

Package ‘xCell2’

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Type Package

Title A Tool for Generic Cell Type Enrichment Analysis

Version 1.0.9

Description xCell2 provides methods for cell type enrichment analysis using cell type signatures.

It includes three main functions -

1. xCell2Train for training custom references objects from bulk or single-cell RNA-seq datasets.
2. xCell2Analysis for conducting the cell type enrichment analysis using the custom reference.
3. xCell2GetLineage for identifying dependencies between different cell types using ontology.

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BlueprintEncode.xCell2Ref

Blueprint and ENCODE Projects Reference

Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(BlueprintEncode.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

- params Linear transformation parameters.
- signatures Gene signatures for cell types.
- dependencies Cell lineage dependencies.
- spill_mat Spillover correction matrix.
- genes_used Genes included in the reference.

Details

Blueprint and ENCODE Projects Reference (human)
A pre-trained xCell2 reference object based on the Blueprint and ENCODE projects datasets.

Source

Martens JHA and Stunnenberg HG (2013); The ENCODE Project Consortium (2012), curated by Aran D (2019); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

dependencies	<i>Access Cell Type Dependencies</i>
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Description

Retrieve or assign hierarchical dependencies between cell types for an [xCell2Object](#).
Retrieve or assign the hierarchical dependencies between cell types for an [xCell2Object](#).

Usage

```
getDeps(object)  
  
setDeps(object) <- value  
  
## S4 method for signature 'xCell2Object'  
getDeps(object)  
  
## S4 replacement method for signature 'xCell2Object'  
setDeps(object) <- value
```

Arguments

object	An xCell2Object .
value	A list of hierarchical dependencies (for the setter).

Value

For ‘getDeps’, a list of hierarchical dependencies. For ‘setDeps<-’, the updated [xCell2Object](#).

For ‘getDeps’, a list of hierarchical dependencies. For ‘setDeps<-’, the updated [xCell2Object](#).

See Also

[xCell2Object-class](#)

[xCell2Object-class](#)

Examples

```
data(DICE_demo.xCell2Ref, package = "xCell2")
setDeps(DICE_demo.xCell2Ref) <- list("Parent" = "ChildType1")
getDeps(DICE_demo.xCell2Ref)
data(DICE_demo.xCell2Ref, package = "xCell2")
setDeps(DICE_demo.xCell2Ref) <- list("ParentType" = "ChildType1")
```

DICE_demo.xCell2Ref *Demo xCell2 Reference Object*

Description

Pre-trained xCell2 reference object based on the DICE dataset.

Usage

```
data(DICE_demo.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

params Linear transformation parameters.

signatures Cell-type-specific gene signatures.

dependencies Cell type lineage dependencies.

spill_mat Spillover correction matrix.

genes_used Genes included in the reference.

Details

Demo xCell2 Reference Object from DICE Subset (human)

A demo xCell2 reference object derived from a subset of the DICE dataset. Suitable for demonstrating the use of xCell2Analysis.

Source

Schmiedel B et al. (2018).

See Also

[xCell2Analysis](#) for enrichment analysis, and [xCell2Train](#) for training custom references.

dice_demo_ref	<i>Subset of the DICE Reference</i>
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Description

Demo reference object derived from the DICE dataset for training xCell2 references.

Usage

```
data(dice_demo_ref, package = "xCell2")
```

Format

A [SummarizedExperiment](#) object.

Details

Subset of the DICE Reference
A subset of the DICE reference stored as a ‘SummarizedExperiment’ object for the xCell 2.0 vignette. This demo reference object demonstrates the use of xCell2Train for generating a custom xCell2 reference.

Source

Schmiedel B et al. (2018).

See Also

[xCell2Train](#) for generating references, and [xCell2Analysis](#) for enrichment analysis.

genesUsed	<i>Access Genes Used</i>
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Description

Retrieve or assign the genes used in training the reference for an [xCell2Object](#).
Retrieve or assign the genes used in training the reference for an [xCell2Object](#).

Usage

