



ESCAPE-NET standard operating procedure (SOP) for user and data management in BC|GENOME

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1 BC|GENOME database platform



The BC|GENOME database platform provided by BC|Platforms is used for data management and statistical analyses of the shared data resources of ESCAPE-NET. The shared database platform has been provided as a deliverable of WP3.

Both the WP2 and WP3 teams have been collaborated to build a secured data management and analysis platform where only authorized users of the ESCAPE-NET project are allowed to use data without risk of either unauthorized changes or unauthorized utilization of the shared data resources.

This standard operating procedure (SOP) document is created to provide necessary information for the ESCAPE-NET researcher to access and analyze the shared resources in BC|GENOME.

In addition to this SOP, please familiarize yourself with documents of

- BCGENOME_Administration_tools.pdf describing tools for data manager
- BCGENOME_User_Guide.pdf describing the tools in BC|GENOME

found at <https://escape-net.github.io/docs/documents/documents.html>

2 Responsibility assignments of users of the ESCAPE-NET shared database platform

BC|GENOME provides toolset for uploading, exporting, filtering and analyzing epidemiological study data. The BC|GENOME graphical user interface accessed using web browser is run on the secure virtual CentOS desktop (i.e. Secure Cloud 575) in the server environment hosted by Computerome at DTU. On this secure desktop data management functionalities are restricted inside the virtual desktop: This means users are not able to download result files, graphs and metadata derived from research data without control of the BC|GENOME administrators.

In Table 1 you can find a summary of tools and responsible assignments of the shared database platform with contact information.

Table 1. Functions and responsibilities for the user and data management in the ESCAPE-NET database platform.

	Function	Work package	Main contact person *	Note
Database platform	Maintenance of BC GENOME	WP3: BC	Päivi / BC support	BC provides BC GENOME, the database platform, and are responsible for the functionality of tools
	Server and calculation environment	WP3: Computerome	Via Päivi / BC support	Computerome provides the server infrastructure
Project management	User Accounts	WP2: RegionH	Simon, Niels	New user accounts
	User permission	WP2: RegionH	Simon, Niels	User permissions and user groups



	File transfer	WP2: RegionH and Computerome /DTU	Simon, Niels	Files transferred onto the server
	Table structures	WP3	Simon / Päivi	Data integration of harmonized data in BC GENOME
	Data uploads	WP2 / BC	Simon / Päivi	Data integration of harmonized data in BC GENOME
Usage of Data management tools in BC GENOME	Data filtering / joining	All	Päivi / BC support	Data management in the secure cloud environment
	New datasets	All	Simon, Niels, Päivi / BC support	See above
	Dataset permissions	All	Simon, Niels, Päivi / BC support	See above
	Data visualization	All	Päivi / BC support	See above
	Data export	All	Päivi / BC support	See above
Data analysis in BC GENOME using research data	Data analysis	All		See above
Data exports from server environment	Export of meta data, analysis results, charts	WP2: RegionH and Computerome /DTU	Simon / Niels /Paulien / Marieke	Export of data from the server environment. <u>Project member who has uploaded data cannot supervise the data exports</u>

* Main contact person:

Simon: simon.mathis.koenig@regionh.dk

Niels: niels.kjaer.stampe@regionh.dk

Paulien: p.c.homma@amc.uva.nl

Marieke: m.t.blom@amc.uva.nl

BC support: support@bcplatforms.com

Päivi: paivi.tikka-kleemola@bcplatforms.com



3 User accounts

For the ESCAPE-NET database platform user need to have user accounts in both Secure Cloud 575 with a 2-factor authentication provided by Computerome and BC|GENOME.

3.1 User profiles

In the ESCAPE-NET project three different user profiles are available (Table 2): Each BC|GENOME database needs to have a database owner for managing both user accounts and user permissions to datasets. The database owner account password is managed by BC support but the account has been assigned to data manager of ESCAPE-NET. Both profiles of database administrator and researcher can be used for daily data management and analysis tasks, but database administrator can create new research user account and monitor system logs.

Table 2. ESCAPE-NET user profiles used in BC|GENOME.

