BD Cellismo™

Data Visualization Tool

More actionable insights. No coding required

BD

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Overview

BD Cellismo™ Data Visualization Tool—now anyone can single cell!

A data visualization tool that does the heavy lifting of secondary bioinformatics data analysis and visualization

Intuitive: Point and click to visualize your data as graphs and plots

Multiomics enabled: Explore single-cell RNA, protein and ATAC datasets with ease

User friendly: No cost of adoption; no coding required

How to access the BD Cellismo™ Data Visualization Tool

1 Navigate to the BD Cellismo™ Data Visualization Tool landing page
Available on the BD Biosciences website under Products > Software & Informatics

2 Provide your information*
Fill out the form with your name, email and institution to access the software

3 Select your operating system
An install file will begin downloading automatically, which you can then install on your computer

4 Install the BD Cellismo™ Data Visualization Tool and agree to the end-user license agreement (EULA)
Accept the Terms and Conditions before use

*will be used to notify you of updates and bug fixes

Input files and system requirements

For WTA or AbSeq data:

- (Preferred) .Cellismo output file from the BD Rhapsody™ Sequence Analysis Pipeline
- Alternative inputs formats:
  - Market exchange (MEX)
  - H5MU/H5AD
  - Seurat .rds
  - Market exchange (MEX) compressed with .zip or tar.gz
  - H5

For ATAC data:

- .Cellismo output file from the BD Rhapsody™ Sequence Analysis Pipeline (V3 or later only)

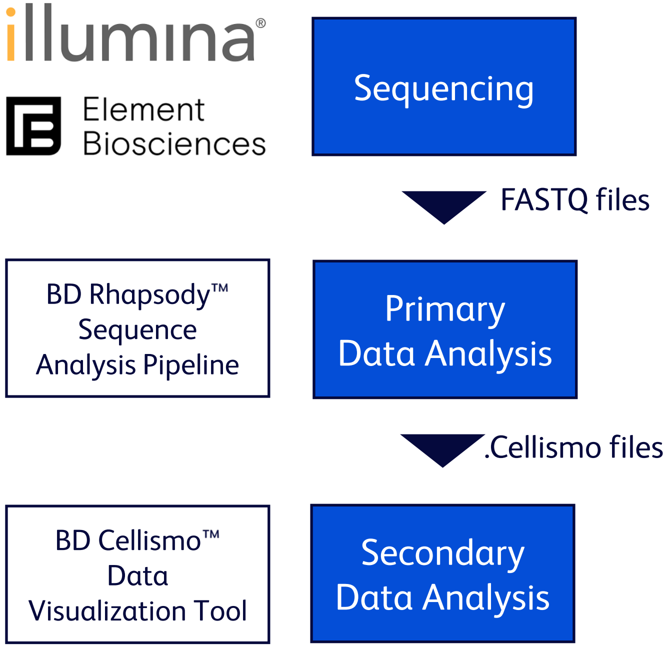
- Windows 10 or later (64-bit)
- MacOS 14 (Sonoma) or later (Intel or Apple silicon chip)
- 8 GB RAM minimum

RNA/AbSeq

- 16 GB RAM for 200,000 cells
- 64 GB RAM for 1M cells

ATAC alone or ATAC multiomic

- 16 GB RAM for 100,000 cells
- 64 GB RAM for 500,000 cells



Features—v1.0, released March 2025

- Load single-cell multiomic data from multiple formats—.Cellismo files, matrix market MEX, Scanpy/Muon or H5AD/H5MU
- Manage multiple single-cell projects and jump between them with a few clicks
- Quality control of single-cell multiomics data (e.g., ribosomal and mitochondrial gene filter) with a visual for the cells being filtered out
- Generate 7 different types of graphs: Dimensionality reduction scatter, Biaxial, Bioproduct correlation, Heatmap, Dot plot, Histogram and Violin plot
- Extensive graph customization with style options (e.g., dot size, opacity, color)
- Save images to a project gallery sidebar and recall them with ease
- Drag gallery images from the sidebar to external applications like Microsoft™ PowerPoint™
- Create new cell annotations by circling cells of interest, running Leiden or K-means clustering or combining existing annotations
- Analyze differential expression between cell groups of interest. Filter genes of interest in a table and view on a Volcano plot
- Generate new dimensionality reduction coordinates
- Supports whole transcriptome or targeted RNA, protein counts with AbSeq/CITE-seq and sample multiplexing

Features—v2.0, released October 2025

Added:

- Support for BD Rhapsody™ ATAC-Seq Assay
  - New modalities: ATAC_PEAKS, ATAC_GENE_ACTIVITY, ATAC_MOTIF
  - Genome browser to view ATAC peaks and ATAC fragments in the context of genomic locations and genes
  - Motif enrichment analysis tool—find transcription factor motifs that are enriched in a given set of peaks, compared to background peaks
  - Peak and RNA expression correlation tool—find peaks whose activity correlate with RNA expression
  - RNA vs ATAC heatmap—see RNA expression and ATAC gene activity correlation for a given cell annotation
  - Ability to combine and reanalyze multiple ATAC datasets
- Doublet detection tool
- Batch correction utility tool, with batch correct counts available to be used in graphing pages
- Integration utility tool
- New cell classification tool, ScType, with the ability to customize marker genes
- Confidence score annotations for cell type classification tools
- Project action recording in the current project page
- Data export options—for R / Seurat, Scanpy (H5AD), Muon (H5MU), FCS and CSV

Features—v2.0, released October 2025 (cont.)

Added (cont.):

- RNA data import option—Seurat RDS
- New DESeq2 method in the Differential Analysis tool
- "Selected Cell Actions" menu on graphing pages, and added "Delete Cells" and "Quick Differential Analysis" options
- Switch to reverse color palette
- Contour lines overlay to biaxial plot
- Options to start project, including flavor of highly variable gene selection, number of highly variable genes and number of PCA/LSI components
- Ability to filter bioproduct dropdown by modality
- Ability to Export and restore app settings

Updated:

- Renamed Differential Expression tool to Differential Analysis and added support for all ATAC modalities
- Cell annotation—Clustering tool to support ATAC modalities
- Dimensionality Reduction utility tool to support ATAC modalities
- Bug fixes

Pricing: Free!

- The BD Cellismo™ Data Visualization Tool is offered free of charge

Why should I use the BD Cellismo™ Data Visualization Tool?

1

Code-free experience: Get to your answers without any coding.

2

Effortless: Interpret data quickly with an intuitive interface.

3

Powerful: Find a combination of valuable tools all in one place.

4

Independence: Get answers on your own without relying on a third-party for analysis.

5

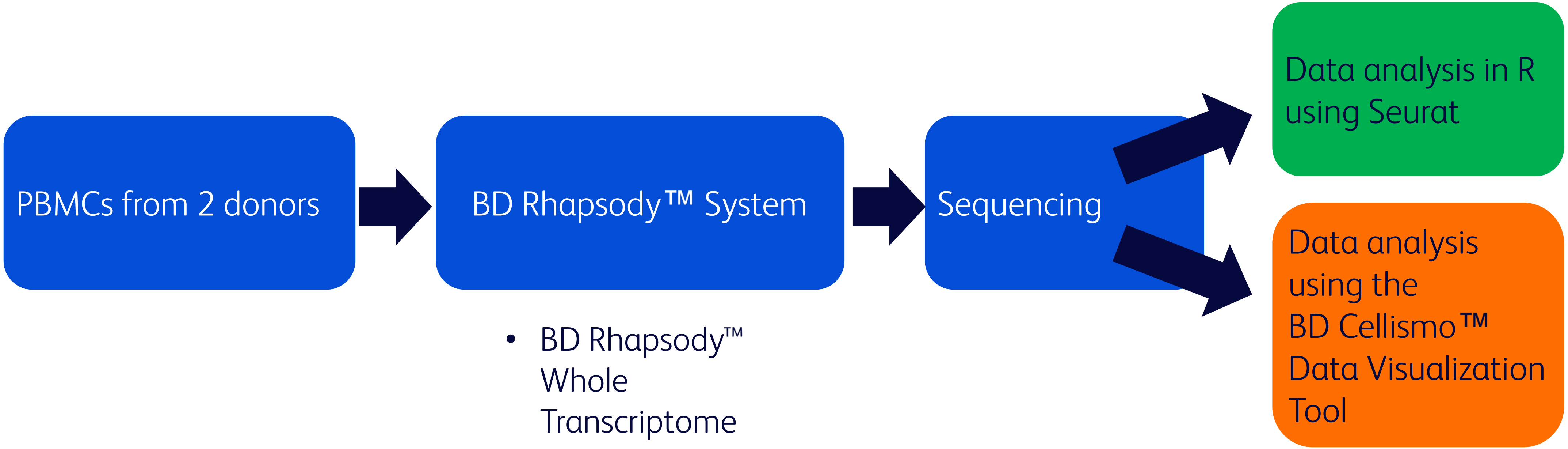
End-to-end support: Get support from getting started to answering any questions.