```

getGenesUsed(object)

setGenesUsed(object) <- value

## S4 method for signature 'xCell2Object'
getGenesUsed(object)

## S4 replacement method for signature 'xCell2Object'
setGenesUsed(object) <- value

```

Arguments

object An [xCell2Object](#).

value A character vector of genes (for the setter).

Value

For ‘getGenesUsed’, a character vector of genes. For ‘setGenesUsed<-’, the updated [xCell2Object](#).

For ‘getGenesUsed’, a character vector of genes. For ‘setGenesUsed<-’, the updated [xCell2Object](#).

See Also

[xCell2Object-class](#)

[xCell2Object-class](#)

Examples

```

data(DICE_demo.xCell2Ref, package = "xCell2")
setGenesUsed(DICE_demo.xCell2Ref) <- c("GeneA", "GeneB", "GeneC")
getGenesUsed(DICE_demo.xCell2Ref)
data(DICE_demo.xCell2Ref, package = "xCell2")
setGenesUsed(DICE_demo.xCell2Ref) <- c("GeneA", "GeneB", "GeneC")

```

ImmGenData.xCell2Ref *Immunologic Genome Project Reference*

Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(ImmGenData.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

params Linear transformation parameters.
signatures Gene signatures for cell types.
dependencies Cell lineage dependencies.
spill_mat Spillover correction matrix.
genes_used Genes included in the reference.

Details

Immunologic Genome Project Reference

A pre-trained xCell2 reference object based on the Immunologic Genome Project dataset.

Source

The Immunological Genome Project Consortium (2008), curated by Aran D (2019); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

ImmuneCompendium.xCell2Ref

Immune Compendium Reference

Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(ImmuneCompendium.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

params Linear transformation parameters.
signatures Gene signatures for cell types.
dependencies Cell lineage dependencies.
spill_mat Spillover correction matrix.
genes_used Genes included in the reference.

Details

Immune Compendium Reference (human)
A pre-trained xCell2 reference object based on the Immune Compendium dataset for immune cell profiling.

Source

Curated by Zaitsev A (2022); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

LM22.xCell2Ref	<i>LM22 Reference</i>
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Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(LM22.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

- params Linear transformation parameters.
- signatures Gene signatures for cell types.
- dependencies Cell lineage dependencies.
- spill_mat Spillover correction matrix.
- genes_used Genes included in the reference.

Details

LM22 Reference (human)
A pre-trained xCell2 reference object based on the LM22 dataset.

Source

Newman AM (2015); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

`mix_demo`*Demo Bulk Gene Expression Data*

Description

Example RNA-Seq data to demonstrate xCell2Analysis.

Usage

```
data(mix_demo, package = "xCell2")
```

Format

A matrix with genes (rows) and samples (columns).

Details

Demo Bulk Gene Expression Data (RNA-Seq)

A demo mixture matrix for bulk RNA-Seq gene expression data. Use this dataset to test xCell2Analysis with pre-trained xCell2 references.

See Also

[xCell2Analysis](#) for enrichment analysis.

`MouseRNAseqData.xCell2Ref`*Mouse RNA-Seq Data Reference*

Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(MouseRNAseqData.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

`params` Linear transformation parameters.

`signatures` Gene signatures for cell types.

`dependencies` Cell lineage dependencies.

`spill_mat` Spillover correction matrix.

`genes_used` Genes included in the reference.

Details

Mouse RNA-Seq Data Reference

A pre-trained xCell2 reference object based on the MouseRNAseqData dataset.

Source

Benayoun B (2019); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

PanCancer.xCell2Ref	<i>PanCancer Reference</i>
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Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(PanCancer.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

params Linear transformation parameters.

signatures Gene signatures for cell types.

dependencies Cell lineage dependencies.

spill_mat Spillover correction matrix.

genes_used Genes included in the reference.

Details

PanCancer Reference (human)

A pre-trained xCell2 reference object based on the PanCancer dataset for cancer-specific analyses.

Source

Nofech-Mozes I (2023); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

params

Access Transformation Parameters

Description

Retrieve or assign linear transformation parameters for an [xCell2Object](#).

Retrieve or assign linear transformation parameters for cell types for an [xCell2Object](#).

Usage

