

# Package ‘Rbec’

November 29, 2024

**Type** Package

**Title** Rbec: a tool for analysis of amplicon sequencing data from synthetic microbial communities

**Version** 1.14.0

**Description** Rbec is a adapted version of DADA2 for analyzing amplicon sequencing data from synthetic communities (SynComs), where the reference sequences for each strain exists. Rbec can not only accurately profile the microbial compositions in SynComs, but also predict the contaminants in SynCom samples.

**License** LGPL-3

**Imports** Rcpp (>= 1.0.6), dada2, ggplot2, readr, doParallel, foreach, grDevices, stats, utils

**LinkingTo** Rcpp

**RoxygenNote** 7.1.1

**biocViews** Sequencing, MicrobialStrain, Microbiome

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

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Contam\_detect

*Reference-based error correction of amplicon sequencing data*

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### Description

This function is designed for predicting the contaminated samples

### Usage

```
Contam_detect(log_file, outdir, outlier_constant=1.5)
```

### Arguments

log_file	the file contains a list of log files of each sample outputted with Rbec function
outdir	output directory
outlier_constant	the multiplier of variance to define the outlier

### Details

Ruben Garrido-Oter's group, Plant-Microbe interaction, Max Planck Institute for Plant Breeding Research

### Value

Returns a plot showing the distribution of percentage of corrected reads across the whole sample set and a summary file recording which samples might be contaminated

### Author(s)

Pengfan Zhang

### Examples

```
#log_file <- system.file("extdata", "rbec_test.list", package = "Rbec")
log_path <- list.files(paste(path.package("Rbec"),
  "extdata/contamination_test", sep="/"),
  recursive=TRUE, full.names=TRUE)
log_file <- tempfile()
writeLines(log_path, log_file)
Contam_detect(log_file, tempdir())
```

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Rbec

*Reference-based error correction of amplicon sequencing data*


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## Description

This function corrects the amplicon sequencing data from synthetic communities where the reference sequences are known a priori

## Usage

```
Rbec(fastq, reference, outdir, threads=1, sampling_size=5000, ascii=33, min_cont_obs_abd=200, min_
```

## Arguments

fastq	the path of the fastq file containing merged amplicon sequencing reads (Ns are not allowed in the reads)
reference	the path of the unique reference sequences, each sequence must be in one line (Ns are not allowed in the sequences)
outdir	the output directory, which should be created by the user
threads	the number of threads used, default 1
sampling_size	the sampling size for calculating the error matrix, default 5000
ascii	ascii characters used to encode phred scores (33 or 64), default 33
min_cont_obs_abd	the minimum observed abundance of unique tags for detecting contamination sequences, default 200
min_cont_abd	the relative abundance of unique tags for detecting contamination sequences that can't be corrected by any of the references, default 0.03
min_E	the minimum expectation of the Poisson distribution for the identification of paralogues, default 0.05
min_P	the minimum P value threshold of the Poisson distribution to correct a read, default 1e-40
ref_seeker	the method for finding the candidate error-producing reference sequence for a tag showing identical lowest K-mer distance to multiple references. 1 for the abundance-based method; 2 for the transition probability-based method, default 1.
cn	the copy number table documenting the copy number of the marker gene in each strain. Rbec will normalize the strain abundance if the copy number is available

## Details

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**Value**

lambda\_final.out the lambda value and pvalue of the Poisson distribution for each read  
error\_matrix\_final.out the error matrix in the final iteration  
strain\_table.txt the strain composition of the sample  
strain\_table\_normalized.txt the copy-number-normalized strain composition of the sample if the copy number table is provided  
contamination\_seq.fna the potential sequences generated by contaminants  
rbec.log percentage of corrected reads, which can be used to predict contaminated samples  
paralogue\_seq.fna paralogue sequences found in each strain except for the reference provided

**Author(s)**

Pengfan Zhang

**Examples**

```
fastq <- system.file("extdata", "test_raw_merged_reads.fastq.gz", package = "Rbec")  
ref <- system.file("extdata", "test_ref.fasta", package = "Rbec")  
Rbec(fastq=fastq, reference=ref, outdir=tempdir(), threads=1, sampling_size=500, ascii=33)
```

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