

# Package 'fraq'

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**Type** Package

**Title** A High-Throughput and Extensible Toolkit for Processing FASTQ Data

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**Description** High-throughput extensible toolkit for processing FASTQ data.  
The goal of this package is to empower users to quickly build out small programmatic 'kernels' to define any FASTQ processing task they may need. Builds on Intel TBB's flow graph to orchestrate concurrent I/O and data processing; throughput can be as fast as compression and disk speed allows. The package also ships with a suite of predefined kernels for common FASTQ tasks.

**License** GPL-3

**biocViews** Software, Infrastructure, Sequencing, DNaseSeq, QualityControl, Alignment

**URL** <https://github.com/traversc/fraq>

**BugReports** <https://github.com/traversc/fraq/issues>

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frac-package

*frac: fastq processing with TBB flow graphs*

---

## Description

frac is a high-throughput toolkit for FASTQ processing. It uses a TBB flow graph to coordinate concurrent I/O and compute, provides prebuilt kernels for common tasks, and lets you extend it by writing custom kernels.

## Details

See individual function help pages for details on each kernel. The README contains a short walkthrough with synthetic data.

## Author(s)

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## See Also

Useful links:

- <https://github.com/traversc/frac>
- Report bugs at <https://github.com/traversc/frac/issues>

---

frac\_align

*Align a query to a target*

---

## Description

Calculate distances between query sequences and a target under a chosen boundary model using Levenshtein or Hamming distance.

**Usage**

```
frac_align(
  query,
  target,
  max_distance = 2147483647L,
  ambiguity_base = "",
  boundary = "contains",
  distance_metric = "lv"
)
```

**Arguments**

query	Character vector or Biostrings XString/XStringSet of query sequences.
target	Character vector or Biostrings XString/XStringSet of target sequences.
max_distance	Integer maximum allowed distance; defaults to .Machine\$integer.max.
ambiguity_base	Single character to treat as ambiguity when matching, or empty string "" to disable; must be length 0 or 1.
boundary	One of "contains", "global", or "starts".
distance_metric	One of "lv" (Levenshtein) or "hm" (Hamming). "hm" requires query and target to be the same length.

**Value**

A data frame with the Biostrings inputs as the first two columns followed by the alignment metadata.

**Examples**

```
frac_align("ACGTNT", "ACGTAT", max_distance = 2L, ambiguity_base = "N",
           boundary = "contains", distance_metric = "lv")
frac_align(Biostrings::DNASTring("ACGT"), Biostrings::DNASTring("ACGA"),
           max_distance = 1L, boundary = "global", distance_metric = "hm")
```

---

frac\_chunk

*Chunk sequencing files into fixed-size batches*


---

**Description**

Split input datasets into sequential chunks. Each chunk is written using output\_prefix suffixed with \_chunk{N} and the format indicated by output\_suffix.

**Usage**

```
frac_chunk(input, output_prefix, output_suffix, chunk_size, nthreads = 1L)
```

**Arguments**

input	Character vector of source files/keys.
output_prefix	Character vector of prefixes used when naming chunked outputs. Must be the same length as input.
output_suffix	Character scalar describing the output format; use "fastq", "frac", "mem", "gz", "zst".
chunk_size	Numeric chunk size in reads; each output chunk contains up to this many records (per input stream).
nthreads	Integer number of worker threads.

**Details**

The suffix mapping follows:

- "fastq" -> .fastq
- "gz" -> .fastq.gz
- "zst" -> .fastq.zst
- "frac" -> .frac
- "mem" -> .mem

**Value**

Invisibly returns NULL after writing all chunked outputs.

**Examples**

```
r1 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 25, read_length = 75)
frac_chunk(r1,
           output_prefix = tempfile("chunked_R1"),
           output_suffix = "fastq",
           chunk_size = 10,
           nthreads = 1L)
```

---

frac\_concat

*Concatenate sequencing files*

---

**Description**

Concatenate one or more FRAQ/FASTQ inputs (plain, .gz, .zst, .frac, or .mem) into a single output file.

**Usage**

```
frac_concat(input, output, nthreads = 1L)
```

**Arguments**

input	Character vector of input paths/keys to concatenate. Mixed formats are supported.
output	Character scalar giving the destination path (or .mem key).
nthreads	Integer number of threads for reading, compression, and writing.

