

**GLEAMviz.org**

The Global Epidemic and Mobility Model



# GLEAMviz SIMULATOR CLIENT MANUAL

Version 7.0



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# INTRODUCTION

This is the manual for the *GLEAMviz Simulator client*, which together with its server-side counterpart constitutes the *GLEAMviz Simulator system*. This system is a scientific application designed for researchers and students in the field of epidemiology who are interested in performing simulations of the spreading of infectious diseases on a global scale. It is based on the *Global Epidemic and Mobility model (GLEAM)*, a stochastic computational model that integrates high-resolution demographic and mobility data, and uses a compartmental approach to define the epidemic characteristics of the infectious disease. More details on this model can be found on <http://www.gleamviz.org> and in Reference [1].

The client application is used to configure the simulations, to submit them for execution by the simulation engine on the server, and to retrieve and visualize the numerical results. The client consists of a few major components and windows: 1) the *Simulation*

- 1.1 RELEASE NOTES
- 1.2 LICENSE
- 1.3 CONDITIONS OF USE
- 1.4 CLIENT INSTALLATION AND REQUIREMENTS
- 1.5 CREDITS

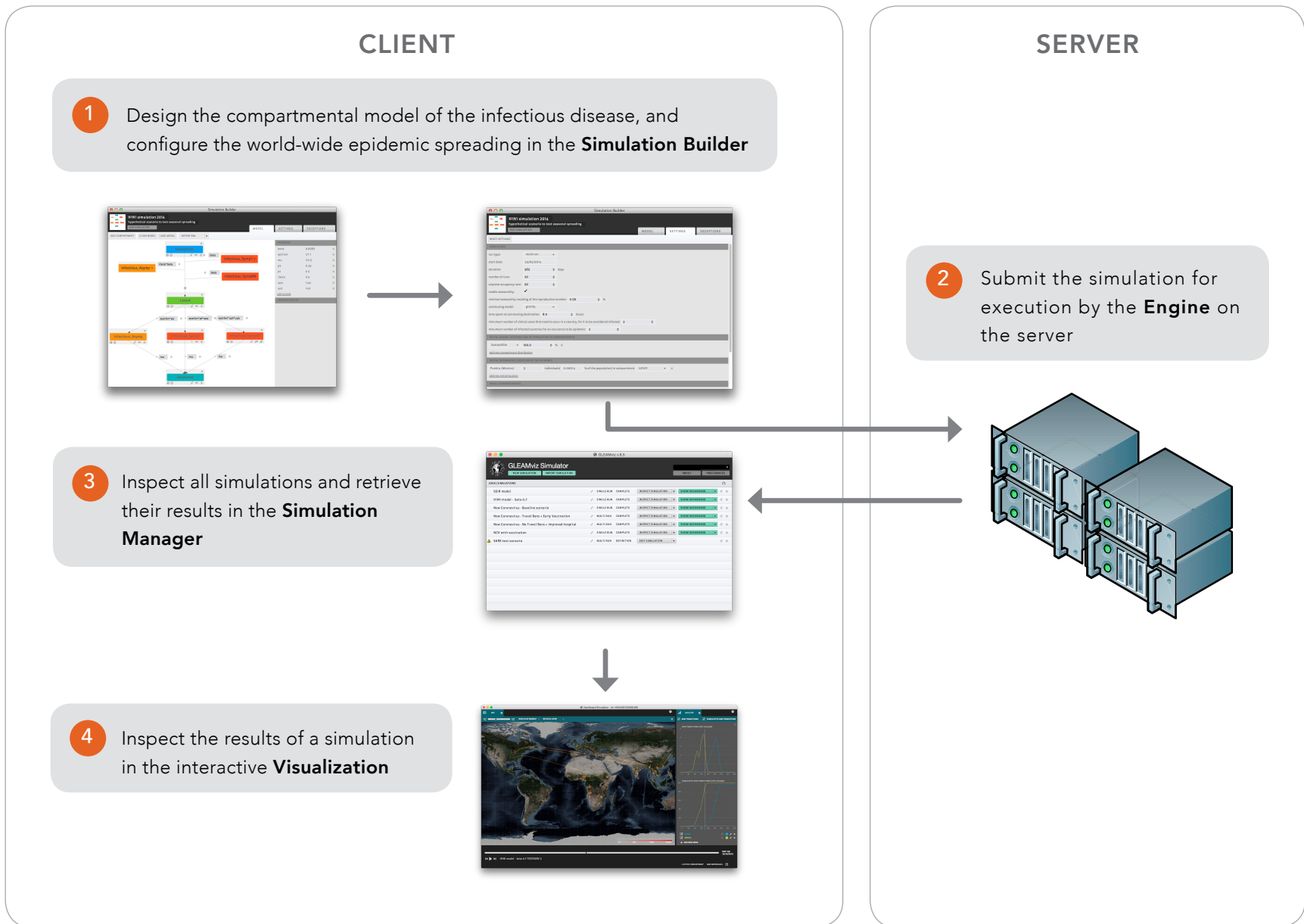


Figure 1.1: Workflow overview and the role of the client and server components.

*Manager*; 2) the *Simulation Builder*; and 3) the *Visualization Dashboard*. Each of these components is described in more detail in the following chapters. The main workflow and the role of the components in this workflow are outlined in the diagram in Figure 1.1.

The usage of the Simulator tool requires users to perform a free registration, and to authenticate on the GLEAMviz server before submitting simulations for execution.

For more information about the *GLEAMviz Simulator* system please refer to the project's web-page: <http://www.gleamviz.org/simulator>.

Version 7.0 of the GLEAMviz Simulator features a major rewriting of the software components handling the simulations' output data. The data format has been changed to a standard format (HDF5) suitable for extending the current output. Some important architectural refactorings have been conducted, bringing together a performance increase. Version 7.0 also features a new widget, the Country Globe, as well as some bug-fixes and improvements.

To convert saved simulations using the old format (up to version 6.9) we are providing a simple tool, distributed together with the main application, called GLEAMconverter; its usage is straightforward, just select the simulations you want to convert and the output directory where to save them.

There are two distinct editions of the *GLEAMviz Simulator client*: the *Public Edition*, which is publicly accessible but has a number of limitations, and the *Unlimited Edition*.

The *Public Edition* of the software application is distributed with the Software-as-a-Service (SaaS) paradigm and is freely usable according to the conditions of use reported below.

## 1.1 RELEASE NOTES

## 1.2 LICENSE

## 1.3 CONDITIONS OF USE

The full system setup, including the server application, can be requested by public institutions and research centers; conditions of use and possible restrictions will be evaluated specifically. If interested, please contact us at: [info@gleamviz.org](mailto:info@gleamviz.org).

All material obtained directly from the simulation products of the *GLEAMviz Simulator*, or further processed, can be published by providing the appropriate credit to the website of the project ([www.gleamviz.org](http://www.gleamviz.org)) and the following publications:

1. **The GLEAMviz computational tool, a publicly available software to explore realistic epidemic spreading scenarios at the global scale.** W. Van den Broeck, C. Gioannini, B. Gonçalves, M. Quaggiotto, V. Colizza, and A. Vespignani. *BMC Infectious Diseases* 11, 37 (2011).
2. **Seasonal transmission potential and activity peaks of the new influenza A(H1N1): a Monte Carlo likelihood analysis based on human mobility.** D. Balcan, H. Hu, B. Gonçalves, P. Bajardi, C. Poletto, J. J. Ramasco, D. Paolotti, N. Perra, M. Tizzoni, W. Van den Broeck, V. Colizza, and A. Vespignani. *BMC Medicine* 7, 45 (2009).
3. **Modeling the spatial spread of infectious diseases: The Global Epidemic and Mobility computational model.** D. Balcan, B. Gonçalves, H. Hu, J. J. Ramasco, V. Colizza, and A. Vespignani. *Journal of Computational Science* 1, 132 (2010).

## 1.4 CLIENT INSTALLATION AND REQUIREMENTS

The GLEAMviz Simulator client version 7.0 is a stand-alone desktop application and can be installed on Windows (7 and later), Mac OS X (10.12 and later) and Linux (glibc version 2.24. or newer) operating systems. A 64bit processor architecture is required.



To install the GLEAMviz Simulator client download the installer program from:

<http://www.gleamviz.org/simulator/client/>

and run it (make sure you have the permission to execute the installer program, according to your OS security settings, and to write in the chosen data directory).

The GLEAMviz client features a built-in updating mechanism that periodically checks for new software updates, and then prompts the user to download and install them when available.

The *Public Edition* of the GLEAMviz client is pre-configured in order to use the GLEAMviz server made available by [gleamviz.org](http://www.gleamviz.org): there is thus no need to install and configure the server to use the client. However, in order to avoid an overload on this server, a number of limitations are enforced in the public client setup. Research groups interested in an unlimited version of the GLEAMviz system are invited to contact us at [info@gleamviz.org](mailto:info@gleamviz.org).

To properly install the GLEAMviz Simulator client, at least 300MB of free disk space is required. Additional disk space will be needed to store locally the output of the performed simulations.

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### THIRD PARTY LIBRARIES AND OTHER ASSETS USED IN THE GLEAMVIZ SIMULATOR CLIENT

World Health Statistics 2009  
[http://www.who.int/gho/publications/  
world\\_health\\_Statistics/en/index.html](http://www.who.int/gho/publications/world_health_Statistics/en/index.html)  
International data base (idb)  
<http://www.census.gov/ipc/www/idb/>  
Blue Marble map by NASA's Earth Observatory  
<http://earthobservatory.nasa.gov>  
Qt development framework  
<http://qt-project.org>  
OpenSceneGraph graphics toolkit  
<http://www.openscenegraph.org>  
BitRock InstallBuilder  
<http://installbuilder.bitrock.com>

# USER REGISTRATION AND LOGIN

## 2.1 LOGIN SCREEN

The *Login screen* interface is shown at first when the GLEAMviz client is launched. The user is asked to authenticate on the system by filling an input form with:

- » username
- » password

Three additional links are present in the Login screen:

- » **register**: brings user to the Register screen, to create a new user
- » **proceed offline**: brings user to the *Simulation Manager* without authenticating (local simulations can still be accessed)
- » **forgot your password?**: brings user to the password reset interface

2.1 LOGIN SCREEN

2.2 REGISTER SCREEN

2.3 FORGOT PASSWORD

## 2.2 REGISTER SCREEN

The *Register screen* interface is used to create a new user's profile on the GLEAMviz system. An input form with the following fields is shown:

- » username
- » email
- » password
- » confirm password

Once the user completes the form, a request is sent to the server to validate the input (for example to check that the chosen username is not already taken). If some fields are not valid the user is shown an error message, otherwise a confirmation message is shown. Upon a valid registration, the user is sent an email to the given address, with a link to follow to confirm the registration request and activate the user account.

## 2.3 FORGOT PASSWORD

To recover a forgotten password, the user has to insert the username and the email given at registration in this form; upon submitting the form, the user will be sent an email with a new valid password to be used for authenticating. Once logged in, the user will be able to change the password by using the standard interface (see section 3.1.1).

# SIMULATION MANAGER

The Simulation Manager window (shown in figure 3.1) is opened after the user performs a successful login, or when the user selects the 'proceed offline' option from the Login screen. This window consists of a menu bar and a list of the user's simulations, organized in different sections.

## 3.1 MENU BAR

The menu bar contains two pairs of buttons and a drop-down menu.

The buttons on the left are related to simulations.

- » **New simulation:** opens the Simulation Builder component, which is used to design a new simulation and execute it.
- » **Import simulation:** opens a dialog window to load a simulation definition from the file system.

The right ones refer to the software application in general.

- » **About:** opens a credits screen.
- » **Preferences:** opens a configuration window. See section 6 below for more details.

