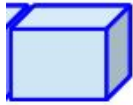


# The *Seurat* Object\* ~~For Dummies~~ For Biologists

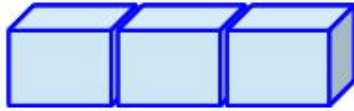
\* v5.x

# Some basic data types in R

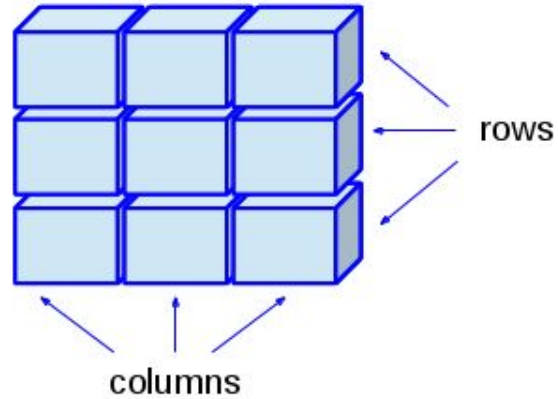
Unit



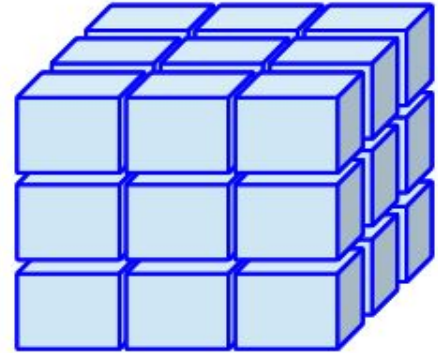
Vector



Matrix

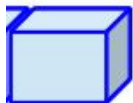


Array



