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 We use this protocol and it's working

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Calculation_and_Normalization_of_Relative_Gene_Abundance

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ABSTRACT

Calculate the relative abundance of gene for metagenome analysis.

- 1 Construction of the bwa index for the gene catalog (MGCA_gene_Catalog.fasta)

Command

Construction of bwa index for fasta sequences

```
bwa index ./MGCA_gene_Catalog.fasta
```

Software

bwa

NAME

- 2 Mapping the clean reads (abc.clean.read1.fq.gz, abc.clean.read2.fq.gz) of each sample to all sequences of the indexed gene catalog

Command

Mapping the reads to fasta files

```
bwa mem -t 20 ./MGCA_gene_Catalog.fasta ./abc.clean.read1.fq.gz 2>  
./abc.clean.read1.fq.gz.log | gzip -> ./abc.clean.read1.fq.gz.sam.gz
```

```
bwa mem -t 20 ./MGCA_gene_Catalog.fasta ./abc.clean.read2.fq.gz 2>  
./abc.clean.read2.fq.gz.log | gzip -> ./abc.clean.read2.fq.gz.sam.gz
```

3

Command

Calculation and normalization of relative gene abundance

```
perl ./bwa_mapping_stat.pl ./abc.clean.read1.fq.gz.sam.gz ./abc.clean.read2.fq.gz.sam.gz --  
out ./abc.clean.fq.gz.sam.gz 2> ./abc.clean.fq.gz.sam.gz.stat.log
```

Software

bwa_mapping_stat.pl

NAME

- 4 Selecting the first and last columns from the output file
(abc.clean.fq.gz.sam.gz..mapping.abundance), which representing the gene id and the
normalized relative abundance of the gene