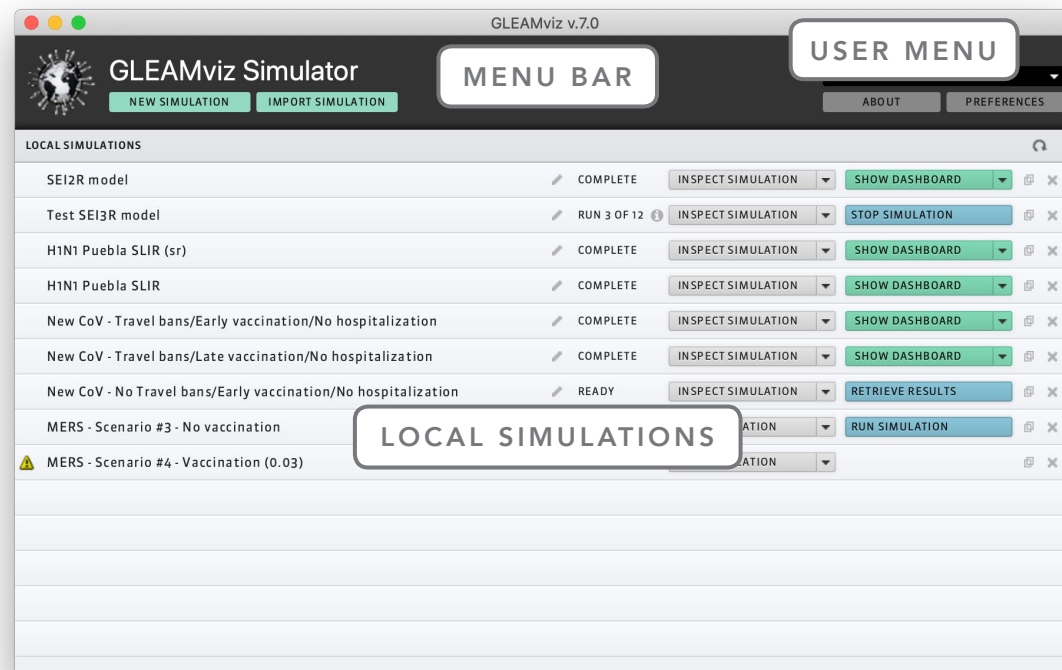


Figure 3.1: Main window with the menu and the simulations' list

The User menu is located above the right side buttons and provides the following options (for authenticated users):

- » **Change email:** to modify the user's email
- » **Change password:** to modify the user's password
- » **Log off:** to log-out from the server and use GLEAMviz Simulator in offline mode.

The change email and change password interfaces ask the user to insert twice the new email address or the new password.

For non authenticated users, the User menu displays the following options:

- » **Register:** to move to the Register screen
- » **Log in:** to move to the Login screen

The *Simulation Manager* window (see figure 3.1) lists the simulations that the user has access to. It is organized in sections relative to the logical position of the simulations.

- » **Local simulations:** lists the locally available simulations that the user has created so far or that have been imported from other sources.
- » **Simulations on GLEAMviz server:** lists the simulations that are available on the GLEAMviz server but are not present locally. This section is shown only if there are simulations on the server which are not present locally; it is useful when logging in with a client different from the one where the simulations were created, to access those simulations from multiple machines.

Each row of each section refers to one simulation, displaying information and actions available:

### 3.1.1 USER MENU

## 3.2 SIMULATIONS MANAGEMENT

### 3.2.1 SIMULATION STATUSES

- » **Title:** title of the simulation. Clicking twice on it (or clicking on the 'edit' icon next to it) allows the user to edit the title. Hovering on the edit icon displays the id of the simulation.
- » **Execution status:** displays the execution status of the simulation (see section 3.2.1).
- » **Simulation Definition menu:** provides access to actions related to the simulation definition. See section 3.2.2.
- » **Simulation Results menu:** provides access to actions related to the execution and the results of a simulation. See section 3.2.3.
- » **Clone Simulation button:** opens the *Simulation Builder* with a new clone of the currently selected simulation.
- » **Remove Simulation button:** clicking this button deletes the selected simulation. Associated results will also be deleted. This action cannot be undone.

A simulation listed in the *Simulation Manager* can be in one of the following statuses, relative to its execution and to the availability of the results:

- » **definition:** the simulation has been created and defined but has not been submitted for execution. If a simulation has not been fully defined (some parameters are missing or some inconsistencies have been detected in the model) an alert icon is shown at the left of the title, and the execution is inhibited.
- » **running:** the execution request has been issued and has been accepted by the server. While the simulation is running this field shows the execution status on the server (run number being computed, final analysis phase, etc..) and an additional tooltip can be visualized with detailed information about the simulation progress.



- » **ready:** the simulation execution has been completed and the output data are ready to be retrieved.
- » **retrieving:** the simulation's output data are being downloaded from the GLEAMviz server.
- » **complete:** the simulation is complete and the output data are locally available.
- » **failed:** the simulation execution failed for some reason.
- » **aborted:** the simulation execution has been interrupted by the user.

The simulation definition menu provides access to actions related to the simulation definition:

- » **Edit / Inspect simulation:** for simulations that have not yet been submitted, the *Edit Simulation* button is shown. Clicking on this button opens the *Simulation Builder* in full editor mode, allowing the user to edit the compartmental model and all the simulation parameters. Once a simulation has been submitted, it can no longer be modified (except for its name and notes). In this case, the *Inspect Simulation* button is shown. It opens a read-only version of the *Simulation Builder*, which shows the model and all the simulation's parameters. It is possible to visualize and save the model and configuration but not to modify it.
- » **Export simulation definition:** exports the simulation definition to an XML file. This file can later be used as the template for a new simulation or it can be shared with other users. Sharing the definition file with others allows them to run a simulation with the same parameters.

### 3.2.2 SIMULATION DEFINITION MENU

### 3.2.3 SIMULATION RESULTS MENU

The simulation results menu provides access to actions related to the execution and the results of a simulation. Different options are available depending on the execution status.

- » **Run simulation:** submits the simulation for execution to the GLEAMviz server.
- » **Stop simulation:** enabled when the execution of the selected simulation is ongoing. Clicking this button allows the user to stop the execution of the simulation.
- » **Retrieve results:** this button is shown for completed simulations. It allows the user to download the results from the server
- » **Cancel retrieving:** is shown while the results of a completed simulation are being downloaded. Clicking the button cancels the data retrieval, reverting the simulation status to "ready".
- » **Show Dashboard:** this option allows the user to access the output visualizations described in section 5 (opening a new window). This button is only shown when simulation results are present.
- » **Export results:** once the results have been retrieved, this button allows the user to export the data, including relevant meta-data and the simulation definition, to a folder. The formatting of this data is detailed in section 8.
- » **Clear results:** this button allows the user to remove the locally stored results from the machine. If the simulation is no longer available on the server, this action resets the simulation to the 'definition' status (and cannot be undone), otherwise it is set to the 'retrieve results' status.

# SIMULATION BUILDER

The *Simulation Builder* window is used to design a simulation, from the compartmental model to the global settings and optional time-dependent exceptions.

The simulation editing window provides a menu header and a number of tabbed panels.

- » **Menu header:** The header contains information and actions related to the simulation as a whole. It contains the simulation name and notes (both editable) and the *Run Simulation button*. This button is enabled when the simulation definition is consistent and error-free. It allows the user to submit the simulation to the server for execution. Clicking this button will close the *Simulation Builder*.
- » **Panels:** Below the header, three tabbed panels labeled “Model”, “Settings”, and “Exceptions” cover three aspects of setting up a simulation. When the information provided in a panel is inconsistent, the “Concerned” tab will

- 4.1 MODEL BUILDER PANEL
- 4.2 SETTINGS PANEL
- 4.3 EXCEPTIONS PANEL

display a warning icon. The inconsistent item will be highlighted with the same icon within that panel.

The panels are described in detail in the following sections.

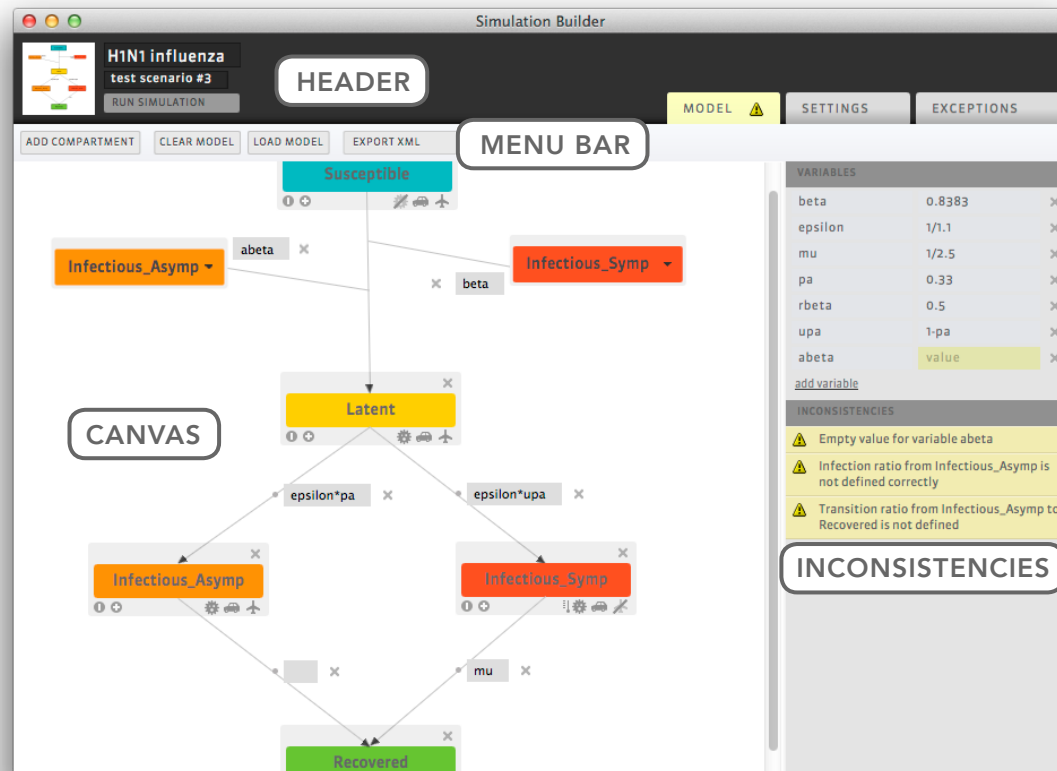


Figure 4.1: Compartmental Model Builder

The *Model Builder* is used to design the *compartmental model* of the infection dynamics. Figure 4.1 identifies the five components of the compartmental Model Builder interface:

- » **Menu bar:** located at the top of the window. It contains buttons to add compartments to the model, to load a model from a file, to clear the model by removing all elements, and to export the model to a file, either as a loadable XML or as an SVG representation of the model diagram.
- » **Canvas:** the *canvas* contains an editable diagram of the compartmental model. It allows the user to move or remove compartments; configure compartment settings; add or remove spontaneous transitions and infection transitions; set transition rates as constant values or simple functions of variables; and add, change, or remove infection source compartments. See below for more details.
- » **Variables list:** this component lists the variables (*name = value pairs*) referenced in the model. New variables can be added by clicking the *add variable* button. Variables can be removed by clicking the cross button on the right-hand side of the variable entry in the list. The name and value of the variables can be edited in the variables list. The values can be algebraic expressions that include references to other variables. Variable names or values with errors are marked in yellow and an explanation of the error is displayed in the inconsistencies list. See section 7 for more details on writing expressions.
- » **Inconsistencies:** this component lists the inconsistencies in the model definition, as determined by the client. These inconsistencies need to be resolved before submitting a simulation.

