

# Application of VAM to 10x PBMC 3k scRNA-seq data using the SCTransform method.

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## 1 Load the VAM package

Loading VAM will also load the required packages MASS and Matrix. Seurat is referenced via suggests so must be directly loaded to enable access to Seurat functions. Note that the sctransform package is also required in this case.

```
> library(VAM)
> library(Seurat)
```

## 2 Load and process the 10x PBMC scRNA-seq data

This example uses the same 10x PBMC scRNA-seq data set that is used in the Seurat Guided Clustering vignette ([https://satijalab.org/seurat/v3.1/pbmc3k\\_tutorial.html](https://satijalab.org/seurat/v3.1/pbmc3k_tutorial.html)). The Cell Ranger files for this data set can be downloaded from [https://s3-us-west-2.amazonaws.com/10x.files/samples/cell/pbmc3k/pbmc3k\\_filtered\\_gene\\_bc\\_matrices.tar.gz](https://s3-us-west-2.amazonaws.com/10x.files/samples/cell/pbmc3k/pbmc3k_filtered_gene_bc_matrices.tar.gz). Except for the use of SCTransform instead of log normalization, the logic here is identical to that found in the Seurat Guided Clustering vignette.

```
> # update the data.dir argument to reflect the local location of the PBMC data
> pbmc.data = Read10X(data.dir = "./filtered_gene_bc_matrices/hg19/")
> pbmc = CreateSeuratObject(counts = pbmc.data, project = "pbmc3k", min.cells = 3,
+   min.features = 200)
> pbmc[["percent.mt"]] = PercentageFeatureSet(pbmc, pattern = "^MT-")
> pbmc = subset(pbmc, subset = nFeature_RNA > 200 & nFeature_RNA < 2500 & percent.mt < 5)
> pbmc = SCTransform(pbmc, verbose=F)
> pbmc = RunPCA(pbmc, npcs=10)
> pbmc = RunUMAP(pbmc, dims = 1:10)
> pbmc
```

```
An object of class Seurat
26233 features across 2638 samples within 2 assays
Active assay: SCT (12519 features, 3000 variable features)
 1 other assay present: RNA
 2 dimensional reductions calculated: pca, umap
```

## 3 Load Ensembl IDs

The Ensembl IDs and gene names must be read in from the genes.tsv file and filtered to match genes left after the quality control steps performed in the prior section.

```

> feature.data = read.delim("./filtered_gene_bc_matrices/hg19/genes.tsv",
+   header = FALSE, stringsAsFactors = FALSE)
> ensembl.ids = feature.data[,1]
> gene.names = feature.data[,2]
> genes.after.QC = rownames(pbmcc@assays$SCT@data)
> indices.to.keep = unlist(sapply(genes.after.QC, function(x) {which(gene.names == x)[1]}))
> ensembl.ids = ensembl.ids[indices.to.keep]
> gene.names = gene.names[indices.to.keep]

```

## 4 Define gene set collection

A gene set collection containing just the BIOCARTA\_BLYMPHOCYTE\_PATHWAY from the MSigDB C2.CP.BIOCARTA collection will be used for this example. To create a version of this gene set that can be used with the PBMC scRNA-seq data, the Entrez IDs from MSigDB were first mapped to Ensembl IDs using the Bioconductor org.Hs.egENSEMBL package and a gene set collection list object required by `vamForSeurat()` was created using the `createGeneSetCollection()` helper function. This helper function filters the original 14 genes down to the 11 that were also contained in the PBMC scRNA-seq data and generates a list whose elements are vectors of gene indices in the scRNA-seq data. To use the VAM method with an entire MSigDB gene set collection (or other collection of pathways), similar logic would be needed to filter genes, determine Ensembl IDs and map these IDs to gene position in the Seurat Assay.

```

> gene.set.name = "BIOCARTA-BLYMPHOCYTE-PATHWAY"
> blymphocyte.gene.ids = c("ENSG00000121594", "ENSG00000005844", "ENSG00000203710",
+ "ENSG00000160255", "ENSG00000117322", "ENSG00000101017", "ENSG00000204287",
+ "ENSG00000198502", "ENSG00000090339", "ENSG00000072694", "ENSG00000081237",
+ "ENSG00000196126", "ENSG00000231021", "ENSG00000230463")
> # Create a collection list for this gene set based on the Ensembl IDs
> gene.set.id.list = list()
> gene.set.id.list[[1]] = blymphocyte.gene.ids
> names(gene.set.id.list)[1] = gene.set.name
> gene.set.id.list

