How to use these modules[*]

Winfried Just[†] Hannah Callender[‡] M. Drew LaMar[§]

December 23, 2015

These modules are similar in format to the modules and projects of our book chapters [1, 2]. In many respects they form a natural continuation of these chapters, but can also be used by students who have not worked through the chapters but are to some extent familiar with disease modeling. We will rely here on the concepts and terminology introduced in the brief overview of network-based models of transmission of infectious diseases that is posted at this web site[1] and we strongly recommend that students read this review before attempting any of the modules.

There is some flexibility regarding the order in which students may want to complete the modules, but some of them rely on material from earlier modules. All such dependencies are indicated in the short descriptions that are given in the list of modules. For selected modules, sample solutions for the exercises are posted at the very end of the module. A complete set of modules with sample solutions can be accessed via a sign-up page through the mirror site at QUBESH Hub.[2]

In most of these modules, you will be working with our NetLogo program IONTW. At the beginning of each module, we will specify parameter settings that will be used for (most of) it. We restrict ourselves to listing the ones that are relevant to the work in a given module. The exercises in each module build on each other and should not be done out of sequence. We will often specify how to change one or two parameters; the tacit assumption is that the other parameter settings will be as in the preceding exercise. If you need to interrupt work on one part and resume at a later time, save the current settings under an appropriate file name by using to **File → Save As**.

Template for batch processing

We will frequently need to run large numbers of simulations in batch processing mode. There is a fixed sequence of steps that you need to follow to set up and run such an

---

[†]Department of Mathematics, Ohio University, Athens, OH 45701 E-mail: mathjust@gmail.com
[‡]University of Portland E-mail: callende@up.edu
[§]The College of William and Mary E-mail: drew.lamar@gmail.com
[1]http://www.ohio.edu/people/just/IONTW
[2]https://qubeshub.org/groups/iontwsolutions/join

experiment. Only four of them change from experiment to experiment. Here we give you the template; in the text of the modules we will only indicate the ones that are marked here with asterisks and described in `typewriter font.` We strongly recommend that you choose choose descriptive file names and keep all output files in a safe place in case you want to return to them later.

- Open **Tools** → **BehaviorSpace**

- ***** `Choose one of the following two options:`

  - Define a **New** experiment.
  - **Edit** an existing experiment.

- Enter a nice suggestive **Experiment name**. Make sure to choose a different name each time so as not to lose previously saved output files from prior experiments.

- **Repetitions:** ***** `Enter number of repetitions`

- **Measure runs using these reporters:**

  ***** `Enter the names of the desired output variables`

- Uncheck **Measure runs at every step**

- **Setup commands:**

  ***** `Enter the commands for initializing each network`

- Click **OK** and then **Run**

- Give instructions for how and where to save the output. Use the option **Table** that gives cleaner output. Unless instructed otherwise, leave the number of **Simultaneous runs in parallel** at its default value. Then click **OK**.

- Next select the directory where you want to save your output. After you click **Save** the simulation starts running.

- A window should appear that has checkboxes **Update view** and **Update plots and monitors.** For best performance, uncheck both and move the speed slider in this window to the extreme right.

- When the window finally disappears, the experiment is completed.

References

[1] Winfried Just, Hannah Callender, and M Drew LaMar. Disease transmission dynamics on networks: Network structure *vs.* disease dynamics. In Raina Robeva, editor, *Algebraic and Discrete Mathematical Methods for Modern Biology*, pages 217–235. Academic Press, 2015.

[2] Winfried Just, Hannah Callender, M Drew LaMar, and Natalia Toporikova. Transmission of infectious diseases: Data, models, and simulations. In Raina Robeva, editor, *Algebraic and Discrete Mathematical Methods for Modern Biology*, pages 193–215. Academic Press, 2015.