

Interactive exploratory analysis with iSEE

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Why (interactive) visualization?

**Quality
assessment**



**Hypothesis
generation/
exploration**



**Result
visualization**

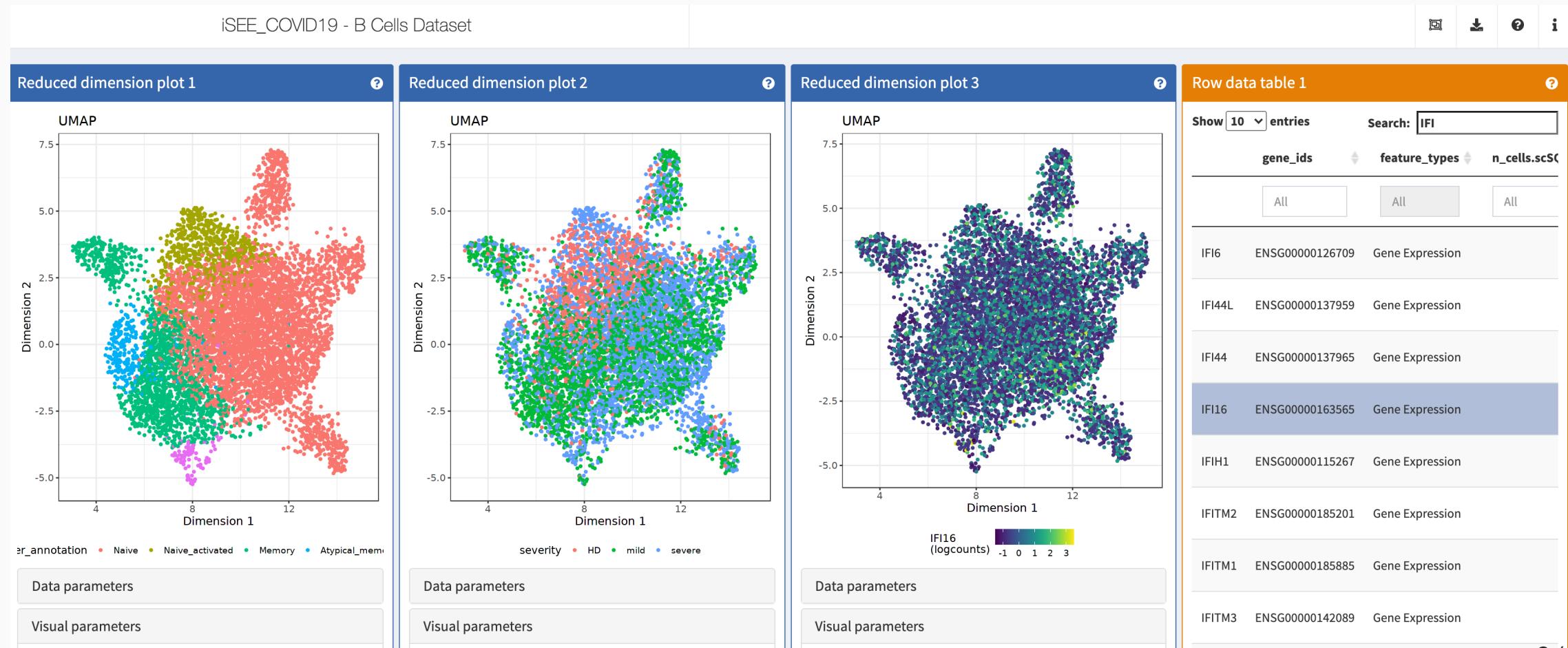


Communication



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.

