

Figure 1 : “Main Window” – Provides the overview of the ForenPopStat and provides the two options, so the user can get started to analyze data by choosing “Analyse Data” or get help by choosing “Get Help?”

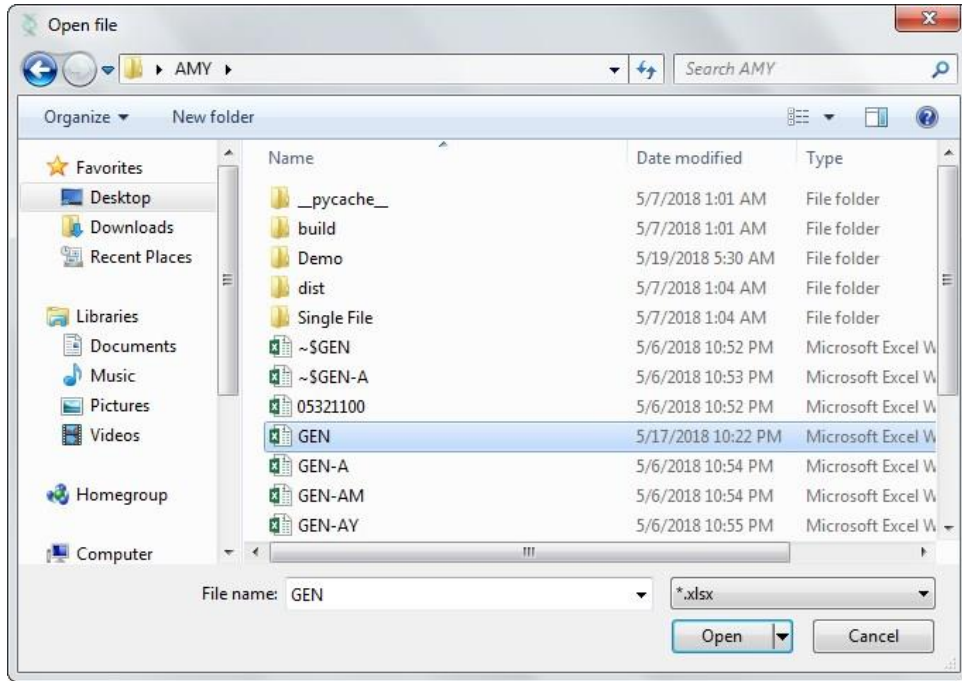


Figure 2 : This window prompts by choosing "Analyze Data" option for choosing the standard input file with ".xlsx" extension (Excel or Spreadsheet file)

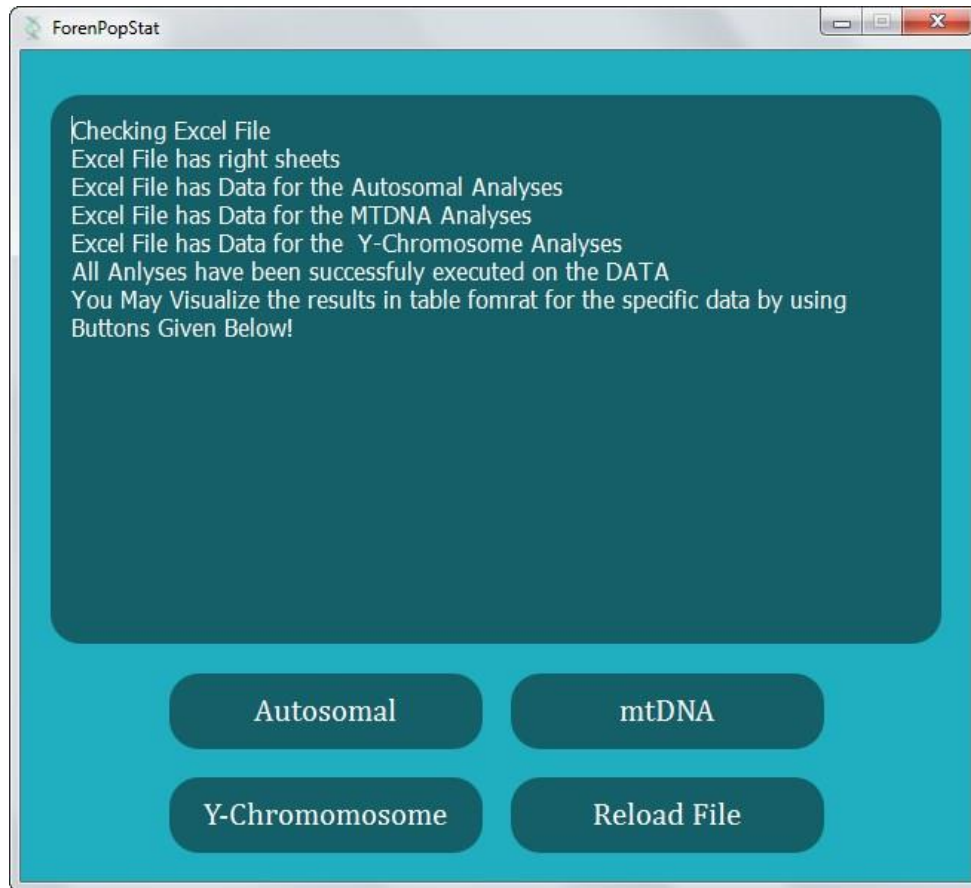


Figure 3 : This window shows the output of the calculation and if there is any error in the input file, it displays those errors. In the bottom, there are four buttons. "**Autosomal**" button leads to the table of autosomal parameters table. "**mtDNA**" button leads to the table of mtDNA parameters table. "**Y-Chromosome**" button leads to the table of Y-Chromosome parameters table. "**Reload File**" provides the opportunity to reselect the file to proceed to analyses.

	Autosomal Parameters	Values
1	Expected Homzygosity	0.3333333333333333
2	Observed Homzygosity	0.6666666666666666
3	Expected Heterozygosity	0.6666666666666667
4	Observed Heterozygosity	0.3333333333333337
5	Matching Probablility	0.18518518518518517
6	Paternity Index	0.75
7	Power of Discrimination	0.8148148148148149
8	Power of Exclusion	0.07818930041152265
9	Polymorphism Informative Conten...	0.5925925925925926

Save Back

Figure 4 : This table shows the results of the calculations of the expected and observed homo- and heterozygosity, Match Probability (PM), Power of Discrimination (PD) and Polymorphism Information Content (PIC) from the autosomal STR data as given in Table 2.

The screenshot shows a software window titled "ForenPopStat". Inside the window, there is a table with two columns: "mtDNA Parameters" and "Values". The table contains five rows of data. Below the table, there are two buttons: "Save" and "Back".

	mtDNA Parameters	Values
1	No. of Samples	14
2	No. of Haplotypes	14
3	Random Match Probability	0.07143142859999997
4	Discrimination Capacity	1.0
5	Haploype Diversity	0.9999969230461538

Figure 5: This window displays the results of calculation of a number of haplotypes, Random Match Probability (PM), Haplotype Diversity and Discriminating Power from mtNDA SNPs data as given in Table 5.

	Y-STRs Parameters	Values
1	No. of Samples	13
2	No. of Haplotypes	7
3	Random Match Probability	0.19526449710000002
4	Discrimination Capacity	0.5384615384615384
5	Haploype Diversity	0.8717967948083333

Save Back

Figure 6 : This window displays the results of calculation of a number of haplotypes, Random Match Probability (PM), Haplotype Diversity and Discriminating Power from Y-STRs data as given in Table 7