

1.) `cd C:\Users\PIP_SNP_V1\Example_User_Manual`

2.) `PIP_SNP_V1.exe -u`

-u or -U: Output this help usage message

-g or -G: The full name of Genotype file

-l or -L: The full name of LD Bin Mapping Result file

-i or -I: The Individual number

-r or -R: The Threshold for the pairwise LD R2

-c or -C: the Correlation Method for a Pairwise Genotypic Markers, 0: Pearson_Correlation_R2; 1: LD_D_R2; Default(>2): Pearson_Correlation_R2

-d or -D: the Detection Method for a Marker Group(LD Block), 0: Right_Breakthrough; 1: Left_Breakthrough; 2: Left and Right Breakthrough; 3: Left or Right Breakthrough; Default(>3) : Right_Breakthrough

-k or -K: the K Nearest Neighbor individuals in The KNN method

-s or -S: the method how to generate the synthesized(binned) genotypic marker, 0: not to synthesize; 1: norm integration of the multiple markers' genotype values; 2: select the optimal one; Default(>2) : norm integration of the multiple markers' genotype values

-o or -O: the full name of Imputing results

3.) `PIP_SNP_V1.exe -g Raw_SNP_Data.txt -l ldmap.txt -o PIP_SNP.txt -i 278 -r 0.8 -c 0 -d 0 -k 10 -s 0`