On the Infectious Diseases in Networks and Their Control

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To obtain a more realistic epidemic model that generalize the most commonly used epidemic models that assume that

- susceptible individuals are equally likely to acquire the infection during an outbreak, and
- the infectious process is markovian.

The last two assumptions the models are analyzed with well known algorithms as the Euler and Euler-Maruyama, from differential equations and Markov process methodology.

Content

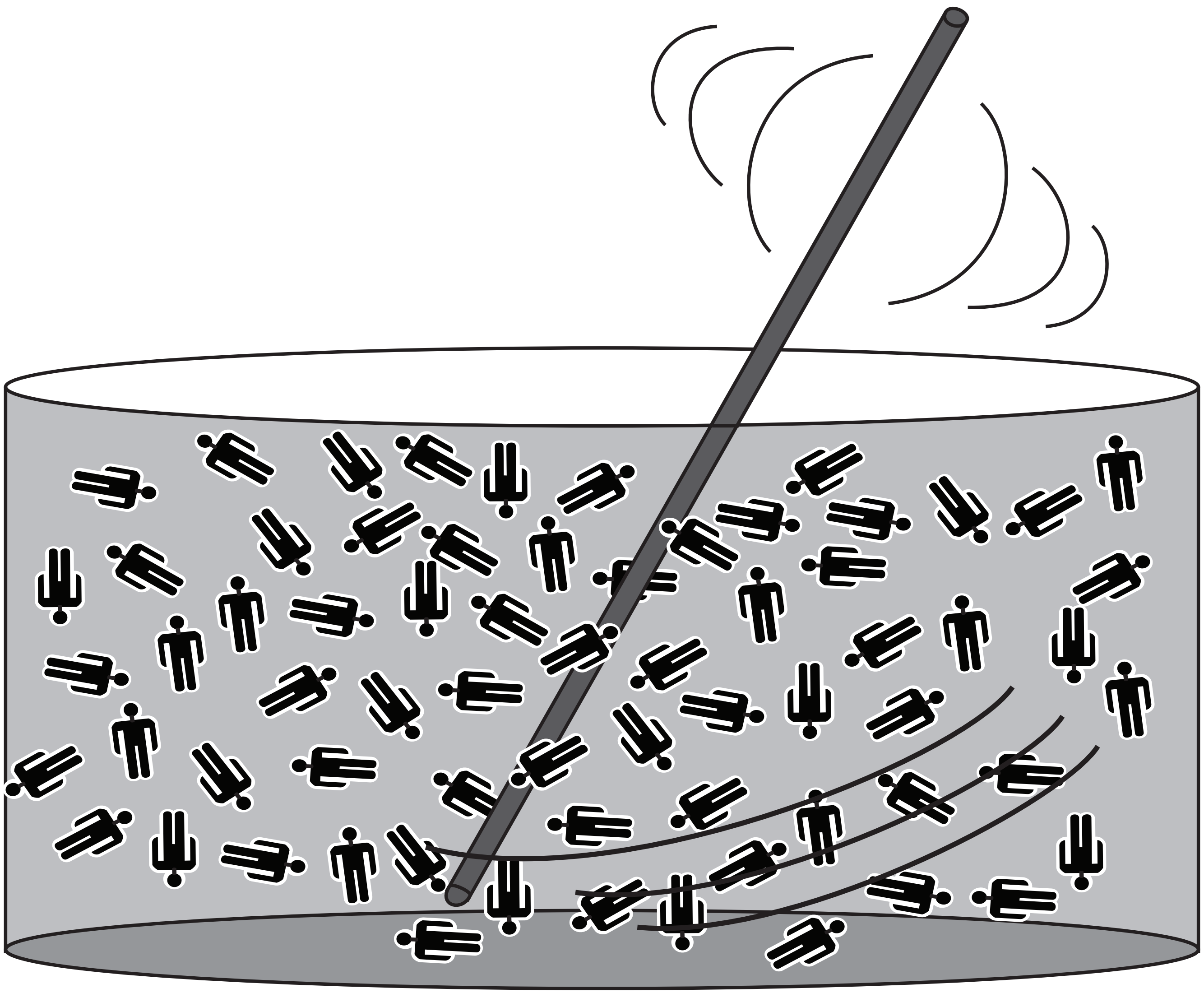
- Background
- Infectious diseases in simple random networks

  Andersson (1998), Molloy and Reed (1995), Newman(2002)
- Hierarchical networks with two populations

  Ramirez-Ramirez and Thompson (a)
- Evolution of infectious process in discrete time
- Control Measures

