



User Manual

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Romeo User Manual

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1 Introduction

1.1 How to read this manual

This manual will guide you through the execution of the steps that will bring you to know and use the features of Romeo, at best. The document is divided in four principal sections:

- **Getting started:** which will provide you the instructions to install and uninstall the software. It also gives you an overview of the main window of Romeo;
- **Set up analysis:** which will guide you through the execution of the necessary steps, that allow you to perform an analysis;
- **Execution of an analysis:** which will provide you the instructions to manage and execute an analysis;
- **Visualization and exportation of results:** which will guide you through the management of the results obtained from the analysis.

The **Glossary** appendix contains definitions of the terms that needs an explanation, for reasons of clarity. These terms are marked in the manual with a subscript “G” in bold.

1.2 Overview

Romeo is an open source tool that can provide the application of cluster analysis to biomedical data. Furthermore, it is possible to extract some features_G of interest from the images and combine them before performing clustering.

This technique is used to automate and facilitate the delineation of anatomical structures and other regions of interest, in medical images. The procedure, can accelerate the processing speed and accuracy of the diagnosis, allowing to locate pathological tissues and measure tissue volumes. It has thus great potential for prevention, prognosis, and treatment.

Below, a schematic representation of the pipeline of analysis of a cluster analysis applied to biomedical image (fig. 1).

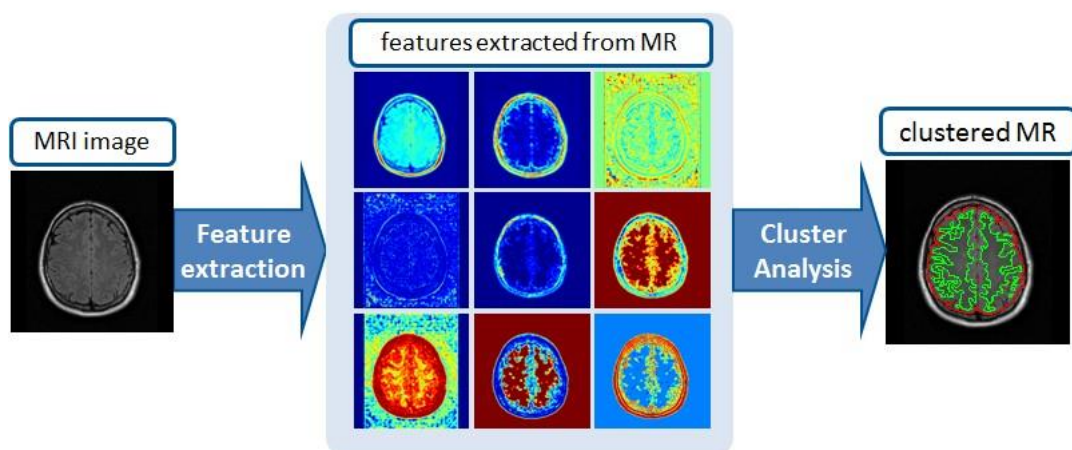


Figure 1: *Feature extraction and Cluster Analysis of a MR image*

1.3 Why Romeo?

- **Intuitive User Interface**
Romeo has an intuitive Graphic User Interface that allows it to be used by expert and not expert ICT users;
- **Various cluster algorithms**
Romeo is the only stand-alone software that integrates three types of Cluster Algorithms by default. In fact, it implements: **K-means**, **Fuzzy C means** and **Hierarchical** algorithms;
- **Supports major data formats**
This tool can work with 2D, 3D, 2D-t and 3D-t images and supports these file formats: .PNG, .JPG, .BPM, .AVI, NIfTI and Analyze 7.5 ;
- **Various feature extractors**
Romeo implements fifteen different Feature Extractors;
- **Independence from file-system**
Once Romeo has imported data, the user has the freedom to change the location of the imported images in its file-system. In fact, the software saves the images inside itself. Once the user wants to export some image results, Romeo asks the path where the files have to be saved.

1.4 Romeo Features

- **Apply mask**
Enables users to import a mask and associate it to another image. That mask, works like a filter of interest on the imported image; in other words, it delimits the region which will be analyzed;
- **Create groups of Subjects**
Enables users to create customized sets of Subjects_G (an image plus its mask), allowing to perform the algorithms on different images simultaneously;
- **Create Protocols**
Enable users to create customized Protocols_G (a set of Feature Extractors plus one or none cluster algorithm_G). Each algorithm can be customized with its own parameters (like window size, GLCM etc...);
- **Create Dataset**
Enables users to create a customized analysis, formed by a group of Subjects_G and one or more Protocols_G. The Dataset_G also memorize the results of the analysis and permits the user to export them;
- **Possibility of extension with other algorithms**
Enables developers to extend the set of feature extractors and cluster algorithms with new ones, compatible with supported format files.

2 Getting started

This section gives an overview of Romeo, including the following paragraphs:

- **Installation and uninstallation**
- **Main window**
- **Environment**

2.1 Installation

This paragraph will guide you through the installation procedure of Romeo.

2.1.1 System requirements

To use the Romeo software, is necessary to have a computer running Windows 7; both 32 and 64 bit architecture are supported. Romeo also needs K-Lite codec pack, provided within the installer; if you already have this codecs, you could step their installation. There is no requirements on the amount of RAM nor on the CPU speed, but few hardware resources could compromise the efficiency of the application.

2.1.2 Installation process

To install the product in your machine, follow these instructions:

- Execute the *RomeoInno.exe* installer, by double clicking it;



Figure 2: *Program installation icon*

- Windows could ask you to confirm the installation, by showing the following dialog: *"Do you want to allow the following program from an unknown publisher to make changes to this computer?"*. Confirm and continue;
- The installation wizard starts. First of all, you must accepts the license agreement (Romeo is distributed under the **GNU General Public License v2.0**). Then select *Next* fig.3;

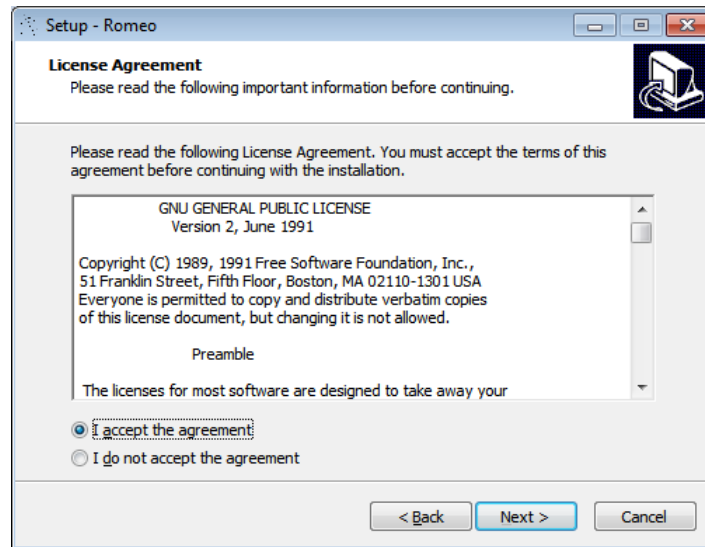


Figure 3: *License agreement*

- Choose the folder in which you want to install Romeo. You can decide to not create a Start Menu folder by checking the flag, as in fig.4. Select *Next*;