**Value**

Invisibly returns NULL after writing the concatenated output.

**Examples**

```
tmp_dir <- tempdir()
inputs <- file.path(tmp_dir, sprintf("reads_%d.fastq", 1:2))
lapply(inputs, generate_random_fastq, n_reads = 10, read_length = 50)
out <- file.path(tmp_dir, "all_reads.fastq.gz")
frac_concat(inputs, out, nthreads = 1L)
```

---

frac\_convert

---

*Convert sequencing files between supported formats*


---

**Description**

Re-encode sequencing files in any supported FRAQ/FASTQ format. Input and output vectors must be the same length.

**Usage**

```
frac_convert(input, output, nthreads = 1L)
```

**Arguments**

input	Character vector of source files/keys.
output	Character vector of destination files/keys, same length as input.
nthreads	Integer number of threads for reading/writing.

**Details**

FIFO pipes (paths ending with `.fifo`) are only available on Unix-like systems; on Windows they are not supported and will trigger an error.

**Value**

Invisibly returns NULL after writing the converted outputs.

## Examples

```
src <- tempfile(fileext = ".fastq")
generate_random_fastq(src, n_reads = 10, read_length = 50)
dest <- tempfile(fileext = ".fastq.gz")
fracount_barcode(src, dest, nthreads = 1L)
```

---

fracount\_barcode     *Count barcodes in FASTQ file(s)*

---

## Description

Count occurrences of provided short barcodes in reads, allowing up to `max_distance` mismatches. Accepts one or more FASTQ files (e.g., R1/R2).

## Usage

```
fracount_barcode(  
  input,  
  barcodes,  
  max_distance = 1L,  
  allow_revcomp = FALSE,  
  nthreads = 1L  
)
```

## Arguments

<code>input</code>	Character vector of one or more input FASTQ file paths (e.g., R1 and R2).
<code>barcodes</code>	Character vector of barcode sequences to count.
<code>max_distance</code>	Integer maximum number of mismatches allowed for a match.
<code>allow_revcomp</code>	Logical; if TRUE, also match reverse complements.
<code>nthreads</code>	Integer number of threads.

## Value

A data frame with counts per barcode.

## Examples

```
r1 <- tempfile(fileext = ".fastq")
r2 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 1000, read_length = 100,
  name_prefix = "read_R1_")
generate_random_fastq(r2, n_reads = 1000, read_length = 100,
  name_prefix = "read_R2_")
short_barcodes <- c("ACGT", "TGCA", "GTAC")
counts <- fracount_barcode(c(r1, r2), short_barcodes, max_distance = 1L,
  allow_revcomp = FALSE, nthreads = 1L)
counts
```

---

`frac_demux`*Demultiplex FASTQ file(s) by barcode prefix*

---

## Description

Write barcode-specific outputs by matching a prefix on the first read of each record. Each output path is formed by substituting {barcode} in the supplied format string.

## Usage

```
frac_demux(input, output_format, barcodes, max_distance = 1L, nthreads = 1L)
```

## Arguments

<code>input</code>	Character vector of one or more input FASTQ file paths (e.g., R1 and R2).
<code>output_format</code>	Character vector of format strings, same length as <code>input</code> . Each string must contain the literal {barcode} placeholder.
<code>barcodes</code>	Character vector of barcode sequences to test as prefixes.
<code>max_distance</code>	Integer maximum Hamming distance allowed between barcode and read prefix.
<code>nthreads</code>	Integer number of threads.

## Details

When no barcode matches, the literal NO\_MATCH is substituted in place of {barcode}. If multiple barcodes match the same read, MULTI\_MATCH is used.

## Value

Invisibly, NULL. Files are written to disk according to `output_format`.

## Examples

```
r1 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 1000, read_length = 100,
  name_prefix = "read_R1_")
out <- tempfile("R1_", fileext = "_{barcode}.fastq")
barcodes <- c("ACGT", "TGCA", "GTAC")
frac_demux(r1, out, barcodes, max_distance = 1L, nthreads = 1L)
```

---

frac_downsample	<i>Downsample FASTQ file(s)</i>
-----------------	---------------------------------

---

## Description

Write deterministically downsampled FASTQ file(s) to disk. input and output must be vectors of the same length (e.g., R1/R2 pairs).