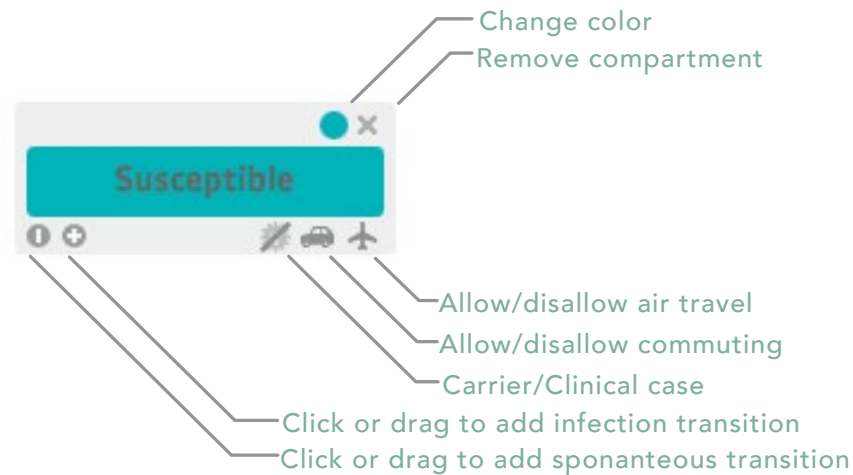
Clicking the *Add compartment* button in the menu will add a new representation of a compartment on the diagram canvas. This compartment will initially have a default

## 4.1 MODEL BUILDER PANEL

### 4.1.1 COMPARTMENTS

name. This name can be changed by clicking on the name in the compartment's representation and entering a new one. Compartments can be repositioned by dragging on the gray area around the colored body of the compartment representation. The color of a compartment can be changed for ease of reference by selecting a color from the color list, which appears when the user clicks on the *change color* button on the compartment representation.

On the gray area below the compartment name, there are five icons that allow the user to add a transition to another compartment, mark the compartment as a carrier or a clinical case, and allow or disallow commuting and air travel for it. Figure 4.2 details the functionality provided by the compartment representation.



**Figure 4.2:** Compartment view

The Carrier/Clinical case icon is used to mark those compartments that are carrying the pathogen and may eventually lead to the disease transmission. It is important to

mark all compartments that might introduce the virus in a population as carrier, even if they have not yet transmitted the infection. For instance, the exposed compartment is a typical example of carrier, as exposed individuals will generally transition to an infectious state that could generate transmission of the disease in the population. A compartment is considered to be a carrier if the virus icon is not barred, and clinical cases are identified by double clicking when the thermometer symbol is shown by side of the virus symbol (see fig.4.1). At least one compartment among the infectious compartments must be defined as corresponding to a clinical case, and this is used by the GLEAM simulation engine to define the conditions for the detection of an outbreak in a given country (see section 4.2).

There are two types of transitions: *infection transitions* and *spontaneous transitions*. Transitions from one compartment to another can be added by dragging the corresponding icon from the source compartment to the target compartment (see Figure 4.2). Dragging a transition icon to an empty point in the canvas will result in the creation of a new compartment and a transition of the selected type connecting it.

When a susceptible individual comes in contact with an infectious one, he/she might contract the infection in accordance with a transmission rate defined by the user. This rate can be an algebraic expression that includes references to other variables. See section 7 for more details on writing expressions.

If the susceptible compartment is denoted by “*S*” and the infectious one is denoted by “*I*”, the expected number of new infections generated under a homogeneous assumption in each sub-population is given by:

$$\beta I \frac{S}{N} \tag{4.1}$$

#### 4.1.2 TRANSITIONS

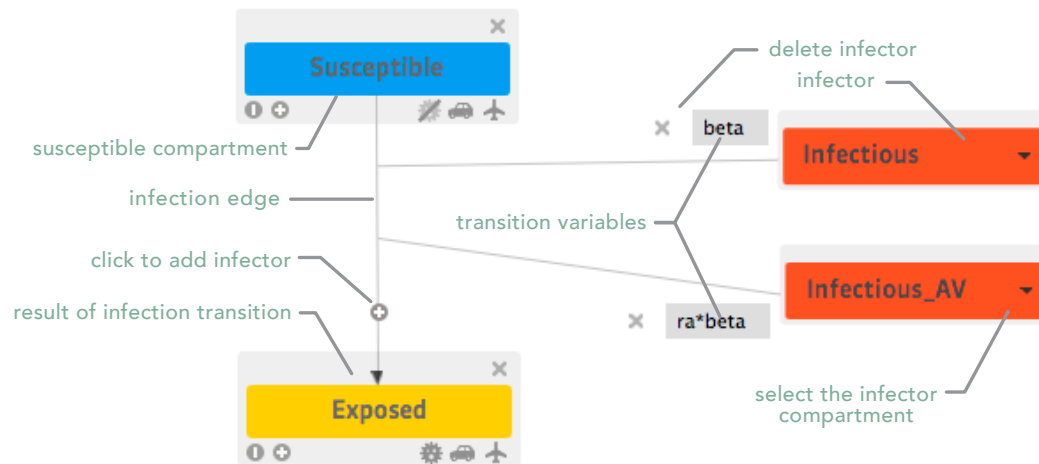


Figure 4.3: Compartment view GUI

where  $\beta$  is the transmission rate set by the user and  $N$  is the total population. Individuals can undergo spontaneous transitions from one compartment to another. Examples include the transition from latent to infectious individuals or from infectious to recovered individuals. The GLEAM simulation engine considers discrete individuals and all transition processes are stochastic, discrete, and modeled through binomial and multinomial processes. For more details, please refer to Ref. [1].

Figure 4.3 provides an overview of the components and functionalities provided for an infection process.

#### 4.1.3 VARIABLES

The user can define one or more variables, which are name–value pairs or name–expression pairs. The transition rate expressions can reference these variables, and the value expression of one variable can reference other variables. These variables are defined in the variables panel on the right side of the Model Builder window.



The name of a variable must start with a letter and can only contain alphabetic, numerical, and underscore characters. The value can be an algebraic expression that includes references to other variables. Variable names or values that do not conform to these rules are marked in yellow. See section 7 for more details on writing expressions.

Before a simulation can be submitted to the server its model must be free of inconsistencies. Any inconsistency that is detected by the GLEAMviz client is listed in the inconsistencies section of the GUI. A model can be saved/loaded to/from a *gvm* XML file if inconsistencies are present, but the simulation cannot be executed.

Examples of inconsistencies are undefined transition rates, invalid transition rate expressions, and circular variable dependencies (see section 7). Note that while the client can determine if a compartmental model is technically consistent, it cannot determine if it makes sense epidemiologically.

The same compartmental model is often used in numerous simulations. Instead of having to recreate this model for each simulation, users can design it once and save it as a file that contains an XML representation of that compartmental model. When configuring subsequent simulations, the compartmental model can then be loaded from such a file and subsequently modified and extended.

The conventional extension for compartmental model files is *gvm*, from GLEEaMvis model. The *gvm* files can be opened in any client and thus can be shared with colleagues. Note that it is also possible to open a *gvd* file (containing a simulation definition) or a *gvs* file (containing a simulation, with or without results) in which case the included compartmental model will be loaded.

#### 4.1.4 INCONSISTENCIES

#### 4.1.5 SAVING AND LOADING COMPARTMENTAL MODELS

#### 4.1.6 EXAMPLES

## 4.2 SETTINGS PANEL

Examples of compartmental models (with .gvm extension) can be downloaded from <http://www.gleamviz.org/simulator/models/>. These examples can be imported into the Model Builder using the Load model button (see Fig. 4.1).

The Settings panel is used to configure the simulation's general parameters, which define the basic scenario for the simulation that will be run by the GLEAMviz server.

On the menu bar, a button is shown:

- » **Reset settings:** resets all the values to the application defaults.

The *Settings* panel interface (shown in figure 4.4) is divided into four sections: *Simulation*, *Initial assignment of population*, *Initial geographic location of the epidemic*, and *Result compartments*.

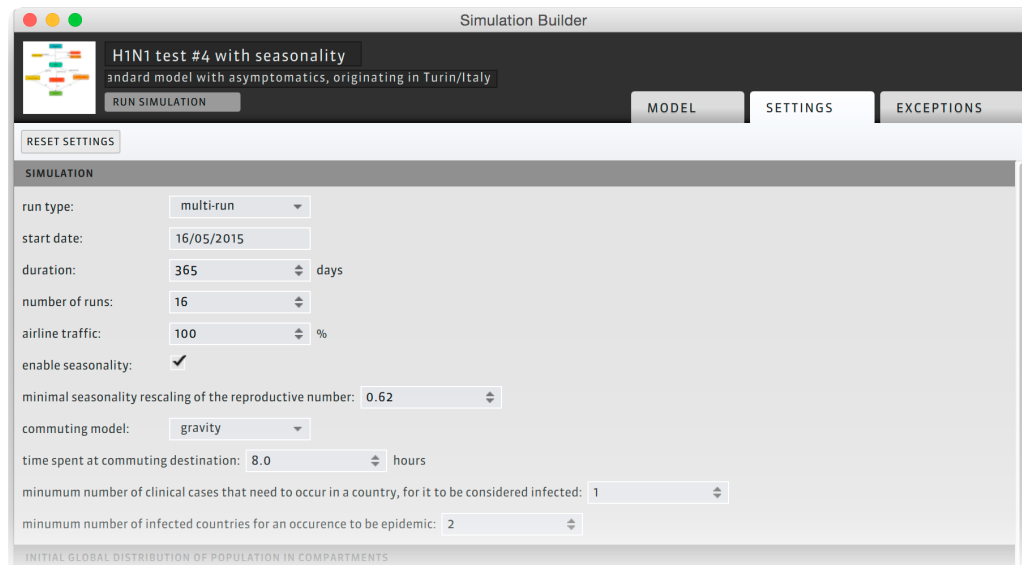


Figure 4.4: Simulation settings

The Simulation panel collects settings concerning the global settings of the simulation:

- » **Type:** single-run (SR) or multi-run (MR).  
A *multi-run simulation* performs multiple simulations (runs) with the same model and settings, and it returns averages and confidence intervals calculated over the set of runs. A *single-run simulation* performs the simulation once. The returned results are the results from that one run and do not include confidence intervals. Unlike the multi-run, the results include data on the concrete transmission of infected individuals between cities, which can be shown as arcs in the visualization.
- » **Start date:** the date at which the epidemic begins.
- » **Duration:** the length of each simulation run expressed in days.
- » **Number of runs (MR only):** the number of stochastic runs starting from the same initial conditions that must be performed and over which the statistics of the simulation results will be performed. Increasing this number results in improved statistics but also in longer computational time.
- » **Airline traffic:** average percentage of passengers with respect to the number of bookings derived from flight data. The default value is 100%. For each simulated flight, the number of passengers is a stochastic variable sampled from a binomial distribution whose mean is given by the airline traffic value times the number of bookings.
- » **Enable seasonality:** if this feature is checked, the GLEAM simulation engine will run simulations considering the seasonality effect on the infection transitions. Seasonality is modeled by rescaling the basic reproduction ratio  $R_0$  by a sinusoidal function  $s_i(t)$ , such that:

$$s_i(t) = \frac{1}{2} \left[ (\alpha_{max} - \alpha_{min}) \sin \left( \frac{2\pi}{365} (t - t_{max,i}) + \frac{\pi}{2} \right) + \alpha_{max} + \alpha_{min} \right] \quad (4.2)$$

where  $i$  refers to the hemisphere considered, following the standard approach adopted in the literature. In the tropical region, the scaling function is equal to 1.0. Along the year, the seasonality scaling function varies from a maximum rescaling,  $\alpha_{max}$ , to a minimum rescaling  $\alpha_{min}$ .  $\alpha_{max}$  is set to 1.1, following previous approaches, whereas  $\alpha_{min}$  is set by the user (see below). The full description of the seasonality modeling is reported in Ref. [1] and its Supplementary Information.