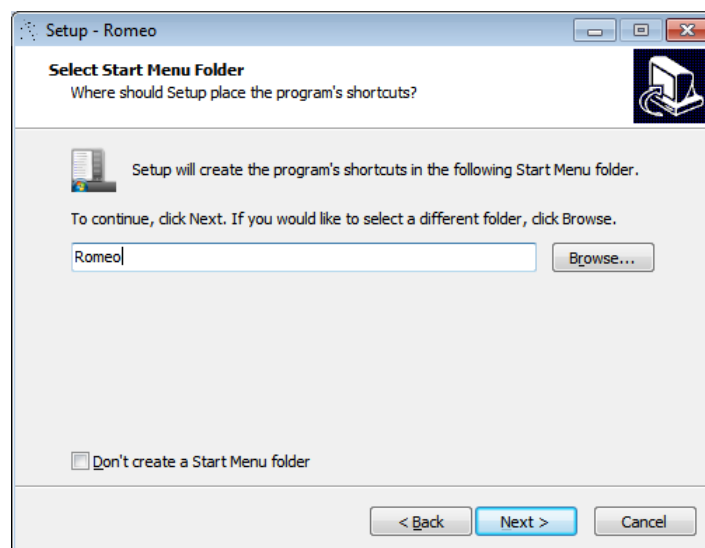


Figure 4: *Choosing the installation folder*

- Choose if you want to create a desktop icon, by clicking the relative flag, then select *Next*;
- Select the *Install* button. The installation will start (fig.5);

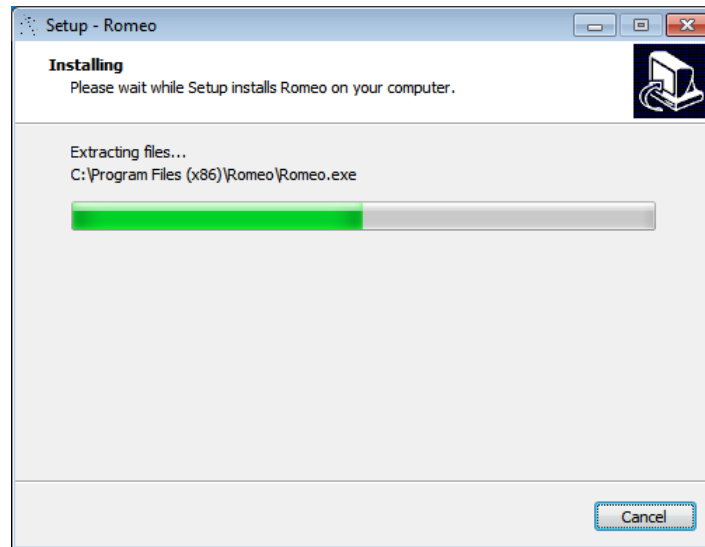


Figure 5: *Installation of Romeo*

- Once it will be completed, you must install the K-Lite codec pack, if they are not already present in the system. Uncheck the "Launch Romeo" flag and check the "Install Codec" one (fig.6). Step the following points otherwise;

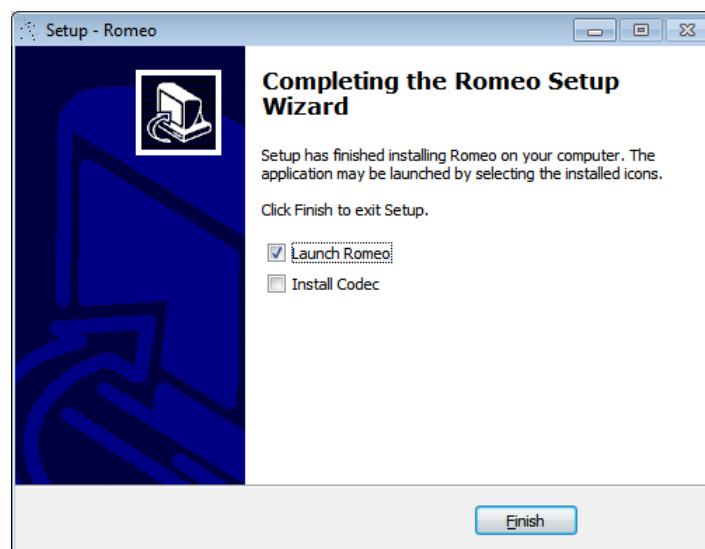


Figure 6: *End installation wizard*

- The installation wizard will appear; select the *Next* button;
- Select the *Simple mode* installation option then confirm with *Next* (fig.7);

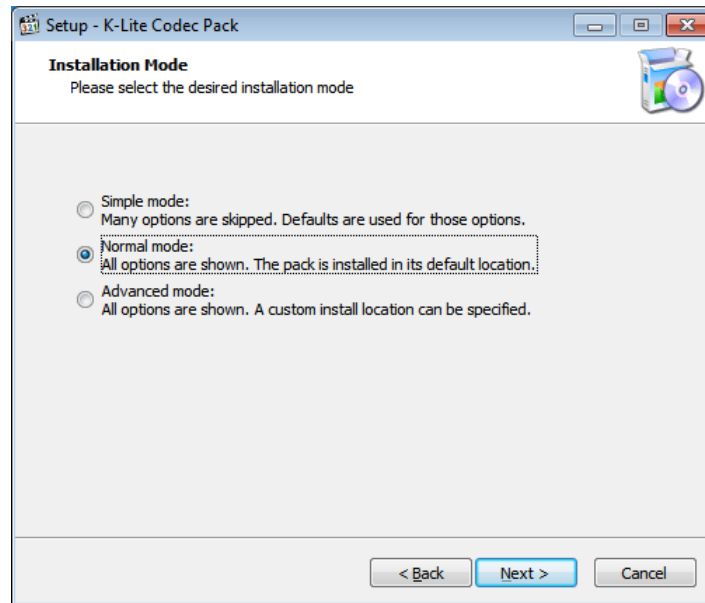


Figure 7: *Choosing the codecs installation mode*

- Continue following the wizard and then confirm the installation. Once it has finished, the *Done* window will appear (fig.8);

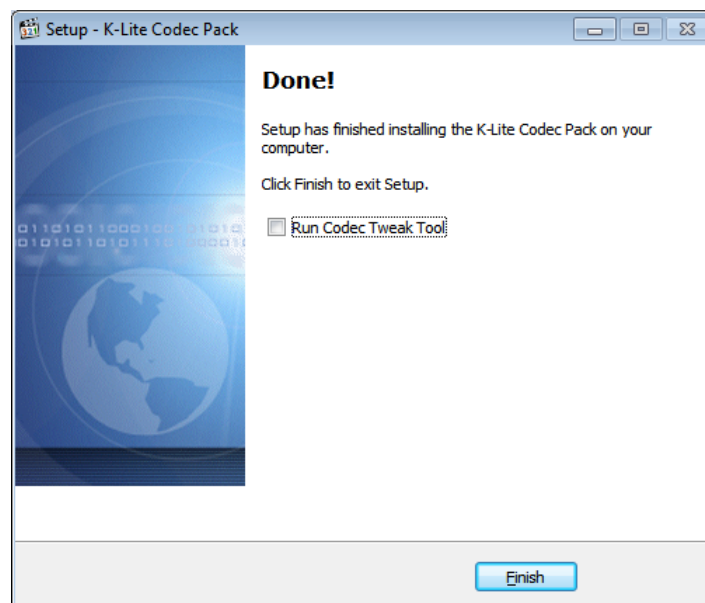






Figure 8: *End codec installation wizard*

2.2 Main window

The Romeo main window includes two major panels. As you can see in fig. 9, the left panel contains a set of buttons, which will allow you to enter the windows that create and manage the entities of the software (Subjects_G, group of Subjects_G, Protocols_G and Datasets_G). The right panel, contains the **Analysis** section which includes two buttons that will bring you respectively to the analysis execution window and the results visualization window. The **More Help** section, instead, includes the links to access the informative materials of the software:

-  Opens the User Manual of Romeo;
-  Brings to the video tutorial of Romeo;
-  Shows the keyboard shortcuts;
-  Shows informations about Romeo and its developers.

