The BioUML platform

QUICK START

GUIDE

BioUML (Biological Universal Modeling Language) is a Java-based platform for collaborative reproducible analysis of omic data and visualisation of biological and medical data. It provides a big set of different methods for analysis, both, self-developed and implemented using literature data. Integration with R/Bioconductor and Galaxy allowed to provide user with significantly extended set of methods.

This quick start guide will introduce you to the basic procedures and basics of working in BioUML (https://ict.biouml.org/bioumlweb/).
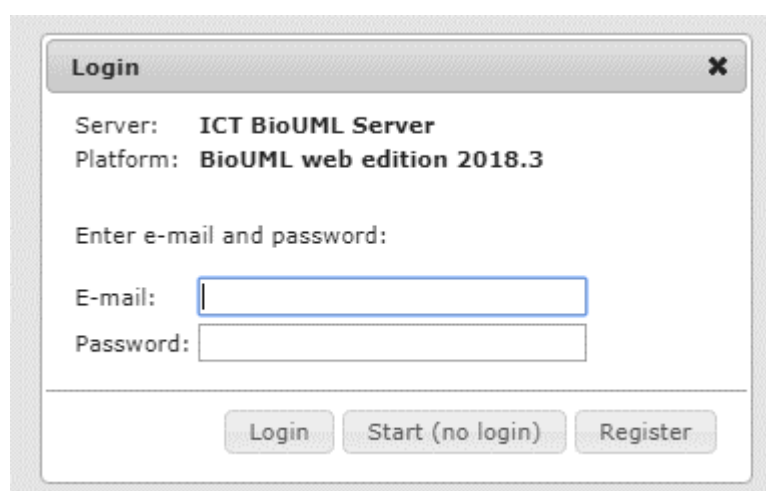
Main topics highlighted in this guide:

- ✓ How do i start working with BioUML?
- ✓ How is the BioUML platform organized?
- ✓ How to work with the BioUML platform?
- ✓ How do I upload my data?
- ✓ How to open/delete a file?
- ✓ Which types of analyses are available?
- ✓ What is a workflow?
- ✓ How to start a workflow?
- ✓ Are there examples on the platform?
- ✓ How to organize project and user data?
- ✓ How to get information about the user account?

How do i start working with BioUML?

Access to BioUML is provided for registered users, but demo access without registration is also available.

Using the link https://ict.biouml.org/bioumlweb/ you will be asked for e-mail (login) and password. If you have no login and password, then you can use 'Start (no login)' entry or click 'Register' for further registration procedure at a BioStore web page.
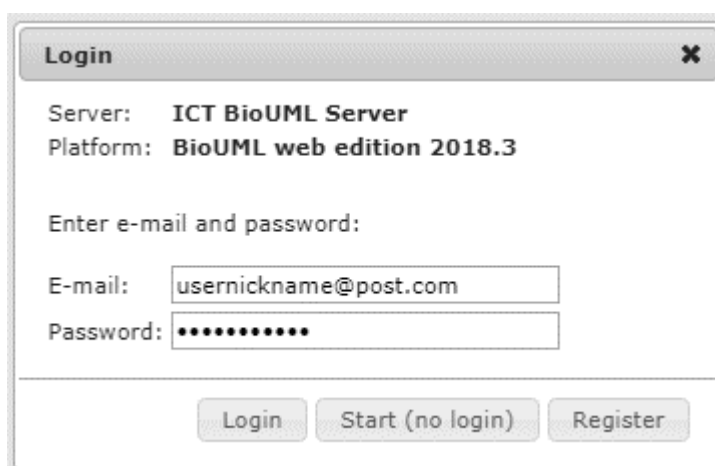