User Profiles in in the ESCAPE-NET project	Description
Database owner	User management, dataset permissions, see the document of BCGENOME_Administration_tool.pdf
Database administrator	Tool for user account creations, monitoring the logs, data management and analysis tools
Researcher	Data management and analysis tools

3.2 Applying for the user account for both Secure Cloud 575 and BC|GENOME

1. When you apply for a user account with a profile of “researcher” send an email to:
 - 1.1. Simon Mathis Kønig (simon.mathis.koenig@regionh.dk) and Niels Kjær Stampe (niels.kjaer.stampe@regionh.dk)
 - 1.2. cc Jacob Tfelt (jacob.tfelt@regionh.dk), Hanno Tan (h.l.tan@amc.uva.nl) and Marieke Blom (m.t.blom@amc.uva.nl)
 - 1.3. with information of your:
 - 1.3.1. Full name
 - 1.3.2. Affiliation as specified in the ESCAPE-NET proposal
 - 1.3.3. E-mail
 - 1.3.4. Mobile phone number with the country code
 - 1.3.5. cc your PI assigned with the ESCAPE-NET project
 - 1.3.6. Inform whether you wish to use either the Google Authenticator application or SMS (Only applicable for users within Denmark) to authenticate your login using your mobile phone
2. When your user request has been approved, you will receive two SMS messages with your passwords:
 - 2.1. one from the HPC team of Secure Cloud 575 and
 - 2.2. one from the ESCAPE-NET database team.



3.3 Login to Computerome's secure cloud desktop and BC|GENOME

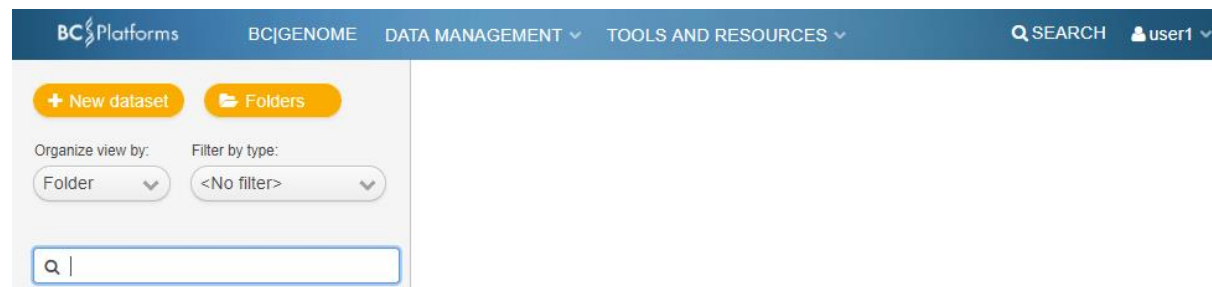
Here's the instructions on how to navigate to BC|GENOME on Computerome's Secure Cloud 575 desktop:

3.3.1 Login to Computerome's secure cloud desktop

1. Familiarize yourself with instructions found in <https://www.computerome.dk/display/CW/How+to+login>, login with user name and password sent by the HPC team. PLEASE do **NOT** change the password on the wiki, it is a shared user.
2. If you have chosen to use Google Authenticator app, then install the application onto your mobile phone
3. Navigate to <https://secureremote.dtu.dk/vpn/index.html> using Chrome or Firefox
4. Type your user name and password sent by the HPC team in Denmark
5. Type the passcode sent via either SMS (from risoe.dtu.dk) or Google authenticator app
6. On the virtual desktop click on the Desktop icon at the top
7. Click on the icon BIOINF Computerome 575 Centos
8. Confirm you want to open Citrix Receiver Launcher. This application will create a secure connection.
9. On the Desktop select Shortcuts / Start
10. You may need to slide the blue screen up to access the active desktop

3.3.2 Login to BC|GENOME and changing your password

1. On the virtual Desktop navigate to Applications / Internet and click the Firefox Web browser open
2. Type URL: <https://risoe-r12-cn518/bcapp/>
3. Type your user name and password provided by Simon, and click Log In
4. You will enter to BC|GENOME dataset navigator.
5. Go to <userID> / Administration on the top right of your browser page





6. On the Profile page click the Edit button to change your password
 - 6.1. Password must have 7 - 32 characters in a combination of upper (A-Z) and lower case letters (a-z) and numbers 0-9 (obs! special characters are not supported)
7. Press Save

4 Working in BC|GENOME

The core of BC|GENOME is the data navigator that can be used to search for datasets you have permissions to (either read or read/write) in BC|GENOME. In addition, each user with either the database administrator or researcher profile can create their own datasets and filtered views, which are subsets in BC|GENOME. However, in Secure Cloud 575 all data exports have been restricted inside the secure cloud desktop thus you need to ask for data transfer service from Simon (simon.mathis.koenig@regionh.dk), for more information please see chapter 4.2.

4.1 BC|GENOME user guide

Table 3 below refers to BC|GENOME's PDF documentation that provides information about the basic usage of the BC|GENOME tools. However, all users are recommended to read the BC|GENOME document entitled BCGENOME_User_Guide.pdf.

