GLEaMviz Simulator
GLEaMviz.org

Client Manual

Version 2.8
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1 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 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 four principal components: 1) the main window with the Simulations History; 2) the Compartmental Model Builder; 3) the Simulation Wizard; and 4) the Visualization windows. Each of these components is described in more detail in the following sections. The main workflow and the role of the components in this workflow is outlined in the diagram in Figure 1.

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

For more information about the GLEaMviz Simulator system please refer to the project’s web-page: http://www.gleamviz.org/simulator.
Design the compartmental model of the infectious disease in the Model Builder.

Configure the simulation of the world-wide epidemic spreading in the Simulation Wizard.

Submit the simulation for execution by the Engine on the server.

Inspect all simulations and retrieve their results in the Simulations History.

Inspect the results of a simulation in the interactive Visualization.

Fig. 1: Workflow overview and the role of the client and server components.
1.1 License

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.

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.

1.2 Conditions of use

All material obtained directly from the simulation products of the GLEaMviz Simulator, or further processed, can be published provided the appropriate credit to the website of the project (www.gleamviz.org) and the following publications:


1.3 Client installation and requirements

The GLEaMviz Simulator client uses the Adobe AIR runtime environment and can thus be installed on recent versions of the following operating systems: Windows (XP, Vista, 7), Mac OS X, and Linux. Please consult http://get.adobe.com/air/ to learn more about operating system support.

The following two steps are required to install the GLEaMviz Simulator client:

1. Download and install the Adobe AIR 2.6 (or higher) runtime software (if not already installed) from:
   http://get.adobe.com/air/

2. Download and install the GLEaMviz Simulator client from:
   http://www.gleamviz.org/simulator/

The GLEaMviz client features a built-in updating mechanism that periodically suggests that the user check for software updates, downloads, and install such updates when they are available.

The Public Edition of the client available from http://www.gleamviz.org/simulator/ is pre-configured to use the GLEaMviz server made available by gleamviz.org. There is thus no need to install the server in order to use this client. However, in order to avoid an overload on this server, a number of limitations are enforced in this setup. Research groups interested in an unlimited version of the GLEaMviz system are invited to contact us at info@gleamviz.org.

To properly install the GLEaMviz Simulator client at least 200Mb of free disk space are required. Additional disk space will be needed to store locally the output of the performed simulations.
1.4 Credits

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Third party libraries and other assets used in the GLEaMviz Simulator system:

Blue Marble map by NASAÕs Earth Observatory
http://earthobservatory.nasa.gov/

Silk Icons
http://www.famfamfam.com/lab/icons/silk/

FZip by Claus Wahlers and Max Herkender
http://codeazur.com.br/lab/fzip/
Contents

Alive PDF
  http://alivepdf.bytearray.org/

FlexLib
  http://code.google.com/p/flexlib/

DashedLine by Trevor McCauley
  http://senocular.com

TweenLite by GreenSock
  http://www.greensock.com/tweenlite/
2 Main window

The main window (shown in figure 2) is opened when the GLEaMviz Simulator client application is launched. This window contains the main menu on the left side, and the Simulations History in the remainder of the window (see section 2.2).

![Main window with menu and Simulations History](image)

Fig. 2: Main window with menu and Simulations History

2.1 Main menu

The main menu can be found on the left side of the main window. It offers the following options:

**Open Model Builder:** Opens the compartmental model builder window, which is used to create or edit a compartmental model of the epidemic characteristics to use in a simulation. See section 3 for more details.

**Open Simulation Wizard:** Opens the simulation wizard window, which is used to define all aspects of a simulation and to submit it for execution on the server. See section 4 for more details.

**Check for updates:** Immediately check for software updates made available over the internet. Note that the client also periodically checks for updates.

**About:** Opens a credits screen. Click the Back button on the credits screen to return to the main content.
Configuration: Opens the configuration window. See section 6 below for more details.

### 2.2 Simulations management

The simulations management interface is located at the right side of the main window (see figure 2). It provides a list of the simulations that the user has created so far. For each simulation it lists the name, the type (single-run or multi-run), the execution status (see section 2.2) and the results status (see section 2.2).

