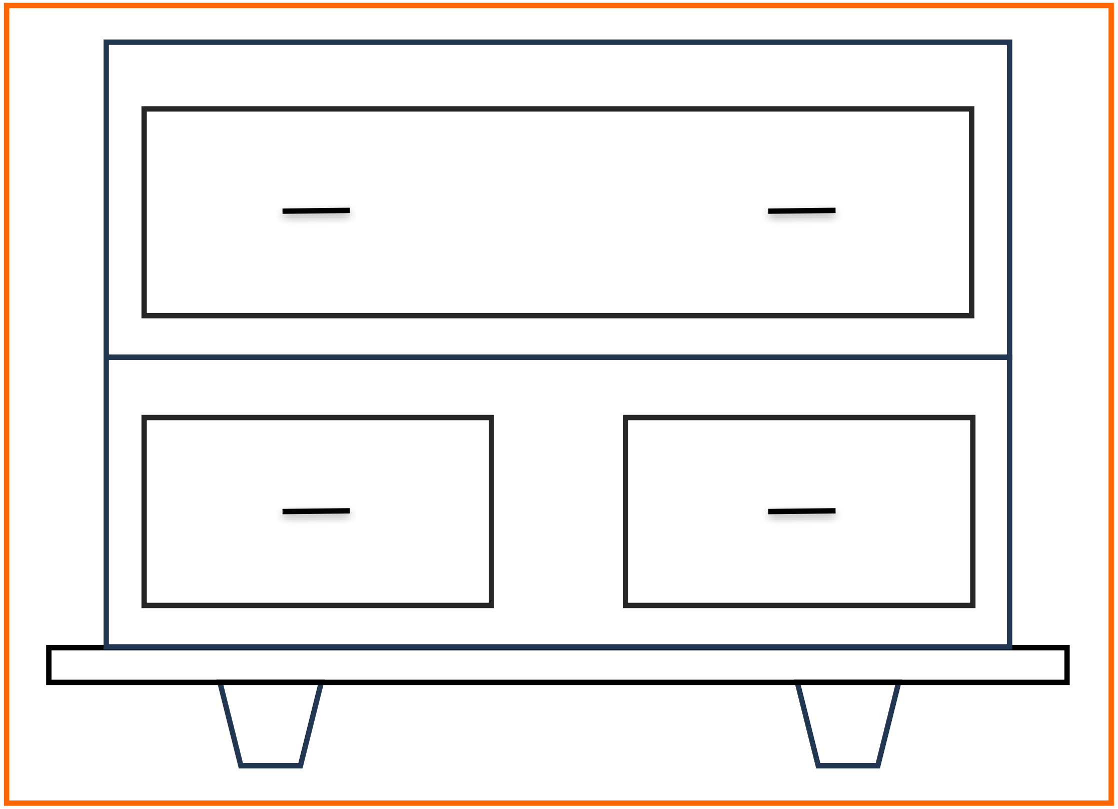
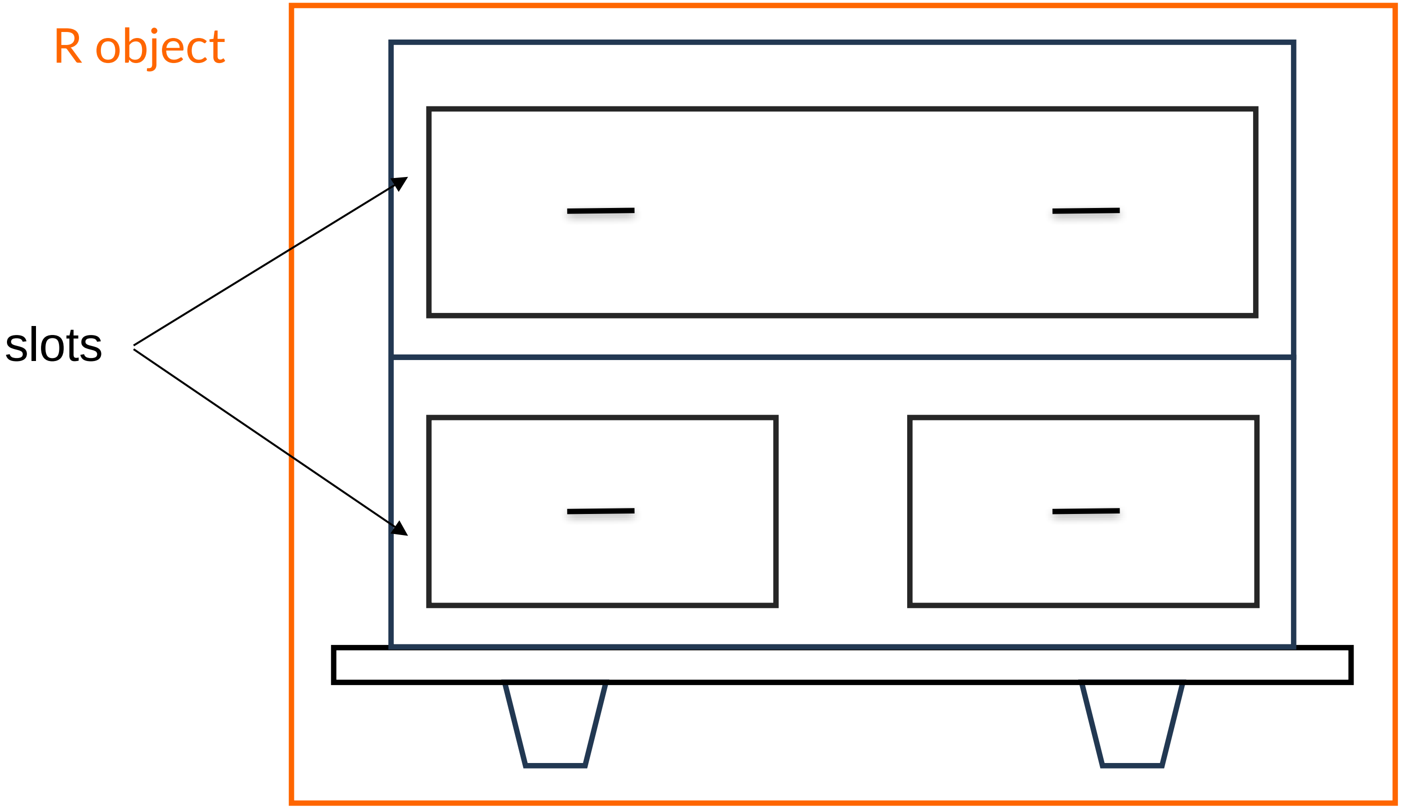
Seurat

