)
    return true
end
```

[29]: `simulateNewPersonEvent (generic function with 1 method)`

[30]:
```
function simulateNewDayEvent(m::Model, e::Event, t::Int, eventSeed::UInt)::Bool
    # Start a new day by advancing DiseaseState
    for p in m.people
        p.diseaseState = nextDiseaseState(p.diseaseState)
        # p.visibleState = p.visibleState # of course; not needed
    end
    return true
end
```

[30]: `simulateNewDayEvent (generic function with 1 method)`

[31]:
```
function simulateTestEvent(m::Model, e::Event, t::Int, eventSeed::UInt)::Bool
    # return consistent (Bool) to be anded with consistent (Bool) for this␣
↪simulation run
    p = e.person
    is_infected = infected(p.diseaseState)   # can transmit same day infected,␣
↪perhaps
    if is_infected
        simulatedTestResult = withProbability(eventSeed, 1, e.testType.P_det)
    else
        simulatedTestResult = withProbability(eventSeed, 2, e.testType.P_FA)
    end
    consistent = Int(simulatedTestResult == e.reportedTestResult)
    return consistent
end
```

[31]: `simulateTestEvent (generic function with 1 method)`

[32]:
```
function simulateSymptomOnsetEvent(m::Model, e::Event, t::Int, eventSeed::UInt)::
↪Bool
    p = e.person
    simulatedSymptomOnsetResult = (!p.asymptomatic && (p.diseaseState ==␣
↪SymptomOnset))
    consistent = Int(simulatedSymptomOnsetResult == e.reportedSymptomOnsetResult)
    return consistent
end
```

[32]: simulateSymptomOnsetEvent (generic function with 1 method)

[33]:
```
function simulateContactEvent(m::Model, e::Event, t::Int, eventSeed::UInt)::Bool
    # An event with several people is equivalent to a number of two-person␣
 ↪contacts
    # This routine has runtime quadratic in number of people in event, so don't␣
 ↪use
    # it for large events.
    # Note that infection won't be transitively propagated within an event:
    # if A infects B in an event, then B won't infect anyone else in that event
    # (because B will be in state I1, which has infectiousness 0).             ␣
 ↪
    subEventCtr = 1
    subEventSeed = unsigned(0)     # to make scope of subEventSeed entire function
    anonymousPerson = Person("",
                             false,
                             DiseaseState(),
                             VisibleState())
    for pui in e.people
        if pui.diseaseState==Susceptible
            for pi in e.people  # infection by known people
                if infected(pi.diseaseState)
                    subEventSeed = subSeed(eventSeed, subEventCtr)
                    subEventCtr += 1
                    simulateTwoPersonContactEvent(m, e, t, pi, pui, subEventSeed)
                end
            end
            for i in 1:e.anonymousNumber # infection by anonymous people
                # set DiseaseState and VisibleState for anonymousPerson
                infectPersonWithProbability(anonymousPerson, t,
                                            e.anonymousInfectedProbability,
                                            subEventSeed)
                # add mask up with probability, too...
                subEventSeed = subSeed(eventSeed, subEventCtr)
                subEventCtr += 1
                simulateTwoPersonContactEvent(m, e, t, anonymousPerson, pui,␣
 ↪subEventSeed)
            end
        end
    end
    return true
end
```

[33]: simulateContactEvent (generic function with 1 method)

[34]:
```
function simulateTwoPersonContactEvent(m,
                                       e::Event,
                                         t::Int,
                                         pi::Person, # infected (source) person
                                         pui::Person,  # uninfected (recipient)␣
↪person
                                         subEventSeed::UInt)

    dose = e.minutes      # in arbitrary units (1 minute six feet away)

    # masks reduce dose by transmission factors
    dose *= pi.visibleState.mask.sourceMaskTransmission
    dose *= pui.visibleState.mask.recipientMaskTransmission

    # multiply dose by infectiousness of source (based on source diseaseState)
    dose *= m.params.infectiousness[Int(pi.diseaseState)]

    # also reduce dose if source is asymptomatic
    pi.asymptomatic && (dose *= m.params.asymptomaticFactor)

    # following is key formula (equivalent to Independent Action Hypothesis)
    transmissionProbability = 1.0 - exp(- dose * m.params.transmissionConstant)

    if withProbability(subEventSeed, 1, transmissionProbability)
        pui.diseaseState = I1            # person pui infected! (if not already)
    end
end
```

[34]:
```
simulateTwoPersonContactEvent (generic function with 1 method)
```

[35]:
```
function simulateStatsEvent(m::Model, e::Event, t::Int, eventSeed::UInt)::Bool
    gatherStats!(m, t)
    return true
end
```

[35]:
```
simulateStatsEvent (generic function with 1 method)
```

[36]:
```
function simulateEvent(m::Model, e::Event, t::Int, eventSeed::UInt)::Bool
    # return true iff all Tes  tEvents and SymptomOnsetEvents
    # have simulated values just as reported
    e isa NewPersonEvent && (return simulateNewPersonEvent(m, e, t, eventSeed))
    e isa NewDayEvent && (return simulateNewDayEvent(m, e, t, eventSeed))   #␣
↪always true
    e isa TestEvent && (return simulateTestEvent(m, e, t, eventSeed))
    e isa SymptomOnsetEvent && (return simulateSymptomOnsetEvent(m, e, t,␣
↪eventSeed))
    e isa ContactEvent && (return simulateContactEvent(m, e, t, eventSeed))
    e isa StatsEvent && (return simulateStatsEvent(m, e, t, eventSeed))
    error("simulateEvent: Illegal event type!")
```

