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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.

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

Construction of bwa index

bwa index ./MGCA_gene_Catalog.fasta

Construction of bwa index for fasta sequences

bwa

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

Bwa mapping

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

Mapping the reads to fasta files

3

Stat of bwa mapping

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

Calculation and normalization of relative gene abundance

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bwa_mapping_stat.pl

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

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