

Implementing System Dynamics

A pure functional correct-by-construction approach in Haskell

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TODO: select journals - ACM Transactions on Modeling and Computer Simulation (TOMACS): <https://tomacs.acm.org/>
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In this short paper we investigate how to implement System Dynamics in the functional programming language Haskell. We use the concept of Functional Reactive Programming which allows to express continuous- and discrete-time systems in a functional way. We show that System Dynamics map very natural to Functional Reactive Programming. Together with Haskell's strong static type system, we arrive at a correct-by-construction implementation which deterministic reproducibility we can guarantee at compile-time.

Additional Key Words and Phrases: System Dynamics, Functional Reactive Programming, Haskell

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1 INTRODUCTION

There exists a large number of simulation packages which allow the convenient creation of System Dynamics simulations by straight-forward visual diagram creation. One simply creates stocks and flows, connects them, specifies the flow-rates and initial parameters and then runs them. An example for such a visual diagram creation in the simulation package AnyLogic can be seen in Figure 1.

The aim of this paper is to look into how System Dynamics can be implemented in raw code without the use of a simulation package. Our language of choice is Haskell because TODO.

We use the well known SIR model [2] from epidemiology to demonstrate our approach.

The contribution of the paper is the demonstration of how a correct-by-construction System Dynamics simulation can be implemented using Haskell.

2 RELATED WORK

TODO: is there some?

3 SIR MODEL

We introduce the SIR model as a motivating example and use-case for our implementation. It is a very well studied and understood compartment model from epidemiology [2] which allows to simulate the dynamics of an infectious disease like influenza, tuberculosis, chicken pox, rubella and measles [1] spreading through a population. In this model, people in a population of size N can be in either one of three states *Susceptible*, *Infected* or *Recovered* at a particular time, where it is assumed that initially there is at least one infected person in the population. People interact *on average* with a given rate of β other people per time-unit and become infected with a given probability γ when interacting with an infected person. When infected, a person recovers *on average* after δ time-units and is then immune to further infections. An interaction between infected persons does not lead to

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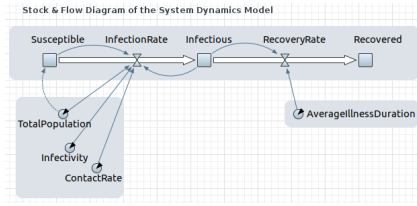


Fig. 1. Visual System Dynamics Diagram in AnyLogic Personal Learning Edition 8.3.1.



Fig. 2. States and transitions in the SIR compartment model.

re-infection, thus these interactions are ignored in this model. This definition gives rise to three compartments with the transitions as seen in Figure 2.

Before looking into how one can simulate this model in an agent-based approach we first explain how to formalize it using System Dynamics (SD) [3]. In SD one models a system through differential equations, allowing to conveniently express continuous systems which change over time. The advantage of a SD solution is that one has an analytically tractable solution against which e.g. agent-based solutions can be validated. The problem is that the more complex a system, the more difficult it is to derive differential equations describing the global system, to a point where it simply becomes impossible. This is the strength of an agent-based approach over SD, which allows to model a system when only the constituting parts and their interactions are known but not the macro behaviour of the whole system. As will be shown later, the agent-based approach exhibits further benefits over SD.

The dynamics of the SIR model can be formalized in SD with the following equations:

TODO: there seems to be an unnerving space after the f letters, can we get rid of them?

$$\frac{dS}{dt} = -infectionRate \quad (1)$$

$$\frac{dI}{dt} = infectionRate - recoveryRate \quad (2)$$

$$\frac{dR}{dt} = recoveryRate \quad (3)$$

$$infectionRate = \frac{I\beta S\gamma}{N} \quad (4)$$

$$recoveryRate = \frac{I}{\delta} \quad (5)$$

Solving these equations is done by integrating over time. In the SD terminology, the integrals are called *Stocks* and the values over which is integrated over time are called *Flows*. At $t = 0$ a single agent is infected because if there wouldn't be any infected agents, the system would immediately reach equilibrium - this is also the formal definition of the steady state of the system: as soon as $I(t) = 0$ the system won't change any more.

