1. cd C:\Users\PIP\_SNP\_V2\Example\_User\_Manual

2.) PIP\_SNP\_V2.exe -u

The usage of input parameter arguments are listed as followings:

-u or -U: Output this help usage message

-g or -G: The full name of Genotype file (Input)

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

-i or -I: The Individual number

-c or -C: the Correlation Method for a Pairwise Genotypic Markers, 0: Pearson\_Correlation\_R2; 1: LD\_D\_R2; Default(>=2): Pearson\_Correlation\_R2

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

-s or -S: the method how to generate the syntesized(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

-o or -O: the full name of Imputing results (Output)

3.) PIP\_SNP\_V2.exe –g Raw\_SNP\_Data.txt –l LD\_Bin\_Map.txt –o PIP\_SNP.txt -i 278 –c 0 –k 10 –s 2