Information and Communication Technologies

EPIWORK

Developing the Framework for an Epidemic Forecast Infrastructure

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D4.3 Public release of the Epidemic Modeling Platform

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Change log

Version	Date	Amended by	Changes

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Public Release of the Epidemic Modelling Platform

Introduction

The main research effort of the Epiwork project is aimed at developing the appropriate framework of tools and knowledge needed for the design and implementation of modeling, computational and ICT tools to forecast epidemic scenarios with a high level of realism and based on data-driven computational models.
Key to the development of such an epidemic forecast infrastructure at the European level is a computational platform that can provide the access to the state-of-the-art modeling approaches to perform data-driven simulations of epidemic out-breaks. Presently, only a few computational tools are available for assessing scenarios, predicting epidemic evolutions, and managing health emergencies that can benefit a broad audience of users including policy makers and health institutions. The approach described in the following aims at optimizing the balance of complex and sophisticated data-driven epidemic modeling at the global scale while maintaining an accessible computational speed and overall flexibility in the description of the simulation scenario, including the compartmental model, transition rates, intervention measures, and outbreak conditions by means of a user-friendly GUI.

During the firs three years of the project, a platform for the computational modeling of infectious disease spread has been designed, implemented and publicly released. The result is a publicly available software system, called "GLEaMviz" (http://www.gleamviz.org) that simulates the spread of emerging human-to-human infectious diseases across the world. This software is a user-friendly tool for the simulation of a case study, test and validation of specific assumption on the spread of a disease, understanding of observed epidemic patterns, study of the effectiveness and results of different intervention strategies, analysis of risk through model scenarios, forecast of newly emerging infectious diseases.
The computational platform deployment and public releasing have been carried on in advance with respect to the planned scheduling because of the exceptional 2009 pandemic event, an opportunity that made the involved teams spend additional effort in the development of realistic modelling software. Since a first public release has already been done, the third year has focused mainly on the integration of the work carried on within the WP2 and WP3 packages, and in the consolidation of the computational platform. We refer to Deliverable D4.2 (second period) for details on the basic features of GLEaMviz while in this Deliverable we will focus more on the further development carried out during the third period of the project.

The GLEaMviz computational platform: general features

The GLEaMviz computational tool is a client-server system made by three components:

- the client application
- the proxy middleware
- the simulation engine

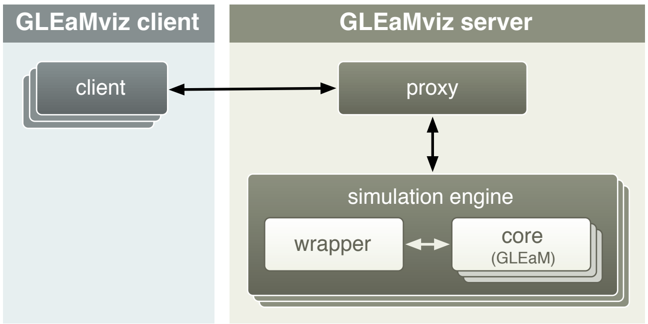

Figure 1: GLEaMviz client, server and middleware

The latter two components constitute the GLEaMviz server.

The simulation engine leverages on the Global Epidemic and Mobility (GLEaM) framework, a stochastic computational scheme that integrates worldwide high-resolution demographic and mobility data to simulate disease spread on the global scale.
Users interact with the GLEaMviz system by means of the client application, whose design aims at maximizing flexibility and usability, allowing to easily setup a simulation (defining the disease compartmental model and configuring the simulation scenario), execute it on the server and visualize the output through dynamic maps and charts.
Multiple clients can use the same server concurrently. A schematic diagram of the workflow between client and server is shown in Figure 2.

