

# Package ‘curatedTBData’

January 30, 2025

**Type** Package

**Title** Curation of existing tuberculosis transcriptomic studies

**Version** 2.3.0

**Description** The curatedTBData is an R package that provides standardized, curated tuberculosis(TB) transcriptomic studies. The initial release of the package contains 49 studies. The curatedTBData package allows users to access tuberculosis transcriptomic efficiently and to make efficient comparison for different TB gene signatures across multiple datasets.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** false

**RoxygenNote** 7.3.1

**Depends** R (>= 4.3.0)

**Imports** AnnotationHub, ExperimentHub, MultiAssayExperiment, rlang,  
stats

**Suggests** BiocStyle, DT, dplyr, HGNCHELPER, knitr, methods, rmarkdown,  
SummarizedExperiment, sva, testthat

**biocViews** ExperimentHub, GEO, Homo\_sapiens\_Data

**URL** <https://github.com/compbiomed/curatedTBData>

**BugReports** <https://github.com/compbiomed/curatedTBData/issues>

**Language** en-US

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/curatedTBData>

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## Contents

.select_assay . . . . .	2
.subset_curatedTBData . . . . .	3
combine_objects . . . . .	3
curatedTBData . . . . .	4
DataSummary . . . . .	5
SignatureInfoTraining . . . . .	7
subset_curatedTBData . . . . .	11
update_gene_symbol . . . . .	12

<b>Index</b>	<b>13</b>
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.select_assay	<i>Select assay based on input list type</i>
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### Description

Select assay based on input list type

### Usage

```
.select_assay(object_list, experiment_name, Subject)
```

### Arguments

object_list	A list of <a href="#">MultiAssayExperiment</a> or <a href="#">SummarizedExperiment</a> objects. The object's assay contain expression data with probes mapped to gene symbol. names(object_list) should not be NULL.
experiment_name	A character/vector of character to choose the name of the assay from the input list of object.
Subject	Boolean. Indicate whether the input is a list of <a href="#">SummarizedExperiment</a> objects.

### Value

A list of selected assays.

---

.subset\_curatedTBData *Subset curatedTBData based on single/multiple conditions*

---

### Description

Subset curatedTBData based on single/multiple conditions

### Usage

```
.subset_curatedTBData(  
  theObject,  
  annotationColName,  
  annotationCondition,  
  assayName  
)
```

### Arguments

theObject      A [SummarizedExperiment](#) or [MultiAssayExperiment](#) object.

annotationColName      A character indicates feature of interest in the object's annotation data.

annotationCondition      A vector of character indicates conditions want to be selected.

assayName      A character indicates the name of the assay from the input object. The default is NULL. When assayName is NULL, the function selects the first assay along assay list.

### Value

A [SummarizedExperiment](#) object containing subjects with desired annotation conditions.

---

combine\_objects      *Merge samples with common gene names from selected studies*

---

### Description

Merge samples with common gene names from selected studies

### Usage

```
combine_objects(object_list, experiment_name, update_genes = TRUE)
```

**Arguments**

object_list	A list of <a href="#">MultiAssayExperiment</a> or <a href="#">SummarizedExperiment</a> objects. The object's assay contain expression data with probes mapped to gene symbol. names(object_list) should not be NULL.
experiment_name	A character/vector of character to choose the name of the assay from the input list of object.
update_genes	Boolean. Indicate whether update the gene symbols using <a href="#">checkGeneSymbols</a> . Default is TRUE.

**Value**

A [SummarizedExperiment](#) object that contains combined data from the input.

**Examples**

```
geo <- c("GSE19435", "GSE19439")
data_list <- curatedTBData(c("GSE19435", "GSE19439"),
                           dry.run = FALSE, curated.only = TRUE)
combine_objects(data_list, experiment_name = "assay_curated")
```

---

curatedTBData

*Import curated Tuberculosis Data*

---

**Description**

A function to access available curated tuberculosis transcriptomic data from the Bioconductor's ExperimentHub services

**Usage**

```
curatedTBData(study_name, dry.run = TRUE, curated.only = TRUE)
```

**Arguments**

study_name	A character or vector of characters that contain name of the studies. When any(study_name == "") == TRUE, the function will return all available studies.
dry.run	Boolean. Indicate the whether downloading resources from the ExperimentHub services. If TRUE (Default), return the names of the available resources to be downloaded. If FALSE, start downloading data.
curated.only	Boolean. Indicate whether downloading resources for the curated version. If TRUE (Default), only download the curated gene expression profile and the clinical annotation information. If FALSE, download both raw and curated resources.

**Value**

A list of [MultiAssayExperiment](#) objects.

