Package 'xCell2'

July 10, 2025

Type Package

Title A Tool for Generic Cell Type Enrichment Analysis

Version 1.0.6

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.

License GPL (>= 3)

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Author Almog Angel [aut, cre] (ORCID: <https://orcid.org/0009-0001-3297-6935>), Dvir Aran [aut] (ORCID: <https://orcid.org/0000-0001-6334-5039>)

Maintainer Almog Angel <`almog.angel@campus.technion.ac.il`>

Contents

`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` *Access Cell Type Dependencies*

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` *Subset of the DICE Reference*

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` *Access Genes Used*

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` *LM22 Reference*

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` *PanCancer Reference*

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` *Access Cell Type Signatures*

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 *Access Spillover Matrix*

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` *Perform Cell Type Enrichment Analysis*

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.
`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` *Identify Cell Type Lineage Dependencies*

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` *xCell2Object Class*

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` *Train Custom xCell2 Reference Object*

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 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)

Almog Angel and Dvir Aran

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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