

# How to Run Simple Models with the Broadwick Framework

“Broadwick Examples”

S. J. Lycett

24 June 2014



University  
of Glasgow

Institute of Biodiversity,  
Animal Health & Comparative Medicine



# Introduction

- Broadwick Framework provides the underlying code for generating and running specific models
- To show how this works, we've generated some examples
  - This morning: running pre-written models
  - This afternoon: how to write your own models

# Broadwick Examples

- Demonstration models have been written in the Broadwick Framework
- They have been compiled (built) together with the Broadwick Framework into one jar file

**BroadwickExamples-1.0-SNAPSHOT.one-jar.jar**

- Files are on the USB stick, or
- Get the files from GitHub (see)  
<http://epicscotland.github.io/broadwick.html>

## EPIC Scotland Modelling

(Github user facing site)

Welcome to the EPIC Scotland Modelling webpages. Here you will find the epidemiological modelling code developed by EPIC members.

Code, built applications, data, and documents are in GitHub repositories: <https://github.com/EPICScotland>

## Projects

### PhylogeneticDataSets

PhylogeneticDataSets contains reference sequence data and trees for pathogens of interest to EPIC. It also contains some R utility script files used to generate the data where applicable.

PhylogeneticDataSets **webpages are live at:** <http://epicscotland.github.io/PhylogeneticDataSets>

(the repository data and html pages are in the **gh-pages** branch of <https://github.com/EPICScotland/PhylogeneticDataSets>)

### Broadwick

#### Main page

<http://epicscotland.github.io/broadwick.html>

#### Broadwick

Broadwick is a java framework for creating and running epidemiological models

Get the code from: <https://github.com/EPICScotland/Broadwick>

#### BroadwickTutorial

BroadwickTutorial contains tutorial materials on how to use the Broadwick Framework, and includes code stubs that you convert into working code as part of the tutorial.

Get the code from <https://github.com/EPICScotland/BroadwickTutorial>

#### BroadwickExamples

BroadwickExamples contains some simple stochastic compartmental models written within the Broadwick framework.

Get the code from <https://github.com/EPICScotland/BroadwickExamples>

#### MovementSimulations

The MovementSimulations repository is for movement simulation code and test data, and contains the AnimalMovementSimulations java project.

Get the code from: <https://github.com/EPICScotland/MovementSimulations>

# Broadwick

## Introduction

Broadwick is a framework for developing sophisticated epidemiological based mathematical models, and consists of several Java libraries and bespoke packages. The components of Broadwick are written in such a way that a scientist may combine them in order to rapidly prototype a model for a new specific scenario.

### Features

- Supports single (e.g. within herd) or structured populations (e.g. multi-species or locations)
- Inclusion of movement over network data (e.g. Cattle movement Tracing System)
- Stochastic Individual Based simulations (including fast approximate options)
- Approximate Bayesian Computation inference for estimating model parameters from data via simulations
- Monte Carol Markov Chain inference for estimating model parameters from data

Get the code from: <https://github.com/EPICScotland/Broadwick>

## BroadwickTutorial



This afternoon

BroadwickTutorial contains tutorial materials on how to use the Broadwick Framework, and includes code stubs that you convert into working code as part of the tutorial.

Instructions for installing Broadwick, and a summary of the tutorial

- [Broadwick Demo Install Instructions.pdf \(April 2014\)](#)
- [MainTutorialTasks.pptx \(17 June 2014\)](#)

Code stubs and Broadwick framework available as zipped files from <https://github.com/EPICScotland/BroadwickTutorial>

There are 9 video tutorials in the [Videos Folder](#) (large files)

- Download Broadwick (video 1)
- Download and install Netbeans (video 2)
- Create a simple SIR Model with Broadwick (video 3)
- Create a Stochastic SIR model (Video 4-7)
- Download Stochastic SIR model code (Video 4a)
- Stochastic flow part 1 - Background to implementation (Video 4)
- Stochastic flow part 2 - Theta events, reading data (Video 5)
- Stochastic flow part 3 - Handling fired events (Video 6)
- Stochastic flow part 4 - Build, run and plot output (video 7)
- Use Multithreading with Broadwick (Video 8)
- Use ABC with Broadwick (Video 9)

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For reference: UML diagram of classes and methods describing how to construct a stochastic model - [Stochastic UML Diagram.pdf](#)

Get the code from <https://github.com/EPICScotland/BroadwickTutorial>

## BroadwickExamples

BroadwickExamples contains some simple stochastic compartmental models written within the Broadwick framework.

To run these you will need the built jar file [BroadwickExamples-1.0-SNAPSHOT.one-jar.jar](#) and the xml configuration files: [Broadwick with \(XXX\).xml](#)

Instructions for running the examples, and an outline of how to write your own (but see the tutorial above for detailed instructions) can be found in the [BroadwickExamples/doc](#) directory:

- [HowTo RunBroadwickExamples QuickStart.pdf \(16 June 2014\)](#)
- [HowTo WriteBroadwickModel QuickStart.pdf \(16 June 2014\)](#)

Get the code from <https://github.com/EPICScotland/BroadwickExamples>

## MovementSimulations

The MovementSimulations repository is for movement simulation code and test data, and contains the AnimalMovementSimulations java project.