The R objects



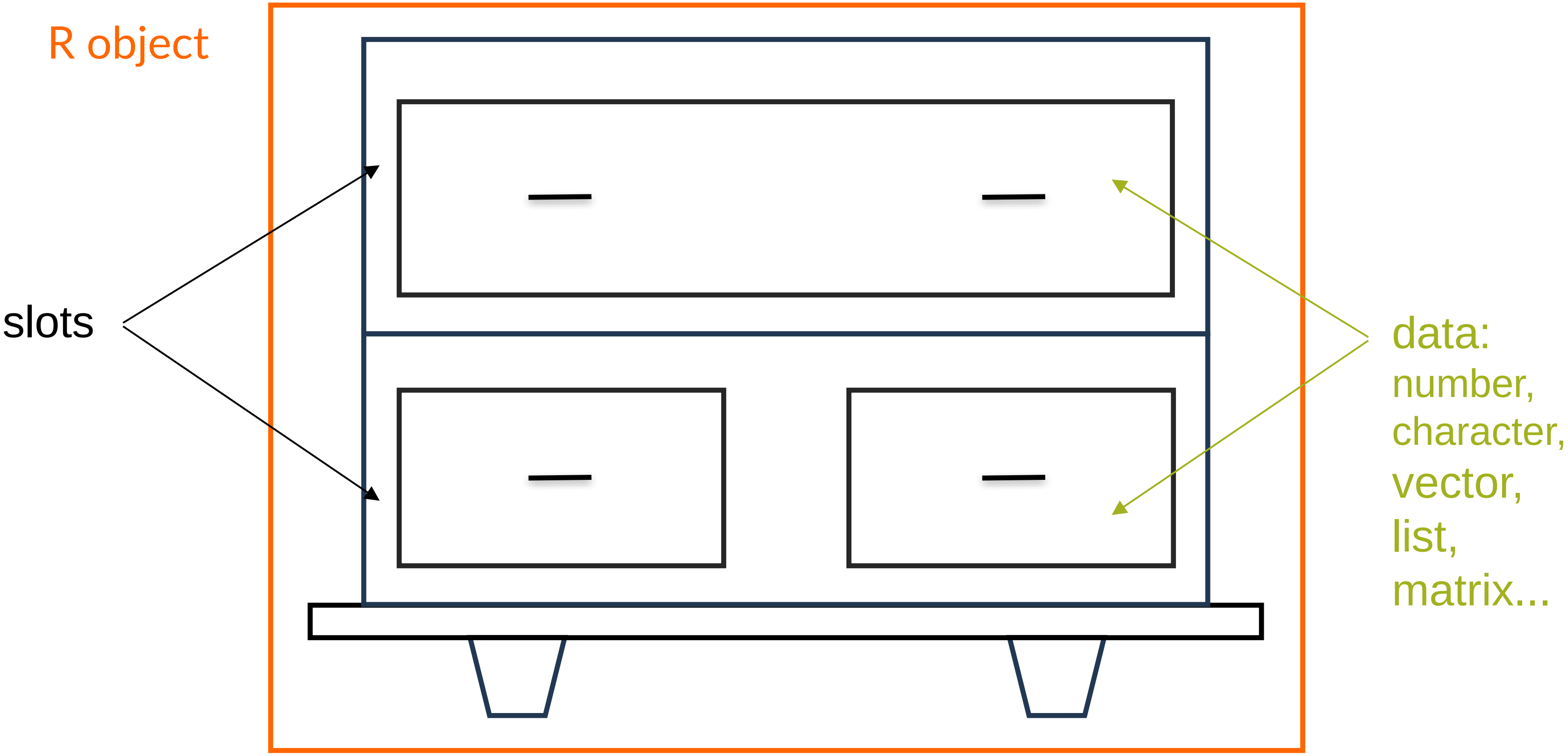
Seurat

The R objects



Seurat

The R objects

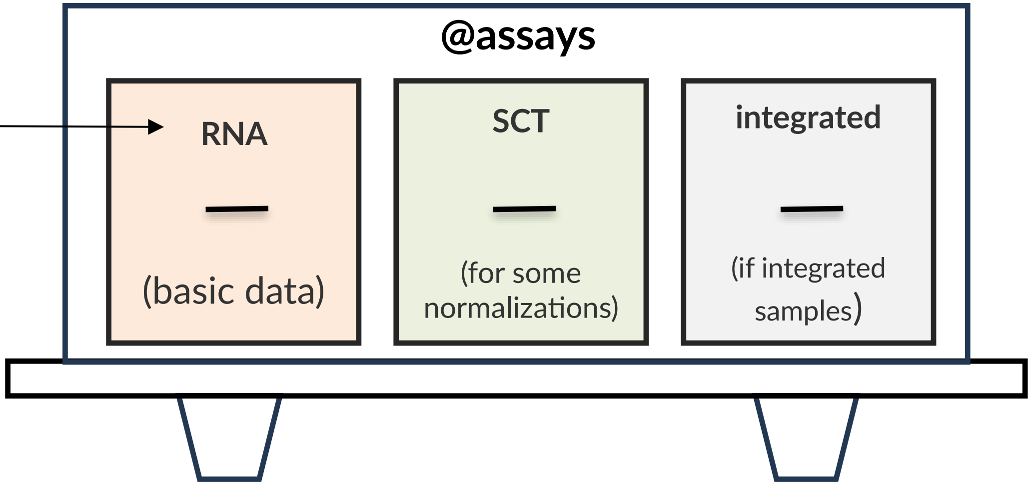


Seurat

The Seurat object

The main components

1 assay contains raw and normalized expression, variable genes...



@assays

RNA

(basic data)

SCT

(for some normalizations)