After registration, you will receive a letter from BioStore – the main server for user registration and subscription processing – with your personal password. To log in you will need your email address and the password. Please, log in here to the platform:
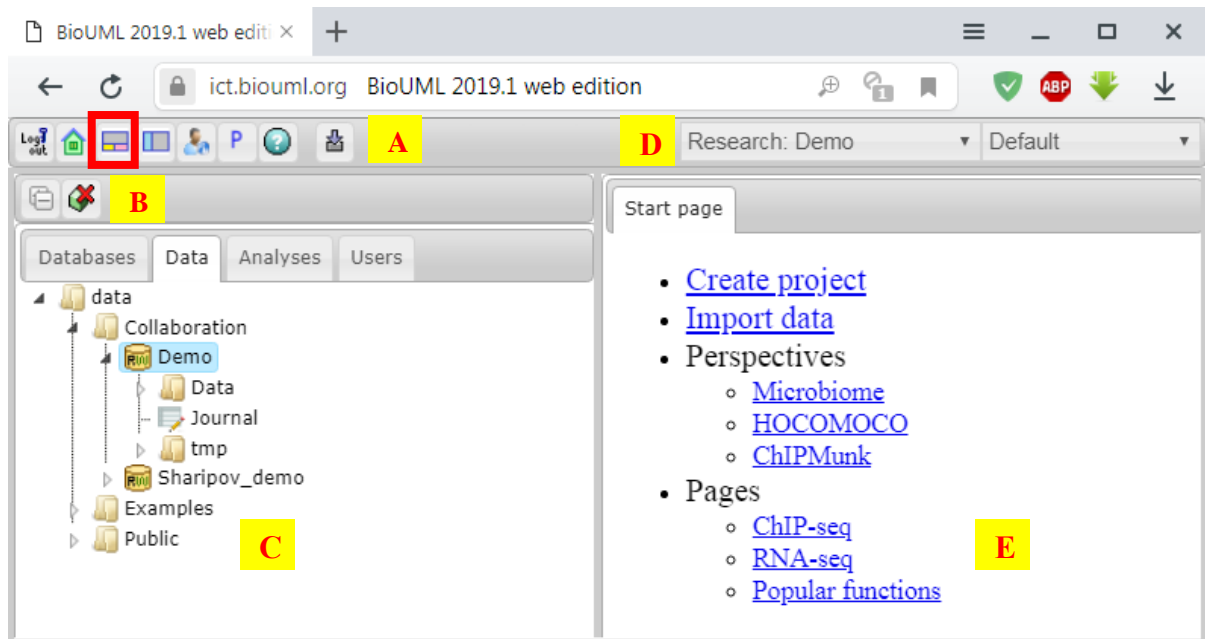
https://ict.biouml.org/bioumlweb/

How is the BioUML platform organized?

When you first log into the BioUML platform, a window opens containing the following areas A-E:


Panel A – a common control panel (toolbar) shows a context-sensitive set of icons for the available operations. "Toggle UI mode" button (red box) will open two bottom panels (see page 4): green – for search and short information about the selected folder or the file, orange – operation field for extended description (if available), graph search, application of scripts (Javascript, R or Math), clipboard, and monitoring of task processing.

Panel A also contains the following buttons: Log out, Start page, Toggle repository (side panel), Account info, Project properties, Help and Import.

Panel B – this is a dynamic panel containing buttons useful for the opened folder. For the project folder, the buttons "Expand/collapse" related to manipulations with folder tree and "Remove project" are available (see below).
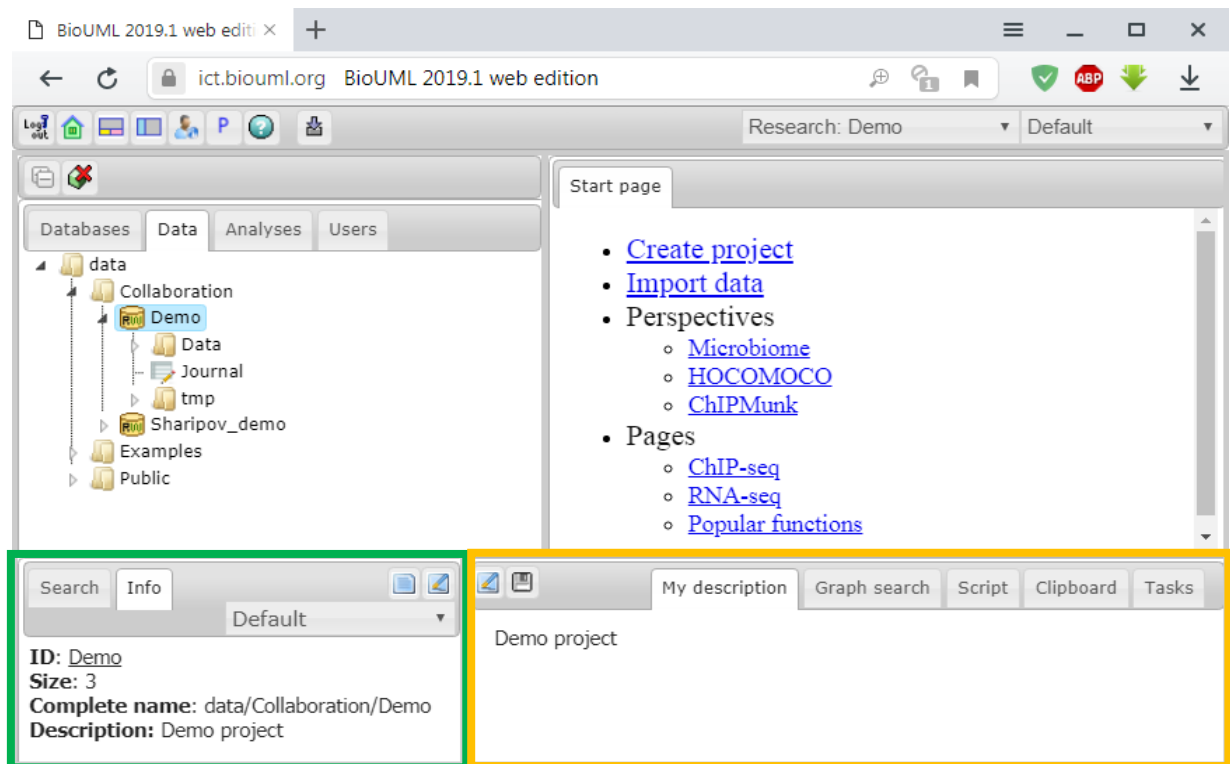
For the folder with experimental data, extended set of tools is available: "Expand/collapse", "New JS script", "New R script", "New workflow", "New folder", "New optimization", "Import", "Export", and "Copy folder" (see below).

