

# Interactive exploratory analysis with iSEE

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# Why (interactive) visualization?

**Quality  
assessment**



**Hypothesis  
generation/  
exploration**



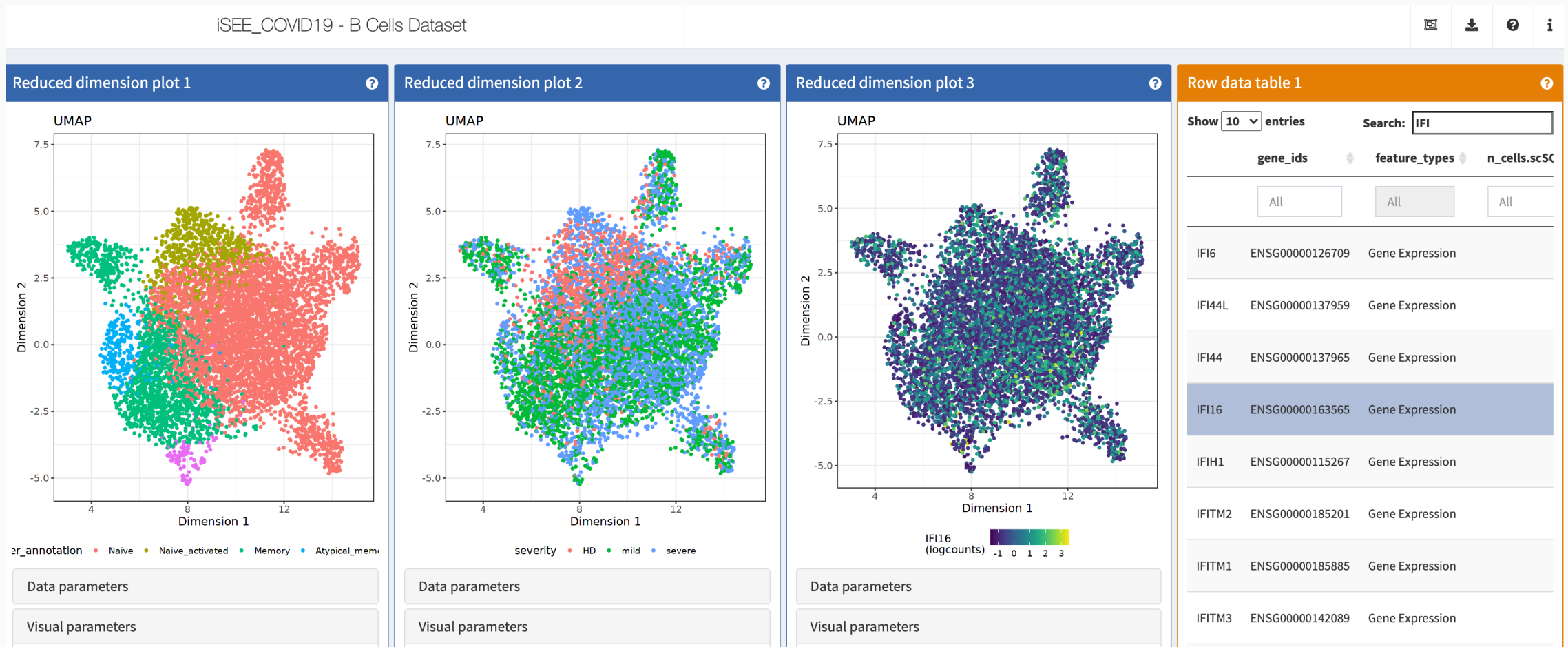
**Result  
visualization**

**Communication**



# What is iSEE?

- An open-source R/Bioconductor package that allows you to easily create customized interactive interfaces for exploring your data and visualize any **pre-calculated** results.



# What is iSEE?

- An open-source R/Bioconductor package that allows you to easily create customized interactive interfaces for exploring your data and visualize any **pre-calculated** results.
- Essentially data type agnostic - any rectangular data can be explored (but it was designed with high-throughput biological data in mind).
- Easy to run (for a suitably formatted data set, more on that shortly):

```
library(iSEE)  
iSEE(sce)
```

- Highly configurable, flexible interface.
- Strong focus on reproducibility, all code to generate displayed figures can be downloaded.

# What about other tools?

- <https://github.com/federicomarini/awesome-expression-browser>

A curated list of software and resources for exploring and visualizing (browsing) expression data, but not only limited to that. Credits for the backbone of the structure go to Sean Davis and his [awesome-single-cell](#) repository.

Contributions welcome!