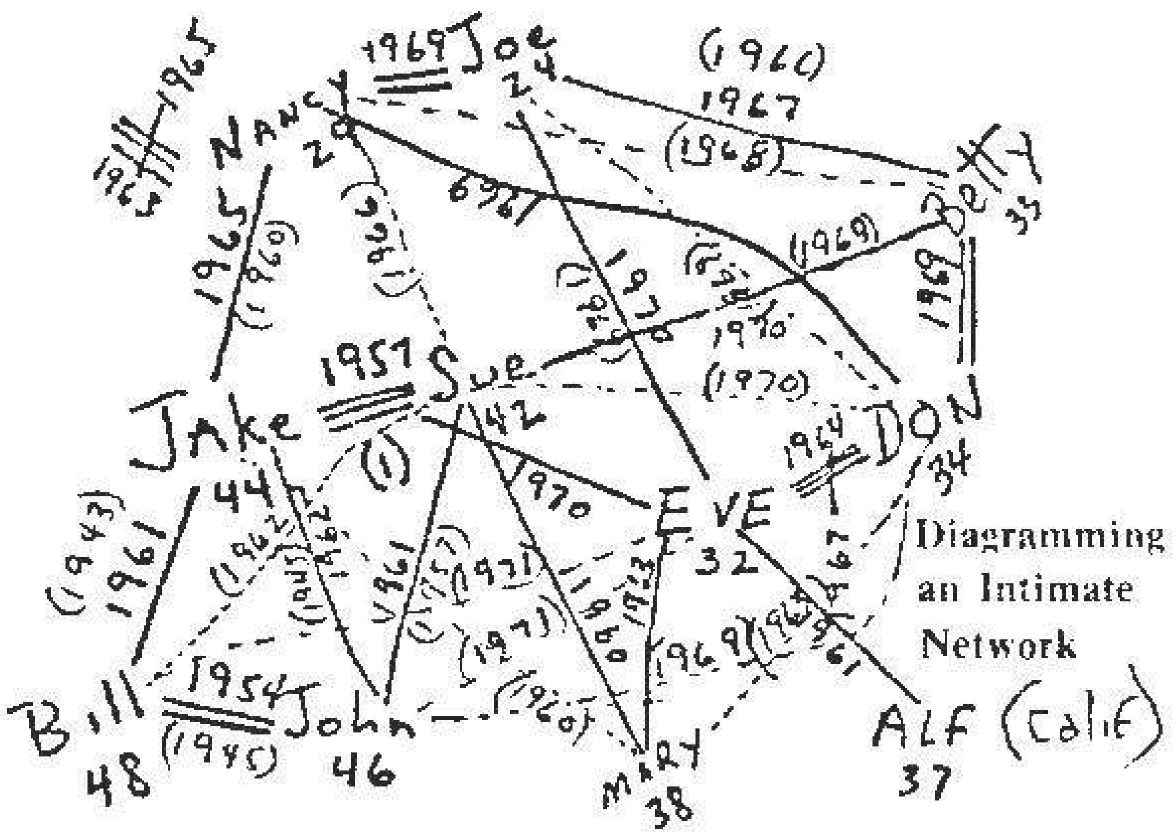
Background

Law of mass action

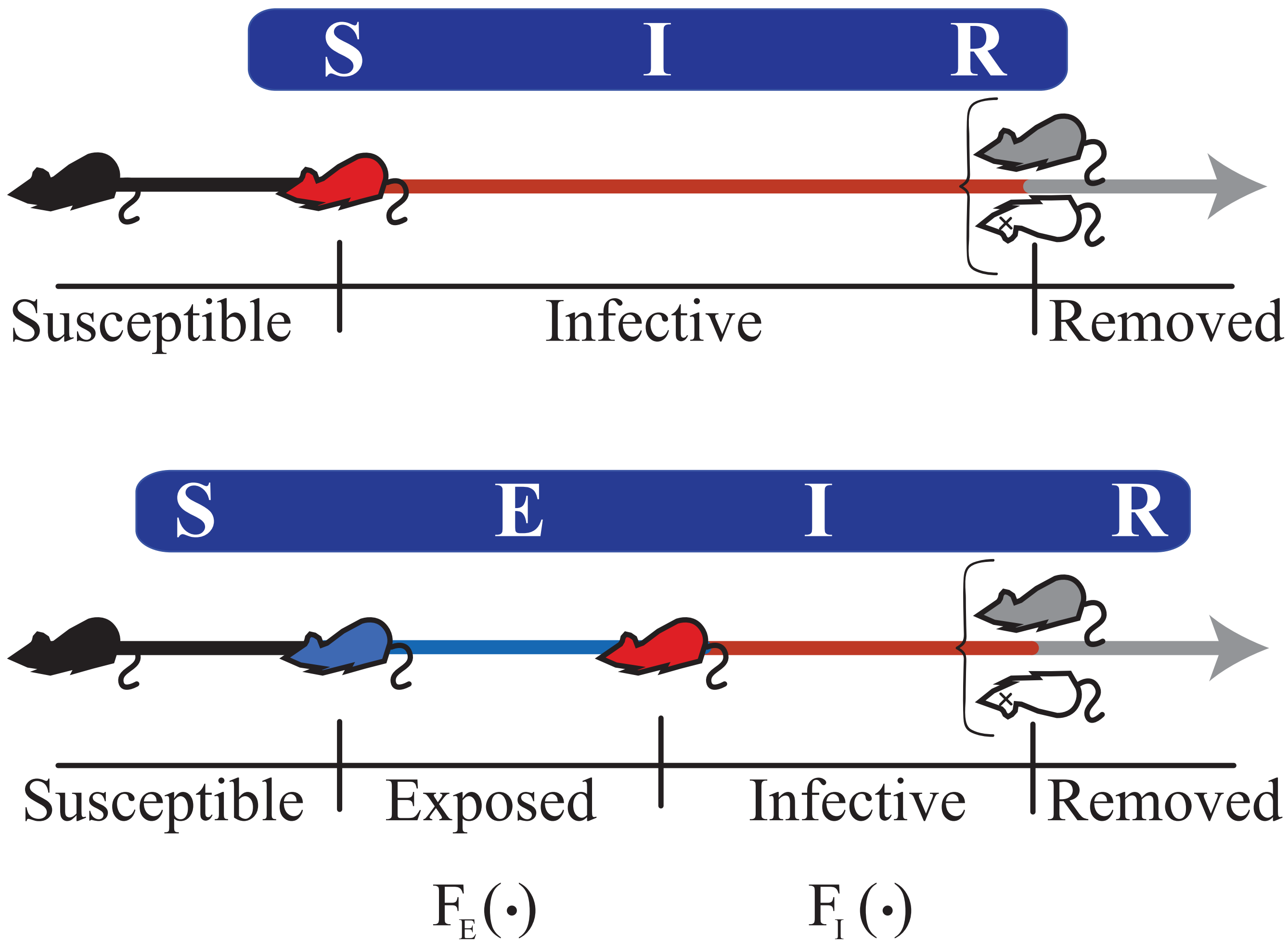


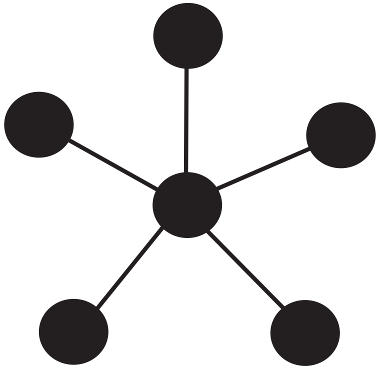
Network of contacts

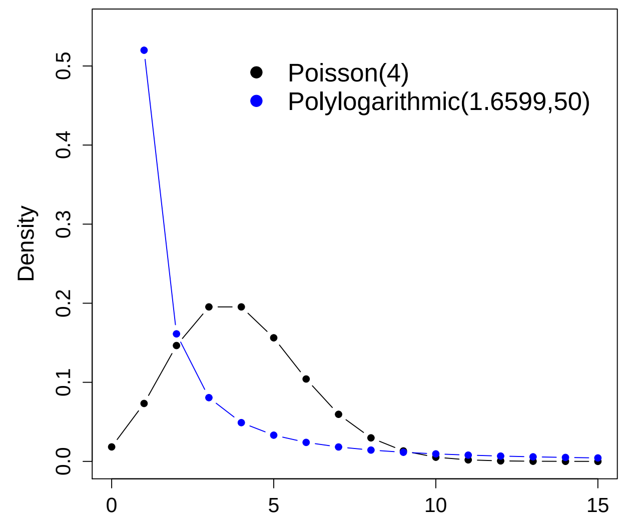
Some infectious diseases are very much affected by the detailed structure of the contacts that can result in transmission.

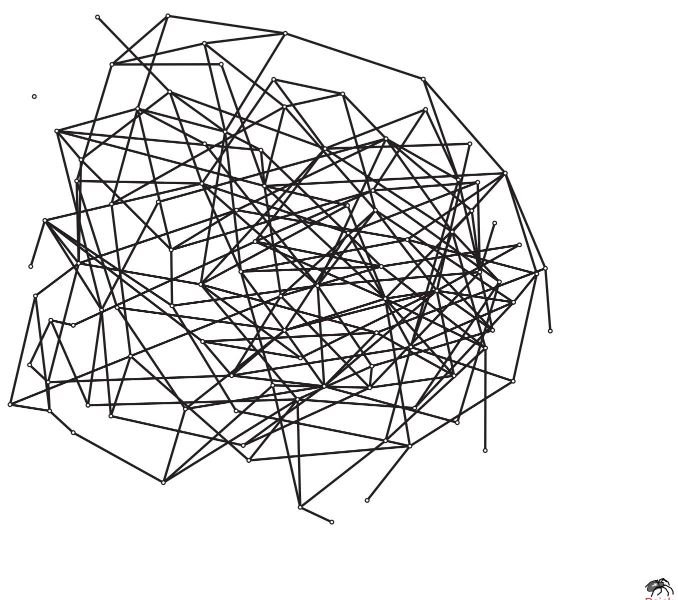


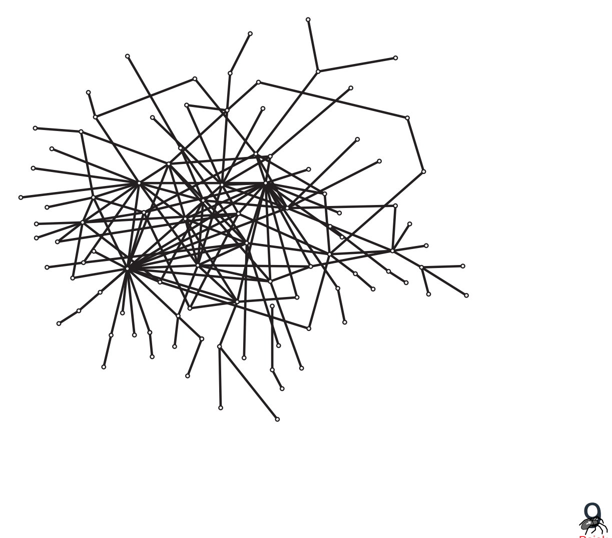
From Luís A. Nunes Amaral's website


S
I
R
Susceptible
Infective
Removed
S
E
I
R
Susceptible
Exposed
Infective
Removed
$F_E(\cdot)$
$F_I(\cdot)$