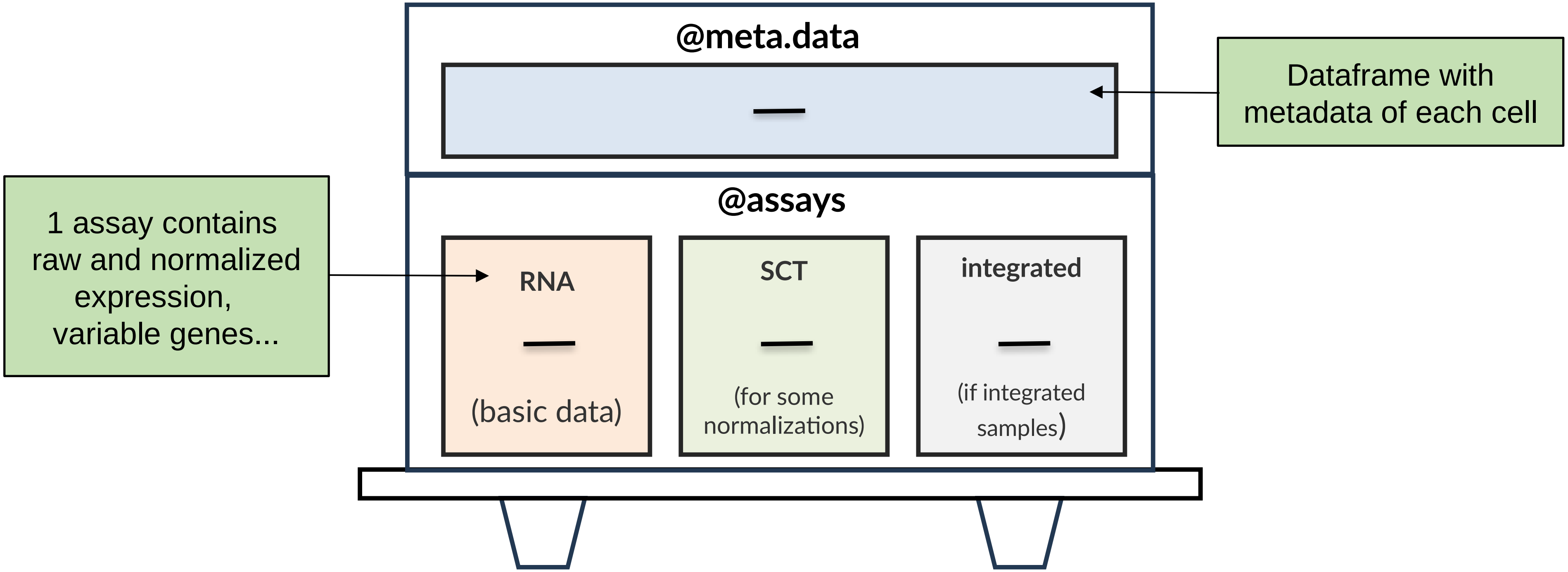
integrated

(if integrated samples)

Seurat

The Seurat object

The main components



1 assay contains raw and normalized expression, variable genes...

@meta.data

Dataframe with metadata of each cell

@assays

RNA

(basic data)

SCT

(for some normalizations)