Panel C – this field contains four chapters: "Databases" (the list of databases available for user, "Data" (tree of folders available for user – repository), "Analyses" (set of useful methods and implemented algorithms), and "Users" (info about users present at the server now). Every chapter contains a structure of tree-type.

Panel D – this field combine two drop-down menus: "Research" and "Perspective". First of them allows to select available research projects (new one can be created via "Create project" on the Start page or in "Account info"). The second one defines sets of tools and options useful for analysis of different types of data.

Panel E – user's working space. With perspective selected by default, user obtains suggestions to create project, import data, select other available perspectives and visit special pages within the BioUML platform with selected sets of methods and algorithms, e.g. for ChIP-seq and RNA-seq analysis.

How to work with the BioUML platform?

Before to start working with BioUML, the user has to create his or her own project by using "Create project" on the Start page or respective button in "Account info".

When you are first time in BioUML, you will see active Data chapter containing the collapsed folders "Collaboration", "Examples", and "Public". Every folder can be opened by double left click of mouse or by pressing small grey triangle on the left.
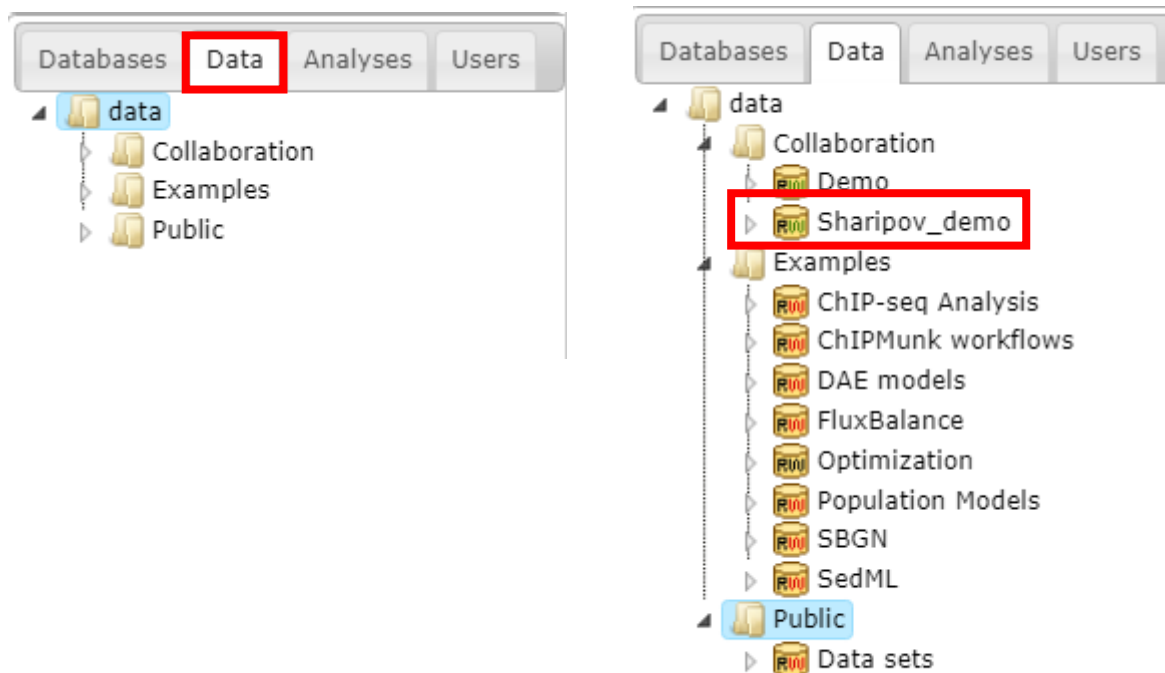

The user's project folders are placed in the "Collaboration" folder (e.g., Sharipov_demo with red box). Every project folder has autogenerated structure: two folders "Data" and "tmp", as well as the "Journal" file containing records of data processing.