# Some more data types in R

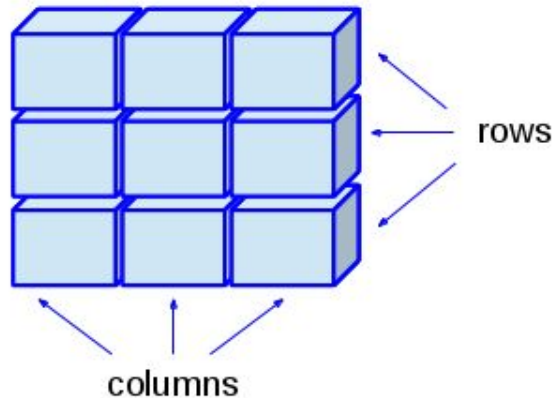
Unit



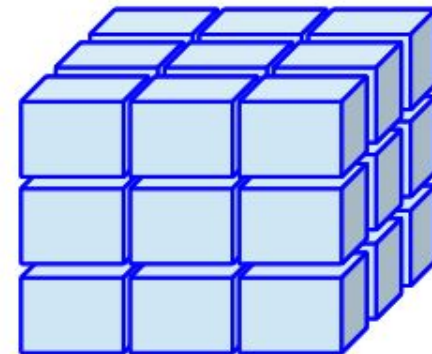
Vector



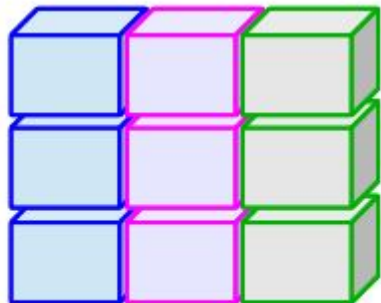
Matrix



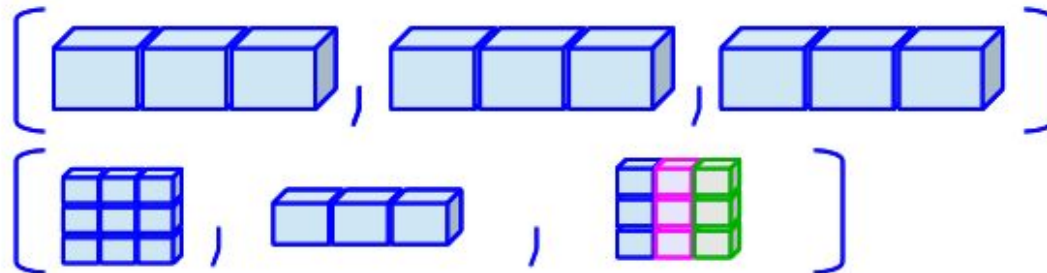
Array



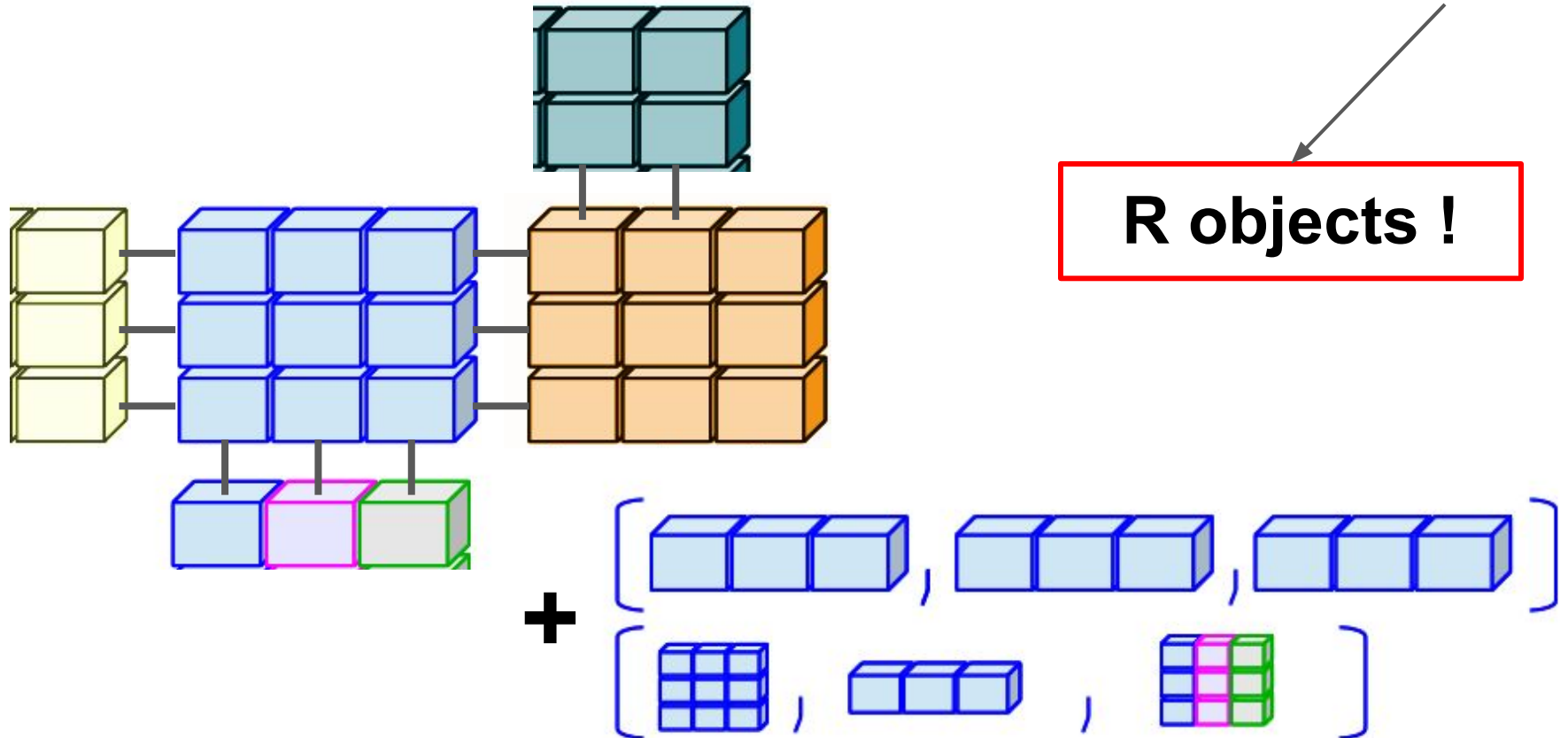
Data Frame  
(Table)



Lists



Add complexity ? Have a structure ? Links between data ?