- » **Minimal seasonality rescaling of the reproductive number:** this option is available only if seasonality is enabled (see above). The value corresponds to the minimum value of the rescaling of the reproductive number, due to seasonality.
- » **Commuting model:** this option allows to specify which model shall be used while computing the number of commuters between neighbouring regions; three options are possible:

**gravity model:** the number of commuters moving from location  $i$  to location  $j$  is given by the gravity law with parameters estimated based on the real commuting data collected from more than 30 countries. According to the model, the number of commuters on any given connection is an increasing function of the populations at the origin and destination and a decreasing function of the distance between them.<sup>1</sup>

**radiation model:** the number of commuters moving from location  $i$  to location  $j$  is given by the radiation model whose input parameter is informed by the real commuting data collected from more than 30 countries. The number of commuters increases with the population at the origin and destination while it decreases with the total population in the surrounding region of the origin.<sup>2</sup>

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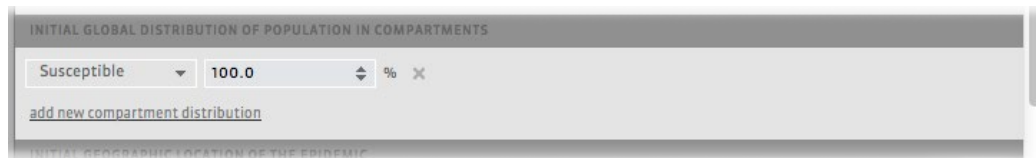
1 Balcan D, Colizza V, Gonçalves B, Hu H, Ramasco JJ, Vespignani A: Multiscale mobility networks and the large scale spreading of infectious diseases. Proc. Natl. Acad. Sci. USA 2009, 106: 21484-21489.

2 Simini F, Gonzalez MC, Maritan A, Barabási AL (2012): A universal model for mobility and migratory patterns. Nature 484: 96-100.

- » **Time spent at the commuting destination (hours):** the average number of hours spent by the commuters at the commuting destination. The default value used is 8 hours, corresponding to the average amount of working time in a day.
- » **Minimum number of clinical cases that need to occur in a country (for it to be considered infected):** this parameter sets the condition for an outbreak in a country.
- » **Minimum number of infected countries (for a global epidemic to be considered to occur):** this parameter sets the condition for the global outbreak. The default value is 2, which corresponds to the requirement that a second country be infected besides the country where the outbreak initially occurs.

This section allows the user to specify the initial conditions for the population of each compartment defined in the model. Populations per compartment are expressed in percentages of the total. Different options can be defined: a fully susceptible population, conditions for partial immunity, etc. These initial conditions are extended to the whole set of sub-populations considered in GLEAM. Clicking the *add new compartment distribution* link will add a new compartment to the list, for which it is possible to define the initial population (see Fig. 4.5). By default, the first compartment added will contain the entire population. In case of multiple compartments, the user must adjust the population distribution in order to total 100%. All other compartments not

#### 4.2.2 INITIAL GLOBAL DISTRIBUTION OF POPULATION IN COMPARTMENTS



**Figure 4.5:** Initial distribution of population into compartments

### 4.2.3 INITIAL GEOGRAPHIC LOCATION OF THE EPIDEMIC

listed in the window are set equal to 0. Compartments can be removed by clicking the X button on the right.

This section of the simulation's setup panel allows the user to define the initial location and quantity of the infectious individuals. Please note that they need not be defined in the initial population assignment section (the previous one), which is a global setting valid for all the census areas worldwide. To add a new epidemic seed, the user can click on the *add new initial location* link. This will add a new line in the list, displaying default values for the epidemic origin. City and compartment of the seed can be selected from the corresponding lists (see figure 4.6). It is possible to add an arbitrary number of epidemic seeds or to remove a previously inserted one by clicking the X button on the right.

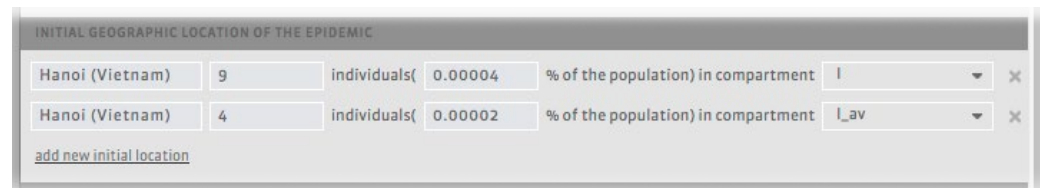


Figure 4.6: Initial geographic location of the epidemic

Infection seeds can be indicated in terms of number of individuals or fraction of the population of the selected basin (census area associated with the city). At least one infectious individual in one city/basin must be specified before proceeding to the next interface.

### 4.2.4 RESULT COMPARTMENTS OF INTEREST

The last section of the *Settings* panel requires selecting the compartments wanted as output, whose data will be shown in the Visualization Window and will be available for local download. The user can select one or more compartments (at most 5 for the

*Public Edition*) to be considered when retrieving and visualizing the results in this client. Depending on this selection, upon simulation completion, the user will be able to visualize the results for all or a subset of the compartments selected here.

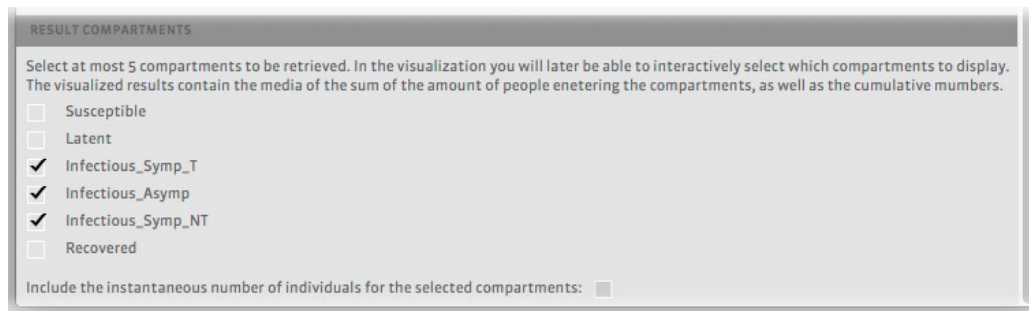


Figure 4.7: Result compartments

The *Exceptions* panel provides a way to specify time and space dependent exceptions of the variable values defined in the compartmental model. On the menu bar, two buttons allow the user to manage exceptions:

- » **Add new exception:** lets users add exceptions to the current simulation.
- » **Clear all exceptions:** removes all the exceptions defined for the simulation.

The exceptions are specified in terms of *rules*, or variable overrides. Each exception lets the user define an alternative value for one or more variables during a specific time-span and for a specific set of geographic units (cities, countries, etc. . . ).

The simulation will use the given alternative variable values:

- » from the selected start date up to and including the selected end date
- » for all the city areas belonging to one of the specified geographical units

## 4.3 EXCEPTIONS PANEL

More than one rule can be specified for each exception.

On the title bar of each exception, the user can adjust the priority when multiple exceptions are defined: higher priority overrides lower priorities, in case of rule overlap.

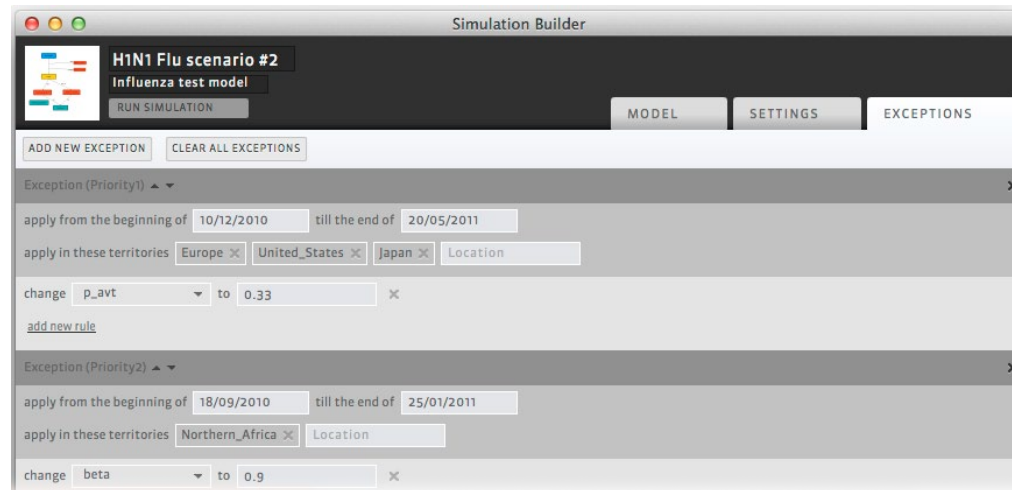


Figure 4.8: Time and space dependent exceptions



# VISUALIZATION COMPONENTS

The *Visualization Dashboard* window is the main component of the GLEAMviz Simulator client that allows the user to see the results of a simulation. The window opens when the user clicks the *Show Dashboard* button in the *Simulation manager*.

For single-run simulations, according to the user's configuration settings, the *Visualization Dashboard* is opened as soon as the simulation has been successfully submitted to the server.

The *Visualization Dashboard* consists of a configurable set of visualization widgets, that can be opened and arranged at will by the user according to the size of the display. The widgets can be moved around and docked, depending on their minimum size. Currently the public edition of the GLEAMviz client supports the following widgets: *Map*, *SPATO*, *Globe*, *Treemap*, *Invasion Tree*, *X3D Globe* and *Analyzer*. Additional widgets might be included in future releases of the software.

- 5.1 Geographic mapping
- 5.2 SPaTo: shortest path tomography
- 5.3 3D globe visualization
- 5.4 Analyzer charts
- 5.5 Treemap
- 5.6 Invasion Tree
- 5.7 X3D Globe

The default *Dashboard* visualization for a standard screen consists of a *Map* and an *Analyzer* widgets, as shown in figure 5.1.

