

# Converting between SCE and Seurat 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	<code>counts(sce_object)</code>	<code>seurat_obj[["RNA"]@counts</code>
Normalized counts matrix	<code>logcounts(sce_object)</code>	<code>seurat_obj[["RNA"]@data</code>
Reduced dimension: PCA matrix	<code>reducedDim(sce_object, "PCA")</code>	<code>seurat_obj\$pca@cell.embeddings</code>
Reduced dimension: UMAP matrix	<code>reducedDim(sce_object, "UMAP")</code>	<code>seurat_obj\$umap@cell.embeddings</code>
Cell-level metadata	<code>colData(sce_object)</code>	<code>seurat_obj@meta.data</code>
Feature (gene)-level metadata	<code>rowData(sce_object)</code>	<code>seurat_obj[["RNA"]@meta.features</code>
Miscellaneous additional metadata	<code>metadata(sce_object)</code>	<code>seurat_obj@misc</code>

Below, we provide some code examples below for how you can accomplish these conversions.

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

```
library(SingleCellExperiment)
```

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## Converting from Seurat to SCE

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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.

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## Converting from SCE to Seurat

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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)
```

## Approaches from `ScPCA`

In addition, this [documentation from the `ScPCA`](#) introduces how to convert `SCE` objects to `Seurat` objects.

Although this documentation was written for `ScPCA` datasets, the steps generally apply to any `SCE` object.

It's worth noting that the example code provided at that link will only retain a single assay (raw `"counts"`) in the new `SCE` object, and it will not retain reduced dimension representations (e.g., PCA or UMAP).

Therefore, this example code is mostly useful at the early stages of processing before you have performed normalization and calculated reduced dimensions.