# Epidemiology Compartmental Modeling Monad Demo

## Version 0.4

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## Introduction

This preliminary notebook aims at giving short, actionable overview of a software monad for rapid specification of Epidemiology Compartmental Modeling (ECM) workflows. Monad's name is "ECMMon", which stands for "**E**pidemiology **C**ompartmental **M**odeling **Mon**ad".

The software monad `ECMMon` is implemented in [AAp6], which relies on [AAp1-AAp4]. The original workflow discussed in [AA4] was implemented in [AAp5].

We use real-life data, The New York Times COVID-19 data, see [NYT1, AA5].

## Load packages

```
In[75]:=   Import["https://raw.githubusercontent.com/antononcube/SystemModeling/master/Projects/Coronavirus-propagation-dynamics/WL/MonadicEpidemiologyCompartmentalModeling.m"];
           Import["https://raw.githubusercontent.com/antononcube/SystemModeling/master/Projects/Coronavirus-propagation-dynamics/WL/MultiSiteModelSimulation.m"]
```

» Importing from GitHub: `HextileBins.m`

» Importing from GitHub: `EpidemiologyModels.m`

» Importing from GitHub: `EpidemiologyModelModifications.m`

» Importing from GitHub: `EpidemiologyModelingSimulationFunctions.m`

» Importing from GitHub: `EpidemiologyModelingSimulationFunctions.m`

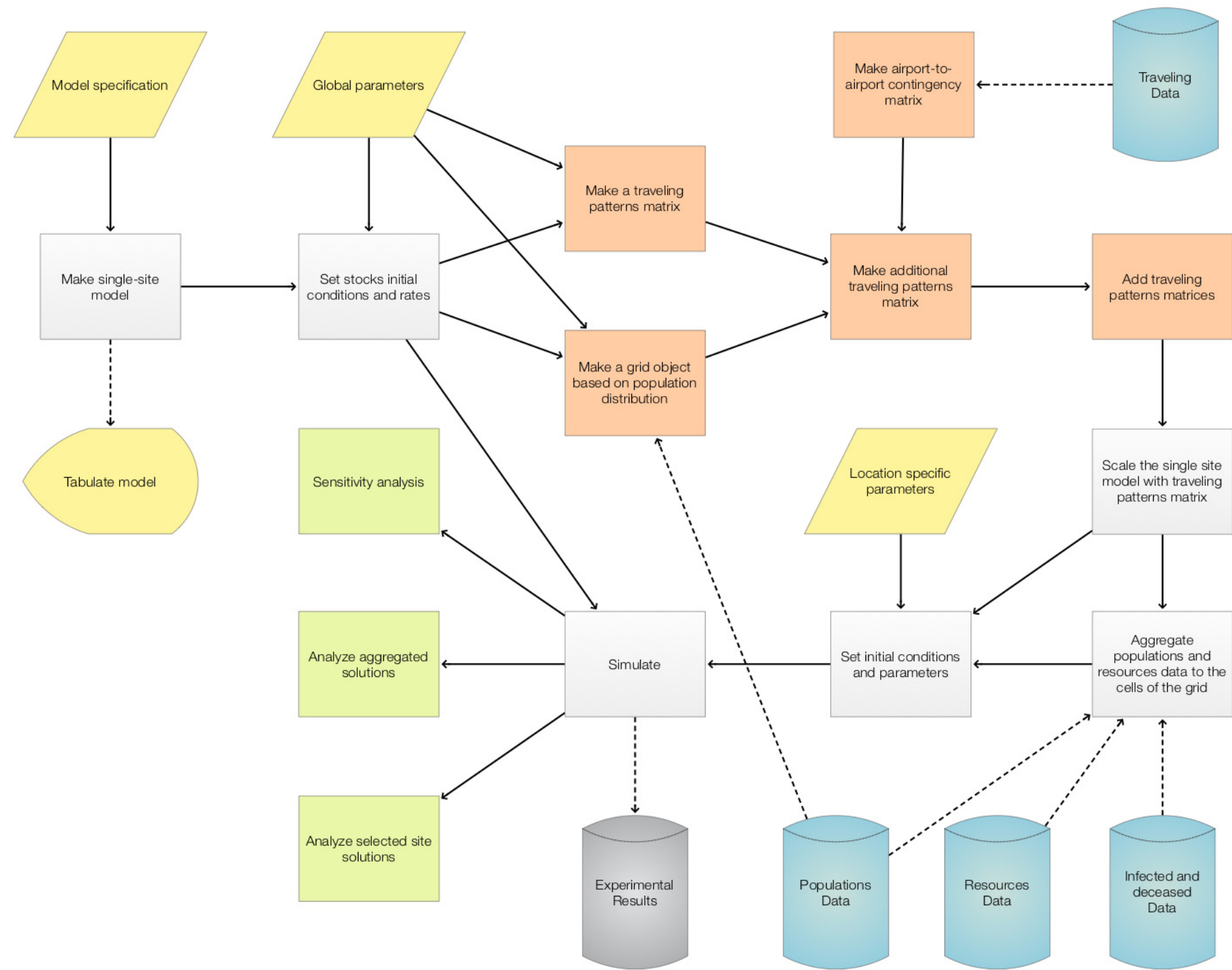» Importing from GitHub: `SystemDynamicsInteractiveInterfacesFunctions.m`

## Ingest data

## General design

### Flow-chart

The following flow-chart visualizes the workflows given below:

```
Import["https://github.com/antononcube/SystemModeling/raw/master/Projects/Coronavirus-propagation-dynamics/ECMMon-workflow.jpeg"]
```



## Two models in the monad

- An ECMMon object can have one or two models. One of the models is a "seed", single-site model from [AAp1], which, if desired, is scaled into a multi-site model, [AA3, AAp2].
- Workflows with only the single-site model are supported.
    - Say, workflows for doing sensitivity analysis, [AA6, BC1].