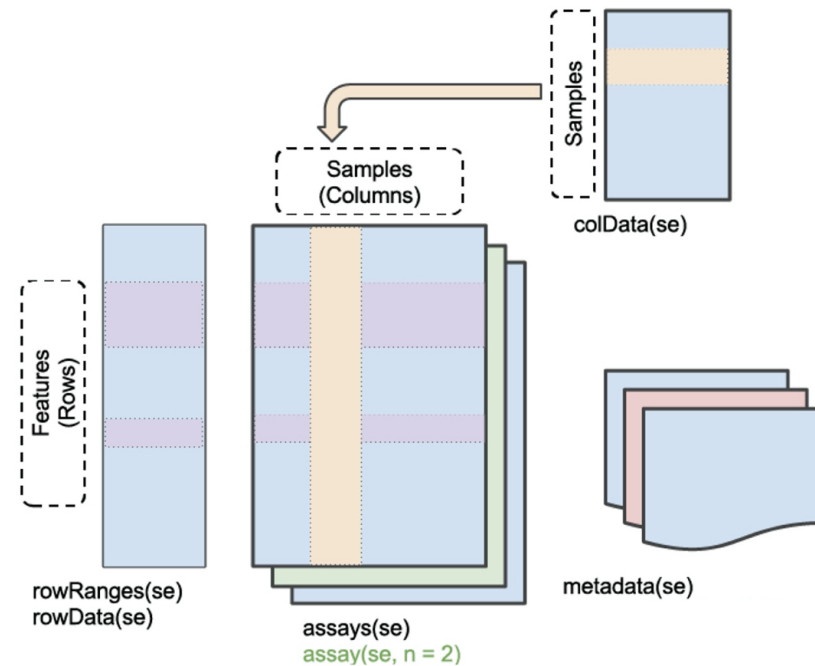
## Software list

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- [AMP RA](#), publicly available RNA-seq and CyTOF for human synovial tissue from patients with rheumatoid arthritis (RA) or osteoarthritis (OA), visualized with Shiny. [bioRxiv](#)
- [AMP SLE](#), publicly available RNA-seq for human kidney biopsies from patients with systemic lupus erythematosus (SLE) patients, visualized with Shiny. [bioRxiv](#)
- [adultHSPC10X](#) as a companion to <https://doi.org/10.1182/blood-2017-12-821413>
- [Allen Brain Atlases](#), Allen Brain Atlases and Data (from the Allen Institute) - for example, referred to in this recent publication on whole brain spatial transcriptomics (<https://www.biorxiv.org/content/10.1101/784181v1>)
- [ALS Spatiotemporal gene expression Atlas](#), companion to the MS <http://science.sciencemag.org/content/364/6435/89>
- [ASAP](#), Automated Single-cell Analysis Pipeline (<https://doi.org/10.1093/bioinformatics/btx337>)
- [Bacnet](#), a user-friendly platform for building multi-omics websites. Described in <https://academic.oup.com/bioinformatics/advance-article/doi/10.1093/bioinformatics/btaa828/5910544>,

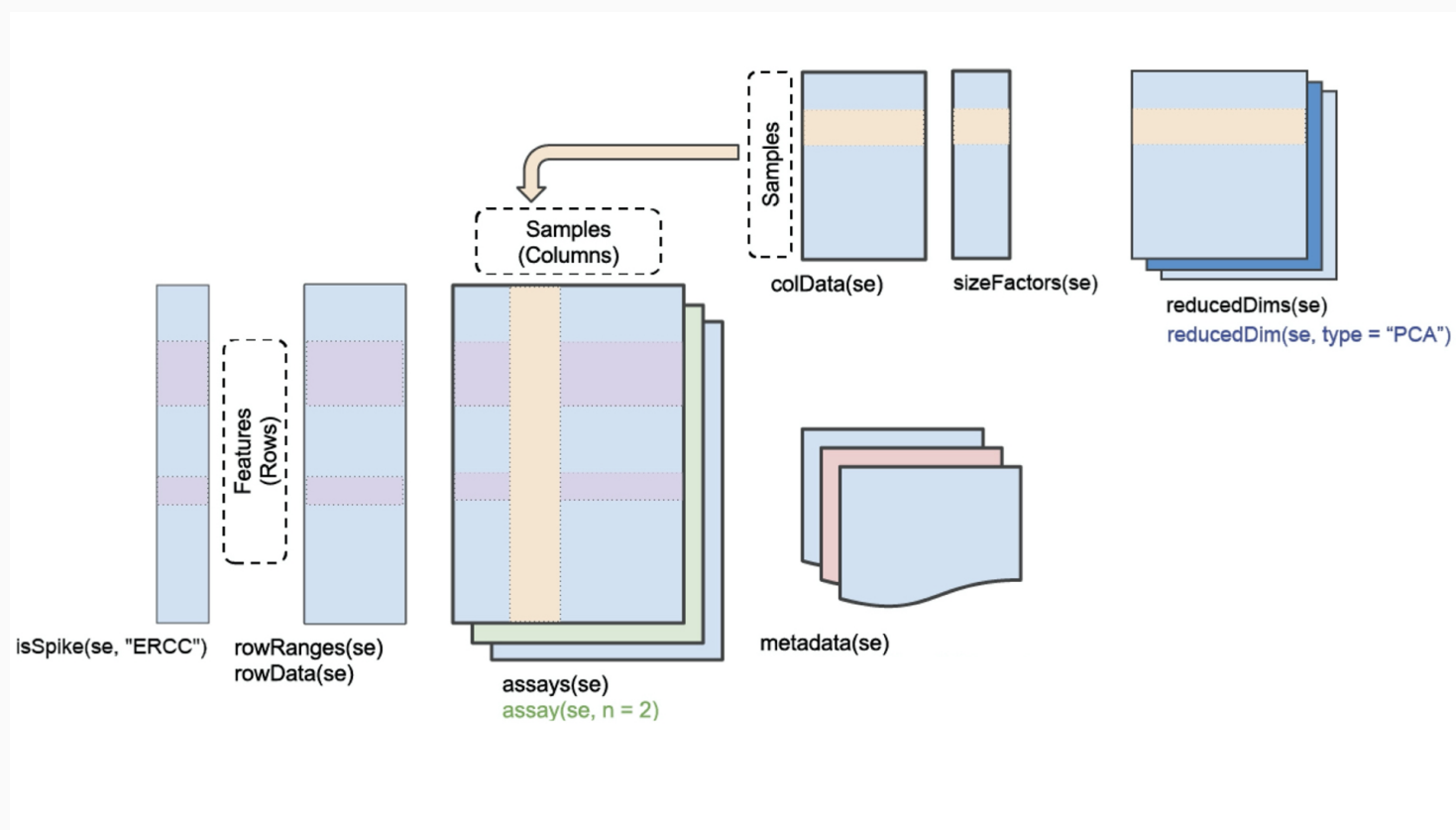
# With what data can iSEE be used?

