Stochastic Modelling of Uncertainties

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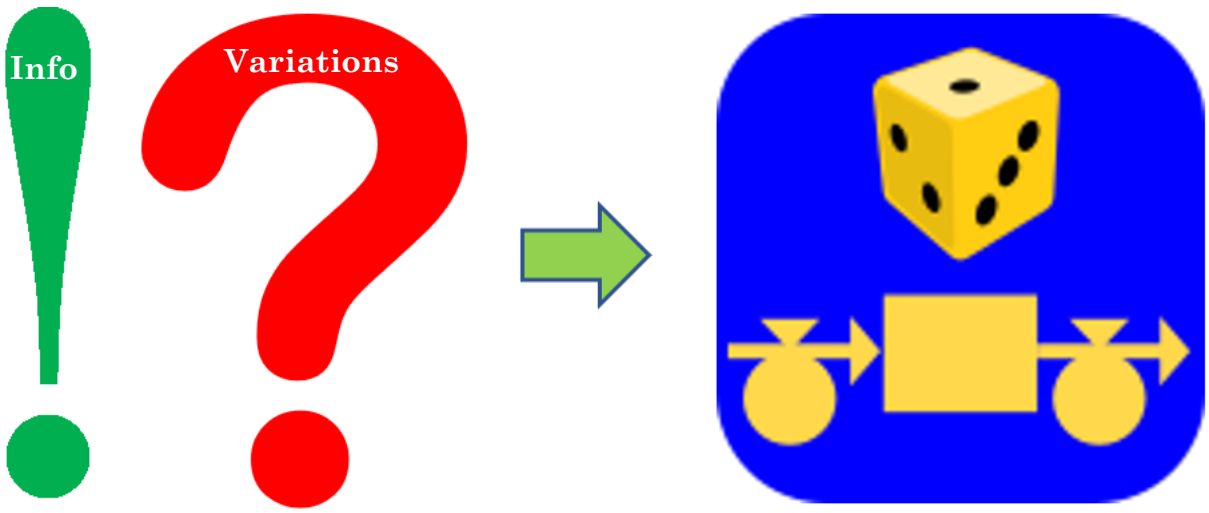
(Is the average of a stochastic model equal to that of a deterministic one?)
(How to model different types of uncertainties and their effects on the model behaviour.)
(Statistics from multiple replications of a stochastic model using the StatRes tool.)



"Stochastics is about including knowledge into the model – not about creating chaos."

Name:	**Date:**
Course:	**Approved:**

1. THE SYSTEM UNDER STUDY (SIR MODEL) AND A DETERMINISTIC MODEL OF IT

1.1 Introduction to epidemic modelling

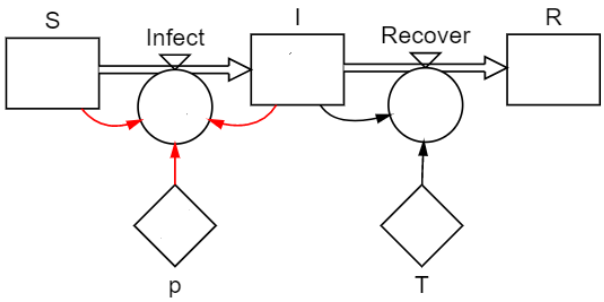
The system to be studied in these exercises is an epidemic. Therefore, we start with this introduction.

After understanding the spreading mechanism by bacteria in the end of the 19th century (and later on also by viruses), W.H. Hamer (1906) formulated the so-called '*mass action principle*' in epidemics that explains that the spread rate of an infectious disease is proportional to the density of the Susceptible and the density of Infectious individuals. In 1908 this was formulated by Ronald Ross as a mathematical model.

In particular, W.O. Kermack and A.G. McKendrick published a number of fundamental papers between 1927 and 1939 where the model consists of a system of three coupled differential equations, which we now call the SIR model. Here, we will study this and similar models by using the powerful tool of simulation.

1.2 The classical SIR model

Here we will first describe the classical SIR model, where S, I and R stands for Susceptible, Infectious, and Recovered individuals. The model structure is shown in Figure 1.



S=S(0); I=I(0); R=R(0) (Initial values)

S = S – DT*Infect

I = I + DT*Infect – DT*Recover

R = R + DT*Recover

Infect = p*S*I (The mass action principle)

Recover = I/T (T is the average time in I)

Figure 1. The classical SIR model. A deterministic, dynamic model based on the stages: Susceptibles (S), Infectious (I) and Recovered (R). To the right, the model in mathematical form.

The key mechanism for the SIR model is the Infection where the number of infected individuals per time unit is proportional to the Number of Susceptibles (that can be infected) and the number of Infectious (that deliver the bacteria or viruses) with a proportion parameter, p, that depends on a number of conditions (behaviour of the studied population, contagiousness, etc.). In mathematical form we have:

Infect = p*S*I (The mass action principle).

The simplest assumption about recovery of the Infectious is that a certain proportion will recover each time unit. However, we here prefer to write this proportion as 1/T, where the time constant, T, is the **sojourn** (stay) **time** in the Infectious stage. The Recovery function then becomes:

Recover = I/T.

The mathematical (numerical) form of the classical SIR model is shown to the right in Figure 1.

A central concept in epidemics is the *Basic Reproductive Rate* (R_0). This is defined as the average number of Susceptibles directly infected by an Infectious individual during his infectious period when entering a Susceptible population. From this, the so-called *Threshold theorem* was formulated.

Threshold theorem: If $R_0 > 1$ there will be an epidemic. (This means that if an infected individual infects more than one susceptible (on average) before recovering, then an epidemic is generated.) From the classical SIR model we get: $R_0 = p*T*S(0)$.