```
end
```

```
[36]: simulateEvent (generic function with 1 method)
```

7.4 Simulation top-level

```
[37]: function simulationRun(m::Model, runSeed::UInt)
          t = 0              # stats counter
          for (i, e) in enumerate(m.events)
              eventSeed = subSeed(runSeed, i)
              e isa StatsEvent && (t += 1)
              !simulateEvent(m, e, t, eventSeed) && break
          end
      end
```

```
[37]: simulationRun (generic function with 1 method)
```

```
[38]: function numberOfStats(events)::Int64
          # return number of StatsEvent
          return length([e for e in events if e isa StatsEvent])
      end
```

```
[38]: numberOfStats (generic function with 1 method)
```

```
[39]: function initPeople!(m::Model)
          # reset DiseaseState and VisibleState of each named person
          for p in m.people
              p.diseaseState = DiseaseState()
              p.visibleState = VisibleState()
          end
      end
```

```
[39]: initPeople! (generic function with 1 method)
```

```
[40]: function initEvents!(m::Model)
          # no-op for now
      end
```

```
[40]: initEvents! (generic function with 1 method)
```

```
[41]: function simulation(m::Model, simulationSeed, runs::Int)
          printfmt("Starting simulation with simulationSeed {:0x} and {} runs\n",
                  simulationSeed, runs)

          # Simulation initialization
          initStats!(m)
```

```
    initEvents!(m)      # no-op
    m.nStats = numberOfStats(m.events)
    initPeople!(m)      # uses m.nDays, so this is last to set up
    simulationSeed = unsigned(simulationSeed)

    # Simulation runs
    for run in 1:runs
        runSeed = subSeed(simulationSeed, run)
        simulationRun(m, runSeed)
    end

    # Print simulation results
    printStats(m, runs)
    println()
    print("Done.")

end
```

```
[41]: simulation (generic function with 1 method)
```

8 Plotting routines

[42]:
```
@nbinclude("SimRiskPlot.ipynb")
```

[42]:
```
simPlot (generic function with 1 method)
```

9 Examples

9.1 Example 1: A one-person one-day model

This simplest-possible example demonstrates adding a person named "Alice" to the model. Here Alice is given an initial probability of infection of 0.200. On day 1, if Alice is infected, she is equally likely to be an infected disease states (I1..ILast). Nothing happens in this example, so at the end of the Alice's infection probability is the same as it was when she first appeared.

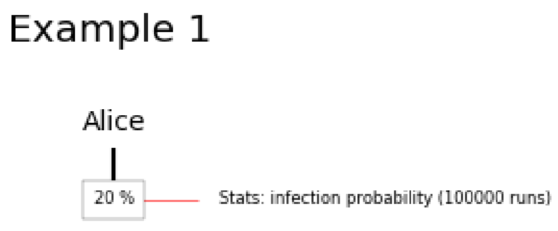
[43]:
```
function example1()::Model
    println("\nExample 1: notePerson")
    m = Model("Example 1")
    notePerson!(m, "Alice", infectedProbability=0.200)
    noteStats!(m)
    return m
end

m = example1()
@time simulation(m, 0, 100000)
# @time simulation(example1(), 0, 100000)
# correct answer is
#     Prob(Alice infected) = 0.200

simPlot(m)
```

```
Example 1: notePerson
Starting simulation with simulationSeed 0 and 100000 runs
  Stats number 1
        Alice:  20046/100000 âĽĹ 0.200

Done.
```



```
  2.845499 seconds (14.17 M allocations: 676.696 MiB, 7.25% gc time)
```

9.2 Example 2: A Two-Day Example

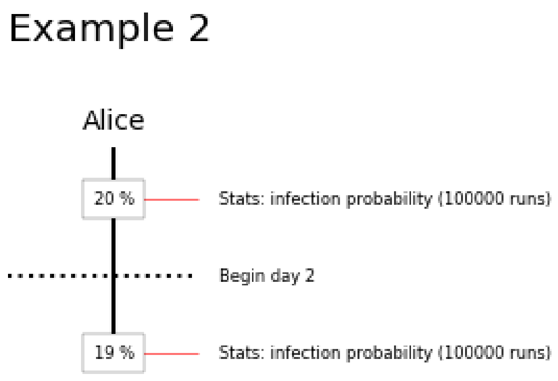
This is identical to example 1, with the addition of a NewDay, which causes a transition to day 2 in the simulation.

[44]:
```
function example2()::Model
    println("Example 2: notePerson and noteNewDay")
    m = Model("Example 2")
    notePerson!(m, "Alice", infectedProbability=0.200)
    noteStats!(m)
    # day 2
    noteNewDay!(m)
    noteStats!(m)
    return m
end

