



A Graphical User Interface for R in a Rich Client Platform for Ecological Modeling

Marcel Austenfeld
University of Kiel

Wolfram Beyschlag
University of Bielefeld

Abstract

For many ecological analyses powerful statistical tools are required for a profound analysis of spatial and time based data sets. In order to avoid many common errors of analysis and data acquisition a graphical user interface can help to focus on the task of the analysis and minimize the time to fulfill certain tasks in a programming language like R. In this paper we present a graphical user interface for R embedded in the ecological modeling software **Bio7** which is based on an Eclipse rich client platform. We demonstrate that within the **Bio7** platform R can not only be effectively combined with Java but also with the powerful components of Eclipse. Additionally we present some custom **Bio7** components which interact with R and make use of some useful advanced concepts and libraries of this connection. Our overview on the **Bio7** R interface also emphasizes a broad applicability for disciplines beyond ecological modelling.

Keywords: rich client platform, ecological modeling, **Rserve**, R, Java.

1. Introduction

In recent years the R platform (R Development Core Team 2012) became a very popular tool for statistical analysis in ecology and ecological modeling not only because of the fact that R is open source but also because of the huge possibilities this platform offers to edit, analyze and shape data for analysis (Petzoldt 2003; Ellner and Guckenheimer 2006; Petzoldt and Rinke 2007; Bolker 2008; Soetaert and Herman 2008; Stevens 2009). The free availability of advanced statistical concepts and a vigor community supports the exploration of the sometimes overwhelming complexity of biotic and abiotic factors within ecological systems. Ecological models can help to explore and predict the impact of certain biotic and abiotic parameters like temperature changes, human induced nutrient enrichment, competitive interactions or the impact of land use changes on a real system. The creation and verification of such models

can be a time consuming and an error-prone task and typically several software tools have to be combined for a complete analysis.

To reduce the time for model creation and analysis for scientists working with environmental data we developed the ecological modeling platform **Bio7** based on a rich client platform (Austenfeld 2009). Eclipse is a very powerful Java integrated development environment (IDE) which offers the possibility to create such a rich client interface (McAffer *et al.* 2010). A rich client platform (RCP) typically consists of a set of components (plugins) which a developer can reuse to create a new application for a complete different task. Building applications on top of Eclipse has the great advantage to profit from the latest and ongoing development in software technology like the modular design of free available plugins which can extend a RCP platform. Also the availability of new graphical user interface (GUI) toolkits like the standard widget toolkit (SWT) are a bonus for the creation of such applications and can even be combined with the default Java GUI toolkits like Swing and JavaFX. SWT itself is the default GUI toolkit for the Eclipse platform (Northover and Wilson 2004; Warner and Harris 2004). For the creation of more advanced graphical user interfaces the rich client concept offers several useful templates which can be combined for an intuitive and flexible custom GUI. Eclipse menus, toolbars, consoles, update components, help facilities and a powerful Eclipse application programming interface (API) can be reused for a custom RCP application. Additionally the application supports the creation of customizable programming language editors and views (customizable GUI containers) which can be statically or dynamically arranged in a so called Perspective. A Perspective is an Eclipse term which describes a configurable superior container for different views and editors and is used in Eclipse to bundle and organize specific development tools for a task. Typically a RCP application embeds several perspectives which can be used to arrange several thematic interfaces for a special purpose e.g., for statistics (see Figure 1).

The application **Bio7** uses the RCP perspective layout concept to arrange different tools for the creation and analysis of ecological models. One custom perspective of **Bio7** embeds useful components to interact with the statistical software R (see Figure 1)

This R interface provides an easy to use and extendable GUI and a link to the other integrated scientific tools and programming languages. Its applicability extends far beyond ecological modelling, where it was primarily developed for.

Since **Bio7** is written in the programming language Java, a special interface to R was integrated to communicate with R. For a bidirectional communication the **Rserve** application is used to set and get values from R and evaluate R code from a R editor or R shell implemented in **Bio7** (Urbanek 2012). **Rserve** provides an interface which can be used by applications to perform computations in R (Urbanek 2003) and can be called directly e.g., from the programming language Java the main programming language of **Bio7**. The connection to R with **Rserve** was chosen because of the speed of a server connection and the flexibility to connect the **Bio7** application not only to a local R instance but also to a remote computer. So it is possible to transfer a heavy load calculation on a remote specialized device on another **Rserve** supported operating system. Most of the operations regarding the interaction with R and **Rserve** are executed by means of a special Eclipse API (Jobs API) which allows to perform the R interactions as background processes in which long running R operations will not block the **Bio7** GUI. The progress of such a job is indicated in the status bar of **Bio7** or in a special progress view in which these jobs can also be cancelled.