Table 3. Key functionalities in BC|GENOME and reference to BCGENOME_User_Guide.pdf

Functions in BC GENOME	Chapter in the user guide
Dataset navigator	2.2. Navigating in BC GENOME
Dataset creation	3.1. Creating a form and datasets
Data upload	3.2. Uploading data
Result folder	3.3. Viewing results and reports
Filtering and joining data	5.2. Subsets
Analysis	5.4. Running analyses in BC GENOME

4.2 Downloading results from BC|GENOME server


Due to the secure cloud environment users of BC|GENOME are not able to transfer any analysis results, metadata information or charts from the server without authorization from the WP2 team. Please confer to

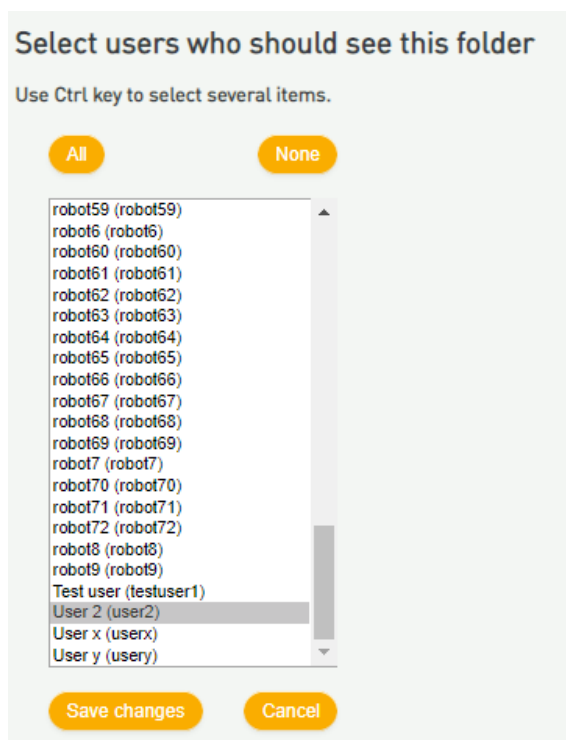



the *Instructions for export of analysis results from the ESCAPE-NET server*, found at <https://escape-net.github.io/docs/documents/documents.html>

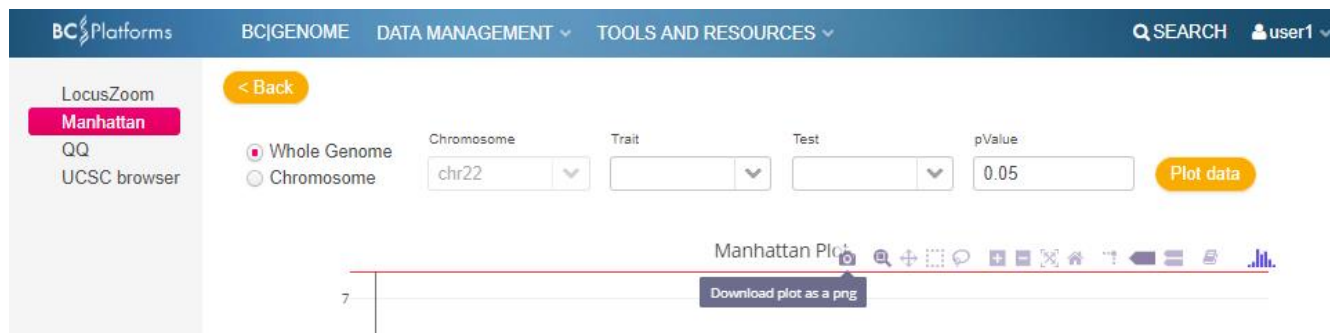
4.2.1 Instructions for researcher working in BC|GENOME

Here are the instructions for sharing your result and chart files to be downloaded from BC|GENOME by data manager of the ESCAPE-NET project. The instructions can be applied also for sharing results and graphs inside BC|GENOME to your colleagues.

1. Sharing a result file
 - 1.1. Navigate to DATA MANAGEMENT > RESULT ARCHIVE and identify your job folder
 - 1.2. Click the small green dot  next to your result file line found in the Share column
 - 1.3. Select the data manager's user account (skonig) and press Save changes



- 1.4. After sharing your file(s) you can see the shared icon  on your result file row
 - 1.5. Contact Simon (simon.mathis.koenig@regionh.dk) with your user name and jobID information so that he knows to ship the files to you.
2. Sharing chart files:
 - 2.1. Either in the a) job folder of DATA MANAGEMENT > RESULT ARCHIVE, or using the b) Charts tools in the DATA tab for your association result dataset (see the screenshot below), or in the c) VISUALIZATION tab you can export (download) charts and graphs