## Usage

```
frac_downsample(input, output, amount, nthreads = 1L)
```

## Arguments

input	Character vector of one or more input FASTQ file paths. Vectors must be the same length as output (e.g., R1 and R2 pairs).
output	Character vector of output FASTQ file paths, same length as input.
amount	Numeric scalar in (0, 1); proportion of reads to retain.
nthreads	Integer number of threads.

## Details

Downsampling is deterministic: given the same inputs, `frac_downsample()` keeps the same records every run while matching the requested proportion as closely as possible.

## Value

Invisibly returns NULL after writing the downsampled outputs.

## Examples

```
r1 <- tempfile(fileext = ".fastq")
r2 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 1000, read_length = 100,
  name_prefix = "read_R1_")
generate_random_fastq(r2, n_reads = 1000, read_length = 100,
  name_prefix = "read_R2_")
out <- c(tempfile(fileext = ".fastq"), tempfile(fileext = ".fastq"))
frac_downsample(c(r1, r2), out, amount = 0.1)
```

---

frac\_fifo\_supported     *Detect FRAQ FIFO support*

---

### Description

Report whether the current build of **frac** was compiled with named pipe (FIFO) support. FIFO outputs (paths ending in `.fifo`) are only available on Unix-like platforms where the build detected `S_IFIFO`.

### Usage

```
frac_fifo_supported()
```

### Details

The result is determined at compile time; reinstalling the package on an operating system that exposes FIFOs is required to enable support.

### Value

Logical scalar indicating whether FIFO inputs/outputs are supported.

### Examples

```
if (frac_fifo_supported()) {  
  message("FIFO streams are available on this platform.")  
} else {  
  message("Use regular files instead of .fifo paths on this build.")  
}
```

---

frac\_mem\_list     *Manage in-memory FASTQ datasets*

---

### Description

`frac_mem_list()` summarizes the `.mem` datasets currently stored in the session. `frac_mem_remove()` deletes one or more `.mem` entries, freeing the associated memory. `frac_mem_load()` is a convenience wrapper around `frac_convert()` that loads on-disk FASTQ/FRAQ inputs into the in-memory store after validating that the outputs end with `.mem`.

The in-memory store lives in the current R session. For consistent results, call the helper functions when no other `frac` jobs are actively writing to the same `.mem` keys.

**Usage**

```
frac_mem_list()

frac_mem_remove(mem_key)

frac_mem_load(input, mem_key, nthreads = 1L)
```

**Arguments**

mem\_key            Character vector of .mem keys to remove.  
input              Character vector of FASTQ/FRAQ paths to load into memory.  
nthreads           Positive integer parallelism for the load.

**Value**

- frac\_mem\_list() returns a data frame with columns mem\_key and n\_reads.
- frac\_mem\_remove() returns a logical vector indicating which keys were removed.
- frac\_mem\_load() returns the target .mem keys invisibly.

**Examples**

```
tmp <- tempfile(fileext = ".fastq")
generate_random_fastq(tmp, n_reads = 100, read_length = 75)
mem_path <- tempfile(fileext = ".mem")
frac_mem_load(tmp, mem_path)
frac_mem_list()
frac_mem_remove(mem_path)
```

---

frac_merge_pairs	<i>Merge paired-end reads into a consensus</i>
------------------	--

---

**Description**

Merge R1/R2 pairs by overlapping sequences (optionally reverse-complementing R2), emitting merged reads and optional unmerged outputs.

**Usage**

```
frac_merge_pairs(
  input,
  output_merged,
  output_unmerged = NULL,
  min_overlap = 12L,
  max_mismatch_rate = 0.1,
  consensus_mode = c("max", "mean", "r1", "r2"),
  trim_overhang = TRUE,
```

```

    revcomp_R2 = TRUE,
    nthreads = 1L
)

```

### Arguments

`input` Character vector of length 2 with input FASTQ paths (R1, R2).

`output_merged` Character scalar path/key receiving merged single-end reads.