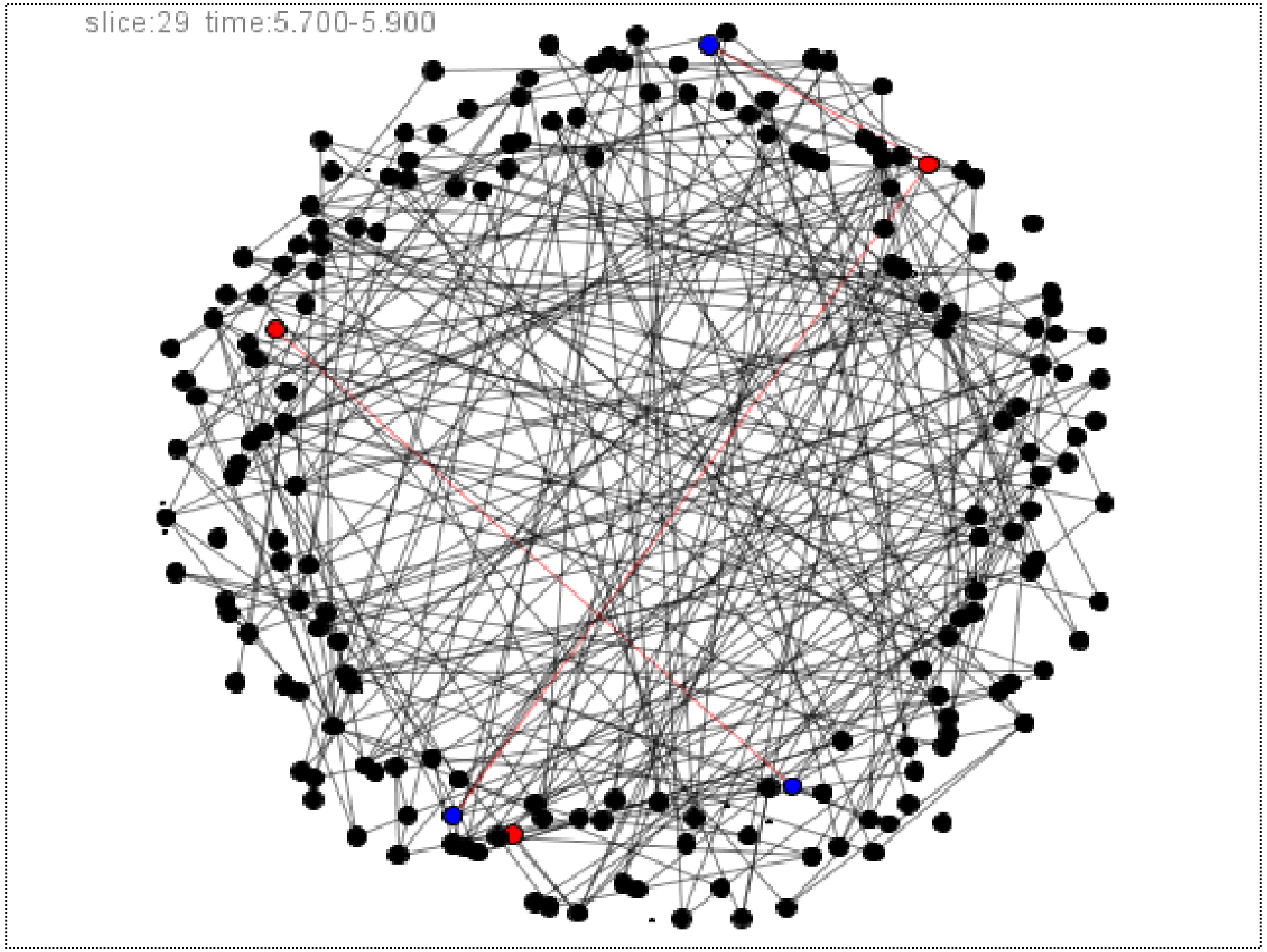



Poisson(4)
Polylogarithmic(1.6599,50)
Density
0.0
0.1
0.2
0.3
0.4
0.5
0
5
10
15


Pajek


Pajek

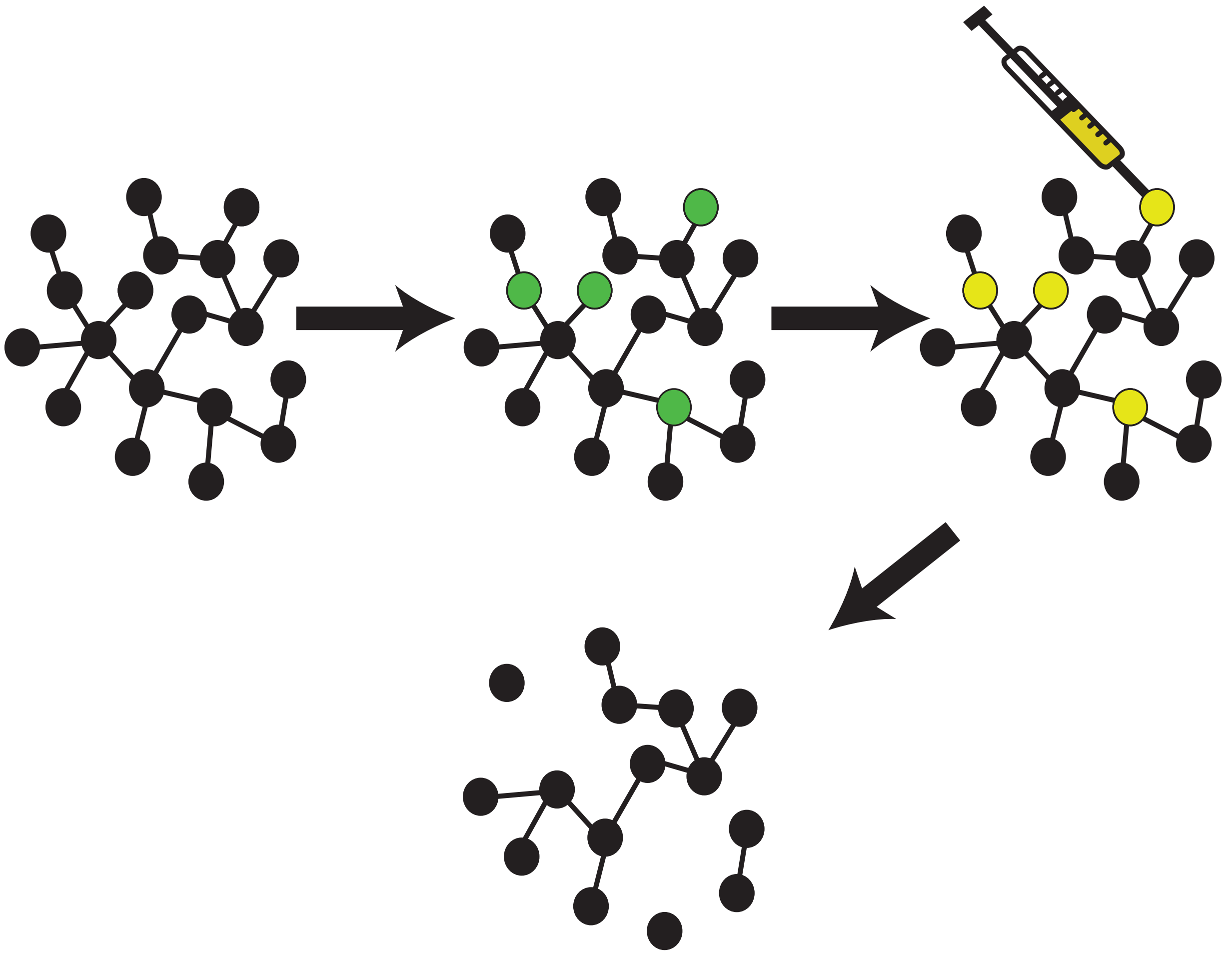
Epidemic in Networks



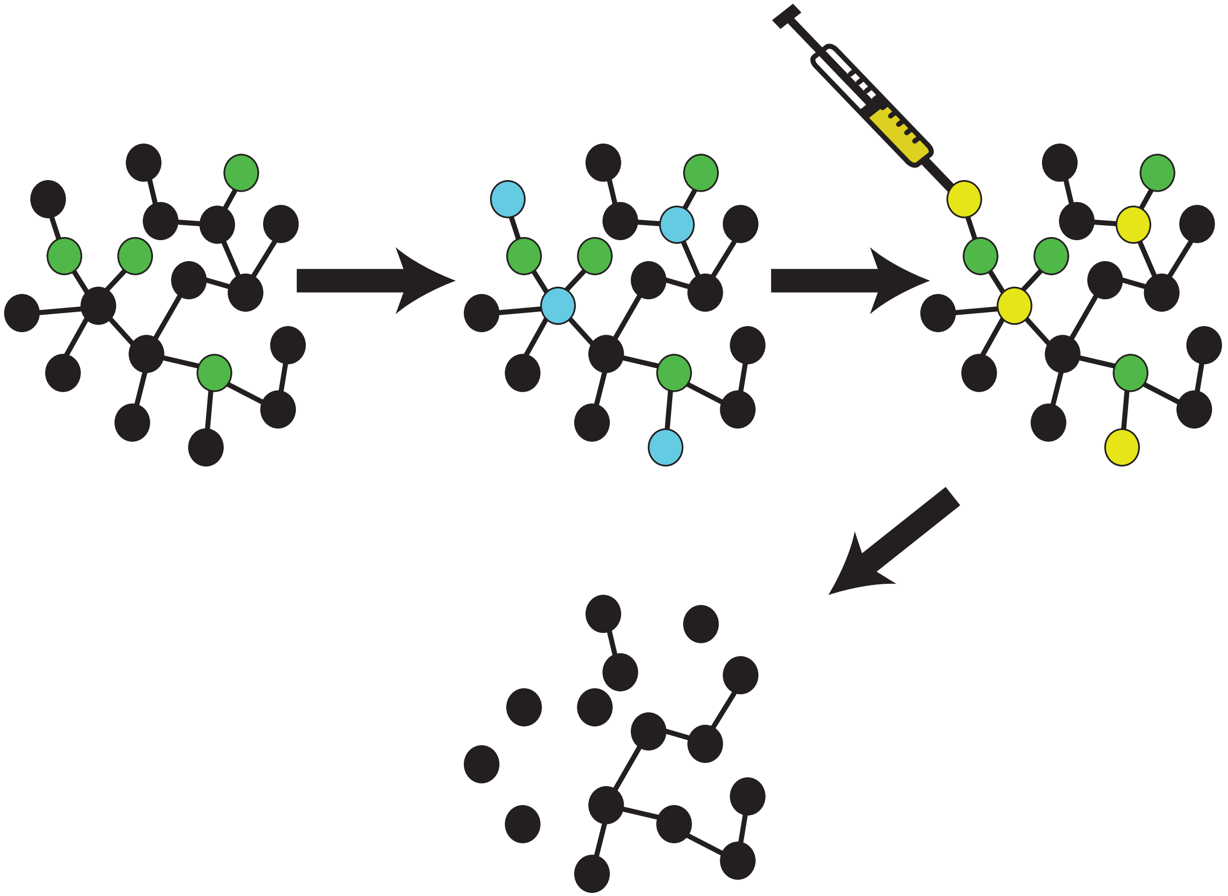
R code visualize with
Social Network Image Animator (Sonia)

Control Measures

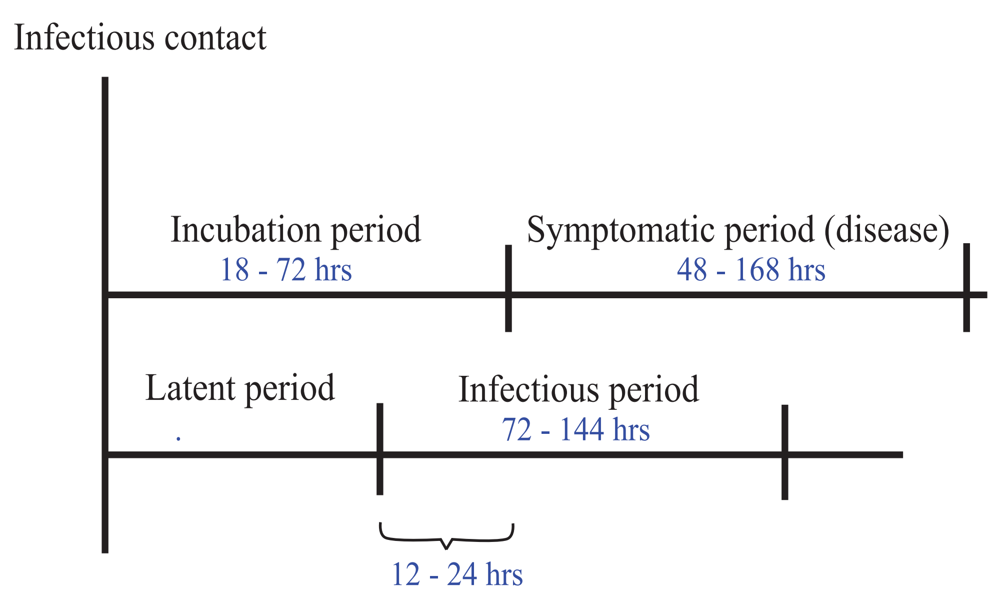
A fraction ν of susceptible individuals is randomly selected and vaccinated prior to an outbreak.