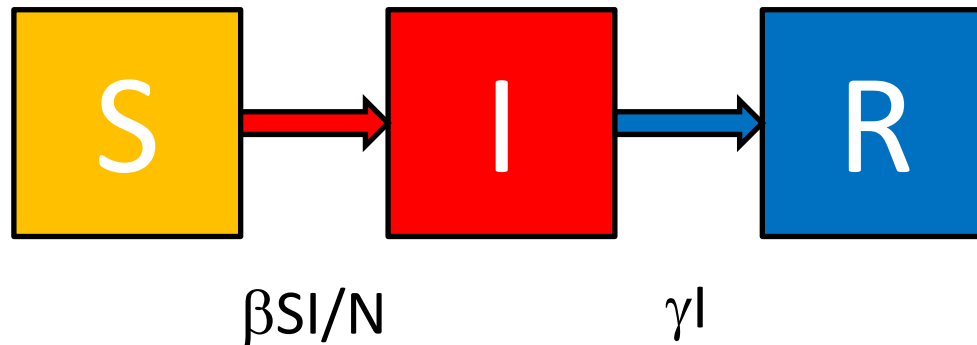
The AnimalMovementSimulations project generates simulated animal movement data for use with Broadwick, and includes for the BroadwickTutorial

Demonstration files



# Simple Compartmental Model

- Assume fixed population of  $N$  individuals
- Model number of Susceptibles ( $S$ ), Infecteds ( $I$ ) and Recovereds ( $R$ ) over time
- Assume that anybody can infect anybody else (if Susceptible)



Infection rate

Recovery rate

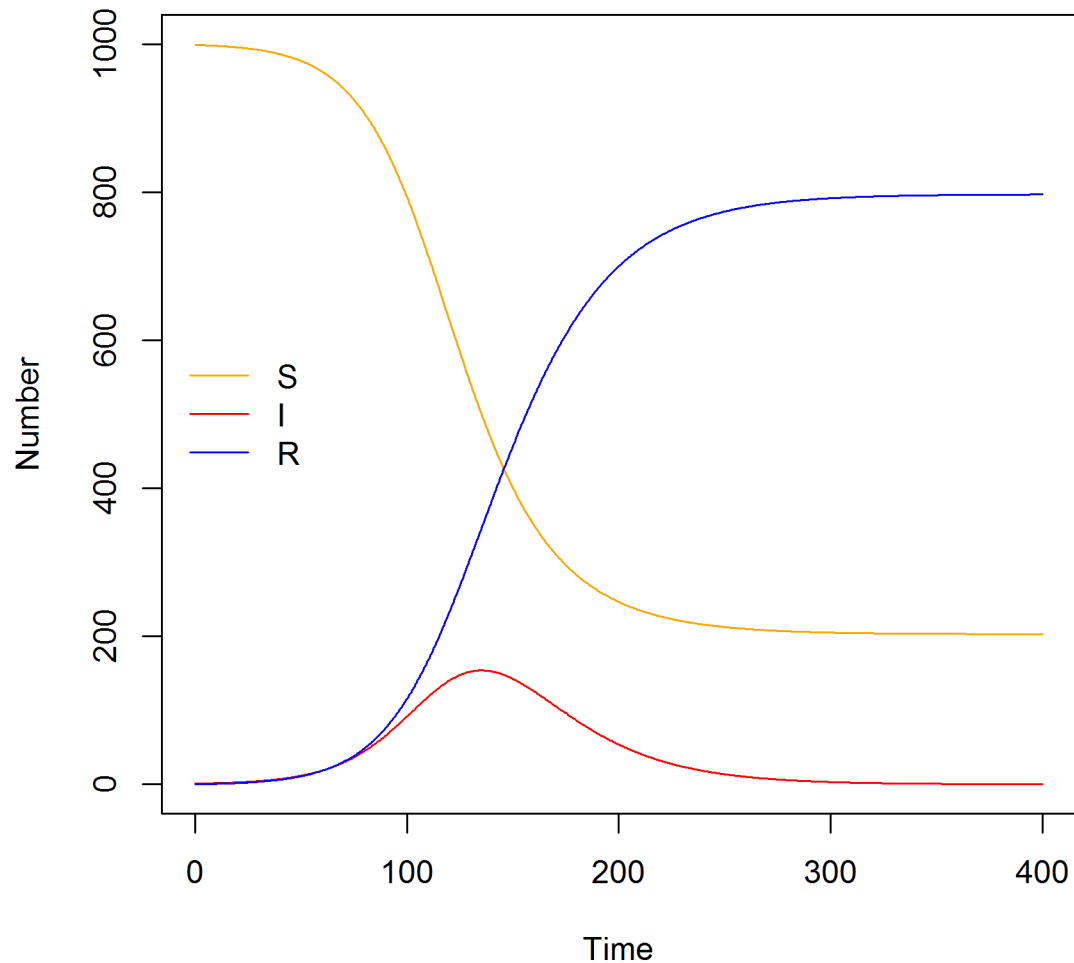
$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

