1. Preparation of data set in XML format

1) Click on link “SCHEME” on the main page and download the file ***data.xlsx***
2) Open the ***data.xlsx*** file and insert your data to particular columns

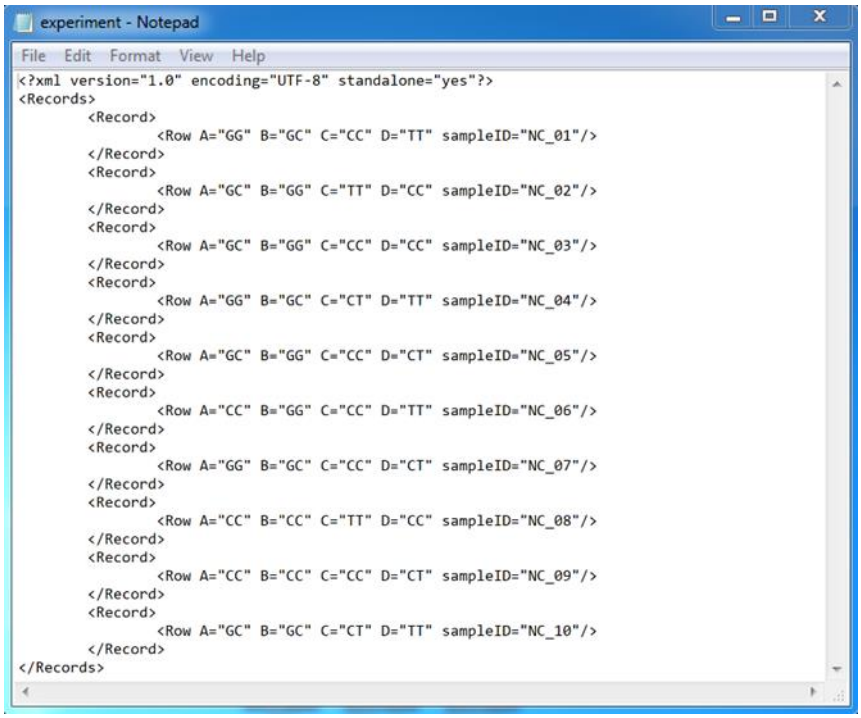
sampleID	SNP 1	SNP 2	SNP 3	SNP 4	SNP 5	SNP 6	SNP 7	SNP 8	SNP 9	SNP 10
NC_01	GG	GC	CC	TT						
NC_02	GC	GG	TT	CC						
NC_03	GC	GG	CC	CC						
NC_04	GG	GC	CT	TT						
NC_05	GC	GG	CC	CT						
NC_06	CC	GG	CC	TT						
NC_07	GG	GC	CC	CT						
NC_08	CC	CC	TT	CC						
NC_09	CC	CC	CC	CT						
NC_10	GC	GC	CT	TT						

1. Sample data set

The order of written alleles for particular SNP must be the same in all samples !!!

3) Open Developer tab. If you do not see the tab, then go to File –> Options –> Customize Ribbon –> Check Developer (for MS Office 365)
4) Click to Developer tab –> Export (in part “XML”) –> Your file name (e.g. *experiment*) –> Export (*experiment.xml* file will be created)

Content of the XML file can be viewed for example in the Notepad (right click on *experiment.xml* -> Open with -> Notepad)



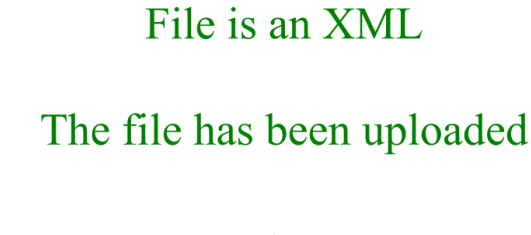
2. An XML file viewed in the Notepad

2. Calculation of haplogenotype combinations using the online application

1) Click Browse –> Choose your XML file (e.g. *experiment.xml*) –> Open –> U P L O A D