The important conclusions from the threshold theorem are: **1)** When the Susceptibles become too few an epidemic will die out. **2)** In a small population *S(0)* (below the threshold size), an epidemic cannot develop. **3)** The larger/denser the population, the larger the risk of an epidemic.

1.3 The SIR family

The SIR concept is very versatile and flexible. The S, I, & R stages could be combined with an Exposed stage (E) where the individual is not yet contagious. Also, loss of immunity of the Recovered individuals (who return to be Susceptible), Deaths in the disease, Birth and Deaths of other reasons, Migration, Vaccination, Recurrent introduction of new Infectious individuals, etc. could now swiftly be modelled. This set of models we call the SIR family, see Figure 2.

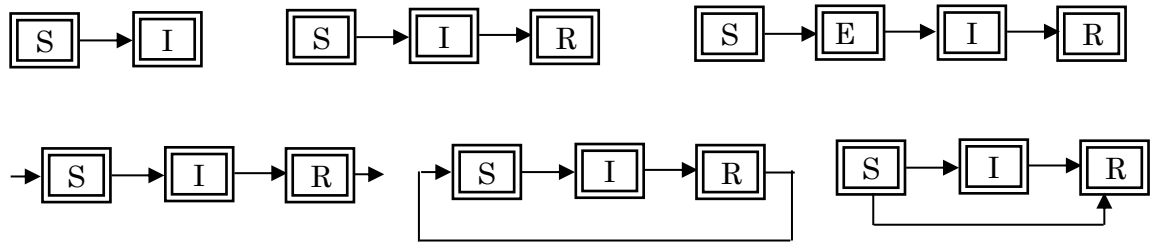


Figure 2. Some members of the SIR family denoted: SI, SIR, SEIR, SIR with births and deaths (or migration), SIRS, and SIR with vaccination. We use double frames to indicate a **stage** and a single frames for a **compartment** (Stock). A stage may contain one or several compartments in series and/or parallel.

1.4 The deterministic SIR model

We will now start with the classical SIR model and investigate how different assumptions about the sojourn time distribution in the *Infectious stage* will affect the epidemic. We will, therefore, model the I-stage by a single compartment (the classical, but absurd assumption that is still common in the literature). (Later on, when exploring Structural uncertainties (in Section 4) we will question this assumption by using several compartments for the I-stage.)

The S stage is just a container that has no defined sojourn time (without infection the susceptibles will remain there). The same is true for the R stage, which is just a counter for the Recovered individuals. In both cases they are to be modelled by a single compartment (Stock).

Exercise 1

Open **StochSD** and start by specifying the ***Time unit*** for your model. E.g. hour, day, week or month. **THEREAFTER, YOU HAVE TO BE CONSISTENT WITH YOUR CHOICE! (**For example, if you choose hours, then the sojourn time, T, becomes 4*24=96 hours.)

Build the classical SIR model in Figure 1. Let the population consist of N=S+I+R = 1001 individuals, where a single individual just has been infectious; i.e. S(0) = 1000, I(0) =1 and R(0) = 0. Set the proportion parameter, p = 0.0003, and the sojourn time constant T = 4 days.

Include a measure of the total epidemic defined as the number of Susceptibles that have got the disease when the epidemic is over; i.e. Epidemic=S(0)-S, where S *at the end of the simulation* will show the remaining individuals in Stage S.

Also, include a calculation of R_0 = S(0)*p*T using an Auxiliary.

To save a lot of execution time, set Length of simulation to a large number, but *include a termination rule* that promptly stops the execution as soon as *the Infectious stage becomes zero* (because then no more individuals can be infected). This is done by linking I to an auxiliary and use the IfThenElse(Test Condition, Value if True, Value if False) function:

IfThenElse([I] < 0.1, Stop(), 0).

However, the Stop() function acts instantaneously why we don't see the values of the last time-step. Therefore, we delay the information about I one time-step so that STOP() acts one time-step later by using the Delay([Primitive], Delay Length, Default Value) function. Thus, including Delay([I], DT(), 1) gives:

IfThenElse(Delay([I], DT(), 1) < 0.1, Stop(), 0)

Also create an Auxiliary named e.g. EndTime that only contains T() - DT() to see the termination time (readjusted one DT) of the epidemic recorded in a Number Box, see Figure 3.

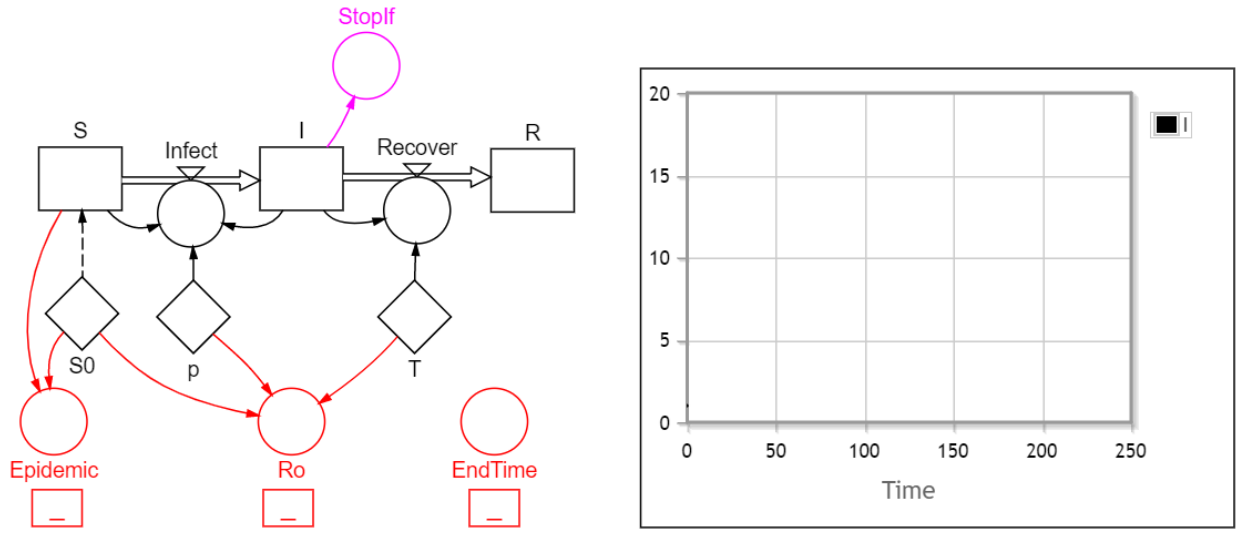


Figure 3. Your model should now look something like this. *Always try to make a proper model!*