6

Continuous improvement: Benefit from regular updates and enhancements to our software.

Performance v1.0

Generate the same data visualization as Seurat using the BD Cellismo™ Data Visualization Tool



PBMCs from 2 donors

BD Rhapsody™ System

Sequencing

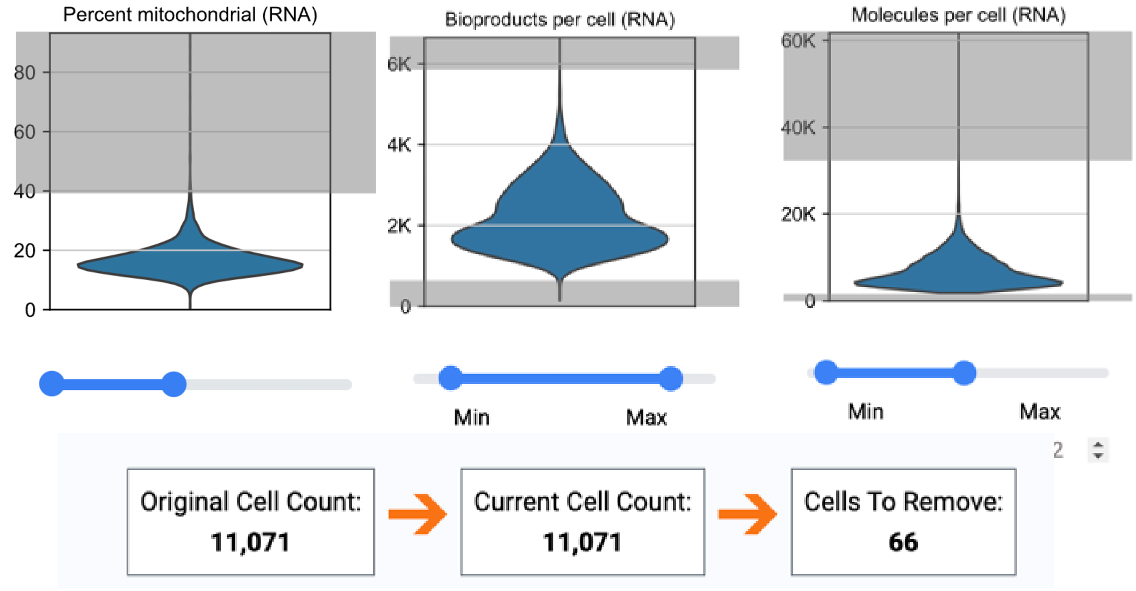
Data analysis in R using Seurat

Data analysis using the BD Cellismo™ Data Visualization Tool

- BD Rhapsody™ Whole Transcriptome Analysis (WTA)
- BD® Single-Cell Multiplexing Kits
- BD® AbSeq Antibody-Oligos (91 markers)

Quality control and filtering out low quality cells

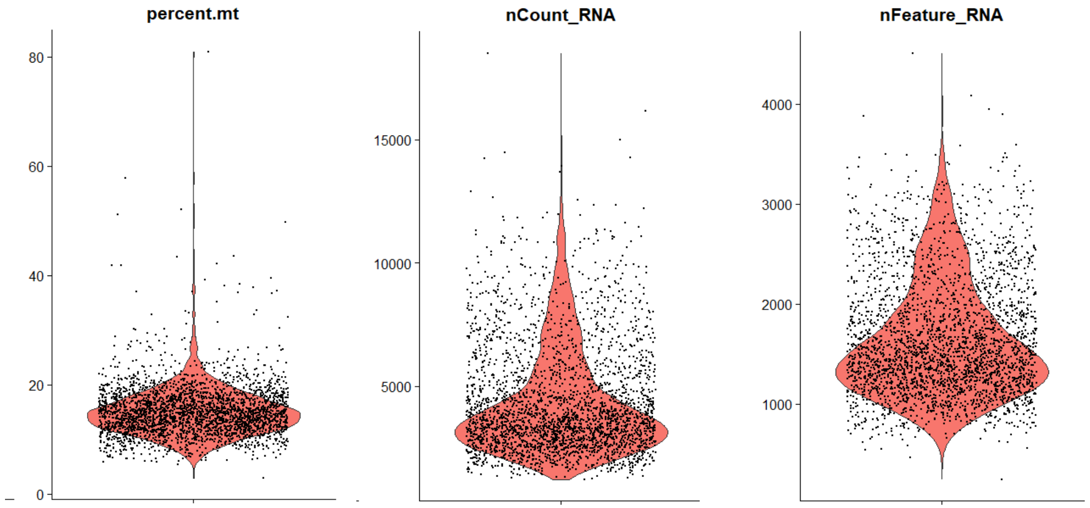
Data analysis using the
BD Cellismo™ Data Visualization Tool