# @time simulation(example2(), 0, 100000)
m = example2()
@time simulation(m, 0, 100000)
# correct answer for end of day 2 is
#     Prob(Alice infected) = 0.20 * 13/14 = 0.1857
# since Alice recovers when entering day 2 with probability 1/14.

simPlot(m)
```

```
Example 2: notePerson and noteNewDay
Starting simulation with simulationSeed 0 and 100000 runs
  Stats number 1
        Alice:  20046/100000 âĽĹ 0.200
  Stats number 2
        Alice:  18647/100000 âĽĹ 0.186
```


Example 2
Alice
20 %
Stats: infection probability (100000 runs)
Begin day 2
19 %
Stats: infection probability (100000 runs)

```
Done.  0.516121 seconds (3.31 M allocations: 73.573 MiB, 2.31% gc time)
```

9.3 Example 3: One person, one day, and one perfect test

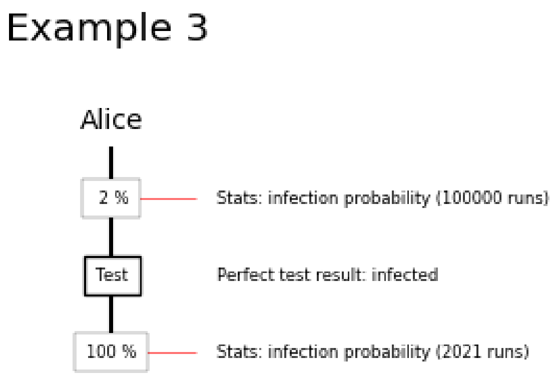
In this example, Alice initially appears with an infection probability of 0.02. But she is immediately tested, and the test result is “true” (infected). So the probability of her being infected, conditioned on this test result, is 1.000.

[45]:
```
function example3()::Model
    println("Example 3: notePerson and noteTest (with perfect test)")
    m = Model("Example 3")
    notePerson!(m, "Alice", infectedProbability=0.020)
    noteStats!(m)
    noteTest!(m, "Alice", PerfectTest, true)    # perfect test returned true here
    noteStats!(m)
    return m
end

m = example3()
@time simulation(m, 0, 100000)
# correct answer for end of day 1 is
#     Prob(Alice infected) = 1.000

simPlot(m)
```

```
Example 3: notePerson and noteTest (with perfect test)
Starting simulation with simulationSeed 0 and 100000 runs
  Stats number 1
        Alice:  2021/100000 âĽĹ 0.020
  Stats number 2
        Alice:  2021/2021 âĽĹ 1.000
```


Example 3
Alice
2 %
Stats: infection probability (100000 runs)
Test
Perfect test result: infected
100 %
Stats: infection probability (2021 runs)

```
Done.  0.344656 seconds (2.03 M allocations: 48.102 MiB, 2.46% gc time)
```

9.4 Example 4: One person, one day, and one imperfect test

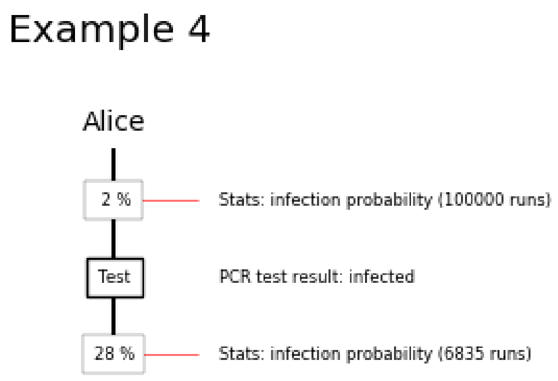
This is the same as example 3, except that the test is now *imperfect*, with a probability of detection (correctly reporting) an infected individual of only ninety-five percent, and a probability of a false alarm (incorrectly reporting an uninfected individual as infected) of five percent. Alice appears on the scene initially with an infection probability of 0.020. She is then tested by an imperfect test, which has a 0.05 false negative rate and a 0.05 false positive rate. The test returns "true" (infected). The chance that Alice is actually infected is only 0.279, due to false positives. (See the next example for the improvement when one has a repeated PCR test.) Many are surprised to see a positive test result from a test that is "95% accurate" have a post-test posterior probability of only 28%.

[46]:
```
function example4()::Model
    println("Example 4: notePerson and noteTest (with imperfect PCR test)")
    m = Model("Example 4")
    notePerson!(m, "Alice", infectedProbability=0.020)
    noteStats!(m)
    noteTest!(m, "Alice", PCRTest, true)    # PCR is imperfect test
    noteStats!(m)
    return m
end

m = example4()
@time simulation(m, 0, 100000)
# corect result here is
#     Prob(Alice infected | TestResult simulated as reported)
#     = 0.020 * 0.95 / (0.020 * 0.95 + 0.980 * 0.05) = 0.279

simPlot(m)
```

```
Example 4: notePerson and noteTest (with imperfect PCR test)
Starting simulation with simulationSeed 0 and 100000 runs
  Stats number 1
        Alice:  2021/100000 âĽĹ 0.020
  Stats number 2
        Alice:  1917/6835 âĽĹ 0.280
```


Example 4
Alice
2 %
Stats: infection probability (100000 runs)
Test
PCR test result: infected
28 %
Stats: infection probability (6835 runs)