How to organize project and user data?

Within the user project's folder (e.g., Sharipov_demo, see below), the Data folder generated automatically is available for storage of analysis results, scripts, etc. To create additional folders, right mouse click will open a menu where you can select "New folder" (see below).
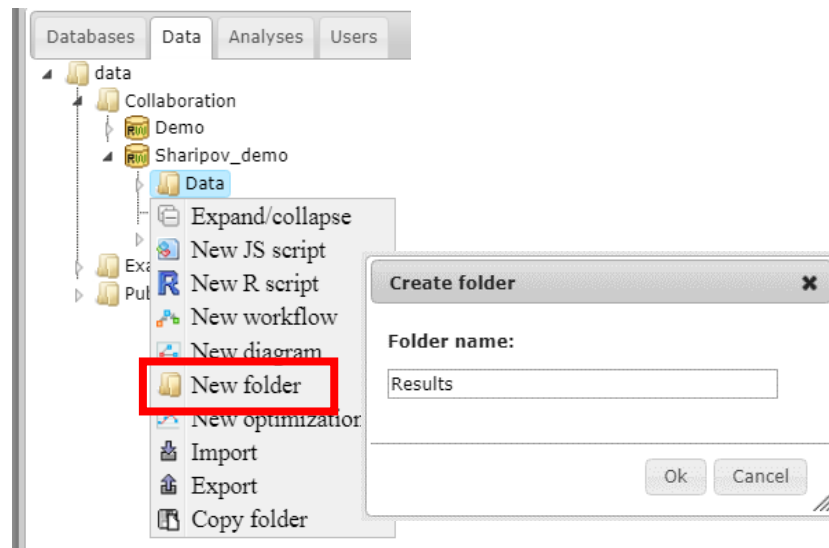
As a result of the research, the user's Data folder will acquire an expanding hierarchical structure. Each workflow or individual method/algorithm that you apply to your data will ask about the folder name for the input location and the placement of the output after the calculations.
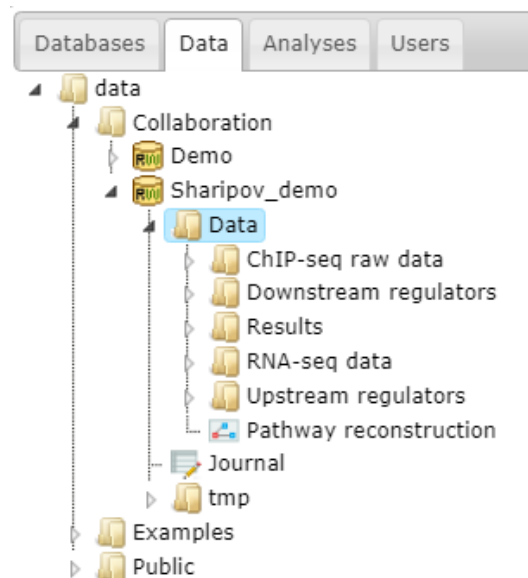
How do I upload my data?

User data can be uploaded/imported by three ways:

1. Find your Data folder (marked blue) and use right click of mouse on it; then press "Import" the window "Import file (upload)" will be opened.

There are four different upload options – sources of files (red boxes): "Computer" (select file from computer), "WebFTP" (use HTTP or FTP address to reach the file for upload), "Repository" (for import of the file that was uploaded to the repository previously) or "Raw" (type or paste file content in the text area).