Set DT=0.1 days and simulate the model. Fill in the results from the Classic SIR model in Table 1.

Table 1. Results from the deterministic SIR and the SI_3R models (rounded to nearest integer).

	Size of epidemic	**Time of epidemic**
Classic SIR model		

Save this deterministic SIR model as '**Det_SIR.ssd**'. ■

Exercise 2

Test the Threshold theorem that says that an epidemic cannot break out if $R_0 = p*T*S(0) < 1$.
This can be reformulated as: $S(0) < 1 /(p*T)$.
What is R_0 and what is the critical value of $S(0)$? **Answer:** R_0 = …… Critical $S(0)$ = ……
Now test this hypothesis by initiating $S(0)$ to *800*, *1000*, and *2000* individuals, respectively and simulate. What do you find? Fill in your results in Table 2.

Table 2. The classical SIR models for a Susceptible population of *800, 1000* and *2000* individuals.

S(0)	Size of epidemic	Size in per cent of the population
800		
1000		
2000		

Does the theory about R_0 agree with your findings from *the classical SIR* model?

Answer: ……

…….. ■

2. USE ALL KNOWLEDGE YOU HAVE ABOUT UNCERTAINTIES

2.1 Uncertainties and randomness

When we model a system under study, we can't know when and how many a radioactive atom decay, customers arrive to a shop, people get infected, or how the weather will develop, etc. This does NOT mean that the studied system behaves in a '*random*' way. It just means that we never have a complete understanding of the system. In modelling, such *uncertainties can be handled in two ways*:

1) Describe the uncertainties (about radioactive decays, arrivals, infections, weather, etc) in average terms. This approach will produce a *deterministic model* that always behaves exactly the same when executed. The downside of this approach is that you drop important information, and replacing omitting will often omit important aspects and produce biased results. (This was more thoroughly discussed and demonstrated in LAB-3.)
2) Collect statistical information about the uncertainty (for example, about the rate of radioactive decays, distribution of arrivals over the day or week arrivals, information about contagiousness and susceptibility, statistics about the weather, etc.). From knowledge or from many observations, you can create probability distributions for 0, 1, 2, 3 … decays, arrivals, infections, temperature, showers of rain, etc. From such a probability distribution, random numbers can be drawn during the execution of the model. We have then a *stochastic model* that will behave differently in each replication. Therefore, we run a stochastic model a large number of times in order to display a spectrum of possible outcomes, which we can analyse with statistical methods and present as: Averages, Standard deviations, Confidence intervals, Min values, max values, Percentiles (e.g. medians and quartiles). In StochSD the tool StatRes will do this for you!

To understand the importance of collecting and using statistical information about uncertainties instead of just using average values, regard the following example.

Example: A barber shop is open 8 hours a day, and the barber can do two customers per hour. The number of customers arriving at the barber shop are on average 16 per day. With a *deterministic model* you would conclude that everything is great. No queues are created and the barber will do 16 haircuts each day.

However, the real world is very different from this. Customers will arrive irregularly. Sometimes the shop is empty, and other times there is a considerable queue why several of the customers will balk. Also, 16 customers per day is just an average that seldom happens. Perhaps the barber will do on average 11 customers a day. Although, we don't know the exact timing of the arrivals, we may still have sufficient statistic information to include into the model to obtain good estimates. □

Stochastic modelling is mainly about including statistical information and to make multiple replications in order to obtain as good estimates as possible and also to estimate the size of uncertainty in these estimates.

2.2 Randomness *within a replication* and over *multiple replications*

It is important to understand that a stochastic model will produce stochastic outcomes that have to be analysed. Here we have to distinguish between:

A) Randomness *within a replication* (Internal statistics). Here the focus is on: The varying queue-length in the barbershop during a day, The varying number of infectious individuals during an epidemic, etc. This can be described in Time Plots, Tables etc., and you can perform a statistical analysis on the tabulated results. You can also use a Counter to sum up the number of customers or infected individuals during the replication. You can also build a so-called Tally to accumulate the busy time of the barber or the queuing time for the customers. Such statistics can be generated by elements and functions created *within the model* and will not be further discussed here.

B) Randomness *over multiple replications* (External statistics). In **StochSD** you can instruct the **StatRes** tool to collect '*end results*' from selected quantities at the end of each of *N* replications. (Note that these *end results* also can be average values, max values, values at specific events, etc. that are collected and calculated during the replication.) After the replications, **StatRes** will calculate and present statistical estimates in form of: *Averages, Standard deviations, Mins, Maxes, Confidence Intervals, Percentiles, etc*. over the *N* replications. These statistics are of two kinds:

B1) Estimates (named: **Avg** in StatRes) and Confidence Intervals (**Conf.Int(Avg)**) around the estimates. For example, *N* replications may give the estimate X=35.4 and the Confidence Interval of X to 33.2 – 37.6 (which also means X = 35.4 ± 2.2). The width of the Confidence Interval depends on what probability ('Confidence level') you want for the '*true value' of* X to *be within* the Confidence Interval. The width of the Confidence Interval will also be smaller if you make more replications, because you then get more information about the model's behaviour.