- Scaling of a single-site model into multi-site is supported and facilitated.

- Workflows for the multi-site model include preliminary model scaling steps and simulation steps.

- After the single-site model is scaled the monad functions use the multi-site model.

- The workflows should be easy to specify and read.

## Single-site model workflow

1. Make a single-site model.

2. Assign stocks initial conditions.

3. Assign rates values.

4. Simulate.

5. Plot results.

6. Go to 2.

## Multi-site model workflow

1. Make a single-site model.

2. Assign initial conditions and rates.

3. Scale the single-site model into a multi-site model.

   3.1. The single-site assigned rates become "global" when the single-site model is scaled.

   3.2. The scaling is based on assumptions for traveling patterns of the populations.

   3.3. There are few alternatives for that scaling:

      3.3.1. Using locations geo-coordinates

      3.3.2. Using regular grids covering a certain area based on in-habited locations geo-coordinates

      3.3.3. Using traveling patterns contingency matrices

      3.3.4. Using "artificial" patterns of certain regular types for qualitative analysis purposes

4. Enhance the multi-site traveling patterns matrix and re-scale the single site model.

   4.1. We might want to combine traveling patterns by ground transportation with traveling patterns by airplanes.

   4.2. For quarantine scenarios this might a less important capability of the monad.

      4.2.1. Hence, this an optional step.

5. Assign stocks initial conditions for each of the sites in multi-scale model.

6. Assign rates for each of the sites.

7. Simulate.

8. Plot global simulation results.

9. Plot simulation results for focus sites.

# Single-site workflow demo

In this section we demonstrate some of the sensitivity analysis discussed in [AA6, BC1].
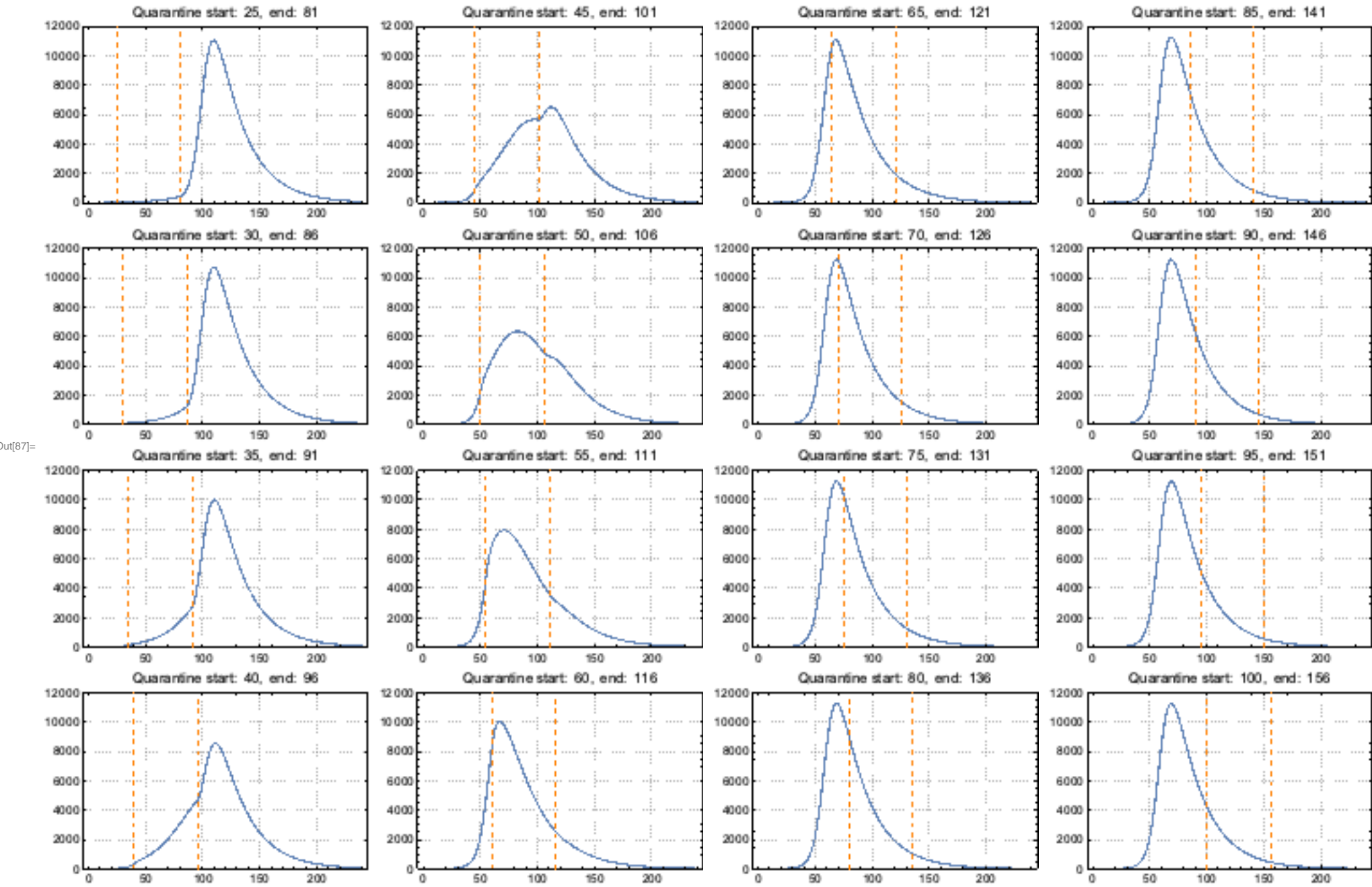
Make a single-site model:

```
In[84]:= model1 = SEI2HREconModel[t, "InitialConditions" → True, "RateRules" → True, "TotalPopulationRepresentation" → "AlgebraicEquation"];
```

