



GenomeCruzer v1.9.0

Quick-Start Guide

Table of Contents

Main Window elements	3
Main toolbar.....	3
3D view.....	3
Tooltips.....	3
Application Modes	3
View mode	3
Analysis mode	3
Changing the active mode.....	4
Navigating in the 3D view	4
Moving the camera	4
Rotating the camera.....	4
Zooming	4
Resetting to the default (“home”) position.....	4
Selection Sets	4
Apply a saved Selection	4
Remove a Selection	4
Hide Unselected Elements	5
Pinning.....	5
Create a new pinning.....	5
Convert a pinning into a selection	5
Pinning from Gene Groups wall	5



Metadata based clustering.....5

 Criteria creation5

 Criterion Editing7

 Criterion Removal8

 Clustering Creation.....8

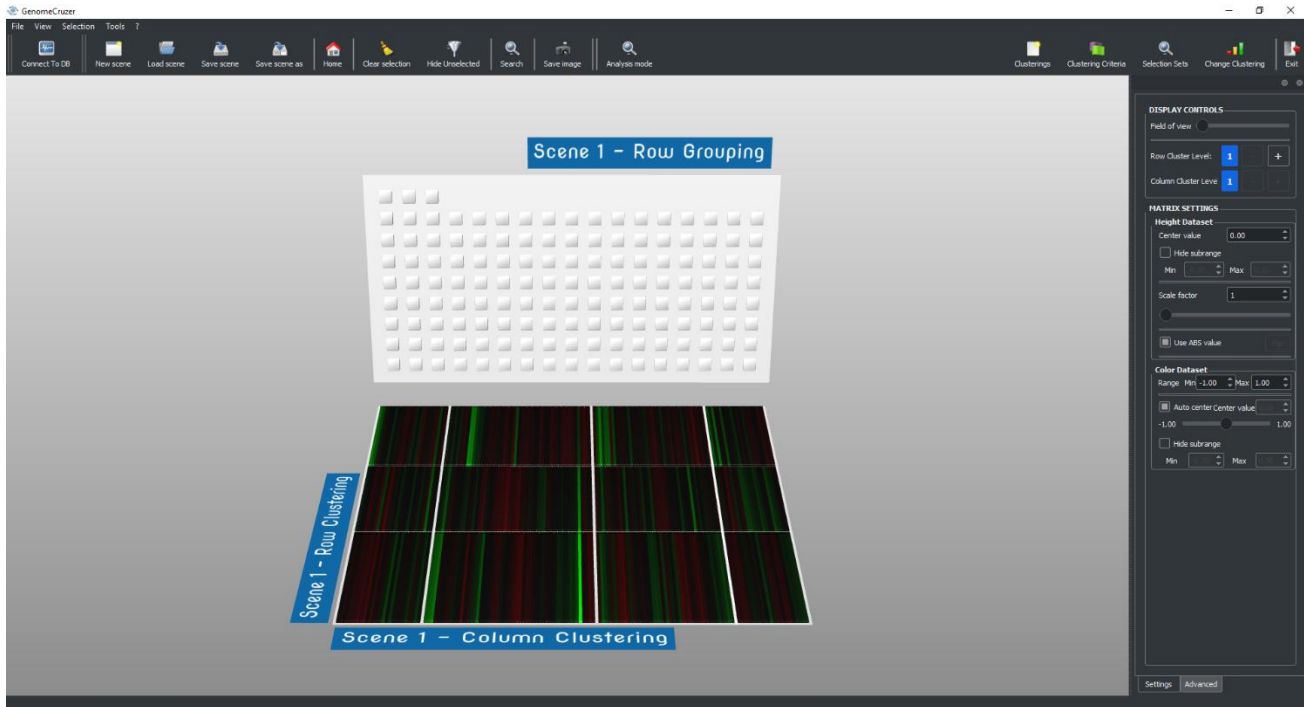
 Clustering Removal8

 Clustering Application8



Main Window elements

When you start GenomeCruzer, the application shows the Main window, from which you can connect to a Database and then load a scene. The image below shows an example view with a loaded scene.



Main toolbar

The application has a toolbar with the main controls, including the “Home” button (see the section on navigation), the clear selection, and the Exit button to quit the program.

3D view

The 3D view is the central part of the window and it shows the 3D scene, with the loaded dataset.

Tooltips

Place the mouse pointer over a data item and after a short while you will get a “tooltip”, a short text message providing detail information about that item (name, current values, etc...).