B2) Variations of the *outcomes* from *N* replications. Then you use Percentiles (**Percentile**). The Standard deviation, Min and Max give you such measures. If you want the interval containing 95 % of the outcomes, then you can remove the smallest 2.5 % of the outcomes and 2.5 % of the highest outcomes by setting the Percentile Box to 2.5 and 97.5, respectively, and read the results in the last column called

Percentile. (The default value for the Percentile box is 50, which means that the Median value is shown.)

EXTREMELY IMPORTANT: *Irrespectively if you deal with internal statistics (within a replication – see A, above) or external statistics (over N replications – see B1 and B2, above),* ***all statistics refer to THE MODEL – NOT TO THE SYSTEM UNDER STUDY!!!*** **That the model is trustworthy is still to be shown!**

2.3 Different types of uncertainties and how to implement them

Now, we will examine the different types of uncertainty and explain how they are to be implemented in a CSS model.

In System Dynamics modelling (e.g. StochSD), different types of uncertainties are associated with different building blocks: Transition uncertainty with a Flow, Initial Value uncertainty with a Stock, Environmental uncertainty with a Parameter, Signal uncertainty with a Link whose distortion or delay is described in an Auxiliary. However, Structural uncertainty refers to the structure of the entire model. See Figure 4.

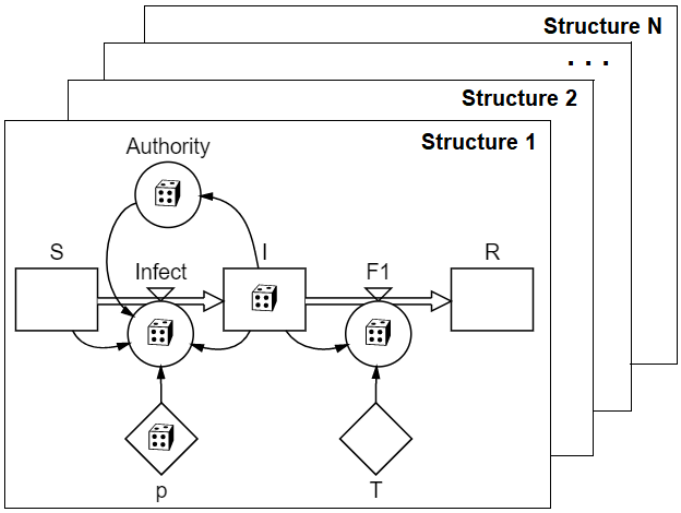


Figure 4. Stochastic uncertainties are handled by Transition stochasticity in Flows, Initial value stochasticity in Stocks, Environmental uncertainty in Parameters, Signal stochasticity of a Link described by an Auxiliary. Further, **Structural uncertainty** is handled by alternative model frameworks, Stage expansion and Attribute expansion.

3. STOCHASTIC UNCERTAINTIES

Stochastic uncertainties are uncertainties that can be handled by statistical means.

3.1 Transition uncertainty (The baseline model)

Transition stochasticity is associated with a Flow. If you know that *events* will happen randomly over time (e.g. customers will arrive randomly), then we have a Poisson process. The method to handle a Poisson process is to draw random numbers from a Poisson distribution that describes the *expected number of events during a time unit*, which we denote Po[x]. Since we prefer to update the model at each DT, the expression becomes Po[DT·x]. (That the x may vary over e.g. day or week is no problem, because the model will be updated in sufficiently small time-steps, DT.) And this argument, DT·x, is the same that is used in a deterministic model (without the Po[ ] surrounding it). Of technical reasons, the flow equation becomes: Flow = Poisson(DT*x)/DT], which in **StochSD** is represented by: Flow = PoFlow(x).

Exercise 3

Open your deterministic SIR model (**Det_SIR.ssd**), and start by saving it as: **Tr_Stoch_SIR.ssd** so you don't destroy your deterministic version. Keep the values of the deterministic model. In particular, check that S(0) is reset to 1000 individuals.

Then include *Transition stochasticity* in the two flows. The Infect flow will then be changed from p*S*I to PoFlow(p*S*I), and the Recover flow from I/T to PoFlow(I/T).

Now you will examine the stochastic model statistically. Set DT=0.1 days, and check that the Length is large enough so that it never will end until the epidemic is over.

Open StatRes, which you find under the Tools menu. Enter the quantities Epidemic and EndTime. Specify 1000 replication and press Run.

Fill in the results at row 2 in Table 3. (Also include the results from the deterministic model that you get from Table 1 at row 1.)

Table 3. Results from deterministic and stochastic SIR models after 1000 replications (rounded to nearest integer).

	MODEL TYPE	Size of epidemic (average and C.I.)	Max epidemic	Duration of epidemic (average and C.I.)
1	**Deterministic SIR model (1 simulation)**			
2	**Trans. stochastic SIR model (BASELINE)**			
3	**Trans. & Initial value stochastic SIR model**			
4	**Trans. & Environmental stochastic SIR model**			
5	**Trans. & Signal stochastic SIR model**			

Now, save your stochastic model (already named).

In the following, we will regard the SIR with only transition stochasticity as our **baseline model** to which we will add other kinds of uncertainties. ■

Some features of StatRes

StatRes also have some other useful facilities. We will here try the *Histogram* and the *Scatter plot* facilities.

Exercise 4

Now we will try some features of StatRes on the performed 1000 replications. First, to see the distribution of the epidemics of different sizes, check the box before the name Epidemic and click the **Histogram** button. This will probably show that the vast majority of the 1000 replications ends with few cases. To see the interesting part better set the 'Lowest' limit to e.g. 30, and the 'Highest' limit to 600, and 'No. bars' to 19 (so that you get a nice width of 30 for the bars).