The **Load simulation** button above the simulations list can be used to load a simulation from a file. This simulation will be added to the list. The **Remove all** button can be used to remove all simulations from the list.

When a simulation is selected in the list, the context-dependent menu below the list will provide information about the selected simulation and options for manipulating that simulation. See section 2.3 for more details.

#### Execution status

The execution status of a simulation can be one of the following:

- **initialized**: The simulation was defined but not yet submitted for execution.
- **start pending**: The execution request has been issued and the client is waiting for a reply from the server.
- **aborted**: The simulation execution has been interrupted by the user.
- **started**: The simulation was successfully submitted and the server is executing it. For single-run simulations the results will be immediately retrieved and, depending on the configuration settings, the Visualization Window will open as soon as the client starts to receive output data from the server. For multi-run simulations the server will be regularly polled in order to check the status of the execution of the pending simulations.
- **complete**: The simulation execution is complete.
- **failed**: The simulation execution failed.
- **stop pending**: A request to stop the simulation was sent to the server. The client is waiting for a reply from the server. If accepted the status will be reverted to initialized.

#### Results status

The results status can be one of the following:

- **none**: No results have yet been retrieved from the server. This status is the only one possible until the simulation has been successfully submitted.
retrieve pending: A request to retrieve the simulation results was sent to the server. The client is waiting for a reply.

retrieving: The results retrieval request was accepted and results are being sent by the server.

stop retrieve pending: A request to stop the results retrieval has been sent to the server. The client is waiting for a reply from the server: if accepted the status will be reverted to none.

complete: The results retrieval is complete.

stored locally: The results have been retrieved and stored on the local machine, ready to be displayed without the need to connect to the server. (This option depends on the configuration settings.)

2.3 Context-dependent menu

The name of the simulation can be edited in the input field at the top of the context-dependent menu.

The following functions are potentially available in the context-dependent panel at the bottom when selecting a single-run (SR) or a multi-run (MR) simulation in the Simulations History.

Submit execution: Enabled when the execution status is initialized. Clicking this button will cause the client to submit the selected simulation for execution.

Stop execution: Enabled when the execution of the selection simulation is ongoing. Clicking this button will cause the client to request to stop the execution of the selected simulation.

Check execution status (MR only): Enabled when the execution of the selected simulation is ongoing. Clicking this button will cause the client to poll the server concerning the execution status of the selected simulation.

Retrieve results (MR only): Enabled when the execution is complete and the results status is none. Clicking this button will cause the client to request the retrieval of the results of the selected simulation.

Visualize results: Enabled when the execution is complete and the results have been completely retrieved (and/or stored locally). Clicking this button will result in the opening of the Visualization Window in which the results of the selected simulation will be visualized.

Export results: Exports all results, including relevant metadata and the simulation definition, to a destination folder chosen by the user. The formatting of this data is detailed in section 8.
Store locally/Do not store locally: Those buttons determine whether the result data of the simulation will be stored by the client on the user’s machine.

Inspect simulation: Opens a read-only version of the Simulation Wizard that shows the model and all the simulation’s parameters. It is possible to visualize and save the configuration but not to modify it.

Clone simulation: Opens the Simulation Wizard with a pre-compiled simulation based on the selected one: the user may edit and modify both the model and/or the initialization parameters to start a new simulation.

Save simulation: Exports the simulation definition to an XML file. This file can later be used as the basis of 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 (SR and MR) or to retrieve the output data of an already completed simulation in order to visualize the results (MR only).

Remove simulation Clicking this button will delete the selected simulation from the Simulations History.
3 Compartmental Model Builder

The Model Builder is used to design the compartmental model of the epidemic characteristics of the simulated infectious disease. The Model Builder window is opened by clicking the Open Model Builder button in the main window menu (see section 2.1), or the Edit model button in the Compartmental model panel in the Simulation Wizard (see section 4.4).

Figure 3 identifies the five components of the compartmental Model Builder interface:

Menu: Located at the top of the window. It contains buttons to add compartments to the model, to save a model to a file, to load a model from a file, or to export a PDF or SVG file that contains a 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 further for more details.
3.1 Compartments

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 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 that 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 clinical case, and allow or disallow commuting and air travel for it.