```
Done.  0.363067 seconds (2.09 M allocations: 49.344 MiB, 2.13% gc time)
```

9.5 Example 5: One person, one day, and a repeated imperfect test

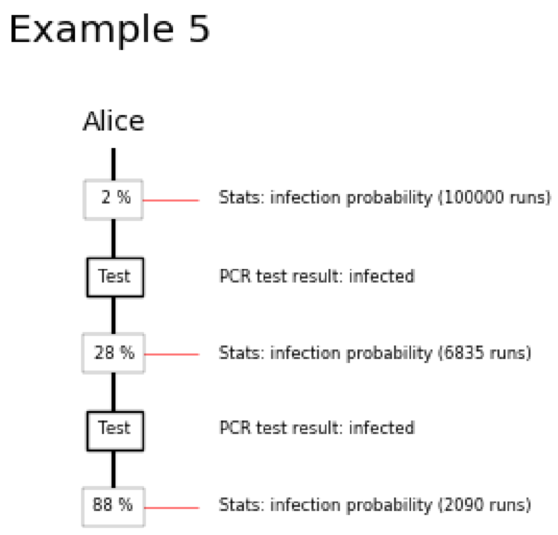
This is the same as example 4, except that the imperfect test is repeated for a second time. The second test also returns "true" (infected). The estimated chance that Alice is actually infected rises from 0.279 to 0.884.

[47]:
```julia
function example5()::Model
    println("Example 5: notePerson and two noteTests (two independent imperfect␣
 ↪PCR tests)")
    m = Model("Example 5")
    notePerson!(m, "Alice", infectedProbability=0.020)
    noteStats!(m)
    noteTest!(m, "Alice", PCRTest, true)    # PCR is imperfect test
    noteStats!(m)
    noteTest!(m, "Alice", PCRTest, true)    # second independent PCR test
    noteStats!(m)
    return m
end

m = example5()
@time simulation(m, 0, 100000)
# corect result here is roughly
#     Prob(Alice infected | TestResult simulated as reported)
#     = 0.020 * 0.95^2 / (0.020 * 0.95^2 + 0.980 * 0.05^2) = 0.884

simPlot(m)
```

```
Example 5: notePerson and two noteTests (two independent imperfect PCR tests)
Starting simulation with simulationSeed 0 and 100000 runs
  Stats number 1
        Alice:  2021/100000 âĽĹ 0.020
  Stats number 2
        Alice:  1917/6835 âĽĹ 0.280
  Stats number 3
        Alice:  1831/2090 âĽĹ 0.876
```


Example 5
Alice
2 %
Stats: infection probability (100000 runs)
Test
PCR test result: infected
28 %
Stats: infection probability (6835 runs)
Test
PCR test result: infected
88 %
Stats: infection probability (2090 runs)

```
Done.  0.388298 seconds (2.15 M allocations: 50.906 MiB, 3.20% gc time)
```

9.6 Example 6: One person, one SymptomOnset

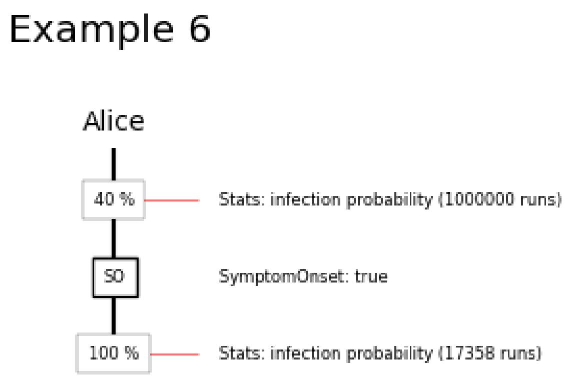
Same as example 4, except replacing a test with symptom onset. The result is similar, except that the number of consistent runs is greatly reduced, as symptom onset can happen only on day 5 of infection in our model, if the person is symptomatic.

[48]:
```
function example6()::Model
    println("Example 6: notePerson and one noteSymptomOnset")
    m = Model("Example 6")
    notePerson!(m, "Alice", infectedProbability=0.400)
    noteStats!(m)
    noteSymptomOnset!(m, "Alice", true)
    noteStats!(m)
    return m
end

m = example6()
@time simulation(m, 0, 1000000)
# 1000000 runs * 0.400 infection rate = 400000 infected
#  400000 infected * 0.600 symptomatic rate = 240000 symptomatic infected
#  240000 symptomatic infected / 14 infected states = 17143 people with symptom␣
 ↪onset

simPlot(m)
```

```
Example 6: notePerson and one noteSymptomOnset
Starting simulation with simulationSeed 0 and 1000000 runs
  Stats number 1
        Alice:  400004/1000000 âĽĹ 0.400
  Stats number 2
        Alice:  17358/17358 âĽĹ 1.000
```


Example 6
Alice
40 %
Stats: infection probability (1000000 runs)
SO
SymptomOnset: true
100 %
Stats: infection probability (17358 runs)

