Package: bulkdeconv (via r-universe)

November 16, 2026

Type Package

Title Cell-Type Deconvolution of Tumor Bulk RNA-Seq Through One Function

Version 0.2.0

Description Runs 24 published cell-type deconvolution and cell-abundance methods for bulk RNA-seq of tumor tissue (human or mouse) through a single function, bulkdeconv(data, expr, species, method). Nineteen methods are implemented in the package and run after installation, with their reference data included; those ported from existing code reproduce the output of the original implementations. The other five need one install step into a private library (their original packages, or for PUREE a downloaded model) and run each in its own R process. Input is checked before anything runs, a registry records what each method needs and how its output can be compared, and results come back in one standard layout with metadata and quality information. Only methods that need no registration are included.

License GPL-3

URL https://daikikumakura.github.io/bulkdeconv/, https://github.com/DaikiKumakura/bulkdeconv

BugReports https://github.com/DaikiKumakura/bulkdeconv/issues

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Depends R (>= 4.1.0)

Imports BiocParallel, callr (>= 3.7.0), MASS, quadprog, sva, tools, utils

Suggests BiocManager, GSVA, pracma, remotes, testthat (>= 3.0.0), withr

biocViews Software, GeneExpression, Transcriptomics

Config/testthat/edition 3

Config/pak/sysreqs libpng-dev libxml2-dev libssl-dev zlib1g-dev

Repository https://daikikumakura.r-universe.dev

Date/Publication 2026-11-16 06:05:16 UTC

RemoteUrl https://github.com/DaikiKumakura/bulkdeconv

RemoteRef HEAD

RemoteSha b38b1aa2151ff4d787a34558b3f9acf2023705f7

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`bulkdeconv` *Cell-type deconvolution of tumor bulk RNA-seq with one function*

Description

Runs one published deconvolution or cell-abundance method on a gene-by-sample table. The input layout is the one `rsemverse::rsem_read()` returns: the first column holds gene symbols and every other column is one sample. The method runs in a separate R process. External methods use the original package at the version recorded in the registry (see `bulkdeconv_install()`).

Usage

```
bulkdeconv(data, expr, species, method, ...)
```

Arguments

`data`	A data frame whose first column is the gene symbol (character) and whose other columns are samples (numeric). A numeric matrix with gene symbols as row names is also accepted. Gene symbols must be unique and every sample must contain at least one nonzero value.
`expr`	`"count"` or `"tpm"`: the scale of the values in `data`. Each method accepts one scale (see `expr_accepted` in `bulkdeconv_methods()`): `"count"` for seqimmucc, `"tpm"` for the others. The wrong one is refused with a message that says so.
`species`	`"human"` or `"mouse"`.
`method`	A method ID; see `bulkdeconv_methods()`.
`...`	Method-specific options, named: `preset` (xcell2, gedit), `cancer_type` (consensus_tme; required for timer), `tissue` (immucellai2, ssmd), `n_permutations` and `seed` (base). Unknown or invalid options are errors.

Details

Use `bulkdeconv_methods()` to check the input scale, minimum sample count and output class. Scores from different methods can have different units. Cohort-dependent scores are interpreted within the run.

All reference data the methods need are installed with the package.

Value

An object of class `bulkdeconv_result`, a list with

- `score`: numeric matrix, samples in rows, features in columns;
- `metadata`: method, species, expr, options, what kind of value the method returns (`output_class`) and how it can be compared (`comparability`), licence, package versions, runtime;
- `qc`: gene and sample counts, signature coverage when the method exposes its genes, and the notes and warnings raised.

Examples

```
## Not run:
# df: first column gene symbols, other columns samples (TPM)
res <- bulkdeconv(df, expr = "tpm", species = "human", method = "quantiseq")
res$score

## End(Not run)
```

`bulkdeconv_install` *Install the packages a method needs into the private library*

Description

Installs the original method packages at the versions recorded in the registry (GitHub packages at a fixed commit) into a private library, so they do not touch your normal library. Interactively it asks before installing.

Usage

```
bulkdeconv_install(method, lib = NULL, ask = interactive())
```

Arguments

`method`	One or more method IDs, or `"all"` for every usable method.
`lib`	Library directory. Default: the first path of the option `bulkdeconv.lib`, else a per-user directory (see Details).
`ask`	Ask for confirmation first. Default: `interactive()`.

Details

The default library is `tools::R_user_dir("bulkdeconv", "data")` plus `lib/R-<major.minor>`. Set `options(bulkdeconv.lib = "path")` to use another place. The packages `remotes` and `BiocManager` are needed for the installation itself.

Value

Invisibly, the library path used.

Examples

```
## Not run:
bulkdeconv_install("quantiseq")
bulkdeconv_install("all")

## End(Not run)
```

`bulkdeconv_methods` *List the methods bulkdeconv can run*

Description

Returns the registry: one row per method, with the species it supports, the expression scale it accepts, what it needs, how its output can be compared, its licence, and whether it is installed in the private library.

Usage

```
bulkdeconv_methods(species = NULL, usable = TRUE)
```

Arguments

`species`	Optional. `"human"` or `"mouse"`; keeps only methods that support it.
`usable`	If `TRUE` (default), drops methods that cannot be run (status `unavailable` or `excluded`).

Value

A data frame with one row per method. `installed` is `TRUE` when every package the method needs is found in the private library or in the normal library paths.

Examples

```
bulkdeconv_methods()
bulkdeconv_methods("mouse")[, c("method", "output_class", "installed")]
```

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