

Supplementary Figure 1

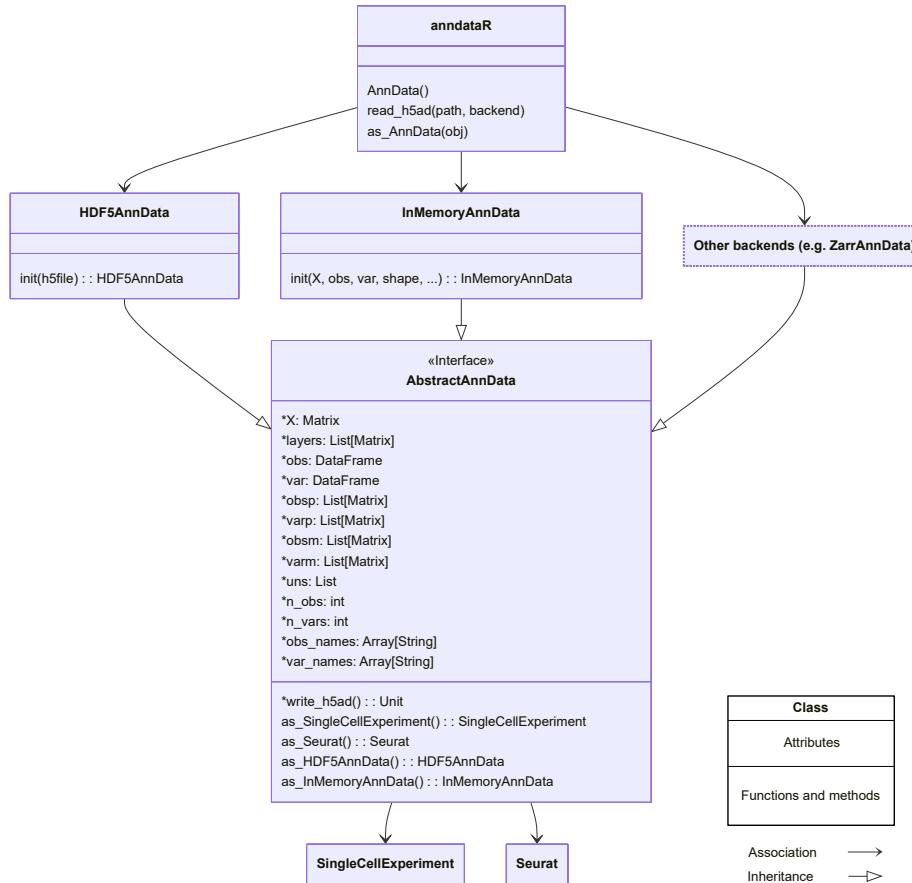


Figure 1: Schematic class diagram of `anndataR`.