**Examples**

```
curatedTBData("GSE39939", dry.run = TRUE)
curatedTBData(c("GSE39939", "GSE39940"), dry.run = FALSE, curated.only = TRUE)
```

---

DataSummary

*Summarized tuberculosis studies included in the curatedTBData*


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**Description**

A dataset containing metadata information of 49 tuberculosis studies. The variables are as follows:

**Usage**

```
data(DataSummary)
```

**Format**

A data frame with 49 rows and 14 variables

**Study** Name of the dataset included in the curatedTBData

**Platform** Sequencing platform information

**GeographicalRegion** Geographical region to which study was conducted

**Tissue** Tissue type of which samples were collected

**Age** Age range of the study

**HIVStatus** Whether dataset contains HIV-infected subjects

**DiagnosisMethod** The diagnostic methods used in the study to identify tuberculosis subtypes

**Control** The number of subjects who were identified as healthy control in the study

**LTBI** The number of subjects with latent tuberculosis infection in the study

**PTB** The number of subjects with active tuberculosis in the study

**OD** The number of subjects with other disease(s) in the study

**Total** Total number of subjects included in the study

**Notes** Additional notes about the study

**GeneralType** Sequencing type of the study (Affymetrix Microarray, Agilent Microarray, Agilent Microarray - Two Color, Illumina Microarray, Illumina RNA-seq, MPEIB Microarray - Two Color, Phalanx Microarray, Phalanx RT-PCR)

**Source**

- **GSE31348:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE31348>
- **GSE36238:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE36238>
- **GSE41055:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE41055>
- **GSE54992:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE54992>
- **GSE73408:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE73408>
- **GSE107731:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE107731>
- **GSE79362:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE79362>
- **GSE84076:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE84076>
- **GSE89403:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE89403>
- **GSE94438:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE94438>
- **GSE107991:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE107991>
- **GSE107992:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE107992>
- **GSE107993:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE107993>
- **GSE107994:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE107994>
- **GSE101705:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE101705>
- **GSE107104:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE107104>
- **GSE112104:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE112104>
- **GSE19435:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19435>
- **GSE19439:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19439>
- **GSE19442:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19442>
- **GSE19443:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19443>
- **GSE19444:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19444>
- **GSE22098:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22098>
- **GSE29536:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE29536>
- **GSE37250:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE37250>
- **GSE39939:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE39939>
- **GSE39940:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE39940>
- **GSE40553:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE40553>
- **GSE42825:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42825>
- **GSE42826:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42826>
- **GSE42827:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42827>
- **GSE42830:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42830>
- **GSE42831:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42831>
- **GSE42832:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42832>
- **GSE50834:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE50834>
- **GSE56153:** <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE56153>

- **GSE69581**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE69581>
- **GSE83456**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE83456>
- **GSE83892**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE83892>
- **GSE25534**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE25534>
- **GSE28623**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE28623>
- **GSE34608**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE34608>
- **GSE62147**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62147>
- **GSE81746**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE81746>
- **GSE62525**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62525>
- **GSE74092**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE74092>
- **GSE6112**: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6112>
- **GSEBruno**: <https://pubmed.ncbi.nlm.nih.gov/28515464/>
- **GSETornheim**: <https://www.ncbi.nlm.nih.gov/Traces/study/?acc=SRP229386>

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SignatureInfoTraining *Summarized results for tuberculosis gene signatures and their corresponding discovery/training studies*

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## Description

A table containing tuberculosis gene signatures with dataset(s) from which they were derived. The variables are as follows:

## Usage

```
data(SignatureInfoTraining)
```

## Format

A data frame with 25 rows and 2 variables:

**TBSignature** Name of the tuberculosis gene signatures

**Study** Name of the dataset

## Source

- **Anderson\_42**: Anderson, Suzanne T., Myrsini Kaforou, Andrew J. Brent, Victoria J. Wright, Claire M. Banwell, George Chagaluka, Amelia C. Crampin, et al. 2014. "Diagnosis of Childhood Tuberculosis and Host RNA Expression in Africa." *The New England Journal of Medicine* 370 (18): 1712-23. [10.1056/NEJMoa1303657](https://doi.org/10.1056/NEJMoa1303657)
- **Anderson\_OD\_51**: Anderson, Suzanne T., Myrsini Kaforou, Andrew J. Brent, Victoria J. Wright, Claire M. Banwell, George Chagaluka, Amelia C. Crampin, et al. 2014. "Diagnosis of Childhood Tuberculosis and Host RNA Expression in Africa." *The New England Journal of Medicine* 370 (18): 1712-23. [10.1056/NEJMoa1303657](https://doi.org/10.1056/NEJMoa1303657)