First a fraction ω of susceptible nodes is randomly chosen. Then a neighbor of each of those nodes is randomly selected and vaccinated.



- With probability γ any infectious node i is detected.
- With probability $\mathbf{q}$ each of its neighbors is identified for vaccination (and vaccinated).
- This detection is done after $\mathbf{m}$ units of time since i is infectious.



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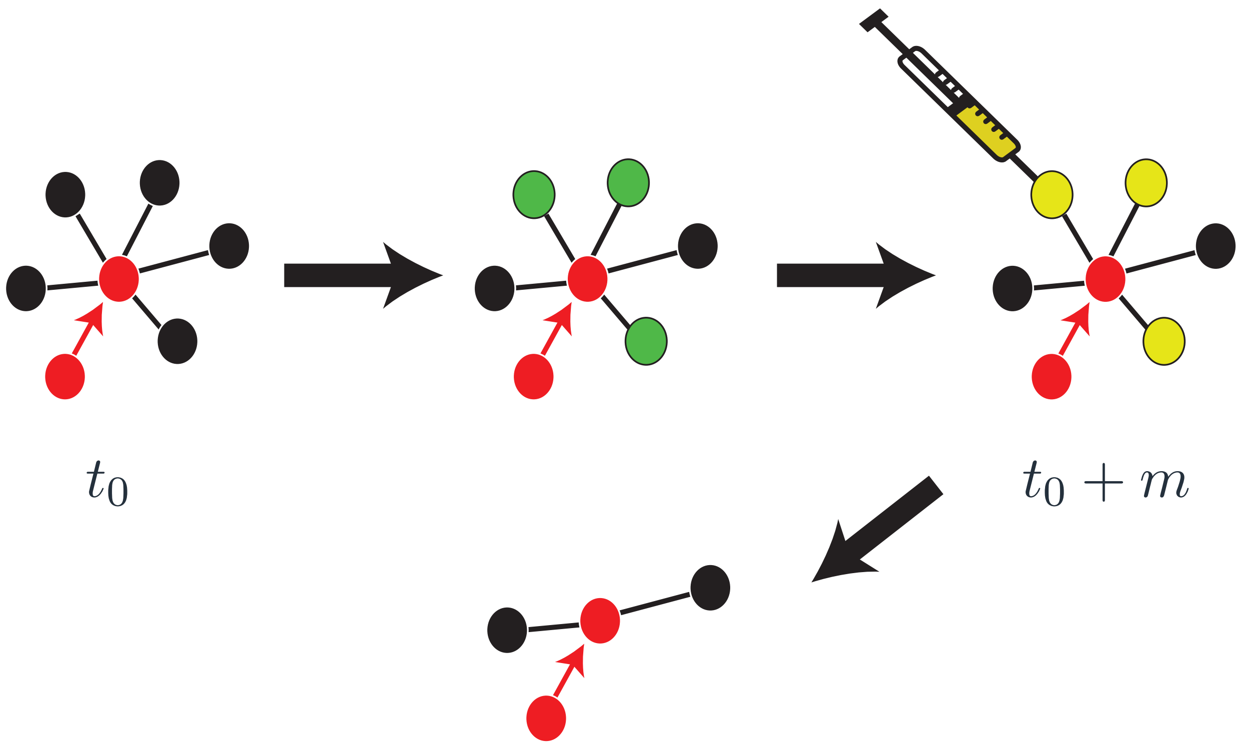
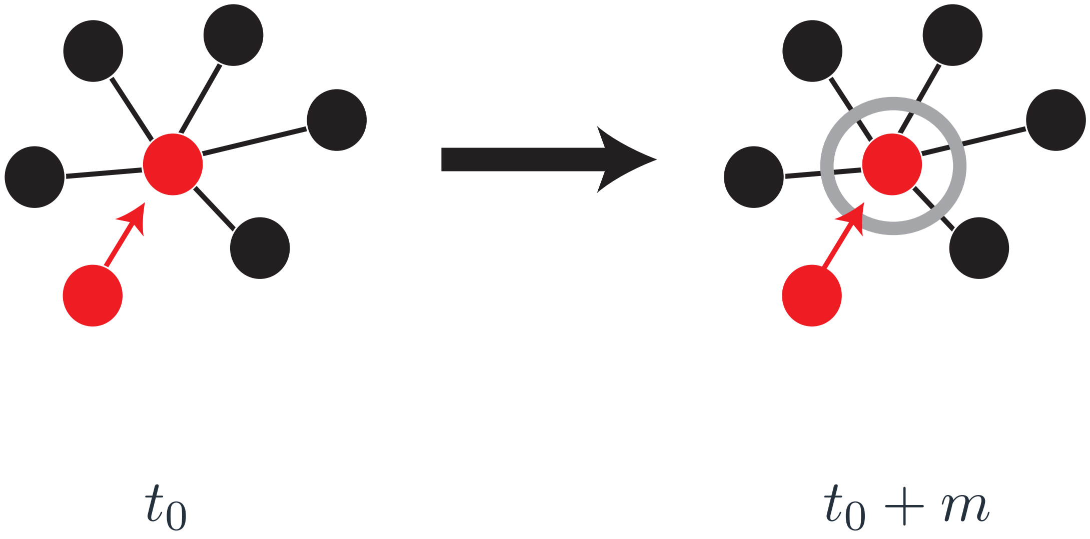


- With probability γ any infectious node i is detected.
- Once detected i is "isolated", reducing its transmission rate by $1 - \alpha \times 100\%$.
- This detection is done after $\mathbf{m}$ units of time since i is infectious.



InfNet-Simulación de redes aleatorias y brotes epidémicos en ellas

Lilia Leticia Ramírez-Ramírez
and Mary E. Thompson

March 30, 2012

¿Como simular una red aleatoria?

Algoritmos

- Havel-Hakim
- Modified Havel-Hakim
- Molloy-Reed
- Selección aleatoria

InfNet

Local.network

- n number of individuals (susceptible and infective)
- distrib is the degree distribution
- param is the distribution parameter (if the function is "fixed" it is a vector of degrees)
- distrib can be "fixed" or "pois" or "ztpois" or "geom" or "nbinom","ztgeom" or "poly.log" or "logarithmic"or "power.law" or "full" (fully connected) or "none" (no element connected)
- one.connection is TRUE when only one connection is allowed between two nodes.
- method specifies the algorithm to build the network: Havel-Hakim ("HH") or Modified Havel-Hakim ("MHH"), Molloy-Reed ("MR") or Random ("Random")

Local.network

```
local.network<-function(n, distrib, param=NULL, one.connection=
TRUE, method="MHH",degree=NULL)
...
list(edges=edges,degree=degree,degree.left=degree.left)
```

connect.two.ln

- Connects two populations (local networks) with the specified degrees using the "MHH" algorithm
- p is the number of individuals in each local network
- degree is in the format of list

```
connect.two.ln<-function(p,degree){
...
list(edges=edges,degree=degree,degree.left=degree.left)}
```

epidemic.sim

- network: network structure (output of global.network)
- ini.infected: number or initial cases in each network
- seir: it is FALSE if model is sir
- ini.infective: number of initially infectives in each network
- obs.time: observation period
- BETA1: parameter of transmission to susceptible
- BETA2: parameter of transmission from an infective
- distrib.lat: distribution of the latent period. The default is poisson resulting in an overal Markov process
- LAMBDA: parameter for the latent period
- distrib.inf: distribution of the infective period. The default is poisson resulting in an overal Markov process

epidemic.sim

- other options are Normal "norm" and lognormal "lnorm".
- GAMMA: parameter of distrib.inf. When distrib.inf is Poisson, it is the reciprocal of the removal rate of infectives. GAMMA is a scalar or vector of length n (Poisson), or a vector of length 2 (normal, lognormal list(c(1,2))) or a matrix of nX2

epidemic.sim

```
epidemic.sim<- function(network=NULL,seir=F,ini.infected=0,
    ini.infective=0,obs.time=0,BETA1,BETA2=1,distrib.lat="norm",
    LAMBDA=NULL,distrib.inf="exp",GAMMA,vac.par=NULL,eff.exp=0,
    eff.inf=0){
....
list(indexes=indexes,time.hist=time.hist,nodes.hist=nodes.hist,
edges.hist=edges.hist,p.hist=p.hist,susp.hist=susp.hist,
infectedp.hist=infectedp.hist,infectivep.hist=infectivep.hist,
remp.hist=remp.hist, n=n)}
```

Ejemplos

```
tempnet<-global.network(1,p=500,distrib="pois",param=2)
epid1<-epidemic.sim(tempnet,ini.infective=1,obs.time=10,BETA=.2,
   distrib.inf="lnorm",GAMMA=list(c(1,.2)))
epid2<-epidemic.sim(tempnet,seir=T,ini.infected=1,obs.time=10,
   BETA=.2,LAMBDA=list(c(1,.1)),GAMMA=.1)
epid3<-epidemic.sim(tempnet,seir=T,ini.infected=1,obs.time=10,
   BETA=.2,distrib.lat="lnorm",LAMBDA=list(c(1,.1)),GAMMA=.1)

tempnet2<-global.network(n=2,p=20,distrib="pois",param=c(2,3),
   distrib.among="pois",param.among=1)
epid21<-epidemic.sim(tempnet2,seir=T,ini.infected=c(2,3),
   obs.time=10,BETA=.2, distrib.lat="norm", LAMBDA=
   list(c(1,.1),c(2,.1)),GAMMA=.2)
epid22<-epidemic.sim(tempnet,ini.infective=1,obs.time=10,BETA1=.2,
   BETA2=c(rep(1,10),rep(.1,10),rep(1000,10)),distrib.inf="lnorm",
   GAMMA=list(c(1,.2)))
```

SIMID: ***SIM**ulation of **I**nfectious **D**isease*

A tool for simulation of infectious disease, enabling spatio-temporal visualization of the dynamics of influenza outbreaks.

