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Select Files

Select Sample List File

Select Input Gene File

Setting Parameters

Min Depth Value	<input type="text" value="4"/>
Region Size	<input type="text" value="500"/>
Region Quaified Value	<input type="text" value="4"/>
DMR_CG_CutOffValue	<input type="text" value="0.2"/>
DMR_CHH_CutOffValue	<input type="text" value="0.2"/>
DMR_CHG_CutOffValue	<input type="text" value="0.2"/>
Heat_CutOffValue	<input type="text" value="0.2"/>
Bin Size	<input type="text" value="1000000"/>
Promotor Range	<input type="text" value="2000"/>

Choosing Options

☐ HeatMap_PCA
 ☐ Enrichment
 ☐ DMG
 ☐ ChrView
 ☐ MetaPlot

Output Selection

☐ Auto shutdown PC

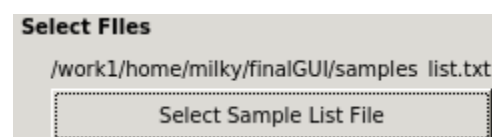
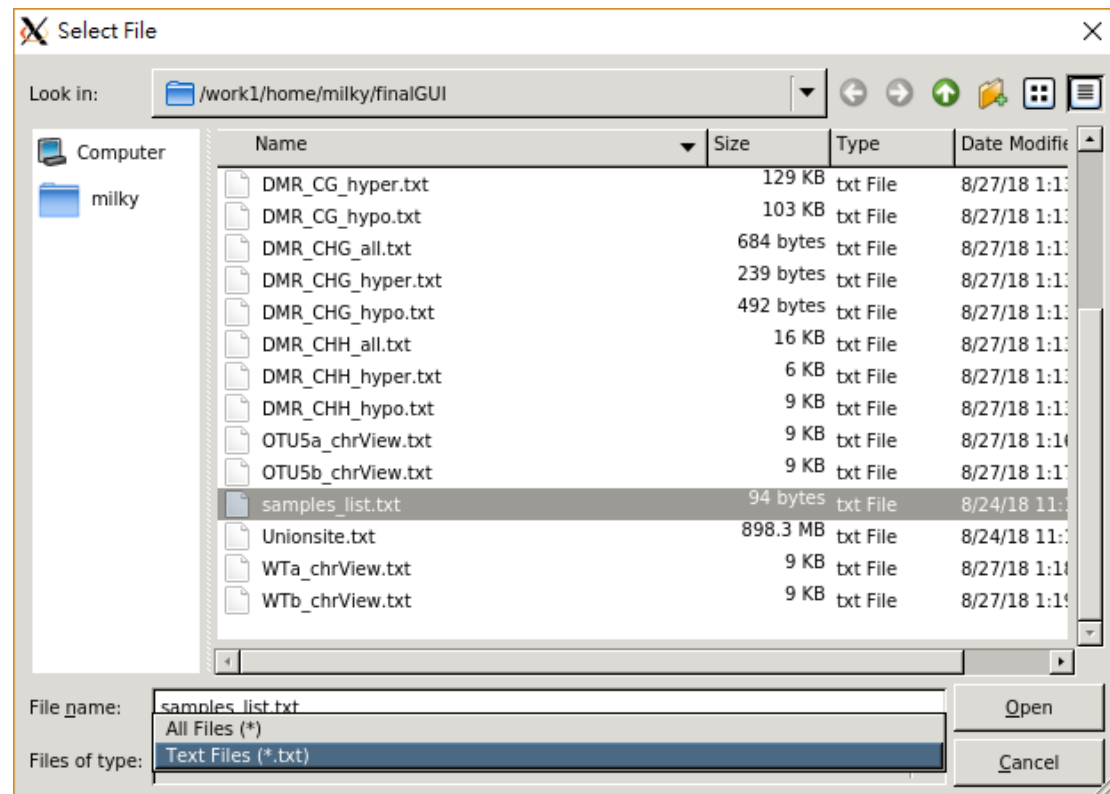
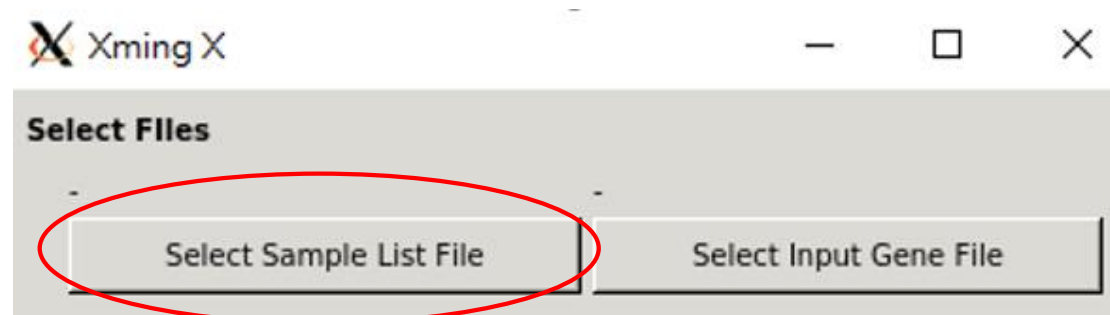
Choose Work Directory