# Deterministic Solution to SIR Model

$N=1000$   $\beta=0.1/N$   $\gamma=0.05$





# Demonstration models

- All use Broadwick Stochastic algorithms
  - Event driven: calculating the probability of infection and recovery for individuals
  - Choice of Gillespie Algorithm or Fixed Step Tau-Leap (approximate Gillespie, faster)
- **BasicSIR**: stochastic SIR model
- **IndividualSIRModel**: stochastic SIR model with named individuals and who-infected-whom
- **NetworkSIRModel**: as above, but individuals only infect each other over a network

# Configuration Files

- Models in the “one-jar” file are run using XML configuration files
  - Broadwick\_with\_DummyModel.xml
  - Broadwick\_with\_BasicSIRModel.xml
  - Broadwick\_with\_IndividualSIRModel.xml
  - Broadwick\_with\_IndividualNetworkModel.xml

# Broadwick\_with\_BasicSIRModel.xml

(Page 1 of 2)

General framework part of configuration file:

```
<?xml version="1.0" encoding="UTF-8" standalone="yes"?>
<project>
  <logs>
    <console>
      <level>info</level>
      <pattern>[%thread] %-5level %msg %n</pattern>
    </console>
    <file>
      <name>epic.basic.basicsirmodel.log</name>
      <level>info</level>
      <pattern>[%thread] %-5level %msg %n</pattern>
      <overwrite>true</overwrite>
    </file>
  </logs>
</project>
```

Broadwick framework  
log file



# Broadwick\_with\_BasicSIRModel.xml

(Page 2 of 2)

Model specific part of configuration file:

```
<models>
  <model id="Broadwick Project">
    <classname>epic.basic.BasicSIRModel</classname>
    <parameter id="filename" value="basicsir_test"/>
    <parameter id="verbose" value="false"/>
    <parameter id="maxTime" value="1000000"/>
    <parameter id="tauStep" value="0"/>
    <parameter id="N" value="1000"/>
    <parameter id="initI" value="1"/>
    <parameter id="beta" value="0.1"/>
    <parameter id="gamma" value="0.05"/>
  </model>
</models>
</project>
```

The model to run

Specific  
parameters for the  
model

# Command Line Operation

- Broadwick is designed to be run from the command line, and/or in batch scripts
- Bring up your command line:
  - Windows: Start -> (search) “prompt” -> command prompt
  - Mac: (Launch Pad) -> Terminal
- Go to the directory of the jar and xml files
- To run a model type this (all one line):

```
java -jar BroadwickExamples-1.0-SNAPSHOT.one-jar.jar  
-c Broadwick_with_BasicSIRModel.xml
```

# **Expected Results**

# Broadwick\_with\_DummyModel.xml

## Command:

```
java -jar BroadwickExamples-1.0-SNAPSHOT.one-jar.jar -c Broadwick_with_DummyModel.xml
```

## Expected results:

lots of:

```
[JarClassLoader] INFO: findResources..
```

```
[main] INFO Running broadwick Version 1.1 Build (SJLDELL - unknown : 2014-06-14 11:49)
```

```
[main] INFO Running broadwick for the following models [Broadwick Project]
```

```
[pool-1-thread-1] INFO Running Broadwick Project [epic.broadwickexamples.DummyModel]
```

```
[pool-1-thread-1] INFO Initialise Dummy Model
```

```
[pool-1-thread-1] INFO Run Dummy Model
```

```
[pool-1-thread-1] INFO stringParam=ABCDEFGG
```

```
[pool-1-thread-1] INFO intParam=1
```

```
[pool-1-thread-1] INFO doubleParam=2.0
```

```
[pool-1-thread-1] INFO Finalise Dummy Model
```

```
[pool-1-thread-1] INFO END
```

```
[main] INFO Simulation complete. 0:00:00.056
```

