

# Manual for Analysis scripts of CROPMETAPOP Sensibility

Analysis:

## **newAnalysis.py**

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19 décembre 2017

## 1 General purpose

These scripts are made to analyse the GenotypeMono.csv file produced by CROPMETAPOP and return several genetic indices :  $\overline{Hs}$ ,  $\overline{Hobs}$ ,  $\overline{Fis}$ ,  $Ht$  and Gst. It outputs each of these indices in .res files.

The script called **analysisNSel.py** analyses the neutral markers, while the script called **analysisSel.py** analyses the selected markers.

It takes a few command-line parameters in input :

1. the path to the folder containing the GenotypeMono.csv file (e.g. /home/\$User/Folder/)
2. the number of replicates of the simulation
3. the number of populations in the simulation
4. the number of markers in the populations
5. the number of alleles of the markers

Be careful, you cannot give to **analysisSel.py** a number of markers lower than 11 !

## 2 Protocol

1. Get all the values for the parameters of the script (this step will be done automatically for the sensibility analysis by the **setGenExpPlanX\*Sel.py** script that will create corresponding launcher file for the analysis)
2. Run the script using Python 3 (**python3 analysis\*Sel.py Path/to/Folder Replicates Populations Markers Alleles**) by replacing the parameters by their respective values
3. The result files are created in the folder of the simulation