```
getParams(object)

setParams(object) <- value

## S4 method for signature 'xCell2Object'
getParams(object)

## S4 replacement method for signature 'xCell2Object'
setParams(object) <- value
```

Arguments

object	An xCell2Object .
value	A data frame of transformation parameters (for the setter).

Value

For ‘getParams’, a data frame of transformation parameters. For ‘setParams<-’, the updated [xCell2Object](#).

For ‘getParams’, a data frame of transformation parameters. For ‘setParams<-’, the updated [xCell2Object](#).

See Also

[xCell2Object-class](#)

[xCell2Object-class](#)

Examples

```
data(DICE_demo.xCell2Ref, package = "xCell2")
setParams(DICE_demo.xCell2Ref) <- data.frame(celltype = "T_cells", a = 0.5, b = 2, m = 1.5)
getParams(DICE_demo.xCell2Ref)
data(DICE_demo.xCell2Ref, package = "xCell2")
setParams(DICE_demo.xCell2Ref) <- data.frame(celltype = "B_cells", a = 0.6, b = 1.8, m = 2.1)
```

signatures	<i>Access Cell Type Signatures</i>
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Description

Retrieve or assign the cell type-specific gene signatures for an [xCell2Object](#).

Retrieve or assign the cell type-specific gene signatures for an [xCell2Object](#).

Usage

```
getSignatures(object)

setSignatures(object) <- value

## S4 method for signature 'xCell2Object'
getSignatures(object)

## S4 replacement method for signature 'xCell2Object'
setSignatures(object) <- value
```

Arguments

object	An xCell2Object .
value	A list of cell type-specific gene signatures (for the setter).

Value

For ‘getSignatures’, a list of cell type-specific gene signatures. For ‘setSignatures<-’, the updated [xCell2Object](#).

For ‘getSignatures’, a list of cell type-specific gene signatures. For ‘setSignatures<-’, the updated [xCell2Object](#).

See Also

[xCell2Object-class](#)

[xCell2Object-class](#)

Examples

```
data(DICE_demo.xCell2Ref, package = "xCell2")
setSignatures(DICE_demo.xCell2Ref) <- list("T_cells" = c("GeneA", "GeneB"), "B_cells" = c("GeneC"))
getSignatures(DICE_demo.xCell2Ref)
data(DICE_demo.xCell2Ref, package = "xCell2")
setSignatures(DICE_demo.xCell2Ref) <- list("T_cells" = c("GeneA", "GeneB"))
```

spillMat	<i>Access Spillover Matrix</i>
----------	--------------------------------

Description

Retrieve or assign the spillover correction matrix for an [xCell2Object](#).

Retrieve or assign the spillover correction matrix for an [xCell2Object](#).

Usage

```
getSpillMat(object)

setSpillMat(object) <- value

## S4 method for signature 'xCell2Object'
getSpillMat(object)

## S4 replacement method for signature 'xCell2Object'
setSpillMat(object) <- value
```

Arguments

object	An xCell2Object .
value	A matrix of spillover correction factors (for the setter).

Value

For ‘getSpillMat’, a matrix of spillover correction factors. For ‘setSpillMat<-’, the updated [xCell2Object](#).

For ‘getSpillMat’, a matrix of spillover correction factors. For ‘setSpillMat<-’, the updated [xCell2Object](#).

See Also

[xCell2Object-class](#)

[xCell2Object-class](#)

Examples