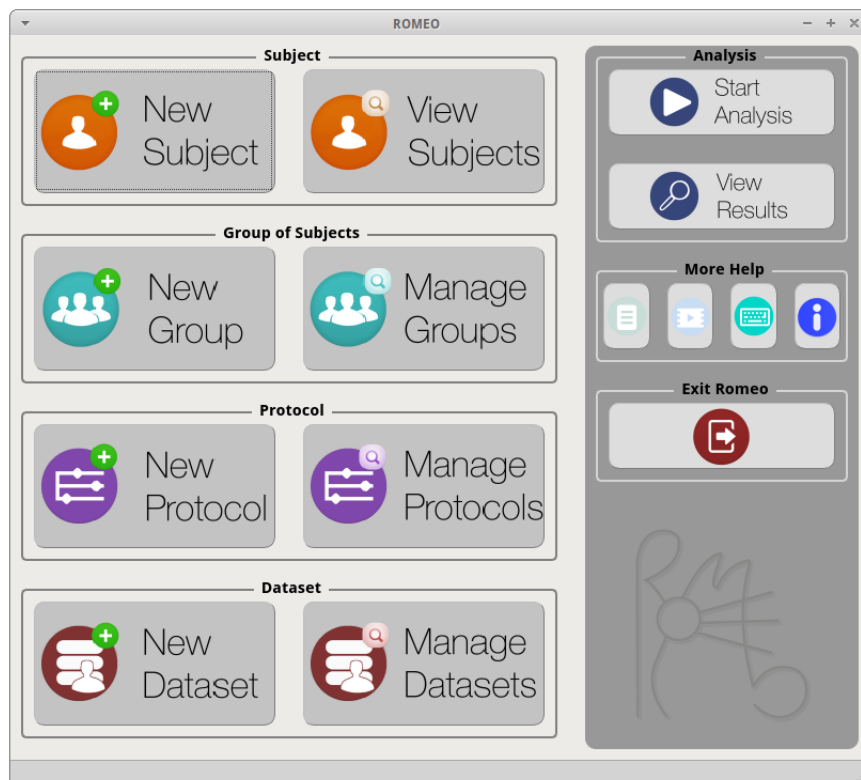


Figure 9: *Main window of Romeo*


2.3 Environment

The windows of Romeo, except the Main Window, have a Menu Toolbar on their top, which includes the direct links to all of the functionalities of Romeo. You can drag and drop this



Figure 10: *Menu Toolbar*

Toolbar on the left or right of the window. Below, the explanation of the various buttons (see fig 10):

-  Brings back to the main window;
-  Leads to the Subject_G creation window (see 3.1.1);
-  Leads to the Subject_G visualization window (see 3.1.2);
-  Leads to the group of Subjects_G creation window (see 3.2.1);
-  Leads to the groups of Subjects_G managing window (see 3.2.2);
-  Leads to the Protocol_G creation window (see 3.3.1);
-  Leads to the Protocols_G managing window (see 3.3.2);
-  Leads to the Dataset_G creation window (see 3.4.1);
-  Leads to the Datasets_G managing window (see 3.4.2);
-  Leads to the Analysis window (see refanalysiswindow);
-  Leads to the Results window (see refresultswindow).
-  Exit from Romeo;

Furthermore, this button is present in every window:



It will provide informations

3 Set up analysis

Once Romeo is properly installed on the computer, you can start to fill it with your data, in order to perform an analysis. Before this, you need to import your images and eventually their relative mask, create your group of Subjects \mathbf{G} , your Protocols \mathbf{G} and your Datasets \mathbf{G} . Please read this section to get more information about these operations.

This chapter contains the following sections:

- About Subjects
- About groups of Subjects
- About Protocols
- About Datasets

3.1 About Subjects

This section contains the procedures to create and manage the Subjects_G.

3.1.1 Create Subject

The creation of a new Subject_G is assigned to the Subjects_G creation window.

From the main window of Romeo, select the *New Subject* button or choose the right one in the toolbar (see 2.3). The Subjects_G creation window (fig. 11), is composed of one panel containing a form in which the user have to insert the information about the Subject_G. In any moment, the user can go back to the main window by selecting the *Back* button.

New Subject - ROMEO

Subject Name *

Brain

Insert the name of the subject.

Type *

2D

Select the type of image.

Add File *

/home/sevenmonkeys/Scrivania/Brain.png

Search..

Select the image to associate subject.

Add Mask (Optional)

Search..

Select mask to apply image.

Back

Save

Figure 11: *Subject creation window*

To create a new Subject_G , follow these instructions:

- From the Subjects_G creation window, type a unique name in the *Subject Name* field. That name will be the name of the Subject_G;
- Select the image type that will be imported in the Subject_G. The type could be: 2D, 3D, 2D-t, 3D-t;
- Select the image to import by selecting the *Search* button next to the *Add File* field and navigating the file system;
- Import a mask_G selecting it by clicking the *Search* button next to the *Add Mask* field and navigating the file system, if necessary;
- Confirm the operation by clicking the *Save* button. Romeo will report an error message if not all the required fields are fulfilled or the name chosen for the Subject_G is already present in Romeo.

3.1.2 Visualize Subjects

The visualization of the details of a Subject_G is assigned to the Subject_G visualization window.

From the main window of Romeo, select the *View Subjects* button or choose the right one in the toolbar (see 2.3). The Subject_G visualization window (fig. 12), is composed of two panels. The left one contains the list of Subjects_G stored in Romeo, ordered by creation data (by default, from the oldest one, to the newest). For each Subject_G it is specified:

- **Name:** the name of the Subject_G;
- **Type:** the type of the Subject_G (2D, 3D, 2D-t, 3D-t);
- **Mask:** display *yes* if a mask was associated to the image, *no* otherwise;
- **Creation date:** the date and time in which the Subject_G was created.

The right panel contains the details of the selected Subject_G. It shows a preview of the image associated to the Subject_G and the list of groups that include such Subject_G. In any moment, the user can go back to the main window by selecting the *Back* button.

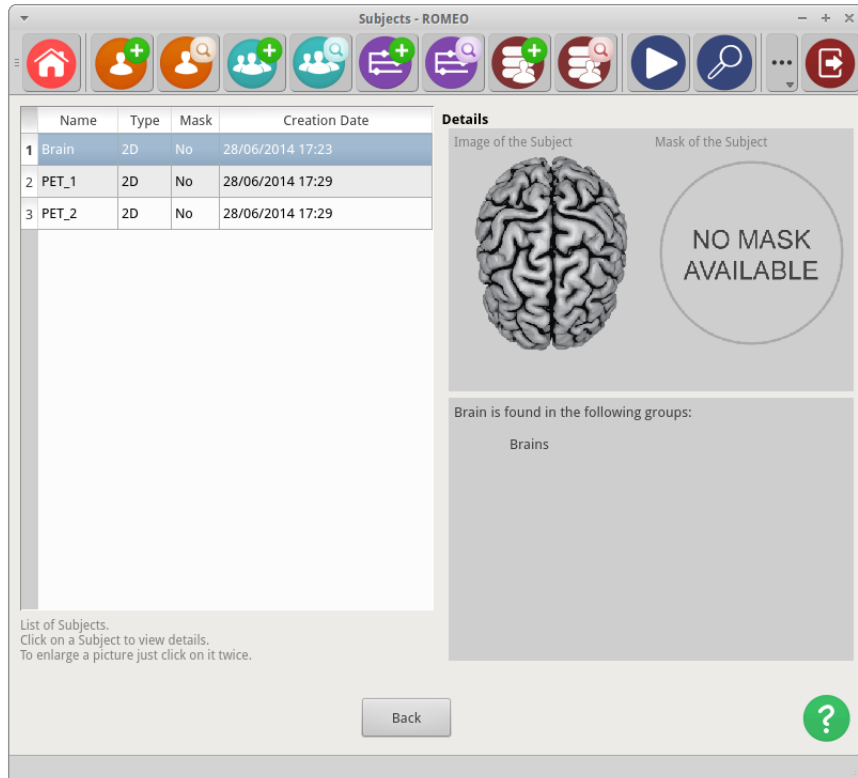


Figure 12: *Subject visualization window*

To visualize the $\text{Subjects}_{\mathbf{G}}$ present into Romeo, follow these instructions:

- From the $\text{Subject}_{\mathbf{G}}$ visualization window, select the $\text{Subject}_{\mathbf{G}}$ of interest, from the list present in the left panel of the window;
- The **Details** panel will show a preview of the image and a list of groups in which this $\text{Subject}_{\mathbf{G}}$ is present.

