

Quick Vignette

Courtney Schiebout, H. Robert Frost

Load Libraries

Libraries “CAMML” (Schiebout and Frost 2022) and “Seurat” (Satija et al. 2015) need to be loaded to carry out this vignette, in addition to several other libraries for data processing and gene set development (Satija et al. 2015; Robinson, McCarthy, and Smyth 2010; Carlson 2023; Liberzon et al. 2011). Packages will also load additional libraries they depend on.

```
library(CAMML)
library(Seurat)
library(SeuratObject)
library(edgeR)
library(org.Hs.eg.db)
library(msigdb)
```

Get Gene Set

Cell type gene sets can be loaded with the `GetGeneSet` function. In this case, we will load “immune.cells” which calls data for 5 immune cell types: T cells, B cells, NK cells, Monocytes, and Hematopoietic Stem Cells (HSCs).

```
gene.set.df <- GetGeneSets(data = "immune.cells")
```

Load Data

For this quick example, we will use “pbmc_small” from Seurat, which will provide a Seurat Object of 80 peripheral blood mononuclear cells (Satija et al. 2015).

```
seurat <- SeuratObject::pbmc_small
seurat <- RunPCA(seurat)
```

```
## Warning in irlba(A = t(x = object), nv = npcs, ...): You're computing too large
## a percentage of total singular values, use a standard svd instead.
```

```
## Warning in irlba(A = t(x = object), nv = npcs, ...): did not converge--results
## might be invalid!; try increasing work or maxit
```

```
## Warning: Requested number is larger than the number of available items (20).
## Setting to 20.
```

```
## Warning: Requested number is larger than the number of available items (20).
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