```
data(DICE_demo.xCell2Ref, package = "xCell2")
spill_mat <- matrix(c(1, 0.1, 0.1, 1), nrow = 2, byrow = TRUE)
rownames(spill_mat) <- colnames(spill_mat) <- c("T_cells", "B_cells")
setSpillMat(DICE_demo.xCell2Ref) <- spill_mat
getSpillMat(DICE_demo.xCell2Ref)
data(DICE_demo.xCell2Ref, package = "xCell2")
spill_mat <- matrix(c(1, 0.05, 0.05, 1), nrow = 2, byrow = TRUE)
rownames(spill_mat) <- colnames(spill_mat) <- c("T_cells", "B_cells")
setSpillMat(DICE_demo.xCell2Ref) <- spill_mat
```

`TabulaMurisBlood.xCell2Ref`*Tabula Muris Blood Reference*

Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(TabulaMurisBlood.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

`params` Linear transformation parameters.

`signatures` Gene signatures for cell types.

`dependencies` Cell lineage dependencies.

`spill_mat` Spillover correction matrix.

`genes_used` Genes included in the reference.

Details

Tabula Muris Blood Reference (mouse)

A pre-trained xCell2 reference object based Tabula Muris dataset.

Source

The Tabula Muris Consortium (2018); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

`TabulaSapiensBlood.xCell2Ref`*Tabula Sapiens Blood Reference*

Description

Pre-trained xCell2 reference for use in xCell2Analysis or extending via xCell2Train.

Usage

```
data(TabulaSapiensBlood.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

`params` Linear transformation parameters.

`signatures` Gene signatures for cell types.

`dependencies` Cell lineage dependencies.

`spill_mat` Spillover correction matrix.

`genes_used` Genes included in the reference.

Details

Tabula Sapiens Blood Reference (human)

A pre-trained xCell2 reference object based on the Tabula Sapiens dataset.

Source

The Tabula Sapiens Consortium (2022); trained by Angel A, et al. (2024).

See Also

[xCell2Analysis](#) and [xCell2Train](#).

`TMECompendium.xCell2Ref`*Tumor Microenvironment Compendium Reference*

Description

Pre-trained xCell2 reference object for analyzing tumor microenvironments.

Usage

```
data(TMECompendium.xCell2Ref, package = "xCell2")
```

Format

An xCell2Object containing:

`params` Linear transformation parameters.

`signatures` Cell-type-specific gene signatures.

`dependencies` Cell type lineage dependencies.

`spill_mat` Spillover correction matrix.

`genes_used` Genes included in the reference.

Details

Tumor Microenvironment Compendium Reference (human)

An xCell2 reference object created from the Tumor Microenvironment Compendium dataset.

Normalized data for training can be accessed at: <https://science.bostongene.com/kassandra/downloads>.

Source

Curated by Zaitsev A (2022) and trained by Angel A, et al. (2024).

References

Zaitsev, A., et al. (2022). Cancer Cell, 40(8), 879-894.

See Also

[xCell2Analysis](#) and [xCell2Train](#).

xCell2Analysis	<i>Perform Cell Type Enrichment Analysis</i>
----------------	--

Description

Estimates the relative enrichment of cell types in a bulk gene expression mixture. This function uses gene signatures from a pre-trained xCell2Object to compute enrichment scores, with options for linear transformation and spillover correction to improve specificity.

Usage

```
xCell2Analysis(
  mix,
  xcell2object,
  minSharedGenes = 0.9,
  rawScores = FALSE,
  spillover = TRUE,
  spilloverAlpha = 0.5,
  BPPARAM = BiocParallel::SerialParam()
)
```

Arguments

mix	A bulk mixture of gene expression matrix (genes in rows, samples in columns). The input should use the same gene annotation system as the reference object. If is RNA-Seq data - normalization by gene length is highly recommended.
xcell2object	A pre-trained reference object of class xCell2Object, created using the xCell2Train function. Pre-trained references are available within the package for common use cases.
minSharedGenes	Minimum fraction of shared genes required between the mixture and the reference object (default: 0.9). If the shared fraction falls below this threshold, the function will stop with an error or warning, as accurate analysis depends on sufficient overlap between the mixture and reference genes.
rawScores	A Boolean indicating whether to return raw enrichment scores (default: FALSE). Raw enrichment scores are computed directly from gene rankings without linear transformation or spillover correction.
spillover	A Boolean to enable spillover correction on the enrichment scores (default: TRUE). Spillover occurs when gene expression patterns overlap between closely related cell types, potentially inflating enrichment scores. Correcting for spillover enhances the specificity of enrichment scores, particularly for related cell types. The strength of this correction can be adjusted using the spilloverAlpha parameter.
spilloverAlpha	A numeric value controlling the strength of spillover correction (default: 0.5). Lower values apply weaker correction, while higher values apply stronger correction. An alpha value of 0.5 is suitable for most cases, but users may tune this parameter based on the similarity of cell types in their reference.