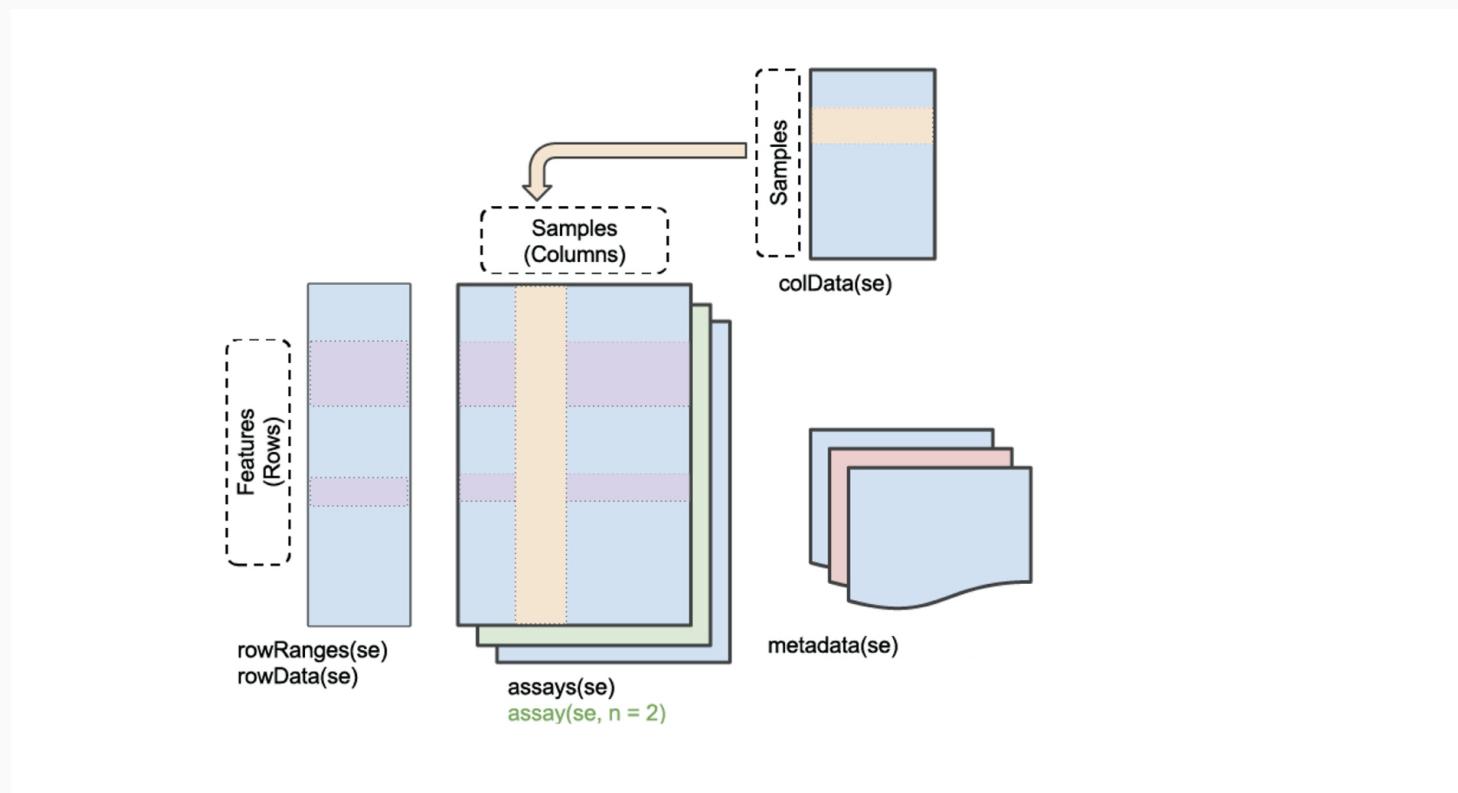
Contributions welcome!