Browser

Start Analysis

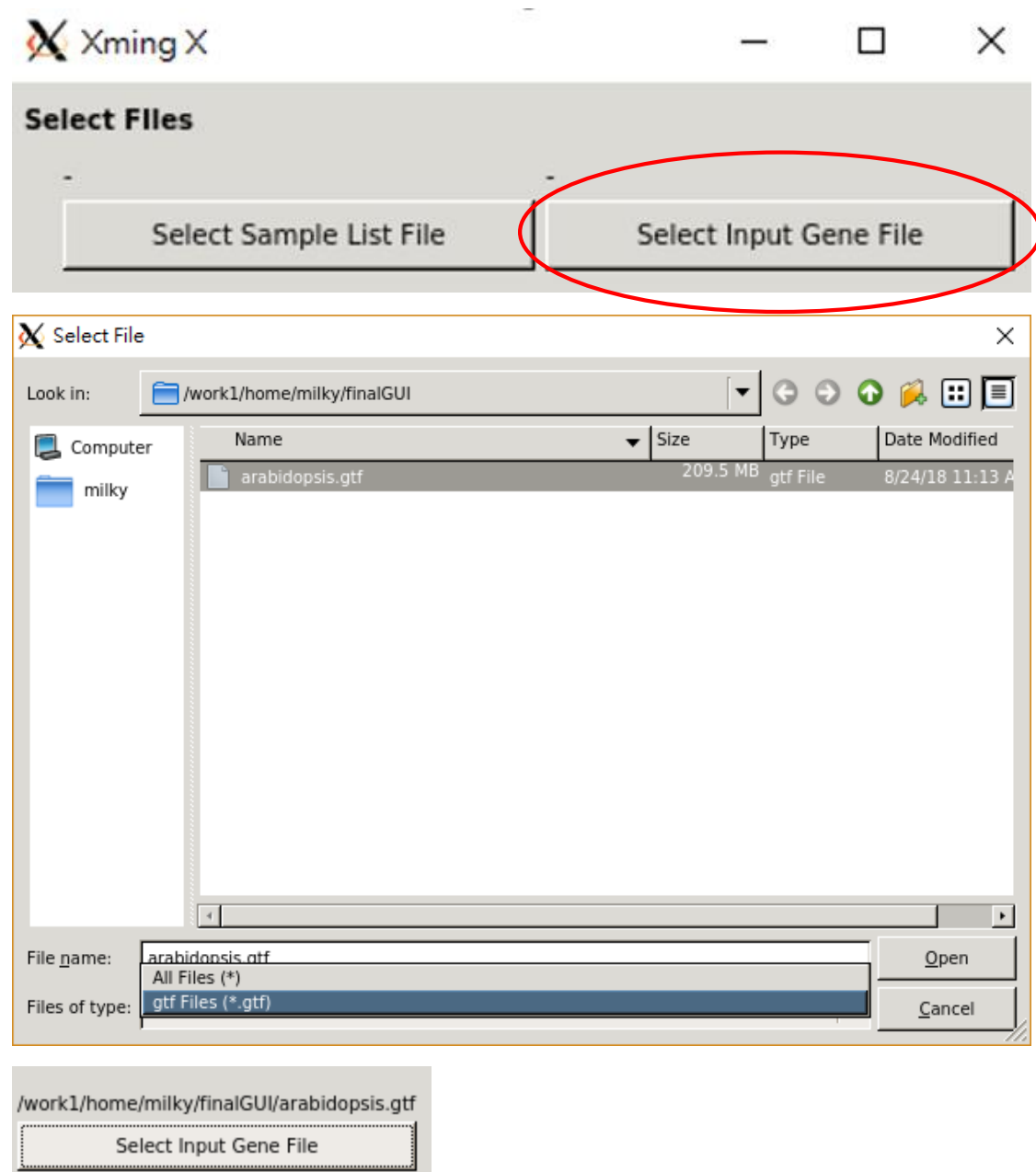
The overview of the tool's GUI

1st step : select sample list file



1. Push Select sample list file
2. Choose your sample list. You can use file filter to help you do this
3. When you selected sample list file, the label will change "-" to your sample list file path, and you can check it

2nd step : select input gene file

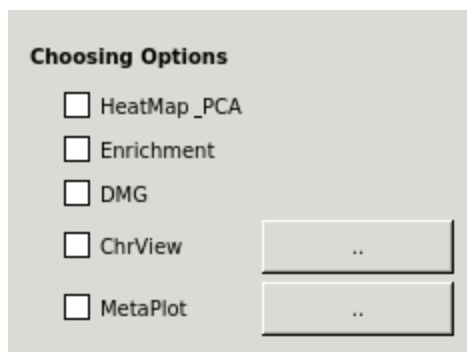


3rd step : setting parameters

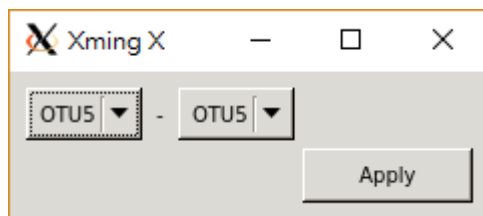
Setteing Parameters	
Min Depth Value	<input type="text" value="4"/>
Region Size	<input type="text" value="500"/>
Region Quaified Value	<input type="text" value="4"/>
DMR_CG_CutOffValue	<input type="text" value="0.2"/>