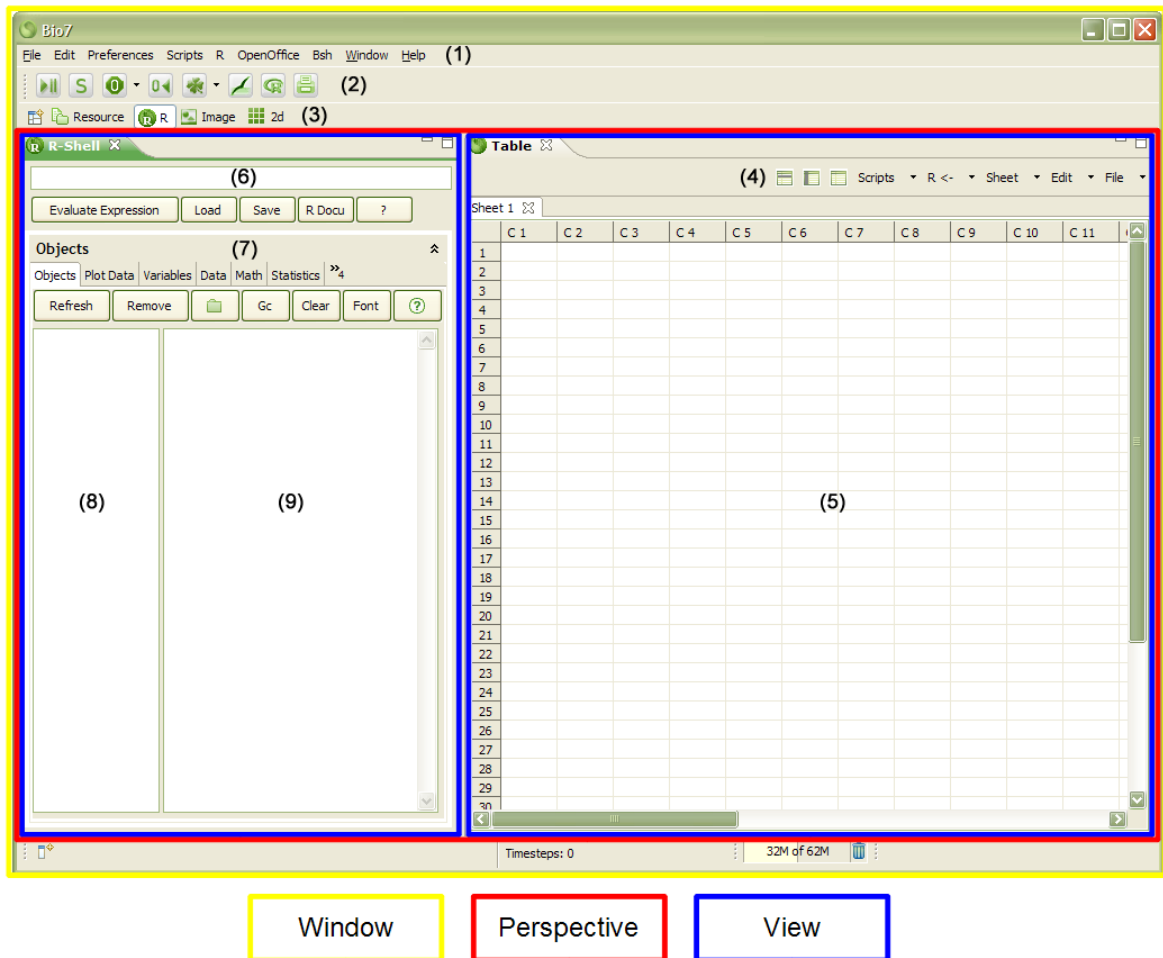


Figure 1: The Eclipse IDE uses “Perspectives” to organize and layout several editors and views (customizable GUI containers) for a specific task. This concept can be reused for a RCP application like **Bio7**. **Bio7** contains several customizable perspectives which can be enabled or opened with actions in the **Perspective Bar** or with the **Window** menu in the main menu bar of **Bio7**. The R perspective of **Bio7** contains two views. The R shell view (left) displays the current R workspace and offers methods and templates to evaluate, edit, plot and transfer data. The **Table** view (right) contains a custom table in which data can be imported, saved, edited or transferred to the R workspace. (1) The main menu bar with an embedded R menu. (2) The main toolbar of **Bio7** with one action to start the **Rserve** connection to R (the action to evaluate R scripts appears here if the R editor is active). (3) The **Perspective Bar** to switch from one perspective to another. Custom perspectives can be saved with an available context menu. (4) Menu and toolbar of the **Table** view with actions to customize the table, import or export data and transfer data to the R workspace. (5) The **Table** view area in which several sheets can be opened side by side. (6) The **Bio7** R shell console in which R expressions can be evaluated. (7) Several tabs with R actions and thematic R templates. (8) A display for the workspace of R (in the first tab) which offers a context menu with several actions to edit, analyze and transfer data. (9) A console (in the first tab) for the display of values and results of R evaluations.

2. The graphical user interface for R

Bio7 embeds several GUI components and evolved over the past years since its first release in 2007 to a full featured R GUI interface. The main R components of **Bio7** are a R menu in the menu bar of **Bio7**, a R editor for source files and a R perspective which embeds a spreadsheet and a custom R console. Furthermore R scripts can be collected in a **Flowchart** editor or extend a specialized scripts menu of **Bio7** for execution. In addition some other **Java** components of **Bio7** can interact dynamically with R data. For example a dynamic **Java** compiler and two **Java** scripting languages (Groovy, BeanShell) which can use the **Rserve** API to get and set values from and to the R workspace and visualize data in available **Bio7** displays. An overview of selected **Bio7** R components is illustrated in Figure 2.

2.1. The R menu

The main R menu of **Bio7** contains custom methods to start the **Rserve** connection, load and



Figure 2: Overview of selected **Bio7** R components and software components which can be used with R.

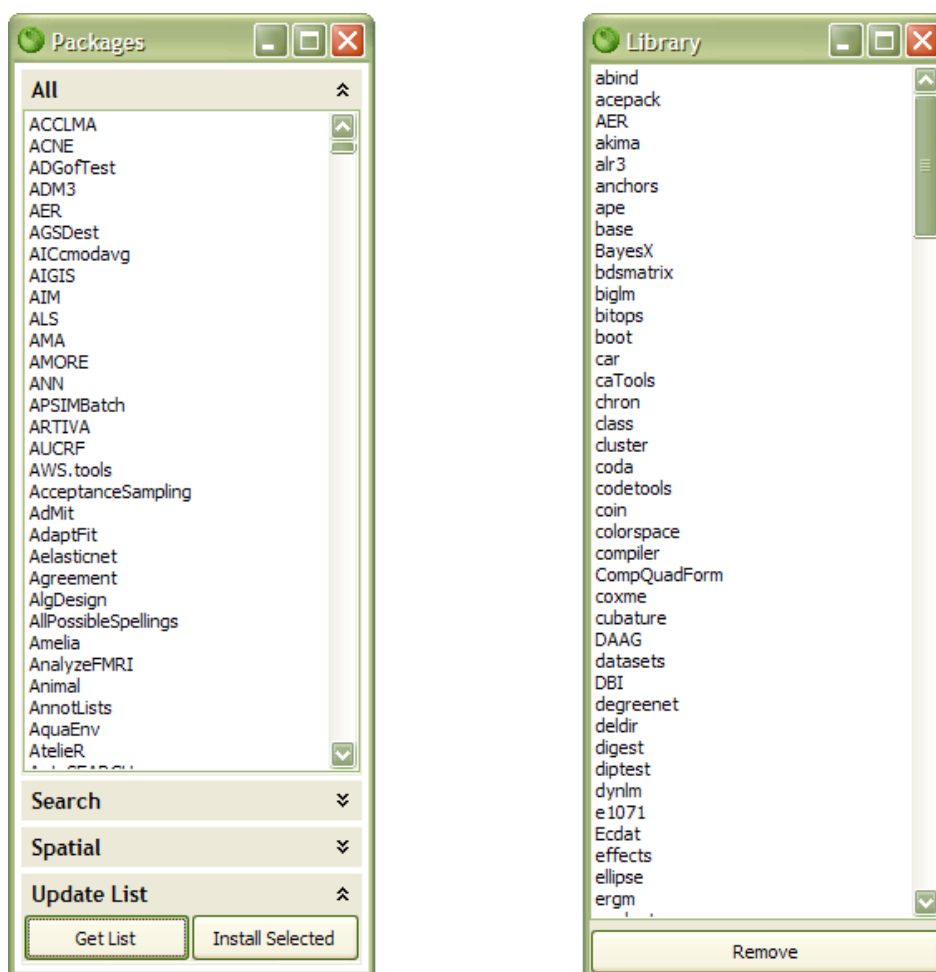


Figure 3: Left – **Bio7** package manager for R to install packages from the internet with a custom search field and a category for selected packages for spatial analysis. Right – Dialog to load and uninstall selected packages.

save R workspaces, evaluate expressions in the R console and delete workspace data. Two custom actions are available to install and load R packages from the internet (see Figure 3). It is also possible to start the regular R GUI (Windows) or shell (Linux) with the current workspace as an option. The R preferences action allows the editing of several adjustments of the R editor, **Rserve** connection (remote, local) and options for the installation of packages. In an available dynamic submenu of the **Scripts** menu of **Bio7** (besides the **R** menu) custom R scripts can be detected and executed if copied in a special available R scripts folder of **Bio7**.