Software list

- [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>,

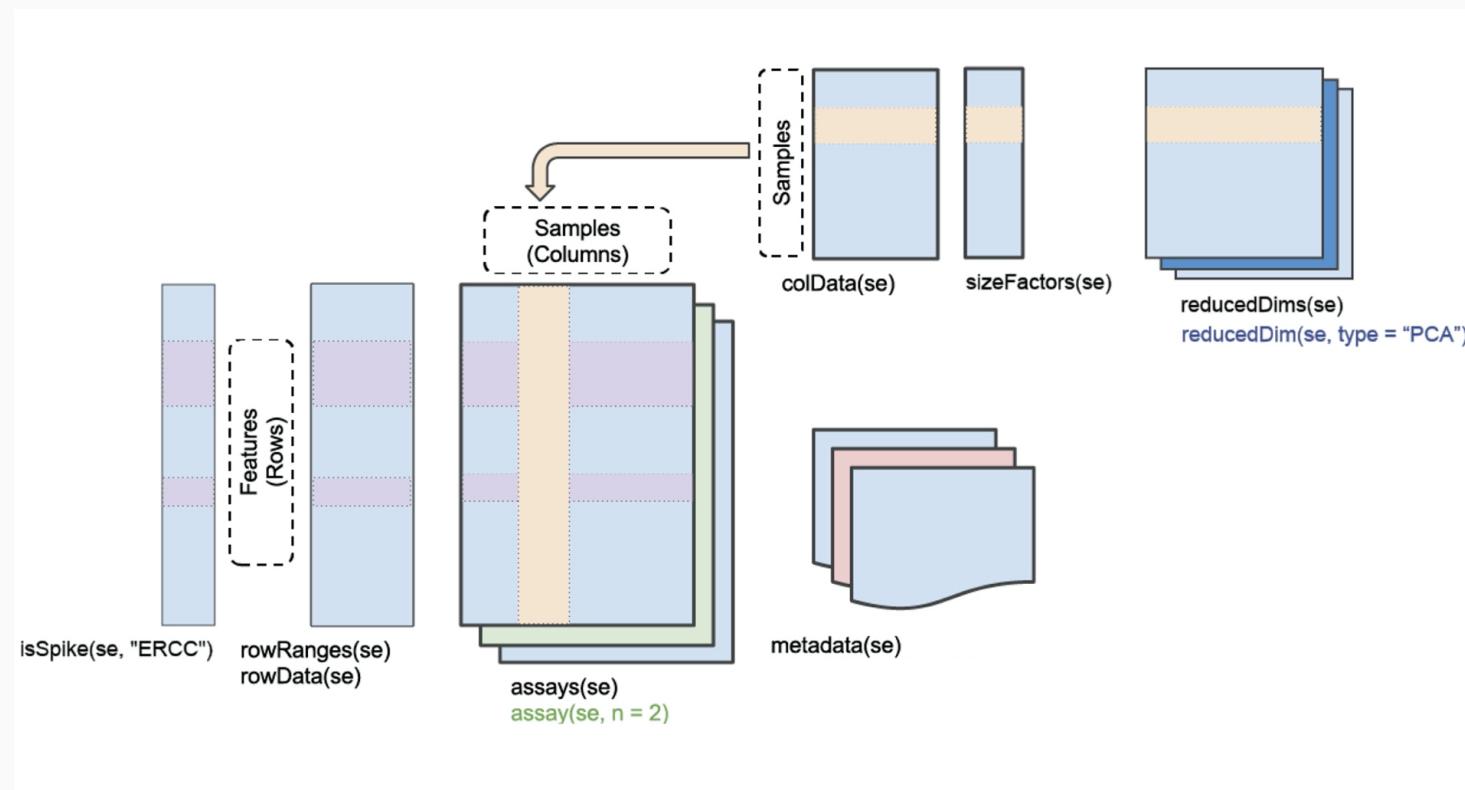
With what data can iSEE be used?