**SUCCESS !**

# Broadwick\_with\_BasicSIRModel.xml

## Command:

```
java -jar BroadwickExamples-1.0-SNAPSHOT.one-jar.jar -c Broadwick_with_BasicSIRModel.xml
```

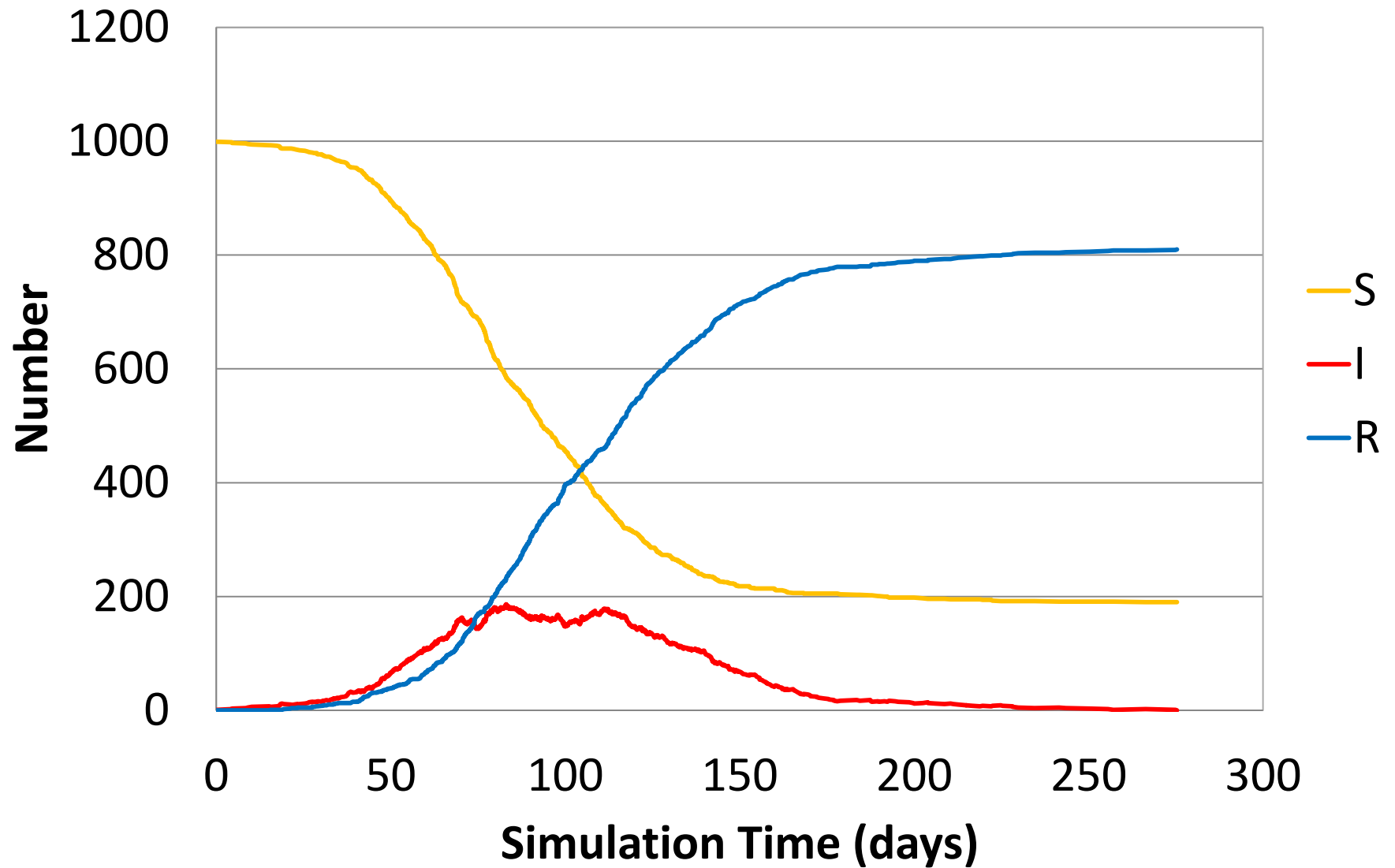
## Expected results – also written to log file epic.basic.BasicSIRModel.log

```
[main] INFO Running broadwick Version 1.1 Build (SJLDELL - unknown : 2014-06-14 11:49)
[main] INFO Running broadwick for the following models [Broadwick Project]
[pool-1-thread-1] INFO Running Broadwick Project [epic.basic.BasicSIRModel]
[pool-1-thread-1] INFO BasicSIRModel - init
[pool-1-thread-1] INFO seed      = 12345
[pool-1-thread-1] INFO maxTime= 1000000.0
[pool-1-thread-1] INFO tauStep  = 0
[pool-1-thread-1] INFO N        = 1000
[pool-1-thread-1] INFO initI    = 1
[pool-1-thread-1] INFO beta     = 0.1
[pool-1-thread-1] INFO gamma    = 0.05
[pool-1-thread-1] INFO BasicSIRModel - run
[pool-1-thread-1] INFO BasicSIRModel - final simulation time = 275.3055756207629
[main] INFO Simulation complete. 0:00:00.246
```

and output file = basicsir\_test.txt



# Basic SIR Model



# Broadwick\_with\_IndividualSIRModel.xml

Command:

```
java -jar BroadwickExamples-1.0-SNAPSHOT.one-jar.jar -c Broadwick_with_IndividualSIRModel.xml
```

