

Program Name: **cf_reh_exact**

Language: SAS/IML

Objective: Computation of exact confidence bounds to the relative excess heterozygosity (REH) exhibited by a SNP genotype distribution

Input:

X1	observed frequency of the homozygous genotype of the first kind
X2	" " " " " " " heterozygotes
X3	observed frequency of the homozygous genotype of the second kind
ALPHA	1 – confidence level
SW	width of search grid
TOL	tolerable difference between the actual and the target value of the function defining the confidence bound
ITMAX	maximum number of iteration steps

Output:

X1	see list of input parameters
X2	" " " " " " " " " "
X3	" " " " " " " " " "
ALPHA	" " " " " " " " " "
SW	" " " " " " " " " "
C_l_exact	lower confidence bound at exact one-sided confidence level 1 – ALPHA
C_r_exact	upper confidence bound " " " " " " " " " " " " " " " "