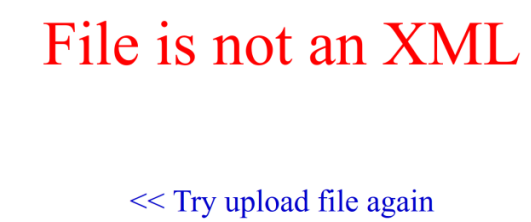
3. Choose the XML file

2) Check file format:
Green color means that uploaded **File is in XML format** = file has xml extension
–> Click Continue



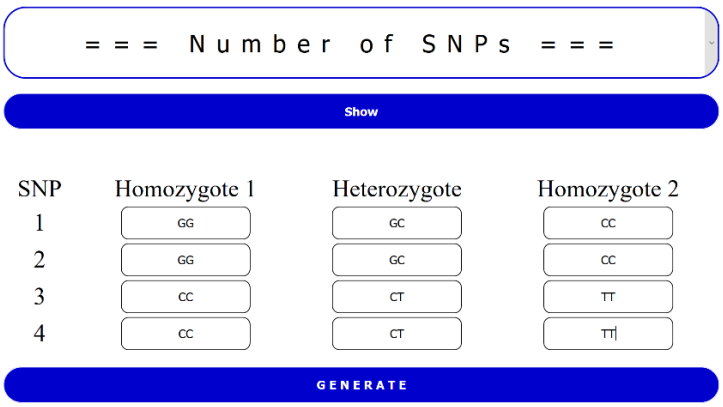
4. Uploaded file is in correct format

Red color means that uploaded **File is not in XML format** = file has not xml extension
–> Check the file and Try upload again



5: Uploaded file is in incorrect format

3) Choose the number of analyzed SNPs –> Show
4) Fill the empty boxes with particular genotypes (the same order of alleles as in the sample data set)
5) –> Click G E N E R A T E



6. Boxes filled with particular genotype combinations

6) After successful calculation click “Download your file”

3. Example of an output of the Haplogenotype Calculator

1) The *xlsx* file - number of sheets corresponds to the number of SNPs.
2) Numbers in columns mean haplogenotypes obtained by combination of SNPs written in the first cell
3) For example: All combinations for SNP 1 and SNP 2 (figure 6) -> GGGG=1, **GGGC=2**, GGCC=3, GCGG=4, GCGC=5, GCCC=6, CCGG=7, CCGC=8, CCCC=9
4) Sample "NC_01" has number 2 haplogenotype for combination of SNP1 with SNP2 -> **GGGC** **(can be compared with figure 1)**

	A	B	C	D	E	F	G
1	Sample ID	SNP 1+2	SNP 1+3	SNP 1+4	SNP 2+3	SNP 2+4	SNP 3+4
2	NC_01	2	1	3	4	6	3
3	NC_02	4	6	4	3	1	7
4	NC_03	4	4	4	1	1	1
5	NC_04	2	2	3	5	6	6
6	NC_05	4	4	5	1	2	2
7	NC_06	7	7	9	1	3	3
8	NC_07	2	1	2	4	5	2
9	NC_08	9	9	7	9	7	7
10	NC_09	9	7	8	7	8	2
11	NC_10	5	5	6	5	6	6

7: Sheet numbered "2" contains combinations of 2 SNPs

	A	B	C	D	E
1	Sample ID	SNP 1+2+3	SNP 1+2+4	SNP 1+3+4	SNP 2+3+4
2	NC_01	4	6	3	12
3	NC_02	12	10	16	7
4	NC_03	10	10	10	1
5	NC_04	5	6	6	15
6	NC_05	10	11	11	2
7	NC_06	19	21	21	3
8	NC_07	4	5	2	11
9	NC_08	27	25	25	25
10	NC_09	25	26	20	20
11	NC_10	14	15	15	15

8: Sheet numbered "3" contains combinations of 3 SNPs

	A	B
1	Sample ID	SNP 1+2+3+4
2	NC_01	12
3	NC_02	34
4	NC_03	28
5	NC_04	15
6	NC_05	29
7	NC_06	57
8	NC_07	11
9	NC_08	79
10	NC_09	74
11	NC_10	42

9. Sheet numbered "4" contains combinations of 4 SNPs