Eileen de Villa, Peel Public Health
Matt McPherson, Infonaut
Lilia Leticia Ramírez Ramírez, University of Waterloo

The Ontario Public Health Convention (TOPHC)
April 7, 2011

Overview

- About SIMID
  - Project Overview
  - How it Works
- Benefits & Challenges
- What's Next

Project Overview

What We Developed

- A tool to enable **visualization of the dynamics of infectious disease outbreaks over time and space**. (starting with **influenza**, including pH1N1 and seasonal influenza)
- A tool that can **educate & inform** public health officials to **create a more effective local infectious disease outbreak planning process**
- A system design paradigm & technology platform **applicable to other health-related urgent responses**

Why We Developed It

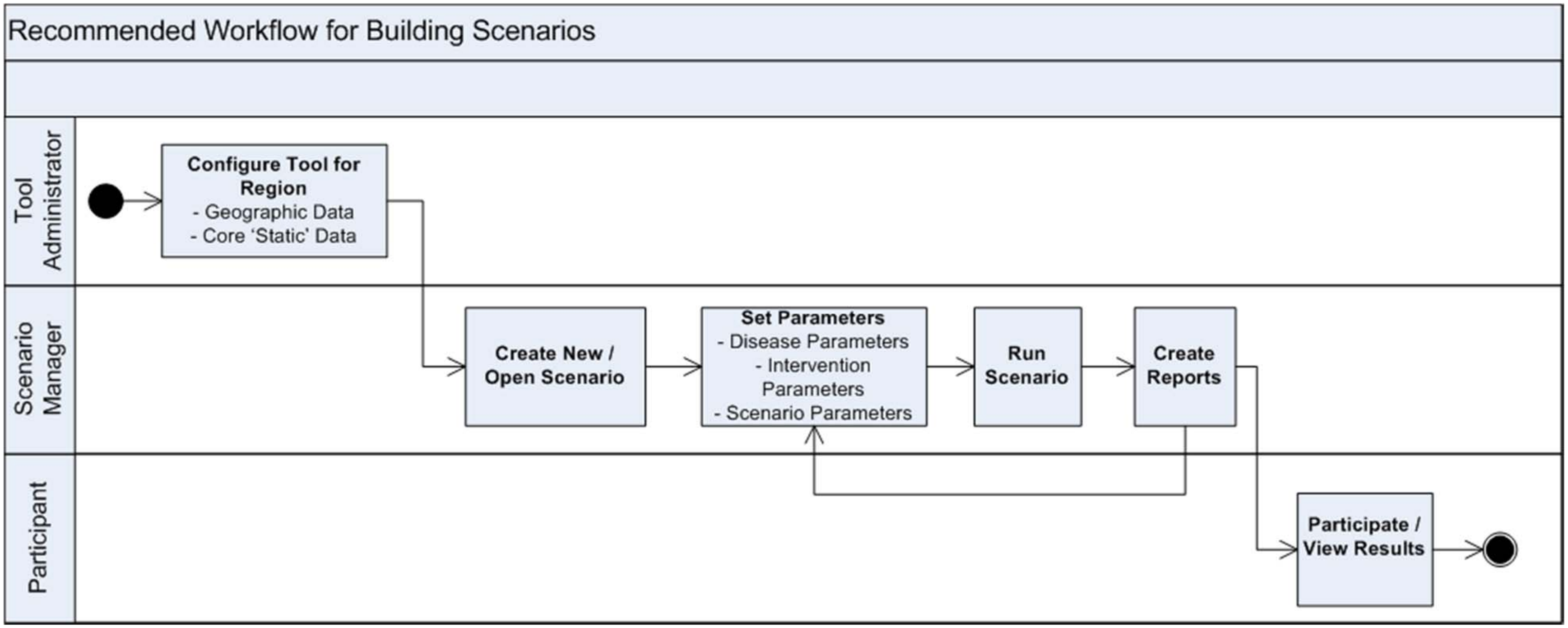
- To **provide public health officials and key decision makers** with more effective local infectious disease outbreak planning tools
- To **create a tool that can be modified** for other infectious disease outbreaks and health-related urgent response
- To **reduce the time required to prepare** for and **respond** to public health emergencies
- Being better prepared for emergencies, including infectious disease outbreaks, **mitigates their negative impact**

Our Vision

"To create a more effective planning process for local infectious disease outbreaks and other disasters by allowing decision makers to visualize the dynamics of the outbreak over time within their own community"

How It Works

Basic Workflow



SIMID Under the Hood – How it Works (1)

- 'Scenario Manager' parameterizes & tests a simulation in **DRAFT**

⬇

- Scenario Manager chooses to **RUN** a simulation

⬇

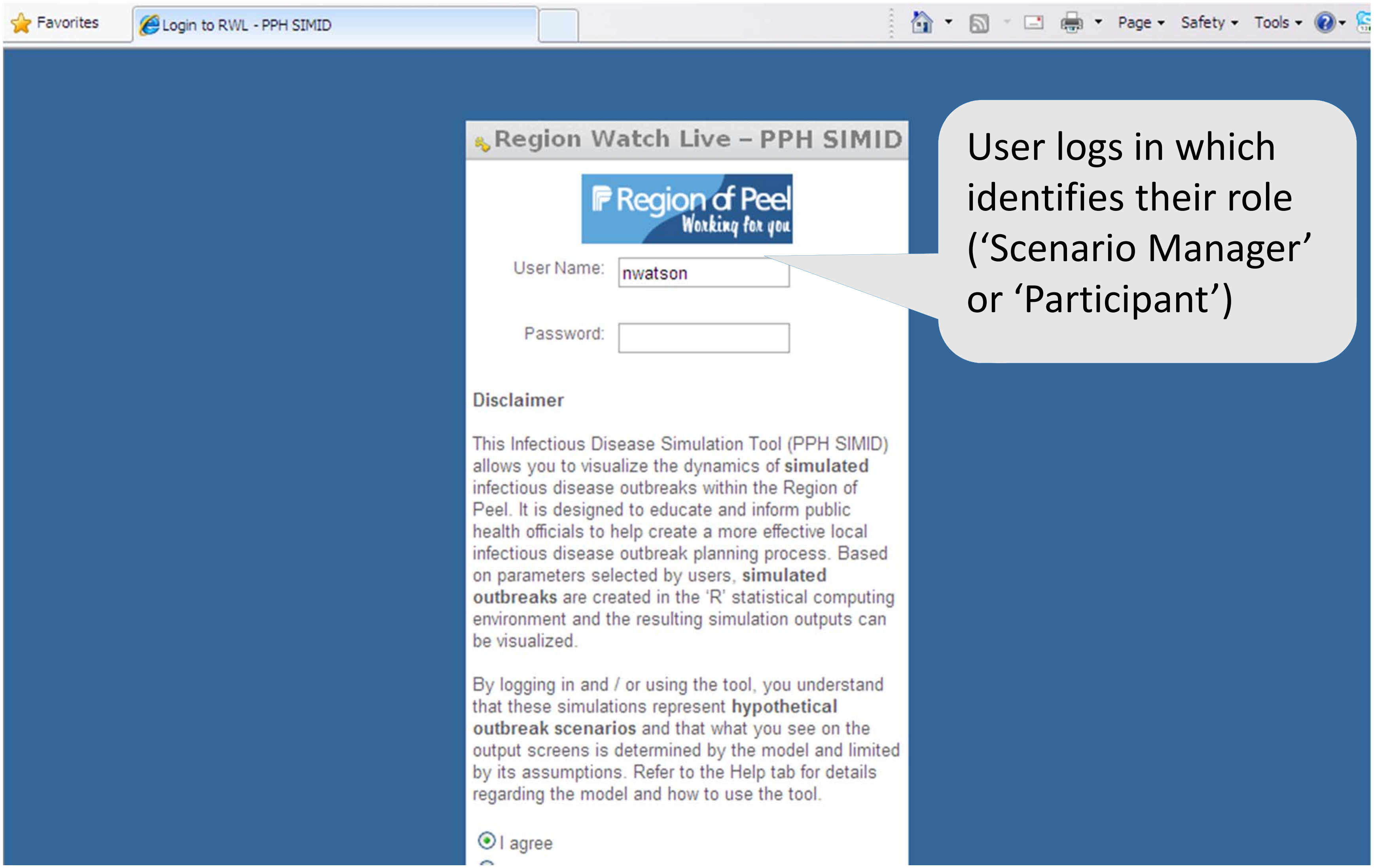
- A **Job Service** tells R software that a simulation is 'waiting' and executes the simulation in R