- Any form of (numeric) rectangular-shaped data (measurements for some form of **features** across a range of **samples**).
- Both features and samples can come with **annotations**/additional information.
- Data must be stored in a `SummarizedExperiment` container (or one of its derivatives, including `SingleCellExperiment` or `DESeqDataSet` ).



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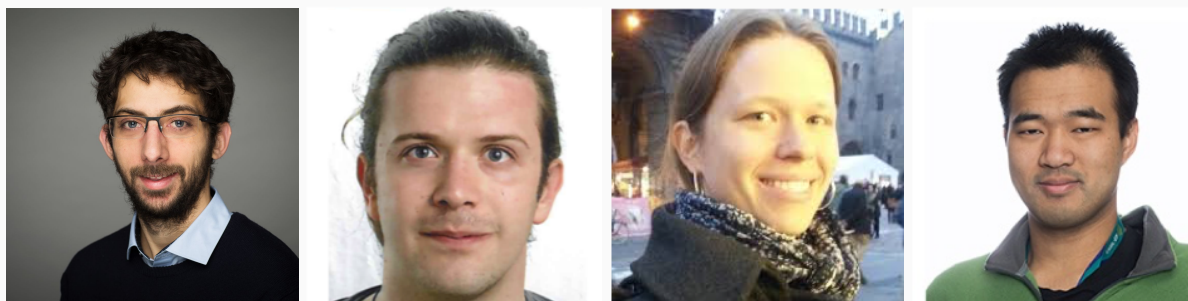
# How to get to a SingleCellExperiment object?

- Many Bioconductor packages directly import data into a `SingleCellExperiment` object (e.g., `DropletUtils::read10xCounts()`) or a `SummarizedExperiment` object (e.g., `tximeta::tximeta()`).
- From an `AnnData` object: use e.g. the `zellkonverter` Bioconductor package.
- From a `Seurat` object: use e.g. `Seurat::as.SingleCellExperiment()`.



# Additional resources

- The bookdown book on *Extending iSEE*: <https://isee.github.io/iSEE-book/>
- Bioconductor landing page: <https://bioconductor.org/packages/iSEE/>
- Publication (F1000Research, 2018): <https://f1000research.com/articles/7-741/v1>
- Deployed examples: <https://marionilab.cruk.cam.ac.uk/>, code at <https://github.com/iSEE/iSEE2018>
  - Further deployments in the [https://github.com/iSEE/iSEE\\_instances](https://github.com/iSEE/iSEE_instances) repo
  - `iSEE` in production: <http://www.teichlab.org/singlecell-treg>, [https://libd.shinyapps.io/tran2020\\_Amyg/](https://libd.shinyapps.io/tran2020_Amyg/), <http://tilatlas.unil.ch/>, [http://shiny.imbei.uni-mainz.de:3838/iSEE\\_covidIT/](http://shiny.imbei.uni-mainz.de:3838/iSEE_covidIT/)
- Development version (bug reports etc): <https://github.com/iSEE/iSEE>
- The `#iSEE` channel in the [Bioconductor slack workspace](#)
- Additional panels and modes in `iSEEu`: <https://bioconductor.org/packages/iSEEu/>



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