Supplementary Figure 2

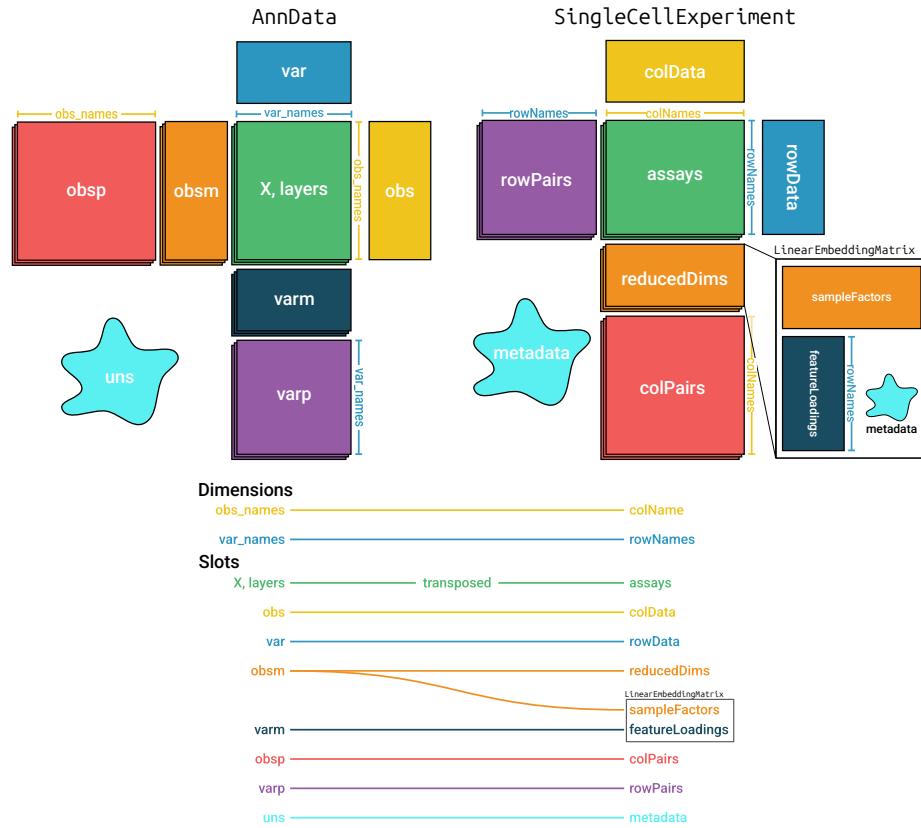


Figure 2: Schematic overview of the default conversion to and from AnnData and SingleCellExperiment objects.

Supplementary Figure 3

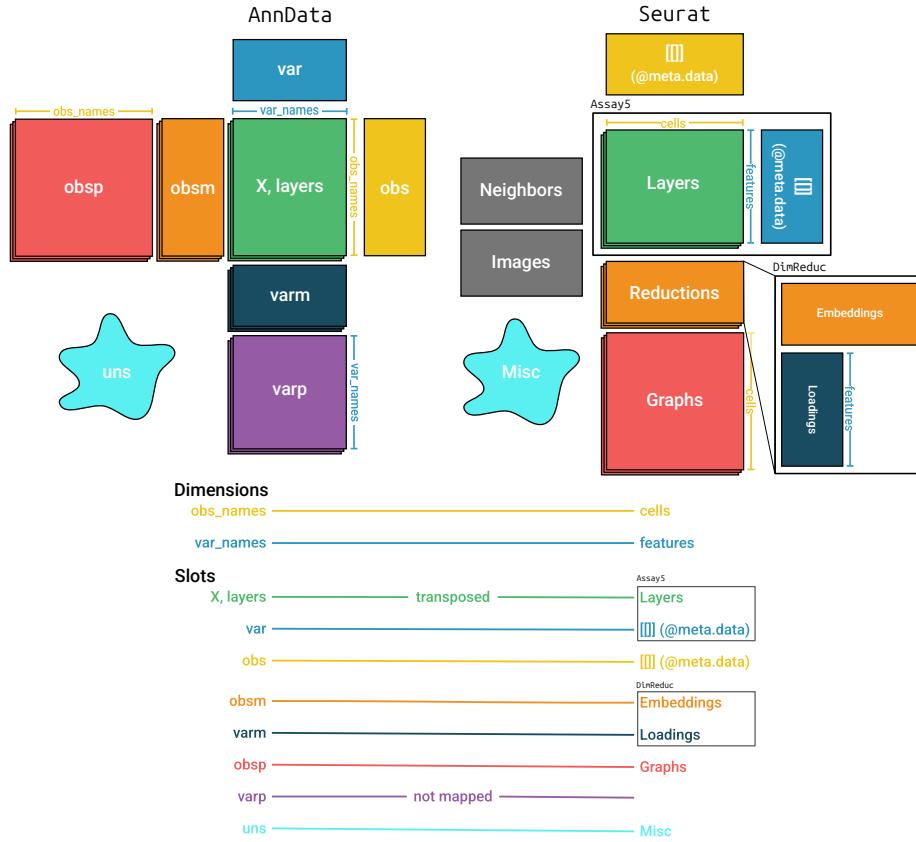


Figure 3: Schematic overview of the default conversion to and from AnnData and Seurat objects. Note that by default, the AnnData `varp` slot will not be converted.

Supplementary Figure 4

Supplementary Table 1

Table 1: This table indicates whether a software tool (anndataR, schard and zellkonverter with the native R reader option) provides certain functionality. For each allowed data type for each AnnData slot, we detail whether the software is capable of 1) representing the data type in R, 2) converting it to an appropriate SingleCellExperiment or Seurat object slot and 3) writing the data type back to an H5AD file.