3.2 About groups of Subjects

This section contains the procedures to create and manage the groups of $\text{Subjects}_{\mathbf{G}}$.

3.2.1 Create a group of Subjects

The creation of a new group of $\text{Subjects}_{\mathbf{G}}$ is assigned to the group of $\text{Subjects}_{\mathbf{G}}$ creation window.

From the main window of Romeo, select the *New Group* button or choose the right one in the toolbar (see 2.3). The group of $\text{Subjects}_{\mathbf{G}}$ creation window (fig. 13) is composed of two panels.

The left one contains the information about the group that is going to be created (Name and Type). The right panel contains the list of $\text{Subjects}_{\mathbf{G}}$ actually stored in Romeo (filtered according to the selected type), plus the utility buttons *Select All* and *Deselect All*. In any moment, the user can go back to the main window by selecting the *Back* button.

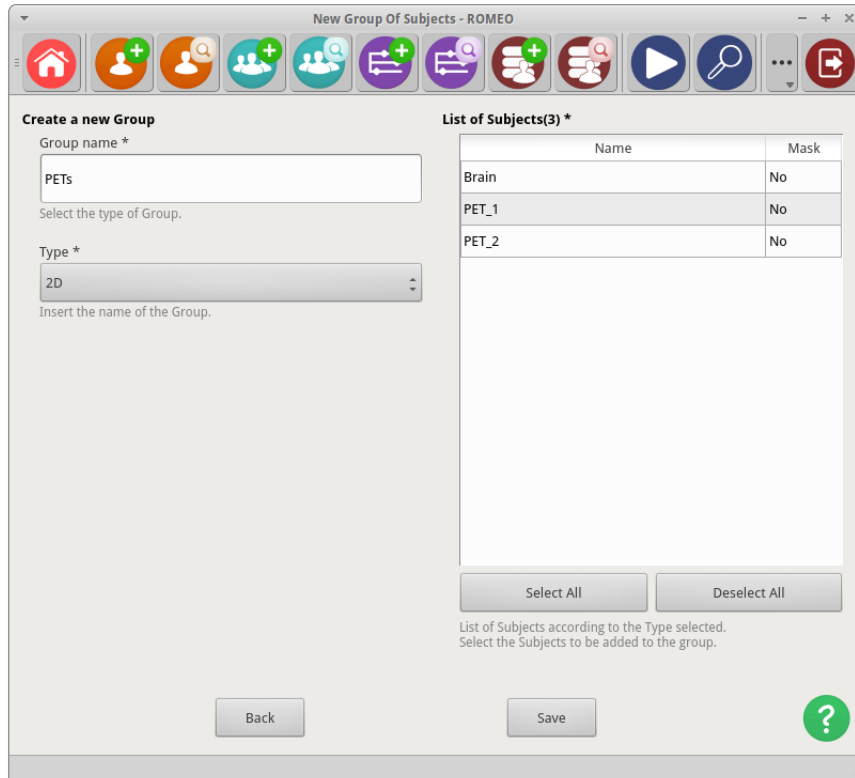


Figure 13: *Group of Subjects creation window*

To create a new group of Subjects_G, follow these instructions:

- From the group of Subjects_G creation window, type a unique name in the *Group name* field. That name will be the name of the group;
- Select the type of the Subjects_G that will be included in the group from the *Type* drop-down menu. A list of Subjects_G with that type, will be listed in the right panel;
- Select the Subjects_G that have to be included into the group, from the list of Subjects_G;
- Confirm the operation by selecting the *Save* button. Romeo will report an error message if the name chosen for the group is already present in Romeo or not all the required fields are fulfilled.

3.2.2 Manage groups of Subjects

Romeo allows the user to visualize the details of the stored groups of Subjects_G and permits their removal or modification. These features are assigned to the groups of Subjects_G managing window.

From the main window of Romeo, select the *Manage Groups* button or choose the right one in the toolbar (see 2.3). The groups of Subjects_G managing window (fig. 14), is composed of two panels. The left one contains the list of the groups of Subjects_G stored in Romeo, ordered by creation data (by default, from the oldest one, to the newest). For each group it is specified:

- **Name:** the name of the group;
- **Type:** the type of the Subjects_G associated with it (2D, 3D, 2D-t, 3D-t);
- **Subjects:** the number of Subjects_G associated with it;
- **Creation Date:** the date and time in which the group of Subjects_G was created.

The right panel contains the details about the Subjects_G of the selected group. In particular, it shows a list with their names and the flags of presence of the mask. In any moment, the user can go back to the main window by selecting the *Back* button.

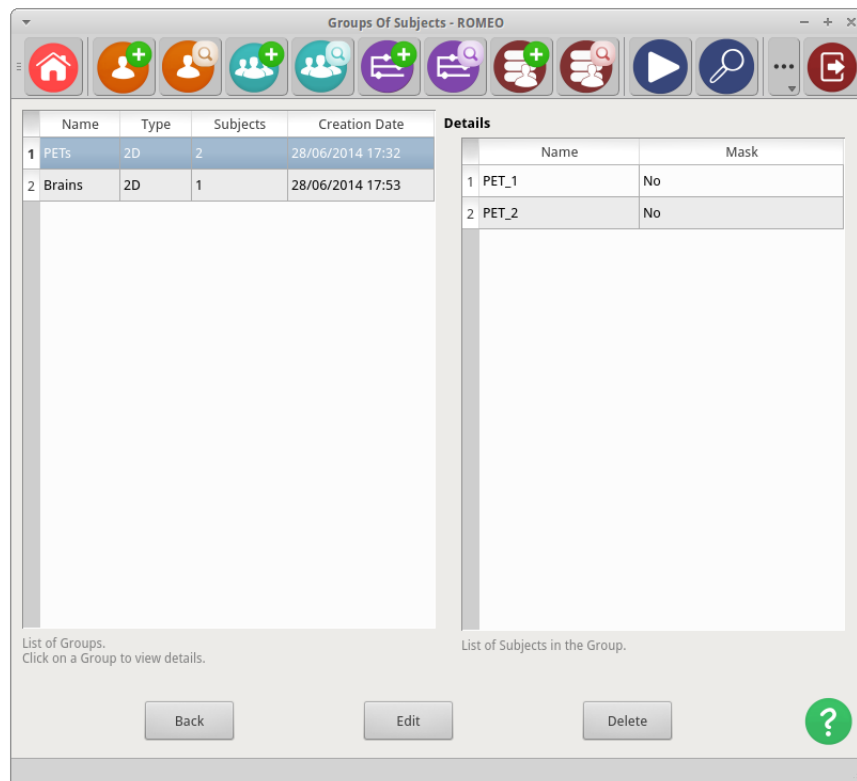


Figure 14: *Groups of Subjects managing window*

Visualize group of Subjects details: to visualize the groups of Subjects_G present into Romeo, follow these instructions:

- Select the group for which you want to view the details, from the list present in the left panel of the window;
- The *Details* panel will show the details of the Subjects_G associated with the group.