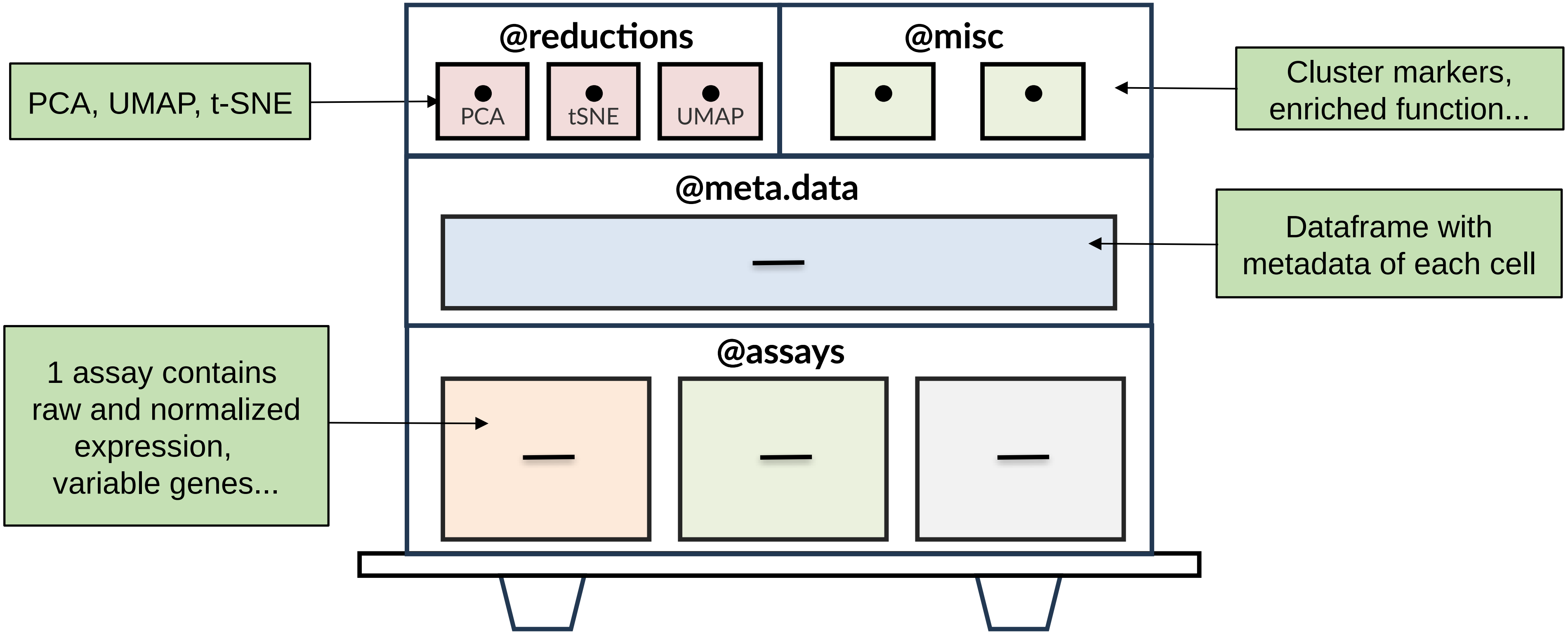
integrated

(if integrated samples)

Seurat

The Seurat object

The main components



PCA, UMAP, t-SNE

Cluster markers, enriched function...