2.2. The R editor

The R editor in **Bio7** comes with functionalities to edit and mark R language expressions and offers several templates (which can be extended in the preferences) for language specific expressions. Since a R plotting device is not directly available with the **Rserve** application (a disadvantage of using **Rserve**) plotting commands can be marked in the R editor and will be displayed in a PDF reader or embedded image application from a temporary created plot

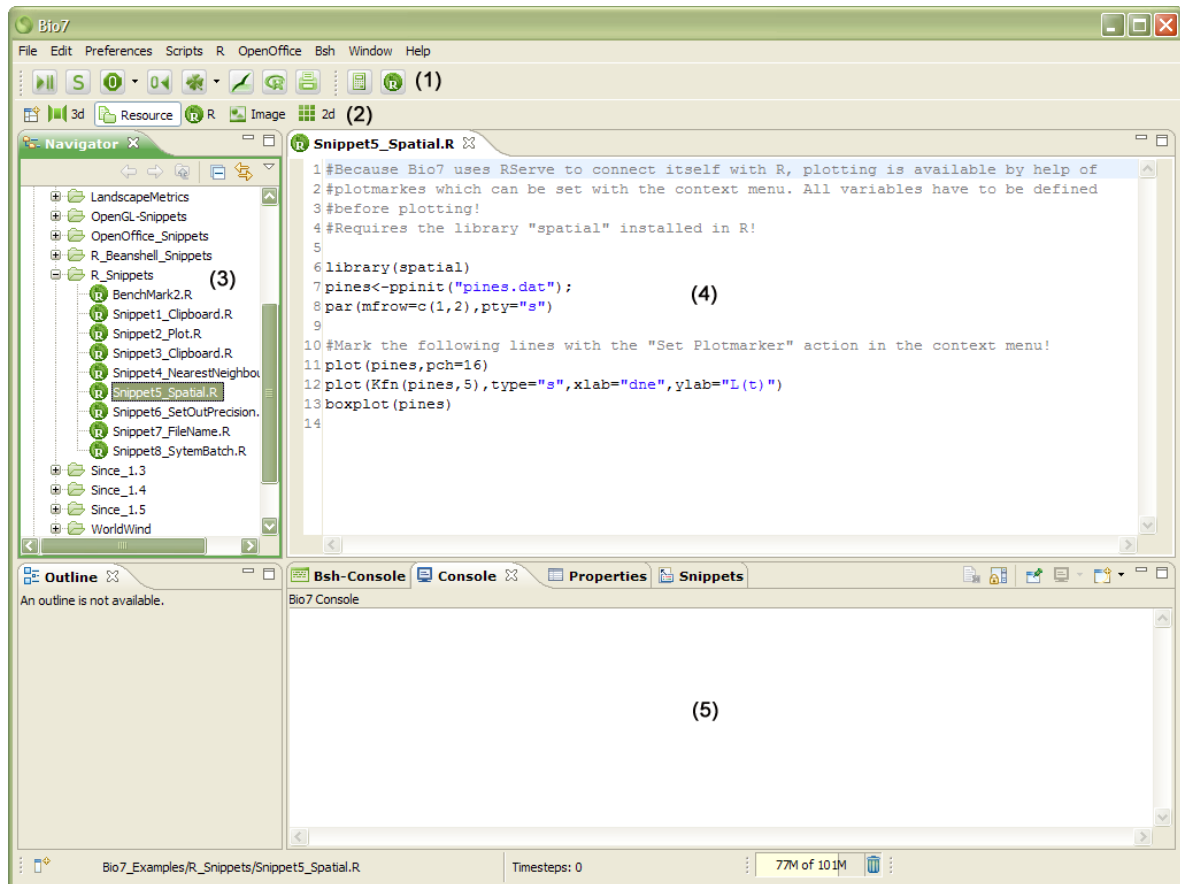


Figure 4: The active **Resource** perspective of **Bio7** with opened R editor actions in the main toolbar (1), the selected **Resource** perspective with the **Perspective Bar** (2), the **Navigator** view (3) and an opened R source file in the R editor (4). The **Navigator** view displays several projects which are stored in the default **Bio7** workspace (a subfolder in the **Bio7** install location). New **Bio7** projects can be created in the **File** menu (**New**) of **Bio7** or with the available context menu of the **Navigator** view. Scripts and **Java** files have to be created in a project (e.g., with the context menu). Opened script and **Java** files can be executed with the editor actions (1) which will be opened with the registered editor in the toolbar of **Bio7**. Evaluated results or expression errors (as well as **Java** and **Java** scripting exceptions) are printed to the default **Bio7** console (5).

file. For the creation, storage, import and export of R script files (and other formats) **Bio7** offers a typical file creation wizard in the **File** menu and a file navigator view (reusable Rich Client Components) which shows the **Bio7** workspace the default storage location for all files in **Bio7**. The default perspective to edit e.g., R files in **Bio7** is the **Resource** perspective which contains e.g., the **Navigator** view, the editor area, a console, a snippets view (e.g., for custom R code snippets) and a property view for files (see Figure 4). The **Navigator** view displays the **Bio7** workspace and offers different methods to export and import files e.g., as a ZIP file.

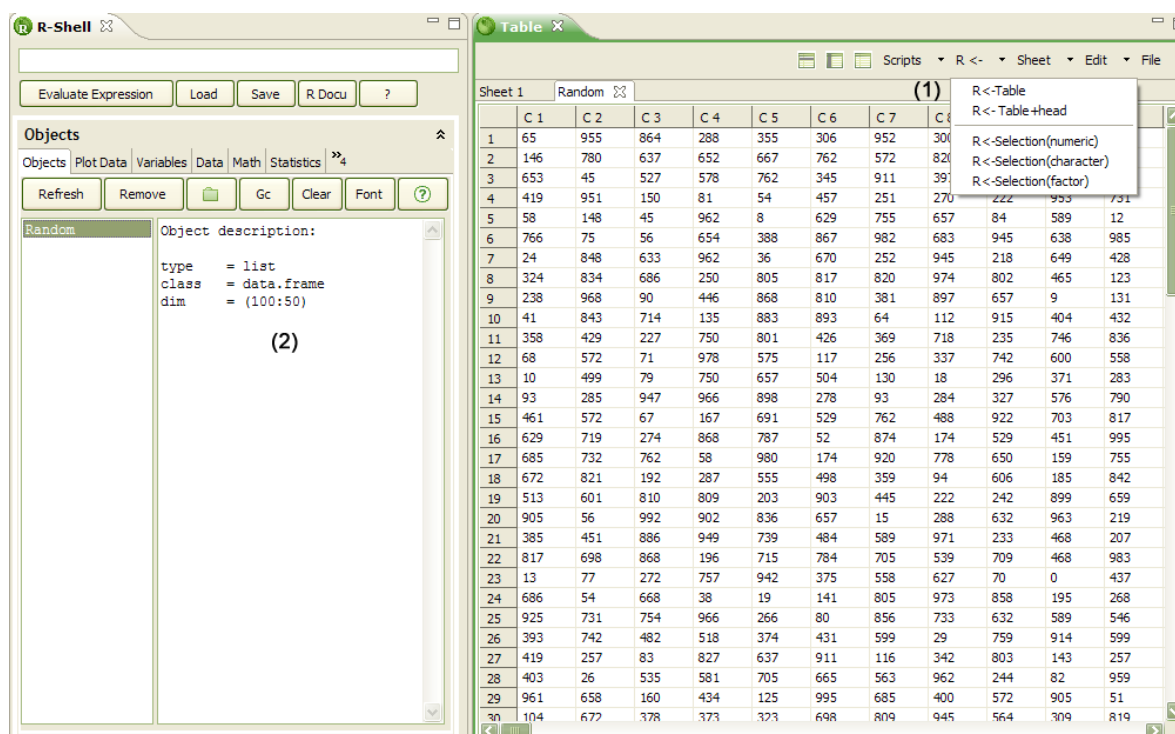


Figure 5: The two views of the R perspective. In the **Table** view (1) several actions are available to transfer data directly to the R workspace as dataframes or vectors of different datatype. Vice versa data of the R workspace can be transferred to new sheets in the **Table** view with actions available in the R shell view (2). A custom **Scripts** menu for Java scripting languages can be extended with custom scripts. The conceptual design of this Perspective separates a view which is extended with Java specific menus and actions (**Table** view) and a view which embeds R specific menus and actions (R shell view).