Expected results – also written to log file epic.sir.IndividualSIRModel.log

```
[main] INFO Running broadwick Version 1.1 Build (SJLDELL - unknown : 2014-06-14 11:49)
[main] INFO Running broadwick for the following models [Broadwick Project]
[pool-1-thread-1] INFO Running Broadwick Project [epic.sir.IndividualSIRModel]
[pool-1-thread-1] INFO IndividualSIRModel - init
[pool-1-thread-1] ERROR Could not find parameter susceptibility in configuration file.
[pool-1-thread-1] INFO Optional parameter susceptibility (=waning immunity) is not set, but this is OK
[pool-1-thread-1] INFO seed      = 12347
[pool-1-thread-1] INFO maxTime= 1000000.0
[pool-1-thread-1] INFO tauStep  = 0
[pool-1-thread-1] INFO N        = 1000
[pool-1-thread-1] INFO initI    = 1
[pool-1-thread-1] INFO IndividualSIRModel - run
[pool-1-thread-1] INFO IndividualSIRModel - final simulation time = 319.6001125147772
[pool-1-thread-1] INFO IndividualSIRModel - SUSCEPTIBLE:249   INFECTED:0   RECOVERED:751
[main] INFO Simulation complete. 0:00:00.356
```

and output files:

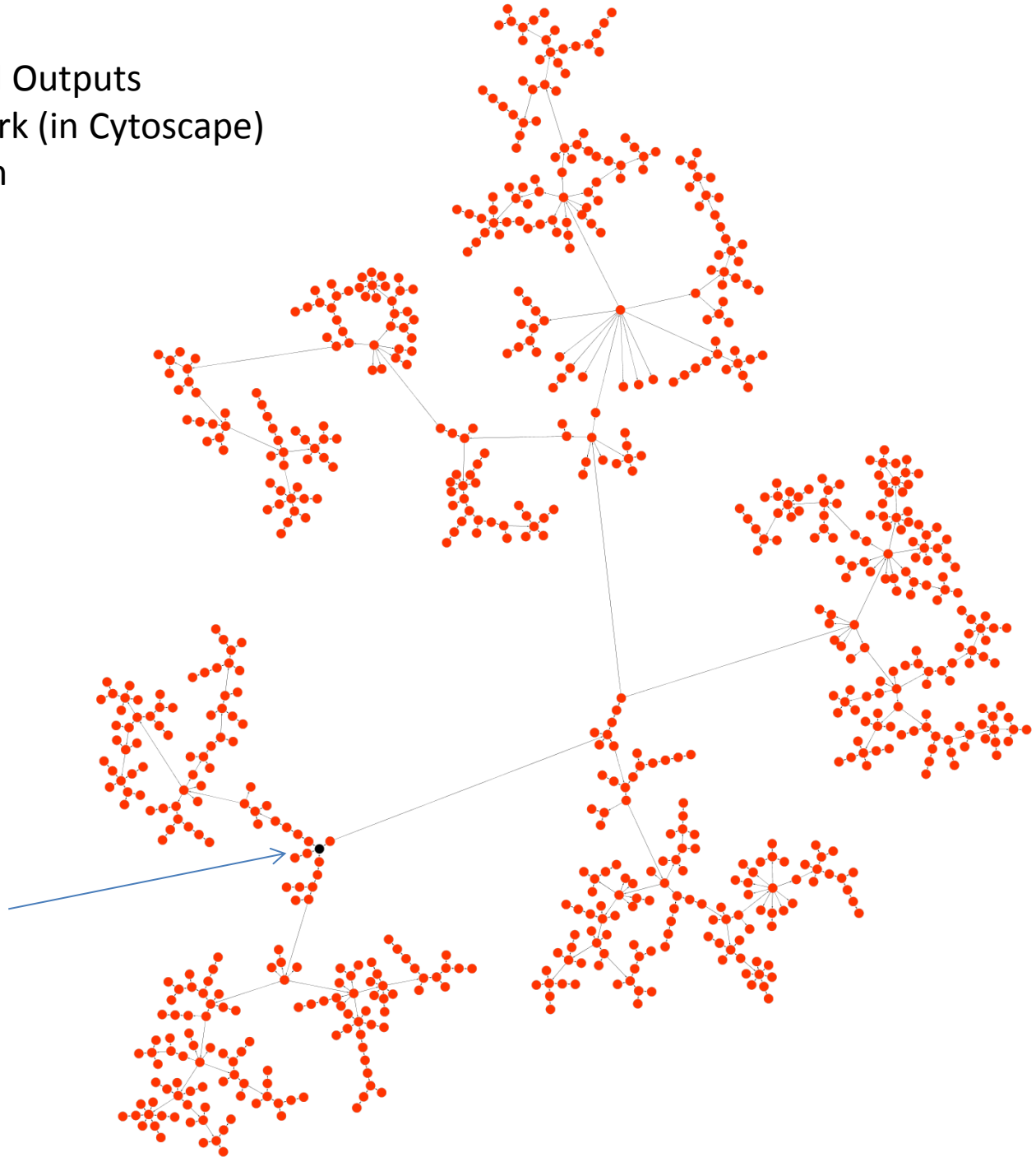
**individualsir\_test\_modelState.txt, individualsir\_test\_transmissions.txt, individualsir\_test\_allEvents.txt**

