We have the human reference genome.

We align our sample using Bam tool which generate the sequence in bam format

The bam sequence is given as an input to samtools and it produces the index file in fasta format.

From the index file we will retrieve the coordinates of mitochondrial chromosome and then using the coordinates we will retrieve the mitochondrial chromosome sequence

To stimulate the data, we will enter the fa.gz file to ART tool and it will give the output in fastq format and alignment in aln fomrat