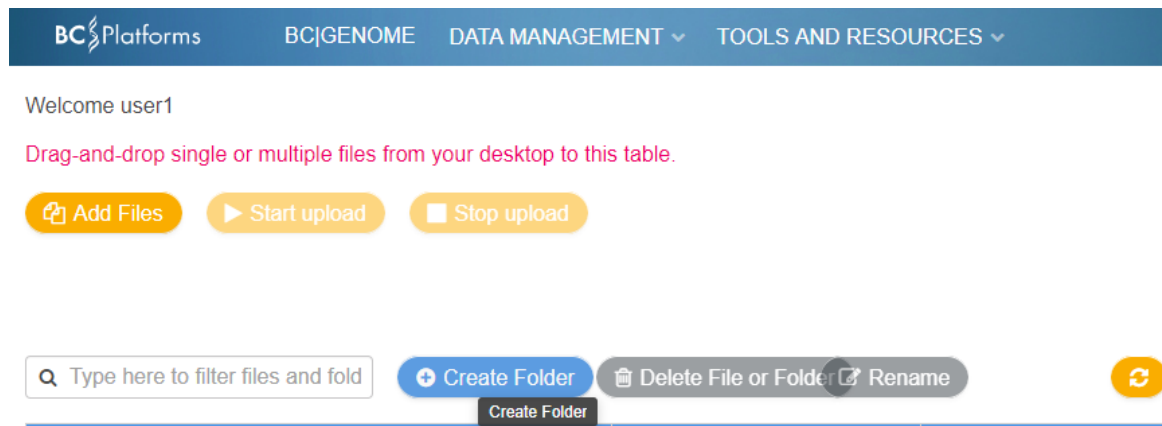


2.2. Download a file onto your Desktop of secure cloud 575. **Please be aware that files will be deleted from the virtual desktop on a regular basis and you should not store any results here.**

2.3. Navigate to TOOLS AND RESOURCES > FILE TRANSFER

2.4. Use the Create Folder button for creating a folder with a descriptive name and date information as shown below


2.5. Click the newly created folder active before using the Add Files button (or Drag and drop files)










2.6. Navigate to DATA MANAGEMENT > RESULT ARCHIVE for sharing the folder with the data manager


2.6.1. Click the Upload folder open

BC Platforms BC GENOME DATA MANAGEMENT	
Result archive	
File name	Description
⌵	Reload current folder (user1)
upload	Transferred files
shared	Results shared by other users

2.6.2. In the upload folder click the share icon  to share the folder with your data manager (skonig) and press the Save changes button

Result archive

Regular folder					
File name	Description	Edit title	Size	Modified	Share
..	Reload current folder (upload)			12:37/30.12.18	
..	Parent folder			10:42/30.12.18	
 user1_export.QjixHM.txt	Regular file		703 bytes	15:39/14.12.18	
 subjects.sample	Regular file		749 bytes	12:52/07.11.18	
 My results some date	Directory		24 KB	12:37/30.12.18	

2.6.3. After sharing your file(s) you can see a shared icon  in your folder

2.6.4. Contact Simon (simon.mathis.koenig@regionh.dk) with your user name and folder information so that he knows to ship the files to you.

5 Jupyter Notebook application

Besides the joint database, hosting consortium data, The ESCAPE-NET server host a main resource for data analysis; the Jupyter Notebook application.

Jupyter Notebook is an operating environment for running blocks of scripts in web graphical user interface, embedded with Markdown cells to create a live document about the script.

Jupyter Notebook is very popular tool amongst Data Scientists, Bioinformaticians and Statisticians, as it provides an interactive environment for organising script-based workflows and work, and allows the authors to include user-friendly HTML commentary, mathematical formulae, etc.

For a overview of the notebook document structure and use, please see <https://jupyter-notebook.readthedocs.io/en/stable/notebook.html#notebook-user-interface>.

5.1 Integration to BC|GENOME

Jupyter Notebook Hub is a service that authenticates and authorises users to use Jupyter Notebooks on BC|GENOME platform. The Hub coordinates generation and management of user notebook servers, each of which lives in their own Docker instance. The Docker instances provide references to user's own files on the BC|GENOME filesystem, like uploaded files, and results from analyses. The Docker space protects the BC|GENOME application server from accidental misuse and runaway scripts.



5.2 Log in to the Jupyter Application

1. Login to Computerome's secure cloud desktop as described in 3.3.1
2. On the virtual Desktop navigate to Applications / Internet and click the Firefox Web browser open
3. Type URL: <https://risoe-r12-cn518/jupyter/>
4. To create a new notebook, click on the "new" menu in the top right and select you preferred language (e.g., R or SAS)