After selection of the source of files, press the "Import all" button to start the uploading procedure.
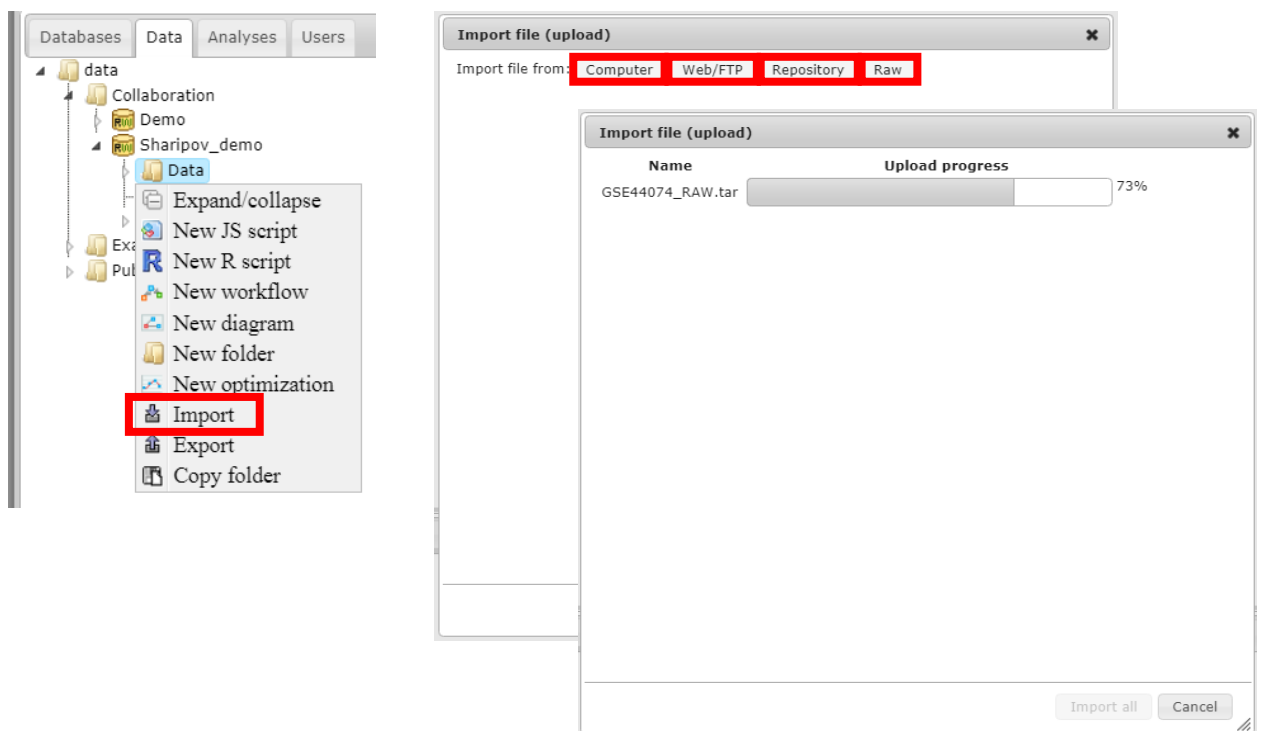
2.   Click the Import button of the common tool bar [⬆] to open the window "Import file (upload)".

3.   Use the chapter "Start page". The second entry of the list is "Import data". Click on it will open the window "Import file (upload)".

How to open/delete a file?

All BioUML tools, methods or algorithms, as well as workflows, will require input file from repository tree (chapter Data). Double click on the selected file will open it in the right panel – user' working space. Right click on the file will provide alternative way for opening: "Open diagram/track/table" option.
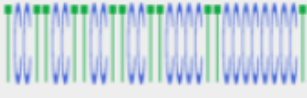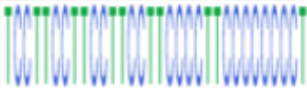
If user wish to delete files then there two ways: use ![delete button] button from the dynamic panel B (page 4) or right click menu and the option "Remove".

Table is a common type of user's data in BioUML. It contains rows and columns. After import or generation, the table content is sorted according to the values of one of its columns. The default column defined for sorting is usually the ID column. The column used as the main for sorting is indicated by a blue arrowhead (red box) (see below).

User can sort the table according to the values of any column in ascending or descending order by clicking on the up- or downwards pointing arrowhead on top of this column, respectively (grey arrowheads for Length and Matrix logo).

If the table is rather big then more than one page will exist. So user will see the counter of kind "Page 1 of 11", as well as buttons "First" (go to the 1st page), "Previous", "Next", and "Last". Number of necessary page can be entered manually via keyboard confirmed by the "Enter" button. All these options will allow navigate within the big table.