Modify a group of Subject: to modify a group, follow these instructions:

- From the groups of Subjects_G managing window, select the group that you want to modify;
- Select the *Edit* button. Romeo will load the fig. 15 window;
- From this window it is possible to add or remove some Subjects_G from the group. Select or deselect the Subjects_G you want to add or remove, from the list in the right panel;
- Confirm the operation by selecting the *Save* button.

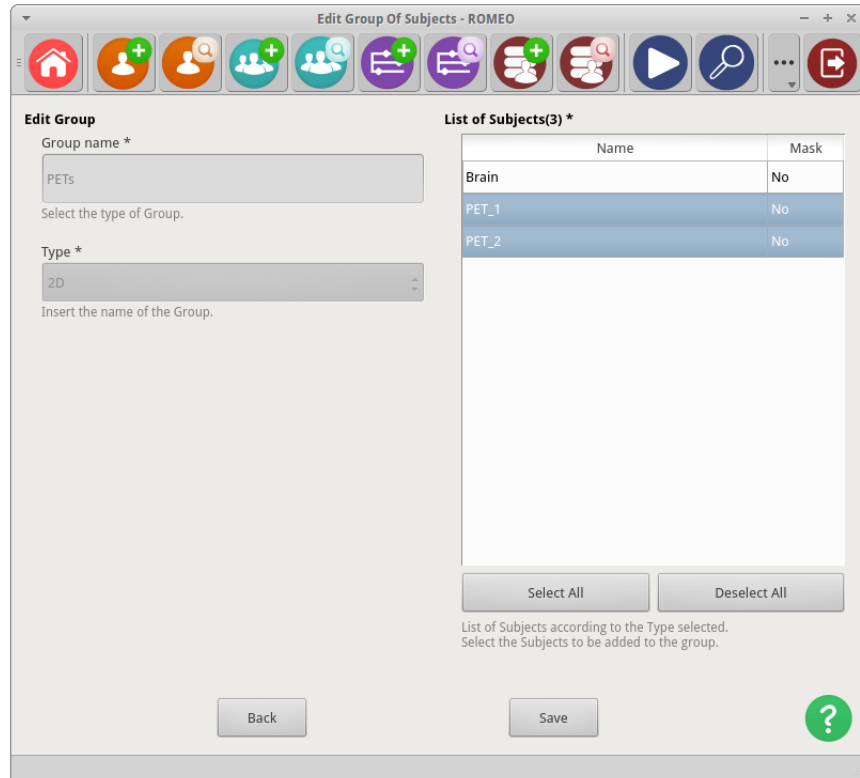


Figure 15: *Editing a Group of Subjects*

Delete a group of Subject: to delete a group of Subjects_G from Romeo, follow these instructions:

- From the groups of Subjects_G managing window, select the group of interest from the list;
- Select the *Delete* button to confirm the removal.

3.3 About Protocols

This section contains the procedures to create and manage the Protocols_G.

3.3.1 Create a Protocol

The creation of a new Protocol_G is assigned to the Protocol_G creation window. From the main window of Romeo, select the *New Protocol* button or choose the right one in the toolbar (see 2.3). The Protocol_G creation window (fig. 16) is composed of three panels.

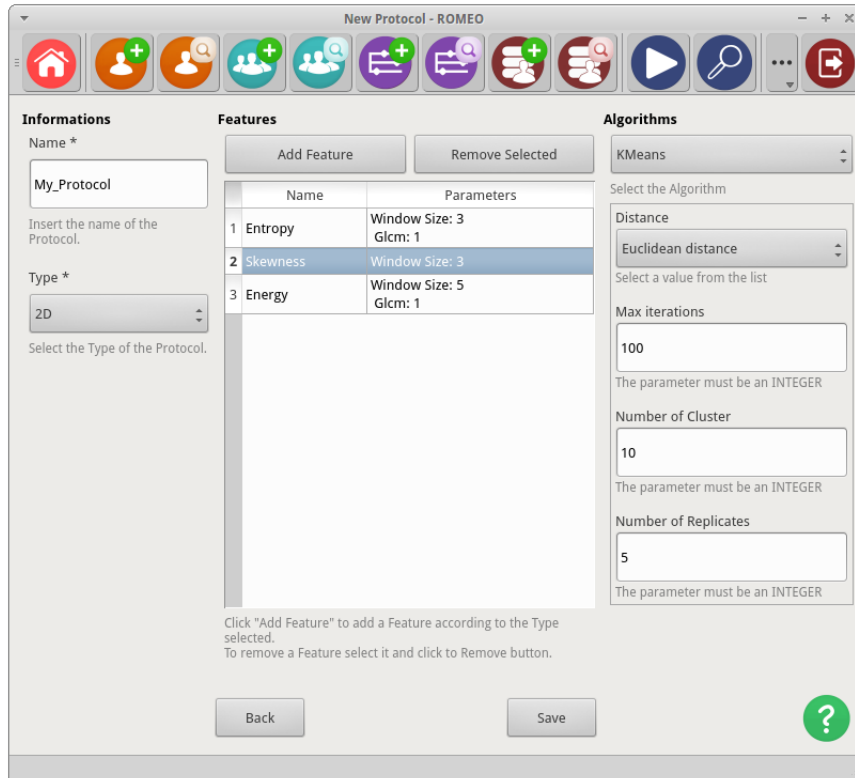


Figure 16: *Protocol creation window*

The left one contains information about the Protocol_G that is going to be created (Name and Type). The center panel eventually contains a list of feature extractors_G that the user has associate to the Protocol_G. Above that list there are the *Add Feature* and the *Remove Selected* buttons. The right one contains the drop-down menu to select the cluster algorithm. In any moment, the user can go back to the main window by selecting the *Back* button. To create a new Protocol_G, follow these instructions:

- From the Protocol_G creation window, type a unique name in the *Name* field. That name will be the name of the Protocol_G;
- Select the type of the Subjects_G on which the Protocol_G will perform from the *Type* drop-down menu;
- To add some feature extractors_G in the Protocol_G, select the *Add Feature* button, and follow these instructions (fig. 17):

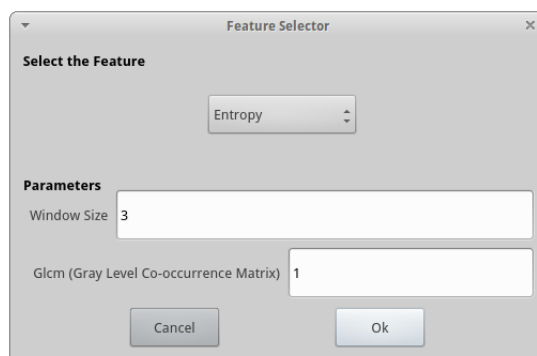


Figure 17: *Feature selector dialog window*

- From the feature selector dialog window, select the feature extractor to include from the drop-down menu. Romeo will show the parameters that have to be setted;
 - Type the necessary parameters for the selected feature or leave the default ones;
 - Select the *Ok* button to confirm the selection.
- To add a cluster algorithm into the Protocol_G, select it from the drop-down menu on the right panel of the window and then set the relative parameters;
 - Select the *Save* button to confirm the operation. Romeo will report an error message if the name chosen for the Protocol_G is already present in Romeo or not all the required fields are properly completed.

3.3.2 Manage Protocols

Romeo allows the user to visualize the details of the stored Protocols_G and permits their removal. These features are assigned to the Protocols_G managing window.