Execute the workflow multiple times with different quarantine starts:

```
In[85]:= qlVar = 56;
lsRes =
  Map[
   ECMMonUnit[] ⟹
     ECMMonSetSingleSiteModel[model1] ⟹
     ECMMonAssignRateRules[
       <|
        aip → 26,
        aincp → 5,
        β[ISSP] → 0.5 * Piecewise[{{1, t < qsd}, {qcrf, qsd ≤ t ≤ qsd + ql}}, 1],
        β[INSP] → 0.5 * Piecewise[{{1, t < qsd}, {qcrf, qsd ≤ t ≤ qsd + ql}}, 1],
        qsd → #,
        ql → qlVar,
        qcrf → 0.25,
        β[HP] → 0.01,
        μ[ISSP] → 0.035 / aip,
        μ[INSP] → 0.01 / aip,
        nhbr[TP] → 3 / 1000,
        lpcr[ISSP, INSP] → 1,
        hscr[ISSP, INSP] → 1
        |>
      ] ⟹
     ECMMonSimulate[365] ⟹
     ECMMonPlotSolutions[{"Infected Severely Symptomatic Population"}, 240, "Together" → True, "Derivatives" → False,
       PlotRange → {0, 12 000}, ImageSize → 250,
       Epilog → {Orange, Dashed, Line[{{#, 0}, {#, 12 000}}], Line[{{# + qlVar, 0}, {# + qlVar, 12 000}}]},
       PlotLabel → Row[{"Quarantine start:", Spacer[5], #, ",", Spacer[5], "end:", Spacer[5], # + qlVar}],
       "Echo" → False] ⟹
     ECMMonTakeValue &, Range[25, 100, 5]];
```

Plot the simulation solutions for "Infected Severely Symptomatic Population":

In[87]:= `Multicolumn[#[[1, 1]] & /@ lsRes, 4]`

Out[87]=



## Multi-site workflow demo

Here we specify a multi-site model workflow over USA data, [WRI2, NYT1].

In[88]:= `model1 = SEI2HRModel[t, "InitialConditions" → True, "RateRules" → True, "TotalPopulationRepresentation" → "AlgebraicEquation"];`

```
In[89]:= ecmObj =
    ECMMonUnit[] ⟹
     ECMMonSetSingleSiteModel[model1] ⟹
     ECMMonAssignRateRules[
      <|
       aip → 26,
       aincp → 5,
       β[ISSP] → 0.5 * Piecewise[{{1, t < qsd}, {qcrf, qsd ≤ t ≤ qsd + ql}}, 1],
       β[INSP] → 0.5 * Piecewise[{{1, t < qsd}, {qcrf, qsd ≤ t ≤ qsd + ql}}, 1],
       qsd → 0,
       ql → 56,
       qcrf → 0.25,
       β[HP] → 0.01,
       μ[ISSP] → 0.035 / aip,
       μ[INSP] → 0.01 / aip,
       nhbr[TP] → 3 / 1000,
       lpcr[ISSP, INSP] → 1,
       hscr[ISSP, INSP] → 1
       |>
      ] ⟹
     ECMMonEcho[Style["Show the single-site model tabulated form:", Bold, Purple]] ⟹
     ECMMonEchoFunctionContext[Magnify[ModelGridTableForm[#singleSiteModel], 0.6] &] ⟹
     ECMMonMakeHexagonalGrid[Keys[aPopulations], 2.5] ⟹
     ECMMonEcho[Style["Show the grid based on population coordinates:", Bold, Purple]] ⟹
     ECMMonPlotGrid["CellIDs" → True, ImageSize → Large] ⟹
     ECMMonExtendByGrid[aPopulations, 0.12] ⟹
     ECMMonAssignInitialConditions[aPopulations, "Total Population", "Default" → 0] ⟹
     ECMMonAssignInitialConditions[DeriveSusceptiblePopulation[aPopulations, aInfected, aDead], "Susceptible Population", "Default" → 0] ⟹
     ECMMonAssignInitialConditions[<||>, "Exposed Population", "Default" → 0] ⟹
     ECMMonAssignInitialConditions[aInfected, "Infected Normally Symptomatic Population", "Default" → 0] ⟹
     ECMMonAssignInitialConditions[<||>, "Infected Severely Symptomatic Population", "Default" → 0] ⟹
     ECMMonEcho[Style["Show total populations initial conditions data:", Bold, Purple]] ⟹
     ECMMonPlotGridHistogram[aPopulations, ImageSize → Large, PlotLabel → "Total populations"] ⟹
     ECMMonEcho[Style["Show infected and deceased initial conditions data:", Bold, Purple]] ⟹
     ECMMonPlotGridHistogram[aInfected, ColorFunction → ColorData["RoseColors"], "ShowDataPoints" → False, ImageSize → Large, PlotLabel → "Infected"] ⟹
     ECMMonPlotGridHistogram[aDead, ColorFunction → ColorData["RoseColors"], "ShowDataPoints" → False, ImageSize → Large, PlotLabel → "Deceased"] ⟹
     ECMMonEcho[Style["Simulate:", Bold, Purple]] ⟹
     ECMMonSimulate[365] ⟹
     ECMMonEcho[Style["Show global population simulation results:", Bold, Purple]] ⟹
     ECMMonPlotSolutions[__ ~~ "Population", 365] ⟹
     ECMMonEcho[Style["Show site simulation results for Miami and New York areas:", Bold, Purple]] ⟹
     ECMMonPlotSiteSolutions[{160, 174}, __ ~~ "Population", 365] ⟹
     ECMMonEcho[Style["Show deceased and hospitalzed populations results for Miami and New York areas:", Bold, Purple]] ⟹
     ECMMonPlotSiteSolutions[{160, 174}, {"Deceased Infected Population", "Hospitalized Population", "Hospital Beds"}, 300, "FocusTime" → 120];
```