- 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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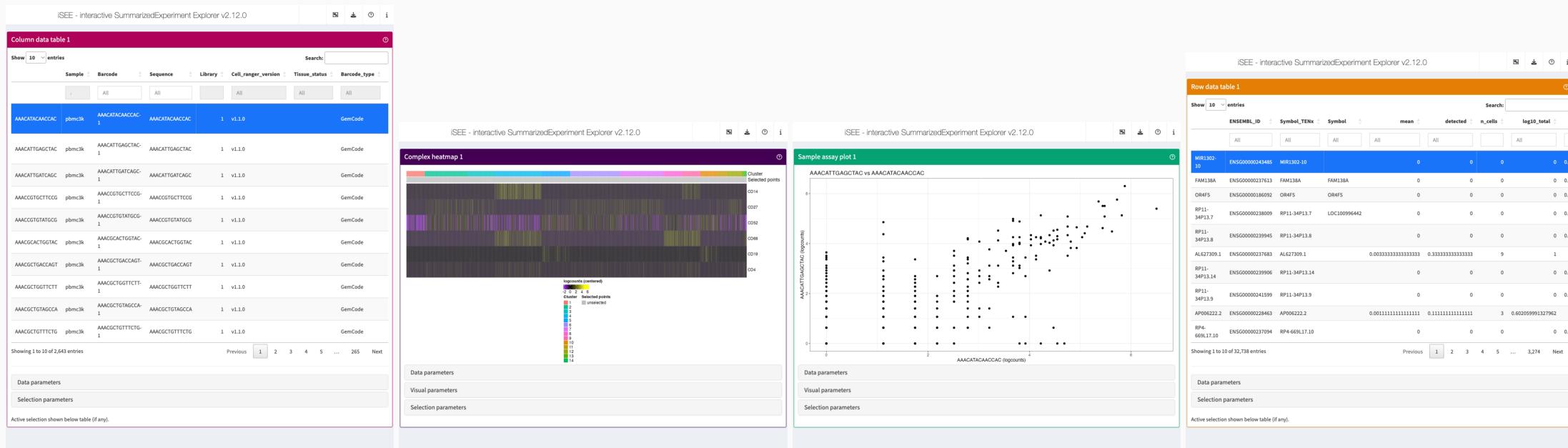
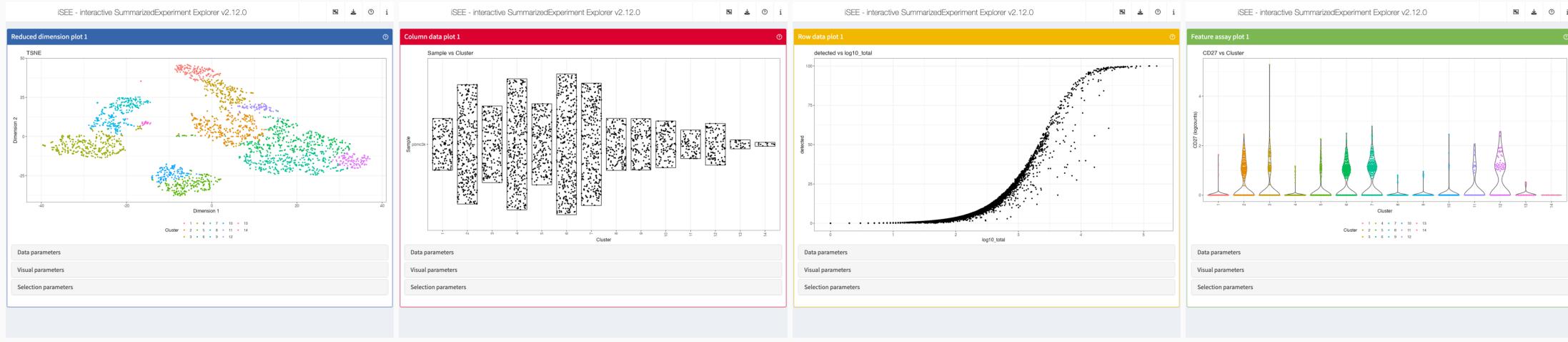
