

Package: perturbMatchData (via r-universe)

September 21, 2026

Title Reference Perturbation Signatures from GEO RNA-seq Experiments

Version 0.99.0

Description Provides the reference perturbation expression signatures used by the perturbMatch package, which ranks the single-gene perturbations whose expression response most resembles a query signature. Each reference signature summarises the differential expression observed after a single-gene perturbation (knockdown, knockout or overexpression) in a human RNA-seq experiment deposited in the Gene Expression Omnibus. Signatures are summarised either by the characteristic direction method or by limma, each with and without surrogate variable analysis batch correction, giving four datasets served as HDF5-backed SummarizedExperiment objects.

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URL <https://github.com/soulj/perturbMatchData>

BugReports <https://github.com/soulj/perturbMatchData/issues>

Encoding UTF-8

biocViews ExperimentHub, ExperimentData, ExpressionData, RNASeqData, SequencingData, Homo_sapiens_Data, GEO

Depends R (>= 4.5.0)

Imports ExperimentHub, HDF5Array, S4Vectors, SummarizedExperiment

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Repository <https://biocstaging.r-universe.dev>

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perturbMatch_reference	<i>The perturbMatchData records on ExperimentHub</i>
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Description

Returns the **ExperimentHub** records prepared by this package. This is a way to inspect what is hosted and what is already cached locally. To work with the data, use the dataset accessors described in [perturbMatchReferenceData](#), which assemble the records into a [SummarizedExperiment](#) for you.

Usage

perturbMatch_reference()

Value

An [ExperimentHub](#) subset of the perturbMatchData records.

See Also

[perturbMatchReferenceData](#) for the dataset accessors.

Examples

perturbMatch_reference()

`perturbMatchReferenceData`*Load a perturbMatch reference dataset*

Description

Retrieve one of the perturbMatch reference expression databases as an HDF5-backed [Summarized-Experiment](#). The assays stay in the ExperimentHub cache and are read from disk on demand.

Usage

```
perturbMatch_chrdir(withAssays = TRUE)
```

```
perturbMatch_chrdir_sva(withAssays = TRUE)
```

```
perturbMatch_limma(withAssays = TRUE)
```

```
perturbMatch_limma_sva(withAssays = TRUE)
```

Arguments

<code>withAssays</code>	Whether the returned object carries the assay data. With FALSE only the gene and signature annotation is retrieved, a few MB rather than gigabytes, enough to browse the available perturbations without fetching the signature matrices.
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Details

`perturbMatch_chrdir` Characteristic direction signatures.

`perturbMatch_chrdir_sva` Characteristic direction, SVA batch-corrected.

`perturbMatch_limma` limma log2 fold-change / pi-score signatures.

`perturbMatch_limma_sva` limma signatures, SVA batch-corrected.

All four are derived from GEO RNA-seq experiments and share a 39,376-gene space, and so also share one gene annotation resource.

The signature matrices are large: 790 MB for `chrdir` and 673 MB for `chrdir_sva`, and 3.1 GB and 2.6 GB for `limma` and `limma_sva`, which carry three assays each. They are downloaded once and then read from the ExperimentHub cache.

Value

A [SummarizedExperiment](#) with HDF5-backed assays.

Examples

```
## which perturbations are available, without the assay data. Only the
## annotation resources are downloaded, a few MB rather than gigabytes
se <- perturbMatch_chrdir(withAssays = FALSE)
head(SummarizedExperiment::colData(se))

## the full dataset, 790 MB of signature matrices on first use
se <- perturbMatch_chrdir()
SummarizedExperiment::assay(se)[1:5, 1:3]
```

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