» **Show the single-site model tabulated form:**

» ⟨ Stocks →

| # | Symbol | Description |
|---|--------|-------------|
| 1 | TP[t] | Total Population |
| 2 | SP[t] | Susceptible Population |
| 3 | EP[t] | Exposed Population |
| 4 | INSP[t] | Infected Normally Symptomatic Population |
| 5 | ISSP[t] | Infected Severely Symptomatic Population |
| 6 | RP[t] | Recovered Population |
| 7 | MLP[t] | Money of Lost Productivity |
| 8 | HP[t] | Hospitalized Population |
| 9 | DIP[t] | Deceased Infected Population |
| 10 | HB[t] | Hospital Beds |
| 11 | MHS[t] | Money for Hospital Services |

, Rates →

| # | Symbol | Description |
|---|--------|-------------|
| 1 | $\mu$[TP] | Population death rate |
| 2 | $\mu$[INSP] | Infected Normally Symptomatic Population death rate |
| 3 | $\mu$[ISSP] | Infected Severely Symptomatic Population death rate |
| 4 | sspf[SP] | Severely Symptomatic Population Fraction |
| 5 | $\beta$[INSP] | Contact rate for the normally symptomatic population |
| 6 | $\beta$[ISSP] | Contact rate for the severely symptomatic population |
| 7 | aip | Average infectious period |
| 8 | aincp | Average incubation period |
| 9 | lpcr[ISSP, INSP] | Lost productivity cost rate (per person per day) |
| 10 | $\mu$[HP] | Hospitalized Population death rate |
| 11 | $\beta$[HP] | Contact rate for the hospitalized population |
| 12 | nhbr[TP] | Number of hospital beds rate |
| 13 | hscr[ISSP, INSP] | Hospital services cost rate (per bed per day) |
| 14 | nhbcr[ISSP, INSP] | Number of hospital beds change rate (per day) |

,

Equations →

| # | Equation |
|---|----------|
| 1 | $TP[t] = Max[0, EP[t] + INSP[t] + ISSP[t] + RP[t] + SP[t]]$ |
| 2 | $SP'[t] = -\frac{HP[t] SP[t] \beta[HP]}{TP[t]} - \frac{INSP[t] SP[t] \beta[INSP]}{TP[t]} - \frac{Max[0,-HP[t]-ISSP[t]] SP[t] \beta[ISSP]}{TP[t]} - SP[t] \mu[TP]$ |
| 3 | $EP'[t] = \frac{HP[t] SP[t] \beta[HP]}{TP[t]} + \frac{INSP[t] SP[t] \beta[INSP]}{TP[t]} + \frac{Max[0,-HP[t]-ISSP[t]] SP[t] \beta[ISSP]}{TP[t]} - EP[t] \left(\frac{1}{aincp} + \mu[TP]\right)$ |
| 4 | $INSP'[t] = -\frac{INSP[t]}{aip} + \frac{EP[t] (1-sspf[SP])}{aincp} - INSP[t] \mu[INSP]$ |
| 5 | $ISSP'[t] = -\frac{ISSP[t]}{aip} + \frac{EP[t] sspf[SP]}{aincp} - HP[t] \mu[HP] - (-HP[t]+ISSP[t]) \mu[ISSP]$ |
| 6 | $HP'[t] = \left( \begin{array}{ll} Min\left[HB[t] - HP[t], \frac{EP[t] sspf[SP]}{aincp}\right] & HP[t] < HB[t] \\ 0 & True \end{array} \right) - \frac{HP[t]}{aip} - HP[t] \mu[HP]$ |
| 7 | $RP'[t] = \frac{INSP[t] - ISSP[t]}{aip} - RP[t] \mu[TP]$ |
| 8 | $DIP'[t] = HP[t] \mu[HP] + INSP[t] \mu[INSP] + (-HP[t]+ISSP[t]) \mu[ISSP]$ |
| 9 | $HB'[t] = HB[t] nhbcr[ISSP, INSP]$ |
| 10 | $MHS'[t] = HP[t] hscr[ISSP, INSP]$ |
| 11 | $MLP'[t] = lpcr[ISSP, INSP] (INSP[t] + ISSP[t] + HP[t] \mu[HP] + INSP[t] \mu[INSP] + (-HP[t]+ISSP[t]) \mu[ISSP])$ |