BPPARAM A [BiocParallelParam](#) instance that determines the parallelization strategy (more in "Details"). Default is `BiocParallel::SerialParam()`.

Details

The `xCell2Analysis` function performs cell type enrichment analysis by leveraging gene signatures from a pre-trained `xCell2Object`. It computes enrichment scores for each cell type in the provided bulk gene expression mixture (`mix`), applies linear transformations, and corrects for spillover. Spillover correction addresses the overlap of gene expression patterns between closely related cell types, improving the specificity of the enrichment scores.

Parallelization with BPPARAM To achieve faster processing by running computations in parallel, `xCell2Analysis` supports parallelization through the BPPARAM parameter. Users can define a parallelization strategy using `BiocParallelParam` from the `BiocParallel` package. For example, [MulticoreParam](#) is suitable for multi-core processing on Linux and macOS, while [SnowParam](#) or [SerialParam](#) are better suited for Windows systems. Refer to the [BiocParallel documentation](#) for further guidance on parallelization strategies.

Relationship with Other Function(s) The pre-trained `xCell2Object` used in `xCell2Analysis` is created via the [xCell2Train](#) function.

Value

A data frame containing the cell type enrichment for each sample in the input matrix, as estimated by `xCell2`. Each row corresponds to a cell type, and each column corresponds to a sample.

Author(s)

Almog Angel and Dvir Aran

See Also

[xCell2Train](#), for creating the reference object used in this analysis.

Examples

```
# For detailed example read xCell2 vignette.

library(xCell2)

# Load pre-trained reference object
data(DICE_demo.xCell2Ref, package = "xCell2")

# Load demo bulk gene expression mixture
data(mix_demo, package = "xCell2")

# Perform cell type enrichment analysis
xcell2_res <- xCell2::xCell2Analysis(
  mix = mix_demo,
  xcell2object = DICE_demo.xCell2Ref
)
```

```
# Parallel processing example with BiocParallel
library(BiocParallel)
parallel_param <- MulticoreParam(workers = 2)
xcell2_res_parallel <- xCell2::xCell2Analysis(
  mix = mix_demo,
  xcell2object = DICE_demo.xCell2Ref,
  BPPARAM = parallel_param
)
```

xCell2GetLineage	<i>Identify Cell Type Lineage Dependencies</i>
------------------	--

Description

Identifies cell type dependencies based on the Cell Ontology, including both descendants and ancestors for each cell type. Enables manual inspection and refinement of lineage relationships to improve biological accuracy in xCell2 analyses.

Usage

```
xCell2GetLineage(labels, outFile = NULL)
```

Arguments

labels	A data frame with the following required columns: "ont": Cell type ontology ID (e.g., "CL:0000545"). Use NA if unavailable. Ontologies can be accessed via EBI Ontology Lookup Service (OLS) or the ontologyIndex package. "label": Cell type name (e.g., "T-helper 1 cell"). "sample": Sample or cell identifier matching column names in the gene expression matrix. "dataset": Dataset or subject source. Use a constant value if not applicable.
outFile	Optional. Output file name for saving dependencies as a TSV file. The file includes columns for "ont", "label", "descendants", and "ancestors". Suitable for manual inspection and refinement before use in downstream analyses.

Details

The xCell2GetLineage function generates lineage relationships for cell types based on the Cell Ontology. These relationships refine lineage-based dependencies, improving the biological relevance of gene signatures. Users can:

- Use the generated TSV file for manual adjustments before training custom references via [xCell2Train](#).
- Skip this step entirely, allowing xCell2Train to infer dependencies automatically.