`output_unmerged` Optional character vector of length 2 for unmerged R1/R2 outputs. Use NULL to drop unmerged pairs.

`min_overlap` Integer minimum overlap required to attempt merging.

`max_mismatch_rate` Numeric maximum mismatch fraction allowed within the overlap.

`consensus_mode` Character string controlling consensus base selection: "max", "mean", "r1", or "r2".

`trim_overhang` Logical; if TRUE, include non-overlapping tails when constructing the merged read.

`revcomp_R2` Logical; if TRUE, reverse-complement R2 before merging.

`nthreads` Integer number of worker threads.

### Details

Qualities are interpreted as PHRED+33.

### Value

A list summarising merge statistics (`merged_reads`, `unmerged_reads`, `mean_insert_size`, etc.).

### Examples

```

r1 <- tempfile(fileext = ".fastq")
r2 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 100, read_length = 100,
  name_prefix = "read_R1_")
generate_random_fastq(r2, n_reads = 100, read_length = 100,
  name_prefix = "read_R2_")
out_merged <- tempfile(fileext = ".fastq")
frac_merge_pairs(c(r1, r2), out_merged, output_unmerged = NULL,
  min_overlap = 20L, max_mismatch_rate = 0.05)

```

frac\_options                      *Get or set FRAQ options*

**Description**

Get or set FRAQ options.

**Usage**

```
frac_options(option, value = NULL)
```

**Arguments**

option	Character string name of the option. Valid options are: "blocksize", "frac_compress_level", "zstd_compress_level", "gzip_compress_level".
value	Optional value to set the option to; if NULL, the current value is returned.

**Value**

The current option value (if input value is NULL) or previous option value.

**Examples**

```
# Get current blocksize
frac_options("blocksize")
# # Set blocksize to 16384
frac_options("blocksize", 16384)
```

frac\_quality\_filter              *Filter reads by whole-read quality*

**Description**

Drop read sets when any mate fails the quality thresholds. Qualities are interpreted as PHRED+33.

**Usage**

```
frac_quality_filter(
  input,
  output,
  min_mean_quality = 20,
  max_low_q_bases = .Machine$integer.max,
  low_q_threshold = 20L,
  nthreads = 1L
)
```

**Arguments**

input	Character vector of one or more input FASTQ file paths. Must be the same length as output.
output	Character vector of output FASTQ paths.
min_mean_quality	Numeric minimum mean base quality required for each mate.
max_low_q_bases	Integer maximum number of bases below low_q_threshold allowed per mate.
low_q_threshold	Integer PHRED cutoff used to count low-quality bases.
nthreads	Integer number of worker threads.

**Details**

Both thresholds are evaluated separately on every mate. If any mate fails, the entire read set is discarded.

**Value**

Invisibly, NULL. Reads are written to output paths for records that pass the filters.

**Examples**

```
r1 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 1000, read_length = 100,
  name_prefix = "read_R1_")
out <- tempfile(fileext = ".fastq")
frac_quality_filter(r1, out, min_mean_quality = 25, max_low_q_bases = 2L,
  low_q_threshold = 20L, nthreads = 1L)
```

---

frac\_rcpp\_template      *Generate an example frac Rcpp script*

---

**Description**

Writes a minimal Rcpp example file showing how to write custom kernels via Rcpp.

**Usage**

```
frac_rcpp_template(output_file)
```

**Arguments**

output_file	Character path where the C++ source file will be written.
-------------	---

**Value**

NULL invisibly.

**Examples**

```
cpp <- tempfile(fileext = ".cpp")
frac_rcpp_template(cpp)
# Rcpp::sourceCpp(cpp) # optionally compile the example
```

---

frac\_shortread                      *Bridge FRAQ formats with ShortReadQ*

---

**Description**

frac\_export\_shortreadq() converts FRAQ/FASTQ inputs into in-memory ShortReadQ objects via frac\_convert. frac\_import\_shortreadq converts ShortReadQ objects to any supported FRAQ format.

