# Read me

# Explanation of the output

You can find it in the output file Output.csv in the directory. Note that this csv file contains a host of useful information e.g.

* SampleID=sample identifier
* DNAmAge=DNA methylation age=predicted age.
* Comment=I only add a comment if a sample looks suspicious.
* noMissingPerSample=number of missing beta values per sample,
* meanMethBySample, minMethBySample=the mean and min beta value before normalization
* predictedGender=predicted gender based on the mean across the X chromosomal markers.
* meanXchromosome= mean beta value across the X chromosomal markers.