

*Program Name:* **cf\_reh\_midp**

*Language:* SAS/IML

*Objective:* Computation of mid-p-value – based confidence bounds to the relative excess heterozygosity (REH) exhibited by a SNP genotype

*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_midp	lower confidence bound at target level (one-sided) 1 – ALPHA
C_r_midp	upper confidence bound " " " " " " " " " "