Which types of analyses are available?
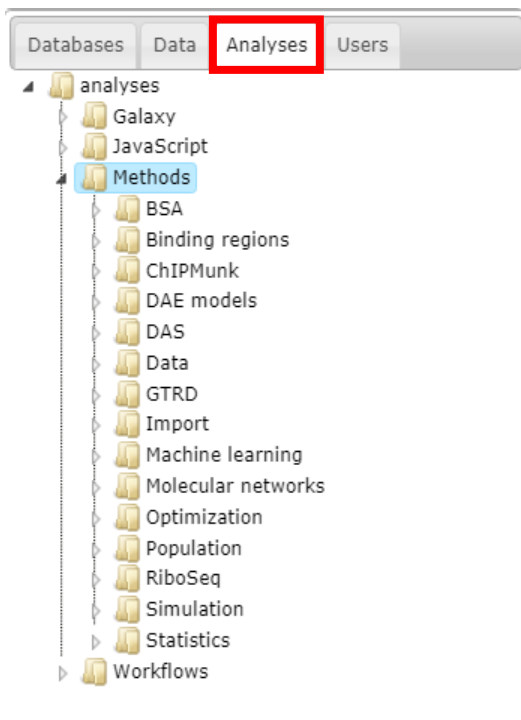
In the tree area (panel C, page 3) user can find the tab "Analyses" (red box) and the "Methods" folder (blue mark) containing links to the implemented in BioUML methods for data analysis. Besides those methods, user can also select the "Galaxy" folder with the respective methods from the Galaxy platform well-known over the world.

Double click on the selected method will open the input mask (see below), where user will be asked to select the input table(s)/file, adjust parameters of analysis and location and the name of the output table/file.
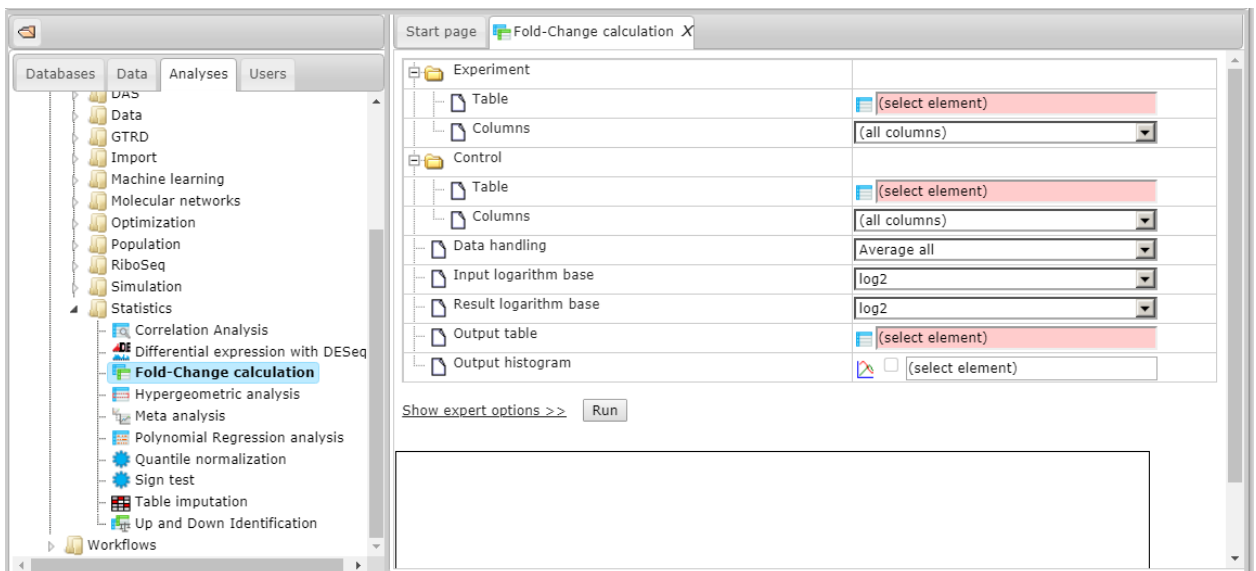
The "Run" button will launch the analysis procedure.

What is a workflow?