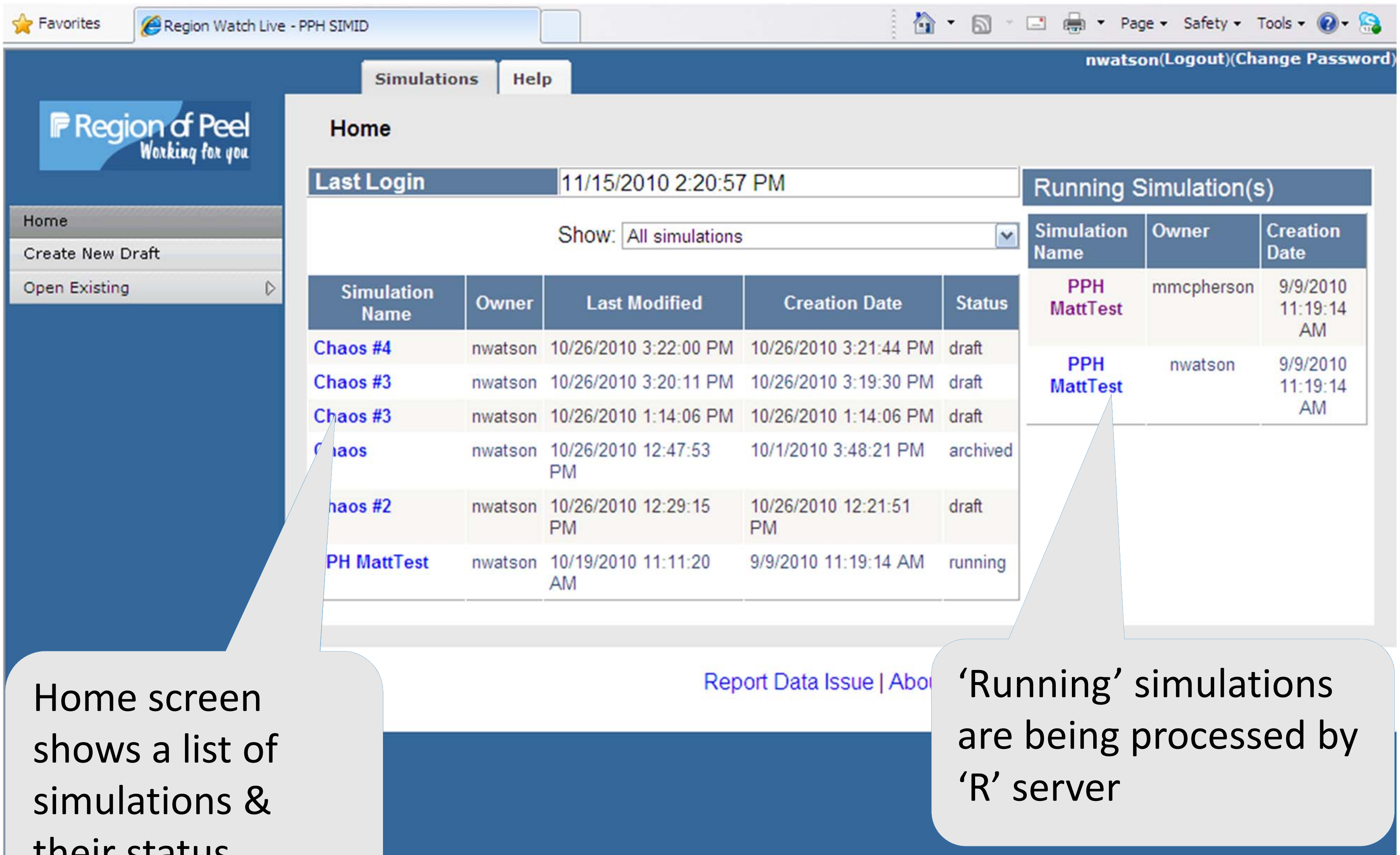
⬇

- When a simulation completes in R, data output is created

SIMID Under the Hood– How it Works (2)

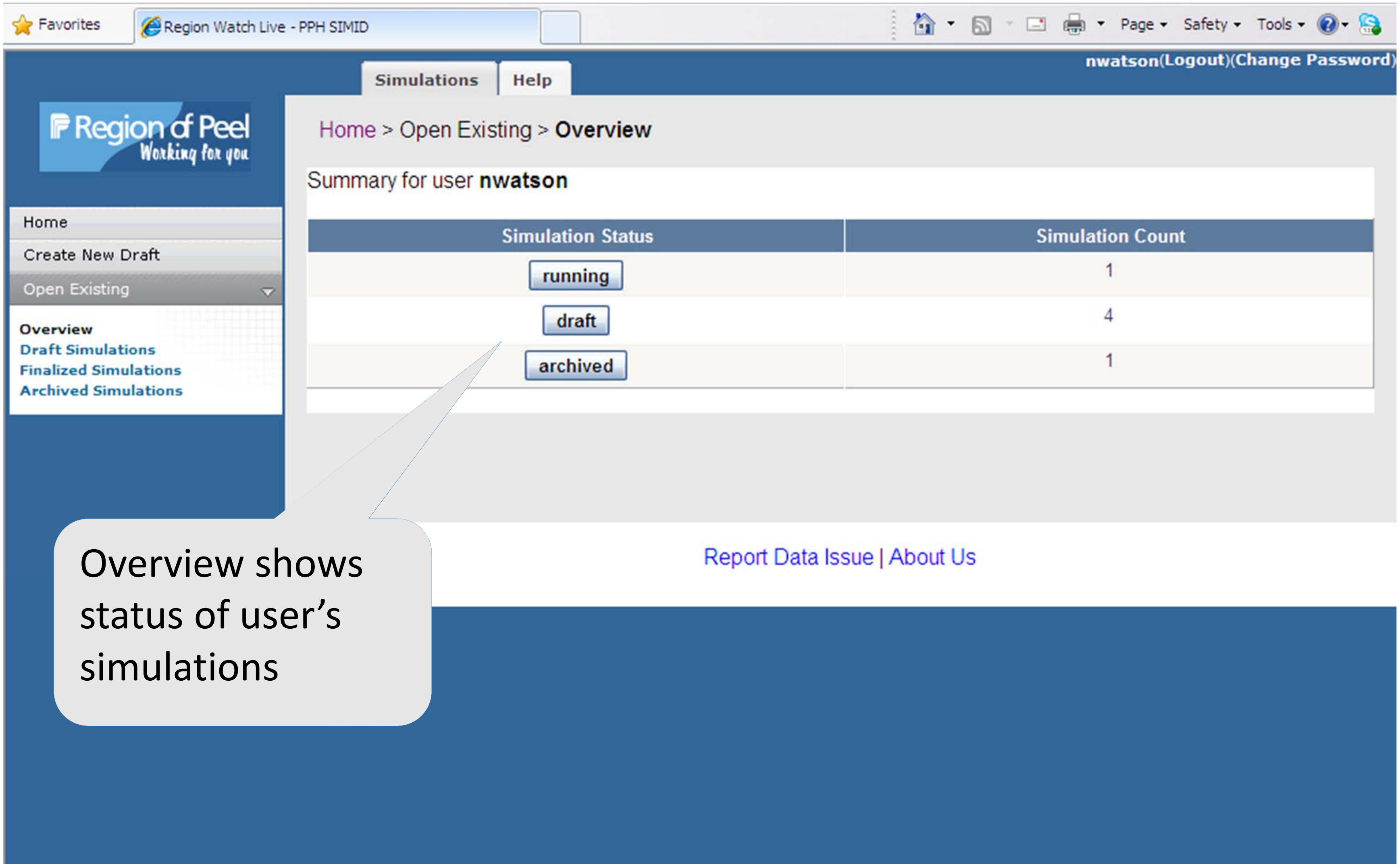
- Job service ‘listens’ to SIMID and determines whether the simulation has completed
- Once completed, Job Service takes a completed output generated by R and imports data into SIMID
- Simulation data is used by SIMID to generate map outputs & other simulation statistics.


Favorites
Login to RWL - PPH SIMID
Page
Safety
Tools
Region Watch Live – PPH SIMID
Region of Peel
Working for you
User Name:
nwatson
Password:
Disclaimer
This Infectious Disease Simulation Tool (PPH SIMID) allows you to visualize the dynamics of **simulated** infectious disease outbreaks within the Region of Peel. It is designed to educate and inform public health officials to help create a more effective local infectious disease outbreak planning process. Based on parameters selected by users, **simulated outbreaks** are created in the 'R' statistical computing environment and the resulting simulation outputs can be visualized.
By logging in and / or using the tool, you understand that these simulations represent **hypothetical outbreak scenarios** and that what you see on the output screens is determined by the model and limited by its assumptions. Refer to the Help tab for details regarding the model and how to use the tool.
I agree
User logs in which identifies their role ('Scenario Manager' or 'Participant')