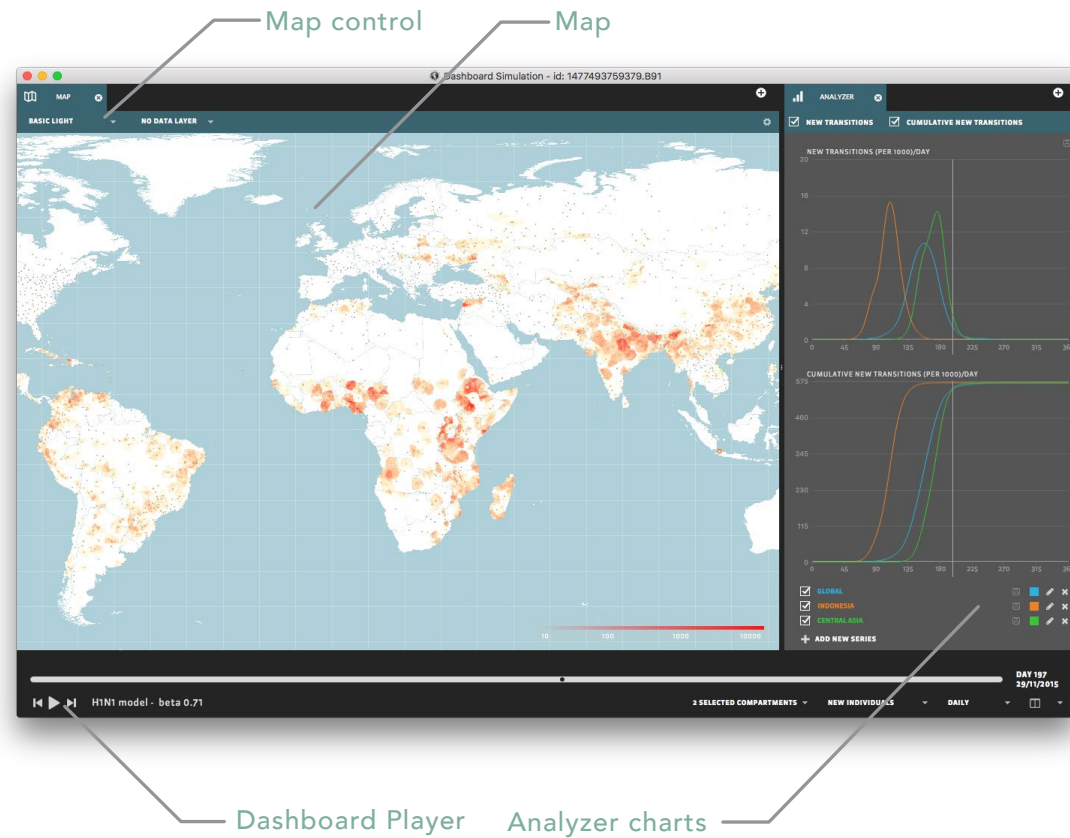


Figure 5.1: Annotated Visualization Window

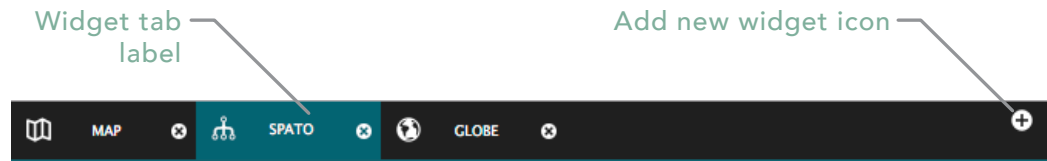


Figure 5.2: Widget tab bar

To add a new widget, click the “+” icon placed in the top-right corner of each tab-widget area (see Figure 5.2) and chose the desired widget type. To drag a widget to a different position click and hold its tab label (where the widget type name is displayed) and then move the mouse pointer to the new location. Widgets can be placed both in existing tab-widget areas and by side of them (between them or close to the window border), in the latter case creating a new tab-widget area. The active drop area is highlighted with a grey rectangle (when multiple dropping options are possible the system cycles through them, the highlighted rectangle showing the current selection). If the dragged widget is too big to fit in the new place the drop area is colored in red, and a drop action results in the widget being displayed in a floating window.

Each widget has a Control bar in the upper part, allowing users to customize the specific visualization.

The *Visualization Dashboard* features a *Dashboard Control* component, at the bottom of the window, which includes the *Player* and the *Compartments Selector* (see Figure 5.3).

The *Player* consists of a slider representing the timeline of the simulation in days, with some buttons to control the data display. The time evolution of the epidemic is represented by showing the results of subsequent days, updating the various widgets accordingly (*Map*, *SPATO*, *Globe*, *Invasion Tree*, *X3D Globe*), and thus obtaining an

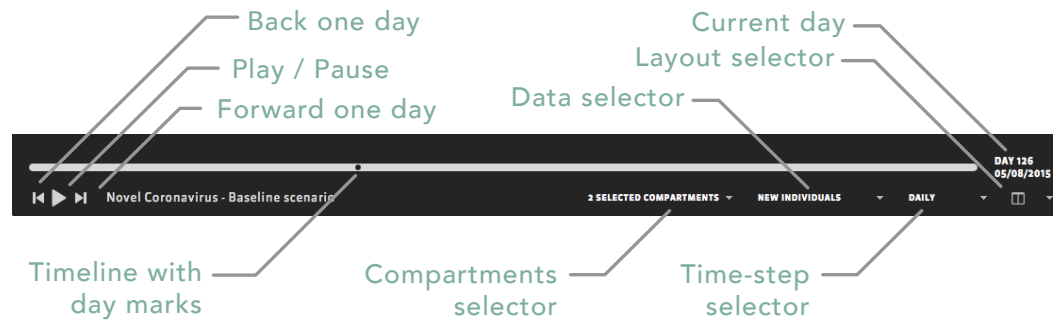


Figure 5.3: Visualization Dashboard Control Component

animation. The user can use the *Play / Pause* button in the *Player* to start or pause this animation. The marker in the timeline marks the current day. Drag this marker or click on the timeline to change the currently selected day. Use the buttons left and right of the *Play / Pause* button to go back or forward one day.

The *Compartments Selector* window (shown in Figure 5.4) provides a menu in which the user needs to select the result compartments (at least one) for which the results should be shown. The visualization widgets (*Map*, *Globe*, *Analyzer*, *X3D Globe*, etc.) will then show the summed results of the selected focus compartments. Note that initially the first “secondary” result compartment is selected as the sole focus compartment.

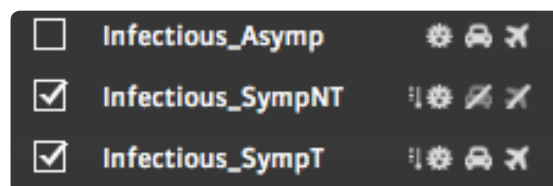


Figure 5.4: Compartments Selector window

The *Data Selector* opens a dialog window that lets the user choose what kind of data to visualize on the *Map*, *Globe* and *SPATO* widgets. It is possible to show the amount of people entering the selected focus

compartments on the current day (New Individuals, which is the default), or the cumulative number of people that entered the selected compartments until the current day (Cumulative New Individuals).

The *Time-step Selector* opens a dialog menu that allows specifying the time aggregation for the output results. By default data are shown as daily steps, as computed by the GLEAMviz engine, but it is also possible to aggregate them weekly or monthly. This allows for instance an easier comparison with official surveillance data. (This selection has no effect on the Treemap widgets).

The *Layout Selector*, in the bottom right of the *Dashboard Control*, lets users choose between some pre-defined layout configurations. The GLEAMviz client automatically tries to select the best fitting configuration according to the size of the display; by using this selector it is possible to change layout and also to save the current custom layout as the default configuration.

The Map widget displays the temporal and geographic evolution of the pandemic by means of a zoomable multi-scale map onto which the results for the selected focus compartment(s) are geographically mapped. These focus compartments are chosen, from the list of result compartments selected in the *Simulation Builder* (see section 4.2.4), by means of the selector window provided in the *Dashboard Control*.

For single-run simulations, the map shows (on top of the map base) the amount of people entering the selected focus compartments on the current day. For multi-run simulations, the corresponding median over the multiple runs is shown. These values are shown using the color scale shown in the overlaying legend (bottom right of the widget). This color scale can be modified in the *Map Settings* (section 5.1.4).

## 5.1 GEOGRAPHIC MAPPING

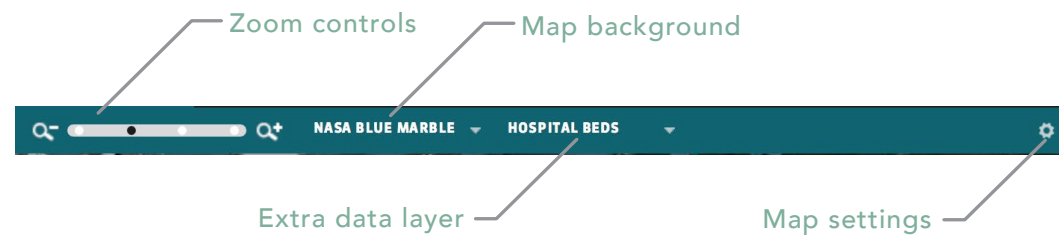
It is also possible to show on the map some extra data that are used by the model but do not depend on the simulated scenario: the population density and the number of hospital beds and physicians per 10,000 inhabitants.

The *Map Control* bar (see figure 5.5) can be used to configure the visualization options by providing widgets to:

- » choose the map background (see section 5.1.1)
- » choose the underlying data layer
- » access the Map Settings menu

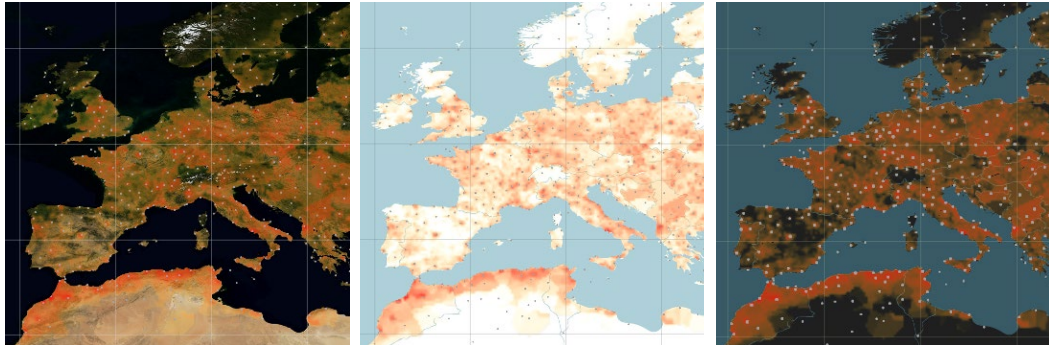
Panning can be done by clicking and dragging the map with the mouse. It's possible to zoom in and out using the mouse wheel.

At any given moment, the map shows the number of new cases or the number of cumulative cases (depending on the option selected in the Infection Data panel in the *Dashboard Control*) for one particular *Current day* or *Current week*, which is specified in the *Dashboard Control*.



**Figure 5.5:** Visualization Window: Map Control bar

Different map background types can be selected, by using the drop-down menu in the *Map control*. Four options are currently available: NASA Blue Marble, Basic Dark, Basic Light, and Natural Earth. Figure 5.6 shows some background examples.



**Figure 5.6:** Visualization Window: Map background types from left to right: Blue Marble Map, Light Map, Dark Map

When moving the cursor on the map, if hovering an area belonging to one of the modeled metapopulations that area is highlighted, and a small popup appears that displays the name of the corresponding city (and the airport code). Clicking on the highlighted basin area opens a larger pop-up like the one shown in figure 5.7. These city info pop-ups provide additional details about that city:

- » the airport code
- » the population of the city basin
- » the country to which the city belongs
- » the average number of hospital beds for 10000 inhabitants (when available)
- » the average number of physicians for 10000 inhabitants (when available)

### 5.1.1 MAP BACKGROUNDS

### 5.1.2 CITY INFO POP-UPS

- » the new and cumulative number of people in the currently selected focus compartments in this city on the current day
- » the age distribution structure of the population in the city area (when available)

Use the *Close* button to close the pop-up or the *Show in new Analyzer* button to open a new *Analyzer* chart with this city as the context. See section 5.4 for more details on the *Analyzer* chart.