2.3. The R perspective

The **Bio7** R perspective by default embeds a Java SWT spreadsheet component (**Table** view) and a R shell view side by side (see Figure 1, Figure 5). With the spreadsheet component external files from e.g., **Excel**, **OpenOffice.org** can be imported with powerful Java libraries, edited in the spreadsheet and then transferred to the R workspace. Some specialized methods of the available **Table** menu offer the possibility to easily transfer the sheet data as different types and in selected portions to R. Vice versa data available in the R workspace can be transferred (as matrices or dataframes) to the **Table** view as a new sheet and e.g., exported to available export formats. Some typical spreadsheet functions help in the creation of data and several tabs can be opened to edit data from different sources.

The R shell view

The R shell view within the R perspective (see Figure 6) is laid out that it can be opened detached in another perspective of **Bio7**. The shell itself consists of several tabs and an expressions text field in which R expressions can be evaluated. In addition the text field can also display a history dialog (up-arrow key). The history data can be saved and opened with

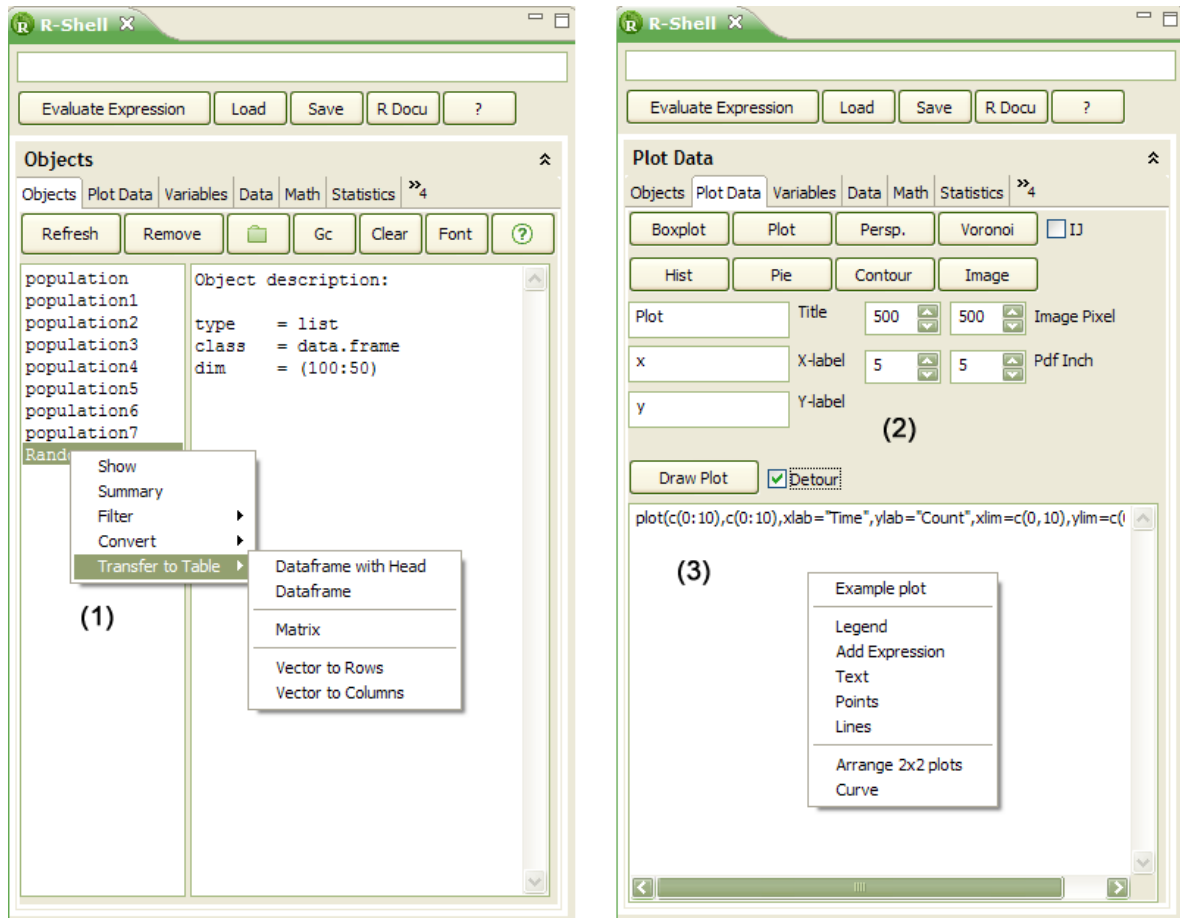


Figure 6: The **Objects** tab of the R shell view (1) with the opened context menu which contains several actions to edit and analyze R data. The activated **Plot Data** tab (2) embeds methods to plot R workspace variables. Selected variables in the **Objects** tab can be plotted with the appropriate plot actions in the **Plot Data** tab (2). In the **Plot Data** tab a textarea is embedded (3) to customize a plot. If the **Detour** option is selected the available plot commands are sent to the enabled textarea for customization. The R commands of the textarea will be interpreted when the **Draw Plot** action is invoked. In the enabled textarea a context menu with templates is available, too.

the available actions below the text field. In the first tab **Objects** some actions are available to refresh the displayed R workspace data, delete variables, store a temporary workspace, trigger the R garbage collection, some options for the display of the R data and a help button with some information about the use of the R shell. In addition the first tab is divided into two displays below the afore mentioned actions. In the left display the R workspace data are displayed and can be selected. Several actions are available with a context menu of the display to show and convert workspace data or transfer data from the R workspace to the afore mentioned spreadsheet. The right display of the first tab visualizes results of evaluated expressions and in addition works like a printing console for R evaluation errors. The second tab **Plot Data** offers actions to plot data in an easy way. Beside the plotting functionality in the R editor this is another possibility in **Bio7** to plot R data which by default is not supported

with an available display in **Rserve** (a counterpart of the R plot display is not supported). Some standard plotting actions can be found in this tab and can be configured with some basic attributes. For a customization of the plotting commands a **Detour** action is available which sends the plotting commands to an intermediate text field for customization (templates are available in the context menu of this text field) and can then be evaluated with another available (**Draw Plot**) action. In addition to the first two tabs of the R shell several other tabs are available with R expression templates in different categories. A click on the displayed expressions opens some context information for the different templates. General this thematic tabs and their embedded templates should help in the selection of appropriate “receipts” for data analysis and manipulation of data.

Usage example

In the following example a simple use of the **Bio7** R functionality is demonstrated. To start an analysis with R in **Bio7** the **Rserve** application has to be started with the **Start Rserve** action in the **Bio7** toolbar to connect **Bio7** with an R installation. After the startup we can create a new Java spreadsheet with random data with the available script action (see Figure 5) in the menu of the **Table** view (**Scripts->Random**). Optionally one can create his own data in the default available sheet. The sheet data can easily transferred to the R workspace with the different actions available in the **R<-** menu. Select the **R<-Table** action to transfer the data as a dataframe to the R workspace. The name of the dataframe is the name of the sheet in the **Table** view. Click on the **Refresh** action in the R shell **Objects** tab for the display of the current workspace. The dataframe is displayed and if selected an object description is given in the console beside the R data view. With the context menu of the R data view we can summarize the data of the selected dataframe (**Summarize**). Optionally we can use the expression text field to apply R commands to the data. To plot the selected data switch to the **Plot Data** tab and press the the **Boxplot** button. By default the plot is opened with the systems default PDF device but can also be opened in the **ImageJ-Canvas** view of **Bio7**.