Figure 4 details the functionality provided by the compartment representation.

3.2 Transitions

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). 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 contracts the infection in accordance with a transmission rate defined by the user. This rate can be an algebraic expression that include 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 subpopulation is given by:

$$\frac{\beta I S}{N}$$  \hspace{1cm} (1)

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].

At least one compartment must be defined as corresponding to a clinical case by clicking the thermometer icon in the compartment interface (see Figure 4). This identifies the clinical cases among the infectious compartments, and is used by the GLEaM simulation engine to define the conditions of an outbreak in a given country (see section 4).

Figure 5 provides an overview of the components and functionalities provided for an infection process.

### 3.3 Variables

The user can define one or more variables, which are name-value-expression pairs. The transition rate expressions can reference these variables, and the value expres-
sion 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 include references to other variables. See section 7 for more details on writing expressions.

### 3.4 Inconsistencies

Before a model can be used in a simulation definition it 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 cannot be saved or submitted as long as inconsistencies appear in this section.

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

### 3.5 Saving and loading compartmental models

Often the same compartmental model is 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.

Note that one can also open a gvs file (see 4.2) that contains a simulation configuration, in which case the included compartmental model will be loaded. The conventional extension for compartmental model files is *gvm*, from GLEaMViz.
model. Note that gvm files can be opened in any client and thus can be shared with colleagues.

### 3.6 Examples

Examples of compartmental models (with .gvm extension) can be downloaded from [http://www.gleamviz.org/simulator-examples/](http://www.gleamviz.org/simulator-examples/). These examples can be imported into the Model Builder using the *Load model* button (see Fig. 3).
4 Simulation Wizard

The Simulation Wizard is the component of the GLEaMviz client used to configure a simulation. Through a sequence of panels, it guides the user through the process of defining all the parameters and settings required by the GLEaMviz simulation engine. When the configuration is complete, the user can submit the simulation for execution by the GLEaMviz engine on the server. Each of the panels in the Simulation Wizard is discussed in more detail from section 4.3 onwards.

4.1 Single-run versus multi-run simulations

The simulation engine can perform two kinds of simulations: a single-run simulation or a multi-run simulation.

A multi-run simulation actually performs multiple simulations –runs– with the same model and settings. The numerical results returned from such a simulation are the averages and the confidence intervals calculated over the set of runs.

A single-run simulation, on the other hand, involves only one run. 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.

4.2 Saving and loading simulation configurations

A complete simulation configuration, including the compartmental model, can be saved as a file that contains an xml representation of the simulation configuration and the compartmental model. Such files can be loaded in the simulation History, or can be used when creating a new simulation based on save one (see the next section). Note that these files can also be shared with colleagues. The conventional extension for compartmental model files is gvs, from GLEaMviz simulation.
4.3 Step 1: Initial options

The first panel, shown in fig. 6, provides the user with three options: Create new single-run simulation; Create new multi-run simulation; and Create new simulation based on saved one.

The first two options let the user create a new simulation from scratch. Note that the type of simulation can actually be changed in the subsequent panel, so the choice between single-run and multi-run is provided here as a non-binding convenience.

The third option lets the user create a new simulation based on a simulation stored in a file. The model and settings loaded from this file can be modified in the subsequent panels.

![Simulation Wizard initial screen](image)

Fig. 6: Simulation Wizard initial screen.
4.4 Step 2: Compartmental model selection and editing

After selecting one of the initial options, the wizard proceeds to the next panel, shown in fig. 7, in which the compartmental model needs to be defined. The user can either (i) design a new compartmental model, or modify the current compartmental model, by selecting Edit model which opens the Model Builder, or (ii) load a model from a gvm file (see section 3.5) by selecting Load model. A small representation of the currently defined model is shown for the user’s convenience.

The name of the simulation can be edited at the top of this and subsequent panels.