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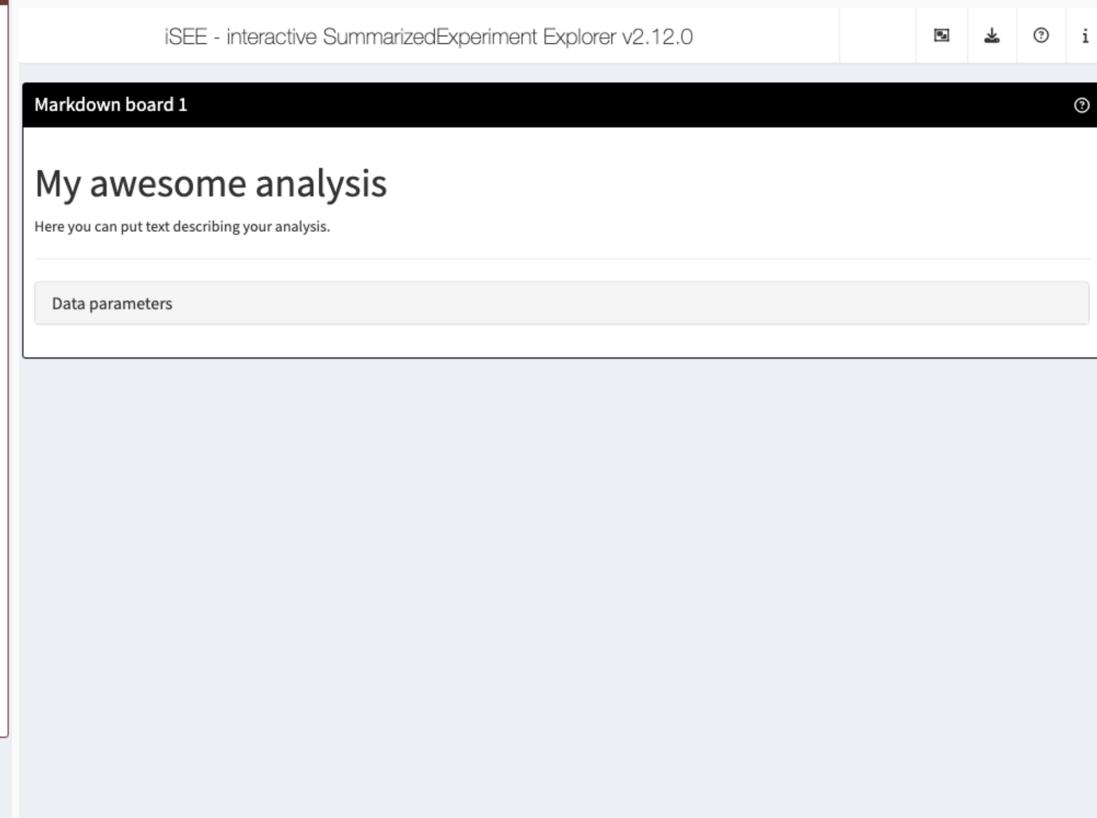
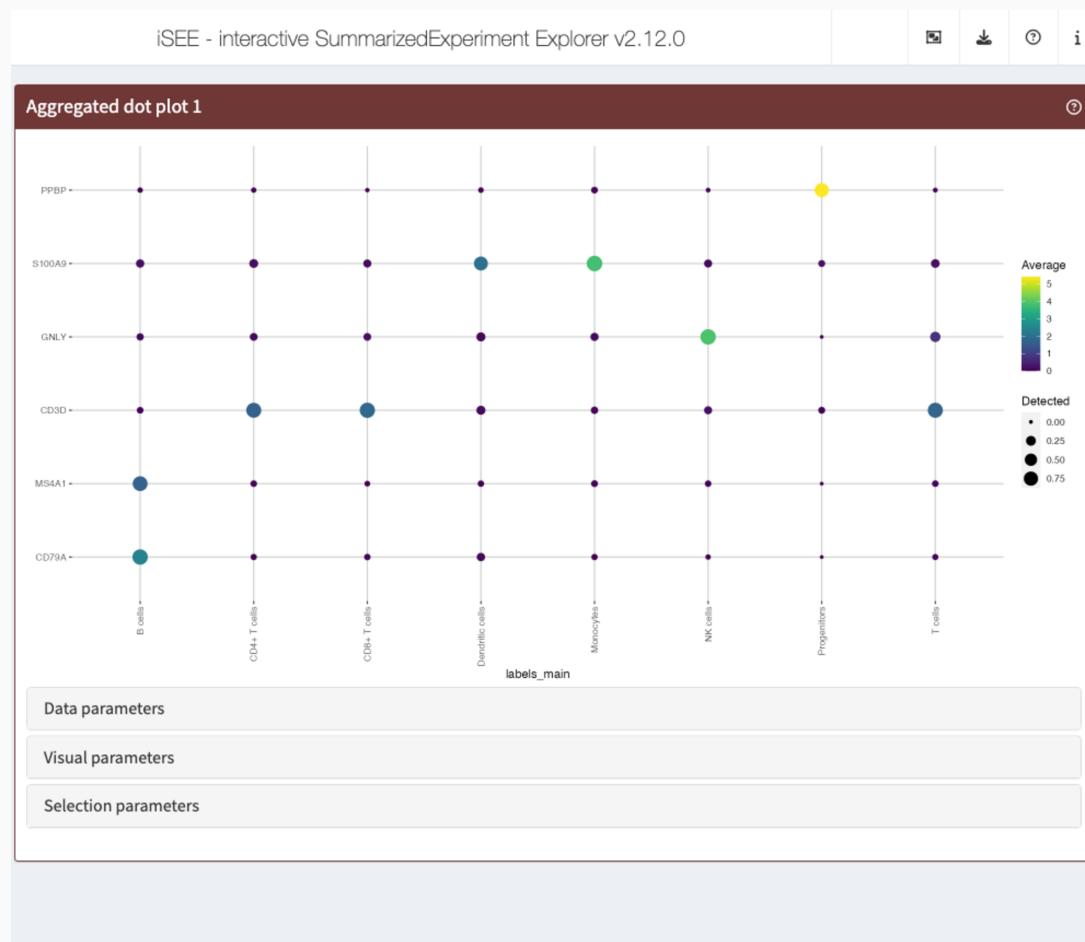
How to get to a `SummarizedExperiment`/`SingleCellExperiment` object?