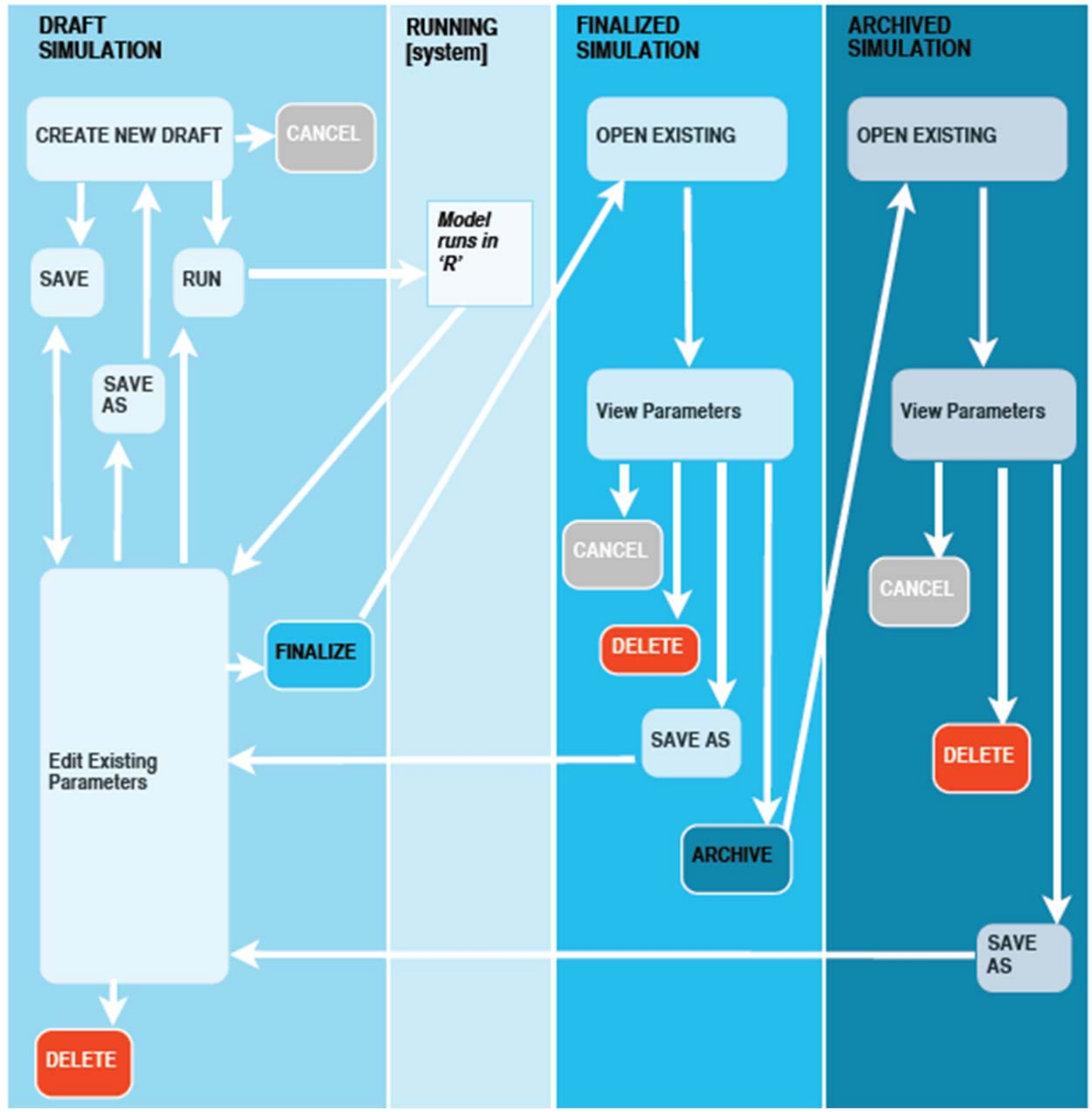
Home screen shows a list of simulations & their status

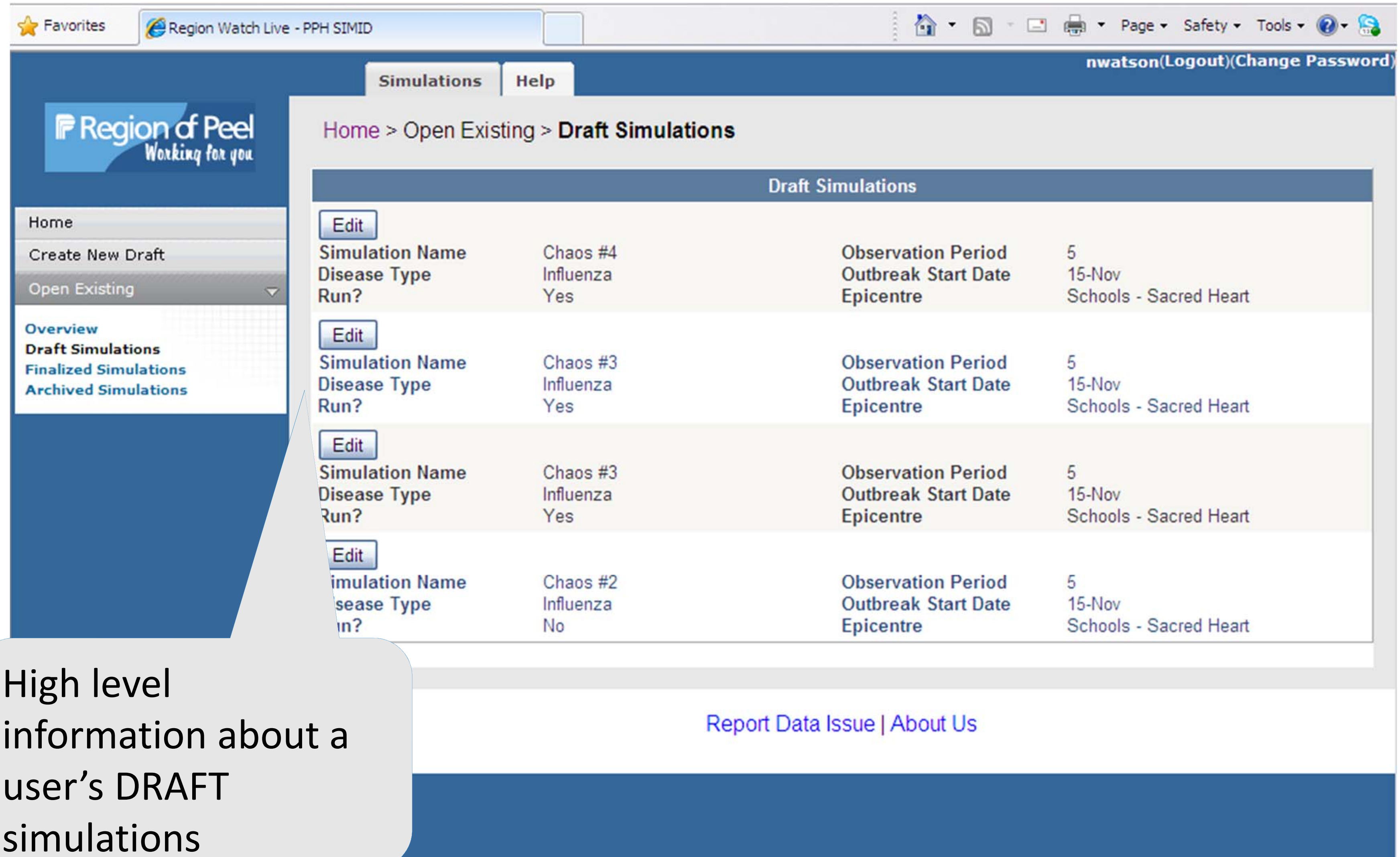
'Running' simulations are being processed by 'R' server


Favorites
Region Watch Live - PPH SIMID
Page Safety Tools
nwatson(Logout)(Change Password)
Simulations
Help
Region of Peel
Working for you
Home
Create New Draft
Open Existing
Overview
Draft Simulations
Finalized Simulations
Archived Simulations
Home > Open Existing > Overview
Summary for user nwatson
Simulation Status
Simulation Count
running
1
draft
4
archived
1
Report Data Issue | About Us
Overview shows status of user's simulations

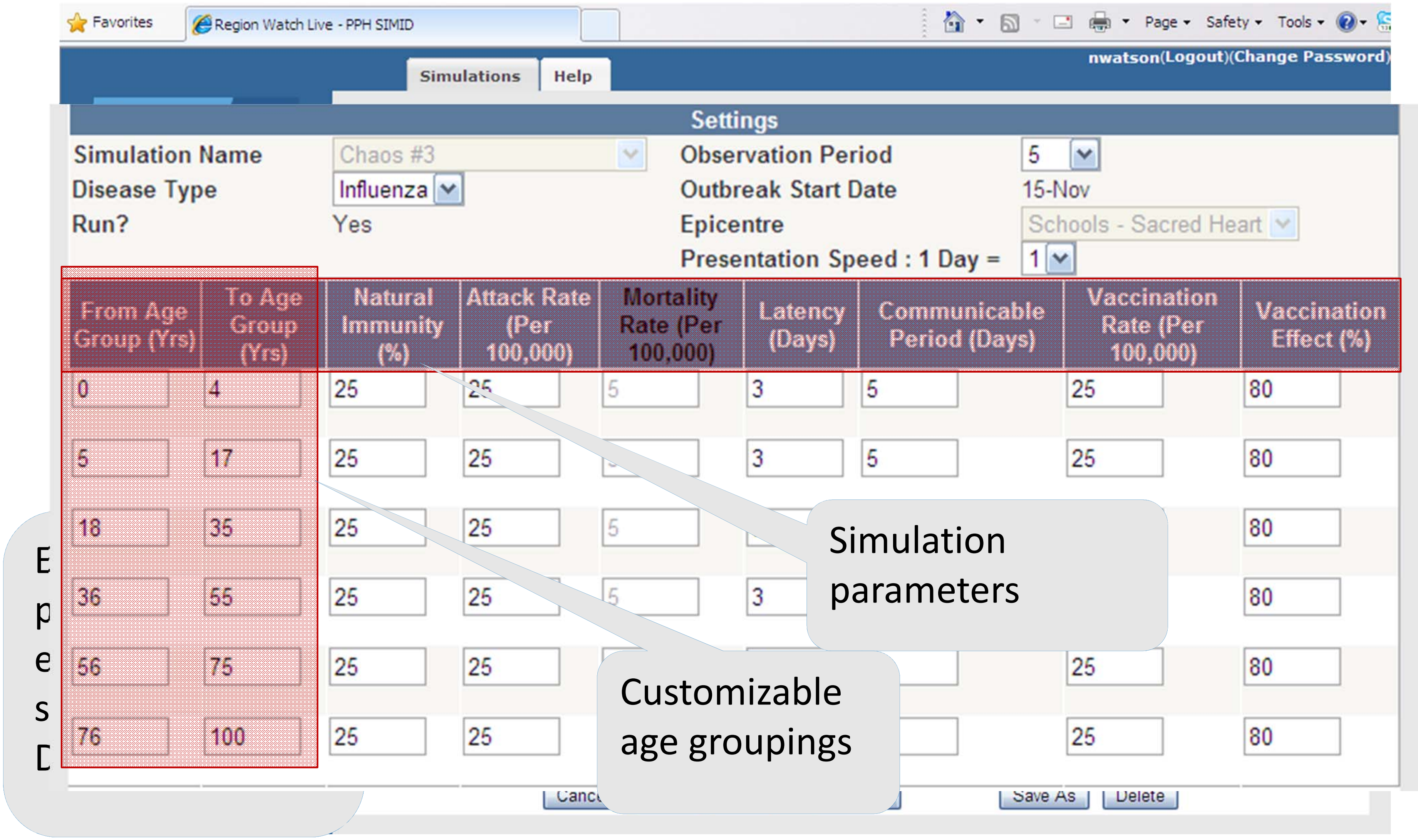
The lifecycle of a simulation, from DRAFT, to RUNNING, to FINALIZED, to ARCHIVED status