From the main window of Romeo, select the *Manage Protocols* button or choose the right one in the toolbar (see 2.3). The Protocols_G managing window (fig. 18) is composed of two panels. The left one contains the list of Protocols_G actually stored in Romeo, while the right one contains the details of the selected Protocol_G. In any moment, the user can go back to the main window by selecting the *Back* button.

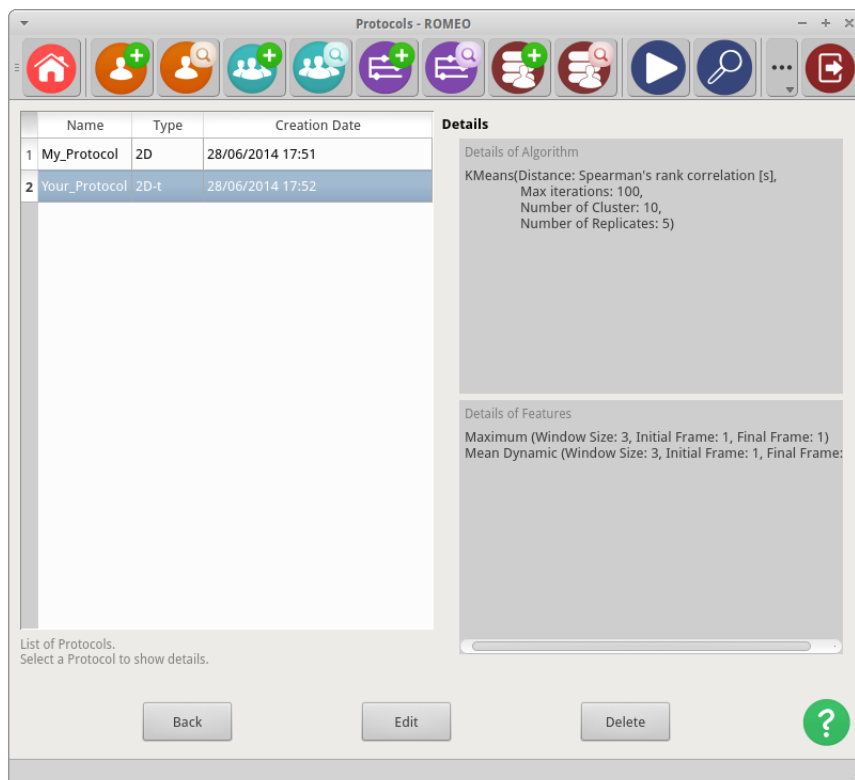


Figure 18: *Protocols managing window*

Visualize Protocol details: to visualize the details of a Protocol_G, follow these instructions:

- From the Protocols_G managing window, select the Protocol_G of interest from the list;

- The details panel will show information about the features extractors \mathbf{G} and/or cluster algorithm \mathbf{G} associated with the Protocol \mathbf{G} .

Modify a Protocol: to modify a Protocol \mathbf{G} , follow these instructions:

- From the Protocols \mathbf{G} managing window, select the one that you want to modify;
- Select the *Edit* button. Romeo will load the fig. 19 window;
- From this window it is possible to add or remove some features and/or change the cluster algorithm of the protocol. To perform these actions, follow the instructions of 3.3.1;
- Confirm the operation by selecting the *Save* button.

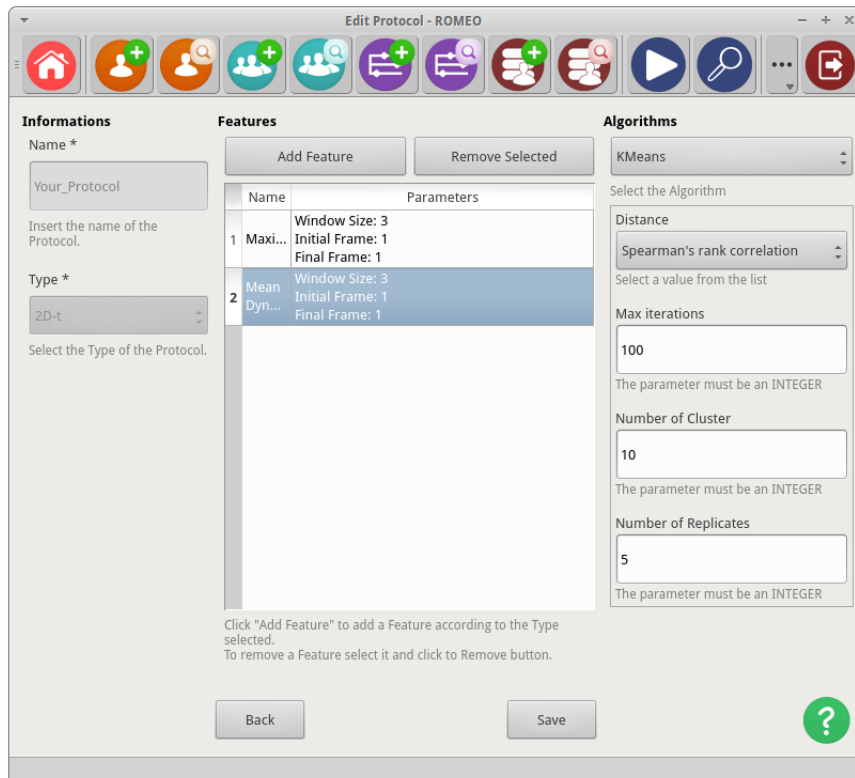


Figure 19: *Editing a Protocol*

Delete a Protocol: to delete a Protocol \mathbf{G} from Romeo, follow these instructions:

- From the Protocols \mathbf{G} managing window, select the Protocol \mathbf{G} of interest from the list;
- Select the *Delete* button to confirm the removal.

3.4 About Datasets

This section contains the procedures to create and manage the Datasets_G.

3.4.1 Create a Dataset

The creation of a new Dataset_G is assigned to the Dataset_G creation window. From the main window of Romeo, select the *New Dataset* button or choose the right one in the toolbar (see 2.3). The Dataset_G creation window (fig. 20), is composed of three panels and a form.

The form allow the user to type the name of the Dataset_G that will be created. The left panel contains the list of groups of Subjects_G actually stored in Romeo, while the center one contains the list of Protocols_G (filtered according to the selected group). The right panel contains the details of the selected group of Subject_G and Protocol_G. In any moment, the user can go back to the main window by selecting the *Back* button. To create a new

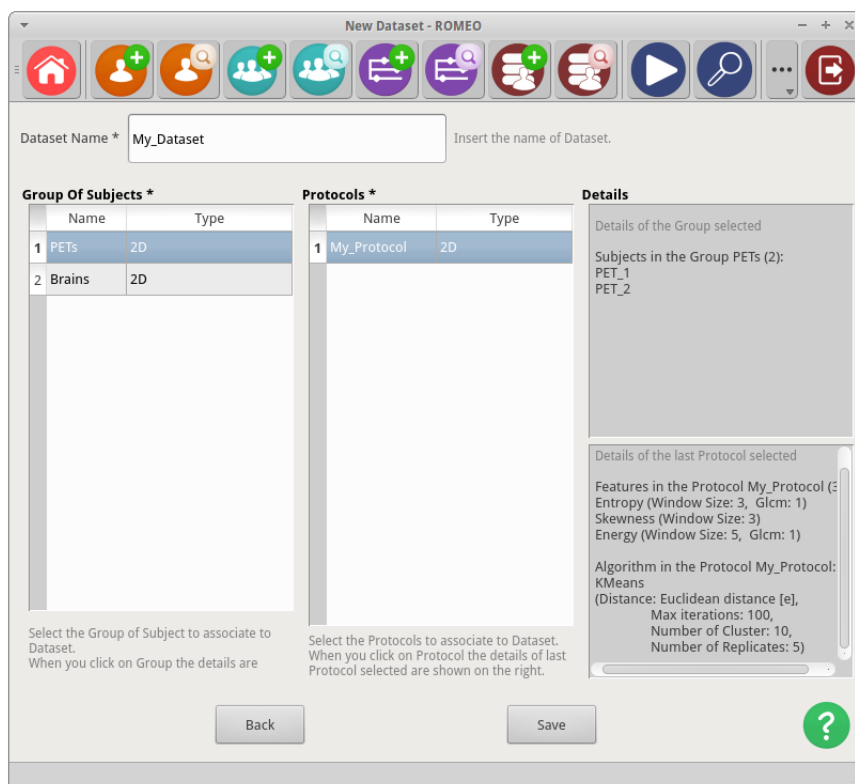


Figure 20: Dataset creation window

Dataset_G, follow these instructions:

- From the Dataset_G creation window, type a unique name in the *Dataset Name* field. That name will be the name of the Dataset_G;
- Select the group of Subjects_G that have to be associated with the Dataset_G from the *Group Of Subjects* panel. Romeo will load the compatible Protocols_G in the *Protocols* panel;
- Select the Protocols_G that have to be associated with the Dataset_G from the *Protocols* panel;
- Select the *Save* button to confirm the operation. Romeo will report an error message if the name chosen for the Dataset is already present in Romeo.

3.4.2 Manage Datasets

Romeo allows the user to visualize the details of the stored Datasets_G and permits their removal. These features are assigned to the Datasets_G managing window.

From the main window of Romeo, select the *Manage Datasets* button or choose the right one in the toolbar (see 2.3). The Datasets_G managing window (fig. 21) is composed of two panels. The left one contains the list of Datasets_G actually stored in Romeo, while the right one contains the details of the group of Subjects_G and Protocols_G associated with the selected Dataset_G. In any moment, the user can go back to the main window by selecting the *Back* button.

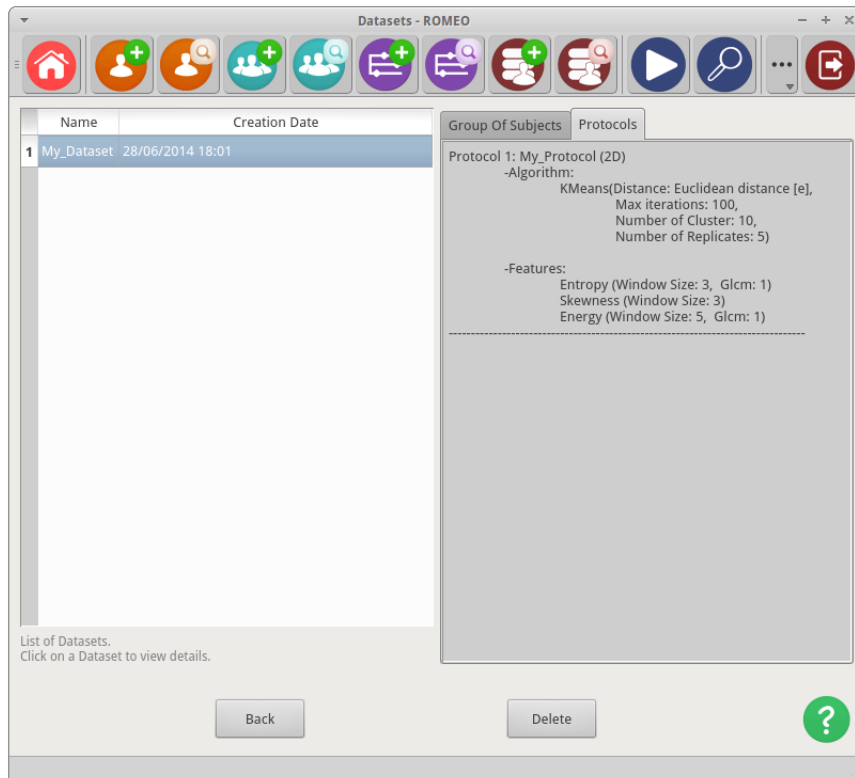


Figure 21: *Datasets managing window*

Visualize Dataset details: to visualize the details of a Dataset_G, follow these instructions:

- From the Datasets_G managing window, select the Dataset_G of interest from the list;
- The details panel will show informations about the groups of Subjects_G and the Protocols_G associated with the Dataset_G.

Delete a Dataset: to delete a Dataset_G from Romeo, follow these instructions:

- From the Datasets_G managing window, select the Dataset_G of interest from the list;
- Select the *Delete* button to confirm the removal.

4 Execution of an analysis

The execution of an analysis is assigned to the analysis window.

From the main window of Romeo, select the *Start Analysis* button or choose the right one in the toolbar (see 2.3). The analysis window (fig. 22), is composed of two panels. The left one contains a drop-down menu, that allow the user to select the Dataset_G of interest. The right one contains an area in which Romeo will show the feature extractors_G associated with the selected Dataset_G. The user can choose which results of the extraction will be saved and/or shown during the analysis, checking the feature extractors_G of interest shown in the right panel. In any moment, the user can go back to the main window by selecting the *Back* button.

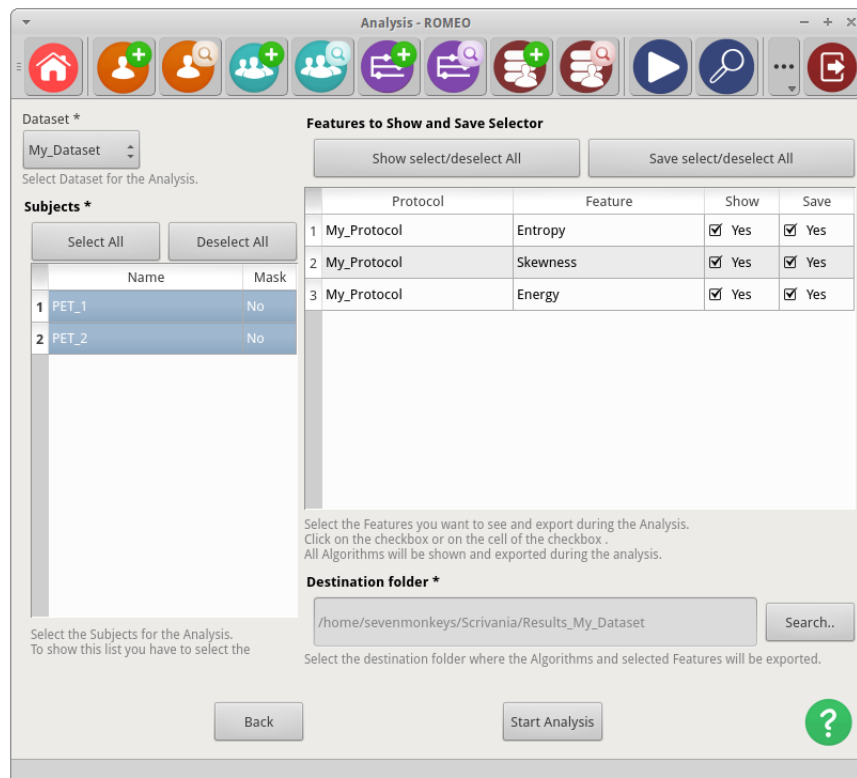


Figure 22: Analysis window

To execute an analysis, follow these instructions:

- From the analysis window, select the Dataset_G of interest from the drop-down menu;
- Select the Subjects_G that you want to analyze from the list in the left panel;
- Check which results of the feature extractors_G will be shown and/or saved in the right panel;
- Select the *Search..* button to indicate the destination folder of the analysis results;
- Select the *Start Analysis* button.