, RateRules →

| # | Symbol | Value |
|---|--------|-------|
| 1 | $\mu$[TP] | $\frac{1}{45625}$ |
| 2 | $\mu$[ISSP] | $\frac{0.035}{aip}$ |
| 3 | $\mu$[INSP] | $\frac{0.01}{aip}$ |
| 4 | $\beta$[ISSP] | $0.5 \left( \begin{array}{ll} 1 & t < qsd \\ qcrf & qsd \le t \le ql + qsd \\ 1 & True \end{array} \right)$ |
| 5 | $\beta$[INSP] | $0.5 \left( \begin{array}{ll} 1 & t < qsd \\ qcrf & qsd \le t \le ql + qsd \\ 1 & True \end{array} \right)$ |
| 6 | aip | 26 |
| 7 | aincp | 5 |
| 8 | sspf[SP] | 0.2 |
| 9 | lpcr[ISSP, INSP] | 1 |
| 10 | $\mu$[HP] | 0.25 $\mu$[ISSP] |
| 11 | $\beta$[HP] | 0.01 |
| 12 | nhbr[TP] | $\frac{3}{1000}$ |
| 13 | nhbcr[ISSP, INSP] | 0 |
| 14 | hscr[ISSP, INSP] | 1 |
| 15 | qsd | 0 |
| 16 | ql | 56 |
| 17 | qcrf | 0.25 |

, InitialConditions →

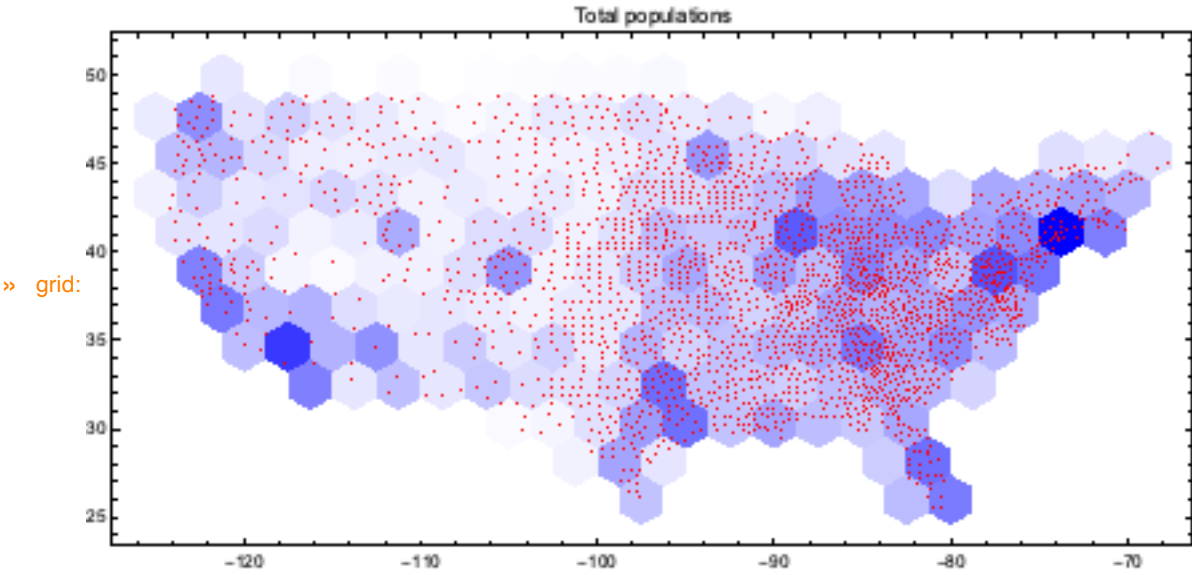| # | Equation |
|---|----------|
| 1 | $SP[0] == 99998$ |
| 2 | $EP[0] == 0$ |
| 3 | $ISSP[0] == 1$ |
| 4 | $INSP[0] == 1$ |
| 5 | $RP[0] == 0$ |
| 6 | $MLP[0] == 0$ |
| 7 | $TP[0] == 100000$ |
| 8 | $HP[0] == 0$ |
| 9 | $DIP[0] == 0$ |
| 10 | $HB[0] == nhbr[TP] TP[0]$ |
| 11 | $MHS[0] == 0$ |