The bars (including the cut-away bar whose value is given in the 'Below' field) shows that the histogram is composed of two parts. A left part of *an almost exponential decline* and a right part of *a hill*. The left part includes those replications where the epidemic gets extinct because of the Infectious recovering before the epidemic 'gained momentum'. *This very real possibility could not happen for the deterministic model*.

Is there a correlation between the size of the epidemic and its duration? To answer this question, check both Epidemic and EndTime, and click the **Scatter Plot** button. What do you see?

Answer: ……..… ■

3.2 Initial Value uncertainty

Initial Value uncertainty is associated with a Stock. The epidemic is initiated by one or several Infectious individuals that bring the disease to the studied population, perhaps after a vacation abroad. However, we will assume that the number of returning Infectious individuals range from 0 to 2, according to an *integer, uniform distribution* (keeping the *average number equal to 1* in order to be compatible with the model used above.) In plain English, The I-compartment will be initiated as 0, 1 or 2 with the same probability.

Exercise 5

Open the **Tr_Stoch_SIR.ssd** model and save a copy of it as as: **Tr_IV_Stoch_SIR.ssd**.

Thus, keep the Transition stochasticities and add *Initial Value stochasticity* to the initial value of I, see Figure 3, above. Now I(0) should have the same probability for 0, 1, or 2 Infectious individuals at Time zero.

One way to do this is by drawing uniformly distributed random numbers between 0 and 3 (actually: 0 < Random Number < 3, so that exact 0 or 3 cannot turn up), which is done by: Rand(0, 3). Then this number is rounded down to its nearest integer (0, 1 or 2) by the Floor() function, giving Floor(Rand(0, 3)).

Repeat the **StatRes** study with 1000 new replications and fill at the appropriate row in Table 3, above.

Did the average size of the epidemic increase or decrease? **Answer:** …….

Did the Standard Deviation of the epidemic increase or decrease? **Answer:** ……..

Save the model. ■

3.3 Environmental uncertainty

Environmental uncertainty is associated with a Parameter. Parameter values (of e.g. wind speed, arrival rate, blood pressure, fertility, currency exchange rate) may change overtime - regularly or unexplained. When we can't foresee these variations, we may have statistics showing:

1) *How frequently the changes occur*. This is in StochSD handled by the function: Fix(Parameter value, Period between changes), where the Parameter value is a random function.

2) *How the changes are statistically distributed*. (Often you then have to use an *empiric distribution*. In StochSD you then use a table-look-up function, which in StochSD is called a Converter.)

Environmental uncertainty has no specific form (like PoFlow(argument) in Transition stochasticity), why you have to model it in accordance with your knowledge about the environmental uncertainty.

Exercise 6

Open the baseline model **Tr_Stoch_SIR.ssd** and save a copy of it as: **Tr_Env_Stoch_SIR.ssd**.

In the SIR model, we assume that the parameter p (which includes the contagiousness and the behaviour of the population) *changes each fifth day*, and that the changes have a *triangular distribution* according ranging from 0.0001 to 0.0005 with the peak frequency value of the distribution at 0.0003. See Figure 5.

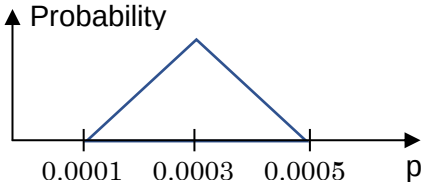


Figure 5. The triangular distribution of the parameter p. (The probability density function (p.d.f.) is completely defined because the area under a p.d.f. is the total probability = 1.)

In StochSD you use the function: RandTriangular(Min_value, Max_value, Peak_ value).

Thus: change p = 0.0003 to p = Fix(RandTriangular(0.0001, 0.0005, 0.0003), 5), where the last parameter of Fix is 5, because Fix then holds the value for 5 days at a time.

Repeat the **StatRes** study with 1000 new replications and fill in the appropriate row in Table 3, above.

Did the average size of the epidemic increase or decrease compared to the BASELINE in Table 3?

Answer: ……

Did the Standard Deviation of the epidemic increase or decrease compared to the BASELINE?

Answer: ……

Save the model. ■

3.4 Signal uncertainty

Signal uncertainty is associated with a Link described by an Auxiliary. Signals are information between different parts of a model. A signal can be both distorted and delayed. Signal uncertainty can include both uncertainty about how the information is handled and uncertainty of how long it takes to collect, analyse and distribute the information.

Exercise 7

Again, open the baseline model **Tr_Stoch_SIR.ssd** and save a copy of it as: **Tr_Signal_Stoch_SIR.ssd**.

Now, we will also include Signal stochasticity into the model. Therefore, we assume that there is an Authority whose behaviour is described by an Auxiliary with this name. The Authority observes the number of Infectious, I. When the I-stage, contains more than 30 individuals, the Authority will issue recommendations to '*wash your hands and avoid visiting sick people'*, which reduces the infectiousness between 20 and 50 per cent according to a uniform distribution. I.e. it affects the infection rate, Infect, by a factor of 1-0.2 = 0.8 to 1-0.5 = 0.5, uniformly distributed as: Rand(0.5, 0.8). Thus, first make an Auxiliary named Authority that is defined as: IfThenElse([I] > 30, Rand(0.5, 0.8), 1). The very last argument is the factor 1 that doesn't change the Infect rate when I ≤ 30.

However, since it takes two days to analyse and deliver the information, we also include a static delay of two days. This means that [I] > 30 is to be replaced by Delay([I], 2) > 30. This gives:
Authority = IfThenElse(Delay([I], 2) > 30, Rand(0.5, 0.8), 1).

