# Converting to/from `SCE` objects

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**This cheatsheet explains how you can convert single-cell experiment data in R between `SingleCellExperiment ( SCE )` and `Seurat` formats.**

## `SCE` vs `Seurat` objects

When converting between `Seurat` and `SCE` objects, it's helpful to know how the different object types store and refer to similar information.

The table below shows different aspects of single-cell objects and how to access the associated data, assuming the default names for each type of single-cell object.

There are several differences between `Seurat` and `SCE` objects that are useful to be aware of when converting them. Importantly, the term `"assay"` refers to different things in `SCE` vs. `Seurat` objects:

- In an `SCE` object, an `assay` is a matrix of counts, with default names `"counts"` for raw counts and `"logcounts"` for normalized counts.
- In a `Seurat` object, an `assay` instead refers to an *experiment*. The default `Seurat` assay is called `"RNA"`, and it is analogous to the "main experiment" in an `SCE` object, which is not given a particular name.
- The `Seurat` count matrices are stored within a given assay (experiment) and have default names of `"counts"` for raw counts and `"data"` for normalized counts.

In addition, by default, `SCE` reduced dimension names are capitalized (e.g., `"PCA"`), and `Seurat` reduced dimension names are in lower case (e.g., `"pca"`).

Always bear in mind that your object(s) may be named differently from the defaults as described here!

| Data aspect | SCE | Seurat |
|---|---|---|
| Raw counts matrix | `counts(sce_object)` | `seurat_obj[["RNA"]]@counts` |
| Normalized counts matrix | `logcounts(sce_object)` | `seurat_obj[["RNA"]]@data` |
| Reduced dimension: PCA matrix | `reducedDim(sce_object, "PCA")` | `seurat_obj$pca@cell.embeddings` |
| Reduced dimension: UMAP matrix | `reducedDim(sce_object, "UMAP")` | `seurat_obj$umap@cell.embeddings` |
| Cell-level metadata | `colData(sce_object)` | `seurat_obj@meta.data` |
| Feature (gene)-level metadata | `rowData(sce_object)` | `seurat_obj[["RNA"]]@meta.features` |
| Miscellaneous additional metadata | `metadata(sce_object)` | `seurat_obj@misc` |

We provide some code examples below for these conversions below.

For all code examples below, it is assumed that the `SingleCellExperiment` library has been loaded into your R environment:

```
library(SingleCellExperiment)
```

# Converting from `Seurat` to `SCE`

The following example code assumes you have a `Seurat` object called `seurat_obj`.

```
# Convert Seurat object to SCE object
sce_object <- Seurat::as.SingleCellExperiment(seurat_obj)
```

By default, all assays (experiments) present in the `Seurat` object will be ported into the new `SCE` object.
Recall, in `Seurat`, an assay refers to an *experiment* which may be associated with multiple count matrices.
To only specify that certain assays are retained, you can optionally provide the argument `assay` with *Seurat assay names* to retain in the `SCE` object, for example:

```
# Convert Seurat object to SCE object, retaining only the 'RNA' experiment (assay)
sce_object <- Seurat::as.SingleCellExperiment(seurat_obj, assay = "RNA")
```

Specifying `assay` is mostly useful if there are alternative experiments, for example from CITE-Seq data, present in the `Seurat` object that you do not want to retain during `SCE` conversion.

# Converting from `SCE` to `Seurat`

The following example code assumes you are starting with an `SCE` object called `sce_object`.

The function `Seurat::as.Seurat()` can be used to convert an `SCE` object into a `Seurat` object and takes the following arguments:

- The `SCE` object to convert
- Optional named arguments with the following defaults:
  - `counts = "counts"` specifies that the `SCE` object contains a `"counts"` assay of normalized counts that should be included during conversion.
  - If there is no `"counts"` assay in the SCE object, set this argument as `counts = NULL` or rename accordingly, e.g. `counts = "whatever_assay_name_you_are_using"`.
  - `data = "logcounts"` specifies that the `SCE` object contains a `"logcounts"` assay of normalized counts that should be included during conversion.
  - If there is no `"logcounts"` assay in the SCE object, set this argument as `data = NULL` or rename accordingly, e.g. `data = "whatever_assay_name_you_are_using"`.
  - `assay = NULL` specifies that, by default, all assays (experiments) will be converted. If there are multiple assays and you wish to only convert, for example, the `"RNA"` assay, set this argument as `assay = "RNA"`.
  - `project = "SingleCellExperiment"` specifies that the `Seurat` object being created will have this associated project name. You can override this with any string of interest, e.g. `project = "sample_XYZ"`.

```
# Convert SCE object to Seurat object, assuming both
#  `counts` and  `logcounts` assays are present
seurat_object <- Seurat::as.Seurat(sce_object)

# Convert SCE object to Seurat object, where the SCE object
#  contains a `counts` but not a `logcounts` assay
seurat_object <- Seurat::as.Seurat(sce_object, data = NULL)
```