Legend:

- x: the software tool can represent, convert, or write this data type
- /: the software tool can not represent, convert, or write this data type
- : the specific data type is not supported in a SingleCellExperiment or Seurat object.

slot	datatype	anndataR (this paper)				schard				zellkonverter (native R reader)			
		in R	to SCE	to Seurat	to H5AD	in R	to SCE	to Seurat	to H5AD	in R	to SCE	to Seurat	to H5AD
X	integer_matrix	x	x	x	x	/	x	x	/	/	x	/	/
	integer_csparse	x	x	x	x	/	x	x	/	/	x	/	/
	integer_rsparse	x	x	x	x	/	x	x	/	/	x	/	/
	float_matrix	x	x	x	x	/	x	x	/	/	x	/	/
	float_csparse	x	x	x	x	/	x	x	/	/	x	/	/
	float_rsparse	x	x	x	x	/	x	x	/	/	x	/	/
	float_matrix_nas	x	x	x	x	/	x	x	/	/	x	/	/
	float_csparse_nas	x	x	x	x	/	x	x	/	/	x	/	/
	float_rsparse_nas	x	x	x	x	/	x	x	/	/	x	/	/
layers	integer_matrix	x	x	x	x	/	/	/	/	/	x	/	/
	integer_csparse	x	x	x	x	/	/	/	/	/	x	/	/
	integer_rsparse	x	x	x	x	/	/	/	/	/	x	/	/
	float_matrix	x	x	x	x	/	/	/	/	/	x	/	/
	float_csparse	x	x	x	x	/	/	/	/	/	x	/	/
	float_rsparse	x	x	x	x	/	/	/	/	/	x	/	/
	float_matrix_nas	x	x	x	x	/	/	/	/	/	x	/	/
	float_csparse_nas	x	x	x	x	/	/	/	/	/	x	/	/
	float_rsparse_nas	x	x	x	x	/	/	/	/	/	x	/	/
	float_matrix_3d	x	-	-	x	/	-	-	/	/	-	-	/
	integer_matrix_3d	x	-	-	x	/	-	-	/	/	-	-	/
obs & var	categorical	x	x	x	x	/	/	/	/	/	x	/	/
	categorical_ordered	x	x	x	x	/	/	/	/	/	x	/	/
	categorical_nas	x	x	x	x	/	/	/	/	/	x	/	/
	categorical_ordered_nas	x	x	x	x	/	/	/	/	/	x	/	/
	string_array	x	x	x	x	/	x	x	/	/	x	/	/
	dense_array	x	x	x	x	/	x	x	/	/	x	/	/
	integer_array	x	x	x	x	/	x	x	/	/	x	/	/

	nullable_integer_array	x x x x	/ / / /	/ x / /
	boolean_array	x x x x	/ x x /	/ x / /
	nullable_boolean_array	x x x x	/ / / /	/ x / /
obsm	integer_matrix	x x x x	/ x x /	/ / / /
	integer_csparse	x x x x	/ / / /	/ / / /
	integer_rsparse	x x x x	/ / / /	/ / / /
	float_matrix	x x x x	/ x x /	/ / / /
	float_csparse	x x x x	/ / / /	/ / / /
	float_rsparse	x x x x	/ / / /	/ / / /
	float_matrix_nas	x x x x	/ x x /	/ / / /
	float_csparse_nas	x x x x	/ / / /	/ / / /
	float_rsparse_nas	x x x x	/ / / /	/ / / /
	dataframe	x - - /	/ / - /	/ / - /
varm	float_matrix_3d	x - - x	/ / - /	/ / - /
	integer_matrix_3d	x - - x	/ / - /	/ / - /
	integer_matrix	x x x x	/ / / /	/ x / /
	integer_csparse	x x x x	/ / / /	/ x / /
	integer_rsparse	x x x x	/ / / /	/ x / /
obsp	float_matrix	x x x x	/ / / /	/ x / /
	float_csparse	x x x x	/ / / /	/ x / /
	float_rsparse	x x x x	/ / / /	/ x / /
	float_matrix_nas	x x x x	/ / / /	/ x / /
	float_csparse_nas	x x x x	/ / / /	/ x / /
	float_rsparse_nas	x x x x	/ / / /	/ x / /
	dataframe	- - /	/ - - /	/ - - /
	float_matrix_3d	x - - x	/ / - /	/ / - /
	integer_matrix_3d	x - - x	/ / - /	/ / - /
	integer_matrix	x x x x	/ / / /	/ x / /
varp	integer_csparse	x x - x	/ / - /	/ / - /
	integer_rsparse	x x - x	/ / - /	/ x - /
	float_matrix	x x - x	/ / - /	/ / - /
	float_csparse	x x - x	/ / - /	/ x - /
	float_rsparse	x x - x	/ / - /	/ x - /
	float_matrix_nas	x x - x	/ / - /	/ / - /
	float_csparse_nas	x x - x	/ / - /	/ x - /
	float_rsparse_nas	x x - x	/ / - /	/ / - /

	float_rsparse_nas	x x - x	/ / - /	/ x - /
	float_matrix_3d	x x - x	/ / - /	/ / - /
	integer_matrix_3d	x x - x	/ / - /	/ / - /
uns	categoricals	x x x x	/ / / /	/ x / /
	matrices	x x x x	/ / / /	/ x / /
	scalars	x x x x	/ / / /	/ x / /
	nested values	x x x x	/ / / /	/ x / /
	nan	x x x x	/ / / /	/ x / /
	None	x x - /	/ / - /	/ / - /