If no ontology IDs ("ont") are provided, the function outputs empty dependencies with a message for user guidance.

Relationship with Other Functions:

- [xCell2Train](#): Incorporates lineage relationships during reference training.
- [xCell2Analysis](#): Uses trained references for enrichment analysis.

Value

If outFile is:

- NULL: Returns a list of dependencies for each cell type, with descendants and ancestors as components.
- Specified: Writes a TSV file and warns the user to inspect and validate results manually.

Author(s)

Almog Angel and Dvir Aran

See Also

[xCell2Train](#) for training custom references with lineage data. [xCell2Analysis](#) for enrichment analysis using trained references. [AnnotationHub](#) to access ontology data. [ontologyIndex](#) to programmatically explore ontologies.

Examples

```
# For detailed examples, see the xCell2 vignette.

library(xCell2)

# Load demo reference object
data(dice_demo_ref, package = "xCell2")

# Prepare labels data frame
dice_labels <- SummarizedExperiment::colData(dice_demo_ref)
dice_labels <- as.data.frame(dice_labels)
dice_labels$ont <- NA
dice_labels$sample <- colnames(dice_demo_ref)
dice_labels$dataset <- "DICE"

# Assign ontology IDs
dice_labels[dice_labels$label == "B cells", ]$ont <- "CL:0000236"
dice_labels[dice_labels$label == "Monocytes", ]$ont <- "CL:0000576"
dice_labels[dice_labels$label == "NK cells", ]$ont <- "CL:0000623"
dice_labels[dice_labels$label == "T cells, CD8+", ]$ont <- "CL:0000625"
dice_labels[dice_labels$label == "T cells, CD4+", ]$ont <- "CL:0000624"
dice_labels[dice_labels$label == "T cells, CD4+, memory", ]$ont <- "CL:0000897"

# Generate cell type lineage dependencies
xCell2::xCell2GetLineage(labels = dice_labels)
```

```
# Manually inspect and adjust saved dependencies for refined lineage relationships
# Use the adjusted file as input to xCell2Train via the `lineageFile` parameter.
```

xCell2Object-class	<i>xCell2Object Class</i>
--------------------	---------------------------

Description

An S4 class to represent the xCell2 reference object. This object contains cell type-specific gene signatures, hierarchical dependencies, linear transformation parameters, spillover correction matrices, and genes used for training.

Slots

signatures A list of cell type-specific gene signatures.

dependencies A list of hierarchical dependencies between cell types.

params A data frame containing linear transformation parameters for cell types.

spill_mat A matrix containing spillover correction factors for cell types.

genes_used A character vector of genes used for training the xCell2 reference object.

xCell2Train	<i>Train Custom xCell2 Reference Object</i>
-------------	---

Description

This function creates a custom reference object for [xCell2Analysis](#), enabling cell type enrichment analysis. It supports references derived from RNA-Seq, microarray, and scRNA-Seq data and can be derived from various tissues and organisms.

Usage

```
xCell2Train(
  ref,
  mix = NULL,
  labels = NULL,
  refType,
  lineageFile = NULL,
  BPPARAM = BiocParallel::SerialParam(),
  useOntology = TRUE,
  returnSignatures = FALSE,
  returnAnalysis = FALSE,
  useSpillover = TRUE,
```

```

    spilloverAlpha = 0.5,
    minPbCells = 30,
    minPbSamples = 10,
    minScGenes = 10000
)

