**Using standalone executable for Linux**

After downloading the file FITS.tar.gz gunzip and untar the file as such

$ gunzip FITS.tar.gz

$ tar -xvf FITS.tar

Now include the FITS folder in your PATH

$ export PATH=path\_of\_FITS\_folder:$PATH

Now you can access commands of FITS from any folder.

For execution you have to pass filename of read-counts csv as a input file. Read-count csv file does not contain header and genomic location i.e. it consist of only data on which imputation is going to perform. Row represents sites and column represent samples/cells in csv file.

To get final imputed matrix, you run two phases1 of FITs using command

$ run\_FITSPhase1.sh input=unimputed.csv output=imputed.csv

It is not necessary to use any option, however for faster executation you could use option

maxLevel= 2

maxLevel can be between 2 to 6 but not less than 2, such as

$ run\_FITSPhase1.sh input=unimputed.csv maxLevel=2 output=imputed.csv

run phase1 of FITS many times, as such

$ run\_FITSPhase1.sh input=unimputed.csv output=imputed.csv

$run\_FITSPhase1.sh input=unimputed.csv output=imputed.csv

$run\_FITSPhase1.sh input=unimputed.csv output=imputed.csv

……………………..

$run\_FITSPhase1.sh input=unimputed.csv output=imputed.csv

after executing Phase-1 many times, run the phase-2 of FITs

$run\_FITSPhase2.sh input=unimputed.csv output=imputed.csv