```
Done.  3.683867 seconds (20.83 M allocations: 487.386 MiB, 1.51% gc time)
```

9.7 Example 7: Two person, one day, close contact

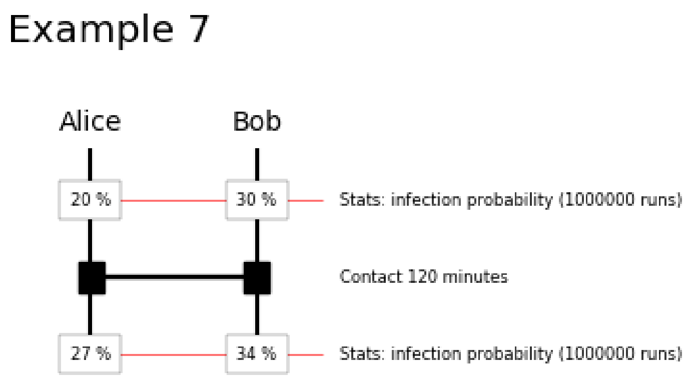
This example has two people, Alice and Bob, who appear on day 1 with initial probabilities of being infected of twenty and thirty percent, respectively. They have a close contact for two hours.

[49]:
```
function example7()::Model
    println("Example 7: notePerson and noteContact")
    m = Model("Example 7")
    notePerson!(m, "Alice", infectedProbability=0.200, maskedProbability=0.0)
    notePerson!(m, "Bob", infectedProbability=0.300, maskedProbability=0.0)
    noteStats!(m)
    noteContact!(m, ["Alice", "Bob"], minutes=120)
    noteStats!(m)
    return m
end

m = example7()
@time simulation(m, 2, 1000000)
# As transmission has probability 1-(1-0.05)^8 = 0.336,
# the correct answer is (for uniform infectiousness, which isn't quite accurate)
#   Prob(Alice infected) = 0.200 + 0.336 * 0.800 * 0.300 = 0.281
#   Prob(Bob infected) = 0.300 + 0.336 * 0.200 * 0.700 = 0.347

simPlot(m)
```

```
Example 7: notePerson and noteContact
Starting simulation with simulationSeed 2 and 1000000 runs
  Stats number 1
        Alice:  200385/1000000 âĽĹ 0.200
        Bob:  298887/1000000 âĽĹ 0.299
  Stats number 2
        Alice:  271633/1000000 âĽĹ 0.272
        Bob:  340775/1000000 âĽĹ 0.341
```


Example 7
Alice
Bob
20 %
30 %
Stats: infection probability (1000000 runs)
Contact 120 minutes
27 %
34 %
Stats: infection probability (1000000 runs)

```
Done.  6.909286 seconds (55.01 M allocations: 1.282 GiB, 1.95% gc time)
```

9.8 Example 8: Twelve person (ten unknown), one day, close contact

This example has two known people, Alice and Bob, who appear on day 1 with initial infection probabilities of twenty and thirty percent, respectively. They have a close contact for two hours, as in Example 7. This close contact now includes ten other people, who are anonymous, and thus assume default parameter settings. (Maybe Alice and Bob were on a bus ride with ten people they didn't know.)

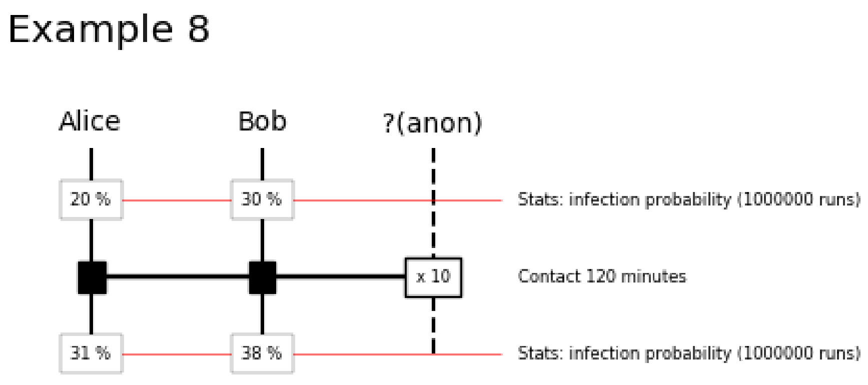
We can see that the final infection probabilities for Alice and Bob increase, compared to Example 7, as one would expect.

[50]:
```
function example8()::Model
    println("Example 8: notePerson and noteContact (with ten unknown parties)")
    m = Model("Example 8")
    notePerson!(m, "Alice", infectedProbability=0.200, maskedProbability=0.0)
    notePerson!(m, "Bob", infectedProbability=0.300, maskedProbability=0.0)
    noteStats!(m)
    noteContact!(m, ["Alice", "Bob"], minutes=120, anonymousNumber=10)
    noteStats!(m)
    return m
end

m = example8()
@time simulation(m, 0, 1000000)

simPlot(m)
```

```
Example 8: notePerson and noteContact (with ten unknown parties)
Starting simulation with simulationSeed 0 and 1000000 runs
  Stats number 1
        Alice:  200019/1000000 âĽĹ 0.200
        Bob:  299737/1000000 âĽĹ 0.300
  Stats number 2
        Alice:  312246/1000000 âĽĹ 0.312
        Bob:  381915/1000000 âĽĹ 0.382
```


Example 8
Alice
Bob
?(anon)
20 %
30 %
Stats: infection probability (1000000 runs)
x 10
Contact 120 minutes
31 %
38 %
Stats: infection probability (1000000 runs)