DMR_CHH_CutOffValue	<input type="text" value="0.2"/>
DMR_CHG_CutOffValue	<input type="text" value="0.2"/>
Heat_CutOffValue	<input type="text" value="0.2"/>
Bin Size	<input type="text" value="1000000"/>
Promotor Range	<input type="text" value="2000"/>

1. The default parameters is already set. You can modify it
2. If you confuse the mean of parameters, you can view the description document

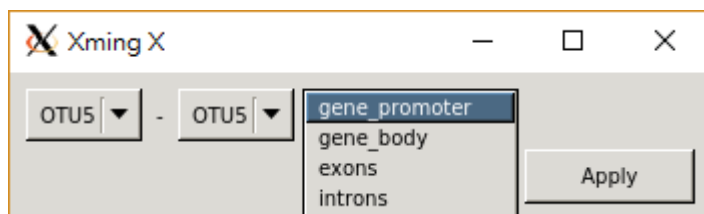
4th step : Choosing which tools you want to use



A dialog box titled "Choosing Options" with a light gray background. It contains five unchecked checkboxes: "HeatMap_PCA", "Enrichment", "DMG", "ChrView", and "MetaPlot". To the right of the "ChrView" and "MetaPlot" checkboxes are two rectangular buttons, each containing two dots " .. ".