# The SeuratObject v5 is a hierarchical data container

- When created from scratch, a Seurat object contains information in **slots** :
  - @ **meta.data** : data frame ; contains metadata **qualifiers** for **barcodes/cells**
  - @ **assays** : a list of containers for count data (assays), the default one named :
    - \$ **RNA** : container of :
      - **layers** = data matrices (feature x barcode) :
        - \$ **counts** : contains **raw** counts (*filled by default*)
        - \$ **data** : contains **normalized** counts (*filled with raw counts by default !*)
        - \$ **scale.data** : contains **scaled** counts (*empty by default*)
      - **meta.data** : data.frame ; contains metadata **qualifiers** for **features**
      - **var.features** : vector ; contains the name of a **selection of features** (based on their **high expression variability**)
    - \$ ...
  - @ **reductions** : a list of containers for **dimension reduction** spaces (PCA, etc). By example :
    - \$ **pca** (component x barcode)
    - \$ ...
  - @ **project.name** : character that defines the **project name**
  - @ **commands** : a freeze of the different **steps** the object underwent, and their **parameter values**
- The content of this object will be increased

# The SeuratObject v5 is a hierarchical data container

---

Seurat-class

*The Seurat Class*

---

## Description

The Seurat object is a representation of single-cell expression data for R; each Seurat object revolves around a set of cells and consists of one or more [Assay](#) objects, or individual representations of expression data (eg. RNA-seq, ATAC-seq, etc). These assays can be reduced from their high-dimensional state to a lower-dimension state and stored as [DimReduc](#) objects. Seurat objects also store additional metadata, both at the cell and feature level (contained within individual assays). The object was designed to be as self-contained as possible, and easily extendable to new methods.

## Slots

`assays` A list of assays for this project

`meta.data` Contains meta-information about each cell, starting with number of features detected (`nFeature`) and the original identity class (`orig.ident`); more information is added using [AddMetaData](#)

`active.assay` Name of the active, or default, assay; settable using [DefaultAssay](#)

`active.ident` The active cluster identity for this Seurat object; settable using [Idents](#)

`graphs` A list of [Graph](#) objects

`neighbors` ...

`reductions` A list of dimensional reduction objects for this object

`images` A list of spatial image objects

`project.name` Name of the project

`misc` A list of miscellaneous information

`version` Version of Seurat this object was built under

`commands` A list of logged commands run on this Seurat object

`tools` A list of miscellaneous data generated by other tools, should be filled by developers only using [Tool<-](#)