During the analysis, a pop up window will show the progress of the computation and in addition the results of the feature extractors_G if selected before. You can navigate through the results with the *Previous* and *Next* buttons (see fig.23).

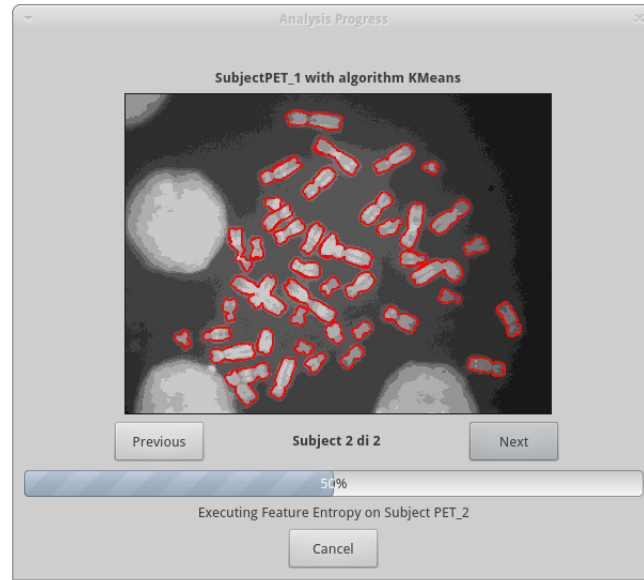


Figure 23: *Progression of an analysis*

5 Visualization of results

The visualization of the results of an analysis, is assigned to the results visualization window. From the main window of Romeo, select the *View Results* button or choose the right one in the toolbar (see 2.3). The results visualization window (fig. 24), is composed by a list of analysis ordered by execution data (by default, from the oldest one, to the newest). For each analysis it is specified:

- **ID:** the ID of the analysis;
- **Completed:** marked *Yes* if it has been completed, *No* otherwise;
- **Dataset:** the name of the Dataset_G analyzed;
- **Subjects Selected:** display the number of Subject_G of the Dataset_G analyzed;
- **Creation date:** the date and time in which the analysis was executed.

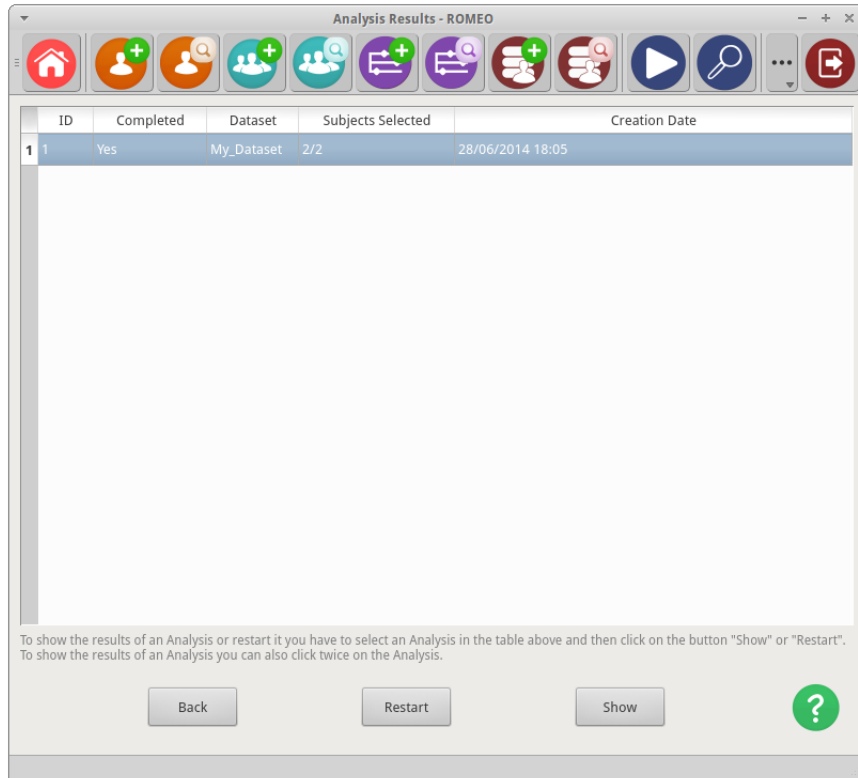


Figure 24: *Results visualization window*

To visualize the results of the executed analysis, follow these instructions:

- From the results visualization window, select the analysis of interest, from the list present in the left panel of the window;
- Select the *Show* button. Romeo will load the fig.25 window;
- Navigate the file system in the left panel of the window to choose which results to visualize.

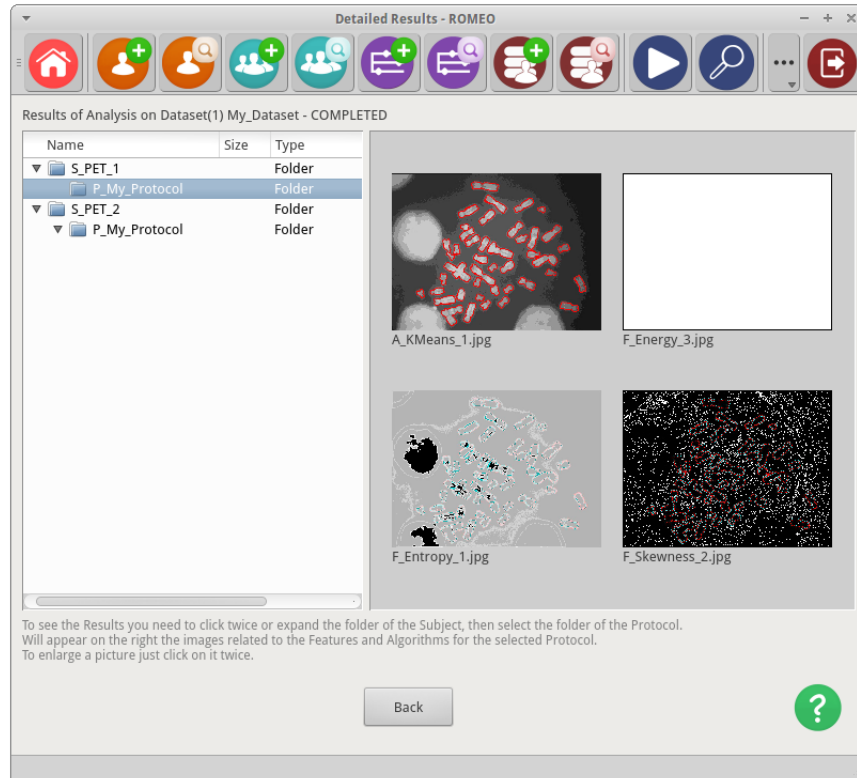


Figure 25: *Detailed results visualization window*

A Glossary

Cluster algorithm

Function that applies a clustering technique to the data (possibly both original image and extracted features_G).

Data

An image that have to be analyzed.

Dataset

Logic abstraction of an analysis. Consists of a group of Subjects_G and a Protocol_G that performs on it. Each Subject_G of the group will may be processed by the Protocol_G during an analysis.

Feature

Information extracted from the image, not present originally. A feature could visually underline, for example, a particular type of tissue.

Feature extractor

Function that calculates a feature_G of interest from the data_G

Mask

A binary image which is used to delimit the region of interest of a data_G that have to be analyzed. The data_G elements whose corresponding mask_G values are zero, are discarded from the analysis.

Protocol

Combination of a set of feature extractors \mathbf{G} (from 0 to N) and one clustering algorithm \mathbf{G} (from 0 to 1). A Protocol is associated to one or more Datasets \mathbf{G} .