2.4. Customization of the R perspective

All available editors and views of **Bio7** can be activated in the available perspectives of the application (with the Window menu in the menu bar of **Bio7**). Additional views and editor files for example can be opened and positioned in the R perspective. This can be interesting when R is used in combination with another integrated tool in **Bio7** like **ImageJ** for the purpose of advanced image analysis with R (see Figure 7). All this created custom perspectives can be saved in the context menu of the **Perspective Bar** for a later session.

3. Using R in the interaction with specialized tools

Additional to the integration of a full featured graphical user interface to R and due to the interaction with R by means of the Java **Rserve** bridge, **Bio7** offers access to several other Java based tools. One of these tools is a **Flowchart** editor (Figure 8) in which R source files can be arranged and executed (beside Java and different script files) to form a reproducible chain of simulation and analysis. The **Flowchart** editor was created with the graphical editing framework (GEF). With GEF it is possible to develop advanced graphical editors e.g., in RCP applications. The graphical visualization is done via the Draw2D framework, which is a

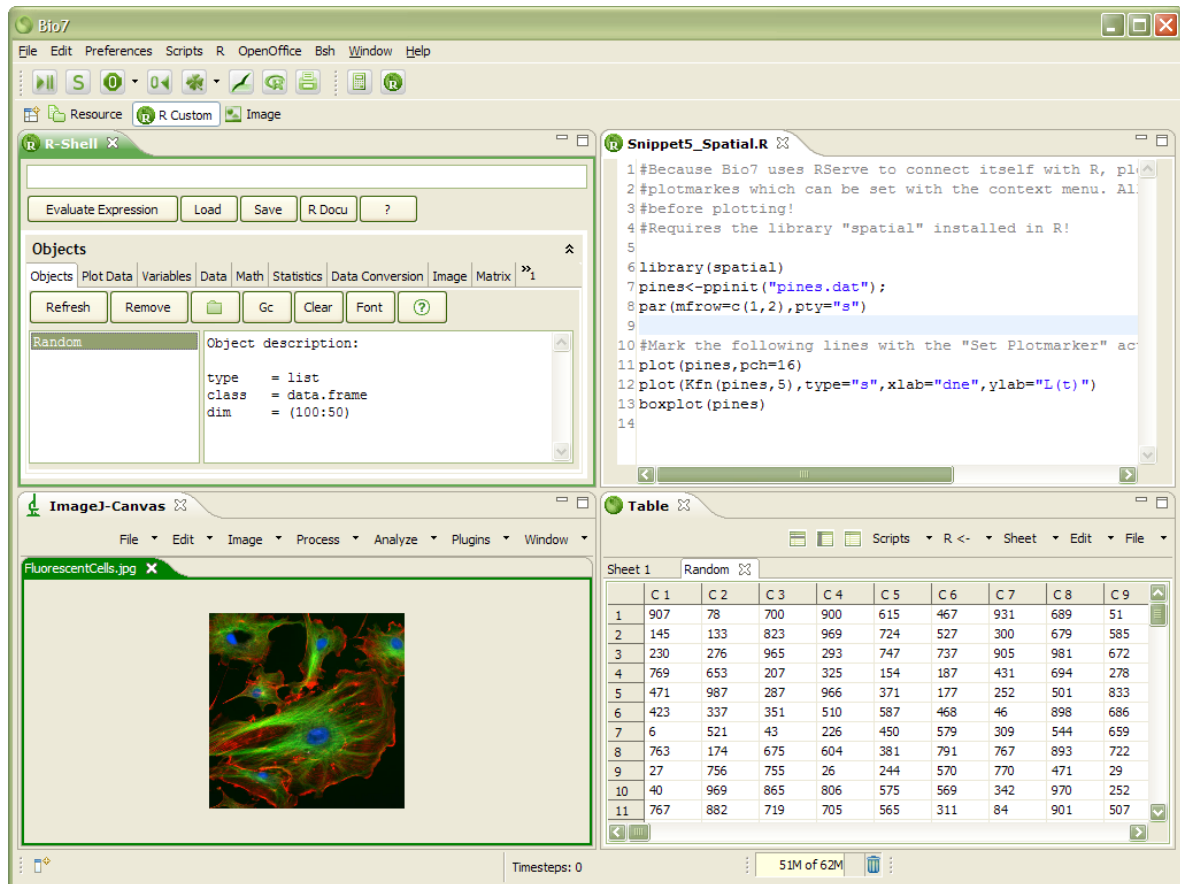


Figure 7: The default R perspective customized with the ImageJ-Canvas view and the editor area of Bio7. All Bio7 views and the editor area can be added to existing perspectives of Bio7 (Window menu). Active custom perspectives can be stored and restored from the Perspective Bar (or Window menu) in Bio7.

standard 2D drawing framework based on SWT (Moore 2004). With the ability of the Bio7 Flowchart editor to handle nested loops and decisions, a dragged model file (e.g., Java, R script) can be executed and the results systematically be analyzed e.g., with the numerous statistical methods of R. The difference to existing general or specialized workflow environment solutions (with bindings to R) like Knime or Kepler (Ludäscher *et al.* 2006; Berthold *et al.* 2006) is the primary purpose of this editor to simplify a sensitivity analysis of ecological models in which the output of different parameterized model runs can be analyzed.

3.1. Using R for image analysis

Bio7 also integrates the popular scientific image analysis tool ImageJ (Rasband 2012; Abramoff *et al.* 2004; Burger and Burge 2008) for the primary purpose to assess geometrical features in digital images (see Figure 9). Several packages are available in R to load and save images and perform image analysis e.g., EBImage (Pau *et al.* 2010). However R still lacks many advanced image analysis capabilities which ImageJ offers by default with a specialized graphical user interface for image editing. Bio7 is also one of the first applications containing special meth-