⟩

» **Show the grid based on population coordinates:**

» grid:
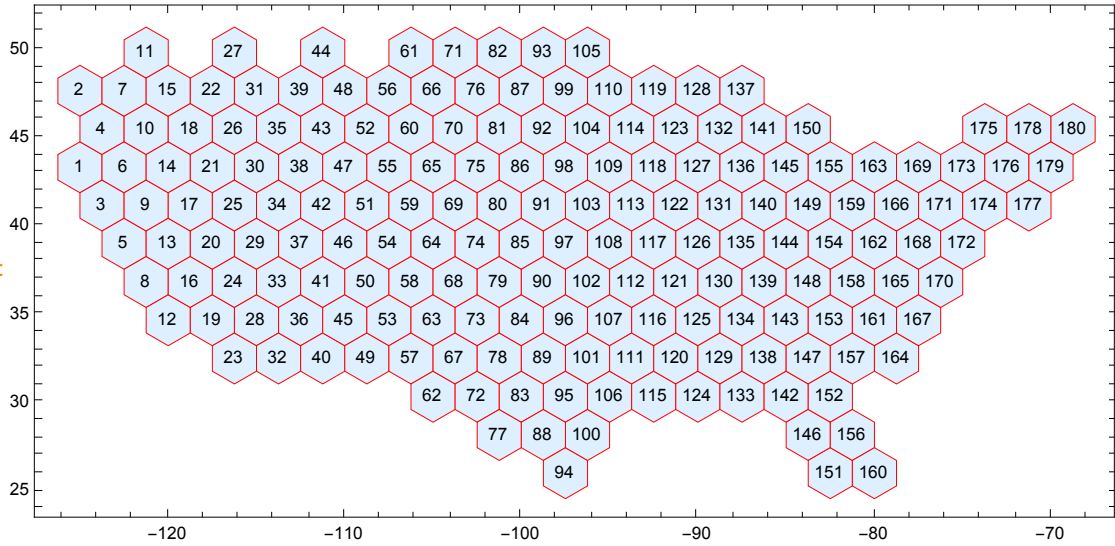


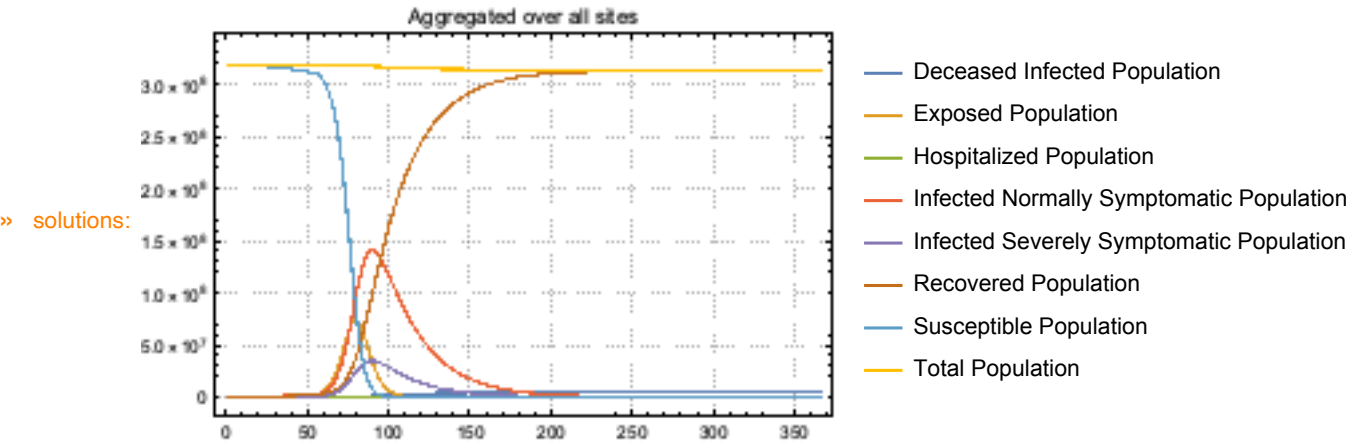» **Show total populations initial conditions data:**

Total populations



» grid:

» **Show infected and deceased initial conditions data:**
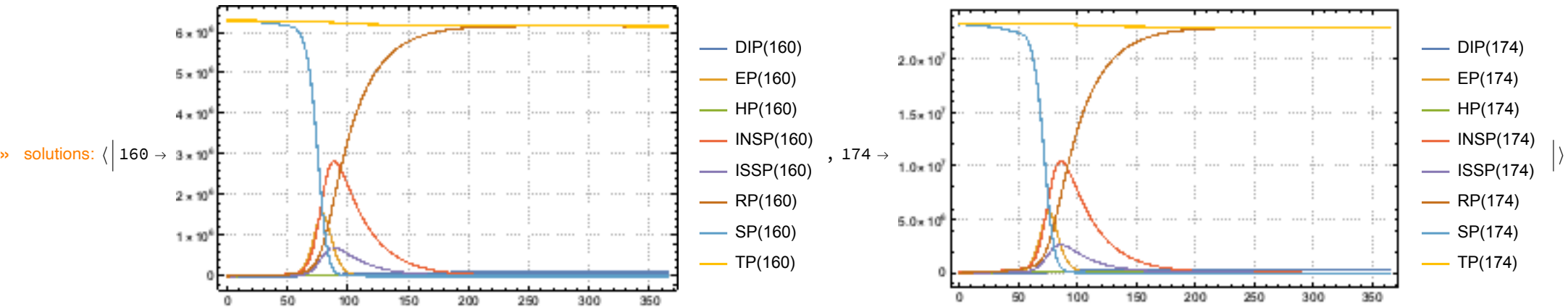
Infected