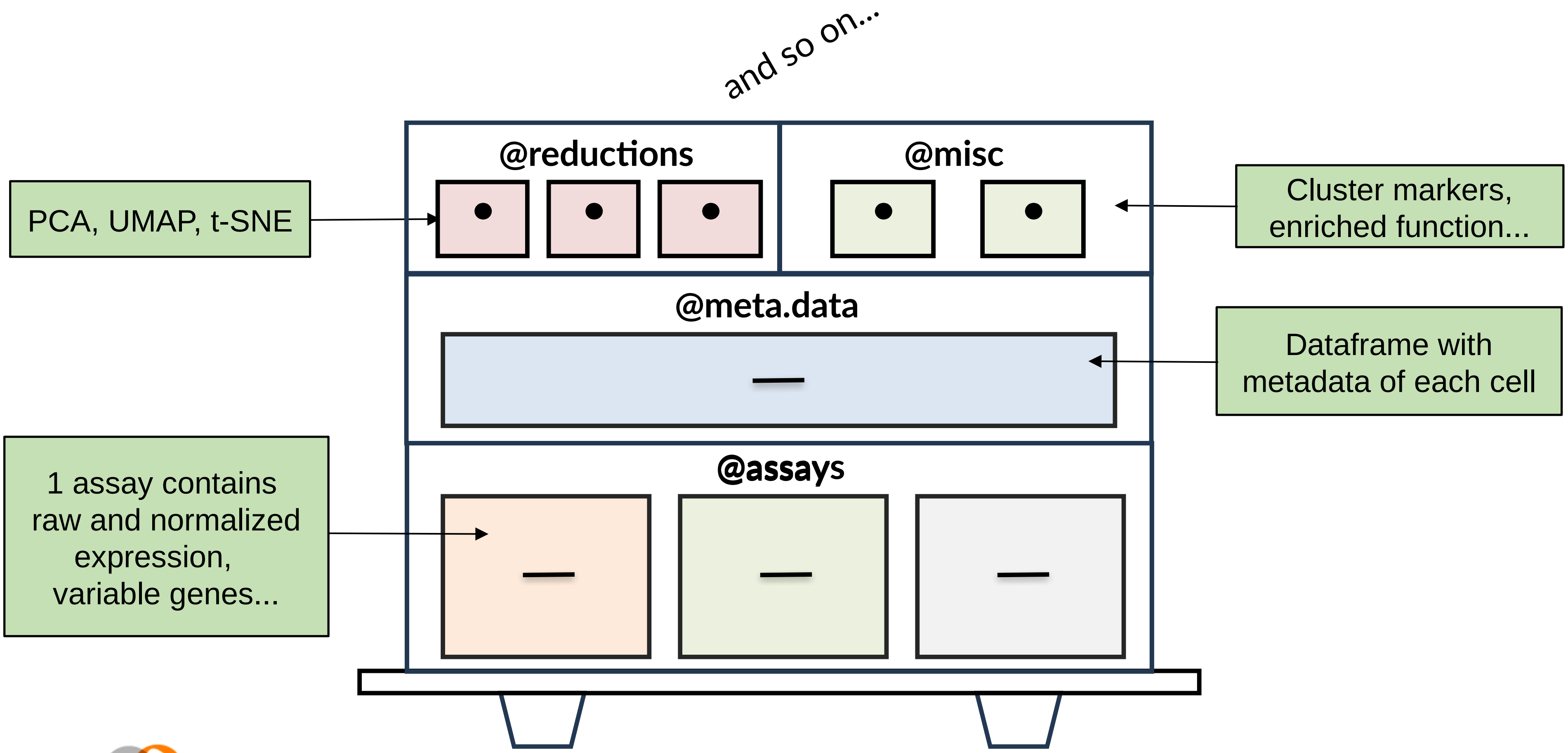
Dataframe with metadata of each cell

1 assay contains raw and normalized expression, variable genes...

Seurat

The Seurat object

The main components