- Use the constructor functions: `SummarizedExperiment()`, `SingleCellExperiment()`, `DESeqDataSet()`,
`DESeqDataSetFromMatrix()`, ...
- 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()`.

Default panels



Some additional iSEEu panels (1)



Some additional iSEEu panels (2)

iSEE - interactive SummarizedExperiment Explorer v2.12.0

Reduced dimension plot 1

TSNE

Dimension 2

Dimension 1

Labels_main:

- B cells
- CD4+ T cells
- Monocytes
- Progenitors
- CD4+ T cells
- Dendritic cells
- NK cells
- T cells

Data parameters

Visual parameters

Selection parameters

147 of 2643 columns in active selection (5.6%)
Transmitting selection to **Dynamic marker table 1**

Dynamic marker table 1

Show 10 entries Search:

	Top	p.value	FDR	summary.logFC
NKG7	1	3.82707813484363e-160	1.25290883978508e-155	4.03792299040721
GZMB	2	1.62101347401e-77	2.65343695560698e-73	3.05201904291836
PRF1	3	3.34350657086276e-68	3.64865727056353e-64	2.2793771574755
GZMA	4	5.72601639771309e-67	4.68645812070829e-63	2.03685758075537
CTSW	5	1.16489080297511e-65	7.62723902155971e-62	1.86101289971994
CST7	6	5.45154910964559e-62	2.9745469125263e-58	2.05343367397107
HLA-C	7	1.7423220827905e-59	8.14859147805644e-56	0.997513102335159
GNLY	8	6.88822582397093e-59	2.8188342128145e-55	3.47023846610855
B2M	9	2.32502589712268e-58	8.45741086888909e-55	0.738172228557924
FGFBP2	10	5.66066123209477e-54	1.85318727416319e-50	2.18921271211894

Showing 1 to 10 of 32,738 entries

Previous 1 2 3 4 5 ... 3,274 Next

Data parameters

Selection parameters

Active selection shown below table (if any).
Receiving selection from **Reduced dimension plot 1**

iSEE - interactive SummarizedExperiment Explorer v2.12.0

Reduced dimension plot 1

TSNE

Dimension 2

Dimension 1

Cluster:

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14

Data parameters

Visual parameters

Selection parameters

147 of 2643 columns in active selection (5.6%)
Transmitting selection to **Dynamic reduced dimension plot 1**

Dynamic reduced dimension plot 1

X

Y

Cluster:

- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8
- 9
- 10
- 11
- 12
- 13
- 14

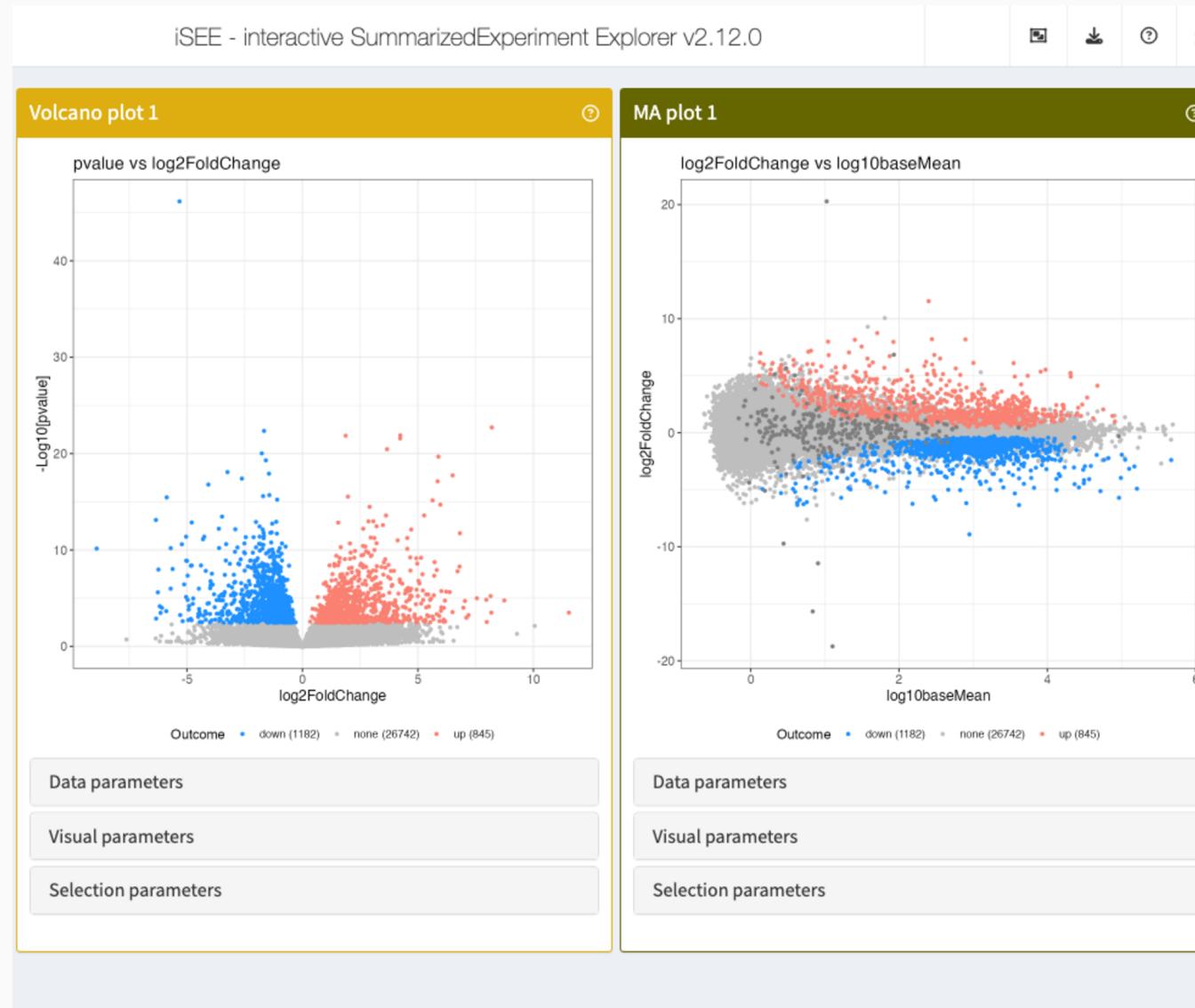
Data parameters

Visual parameters

Selection parameters

Receiving selection from **Reduced dimension plot 1**

Some additional iSEEu panels (3)



