ChIMP Vignette

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Load Libraries

Libraries "CAMML" (Schiebout and Frost 2022) and "Seurat" (Satija et al. 2015) need to be loaded to carry out this vignette. Packages will also load additional libraries they depend on.

```
library(CAMML)
library(Seurat)
library(dplyr)
```

Data Processing

The following code outlines how the joint scRNA-seq/CITE-seq data from Lawlor, et al. (2021) (Lawlor et al. 2021), available on the 10X Genomics website, was processed for further analysis.

```
#load data
malt <- Read10X("raw_feature_bc_matrix/")
```

```
## 10X data contains more than one type and is being returned as a list containing matrices of each typ
```

```
#isolate the RNA data and make it a Seurat Object
malt.data <- malt$`Gene Expression`
seurat <- CreateSeuratObject(counts = malt.data,  min.cells=10,min.features=100)

#filter for mitochondrial genes
seurat[["percent.mt"]] <- PercentageFeatureSet(seurat, pattern = "^MT-")
seurat <- subset(seurat, subset = percent.mt < 10)

#normalize and scale the RNA data
seurat <- NormalizeData(seurat)
```

```
## Normalizing layer: counts
```

```
seurat <- FindVariableFeatures(seurat, selection.method = "vst", nfeatures = 2000)
```

```
## Finding variable features for layer counts
```

```
seurat <- ScaleData(seurat)
```

```
## Centering and scaling data matrix
```

```
#cluster and visualize
seurat <- RunPCA(seurat)
```

```
## PC_ 1
## Positive:  PCLAF, MKI67, RGS13, TYMS, MYBL2, CDK1, ZWINT, RRM2, UBE2C, AURKB
##     TK1, GRN, PKM, TOP2A, BIRC5, ACTB, CCNB2, PHGDH, DHFR, LMO2
##     NUF2, CST3, SPC25, CTSH, SERPINA9, ASPM, GTSE1, CDT1, SHCBP1, MAD2L1
## Negative:  ANXA1, GPR171, GZMK, CCL5, CD8A, SPRY1, GZMA, GTSCR1, RTKN2, TRGC2
```