![Fig. 7: Compartmental model selection.](image)
4.5  Step 3: Simulation parameters

Having selected a model, the user is asked to define the basic scenario for the simulation that will be run by the GLEaM simulation server. The relative interface (shown in figure 8) asks the user for the following parameters:

**Fig. 8:** Basic scenario parameters.

**Type:** single-run (SR) or multi-run (MR). This value is already set depending on how the Simulation Wizard was invoked, but the user can change it if desired.

**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 (to be defined in a following window) 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.

**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

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

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

p. 20
1.0. Along the year the seasonality scaling function varies from a maximum rescaling, \( \alpha_{\text{max}} \), to a minimum rescaling \( \alpha_{\text{min}} \). \( \alpha_{\text{max}} \) is set to 1.1, following previous approaches, whereas \( \alpha_{\text{min}} \) 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.

**Airplane occupancy rate:** the average percentage of seats occupied in each flight. For each simulated flight, the number of passengers is a stochastic variable given by \( C(\alpha + (1 - \alpha)\eta) \), where \( C \) is the number of seats on the plane, \( \alpha \) is the occupancy rate and \( \eta \) is a random variable between \(-1 \) and \(1\). The default value for the air loaded travel used in the simulator is 90\%, consistent with current official airline transportation data.

**Time spent at the commuting destination (hours):** average number of hours spent by the commuters at the commuting destination. The default value used is 8 hours, corresponding to the average 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 of a second country to be infected besides the country where the outbreak initially occurs.
4.6 Step 4: Time-dependent variable overrides

Here the user can specify time-dependent values for the variables defined in the compartmental model. These values are specified in terms of variable overrides. Each of these applies for the selected variable, from the selected start date and up to and including the selected end date. During this period, the simulation will use the given alternate value. The alternative value can be an algebraic expression that includes references to other variables\(^1\). See section 7 for more details on writing expressions.

Use the Add variable override button to add a new override. It is possible to specify multiple overrides for the same variable. When the periods of these overrides overlap, then the override that is positioned higher in the list has precedence. The overrides can be reordered by clicking on the small up or down arrows on the right side of the override forms.

![Time-dependent variable overrides](image)

Fig. 9: Time dependent variable overrides.

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\(^1\) Note that the client considers all expressions when checking for circular dependencies among variables. So while in principle it could be OK to have variable \(v_1\) reference variable \(v_2\) in one override, and having \(v_2\) reference \(v_1\) in another override, the client will signal an inconsistency that needs to be resolved.
4.7 Step 5: Initial assignment of population

On this page the user needs 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 subpopulations considered in GLEaM.

Fig. 10: Initial distribution of population into compartments.

Clicking the Add compartment button will add a new compartment to the list, for which it is possible to define the initial population (see Fig. 10). 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 listed in the window are set equal to 0. Compartments can be removed by selecting them and then clicking the Remove compartment button.
4.8 Step 6: Initial geographic location of the epidemic

The next step in the simulation’s setup is to define the initial location and quantity of the infectious individuals. Please note that they need not to be defined in the initial population assignment interface (the previous step), which is a global setting valid for all the census areas worldwide.

![Image of epidemic location interface](image)

Fig. 11: Initial geographic location of the epidemic.

To add a new epidemic seed the user can click on the *Add seed* button. 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 11). It is possible to add an arbitrary number of epidemic seeds, or to remove a previously inserted one by means of the *Remove seed* button.

Infection seeds can be indicated in terms of number of individuals or in terms of fraction of the population of the selected basin (census area associated to the city). At least one infectious individual in one city/basin must be specified before proceeding to the next interface.
4.9 Step 7: Select result compartments of interest

The next and final step is the selection of the compartments that the user wants 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 (at most 5 for the Public Edition) compartments to be considered when retrieving and visualizing the results in this client. In the visualization window will then be able to visualize the results for all or a subset of the compartments selected here.

Any of the previous selections can be modified by pressing the “Back” button and moving through the Simulation Wizard interfaces. Clicking the Submit button will send the whole simulation settings to the server for computation. The submitted simulation will be added to the Simulations History list in the main window and the Simulation Wizard window will be closed.