The Authority, must of course have a Link from the number of Infectious, I, to the Authority, and another link must go from the Authority to Infect. (This closed loop includes more dynamics to the model. For example, information about the number of Infectious, I, delayed by two days could, in principle, generate oscillations.) How the Authority is linked in is seen in Figure 4, above.

Repeat the **StatRes** study with 1000 new replications and fill in the appropriate row in Table 3, above.

Did the average size of the epidemic increase or decrease compared to the BASELINE?

Answer: ……

Did the Standard Deviation of the epidemic increase or decrease compared to the BASELINE?

Answer: ……

Save the model. ■

4. STRUCTURAL UNCERTAINTY

Structural uncertainty refers to the structure of the model. There are three aspects of it:

a. Framework uncertainty (Layout of stages and flows)
Uncertainty about the structure and mechanisms of the system under study implies uncertainty about how to structure the model. For an epidemic model study, it is not trivial to find a proper model structure. Already within the SIR family you will find a large number of structures such as SI, SIR, SEIR where the disease is subdivided in different number of stages, or SEIRS and SIR with vaccination where flows are included from R to S and from S to R, respectively. See Figure 2, above.

b. Stage expansion (Stage-to-Compartments expansion)
This is about creating a realistic sojourn time distribution. A stage represented by a single compartment will produce an exponential sojourn time, which works to describe e.g. a radioactive decay process, but not for describing the duration of a child stage or a sickness stage. In the general case, a stage has to be modelled by a structure of compartments in series and/or parallel. Here we will only study the case where the I-stage is represented by *three* serial compartments. We will denote this model SI_3R.

Attribute expansion (Requires coupled sub-models for each combination of attributes)
In modelling the *attributes* may play an important role for the behaviour of an individual. Therefore, it may be important to describe individuals differently (often with only different parameter values, but sometimes also with different substructures). For example, important attributes may be *age* (e.g. Child, Adult, Old) or *sex* (Male, Female) or *smoking habit* (Smoker, Non-smoker).

In CSS models (where the individuals are reduced to *numbers* contained in different compartments) the compartment can only hold individuals with the same *combination* of attributes. For example, Adult-Male-Smoker. In this example we therefore need $3\times2\times2=12$ instances of the compartment to hold all possible combinations. For a very heterogeneous population (many necessary attributes) the model can be huge, and the amount of data needed may be gigantic. Below, we will only include the attribute *sex* (Male, Female).

The effect of **structural uncertainties** can be studied by investigating how well candidate models works for explaining e.g. a real epidemic.

4.1 Framework uncertainty – SIR or SEIR model?

Now assume that we are uncertain about whether an infected person almost immediately becomes infectious (SIR) or if it takes an incubation period before the individual becomes infectious (SEIR where E stands for exposed -but not jet contagious). Therefore, you will now investigate the effects of a SEIR model, where we include an Exposed E-stage.

Exercise 8

Open the baseline model **Tr_Stoch_SIR.ssd** and save a copy of it as: **Tr_Stoch_SEIR.ssd**.

Include The E-stage as a single compartment according to Figure 6. The e-stage has an average sojourn time $T_e = 3$ days. (We have here also renamed the sojourn time for the I-stage to T_i of cosmetic reasons.)

Note that the StopIf criterion now is that *both* E and I are empty for the epidemic to be over.

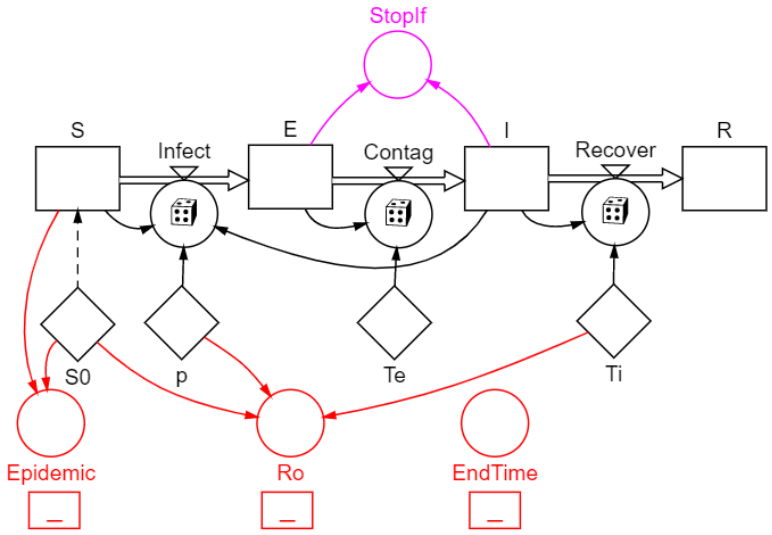


Figure 6. An epidemic SEIR model where an exposed E-stage is included.

Repeat the **StatRes** study with 1000 new replications and fill in row 2 in Table 4, below.

Also, include the *baseline results* from **Tr_Stoch_SIR.ssd**, which you find in Table 3, above.

Table 4. Results from structural uncertainties after 1000 replications (rounded to nearest integer).

	MODEL TYPE	Size of epidemic (average and C.I.)	Max epidemic	Duration of epidemic (average and C.I.)
1	**Trans. stochastic SIR model (BASELINE)**			
2	**Transition stochastic SIER model**			
3	**Transition stochastic SI_3R model**			
4	**Transition stochastic 2SIR model**			

Did the average size of the epidemic increase or decrease compared to baseline?

Answer: ……

Did the duration of the epidemic increase or decrease compared to baseline?