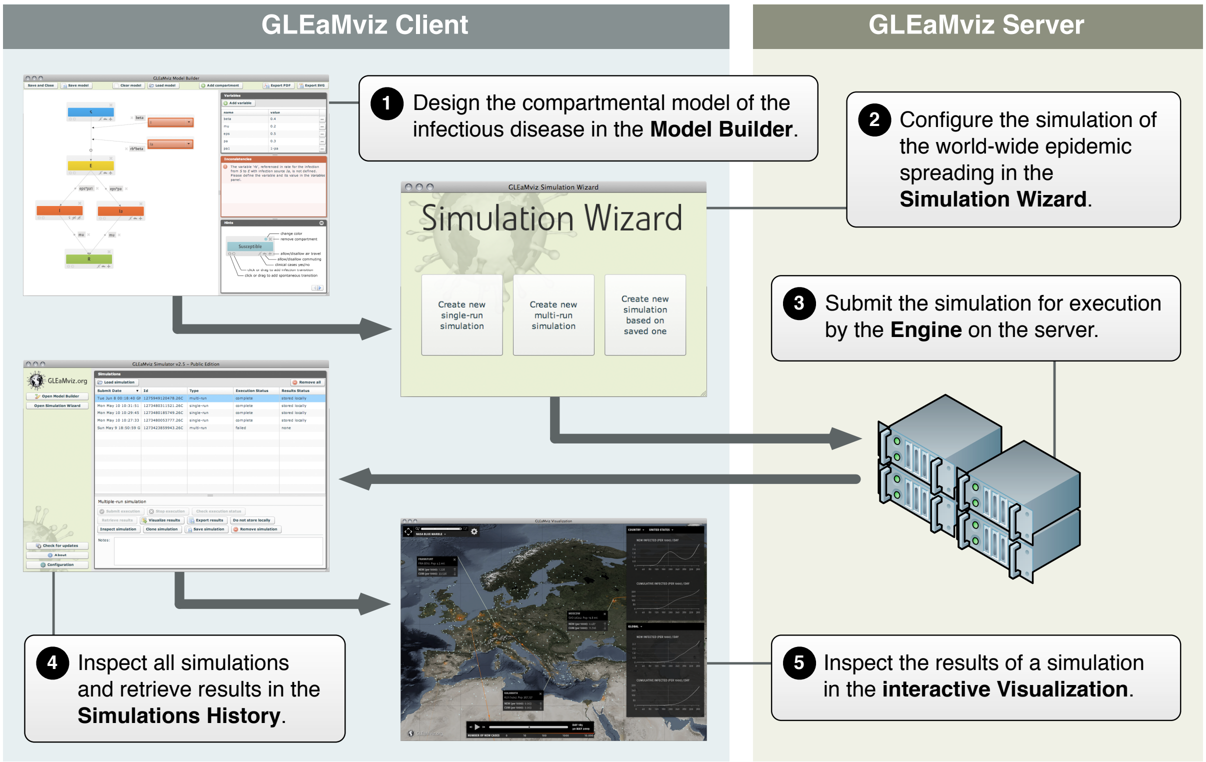

Figure 2: GLEaM workflow

This client-server model allows for full flexibility in its deployment; the client and server can be installed on the same machine, or on different machines connected by a local area network or the Internet.

The GLEaMviz server: progress beyond the objectives

The GLEaMviz simulation engine uses a stochastic meta-population approach that considers data-driven schemes for the short-range and long-range mobility of individuals at the inter-population level, coupled with coarse-grained techniques to describe the infection dynamics within each subpopulation. The basic mechanism for epidemic propagation occurs at multiple scales. Individuals interact within each subpopulation and may contract the disease if an outbreak is taking place in that subpopulation. By travelling while infected, individuals can carry the pathogen to a non-infected region of the world, thus starting a new outbreak and shaping the spatial spread of the disease. The details of the data-driven model and its features have been previously described in D4.2.

After the first public release, the server component of the GLEaMviz computational platform has been refactored, in order to allow for a more flexible and scalable infrastructure and thus to enhance the potential level of integration with other systems. The communication between server and client, which used to make use of a custom protocol, has been re-implemented using a standard "XML over HTTP" protocol, following the REST paradigm. The data representation of simulations has been redesigned accordingly, allowing a consistent storage and management through the whole pipeline, form the server to the client and to external interfacing systems. In the context of this restructuring the management of the simulations client side has been rethought, following a document-oriented approach that makes simpler the filing, storing and sharing of simulations by the users. The new platform authenticates users upon an LDAP directory.

The engine component of the GLEaMviz computational platform, which implements the Global Epidemic and Mobility model (GLEaM), has been rewritten according to a modular and extensible engineering, resulting in a significantly faster computation. The engine component is coded as a Python program with additional modules; all the computational expensive tasks are then performed by embedded FORTRAN routines directly callable by the main program.