```
Done.  7.230288 seconds (55.00 M allocations: 1.282 GiB, 1.94% gc time)
```

9.9 Example 9: Three named people, four anonymous people, two tests, and a NewDay

(Explained above; this is the introductory example.)

[51]:
```julia
function example9()::Model
    m = Model("Example 9")
    # day 1
    notePerson!(m, "me", infectedProbability=0.00, maskedProbability=0.500)
    notePerson!(m, "Jack", infectedProbability=0.05, maskedProbability=0.000)
    notePerson!(m, "Jill", infectedProbability=0.10, maskedProbability=1.00)
    noteStats!(m)
    noteContact!(m, ["me", "Jack"], minutes=120)
    noteContact!(m, ["me", "Jill"], anonymousNumber=4, minutes=60)
    # day 2
    noteNewDay!(m)
    noteStats!(m)
    noteTest!(m, "Jack", PCRTest, true)
    noteTest!(m, "Jill", PCRTest, false)
    noteStats!(m)
    return m
end
```

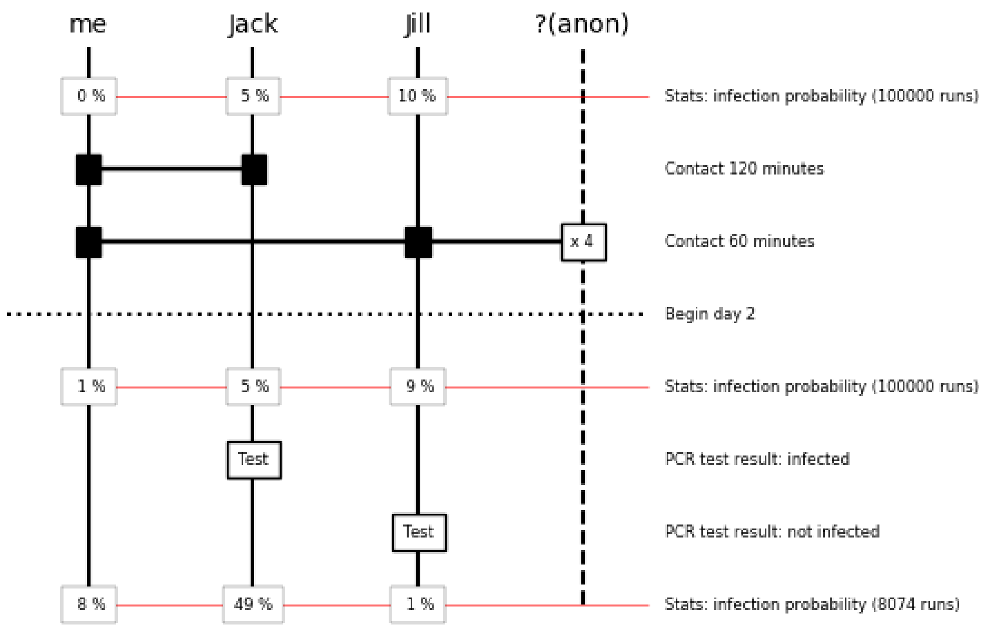
[51]:
```
example9 (generic function with 1 method)
```

[52]:
```julia
m = example9()
@time simulation(m, 1, 100000)

simPlot(m, save="example9")
```

```
Starting simulation with simulationSeed 1 and 100000 runs
  Stats number 1
        me:  0/100000 âĽĹ 0.000
        Jack:  5057/100000 âĽĹ 0.051
        Jill:  10149/100000 âĽĹ 0.101
  Stats number 2
        me:  1407/100000 âĽĹ 0.014
        Jack:  4701/100000 âĽĹ 0.047
        Jill:  9499/100000 âĽĹ 0.095
  Stats number 3
        me:  675/8074 âĽĹ 0.084
        Jack:  3916/8074 âĽĹ 0.485
        Jill:  52/8074 âĽĹ 0.006
```

Example 9


me
Jack
Jill
?(anon)
0 %
5 %
10 %
Stats: infection probability (100000 runs)
Contact 120 minutes
x 4
Contact 60 minutes
Begin day 2
1 %
5 %
9 %
Stats: infection probability (100000 runs)
Test
PCR test result: infected
Test
PCR test result: not infected
8 %
49 %
1 %
Stats: infection probability (8074 runs)