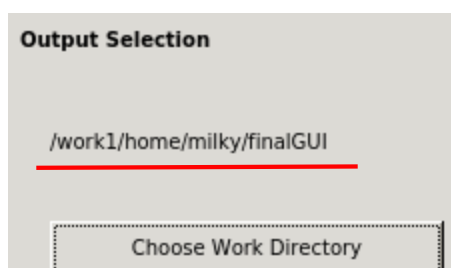
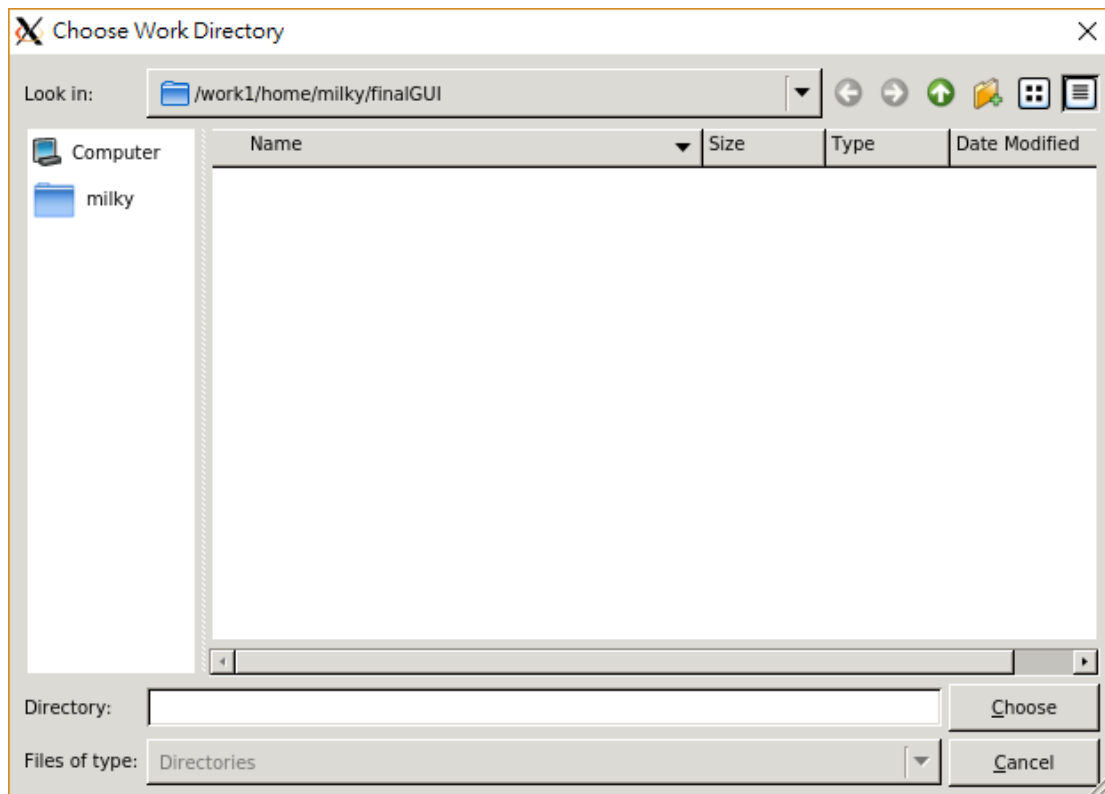
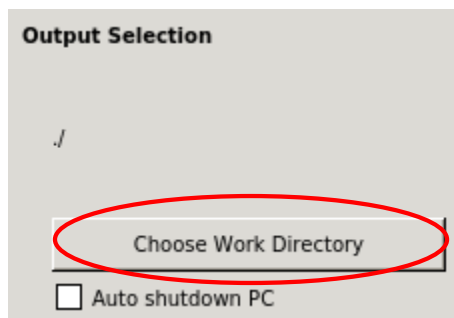
A window titled "Xming X" with standard window controls (minimize, maximize, close). It features two dropdown menus, both currently set to "OTU5", separated by a minus sign "-". Below these is an "Apply" button.