» grid:

Deceased



» grid:
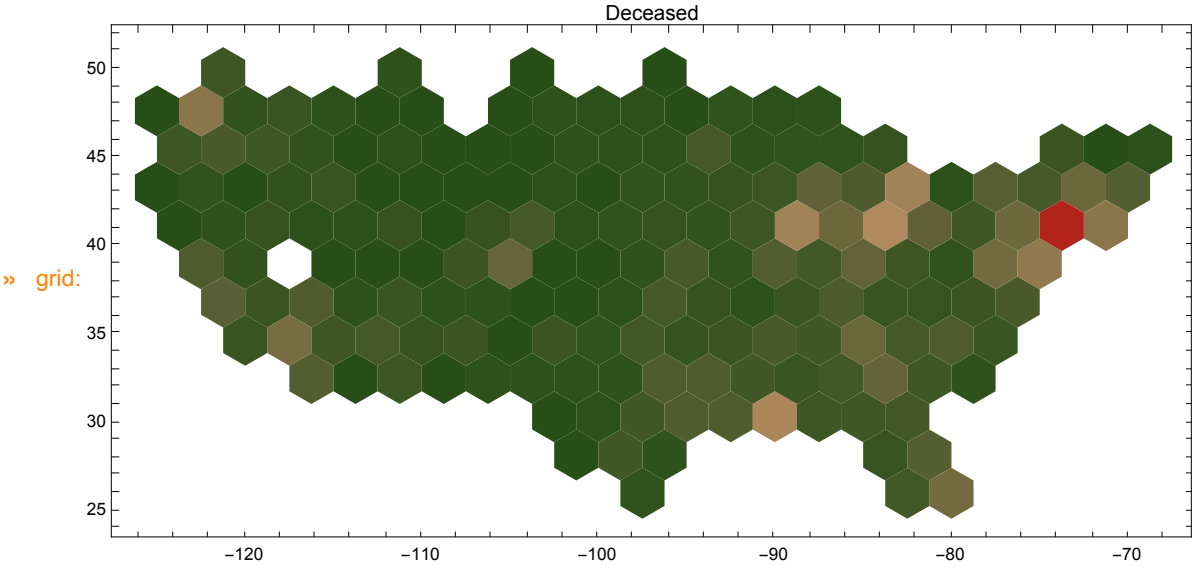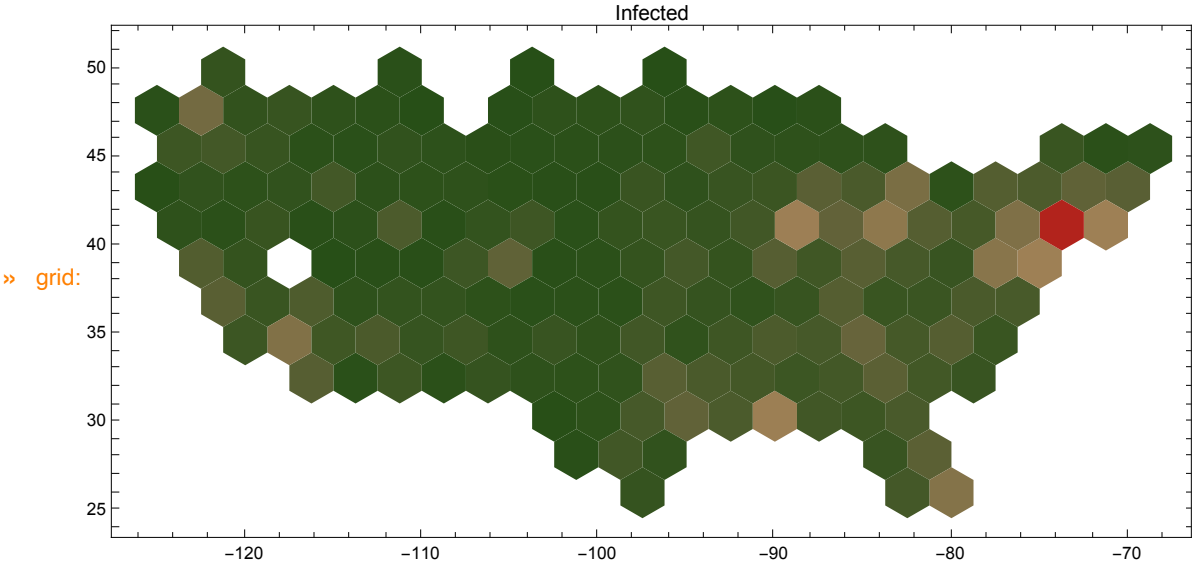
» **Simulate:**

▪▪▪ **NDSolve**: NDSolve has computed initial values that give a zero residual for the differential−algebraic system, but some components are different from those specified. If you need them to be satisfied, giving initial conditions for all dependent variables and their derivatives is recommended.