# Individual SIR Model Outputs

- \*ModelState.txt
  - Numbers of S, I, R over time
- \*allEvents.txt
  - Record of all events, e.g.:
    - Time, Event Name, From:State -> To:State
    - 20.26,INFECTION,IA000000059:INFECTED -> IA000000132:INFECTED
    - 21.23,RECOVERY,IA000000260:INFECTED -> IA000000260:RECOVERED
- \*transmissions.txt
  - Record of the transmission events (who infected whom) only

Individual SIR Model Outputs  
Transmission Network (in Cytoscape)  
Who infected Whom

Index case  
(black)



# Broadwick\_with\_IndividualNetworkModel.xml

Command:

(example\_UK\_cities.txt, example\_UK\_cities\_links.txt must be in the same directory as the jar file)  
java -jar BroadwickExamples-1.0-SNAPSHOT.one-jar.jar -c Broadwick\_with\_IndividualNetworkModel.xml

## Expected results – also written to log file epic.sir.IndividualNetworkModel.log

```
[main] INFO Running broadwick Version 1.1 Build (SJLDELL - unknown : 2014-06-14 11:49)
[main] INFO Running broadwick for the following models [Broadwick Project]
[pool-1-thread-1] INFO Running Broadwick Project [epic.network.IndividualNetworkModel]
[pool-1-thread-1] INFO IndividualNetworkModel - init
[pool-1-thread-1] ERROR Could not find parameter susceptibility in configuration file.
[pool-1-thread-1] INFO Optional parameter susceptibility (=waning immunity) is not set, but this is OK
[pool-1-thread-1] INFO Network Model locationsFile = example_UK_cities.csv
[pool-1-thread-1] INFO Network Model linksFile = example_UK_cities_links.csv
[pool-1-thread-1] INFO Network Model locationType = LATLONG
[pool-1-thread-1] INFO 170 locations read from file
[pool-1-thread-1] INFO 181 links read from file
[pool-1-thread-1] INFO Initialising infection from CN000111,Stoke-on-Trent,53.0,-2.13
[pool-1-thread-1] INFO Number of susceptibles in network = 106
[pool-1-thread-1] INFO Number of infecteds in network = 1
[pool-1-thread-1] INFO seed = 12349
[pool-1-thread-1] INFO maxTime          = 1000000.0
[pool-1-thread-1] INFO tauStep              = 0
[pool-1-thread-1] INFO N              = 107
[pool-1-thread-1] INFO initI          = 1
[pool-1-thread-1] INFO IndividualNetworkModel - run
[pool-1-thread-1] INFO IndividualNetworkModel - final simulation time = 152.54159155869897
[pool-1-thread-1] INFO IndividualNetworkModel - SUSCEPTIBLE:3      EXPOSED:0    INFECTED:0    RECOVERED:104
[main] INFO Simulation complete. 0:00:00.710
```

