split_library_log_parser Documentation Release 1.0

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Contents

1	Why should I need this?	3
2	Usage	5
3	Dependencies	7

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Contents 1

2 Contents

Why should I need this?

When using QIIME, one of the first steps is the split_libraries_fastq.py script which performs demultiplexing of Fastq sequence data where barcodes and sequences are contained in two separate fastq files, while also doing some basic quality testing.

This step creates a log file, *split_library_log.txt*, which contains statistics about the number of reads per sample that passed the various tests and manipulations.

parse_split_library_log.R converts this text file into a tsv table, which is more convenient for comparison between the samples etc.

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CHAPTER 2

Usage

Simple! Just execute the following::

```
Rscript parse_split_library_log.R \
--input split_library_log.txt \
--output split_library_log.tsv
```

Where:

--input file Path to split_library_log.txt--output file Path to tab-delimited output file

6 Chapter 2. Usage

CHAPTER 3

Dependencies

Please make sure you have the following libraries installed in your R version:

- magrittr
- optparse
- tools