Application Modes

GenomeCruzer has two different application modes: *View* and *Analysis*.

View mode

The View mode lets you explore your dataset. It creates a 3D representation of the input values and allows navigating through it, seeing different level of details as needed (from cluster/group nodes to single values). It displays two datasets simultaneously, one defining the colors of the 3D items, the other their height.

Analysis mode

The Analysis mode provides a 3D space in which you can perform statistical analysis on your datasets, by selecting group of rows or columns and computing values on related items. You can choose the operation to apply (average, median, standard deviation, ...) and you can select the dataset to work with. The analysis mode shows only one dataset at a time: you can easily switch between them as needed.



Changing the active mode

To change the active mode from View to Analysis, use the “Analysis Mode” button in the main toolbar. When in Analysis mode, the same button has a different icon and it lets you go back to View mode.

Navigating in the 3D view

Navigation through the 3D view is controlled by the mouse. Each type of movements is initiated by clicking a button and then dragging the mouse. It is important to click on a geometry item, so the movement will happen around the picked point. If you click on an empty part of the scene (the background), controlling the movement may be less intuitive.

Moving the camera

Press the RIGHT mouse button and, while holding it pressed, drag the mouse. Your point of view will move with respect to the point you have clicked on.

Rotating the camera

Press the LEFT mouse button and, while holding it pressed, drag the mouse. Your point of view will rotate around the point you have clicked on.

Zooming

Press both the LEFT and RIGHT mouse buttons simultaneously and, while holding them pressed, move the mouse up or down to zoom in or out.

If you have a wheel mouse, you can use the wheel for the same purpose.

Resetting to the default (“home”) position

Press the spacebar to move the camera back to the default position. This is also called the “home” position. There is also a button in the main toolbar for this action.

Selection Sets

In Analysis mode, GenomeCruzer v1.7 allows you to save and load a selection of a set of nodes (Selection Set)

Create a new Selection

Select a new node with DOUBLE CLICK and add the desired nodes by CTRL-LEFT mouse button. To remove a node from the current selection, ALT-LEFT click on it. To clear the selection, double click on a point outside the walls.

If you DOUBLE-CLICK or CTRL-LEFT click on the opposite wall, the current selection will be cleared and a new one will be created on the opposite wall.

When you have selected all the desired nodes, click on the “Selection Sets” button in the Main Toolbar. A dialog window will open, showing the available selections for the current scene. Fill in the required information and click on the “Save” button in the dialog to create the selection.

Please note that the new selection will not be permanently stored in the database until you save the current scene.

Apply a saved Selection

The “Selection Sets” dialog holds the set of all the selections saved for the current scenes. To apply one of them, select it from the list and press Apply.

Remove a Selection

A selection can be removed from the set of available selections: in order to do so, select it from the list and press Remove. Note that the selection will not be permanently deleted from the database until you save the current scene.



Hide Unselected Elements

In Analysis mode, it is possible to hide some parts of the scene: In order to do so, select the parts that you want to maintain visible and click on “Hide Unselected” button. The unselected elements (on the same wall as the current selection) will be hidden from the view.

From here, it is possible to change the selection, create a new one (but the set of visible nodes will not be modified) and to create pinning on top of the selection.

To show the hidden nodes, click on “Show All” button

Pinning

In Analysis mode, a “pinning” feature is available besides the regular selection.

When a selection is active on a wall, you can “pin” a set of nodes on the opposite wall. This allows to “highlight” nodes affected by a calculation without clearing the selection itself.

To activate the pinning mode, click on the “Pinning” radio button when calculation results are available on either wall.

Create a new pinning

When pinning mode is activated, you can add nodes to a pinning in the same way used for the normal selection: DOUBLE-CLICK to create a new selection, CTRL-LEFT click to add nodes to the current selections, ALT-LEFT click to remove a node from a set of pinning nodes.

Convert a pinning into a selection

Pinned nodes are not permanently saved into the database, but they can be converted into a Selection Set and saved. In order to do so, click on the “Convert to Selection” button in the Analysis Preferences dialog when a pinning is active in the scene.

Pinning from Gene Groups wall

When at least a node from the Samples wall is selected in the scene and pinning mode is active, selecting a gene group from the Gene Groups wall will create a pinning on the floor. It is possible to modify this pinning adding/removing nodes from it and to convert it into a Selection, in the same way as the manual pinning.

Metadata based clustering

GenomeCruzer v1.7 allows the user to create, edit and save clusterings at runtime: these clusterings are based on the metadata attached to the genes and to the samples.