This last interface of the Simulation Wizard shows also a Save simulation button that allows the user to save the simulation’s definition to a local file. This file may then be imported by a GLEaMviz simulator client as a pre-defined simulation.
5 Visualization Window

The Visualization Window is the 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 Visualize results button in the context dependent menu; this action automatically fires the results retrieval if data has not been downloaded yet. For single-run simulations, according to the user’s configuration settings, the Visualization Window is opened as soon as the simulation has been successfully submitted to the server. The visualization consists of a Map with the temporal and geographic mapping of the results, the Map Control, the Play Control, and a number of Charts Panels; all identified in figure 13.

Fig. 13: Annotated Visualization Window

5.1 Geographic mapping

The geographic mapping involves a zoomable multi-scale map onto which the results for the selected focus compartment(s) are geographically mapped. These focus compartments are selected from among the result compartments selected in the Wizard (see section 4.9) by means of the drop-down menu provided in the
Map Control, as shown in figure 14. In this menu the user needs to select the result compartments (at least one) for which the results should be shown, and click on "APPLY" to apply the selection. The mapping and charts 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.

Note that results retrieved by the GLEaMviz Simulator client version 2.6 or older, are not available separately for each result compartment. It will consequently not be possible to select focus compartments for such results. Resubmit a clone to obtain separate results.

Fig. 14: Visualization Window: focus compartments selection drop-down menu

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 legend of the Play Control, see figure 16. This color scale can be modified in the Map Settings as detailed in section 5.5.

The Map Control (see figure 15) can be used to zoom in and out and pan the map. Panning can also be done by dragging the map with the mouse. When double-clicking on a specific location on the map, then the map refocusses on this location.

Fig. 15: Visualization Window: Map Control details

At any given moment, the map shows the number of new cases for one particular Current day, which is specified on the Play Control as shown in figure 16. The time evolution of the epidemic is represented by showing the results of subsequent days by updating the mapping accordingly, and as such obtaining an animation. The user can use the the Play / Pause button in the Play Control to start or pause...
5.2 Map backgrounds

One of three map background types, shown in figure 17, can be selected by means of the Map Settings (see section 5.5) or the map’s context menu (right-mouse-click or ctrl-click on the map to open this menu).

![Map background types](image)

Fig. 17: Visualization Window: Map background types, from left to right: Blue Marble Map, Light Map, Dark Map.

5.3 City Info Pop-ups

When the city markers are shown (which can be controlled in the Map Settings detailed in section 5.5), moving the cursor over a city marker causes a small popup to appear that gives the name of that city. Clicking on a city marker opens a larger pop-up like the one shown in figure 18. These city info pop-ups provide additional details about that city, i.e., the airport code (BRU in the example), the system id of the city (378), the population of the city basin (Pop: 2.4 mil.), and the new and cumulative number of people in the currently selected focus compartments of this city on the current day. Use the Close button to close the pop-up, or the Show in
new Charts Panel button to open a new Charts Panel with this city as the context. See section 5.6 for more details on the Charts Panels.

Fig. 18: Visualization Window: City info pop-up.

5.4 Infection transport

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. Such transportation is marked by means of a directed edge from the city of origin to the destination city, as shown in figure 19.

Note that this visualization is mostly significant when the displayed output quantity is made by one or more infectious compartments, in which case the edges show the actual seeding of the infection. Also note that the evolution of the epidemic depends strongly on the model definition, 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 then no seeding flight will be shown in this case.

5.5 Map Settings

Various aspects of the visualization can be controlled through the Map Settings menu, which appears (and disappears) after clicking on the gear icon in the Map Control shown in figure 15. This menu consists of a number of collapsible panels, some of which are shown in figure 20.
Fig. 19: Visualization Window: single-run simulation with seeding flights

Fig. 20: Visualization Window: Settings menu
5.6 Charts Panels

Each Charts Panel, as shown in figure 21, contains two charts. The top chart shows the number of new individuals per 1000 in the selected focus compartments for the Charts Panel’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 Context selection menu at the top of each Charts Panel lets the user choose the context for which the corresponding charts show the results data. This context is either: global, hemispheric, continental, regional, by country, or by city. When opening a Visualization window the upper Charts Panel display the data for the country where the first infection seed was set, while the lower panel shows the global results.