```
Done.  1.362576 seconds (9.49 M allocations: 231.043 MiB, 2.31% gc time)
```

9.10 Example 10: a complex thirteen-person example

This example has three known people: Alice, Bob, and Charles, and ten anonymous people. The example proceeds for three days, and has four contact events.

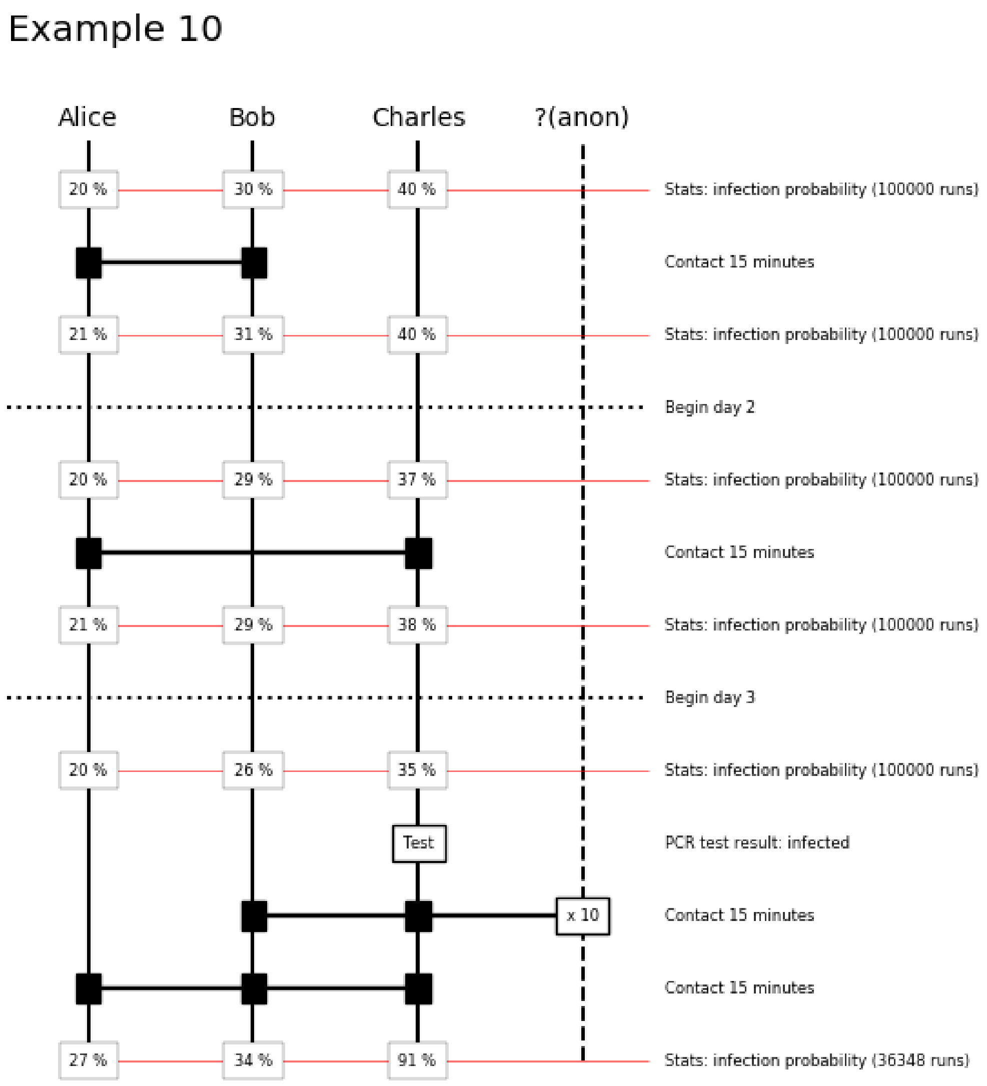
[53]:
```
function example10()::Model
    m = Model("Example 10")
    # day 1
    notePerson!(m, "Alice", infectedProbability=0.200, maskedProbability=0.00)
    notePerson!(m, "Bob", infectedProbability=0.300, maskedProbability=0.00)
    notePerson!(m, "Charles", infectedProbability=0.400, maskedProbability=0.00)
    noteStats!(m)
    noteContact!(m, ["Alice", "Bob"], minutes=15)
    noteStats!(m)
    # day 2
    noteNewDay!(m)
    noteStats!(m)
    noteContact!(m, ["Alice", "Charles"], minutes=15)
    noteStats!(m)
    # day 3
    noteNewDay!(m)
    noteStats!(m)
    noteTest!(m, "Charles", PCRTest, true)
    noteContact!(m, ["Bob", "Charles"], minutes=15, anonymousNumber=10)
    noteContact!(m, ["Alice", "Bob", "Charles"], minutes=15)
    noteStats!(m)
    return m
end

m = example10()
@time simulation(m, 1, 100000)

simPlot(m)
```

```
Starting simulation with simulationSeed 1 and 100000 runs
  Stats number 1
        Alice:  19954/100000 âĽĹ 0.200
        Bob:  30140/100000 âĽĹ 0.301
        Charles:  39957/100000 âĽĹ 0.400
  Stats number 2
        Alice:  21064/100000 âĽĹ 0.211
        Bob:  30772/100000 âĽĹ 0.308
        Charles:  39957/100000 âĽĹ 0.400
  Stats number 3
        Alice:  19611/100000 âĽĹ 0.196
        Bob:  28643/100000 âĽĹ 0.286
        Charles:  37139/100000 âĽĹ 0.371
  Stats number 4
```