```

Arguments

ref	A reference gene expression matrix (genes in rows, samples/cells in columns) or a SummarizedExperiment/SingleCellExperiment object with expression data in the assays slot. Valid Assays: "tpm" Transcripts Per Million (recommended for RNA-Seq). "logcounts" Log-transformed normalized counts. "normcounts" Normalized counts. "counts" Raw counts (required for microarray references). Notes: • If is RNA-Seq data - normalization by gene length is highly recommended. • If multiple assays exist, "tpm" is prioritized. • For microarray data, the "counts" assay must be used.
mix	A bulk mixture of gene expression matrix (genes in rows, samples in columns) (optional). This parameter is required if returnAnalysis is set to TRUE, as it is used for enrichment analysis.
labels	A data frame with the following columns: • "ont": The cell type ontology ID (e.g., "CL:0000545"). Set to NA if not available. Ontologies can be found at EBI Ontology Lookup Service (OLS) or by using the ontologyIndex package. • "label": The cell type name (e.g., "T-helper 1 cell"). • "sample": The sample or cell identifier, matching column names in the reference matrix. • "dataset": The dataset source for each sample. If not applicable, use a constant value for all samples. If ref is a SummarizedExperiment or SingleCellExperiment object, this parameter can be used to **override** the default labels extracted from colData(ref).
refType	The type of reference data: "rnaseq" for RNA-Seq, "array" for microarray, or "sc" for scRNA-Seq.
lineageFile	Path to a manually curated cell type lineage file generated with xCell2GetLineage (optional).
BPPARAM	A BiocParallelParam instance that determines the parallelization strategy (more in "Details"). Default is BiocParallel::SerialParam().
useOntology	A Boolean indicating whether to use ontological integration for cell type dependencies (default: TRUE). Lineage relationships are determined using the Cell Ontology (CL). Users can refine these dependencies with xCell2GetLineage and provide them via the lineageFile parameter.

returnSignatures	A Boolean to return only cell type signatures (default: FALSE).
returnAnalysis	A Boolean to return xCell2Analysis results instead of a reference object (default: FALSE).
useSpillover	A Boolean to use spillover correction during analysis when returnAnalysis is TRUE (default: TRUE). Spillover correction enhances the specificity of enrichment scores by accounting for overlaps between cell types.
spilloverAlpha	Numeric value controlling spillover correction strength (default: 0.5). Lower values apply weaker correction, while higher values apply stronger correction.
minPbCells	Minimum number of cells in a pseudo-bulk sample for scRNA-Seq references (default: 30).
minPbSamples	Minimum number of pseudo-bulk samples for scRNA-Seq references (default: 10).
minScGenes	Minimum number of genes for pseudo-bulk samples for scRNA-Seq references (default: 1e4).

Details

Ontological Integration: Ontological integration (useOntology) leverages hierarchical cell type relationships to ensure biologically meaningful signatures. Dependencies can be refined using [xCell2GetLineage](#), which generates lineage files for manual review.

Spillover Correction: Spillover correction enhances the specificity of enrichment scores by reducing overlaps between related cell types. Use the spilloverAlpha parameter to tune the strength of correction.

Contribute Your xCell2 Reference Object: Users are encouraged to share their reference objects via the [xCell2 Reference Repository](#).

Value

An xCell2Object containing:

- **signatures:** Cell type-specific gene signatures.
- **dependencies:** Lineage-based dependencies.
- **params:** Linear transformation parameters.
- **spill_mat:** A spillover correction matrix.
- **genes_used:** Genes used for training.

Author(s)

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See Also

[xCell2Analysis](#), for enrichment analysis. [xCell2GetLineage](#), for refining cell type dependencies.

Examples

```
library(xCell2)
data(dice_demo_ref, package = "xCell2")
dice_ref <- SummarizedExperiment::assay(dice_demo_ref, "logcounts")
colnames(dice_ref) <- make.unique(colnames(dice_ref))
dice_labels <- as.data.frame(SummarizedExperiment::colData(dice_demo_ref))
dice_labels$ont <- NA
dice_labels$sample <- colnames(dice_ref)
dice_labels$dataset <- "DICE"
DICE.xCell2Ref <- xCell2::xCell2Train(ref = dice_ref, labels = dice_labels, refType = "rnaseq")

# Parallel processing example with BiocParallel
library(BiocParallel)
parallel_param <- MulticoreParam(workers = 2)
DICE.xCell2Ref <- xCell2::xCell2Train(ref = dice_ref, labels = dice_labels, refType = "rnaseq",
  BPPARAM = parallel_param)
```

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