# Individual Network Model Outputs

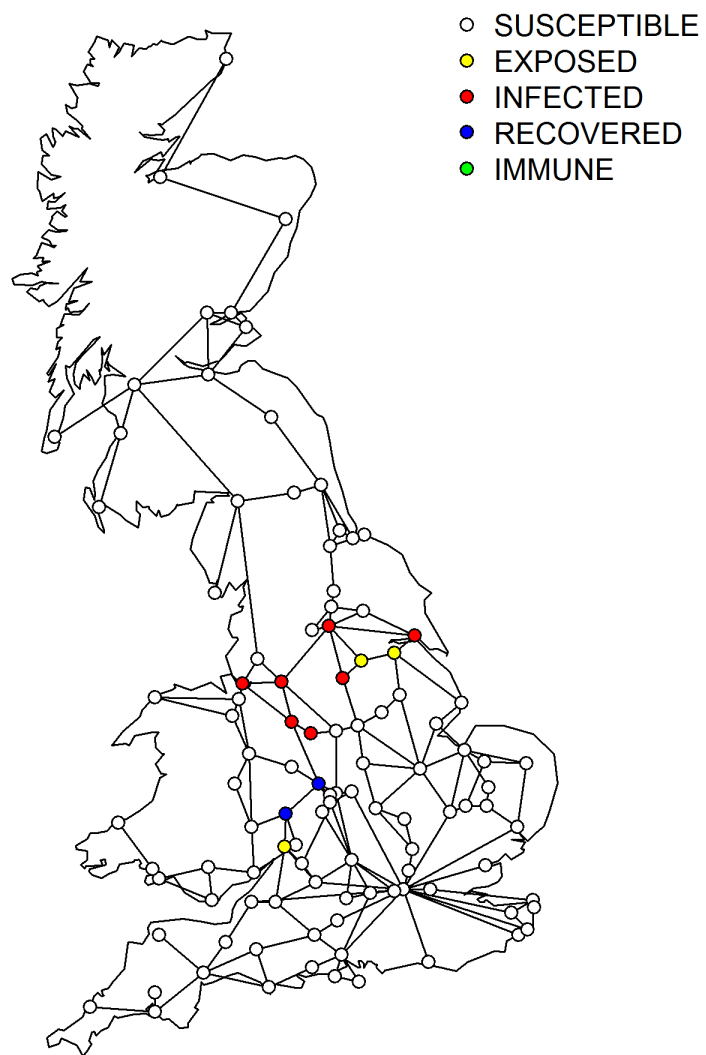
- \*modelState.txt, \*allEvents.txt, \*transmissions.txt
  - Same as in Individual SIR Model outputs
- \*locations.txt
  - The locations of the network nodes (one line = one vertex):  
Name,Location,Latitude,Longitude  
CN000144,Edinburgh,55.95,-3.35  
CN000145,Glasgow,55.8667,-4.43333  
CN000146,Inverness,57.5333,-4.05
- \*initialNetwork.net
  - The (undirected) links between the network nodes (one line = one edge):  
Name,Location,Latitude,Longitude,Name,Location,Latitude,Longitude  
CN000145,Glasgow,55.8667,-4.43333,CN000142,Campbeltown,55.4333,-5.6
- \*individualStates\_initial.txt, \*individualStates\_final.txt,  
\*individualStates\_[number].txt
  - The infection state of each network node at each simulation step (one file per step), e.g:  
Name,Location,Latitude,Longitude,State  
CN000144,Edinburgh,55.95,-3.35,SUSCEPTIBLE

individualnetwork\_test\_individualStates\_initial.txt



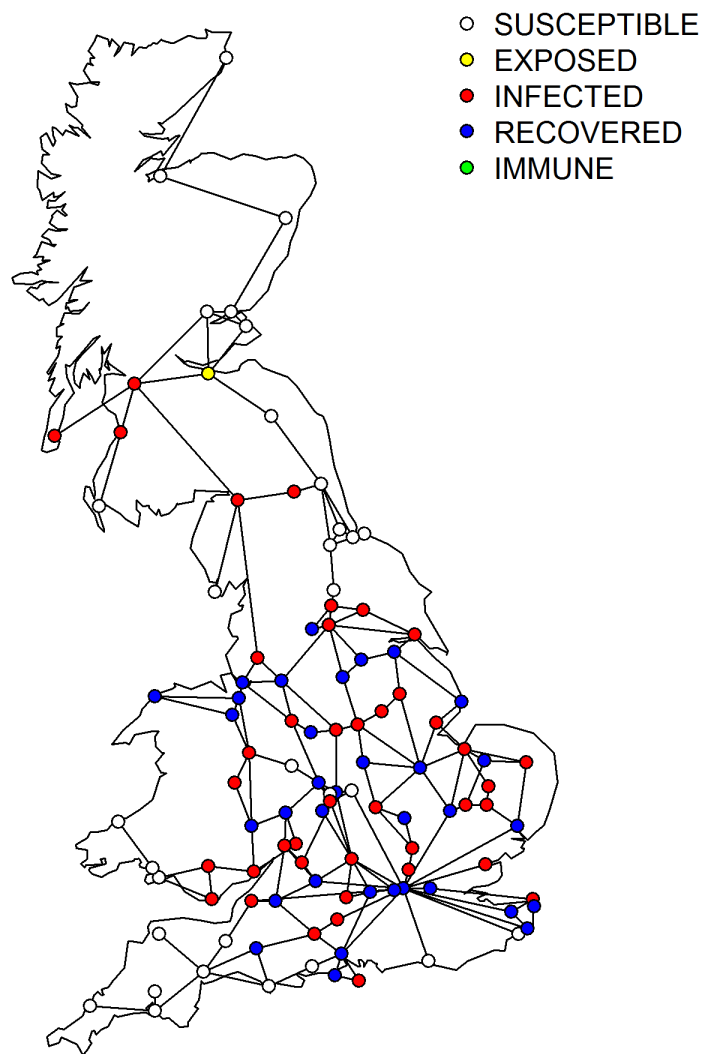
Plot individual states output using R script: plotGBDiseaseMap.R (one image per step)