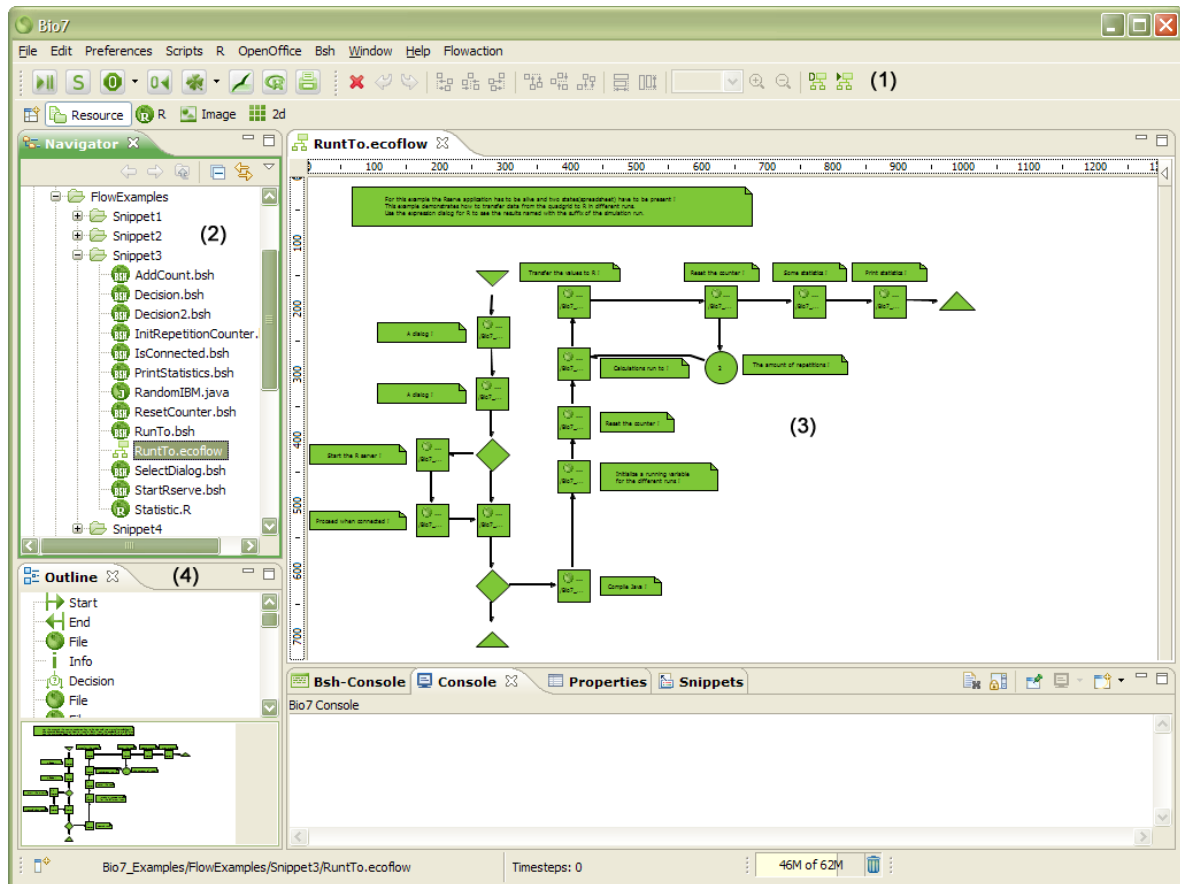


Figure 8: The Flowchart editor of **Bio7** with several R source files to analyze simulation data. With the main Flow actions (1) a flow can be verified and executed. Files of different filetypes can be dragged from the Navigator view (2) to the Flowchart editor (3) and then executed or evaluated in an ordered sequence. In the context menu of the Flowchart editor several actions are available e.g., to visualize the current progress of the flow (Debug Mode). In the Outline view (4) an overview of the current flow is given and can be used to navigate to parts of the flow.

ods to effectively transfer image data (as matrices or vectors) from **ImageJ** directly into R (without producing intermediate files). Vice versa vector or matrix data created in R can be transferred back efficiently to **ImageJ** for the creation and analysis of images (e.g., float, RGB, and grayscale images). In addition coordinates from single and multiple selections in images as well as specific geometrical particle measurements results of **ImageJ** can be transferred to R directly to perform advanced morphometrics on selected image shapes or to perform advanced multivariate analysis of image data in R. One typical application of this **ImageJ** to R feature is the possibility to perform a unsupervised or supervised classification of transferred image data in R and to display the results in **ImageJ** (e.g., to analyze plant structures or the composition of plant species in a digital image, see Figure 9). The combination of both applications greatly reduces the time for a profound statistical analysis of image data and avoids many mistakes and misconceptions in this process.

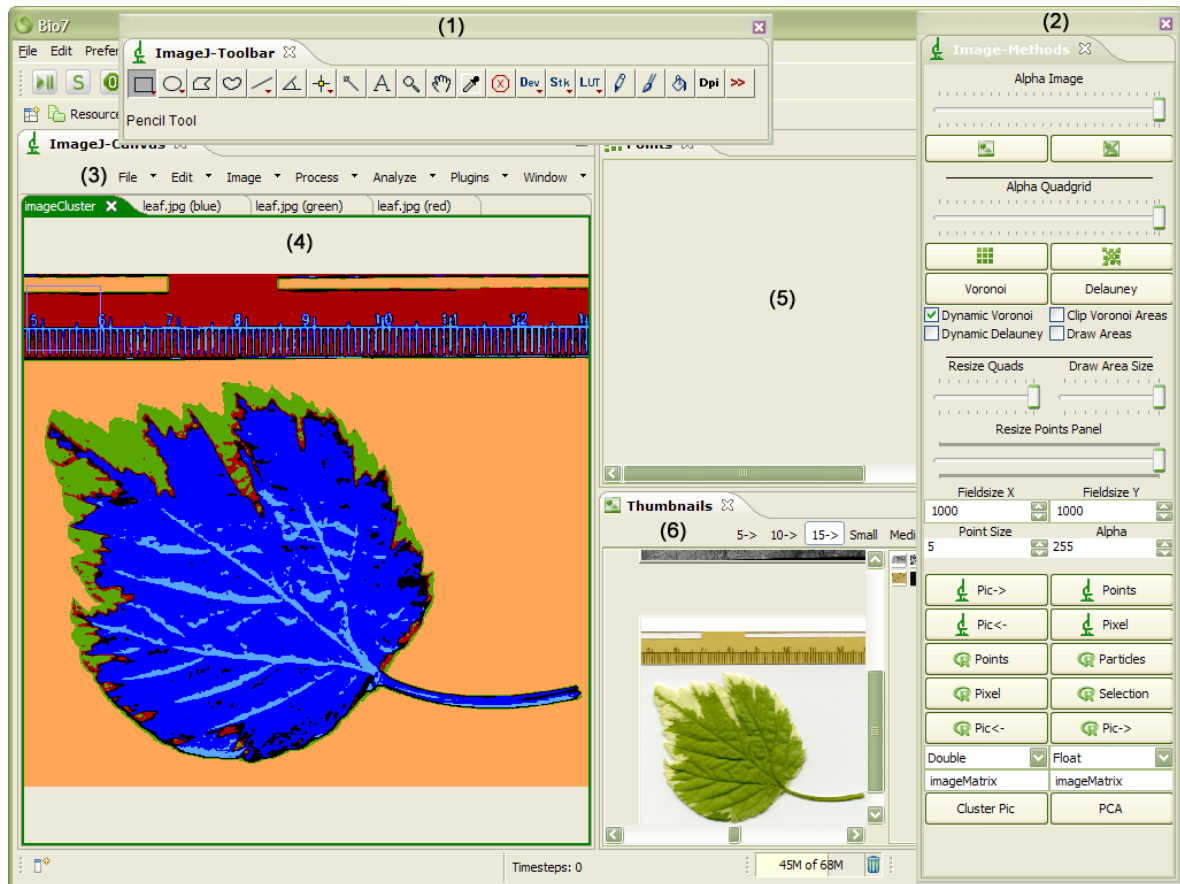


Figure 9: The Image perspective of **Bio7** with the opened **ImageJ-Toolbar** (1) and the **Image-Methods** view (2) which both can be opened with the **Window** menu of the **ImageJ-Canvas** view (3). The detached **Image-Methods** view contains several actions to transfer the current image data in R supported data types to the R workspace. Data in the R workspace can easily transferred back to **ImageJ** as different types of images. The left displayed image in the **ImageJ-Canvas** view (4) shows the R clustering result of R, G, B image data from an example image available from the internet. With the cluster result several parts of the image can be morphologically or statistically analyzed in R or in **ImageJ**. In addition the perspective contains a panel (**Points** view) for spatial 2D simulations (5) and a thumbnail browser (6) to preview and open **ImageJ** supported image types of a directory.