The middleware component of the GLEaMviz computational platform takes care of the interaction between the clients and the actual computational engine, handling the user management and the simulation requests, and controlling the engine's execution. This component has been fully redesigned, accordingly to the communication protocol change, and is now enabling the LDAP based authentication of users. The middleware component implementation is based on the Django Web framework (https://www.djangoproject.com/) and the PostgreSQL database (http://www.postgresql.org/) to handle user management and simulations management. The middleware component is now designed in a way that makes the GLEaMviz server potentially suitable for interfacing with various client types.

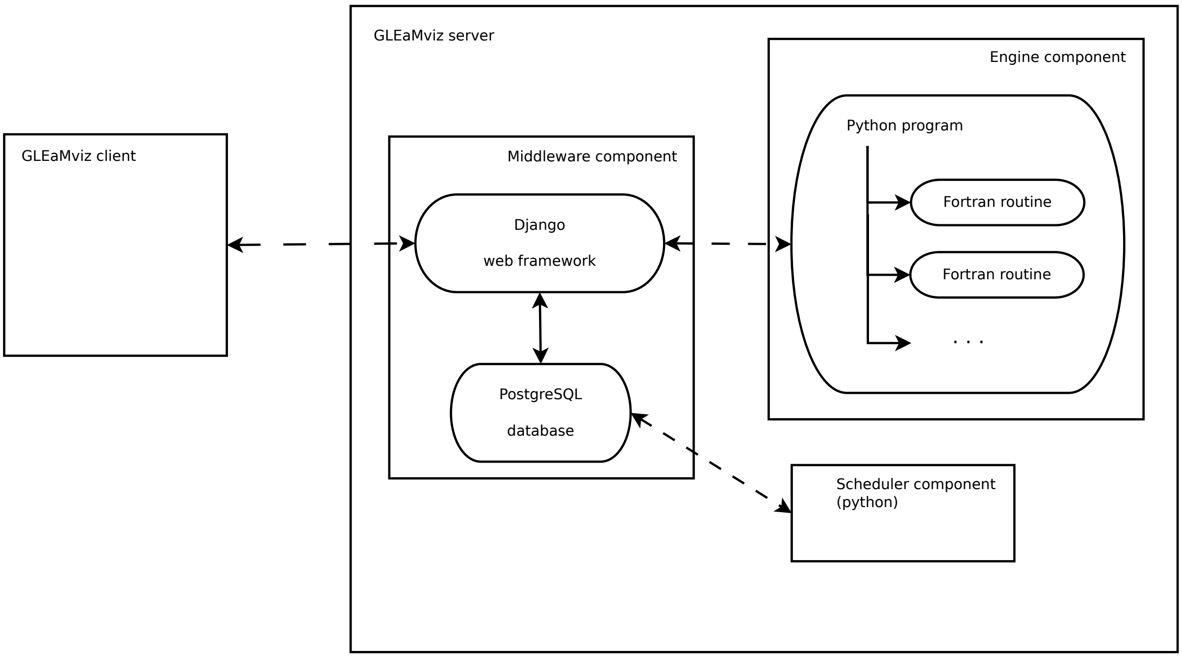

Figure 3: new design of the middleware

The GLEaMviz client

The GLEaMviz client application provides GUIs for its four main functions: 1) the design of compartmental models that define the infection dynamics; 2) the configuration of the simulation parameters; 3) the visualization of the simulation results; and 4) the management of the user's collection of simulations. The client can be installed on recent versions of the Microsoft Windows and Mac OS X operating systems.

Many kinds of human-to-human infectious diseases can be modeled, in particular respiratory and influenza-like diseases. For a detailed description of the basic interfaces of the GLEaMviz client please refer to deliverable D4.2.

With respect to the first public release described in D4.2 the GUI of the client application has been improved and extended. A study on usability and ergonomics of the interface has been carried on by design experts, leading to a redesign of the simulation management and setup windows. The simulation wizard, used to design new simulations, has been completely rewritten and has been integrated with the model builder in a tabbed panel interface. New functionalities to allow for time-dependent exceptions in variables values, and thus to simulate global scale time-dependent interventions like vaccinations or drug treatments etc. have been included in the setup interface, exploiting the flexibility and modularity of the engine component.