Workflow in BioUML is a conveyor of linked methods to perform a bioinformatic analysis in one click. The picture below presents an overview of a workflow for genome assembly using SPAdes.
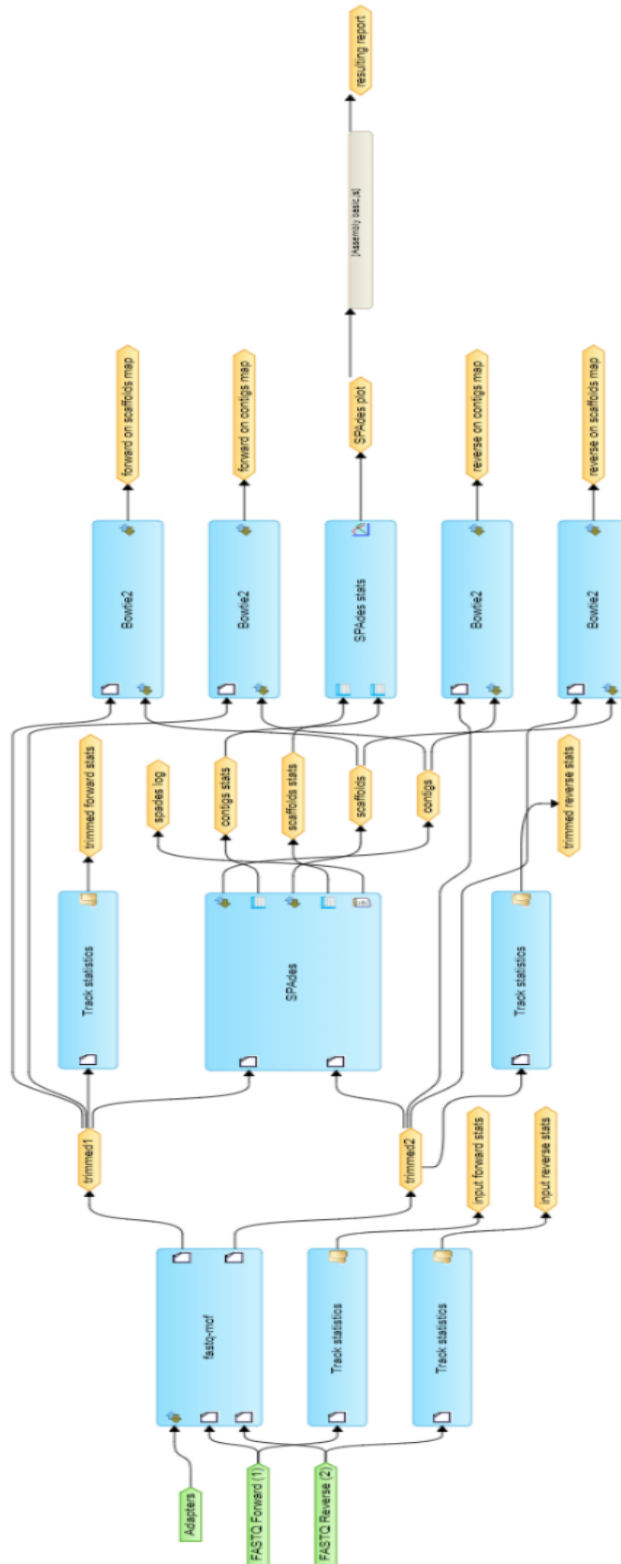
Green boxes denote input files, user-defined inputs. The light blue boxes are methods/algorithms of the conveyor (workflow "bricks"). Yellow boxes represent autogenerated files (intermediates) or output files.
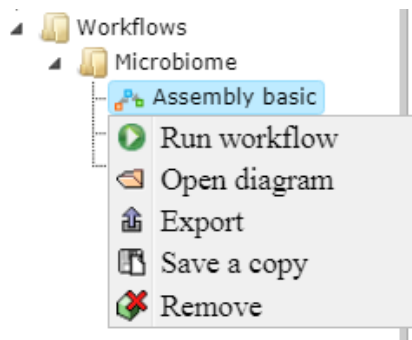
How to start a workflow?

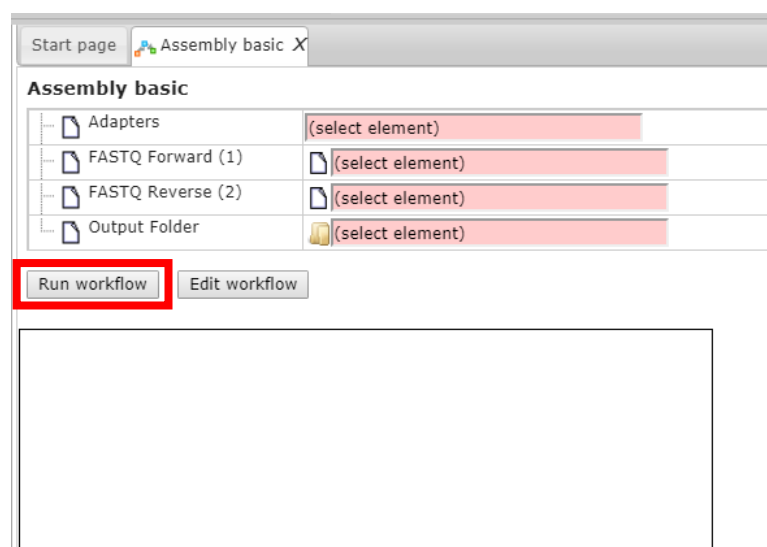After selection of the appropriate workflow it can be started by two ways:

- via the button "Run workflow" in the dynamic panel of the "Workflows" folder (see below);

- via right click menu on the workflow name (blue mark) in the list (see below):