Answer: ……

Save the model. ■

4.2 Stage expansion of the SIR model – a SI_3R model?

A single compartment to describe the Infectious stage means that the sojourn time is exponentially distributed; i.e. that the most probable duration in the Infectious stage is almost zero but with a very small probability of a very long duration. Real diseases don't have such a distribution. A more realistic description is that most Infectious individuals will have a duration that is closer to the sojourn time, *T*, and only a few will have a considerably smaller

or larger duration. To achieve this, we now model the Infectious stage by three serial compartments.

Exercise 9

Open the baseline model **Tr_Stoch_SIR.ssd** and save a copy of it as: **Tr_Stoch_SI3R.ssd**.

Use a copy of the SIR model and reconstruct it to a SI_3R model; i.e. the *I-stage* should now have three serial compartments named I1, I2 and I3, where I1=1, I2=0 and I3=0. Also include an auxiliary I=I1+I2+I3 that sums up the total content of the I-stage. See Figure 7.

To keep the value of the sojourn time, T, in the Infectious stage (I1+I2+I3) the same, you have to divide the old T value by 3.

Important: A time-step must be significantly shorter that the smallest time constant in the model. The shortest time constant in the SIR model was T, but in SI_3R it was T/3, which somewhat may affect the results. So, reduce DT by at least a factor 3; e.g. use DT=0.025.

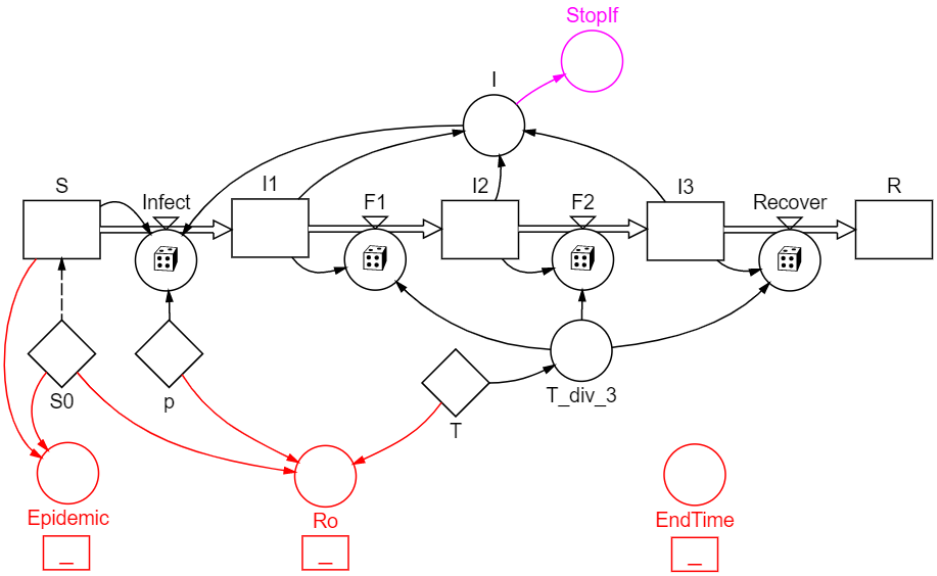


Figure 7. A stochastic SI_3R model. Here the I-stages is composed by three serial Stocks I1, I2 and I3 summed up to I=I1+I2+I3.

Make a simulation and fill in the SI_3R result at row 3 in Table 4, above. What did you find out about Epidemic and EndTime?

Answer: ……

……

Save this model. ■

4.3 Attribute expansion of the SIR model

Attributes are simple to handle in *micro modelling*. However, in *macro modelling* the aggregation of individuals in stages/compartments with the same attributes requires a sub-model for each *combination of attributes*, and an often-tricky coupling between these sub-models. This makes a CSS model both large and complicated for many attributes to consider.

Micro models grow (particularly in execution time) with the number of entities (e.g. individuals), while macro models grow (in size and execution time) with the number of attribute combinations. Therefore, if many attributes are *necessary* in your conceptual model and the 'population' is not to large, you might consider to use a micro model.

Exercise 10

In this exercise you will investigate the epidemic SIR model with the attribute: Sex {male, Female}, where we assume that the males (indexed by 'm') are more vulnerable to the disease (larger p) and have a longer sojourn time as infectious (larger T) than the females (indexed 'f).

Open the baseline model **Tr_Stoch_SIR.ssd** and save a copy of it as: **Tr_Stoch_2SIR.ssd**.

Use the copy of the SIR model and double it so that you have one sub-model for the males and one for the females, see Figure 8.

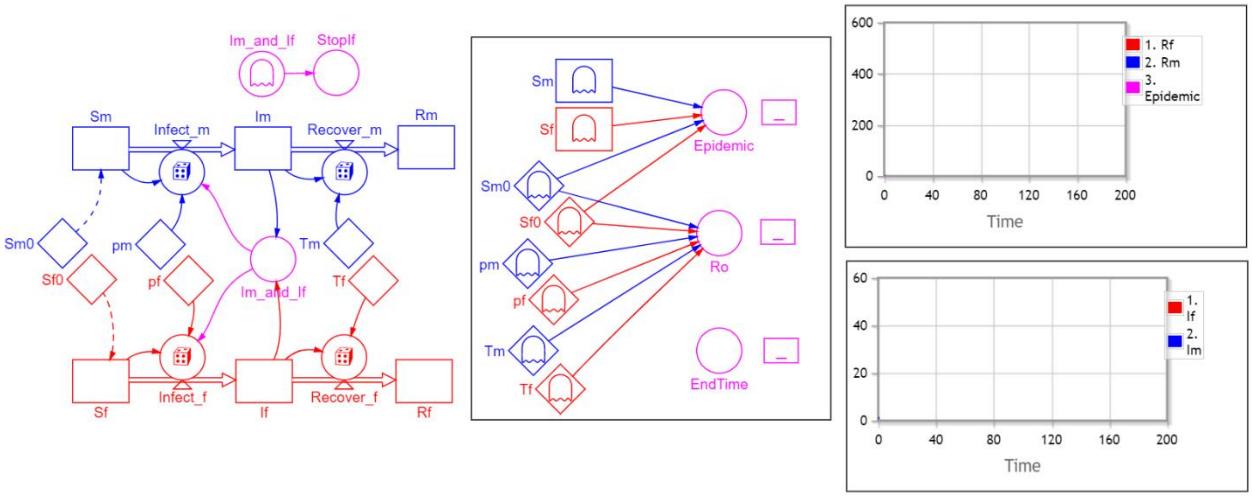


Figure 8. Attribute expansion. The SIR model with the attribute *sex* (Male, female).