**Usage**

```
frac_export_shortreadq(input, nthreads = 1L, tmpdir = tmpdir())

frac_import_shortreadq(shortreadq, output, nthreads = 1L, tmpdir = tmpdir())
```

**Arguments**

input	Character vector of input paths/keys accepted by <a href="#">frac_convert()</a> .
nthreads	Positive integer passed to frac_convert.
tmpdir	Directory used for staging temporary files.
shortreadq	A ShortReadQ or list of ShortReadQ objects to be written via FRAQ encoders.
output	Character vector of destination paths/keys, same length as shortreadq.

**Value**

- frac\_export\_shortreadq() returns a single ShortReadQ when input has length 1, otherwise a list of ShortReadQ objects.
- frac\_import\_shortreadq() invisibly returns the normalized output vector after conversion.

**See Also**

[ShortRead::readFastq\(\)](#), [ShortRead::writeFastq\(\)](#), [frac\\_convert\(\)](#)

**Examples**

```
fq <- tempfile(fileext = ".fastq")
generate_random_fastq(fq, n_reads = 10, read_length = 50)
frac_path <- tempfile(fileext = ".frac")
frac_convert(fq, frac_path)

reads <- frac_export_shortreadq(frac_path)
roundtrip_fastq <- tempfile(fileext = ".fastq")
frac_import_shortreadq(reads, roundtrip_fastq)
stopifnot(file.exists(roundtrip_fastq))
```

frac\_slice

*Slice reads by index or limit***Description**

Write a subset of reads from input to output, either the first `limit` reads or specific zero-based indices in `select`.

**Usage**

```
frac_slice(input, output, limit = NULL, select = NULL, nthreads = 1L)
```

**Arguments**

<code>input</code>	Character vector of source files/keys.
<code>output</code>	Character vector of destination files/keys, same length as <code>input</code> .
<code>limit</code>	Numeric scalar; keep the first <code>limit</code> reads (per record index). Defaults to <code>NULL</code> .
<code>select</code>	Numeric vector of zero-based indices to keep. Defaults to <code>NULL</code> .
<code>nthreads</code>	Integer number of threads for reading/writing.

**Details**

Exactly one of `limit` or `select` must be supplied.

**Value**

Invisibly returns `NULL` after writing the selected reads.

**Examples**

```
src <- tempfile(fileext = ".fastq")
generate_random_fastq(src, n_reads = 10, read_length = 50)
dest <- tempfile(fileext = ".fastq")
frac_slice(src, dest, limit = 5)
```

---

frac_summary	<i>Summarize FASTQ quality metrics (single- or paired-end)</i>
--------------	--

---

### Description

Compute QC summaries for single- or paired-end FASTQ files. When two inputs are provided, R1 and R2 are summarized separately and an insert-size histogram is reported (estimated from R1 vs reverse-complemented R2 overlap).

### Usage

```
frac_summary(
  input,
  phred33 = TRUE,
  min_overlap = 12L,
  max_mismatch_rate = 0.1,
  limit = 0L,
  nthreads = 1L
)
```

### Arguments

input	Character vector of length 1 or 2 with input FASTQ paths. Length 1 = single-end; length 2 = paired-end (first element maps to R1, second to R2).
phred33	Logical; TRUE if qualities are PHRED+33, FALSE for PHRED+64.
min_overlap	Integer minimum overlap used for insert-size estimation (paired-end only).
max_mismatch_rate	Numeric between 0 and 1 (inclusive); maximum allowed mismatch rate within the overlapped region (paired-end only).
limit	Numeric cap on the number of read sets to process. Use 0 to process all available reads.
nthreads	Integer number of threads.

### Details

Outputs per-mate tables:

- `basic_stats_R{1,2}`: total sequences, total bases, min/mean/max length, GC percent.
- `per_base_quality_R{1,2}`: mean PHRED by 1-based position (with counts).
- `per_base_content_R{1,2}`: long format base usage by position (A/C/G/T/N/other).
- `length_distribution_R{1,2}`: histogram of sequence lengths.
- `avg_read_quality_R{1,2}`: histogram of rounded per-read average quality (columns avg\_quality, count).

For paired-end inputs, `insert_size` is included when overlaps are found.

**Value**

A named list of data frames. For single-end: R1-only tables. For paired-end: R1/R2 tables plus optional insert\_size. Each mate includes basic\_stats, per-base quality/content, length distributions, and average read quality histograms.