individualnetwork\_test\_individualStates\_000000020.txt

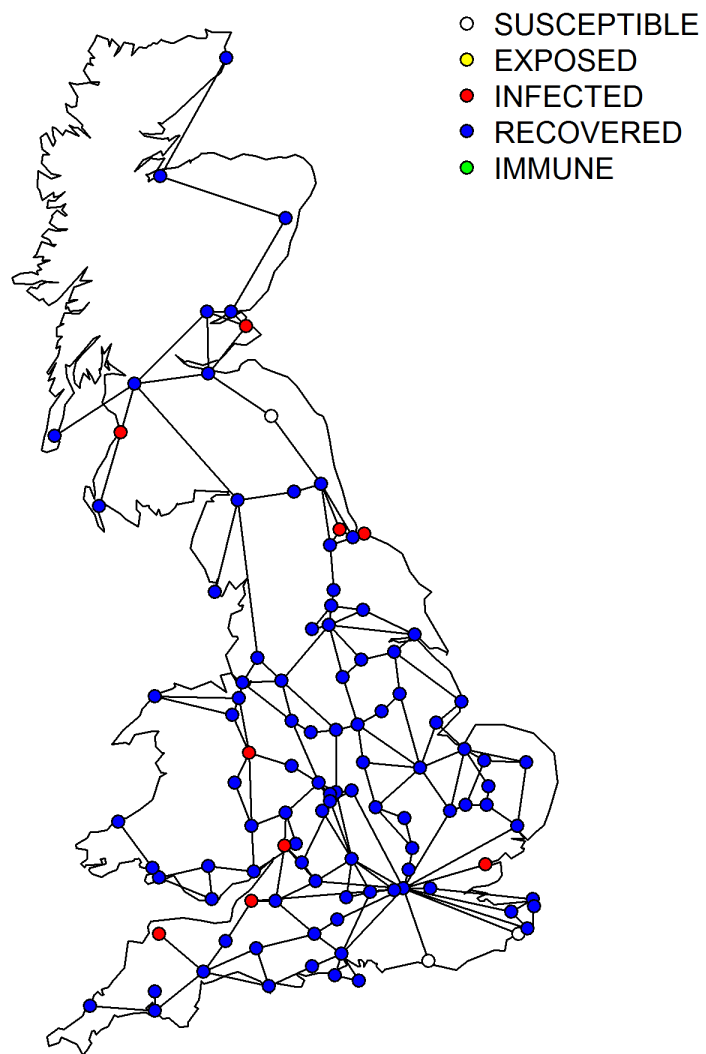




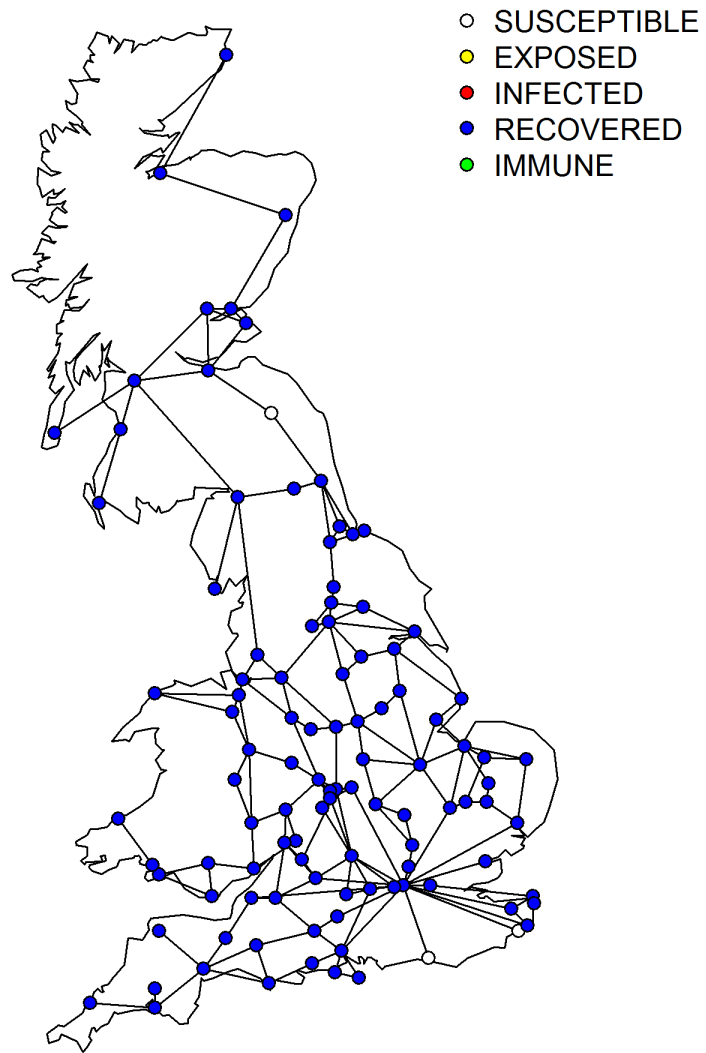
individualnetwork\_test\_individualStates\_000000182.txt



individualnetwork\_test\_individualStates\_000000300.txt



# individualnetwork\_test\_individualStates\_final.txt



# Next Steps

**Broadwick Tutorial**

**How to write your own models**

**This afternoon**



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