The same "Xming X" window as above, but with the second dropdown menu open. The menu is expanded to show four options: "gene_promoter" (highlighted in blue), "gene_body", "exons", and "introns". The "Apply" button remains visible to the right.

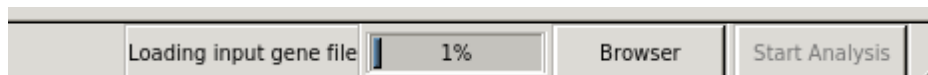
1. Check the box only
2. Chromosome view have a function that viewing the two group of samples mean methylation difference. So users who using this tool must set which group of samples mean minus which group of samples mean
3. Metaplot also have similar function. Other than this, metaplot also need user assign one genomic feature, so users can choose it through the combo box

5th step : setting output options



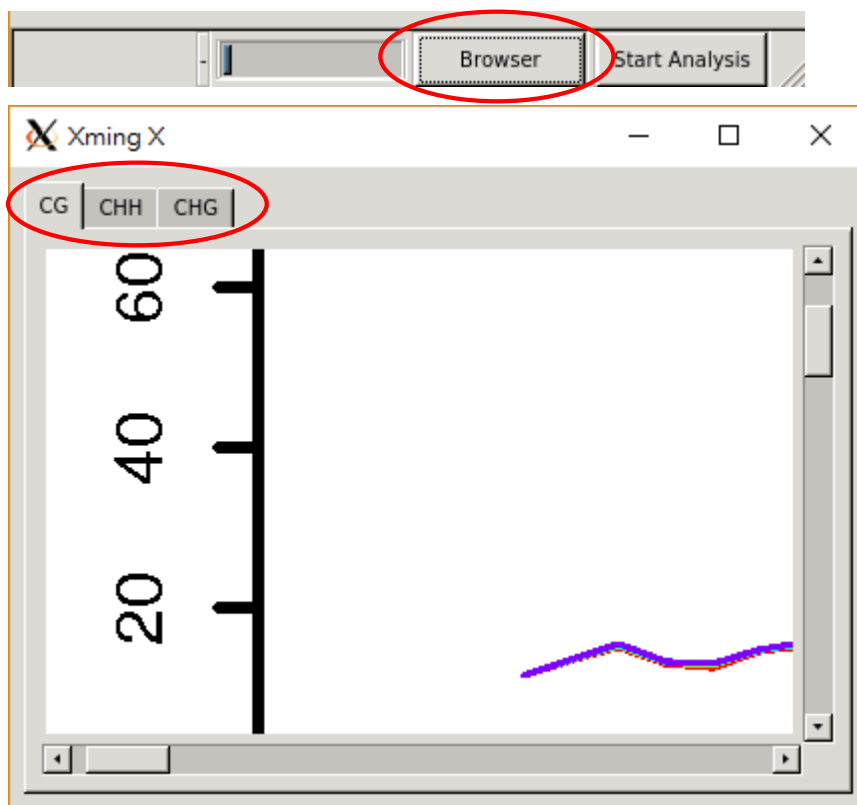
1. Setting the directory which you want output file save in it
2. After choosing directory, you can see this directory path on the label, and you can check it
3. If you want to sleep or do other things, you can choose the function auto shutdown PC, it will close your computer when analysis is complete. Using this function, you may check your permission first, if user have not enough permission, this function may not work

6th step : run it



1. When you start the analysis, there will show the instant progress at the bottom of window, so you can check the current progress in any time

7th step : View the analysis result



1. When analysis is done, you can use a simple browser to view the report (figure)
2. The browser classifies reports by methylation type, so you can switch it through the list button
3. At the same time, the report (output files) containing the non-figure report are totally saved in the directory which you set