@ assays

\$ RNA

@ var.features

@ meta.features

Features

@ counts = raw

@ data = raw/normalized

@ scale.data =  
scaled/regressed

Barcodes

Barcodes

@ meta.data

Annotations / metrics

@ reductions

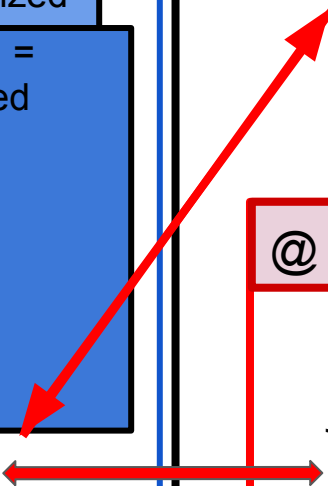
\$ pca

Barcodes

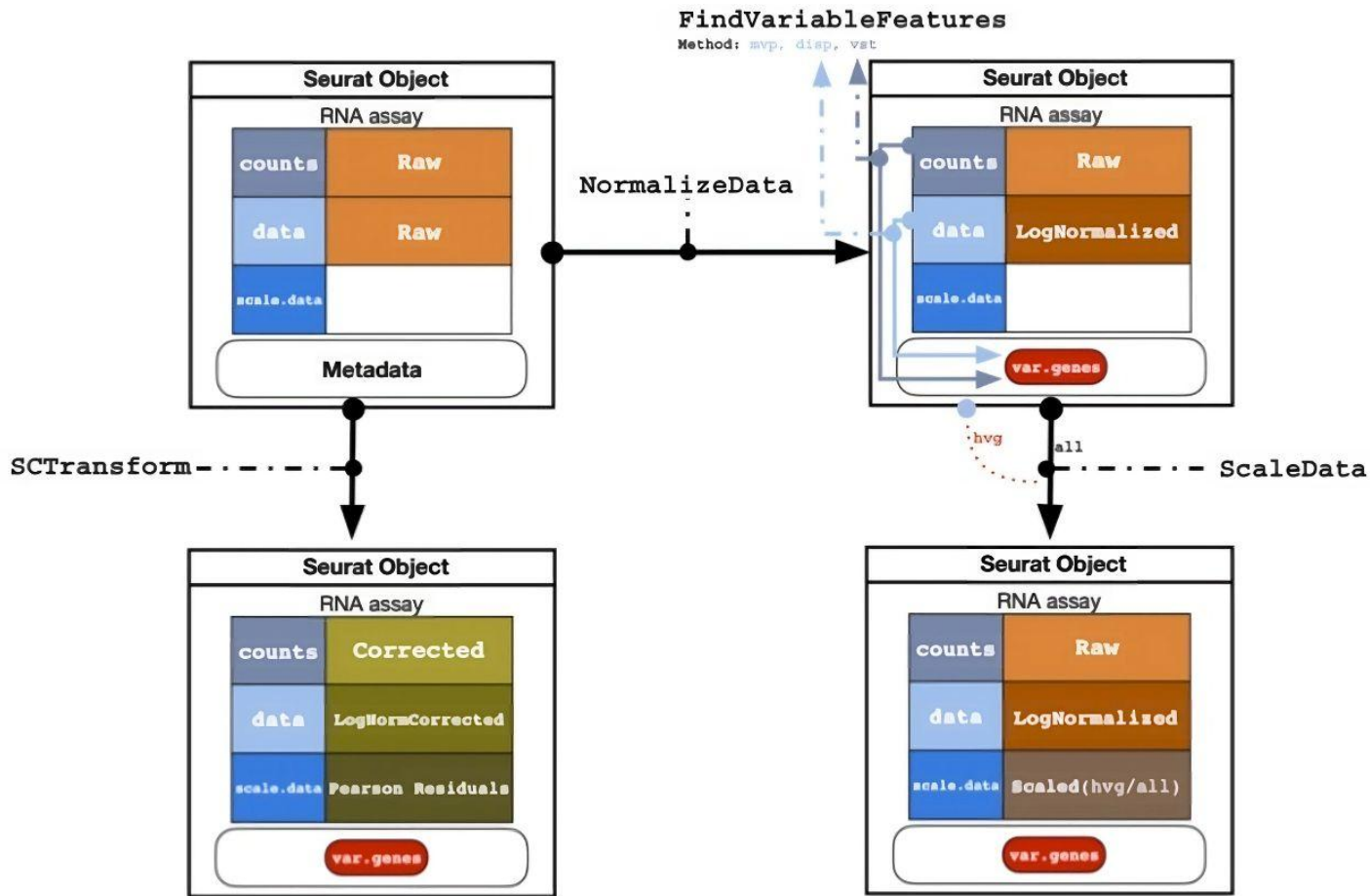
Components

@ project.name

@ commands

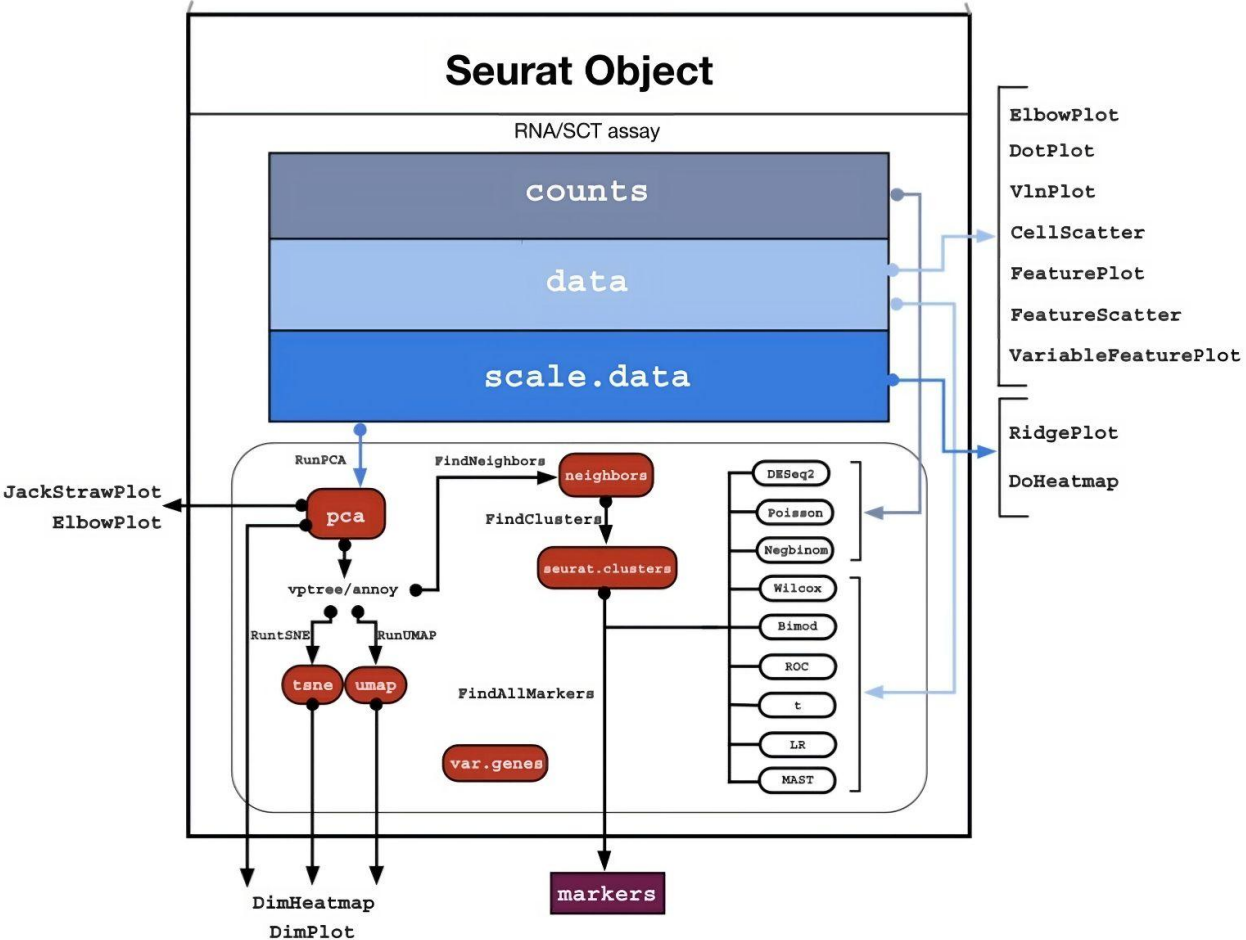


# Cheat sheet : Seurat object evolution through analysis





# Cheat sheet : Interaction of content with analysis steps



Source : X @the HumanBorch

# ! WARNING !

- Current (as of 2023/10) Seurat object format is **v4**
- Newest version (**v5**) is expected to be released **very soon**
  - @ **Seurat** package (contains functions) v5 submitted to CRAN (not released yet)
  - @ **SeuratObject** package (contains the Seurat object specifications) is already available :
    - \$ <https://cran.r-project.org/web/packages/SeuratObject/index.html>
- This new object version will have multiple modifications to its structure
  - @ Introduction of **layers**
- Consequently, some of the explanations given in this presentation may soon be **obsolete**, at least *partially*
- However, the v5 object structure should be **compatible** with v4.