» **Show global population simulation results:**

» solutions:



Aggregated over all sites

- Deceased Infected Population
- Exposed Population
- Hospitalized Population
- Infected Normally Symptomatic Population
- Infected Severely Symptomatic Population
- Recovered Population
- Susceptible Population
- Total Population

» **Show site simulation results for Miami and New York areas:**

» solutions: ⟨ | 160 →



- DIP(160)
- EP(160)
- HP(160)
- INSP(160)
- ISSP(160)
- RP(160)
- SP(160)
- TP(160)

, 174 →



- DIP(174)
- EP(174)
- HP(174)
- INSP(174)
- ISSP(174)
- RP(174)
- SP(174)
- TP(174)

| ⟩

» **Show deceased and hospitalzed populations results for Miami and New York areas:**

» solutions: ⟨ | 160 →



- DIP(160)
- HB(160)
- HP(160)

, 174 →



- DIP(174)
- HB(174)
- HP(174)

| ⟩
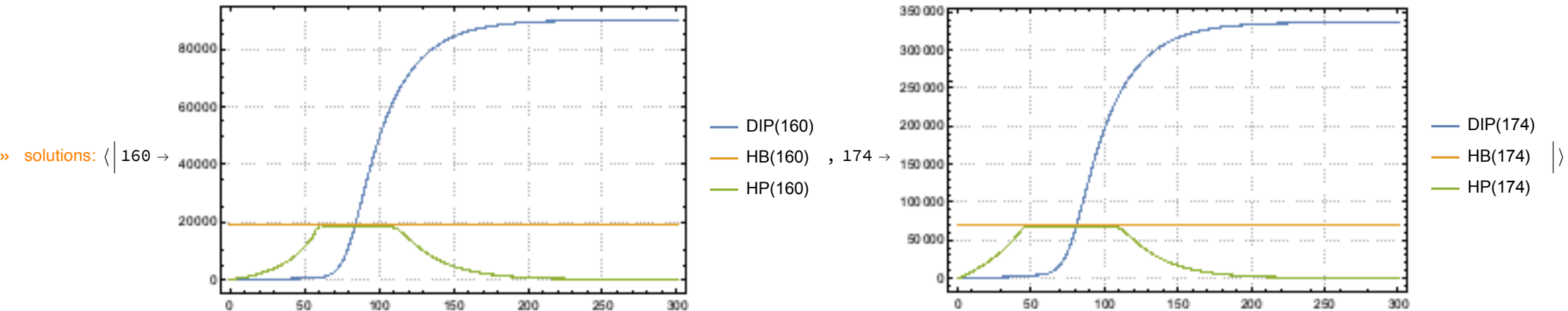
# References

## Articles

[Wk1] Wikipedia entry, "Compartmental models in epidemiology".

[Wl2] Wikipedia entry, "Coronavirus disease 2019".

[HH1] Herbert W. Hethcote (2000). "The Mathematics of Infectious Diseases". SIAM Review. 42 (4): 599–653. Bibcode:2000SIAMR..42..599H. doi:10.1137/s0036144500371907.

[BC1] Lucia Breierova, Mark Choudhari, An Introduction to Sensitivity Analysis, (1996), Massachusetts Institute of Technology.

[AA1] Anton Antonov, "Coronavirus propagation modeling considerations", (2020), SystemModeling at GitHub.

[AA2] Anton Antonov, "Basic experiments workflow for simple epidemiological models", (2020), SystemModeling at GitHub.

[AA3] Anton Antonov, "Scaling of Epidemiology Models with Multi-site Compartments", (2020), SystemModeling at GitHub.

[AA4] Anton Antonov, "WirVsVirus hackathon multi-site SEI2R over a hexagonal grid graph", (2020), SystemModeling at GitHub.

[AA5] Anton Antonov, "NY Times COVID-19 data visualization", (2020), SystemModeling at GitHub.

[AA6] Anton Antonov, "SEI2HR model with quarantine scenarios", (2020), SystemModeling at GitHub.

[AA7] Anton Antonov, "SEI2HR-Econ model with quarantine and supplies scenarios", (2020), SystemModeling at GitHub.

## Repositories, packages

[WRI1] Wolfram Research, Inc., "Epidemic Data for Novel Coronavirus COVID-19", WolframCloud.

[WRI2] Wolfram Research Inc., USA county records, (2020), System Modeling at GitHub.

[NYT1] The New York Times, Coronavirus (Covid-19) Data in the United States, (2020), GitHub.

[AAr1] Anton Antonov, Coronavirus propagation dynamics project, (2020), SystemModeling at GitHub.

[AAp1] Anton Antonov, "Epidemiology models Mathematica package", (2020), SystemModeling at GitHub.

[AAp2] Anton Antonov, "Epidemiology models modifications Mathematica package", (2020), SystemModeling at GitHub.

[AAp3] Anton Antonov, "Epidemiology modeling visualization functions Mathematica package", (2020), SystemModeling at GitHub.

[AAp4] Anton Antonov, "System dynamics interactive interfaces functions Mathematica package", (2020), SystemModeling at GitHub.

[AAp5] Anton Antonov, "Multi-site model simulation Mathematica package", (2020), SystemModeling at GitHub.

[AAp6] Anton Antonov, "Monadic Epidemiology Compartmental Modeling Mathematica package", (2020), SystemModeling at GitHub.