Some additional iSEEu panels (4)

iSEE - interactive SummarizedExperiment Explorer v2.12.0

Feature set table 1

Show 10 entries

Search:

TERM
type II interferon
GO:0032609 type II interferon production
GO:0032649 regulation of type II interferon production
GO:0032729 positive regulation of type II interferon production
GO:0034341 response to type II interferon
GO:0071346 cellular response to type II interferon
GO:0060330 regulation of response to type II interferon
GO:0060331 negative regulation of response to type II interferon
GO:0060333 type II interferon-mediated signaling pathway
GO:0060334 regulation of type II interferon-mediated signaling pathway
GO:0060336 negative regulation of type II interferon-mediated signaling pathway

Showing 1 to 10 of 16 entries (filtered from 22,934 total entries)

Previous 1 2 Next

Data parameters

132 of 29060 rows in active selection (0.5%)
Transmitting selection to Row data table 1
Transmitting selection to MA plot 1

Row data table 1

Show 10 entries

Search:

gene_id	SYMBOL	
All	A	
CX3CL1	ENSG0000006210.6	CX3CL1
CCL26	ENSG0000006606.8	CCL26
NOS2	ENSG0000007171.17	NOS2
NUB1	ENSG0000013374.16	NUB1
WAS	ENSG0000015285.10	WAS
SLC11A1	ENSG0000018280.16	SLC11A1
CD74	ENSG0000019582.14	CD74
NR1H3	ENSG0000025434.18	NR1H3
VIM	ENSG0000026025.15	VIM
IFNGR1	ENSG0000027697.14	IFNGR1

Showing 1 to 10 of 132 entries

Previous 1 2 3 4 5 ... 14 Next

Data parameters

Selection parameters

Receiving selection from Feature set table 1

MA plot 1

log2FoldChange vs log10baseMean

Row selection • active = unselected

Data parameters

Visual parameters

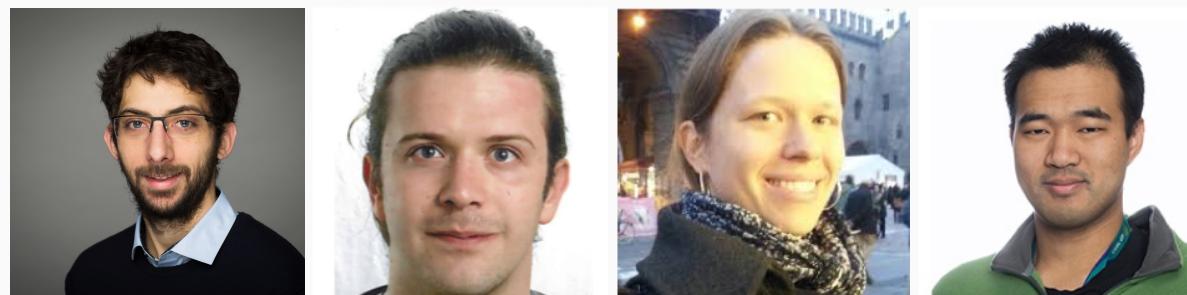
Selection parameters

Receiving selection from Feature set table 1

Active selection shown below table (if any). Receiving selection from Feature set table 1

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 repo
 - `iSEE` in production: <http://www.teichlab.org/singlecell-treg>, https://libd.shinyapps.io/tran2020_Amyg/,
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/>



Kevin Rue-Albrecht, Federico Marini, Charlotte Soneson, Aaron Lun