Metadata for a gene or a sample are defined as a Json string composed of a sequence of pairs <property, value>.

Criteria creation

Metadata clusterings are based on one or more criteria which need to be manually inserted in GenomeCruzer. Criteria definition is handled in GenomeCruzer clicking on the “ClusteringCriteria” button in the top right part of the GenomeCruzer window.

A dialog opens, showing the available criteria and the possibility to Edit/Remove them, or to create a new one. Clicking on the “Add” button opens a new dialog window (see Figure 2), from which it is possible to specify the name which will identify the criterion, the property which will be used to subdivide the elements, whether it will be applied to rows or columns. The criterion itself will be defined with a JSON string structured as follows:



```
[
{
  "name" : "cluster_name_1",
  "descr" : "cluster_description"
},
{
  "name" : "cluster_name_2",
  "descr" : "cluster_description"
}
]
```

The clustering description depends on the type of the criterion. Three criterion types are present: Enum, Boolean, Numeric.

Enum: the elements in that cluster must match the string in "cluster_description". If an element does not match to any of the descriptions, it will be labeled as "undefined".

Example: in case we want to subdivide the patients depending on their gender, here is what the description of the criterion would look like:

```
[
  {
    "name" : "Male",
    "descr" : "MALE"
  },
  {
    "name" : "Female",
    "descr" : "FEMALE"
  }
]
```

Boolean: each element can have two values ("true" and "false"). If a value is not specified for that property on an element, it will be labeled as "undefined".

Example: if we want to subdivide the patients depending on whether they smoke or not, the description would look like this:

```
[
  {
    "name" : "Smoker",
    "descr" : "true"
  },
  {
```



```

        "name" : "Not smoker",
        "descr" : "false"
    }
]

```

Numeric: in this case, each cluster will be defined by a range of values rather than a single value. The “Descr” field in this case is an array of two values ([min, max]) and each element will belong to that cluster if its value for that property lies between min and max. If the value does not fall in any of the ranges, it will be labeled as “undefined”.

Example: in case we want to subdivide the patients depending on their age, the criterion would be specified similarly to the following:

```

[
    {
        "name" : "A",
        "descr" : [1, 20]
    },
    {
        "name" : "B",
        "descr" : [21, 40]
    },
    {
        "name" : "C",
        "descr" : [41, 60]
    },
    {
        "name" : "D",
        "descr" : [61, 80]
    },
    {
        "name" : "E",
        "descr" : [81, 100]
    }
]

```

Criterion Editing

Once a criterion is created, it is possible to edit it: to do this, highlight it and click on the “Edit” button on the bottom right part of the Criteria Dialog Window. If the criterion is used in some clustering, a popup will be opened to warn the user. Then the same window as Figure 2 is opened, with the fields already filled with the criterion data. When the user clicks the “Ok” button, the criterion information is updated



Criterion Removal

It is possible to remove a criterion, as long as it is not used by any metadata-base clustering: to do so, select the criterion in the interface and click on “Remove”. If the criterion is in use, a popup will inform the user that the criterion can't be deleted and nothing will be changed.

Clustering Creation

Clicking on the “Clusterings” button on the top-right part of the GenomeCruzer interface opens the Clustering dialog: from here it is possible to create/delete/edit metadata-based clusterings.

When adding (“Add” button) or editing (“Edit” button) a clustering, a new dialog window is opened to allow the user to insert the clustering data (see Figure 3). When the clustering is created, the user can specify whether it can be applied on rows or on columns (this can't be modified). clicking on the “Add Level” button adds a new clustering level: a new row is inserted in the description panel, and the user can adjust its criterion, delete it and/or change its position in the panel (clicking on the “Move Up” button).

When the user is satisfied with the clustering, it can be saved by clicking on the “Ok” button. The clustering definition window will be closed and the user will go back to the Available Clusterings window.

Clustering Removal

In order to remove a metadata-based clustering, select it in the list and click on “Delete”.

Clustering Application

To apply a metadata-based clustering, it is necessary to click on “Change Clustering” button. This opens a dialog showing all the available clusterings for the rows and for the columns (both metadata-based and not metadata-based).

Select the desired clustering from the dropdown menu and click ok to apply it to the current scene. If the clustering is malformed, a warning is shown on screen and no clustering is assigned to the selected wall (i.e. all the elements will be in the same tile), otherwise the selected clustering will be applied on the correct wall and visualized accordingly.