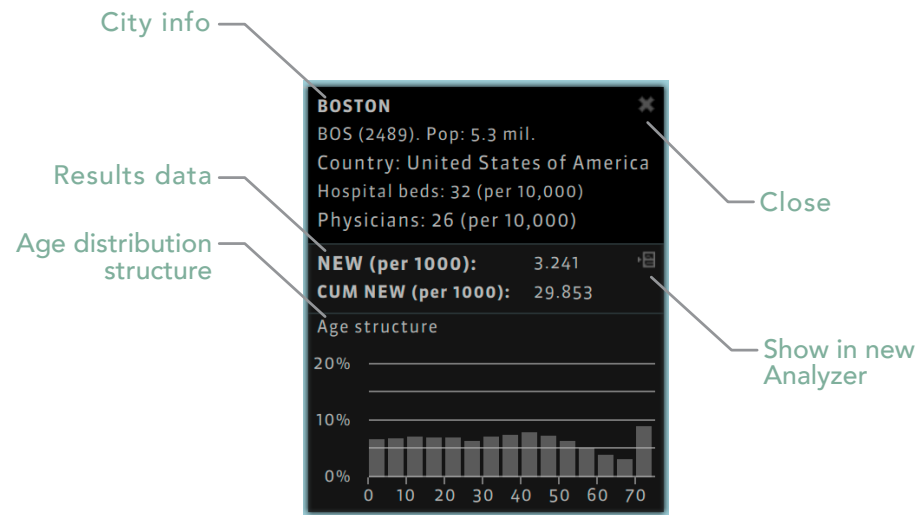


Figure 5.7: Visualization Window: City info pop-up

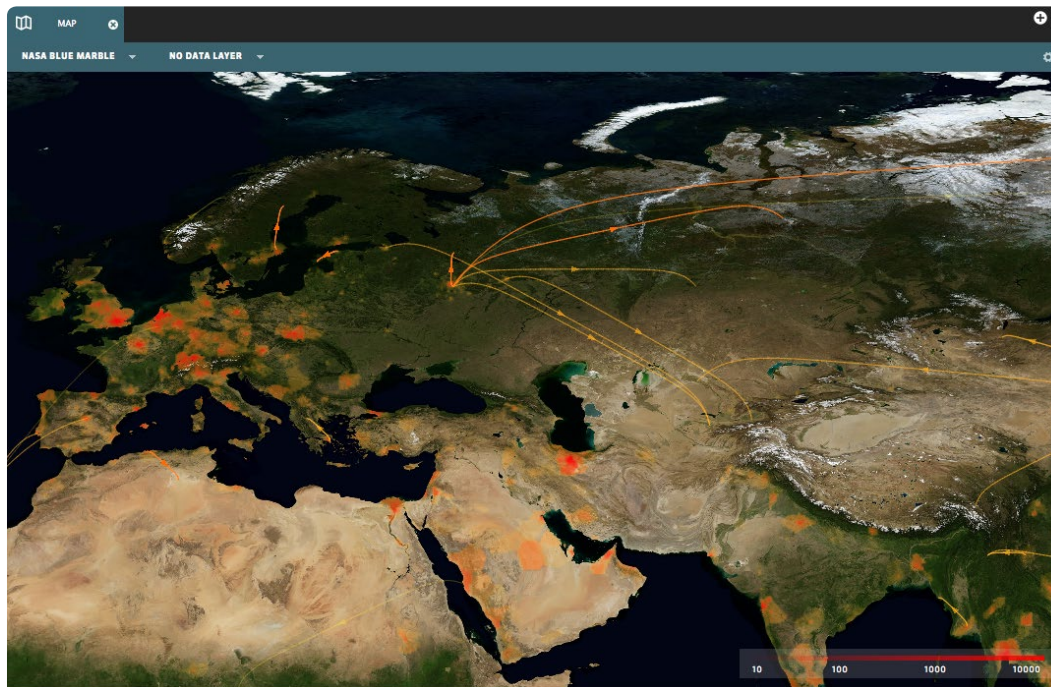
### 5.1.3 AREA SELECTION (ANALYZER)

It is possible to select an arbitrary rectangular area by clicking the map, holding down the Ctrl key (Command on Mac), and dragging the mouse pointer to a new place. This will result in opening a pop-up window with an *Analyzer* widget displaying the new and cumulative cases per 1000 over time for the compartments specified by the *Compartments Selector* in the selected area.



For single-run simulations, the transportation of “seeding” individuals can be shown. A seed is the first occurrence of an individual belonging to the selected focus compartment(s) flying to a particular city. Seeding can only be shown for compartments carrying the infectious pathogen. Such transportation is marked by means of a directed edge from the city of origin to the destination city, as shown in figure 5.8. The infection seeding can be displayed only when daily time aggregation is selected in the *Dashboard Control*.

Note that the evolution of the epidemic depends strongly on the model definition,



**Figure 5.8:** Geographic mapping window: single-run simulation with seeding flights

### 5.1.5 MAP SETTINGS

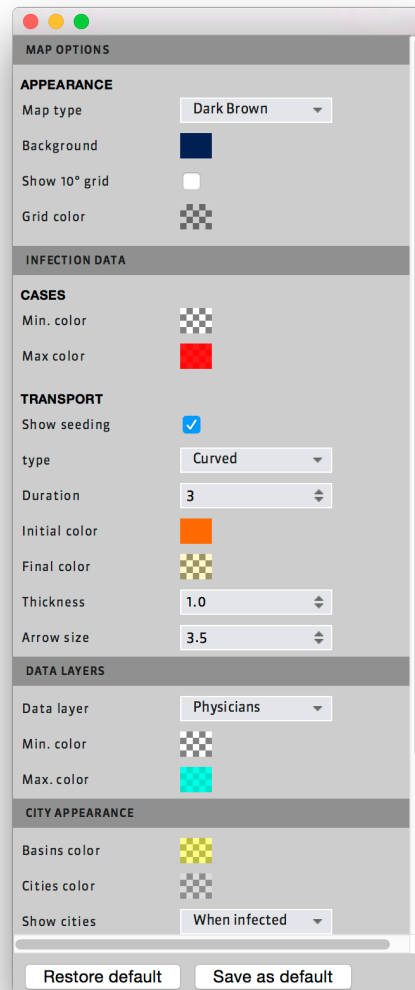


Figure 5.9: Geographic mapping window: Settings

and it could be possible that some city becomes infected by a traveling latent individual that develops the disease after arrival in the destination city. If only infectious compartments were selected as the current focus compartments, in this case, no seeding flight will be shown.

Various aspects of the visualization can be controlled through the *Map Settings* menu, which appears at the top right corner of the window, within the *Map Control* shown in figure 5.5. This menu consists of a number of sections:

- » Map options
- » Infection data
- » Data layers
- » City appearance

as shown in figure 5.9, allowing the user to customize the map appearance by choosing if and how to display various items (color, size, etc. . . ).

## 5.2 SPATO: SHORTEST PATH TOMOGRAPHY

This visualization is based on the SPaTo Visual Explorer (<http://www.spato.net>), an interactive software tool for the visualization and exploration of complex networks. By reducing a network (here the transportation network) to the shortest-path tree of a selected root node (here initially the source of the infection), we obtain a local but simpler view of the network that can be easily visualized.

This visualization allows the user to switch between a geographic mapping of the transportation hubs (as shown in figure 5.11) and a concentric mapping of the hubs

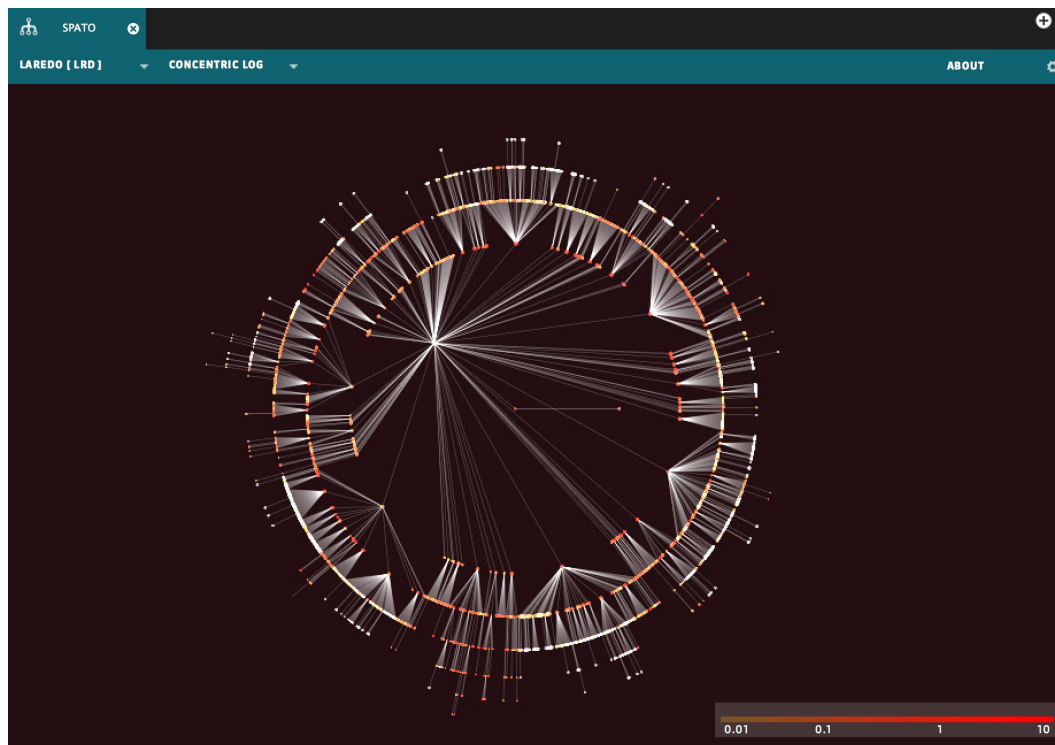
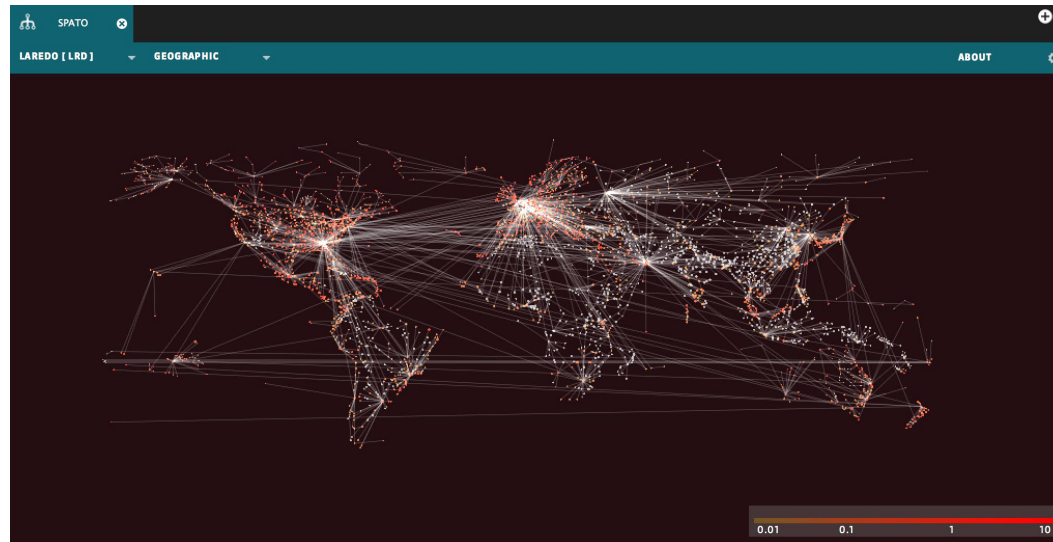


Figure 5.10: SPaTo visualization window: Concentric layout



**Figure 5.11:** SPaTo visualization window: Geographic layout

according to the shortest distance (in terms of transportation steps) between the hubs and the root hub (as shown in figure 5.10). In both views, the shortest-path tree among the nodes is rendered by means of edges. The ability to quickly change the root node allows to explore the network from different perspectives. It is possible to select any hub as the root node by clicking on it. It is possible to pan the graph visualization by dragging the mouse pointer, and zoom in/out by using the mouse wheel.

The method and original software were developed by Christian Thiemann in the research group of Dirk Brockmann at Northwestern University and the Max Planck Institute [see [www.spato.net](http://www.spato.net)].