**Examples**

```
# Single-end example
r1 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 1000, read_length = 100,
  name_prefix = "read_R1_")
res_se <- frac_summary(r1, nthreads = 1L)
res_se$basic_stats_R1

# Paired-end example
r1 <- tempfile(fileext = ".fastq"); r2 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 1000, read_length = 100,
  name_prefix = "read_R1_")
generate_random_fastq(r2, n_reads = 1000, read_length = 100,
  name_prefix = "read_R2_")
res_pe <- frac_summary(c(r1, r2), nthreads = 1L)
res_pe$basic_stats_R1
# dplyr example using pipes
# library(dplyr)
# res_pe$insert_size %>% arrange(desc(count)) %>% head()
```

---

frac\_trim\_adapters      *Trim adapters from FASTQ file(s)*

---

**Description**

Trim occurrences of adapter sequence(s) at the start of the first fastq input. input and output must be vectors of the same length (e.g., R1/R2 pairs). Adapters will be trimmed only for the first fastq, but all inputs will be filtered if filter\_untrimmed is TRUE.

**Usage**

```
frac_trim_adapters(
  input,
  output,
  adapters,
  max_distance = 1L,
  filter_untrimmed = TRUE,
  nthreads = 1L
)
```

**Arguments**

input	Character vector of one or more input FASTQ file paths. Vectors must be the same length as output (e.g., R1 and R2 pairs).
output	Character vector of output FASTQ file paths, same length as input.
adapters	Character vector of adapter sequences to trim. Adapters are given priority based on the order they appear.
max_distance	Integer maximum number of mismatches for adapter matching.
filter_untrimmed	Logical; if TRUE, drop reads with no trim.
nthreads	Integer number of threads.

**Value**

A data frame of counts of trimmed adapters.

**Examples**

```
r1 <- tempfile(fileext = ".fastq")
r2 <- tempfile(fileext = ".fastq")
generate_random_fastq(r1, n_reads = 1000, read_length = 100,
  name_prefix = "read_R1_")
generate_random_fastq(r2, n_reads = 1000, read_length = 100,
  name_prefix = "read_R2_")
out <- c(tempfile(fileext = ".fastq"), tempfile(fileext = ".fastq"))
adapters <- c("ACGT", "TGCA", "GTAC")
frac_trim_adapters(c(r1, r2), out, adapters, max_distance = 1L,
  filter_untrimmed = TRUE, nthreads = 1L)
```

---

generate\_random\_fastq *Generate a random FASTQ file (optionally gzipped)*

---

**Description**

Creates a synthetic FASTQ file with random DNA sequences and Illumina-like Phred+33 quality strings (high early-cycle quality with a gentle tail drop). If output\_file ends with .gz, the file is written gzip-compressed via a connection.

**Usage**

```
generate_random_fastq(
  output_file,
  n_reads = 1e+05,
  read_length = 100,
  name_prefix = "read_"
)
```

**Arguments**

output_file	Character vector of length 1 (single-end) or 2 (paired-end) outputs. .gz suffixes create gzip-compressed files; otherwise plain-text FASTQ is written.
n_reads	Integer number of reads to generate. Default 1e5.
read_length	Integer read length (number of bases per read). Default 100.
name_prefix	Character prefix for read names. Default "read_".

**Details**

Each read comprises four lines: header, sequence, +, and quality. Headers are generated as @<name\_prefix><index>. Sequences are sampled uniformly from ACGT. Qualities follow a tapered profile that starts near Q37 and falls toward the low 30s, with occasional low-quality spikes to mimic typical Illumina output.

**Value**

Invisibly returns the path(s) written in output\_file.

**Examples**

```
# Example: small test files
tmp_fastq <- tempfile(fileext = ".fastq")
tmp_fastq_gz <- tempfile(fileext = ".fastq.gz")

# Create plain FASTQ (500 reads, length 100)
generate_random_fastq(tmp_fastq, n_reads = 500, read_length = 100)

# Create gzipped FASTQ (500 reads, length 100)
generate_random_fastq(tmp_fastq_gz, n_reads = 500, read_length = 100)

# Paired-end example with overlapping mates
generate_random_fastq(c(tmp_fastq, tmp_fastq_gz),
                      n_reads = 100,
                      read_length = 150)
```

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