"Run workflow" will open the form with the input and output parameters (see below). Two ways for selection of elements also possible: 1) drag-and-drop from the folder tree for input; 2) click on red fields and selection of files or folders via pop-up menu. When everything is correct, press the button "Run workflow" (red box).
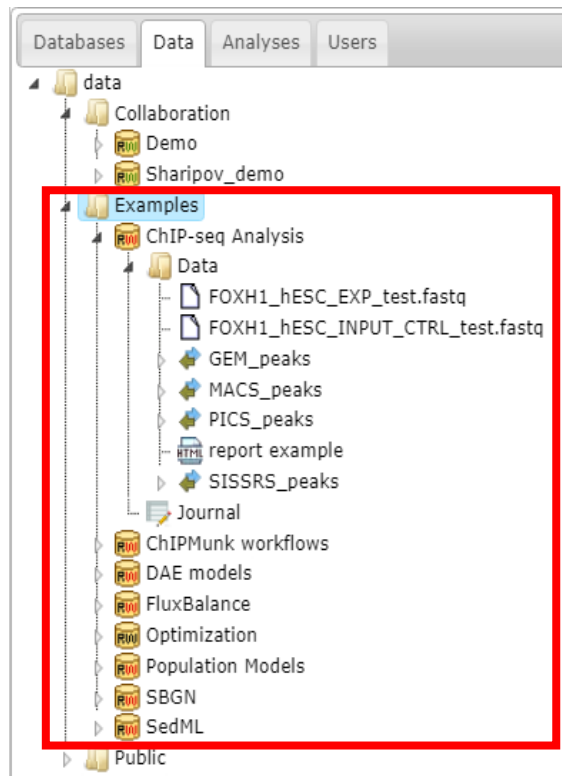
Are there examples on the platform?

In the folder tree "Data", there is a set of examples of the BioUML application for data analysis (red box). Examples include data from different ChIP-seq analysis, using ChIPMunk method, DAE and population-based models, etc.
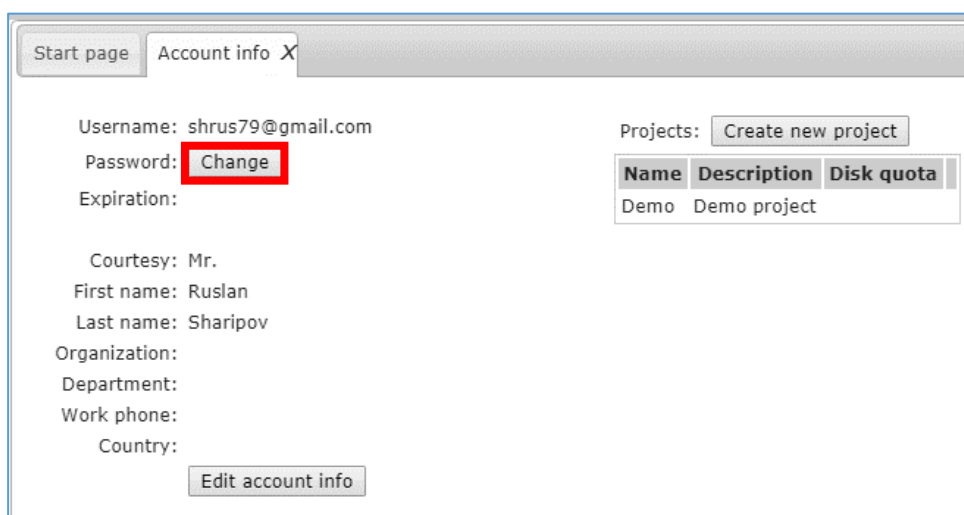
How to get information about the user account?

Your first password for the BioUML platform is generated and visualized automatically at the moment of registration, as well as sent to you by email. After logging in to the platform, you can change your password and edit your personal information.

To get information about your account, click the "Account Info" icon (red box) on the control panel in the top menu.
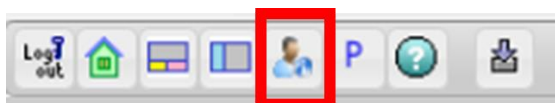
On the right panel you will see the account information.

"Change" button (red box) will help you to change your default password.

"Create new project" button allows to create your own research project that can be chosen further in drop-down menu "Research".

Let's work together

1. [Log in](Log in) to the platform

2. Select and import your own datasets

3. Process your data by using sophisticated set of tools (either workflows or single methods/algorithms)

4. Save your results

5. Collaborate with your colleagues worldwide

For any further questions/suggestions/problems, please, do not hesitate to contact:

contact_info@biosoft.ru

support@biouml.org (customer support)

Useful links:

http://landing.biouml.org

http://wiki.biouml.org/