PCA, UMAP, t-SNE

Cluster markers, enriched function...

Dataframe with metadata of each cell

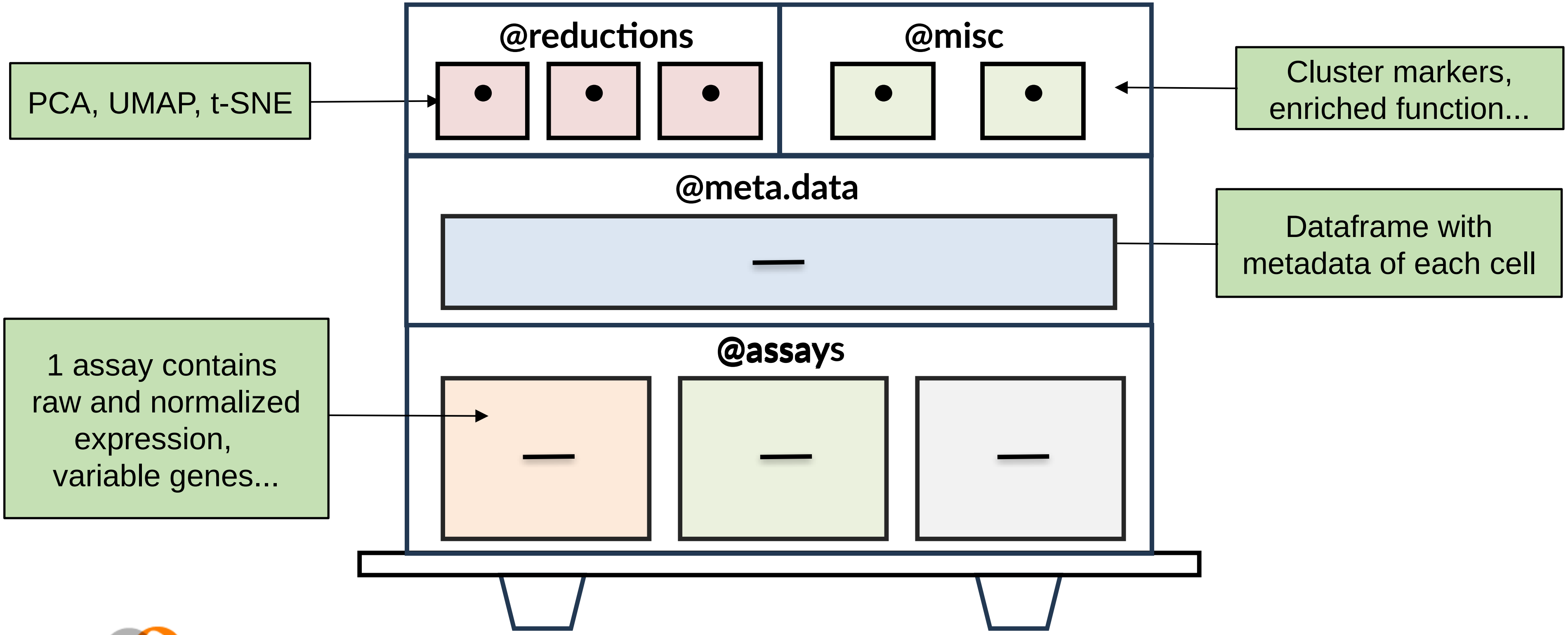
1 assay contains raw and normalized expression, variable genes...

