Database working-session – Amsterdam

1. Follow the instructions in the SOP (https://escape-net.github.io/texts/EscapeNet_SOP.pdf) on how to login to the secure cloud 575 and the BC|GENOME app.

BC|GENOME

2. Explore the various tools and function in BC|GENOME. We can recommend you to have a look at the following chapters in the BC|GENOME user guide (https://escape-net.github.io/texts/BCGENOME_User%20Guide_Dec2018.pdf):

    a. Navigating in BC|GENOME (2.2)
    b. Working with data in BC|GENOME
        i. Creating a dataset (5.1)
        ii. Subsets (5.2)
        iii. Viewing the distribution of data values (5.3)
        iv. Running analyses in BC|GENOME (5.4) (PLINK)
    c. Result archive (6)

3. For hand-on experience purposes we have created the three datasets in the folder **EscN Demo** found in the **DATASET NAVIGATOR** in BC|GENOME. All users have read permission to the demo datasets. Additionally, demo data sets for GWAS studies are found in the folder **Demo data**, with affection status, pedigrees, phenotypes, and snp's.

Jupyter Notebook – analysis environment

4. Access the **Jupyter Hub** analysis environment, by typing the URL https://risoe-r12-cn518/jupyter/ in the web-browser of the virtual desktop
5. For information on what Jypyter Notebooks are and how they are used, please see https://escape-net.github.io/docs/jupyter
6. Check out the Jupyter Notebook example on how to import data from BC|GENOME into the analysis environment - found in the BC|GENOME app, under **DATA MANAGEMENT / RESULT ARCHIVE**: shared / skonig