

# HOW TO FORMAT INPUT FILE

Input file is composed of several spreadsheets, one for each marker. Each spreadsheet is named after the marker, and formatted as follows:

- Topmost number of column A (A1) is the number of marker alleles. The rest of the column serves for identification purposes only.
- Columns B and C reflect population groups, and populations within each group, respectively.
- Column D contains the number of individuals of each population.
- Columns E onwards contain the name of each allele (heading) and its frequency in every population.
- Therefore, the total number of columns for each marker must be  $A1+4$ .



# HOW TO FORMAT PROFILE TO CLASSIFY

Marker information is separated by slashes, both alleles of each marker by commas. Uncalled alleles are represented by n or N.

For instance, in the first example file (51 populations within 7 groups), marker names are:

D1S1679, D2S427, D3S2406, D3S4545, D5S1457, D7S2201, D9S1118,  
D11S1304, D12S297, D14S1426, D15S822, D21S1432.

Therefore, a possible profile would be:

163,152/251,243/294,343/192,233/103,119/101,97/157,143/192,172/  
241,245/150,N/310,246/140,131.

# HOW TO PROCEED

- Input number of populations, input population spreadsheet document, and click on the "next step" button.
- You will then be presented with data tables for all markers. Have a attentive look at the information which has been read. If you agree with what you see, click on "next step" to input the profile to classify.
- Then click on "next step" to obtain classification, provided your profile is classifiable.