Seurat

The Seurat object

The main components

Seurat object are a little more complicated. We will see the details during pratical sessions



PCA, UMAP, t-SNE

Cluster markers, enriched function...

Dataframe with metadata of each cell

1 assay contains raw and normalized expression, variable genes...

Seurat

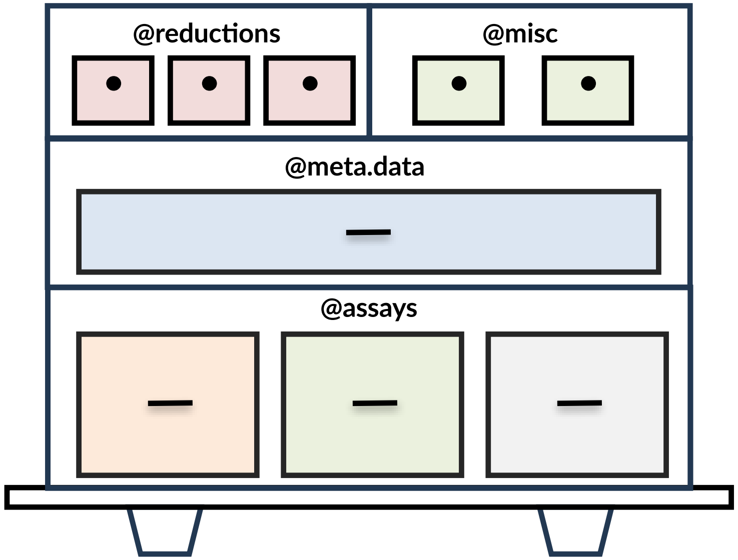
The Seurat object

Access the components

Access a slot:

- **@** operator: e.g. : access metadata

```
seurat_object@meta.data
```



Seurat

The Seurat object

Access the components

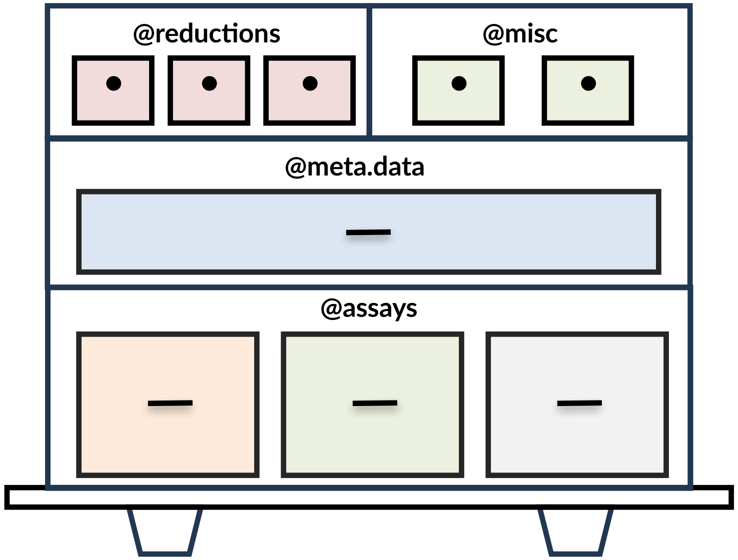
Access a slot:

- **@** operator: e.g. : access metadata

`seurat_object@meta.data`

In practice, Seurat was implmented so that you can browse it with a succession of **@** and **$**.