```

```

$`BIOCARTA-BLYMPHOCYTE-PATHWAY`
 [1] "ENSG00000121594" "ENSG00000005844" "ENSG00000203710" "ENSG00000160255"
 [5] "ENSG00000117322" "ENSG00000101017" "ENSG00000204287" "ENSG00000198502"
 [9] "ENSG00000090339" "ENSG00000072694" "ENSG00000081237" "ENSG00000196126"
[13] "ENSG00000231021" "ENSG00000230463"

```

```

> # Create the list of gene indices required by vamForSeurat()
> (gene.set.collection = createGeneSetCollection(gene.ids=ensembl.ids,
+   gene.set.collection=gene.set.id.list))

```

```

$`BIOCARTA-BLYMPHOCYTE-PATHWAY`
ENSG00000005844 ENSG00000203710 ENSG00000160255 ENSG00000117322 ENSG00000101017
          9477              1122              12482              1121              10961
ENSG00000204287 ENSG00000198502 ENSG00000090339 ENSG00000072694 ENSG00000081237
          3985              3986              11280              944              1062
ENSG00000196126
          3987

```

```
> blymphocyte.gene.indices = gene.set.collection[[1]]
> (blymphocyte.gene.names = gene.names[blymphocyte.gene.indices])

[1] "ITGAL"      "CR1"        "ITGB2"      "CR2"        "CD40"       "HLA-DRA"
[7] "HLA-DRB5"   "ICAM1"      "FCGR2B"     "PTPRC"      "HLA-DRB1"
```

## 5 Execute VAM method

Since the scRNA-seq data has been processed using Seurat, we execute VAM using the `vamForSeurat()` function. We have set `return.dist=T` so that the squared adjusted Mahalanobis distances will be returned in a "VAMdist" Assay.

```
> pbmc = vamForSeurat(seurat.data=pbmc,
+   gene.set.collection=gene.set.collection,
+   center=F, gamma=T, sample.cov=F, return.dist=T)
```

Look at the first few entries in the "VAMdist" and "VAMcdf" Assays.

```
> pbmc@assays$VAMdist[1,1:10]
```

```
1 x 10 sparse Matrix of class "dgCMatrix"
```

```
BIOCARTA-BLYMPHOCYTE-PATHWAY 8.376617 143.7326 2.716563 186.538 57.66302
```

```
BIOCARTA-BLYMPHOCYTE-PATHWAY 2.887088 22.46748 . 37.82066 13.81838
```

```
> pbmc@assays$VAMcdf[1,1:10]
```

```
1 x 10 sparse Matrix of class "dgCMatrix"
```

```
BIOCARTA-BLYMPHOCYTE-PATHWAY 0.1253705 0.9283303 0.03948378 0.9681246 0.640518
```

```
BIOCARTA-BLYMPHOCYTE-PATHWAY 0.04208422 0.3167245 . 0.4823162 0.2037744
```

## 6 Visualize VAM scores

Visualize VAM scores using Seurat `FeaturePlot()`. The default Assay must first be changed to "VAMcdf".

```
> DefaultAssay(object = pbmc) = "VAMcdf"
> FeaturePlot(pbmc, reduction="umap", features=gene.set.name)
```

# BIOCARTA-BLYMPHOCYTE-PATHWAY