```
      Alice:  21055/100000 âĽĹ 0.211
      Bob:  28643/100000 âĽĹ 0.286
      Charles:  37737/100000 âĽĹ 0.377
Stats number 5
      Alice:  19626/100000 âĽĹ 0.196
      Bob:  26483/100000 âĽĹ 0.265
      Charles:  34840/100000 âĽĹ 0.348
Stats number 6
      Alice:  9884/36348 âĽĹ 0.272
      Bob:  12215/36348 âĽĹ 0.336
      Charles:  33224/36348 âĽĹ 0.914
```


Example 10
Alice
Bob
Charles
?(anon)
20 %
30 %
40 %
Stats: infection probability (100000 runs)
Contact 15 minutes
21 %
31 %
40 %
Stats: infection probability (100000 runs)
Begin day 2
20 %
29 %
37 %
Stats: infection probability (100000 runs)
Contact 15 minutes
21 %
29 %
38 %
Stats: infection probability (100000 runs)
Begin day 3
20 %
26 %
35 %
Stats: infection probability (100000 runs)
Test
PCR test result: infected
x 10
Contact 15 minutes
Contact 15 minutes
27 %
34 %
91 %
Stats: infection probability (36348 runs)

```
Done.  2.483053 seconds (19.90 M allocations: 469.296 MiB, 2.82% gc time)
```

9.11 Example 11: Can a PCR positive test be cleared by a subsequent negative test?

An example motivated by this article: (https://medical.mit.edu/covid-19-updates/2020/11/pcr-test-result).

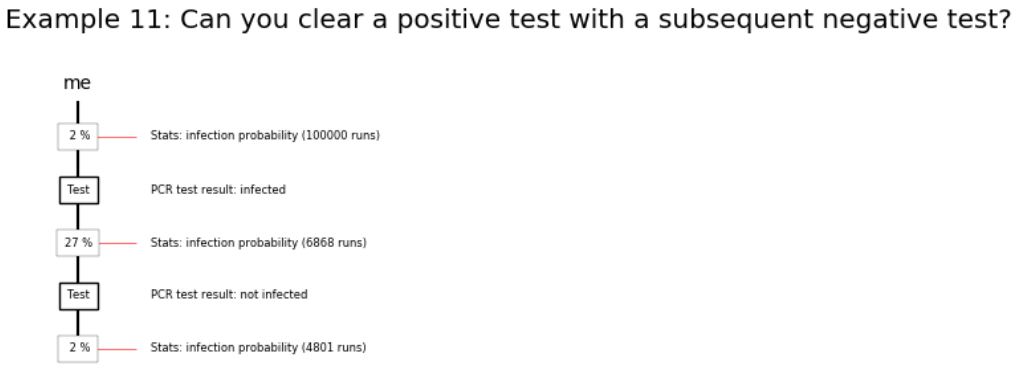
The short answer is “yes”. That is to say, you can combine the results of more than one test to get a final probability of infection. In our case, where a PCR test has equal values for “miss probability” $(1 - P_{DET})$ and “false alarm probability” (P_{FA}) then one negative test exactly cancels one positive test, so you might want *two* negative tests to conclude an overall “negative” result.

[54]:
```
function example11()
    m = Model("Example 11: Can you clear a positive test with a subsequent␣
 ↪negative test?")
    notePerson!(m, "me", infectedProbability=0.02)
    noteStats!(m)
    noteTest!(m, "me", PCRTest, true)
    noteStats!(m)
    noteTest!(m, "me", PCRTest, false)
    noteStats!(m)
    return m
end

m = example11()
@time simulation(m, 1, 100000)

simPlot(m)
```

```
Starting simulation with simulationSeed 1 and 100000 runs
  Stats number 1
        me:  1948/100000 âĽĹ 0.019
  Stats number 2
        me:  1857/6868 âĽĹ 0.270
  Stats number 3
        me:  83/4801 âĽĹ 0.017
```


Example 11: Can you clear a positive test with a subsequent negative test?
me
2 %
Stats: infection probability (100000 runs)
Test
PCR test result: infected
27 %
Stats: infection probability (6868 runs)
Test
PCR test result: not infected
2 %
Stats: infection probability (4801 runs)

```
Done.  0.379335 seconds (2.19 M allocations: 51.705 MiB, 1.97% gc time)
```

10 Notes

Each simulation run could have different parameters, not just a different simulation seed (see SafeBlues video).

11 Related Work

SafeBlues

COVID-19 Indoor Safety Guideline

SimAEN (Lincoln Laboratory) – to appear.

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The code here is freely usable by others (under the MIT License).

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