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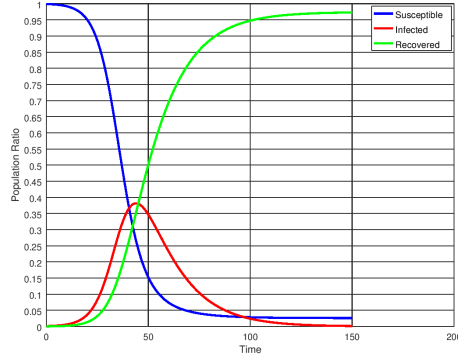


Fig. 3. Dynamics of the SIR compartment model. Population Size $N = 1,000$, contact rate $\beta = \frac{1}{5}$, infection probability $\gamma = 0.05$, illness duration $\delta = 15$ with initially 1 infected agent. Simulation run for 150 time-steps.

$$S(t) = N - I(0) + \int_0^t -infectionRate \, dt \quad (6)$$

$$I(0) = 1 \quad (7)$$

$$I(t) = \int_0^t infectionRate - recoveryRate \, dt \quad (8)$$

$$R(t) = \int_0^t recoveryRate \, dt \quad (9)$$

Running the SD simulation over time results in the dynamics as shown in Figure 3 with the given variables.

4 A CORRECT-BY-CONSTRUCTION IMPLEMENTATION

In this section we develop a correct-by-construction implementation step-by-step¹.

The constant parameters *populationSize*, *infectedCount*, *contactRate*, *infectivity*, *illnessDuration* are defined globally and omitted for clarity.

```
type SIRStep = (Time, Double, Double, Double)

sir :: SF () SIRStep
sir = loopPre (0, initSus, initInf, initRec) sirFeedback
  where
    initSus = populationSize - infectedCount
    initInf = infectedCount
    initRec = 0

    sirFeedback :: SF ((), SIRStep) (SIRStep, SIRStep)
    sirFeedback = proc (_, (_, s, i, _)) -> do
      let infectionRate = (i * contactRate * s * infectivity) / populationSize
          recoveryRate = i / illnessDuration

      t <- time -< ()
```

¹The whole code, including visualisation and exporter to Matlab, is freely available on the Git Repository <https://github.com/thalerjonathan/phd/tree/master/public/sdhaskell/SIR>

```

148
149   s' <- (initSus+) ^<< integral -< (-infectionRate)
150   i' <- (initInf+) ^<< integral -< (infectionRate - recoveryRate)
151   r' <- (initRec+) ^<< integral -< recoveryRate
152
153   returnA -< dupe (t, s', i', r')
154
155   dupe :: a -> (a, a)
156   dupe a = (a, a)
157
158   runSD :: Time -> DTime -> [SIRStep]
159   runSD t dt = embed sir ((), steps)
160   where
161     steps = replicate (floor (t / dt)) (dt, Nothing)

```

5 DISCUSSION

TODO: argue why it is correct-by-construction, why reproducible guaranteed at compile-time,... support our initial hypothesis and claims from introduction

6 CONCLUSION

TODO: wow its so super

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REFERENCES

- [1] Richard H. Enns. 2010. *It's a Nonlinear World* (1st ed.). Springer Publishing Company, Incorporated.
- [2] W. O. Kermack and A. G. McKendrick. 1927. A Contribution to the Mathematical Theory of Epidemics. *Proceedings of the Royal Society of London A: Mathematical, Physical and Engineering Sciences* 115, 772 (Aug. 1927), 700–721. <https://doi.org/10.1098/rspa.1927.0118>
- [3] Donald E. Porter. 1962. Industrial Dynamics. Jay Forrester. M.I.T. Press, Cambridge, Mass.; Wiley, New York, 1961. xv + 464 pp. Illus. \$18. *Science* 135, 3502 (Feb. 1962), 426–427. <https://doi.org/10.1126/science.135.3502.426-a>

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