Example using R for image analysis

Switch to the Image perspective and open the available **ImageJ** leaf example from the internet with the **ImageJ-Canvas** menu (**File**->**Open Samples**->**leaf.jpg**). Start the **Rserve** application for a connection to R. Open the **ImageJ-Toolbar** view and the **Image-Methods** view from the **ImageJ-Canvas** menu (**Window**->**ImageJ-Toolbar** and **Window**->**Bio7-Toolbar**). Split the image in it's R, G, B components (**Image**->**Colour**->**Split Channels**) and then select the **Cluster Pic** action in the **Image-Methods** view. Optionally you can select a different memory efficient transfer type (byte for this example would be sufficient) in the **Image-Methods** view. In the cluster dialog select the afore created R, G , B images (transfer the selected images to

the right component of the split panel with the available action) and a sufficient number of clusters for the image (e.g., 6 centers). Press **OK** to confirm the cluster operation. The images are transferred to R and clustered with the **clara** method of the **cluster** package of R (for details about this method consult the package documentation). After the clustering process in R the resulted image matrix is automatically transferred back to the **ImageJ-Canvas** view and can be coloured with the LUT (look up tables) actions in the **ImageJ-Toolbar**. The different cluster areas can be measured with **ImageJ**. Another way to measure the area of the clustered pixel data is to use R. The clustered image data can be transferred to R with the **Pic<-** action in the **Image-Methods** view. To transfer only parts of the image (selections e.g., to exclude regions) we can use the **Pixel** action in the **Image-Methods** view. Before the transfer select a part of the image with one of the different available selection methods in the **ImageJ-Toolbar** view. Press the **Pixel** action to open the transfer dialog. Select **No** to transfer only the selected pixels of the active image. The image (cluster) data can now be summarized and the pixel area can be measured (count of cluster data) in the R shell of **Bio7**.

3.2. Java and R

The use of Java in combination with R by means of an interface like **Rserve** offers numerous other useful implementations e.g., to visualize data from R in the different **Bio7** panels. Because of the speed of this connection it is for example possible to reuse existing advanced specialized libraries of Java to draw R data not only statically but also dynamically on different available **Bio7** panels. For instance the embedded Java Compiler of **Bio7** can dynamically compile Java OpenGL commands (see Figure 12) to draw R data in 3D (see Figure 11) or to draw georeferenced data on a Java virtual 3D globe (see Figure 10).

The **Rserve** API is accessible by the dynamic Java compiler and the scripting languages of **Bio7**.

Example: Interaction of Java and R

The following simplified code (Figure 12) demonstrates an access to R methods and data with Java to produce the dynamic visualization of 3D data of Figure 11.

To use this code a new project has to be created in the **Bio7** workspace. Switch to the **Resource Perspective** (see Figure 4) in the **Perspective Bar** and then select **File->New** in the main menubar of **Bio7**.

In the opened File Wizard dialog select **General->Project** to create a new project in the **Bio7** workspace. Choose an appropriate name for the project and then press the **Finish** action to create the project. In this project you can now create a Java OpenGL file (a Java template with necessary methods to get the OpenGL drawing context).

Select **File->New** and select in the File Wizard **Bio7->Java OpenGL File** to create a new Java file with default defined OpenGL methods. The Listing can be copied over the afore created file. Optionally download the formatted file from <https://github.com/Bio7/Bio7> (the file can be downloaded and copied to the afore created project of **Bio7** without the necessity to create a new Java OpenGL file).

To execute the file start the **Rserve** application in the toolbar of **Bio7** (see Figure 1) and open the 3d perspective with the **Open Perspective** action in the **Perspective Bar** (or with the **Window->Open Perspective->Other...** action in the main menu of **Bio7**).

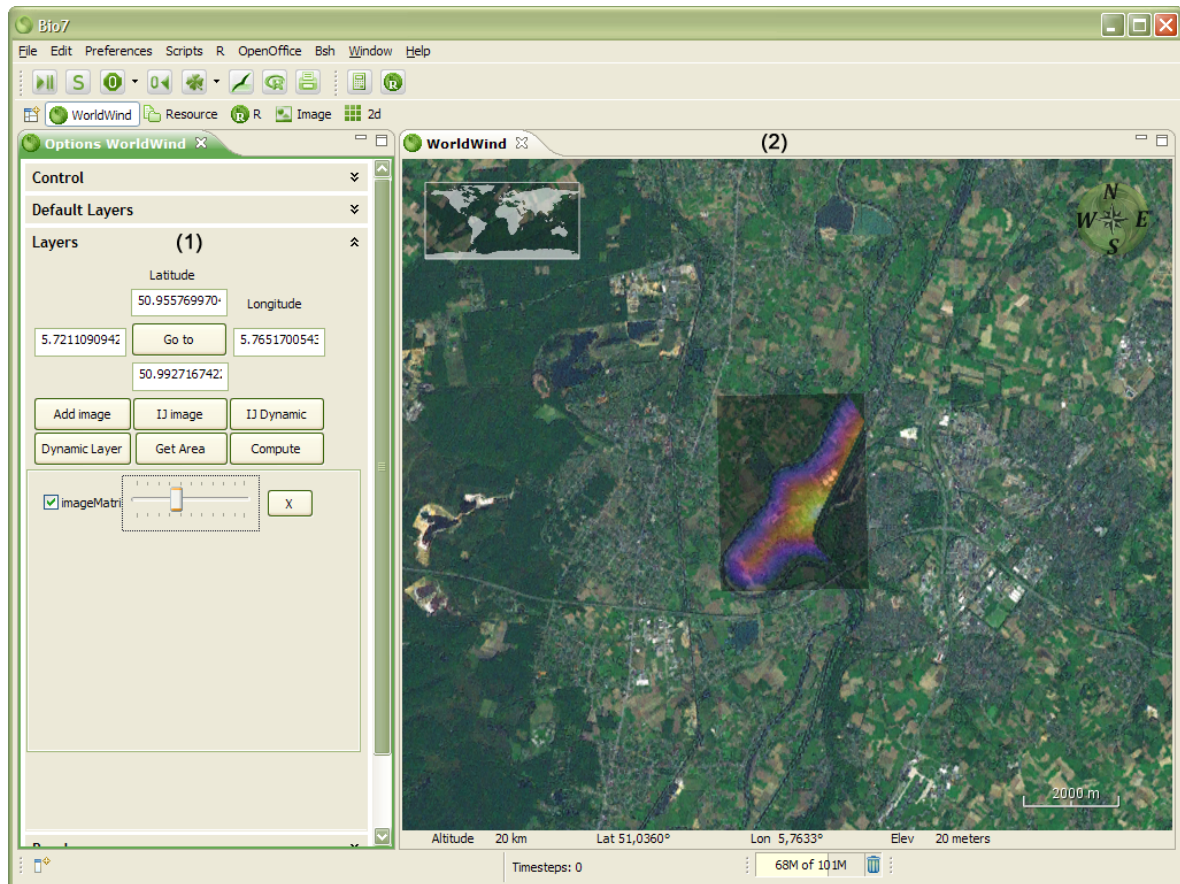


Figure 10: The WorldWind perspective with the Options WorldWind view (1) and the WorldWind view (2). The Options WorldWind view contains several expandable panels with custom actions to control the behaviour of the WorldWind 3D globe. In the WorldWind view georeferenced data (Meuse data) from R is displayed and plotted with accurate coordinates on the embedded virtual 3D globe. The meuse data set used here as an example is a data set comprising of four heavy metals measured in the top soil in a food plain along the river Meuse (Netherlands; Lat: 50.9703 Lon: 5.7415 – WGS 84). Example adapted from [Pebesma \(2004\)](#).

Extend the Time item in the Options Space view (left view) and press the Start button for the visualization (see Figure 11).

In a very similar way scripts can be created with the available scripting languages to evaluate R expressions or send data from Java to R (or vice versa).