This visualization widget contains a 3D globe. The rotation of the globe can be manipulated by a mouse, while the zoom level can be adjusted using the mouse wheel. Similar to the 2D map, this visualization shows the number of new cases or cumulative cases as a color coded texture on top of the base texture. For single-run simulations, "seeding" individuals are shown as 3D edges with arrows.

### 5.3 3D GLOBE VISUALIZATION

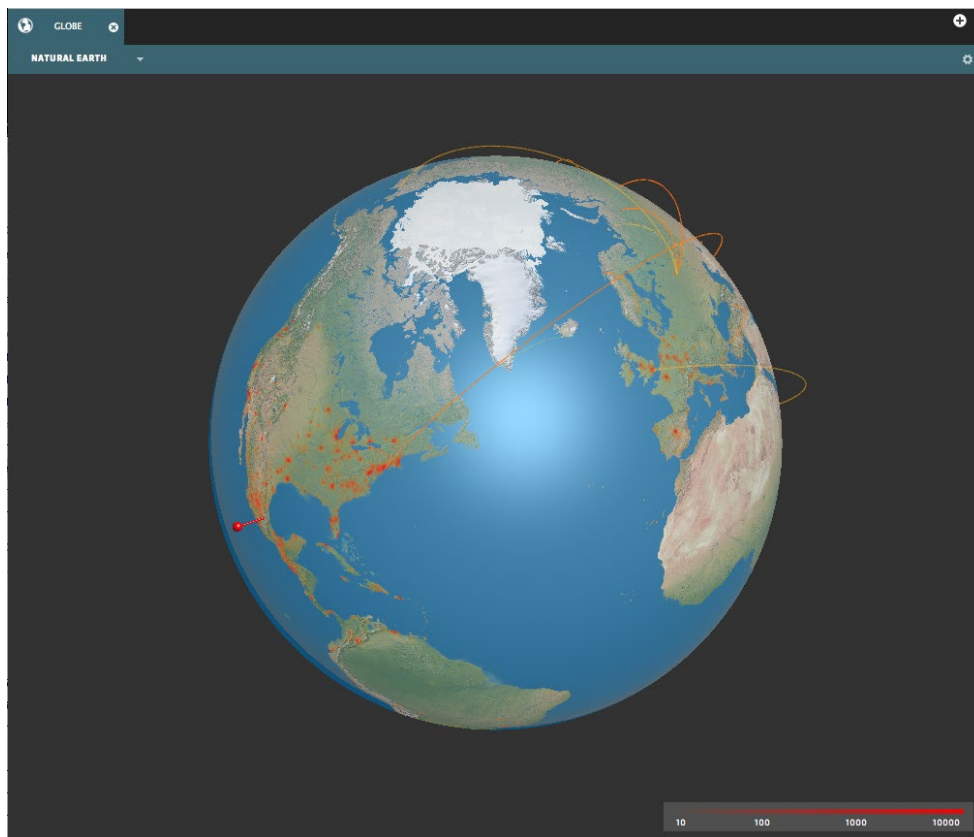


Figure 5.12: Globe visualization

## 5.4 ANALYZER

The temporal mapping of the evolution of the epidemic spreading is controlled through the *Dashboard Control* component of the *Dashboard* window, as for the *Map* and *SPATO* widgets. The *Globe Control* bar allows the user to change the background style for the Earth's surface: the same options available for the *Map*, as in section 5.1.1, are available for the *Globe* widget. Some other visualization options can be configured by means of the settings window that is opened by clicking the gear icon in the top-right corner (coloring, etc.).

The *Analyzer* widget, as shown in figure 5.13, contains two plot charts. The top chart shows the number of new individuals per 1000 in the selected focus compartments for the *Analyzer's* context over time. The bottom chart shows the cumulative number of new individuals per 1000 over time. For multi-run simulations, the median values of the multiple runs and the corresponding 95% confidence intervals are shown. The charts can display up to five data series, which can be specified using the controls at the bottom of the charts. It is possible to show only the plot for the new individuals or only the cumulative one by selecting/unselecting the corresponding check-boxes in the *Control* bar placed on top.

The *Context selection menu* at the bottom of the widget lets the user choose the data series for which the corresponding charts show the results. It is possible to add new series (up to a maximum of five per chart), specifying for each of them the Geographic Area (either *global*, *hemispheric*, *continental*, *regional*, *by country*, or *by city*, a city representing the whole census area centered around the given city), the compartments of interest, and the color of the curve. Unless modified by the user, each curve displays the data for the compartments selected in the *Compartments Selector*. For each series there is a check-box to show or hide the curve, and a set of icons allowing



Figure 5.13: Visualization Window: Analyzer charts

to save the corresponding data, to change the curve color, to modify the data source, and to remove the corresponding curve from the chart. (See Figure 5.13).

The vertical line marks the day currently shown on the map. By clicking on the graph, it is also possible to have the Dashboard display the state of the epidemic at the corresponding day.

By using the Time-step Selector it is possible to display the epidemic curves as a sequence of weekly or monthly steps. If the initial and/or final step is incomplete (i.e. only ten days of the last month are being simulated) the corresponding segment of the curve is an interpolation based on the available data, and is displayed using a different color (a desaturated version of the color chosen for the curve).

When exporting data from a single series (by clicking the save icon), it is exported to a tab-separated values (TSV) file. There are three columns of data for a single-run simulation and seven for a multi-run simulation. The first column is, in both cases, the *Time-step*, i.e., the day offset since the start of the simulation. For a single-run simulation, the second and third columns contain the number of new individuals per 1000 in the selected focus compartments for the current series, and the cumulative number of new individuals, respectively. For a multi-run simulation, the second to seventh columns respectively contain: the median number of new cases; the corresponding lower and upper 95% confidence interval boundary values; the cumulative median; and its lower and upper confidence interval boundary values. The comments at the top of the file contain relevant meta-data describing the context and the focus compartments.

The whole set of data series shown in the *Analyzer* can be exported by clicking the *Export data* button close to the top-right corner of the widget. In this case the user is prompted for a directory, where to save a file with the same structure described above for each series displayed in the *Analyzer*.

If two (or more) *Analyzers* are open, it is possible to click and drag one series from one *Analyzer* widget to the other. To do so, just click and drag on the series' name; when hovering a droppable area of the target widget the corresponding Context section area will be highlighted and releasing the mouse button will move the curve.



No more than five series can be displayed in each Analyzer, so trying to drop a new series when five are already shown will fail.

This widget can be visualized when the simulation is complete and displays the final size of the epidemic by means of colored rectangles whose area is proportional to the cumulative number of new transitions at the end of the simulation in each geographical region (Figure 5.14). When opening the tool the visualization is set to the global scale, and continents are shown together with their internal subdivision in regions (according to the United Nations geoscheme).

## 5.5 TREEMAP

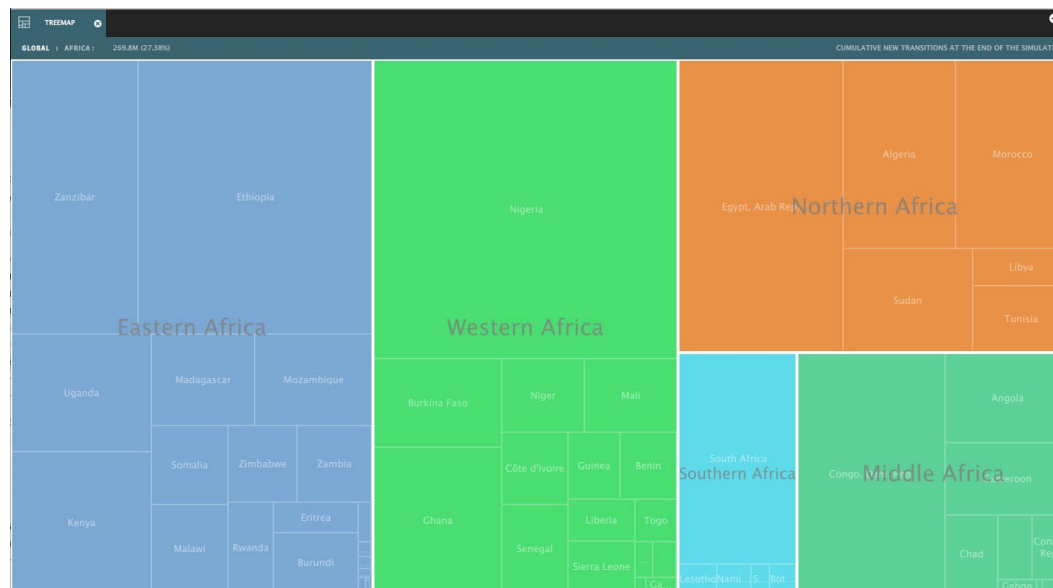


Figure 5.14: Visualization Window: the Treemap widget

## 5.6 INVASION TREE

Hovering a rectangle with the mouse opens an info popup reporting the total number of new transitions and the percentage over the total population for both the higher and lower level areas. By clicking on a rectangle it's possible to "zoom-in" and display an analogous representation for a specific continent: in this case the UN regions are shown together with their internal subdivision in countries. Eventually, by clicking and zooming once more the selected region is expanded, showing the countries together with their internal subdivision in city basins. The Control bar lists the geographical regions selected, allowing to easily return to a higher level, and displays the total number of new transitions and the percentage over the total population for the current selection.

This visualization shows the invasion tree of the simulation, allowing users to explore the geographical diffusion of the pathogen over time from one city basin to the other. The links connect the source and the target subpopulation for any infection occurring in a city previously unaffected. Different colors are used to distinguish between cities invaded by means of long-range traveling (flights) or by close range commuting.

A slider in the Control bar lets users adjust the time interval for which the invasion links are shown on the geographical display: the interval can range from one day up to the total duration of the simulation, and the links actually shown are all those occurring in a time interval that long up to the current day (that is the day indicated in the *Dashboard Player*).

The Control bar also provides two drop-down selection dialogs. The first one allows the user to change the background style: the same options available for the *Map*, as in section 5.1.1, are available for the *Invasion Tree*, with the extra option of showing no background map. The second drop-down dialog can be used to show the invasion

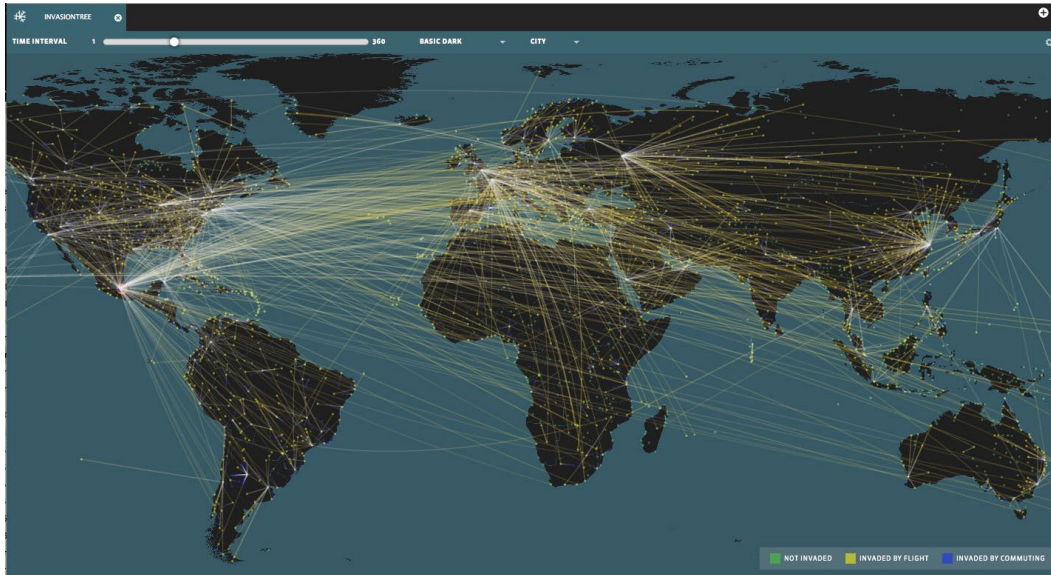


Figure 5.15: Visualization Window: the Invasion tree widget

tree at the country level, for single-run simulations only.