`seurat_obj@reductions$umap`



Seurat

The Seurat object

Access the components

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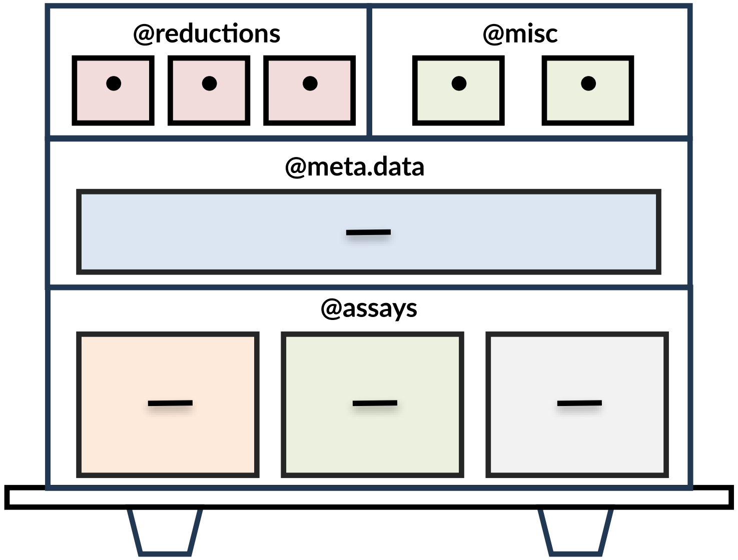
```
seurat_object@meta.data
```

In practice, Seurat was implmented so that you can browse it with a succession of **@** and **$**.

```
seurat_obj@reductions$umap
```

- Acces methods if implemented:
  e.g. access an assay called "RNA":

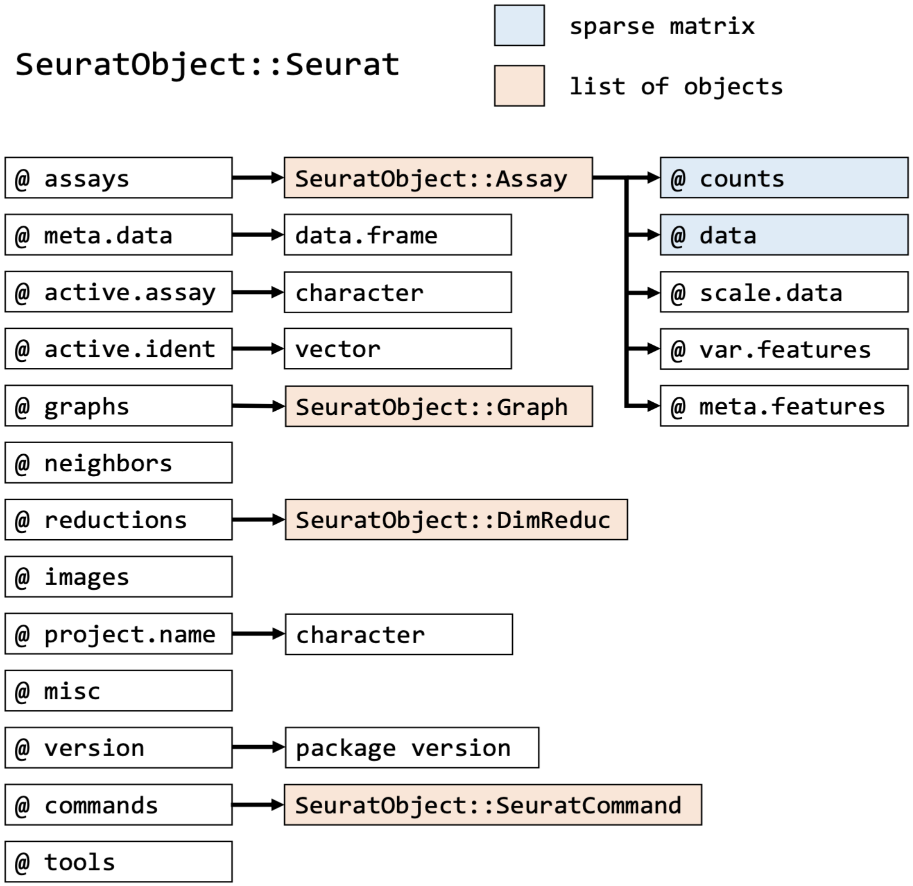
```
GetAssay(seurat_object, assay = "RNA")
```



Seurat

The Seurat object

The whole object



SeuratObject::Seurat

🟦 sparse matrix

🟧 list of objects

@ assays → SeuratObject::Assay
@ meta.data → data.frame
@ active.assay → character
@ active.ident → vector
@ graphs → SeuratObject::Graph
@ neighbors
@ reductions → SeuratObject::DimReduc
@ images
@ project.name → character
@ misc
@ version → package version
@ commands → SeuratObject::SeuratCommand
@ tools

SeuratObject::Assay →
@ counts
@ data
@ scale.data
@ var.features
@ meta.features