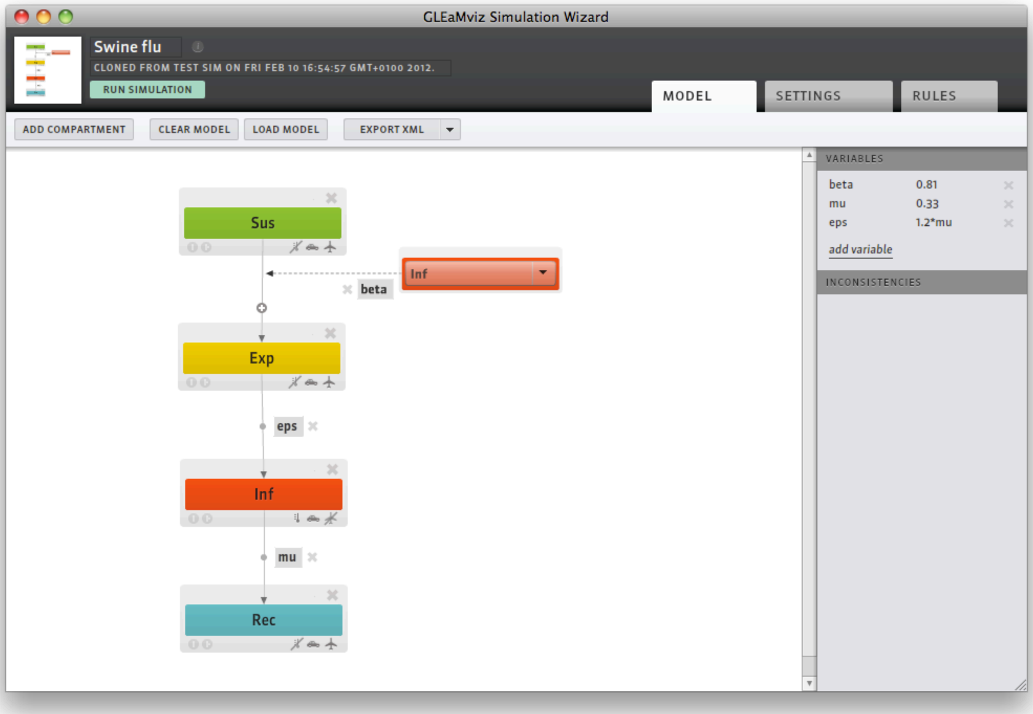

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Figure 4: new GLEaMviz client

The SPATO algorithm and visualization approach previously developed within WP2 by the MPG group have been integrated directly into the GLEaMviz client. It is now possible to visualize the results of a simulation by displaying the spreading of a global-scale epidemic upon a shortest-path representation of the airline transportation network, with different rescaling options. The same simulation can thus be visualized simultaneously in terms of geographical mapping and in terms of topological network representation.