Since males are infecting both males and females and females also are infecting both males and females, it is necessary to couple the infection mechanism (p·S·I) between the sexes. Therefore, include an Auxiliary named Im_and_If defined as: Im+If that represent the total number of infectious individuals. The infectious mechanisms then become:

Infect_m = PoFlow(pm*Sm*Im_and_If) and Infect_f = PoFlow(pf*Sf*Im_and_If), see Figure 8.

We still want the population size be the same and to start with a single infected person. Thus, set:

Sm(0) = Sf(0) = 500, Im=1 & If=0.

Further, to keep the *average values* for males + females (p=0.0003 and T=4 days) we assume:

pm = 0.0004 & pf = 0.0002, and Tm = 5 & Tf = 3 days.

Also note that the breaking criterium StopIf must check that Im_and_If < 0.5.

To avoid messing up the model with a number of crossing links – use Ghosts to calculate Epidemic, Ro and EndTime, as in Figure 8.

Repeat the **StatRes** study with 1000 new replications and fill in the results at row 4 in Table 4, above.

Also make a few simulations until you get a significant epidemic, and sketch the behaviours in the diagrams of Figure 8.

What did you find out about how the epidemic hits males and females?

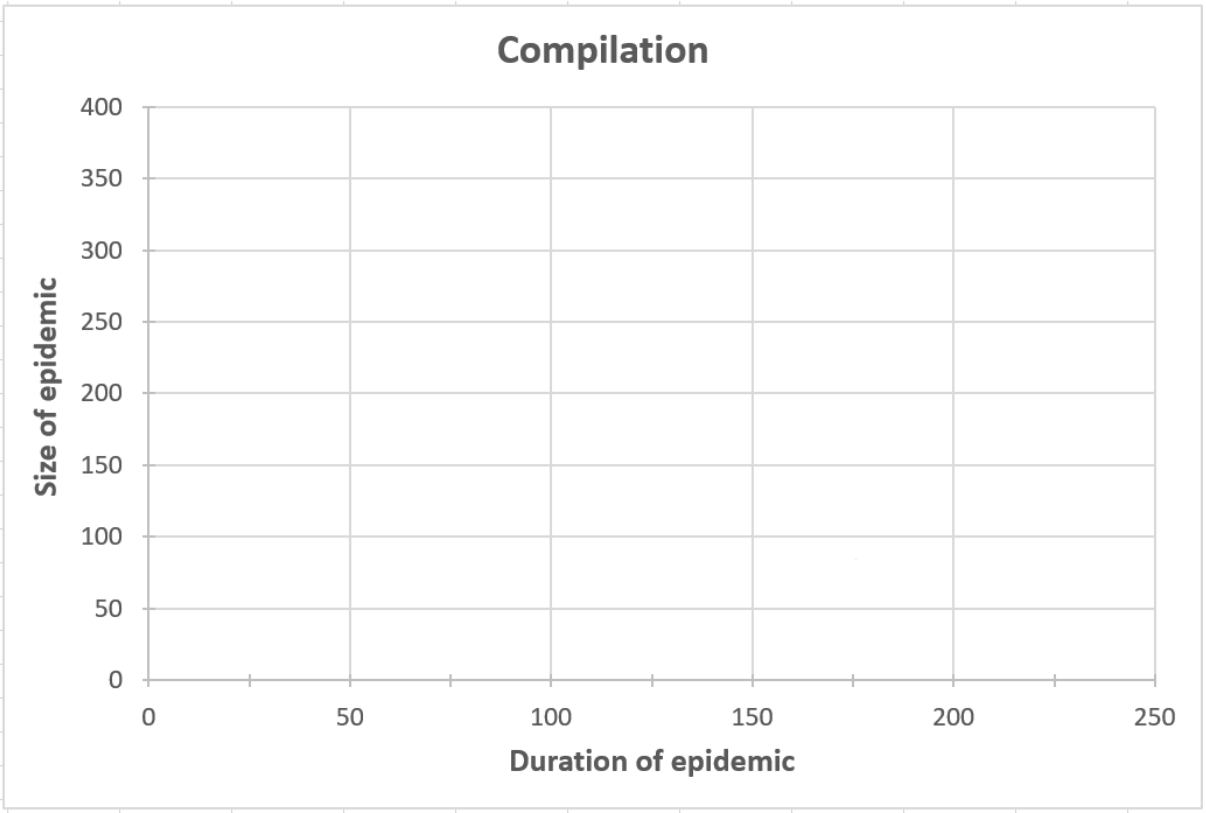
Answer: ……

……

Save this model. ■

5. Compilation of results

Finally, compile the results from Tables 3 and 4 with respect to (Size, Duration) of the epidemic in the diagram, below. Also mark the eight dots with: Det_SIR, Tr_SIR, Tr_IV_SIR, Tr_Env_SIR, Signal_SIR, Tr_SEIR, Tr_SI_3R and 2SIR, respectively.



Comment: …….

……..……...

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