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- **Berry\_OD\_86**: Berry, Matthew P. R., Christine M. Graham, Finlay W. McNab, Zhaohui Xu, Susannah A. A. Bloch, Tolu Oni, Katalin A. Wilkinson, et al. 2010. "An Interferon-Inducible Neutrophil-Driven Blood Transcriptional Signature in Human Tuberculosis." *Nature* 466 (7309): 973-77. [10.1038/nature09247](https://doi.org/10.1038/nature09247)
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- **Esmail\_82**: Esmail, Hanif, Rachel P. Lai, Maia Lesosky, Katalin A. Wilkinson, Christine M. Graham, Stuart Horswell, Anna K. Coussens, Clifton E. Barry 3rd, Anne O'Garra, and Robert J. Wilkinson. 2018. "Complement Pathway Gene Activation and Rising Circulating Immune Complexes Characterize Early Disease in HIV-Associated Tuberculosis." *Proceedings of the National Academy of Sciences of the United States of America* 115 (5): E964-73. [10.1073/pnas.1711853115](https://doi.org/10.1073/pnas.1711853115)
- **Esmail\_203**: Esmail, Hanif, Rachel P. Lai, Maia Lesosky, Katalin A. Wilkinson, Christine M. Graham, Stuart Horswell, Anna K. Coussens, Clifton E. Barry 3rd, Anne O'Garra, and Robert J. Wilkinson. 2018. "Complement Pathway Gene Activation and Rising Circulating Immune Complexes Characterize Early Disease in HIV-Associated Tuberculosis." *Proceedings of the National Academy of Sciences of the United States of America* 115 (5): E964-73. [10.1073/pnas.1711853115](https://doi.org/10.1073/pnas.1711853115)
- **Esmail\_OD\_893**: Esmail, Hanif, Rachel P. Lai, Maia Lesosky, Katalin A. Wilkinson, Christine M. Graham, Stuart Horswell, Anna K. Coussens, Clifton E. Barry 3rd, Anne O'Garra, and Robert J. Wilkinson. 2018. "Complement Pathway Gene Activation and Rising Circulating Immune Complexes Characterize Early Disease in HIV-Associated Tuberculosis." *Proceedings of the National Academy of Sciences of the United States of America* 115 (5): E964-73. [10.1073/pnas.1711853115](https://doi.org/10.1073/pnas.1711853115)
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  - **Leong\_RISK\_29:** Leong, S., Zhao, Y., Ribeiro-Rodrigues, R., Jones-López, E. C., Acuña-Villaorduña, C., Rodrigues, P. M., Palaci, M., Alland, D., Dietze, R., Ellner, J. J., Johnson, W. E., Salgame, P., Cross-validation of existing signatures and derivation of a novel 29-gene transcriptomic signature predictive of progression to TB in a Brazilian cohort of household contacts of pulmonary TB. *Tuberculosis (Edinb)*. 2020 Jan;120:101898. [10.1016/j.tube.2020.101898](https://doi.org/10.1016/j.tube.2020.101898)
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---

subset\_curatedTBData *Subset curatedTBData based on single/multiple conditions*

---

## Description

The function selects desired samples from curatedTBData database based pre-specified conditions

## Usage

```
subset_curatedTBData(  
  theObject,  
  annotationColName,  
  annotationCondition,  
  assayName = NULL  
)
```

## Arguments

**theObject** A [SummarizedExperiment](#) or [MultiAssayExperiment](#) object.

**annotationColName** A character indicates feature of interest in the object's annotation data.

**annotationCondition** A vector of character indicates conditions want to be selected.

**assayName** A character indicates the name of the assay from the input object. The default is NULL. When assayName is NULL, the function selects the first assay along assay list.

## Value

A [SummarizedExperiment](#) object containing subjects with desired annotation conditions.

## Examples

```
obj <- curatedTBData("GSE74092", dry.run = FALSE, curated.only = TRUE)  
subset_curatedTBData(obj[[1]], annotationColName = "TBstatus",  
  annotationCondition = c("Control", "PTB"))
```

---

update\_gene\_symbol      *Update gene names from input data*

---

**Description**

Update gene names from input data

**Usage**

```
update_gene_symbol(dat_exprs)
```

**Arguments**

dat\_exprs      A `data.frame` with row names as gene symbols to be updated.

**Value**

A `data.frame` with updated gene symbol as row names.

# Index

## \* **datasets**

- DataSummary, [5](#)
- SignatureInfoTraining, [7](#)
- .select\_assay, [2](#)
- .subset\_curatedTBData, [3](#)
  
- checkGeneSymbols, [4](#)
- combine\_objects, [3](#)
- curatedTBData, [4](#)
  
- DataSummary, [5](#)
  
- MultiAssayExperiment, [2-4](#), [11](#)
  
- SignatureInfoTraining, [7](#)
- subset\_curatedTBData, [11](#)
- SummarizedExperiment, [2-4](#), [11](#)
  
- update\_gene\_symbol, [12](#)