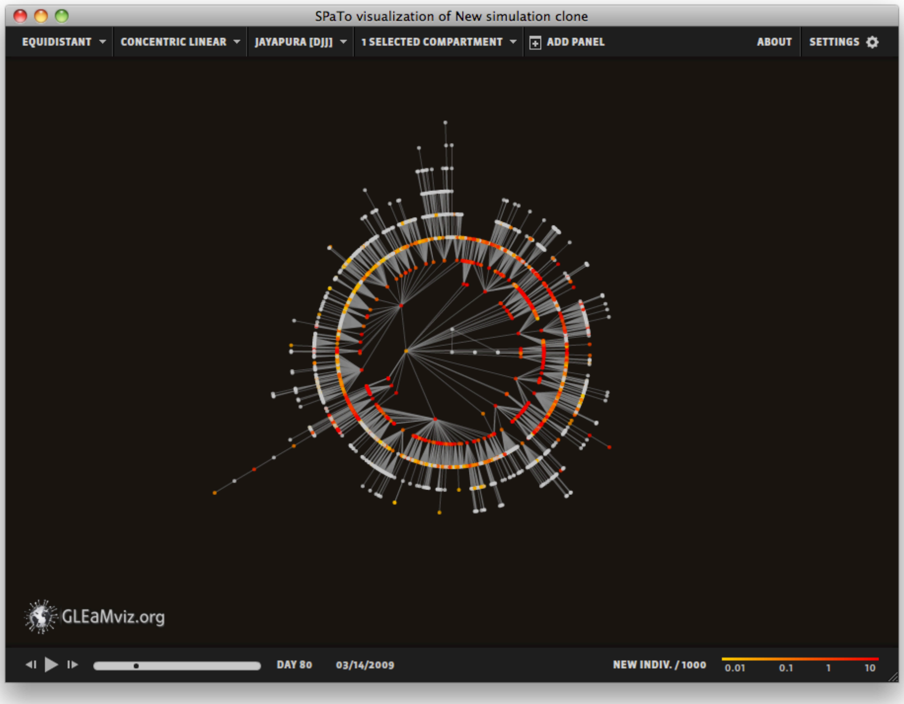

Figure 5: SPATO visualization

Another new option has been added to the visualization component of the GLEaMviz client application. In addition to the default map visualization and the SPATO (http://www.spato.net) visualization is now possible to access a third visualization option, where the disease spreading is displayed on a 3D representation of the Earth.

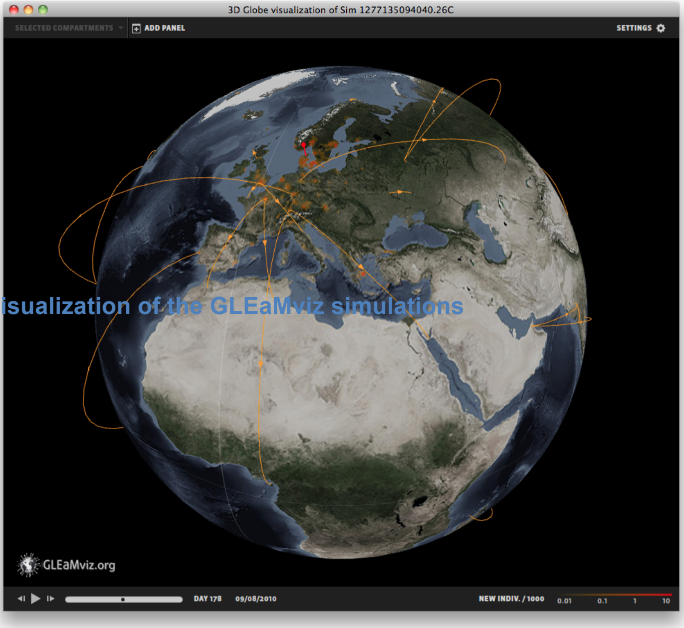

Figure 6: 3D visualization of the GLEaMviz simulations

Chart panels plotting the number of new cases and cumulative new cases for each geographical region can now also be added in any number to every visualization component.

The new client can be downloaded from: http://www.gleamviz.org/simulator/. The new features have been documented in the updated version of the manual, which can be found at the address: http://www.gleamviz.org/simulator/GLEaMviz_client_manual.pdf

Conclusions

GLEaM is under continuous development and so far it has been used: to assess the role of short-range and long-range mobility in epidemic spread [2]; to retrospectively analyze the SARS outbreak of 2002-2003 in order to investigate the predictive power of the model [4]; to explore global health strategies for controlling an emerging influenza pandemic with pharmaceutical interventions under logistical constraints [3]; estimate the seasonal transmission potential of the 2009 H1N1 influenza pandemic during the early phase of the outbreak to provide predictions for the activity peaks in the Northern Hemisphere [1, 8]; and more recently to assess the ecotoxicologic risks of a pandemic influenza medical response [10].

Computer-based simulations provide an additional instrument for emerging infectious-disease preparedness and control, allowing the exploration of diverse scenarios and the evaluation of the impact and efficacy of various intervention strategies.

The Epidemic Modeling Platform, developed in the scope of Epiwork Work Package 4 and here presented, is a computational tool for the simulation of emerging ILI infectious diseases at the global scale based on a data-driven spatial epidemic and mobility model that offers an innovative solution in terms of flexibility, realism, and computational efficiency, and provides access to sophisticated computational models in teaching/training settings and in the use and exploitation of large-scale simulations in public health scenario analysis.

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