Simulation Lifecycle



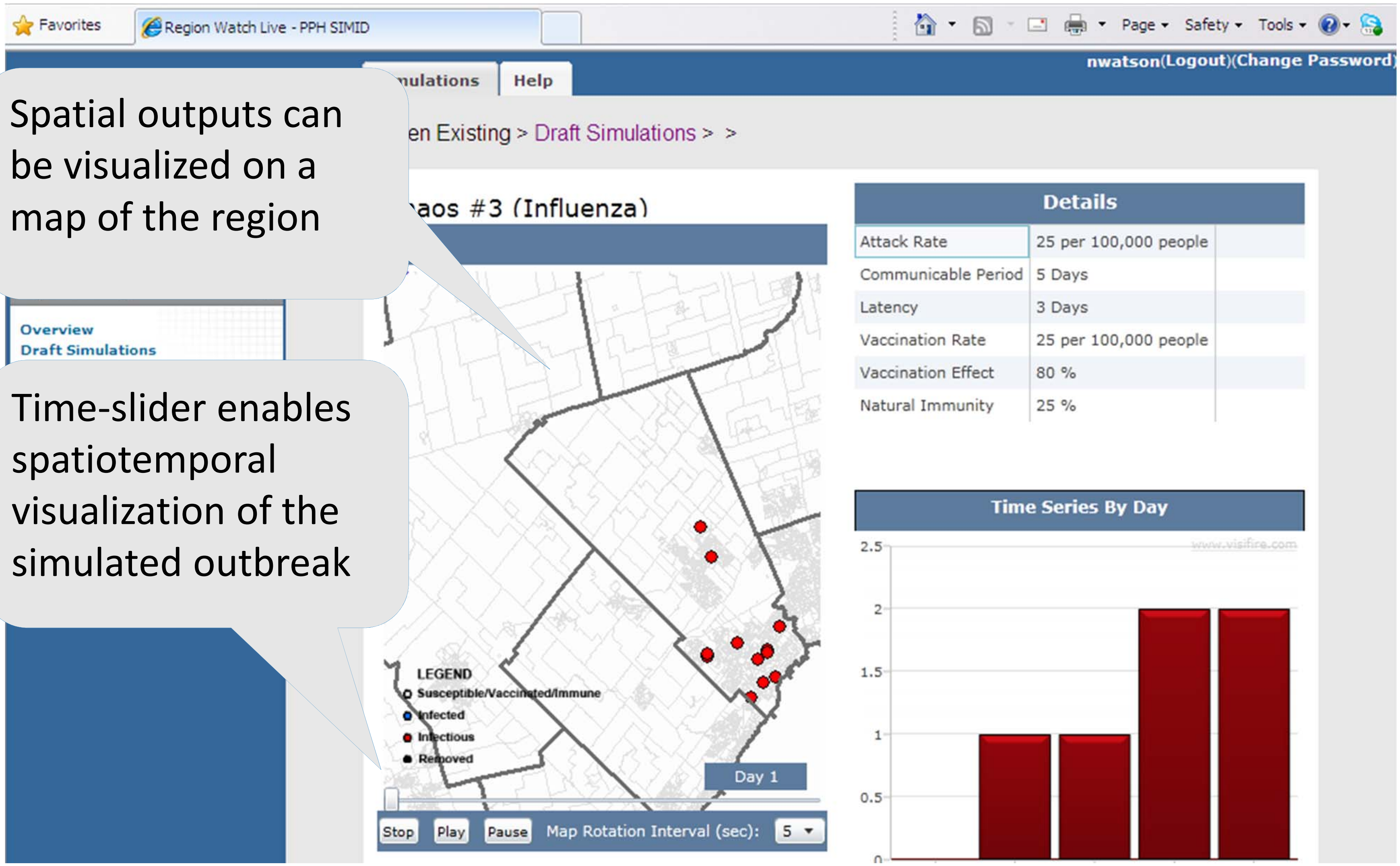


High level information about a user's DRAFT simulations


Favorites
Region Watch Live - PPH SIMID
Page
Safety
Tools
nwatson(Logout)(Change Password)
Simulations
Help
Settings
Simulation Name
Chaos #3
Observation Period
5
Disease Type
Influenza
Outbreak Start Date
15-Nov
Run?
Yes
Epicentre
Schools - Sacred Heart
Presentation Speed : 1 Day =
1
From Age Group (Yrs)
To Age Group (Yrs)
Natural Immunity (%)
Attack Rate (Per 100,000)
Mortality Rate (Per 100,000)
Latency (Days)
Communicable Period (Days)
Vaccination Rate (Per 100,000)
Vaccination Effect (%)
Save As
Delete
Simulation parameters
Customizable age groupings

Spatial outputs can be visualized on a map of the region

Time-slider enables spatiotemporal visualization of the simulated outbreak



About the Model Used

- Network Model developed in collaboration with University of Waterloo

- For details of the model see:

  Ramírez Ramírez, L. L. (2008) “On the dynamics of infectious diseases in non-homogeneous populations” (http://uwspace.uwaterloo.ca/bitstream/10012/4054/1/llramireThesis.pdf)

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Benefits

Benefits (1)

Modeling for 'Non-Modelers'

Complex disease models developed in 'R' language can be parameterized, run and visualized **by field personnel** who are designated 'Scenario Managers'

Collaborative Modeling

Scenario Managers can explore simulations, change parameters and then **share outputs** with designated 'Participants'

Potential End-Users ('Participants')

- **Public Health**
  - Epidemiologists
  - MOH Personnel
  - Emergency Planners
  - Infection Control Specialists
  - Surveillance Managers
  - Front Line Case Management Staff
- **Institutions**
  - Emergency Site Managers
  - Infection Control (Acute care)
  - Infection Control (LTC)
  - Institutional Planners
  - Emergency Room surge capacity Managers
  - Hospital Administrators
  - LTC Facility Administrators
- **Municipalities**
  - Emergency Services (911)
  - Emergency Management
  - Municipal Operations Centre
  - Public Works
  - Emergency Medical Services
  - Municipal Planners
  - RICN Coordinators

Benefits (2)

Enhanced Table-Top Exercises

Simulations can be developed to support 'table-top' exercises with high-fidelity scenarios

Cultivates a 'Learning Organization'

Creates intra/inter-organizational knowledge by testing assumptions and exploring 'What if' scenarios, e.g.:

- contrasting simulated interventions
- evaluating response times
- quantifying costs

Benefits (3)

Expandable Platform

Can be expanded to accommodate:

- Additional parameters for influenza, including interventions;
- Additional influenza models developed with R language
- Models for additional disease types and others health-related emergency response

Challenges

Challenges (1)

“All Models Are Wrong, Some Are Useful”[1]

Modeling by nature is an exercise in uncertainty… the model is not predictive

Challenge setting user expectations with respect to the limitations of the model vs. real world events

Our approach was to create a learning tool capable of creating a range of possible ‘What if’ scenarios for organizational learning

1. Attributed to George E.P. Box

Challenges (2)

Complexity & Knowledge Translation

Knowledge translation among a wide variety of highly specialized professionals: e.g. **mathematical modelers**, **developers**, **epidemiologists**, **public health practitioners**

Technological Changes

Technological changes during the design phase dictated a change in some system components… impacting our workplan, resource requirements and the effort involved

Challenges (3)

Pandemic H1N1 response

Key project collaborators were occupied with the pandemic H1N1 response

Collaborators managing a real event find it hard to find time to plan for an imaginary event

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Next Steps (1)

Further Testing

Due to some of the challenges mentioned, our team was unable to complete thorough pilot testing

Consume Additional Influenza Models

SIMID platform is designed for reuse including:

- System architecture
- ‘Job service’ that integrates GIS & ‘R’
- System development methodology
- Geo-processing service

Next Steps (2)

Customize for Additional Disease Types

Reuse capabilities offer a collaborative platform for public health emergency planning, e.g.:

- Infectious Diseases
- Environmental Health
- CBRN (Chemical, Biological, Radiological & Nuclear)

Opportunity for Expanding the Tool for Other Communicable Diseases / Urgent Response

Next Steps (3)

Identify Additional Partners, including:

- **Hosting Partner – *Need to 'Find a Home'***
- Additional Sources of Funding
- Additional End-Users / Emergency Planners at the local level

Opportunity for Deployment in Other Jurisdictions

Acknowledgements

Region of Peel / Peel Public Health	University of Waterloo	Infonaut Inc.
Danielle Steinman Monali Varia	Yulia Gel Matthew Lok Mary Thompson	Colin Furness Niall Wallace Neil Watson Jane Yu

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Kieran Moore Adam Van Dijk	Natasha Crowcroft Steven Johnson Cary Luner Jemila Seid Hamid Haranadha Puttur Adrian Rose Jim Tom	

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