When the *Dashboard Player* is stopped, the *Invasion Tree* widget displays a looping animation of the invasion patterns, by highlighting every link with a moving dot from the source city/country to the target one. Selecting a single city/country the visualization shows both the path from the seeding origin to the selected point, and the cascading tree of cities/countries invaded through the selected one.

Some other visualization options can be configured by means of the settings window that is opened by clicking the gear icon in the top-right corner (coloring, etc.).

## 5.7 X3D GLOBE

This widget displays a 3D globe similar to the Globe widget, but focuses on the new transitions at the country level. The number of new transitions per 1000 for each country are shown as 3D extrusions from the country surface, according to the compartments indicated in the *Compartments Selector*. The shapes are also colored according to the relative values.

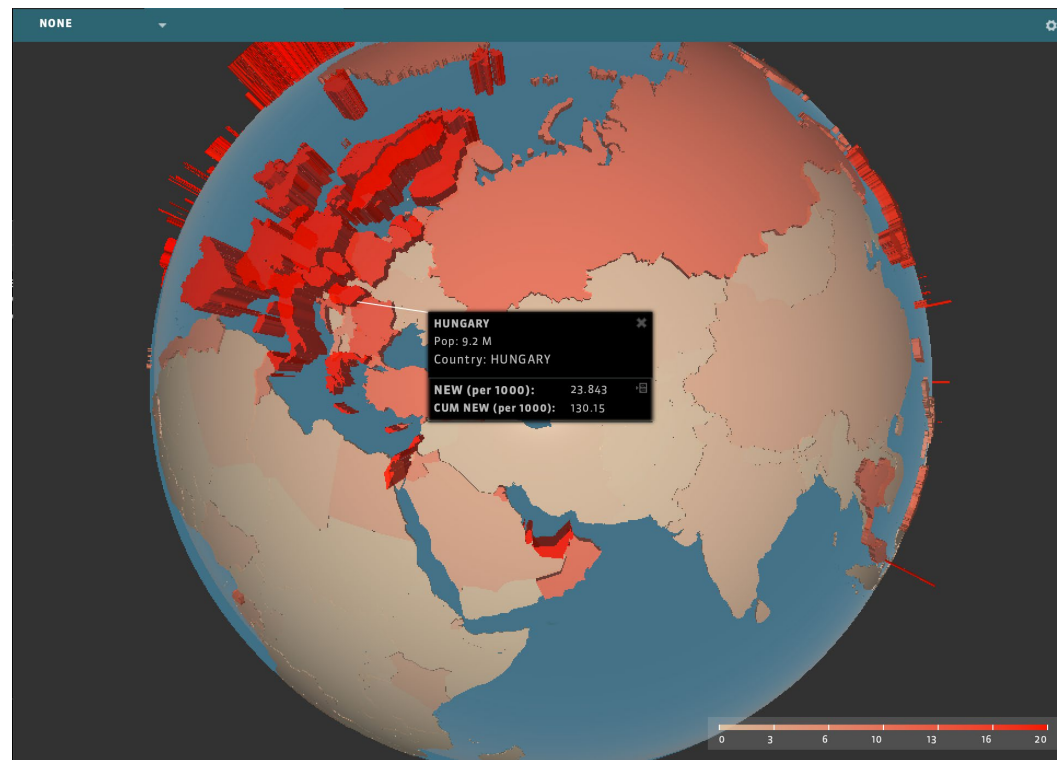


Figure 5.16: X3D Globe

The rotation of the globe can be manipulated by clicking and dragging the mouse, while the zoom level can be adjusted with the mouse wheel. When zooming in and out the visualization adapts the scale of the extrusion for a better perception. It is also possible to adjust the scale factor in the widget configuration settings, as well as other options (coloring...), while the Control bar allows to apply a background for the Earth's surface, with the same options available in the Map widget.

When moving the cursor on the globe, if hovering an area belonging to one of the countries, that country is highlighted, and a small popup appears displaying its name. Clicking on the highlighted country area opens a larger pop-up providing additional details:

- » the population of the country
- » the new and cumulative number of people in the currently selected focus compartments in that country on the current day

Use the Close button to close the pop-up or the Show in new Analyzer button to open a new Analyzer chart with this country as the context. See section 5.4 for more details on the Analyzer chart.

# 06

## PREFERENCES WINDOW

The configuration window (shown in figure 6.1) is opened by clicking on the *Preferences* button in the main window menu bar (see section 3.1).

The preferences window allows the user to manually check for software updates and to configure the application behavior (interaction with the GLEAMviz server, simulations' management, visualization and animation settings, etc.)

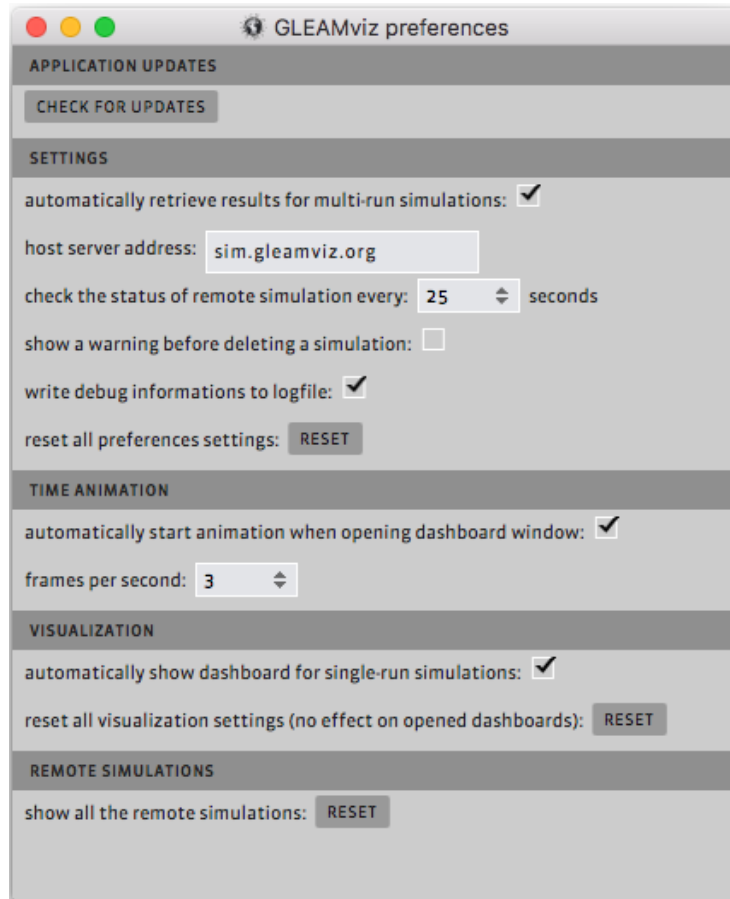


Figure 6.1: Preferences window

# 07

## ALGEBRAIC EXPRESSIONS

Algebraic expressions can be provided for:

1. the values for the variables defined in the compartmental model (see section 4.1.3).
2. the rates of a transition specified in the compartmental model (see section 4.1.2).

A valid algebraic expression consists of numbers, variable references, operators, and parenthesis.

- » Numbers: The numbers can be integers<sup>1</sup> or decimals and can be written using a scientific notation. Examples of valid numbers are: 123; 1.23; .123; 1e23; 1.23e4; 1.23e+4; 1.23e-4; 1.23E4; 1.23E+4; 1.23E-4.
- » Variable References: A variable reference should be a name of another variable defined in the compartmental model. There must be no circular

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<sup>1</sup> Integer numbers are cast to decimals. The expression 1/2 will thus be properly evaluated as .5.



dependencies among the variables. A circular dependency exists when a variable directly or indirectly references itself.

» Operators: The allowed operators are: + (addition); - (subtraction); \* (multiplication); and / (division). The standard operator precedence applies, from highest to lowest precedence:

1. terms inside parentheses
2. multiplication and division, as they appear left to right
3. addition and subtraction, as they appear left to right

The GLEAMviz client checks to see if expressions are valid and no circular dependencies exist<sup>2</sup> and provides more information on invalid expressions.

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<sup>2</sup> The GLEAMviz client considers all references independent of the periods in which they are valid when checking for circular dependencies. GLEAMviz could report a circular dependency when in principle there might not be one. Please use intermediate variables in such situations.

## RESULTS DATA RETRIEVAL

The GLEAMviz Simulator client allows the user to export the results of the simulations that have been successfully completed and retrieved by selecting the *Export results* option in the simulation's drop-down menu. The user is first prompted to select a local directory in which the data will be exported. A new folder will then be created including the following files and sub-directories:

**simulation.gvd:** the XML simulation definition (including the model specification, the parameters settings, and the initial conditions), which can be used as an import file in the Simulation Builder;

**md\_cities.tsv:** the meta-data for the cities-level aggregated output, mapping the numerical identifiers used for the actual output files;

**md\_countries.tsv:** the meta-data for the countries-level aggregated output, mapping the numerical identifiers used for the actual output files;

**md\_regions.tsv:** the meta-data for the regions-level aggregated output, mapping the numerical identifiers used for the actual output files;

**md\_continents.tsv:** the meta-data for the continents-level aggregated output, mapping the numerical identifiers used for the actual output files;

**md\_hemispheres.tsv:** the meta-data for the hemispheres-level aggregated output, mapping the numerical identifiers used for the actual output files;

**cities:** a directory containing one .tsv output file for each city - result compartment combination, named with the city ID followed by a dash and the index of the focus compartment in the result compartments list as defined in the meta-data files;

**countries:** a directory containing one .tsv output file for each country - result compartment combination, named with the country ID followed by a dash and the index of the result compartment as defined in the meta-data files;

**regions:** a directory containing one .tsv output file for each region - result compartment combination, named with the region ID followed by a dash and the index of the result compartment as defined in the meta-data files;

**continents:** a directory containing one .tsv output file for each continent - result compartment combination, named with the continent ID followed by a dash and the index of the result compartment as defined in the meta-data files;

**hemispheres:** a directory containing one .tsv output file for each hemisphere – result compartment combination, named with the hemisphere ID followed by a dash and the index of the result compartment as defined in the meta-data files;

**global:** a directory containing one .tsv output file for each result compartment, named as "0-" followed by the index of the result compartment as defined in the meta-data files;

**seedings.tsv:** for single-run simulations only; a file that contains the seeding data (see section 5.1.3). This file contains four columns: the first contains the day offset since the beginning of the simulation, the second and third columns contain the source and target city IDs, the fourth column contains a bit-mask (represented as an integer) in which the n-th lowest bit is 1 if the seeding concerns an individual in the n-th result compartment.

All the .tsv files are Tab Separated Values (TSV) files.

The output TSV files contain three columns for single-run simulations and seven for multi-run (MR) simulations. The file columns, listed in order, represent the following quantities:

- » the time step, corresponding to the day of the simulation, starting from 0;
- » the new number of individuals per 1000;
- » the lower bound of the relative 95% confidence interval of the stochastic realization (multi-run only);
- » the upper bound of the relative 95% confidence interval of the stochastic realization (multi-run only);
- » the cumulative number of individuals per 1000;
- » the lower bound of the relative 95% confidence interval of the stochastic realization (multi-run only);
- » the upper bound of the relative 95% confidence interval of the stochastic realization (multi-run only).

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