4. Outlook

The graphical user interface for R in an ecological modeling platform represents an ongoing effort to simplify the use of the powerful statistical package R. Initially developed for ecological model verification and analysis, it evolved over the past years to a full featured R GUI useful for a broad scientific context. The R interface of **Bio7** is not only well suited for experienced

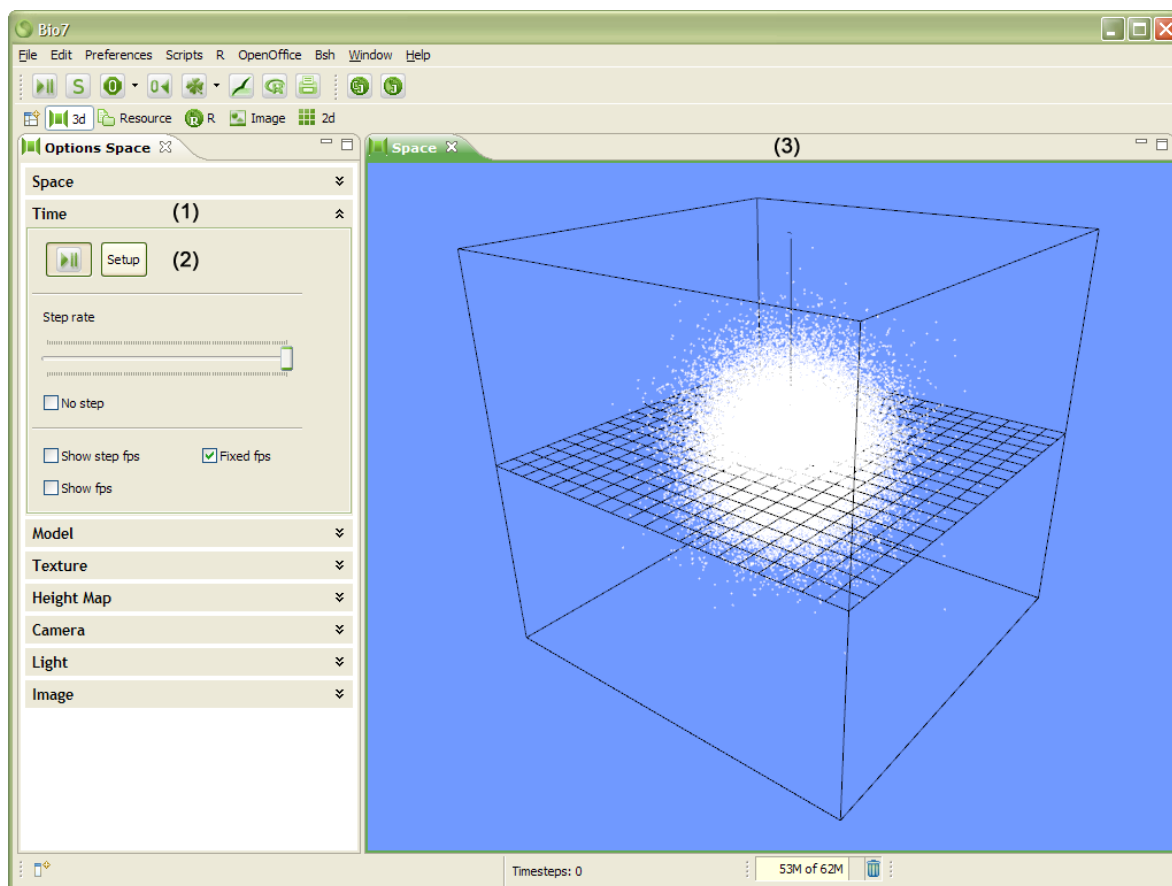


Figure 11: The 3d perspective with the Options Space view (1), the extended Time panel (2) of the view and the Space view (3). The screenshot shows R data dynamically visualized with Java and OpenGL in the Space view (3). Several actions are available in the Options Space view. In the Time panel (2) the custom OpenGL context (the OpenGL commands in the `ecomain` method – see Figure 12) can be enabled with the Start/Pause action.

R users who want to use the advanced concepts of the Java – R interaction but also for unexperienced users who can profit from the advanced R usability.

The basis for the graphical user interface is the highly modular and extensible Eclipse rich client platform which offers plugins and tools for the creation of advanced interfaces. In addition applications built upon this platform profit from the ongoing improvements of new plugins and interfaces which often reflect the latest development of software design.

For the communication between R and Bio7 (Java) the Rserve application is used. Beside of some above mentioned disadvantages a great advantage of this Server–Client connection is the possibility to transfer calculations and data to a more powerful or specialized remote computer optional running a different Operating System. A future perspective of Bio7 in connection with Rserve could be the GUI support of several connections and remote machines to distribute calculation intensive tasks.

With the interface of Rserve many powerful Java applications can be combined with R thus supporting an easier access to specialized libraries in areas where R lacks until now the func-

```

import static com.eco.bio7.spatial.SpatialUtil.*;

/*Java container (arrays) for the data created with R!*/
int[] x;
int[] y;
int[] z;

/*The main method with the OpenGL context can be triggered
in different time intervals!*/
public void ecomain(GL gl, GLU glu, GLUT glut) {
/*After a specified time intervall the data is created!*/
if (canStep()) {
/*Method to dynamically create the data in R!*/
    createRData();
}
/*Rendering of the data with OpenGL!*/
if (x != null && y != null && z != null) {
    for (int i = 0; i < z.length; i++) {
        /*OpenGL commands to render the data as primitive points!*/
        gl.glPushMatrix();
        gl.glPointSize(1);
        gl.glDisable(GL.GL_LIGHTING);
        gl.glColor4f(1.0f, 1.0f, 1.0f, 1.0f);
        gl.glBegin(GL.GL_POINTS);
        gl.glVertex3i(x[i], y[i], z[i]);
        gl.glEnd();
        gl.glEnable(GL.GL_LIGHTING);
        gl.glPopMatrix();
    }
}
}
public void createRData(){
RConnection c=RServe.getConnection();
if (c!=null) {
    try {
        /*Creation of random data in R and the transfer to the Java arrays!*/
        x = c.eval("rnorm(100000)*100").asIntegers();
        y = c.eval("rnorm(100000)*100").asIntegers();
        z = c.eval("rnorm(100000)*100").asIntegers();
    }
    catch (RserveException rse) {
        /*error!*/
    }
    catch (REXPMismatchException mme) {
        /*error!*/
    }
}
}
}

```

Figure 12: Java source to produce the dynamic visualization of 3D data of Figure 11.

tionality of such specialized tools. In combination with the flexible layout of an RCP application and the many plugins available for Eclipse which can be reused for RCP applications new and manifold useful functionality can easily be integrated into **Bio7**. In future releases of **Bio7** the R interface will be extended with more useful functionality and options.

The **Bio7** development will definitely benefit from the ongoing improvement of new Eclipse RCP concepts for the upcoming Eclipse Release 4.x which will simplify the development and extend the functionality of RCP applications and plugins. The primary goal of all these efforts is a more reliable and easy to use Ecological Modeling platform in which R plays a fundamental role to detect patterns within the complexity of ecological systems.

Bio7 is an open-source application available for Windows, Linux and OS X which can be downloaded freely together with all documentation materials from the **Bio7** project website (<http://bio7.org/>) or the associated SourceForge project website (<http://SourceForge.net/projects/bio7/>).

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Affiliation:

Marcel Austenfeld
University of Kiel
Leibnizstr. 3
24118 Kiel, Germany
E-mail: maustenfeld@uv.uni-kiel.de
URL: <http://bio7.org/>

Wolfram Beyschlag
Department of Experimental and System Ecology
University of Bielefeld
Universitätsstraße 25
33615 Bielefeld, Germany
E-mail: w.beyschlag@uni-bielefeld.de
URL: <http://www.uni-bielefeld.de/biologie/Oekosystembiologie/>