

Manual for split_fastq_paired_reads.pl

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February 2012

Summary:

The program `split_fastq_paired_reads.pl` splits a fastq files with paired reads into two files containing first and second reads of each pair, respectively. Useful for downstream programs that need paired reads in separate files for first and second reads from each pair.

Usage: `split_fastq_paired_reads.pl file.fastq`

Read order in the input file:

pair1_read1
pair1_read2
pair2_read1
pair2_read2
...

Read order in the output files:

a) `file.fastq_read1.fastq`
pair1_read1
pair2_read1
...

b) `file.fastq_read2.fastq`
pair1_read2
pair2_read2
....

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