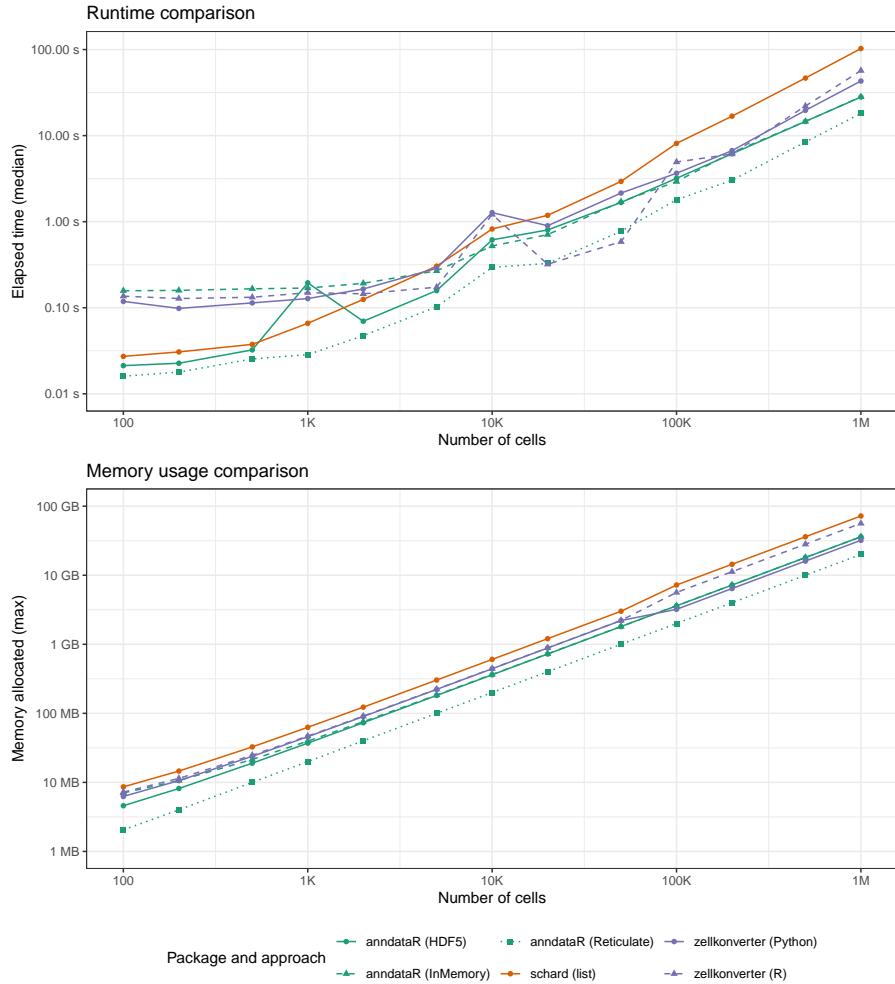


Figure 4: Runtime and memory benchmark for reading an H5AD file and computing the sum of the expression matrix. **Top:** Median elapsed time. **Bottom:** Maximum memory allocated. We compared three anndataR backends (In-Memory, HDF5, and Reticulate), two zellkonverter backends (native R reader and Python/basilisk reader), and schard (list export). Synthetic datasets were generated with `dummy_anndata` containing 20 000 genes and between 100 and 1 000 000 cells at approximately logarithmic intervals, with a sparse expression matrix (density 5%). Each benchmark iteration reads the H5AD file and computes the sum of the X matrix; anndataR and schard access the X slot directly, whereas zellkonverter returns a `SingleCellExperiment` object and is therefore expected to incur slightly higher overhead. Timings report the median of at least 3 iterations. Benchmarks were run on a machine with an AMD Ryzen 9 5950X (16 cores, 32 threads) and 126 GiB RAM, running Fedora Linux 42. Software versions: R 4.5.2, Python 3.13.11, anndataR 1.1.0, zellkonverter 1.20.1, schard 0.0.1, anndata 0.11.4, rhdf5 2.54.1. The full environment is documented in the repository at `runtime_benchmark/session_info.txt`.