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

A Charts Panel can be repositioned by dragging the panel’s title bar. A Charts Panel can be closed by clicking the Close button or by selecting Close Panel from the panel’s context menu (right-mouse-click or ctrl-click on the panel to open this menu). Additional Charts Panels can be added by selecting Add Charts Panel in the Panel Options section of the Map Settings, or in the context menu of the map or a Charts Panel.

![Fig. 21: Visualization Window: Charts Panel](image)

The results data shown in a Charts Panel can be exported separately by clicking the Export data button or by selecting Export Charts Data from the panel’s context.
The data is exported to a single 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 Timestep, i.e., the day offset since the start of the simulation. For a single-run simulation the second and third columns contain respectively the number of new individuals per 1000 in the selected focus compartments for the Charts Panel’s context, and the cumulative number of new individuals. 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.
6 Configuration window

The configuration window (shown in figure 22) is opened by clicking on the Configuration button in the main window menu (see section 2.1).

![Fig. 22: Configuration window: General section](image)

The following panels are provided in the configuration window:

- **Visualization**: Configure the behaviour of the Visualization Window and the epidemiics evolution animation.

- **Server settings**: Configure the host and port of the GLEaMviz Simulator server, enable/disable the autoconnect flag and manually connect or disconnect.

- **System settings**: Specify whether to store the results of the simulations locally and define the execution status polling interval.
7 Algebraic expressions

Algebraic expressions can be provided for:

1. the values for the variables defined in the compartmental model (see section 3.3).
2. the rates of a transition specified in the compartmental model (see section 3.2).
3. the alternative values of a time-dependent variable overrides specified in the Simulation Wizard (see section 4.6).

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

**Numbers** The numbers can be integers or decimals and can be written using scientific notation. Examples of valid numbers are: 123; 1.23; 0.123; 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 dependencies among the variables. A circular dependency exist 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; and
3. addition and subtraction, as they appear left to right.

The GLEaMviz client checks whether expressions are valid and no circular dependencies exist and provides more information on invalid expressions.

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2 Integer numbers are cast to decimals. The expression 1/2 will thus be properly evaluated as .5.
3 The GLEaMviz client considers all references independent of the periods in which they are valid when checking for circular dependencies. GLEaMviz would could report a circular dependency when in principle there might not be one. Please use intermediate variables in such situations.
Contents

8 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 clicking on the Export results button in the Simulations History. The user is first prompted to select a local directory in which the following files and subdirectories will be stored.

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

md_cities.tsv: the metadata for the cities-level aggregated output, mapping the numerical identifiers used for the actual output files;

md_countries.tsv: the metadata for the countries-level aggregated output, mapping the numerical identifiers used for the actual output files;

md_regions.tsv: the metadata for the regions-level aggregated output, mapping the numerical identifiers used for the actual output files;

md_continents.tsv: the metadata for the continents-level aggregated output, mapping the numerical identifiers used for the actual output files;

md_hemispheres.tsv: the metadata 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 metadata 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 metadata 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 metadata 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 metadata 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 metadata 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 metadata files;

seedings.tsv: for single-run simulations only; a file that contains the seeding data (see section 5.5). This tab separated values file contains four columns. The first contains the day offset since the beginning of the simulation. The second and third columns contain respectively 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 (except seedings.tsv) 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).

Note that results retrieved by the GLEaMviz Simulator client version 2.6 or older, are not available separately for each result compartment. When exporting this data there will consequently be only one file for each city, region, etc.

References

[1] Duygu Balcan, Hao Hu, Bruno Gonçalves, Paolo Bajardi, Chiara Poletto, José J. Ramasco, Daniela Paolotti, Nicola Perra, Michele Tizzoni, Wouter Van den Broeck, Vittoria Colizza, and Alessandro Vespignani. Seasonal transmission potential and activity peaks of the new influenza a(h1n1): a monte carlo likelihood analysis based on human mobility. BMC Medicine, 7(45), September 2009. 2, 14, 21