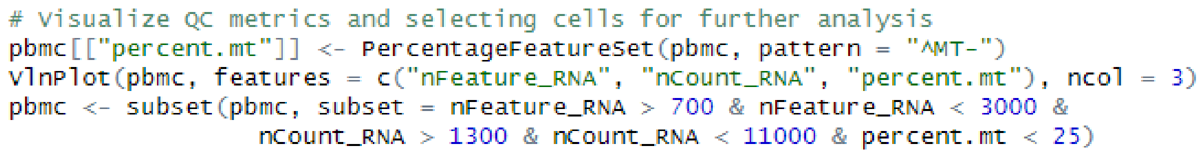


Original Cell Count: **11,071** → Current Cell Count: **11,071** → Cells To Remove: **66**

- Interactive cell filtering based on molecules and bioproducts (for both RNA and protein modalities)
- Control over cell removal count by changing QC parameters
- Cell Filter Modality based on included mitochondrial gene percentage, which can also be used for QC

Data analysis in R
using Seurat

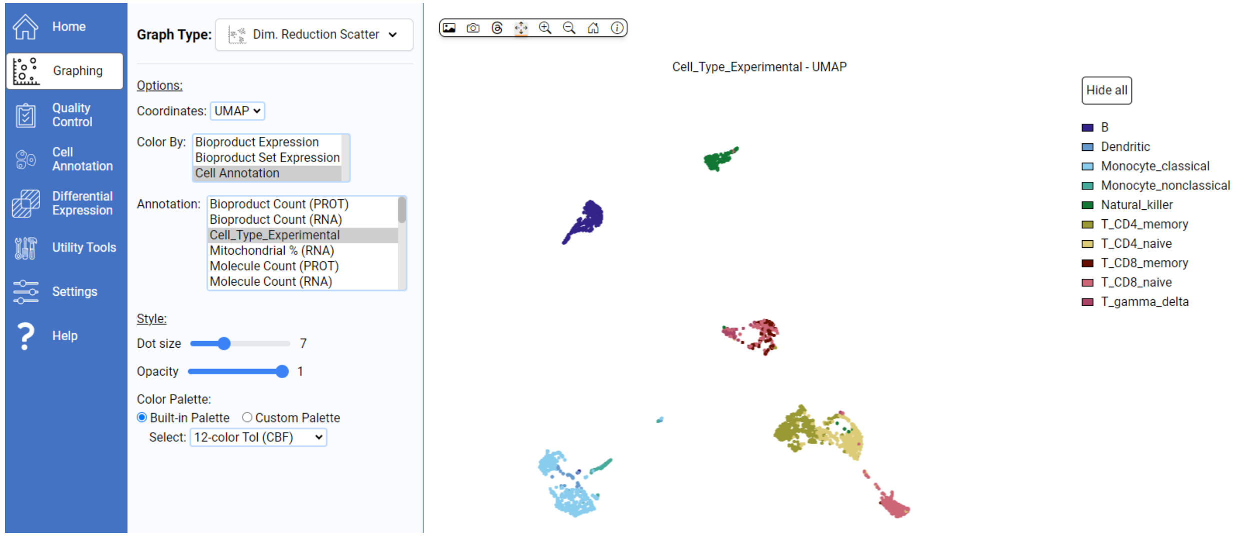




```
# Visualize QC metrics and selecting cells for further analysis
pbmc[["percent.mt"]] <- PercentageFeatureSet(pbmc, pattern = "^MT-")
VlnPlot(pbmc, features = c("nFeature_RNA", "nCount_RNA", "percent.mt"), ncol = 3)
pbmc <- subset(pbmc, subset = nFeature_RNA > 700 & nFeature_RNA < 3000 &
                 nCount_RNA > 1300 & nCount_RNA < 11000 & percent.mt < 25)
```

Dimensional reduction (UMAP/tSNE)

Data analysis using the BD Cellismo™ Data Visualization Tool



Graph Type: Dim. Reduction Scatter

Options:

Coordinates: UMAP

Color By: Bioproduct Expression / Bioproduct Set Expression / Cell Annotation

Annotation: Bioproduct Count (PROT) / Bioproduct Count (RNA) / Cell_Type_Experimental / Mitochondrial % (RNA) / Molecule Count (PROT) / Molecule Count (RNA)

Style:

Dot size 7

Opacity 1

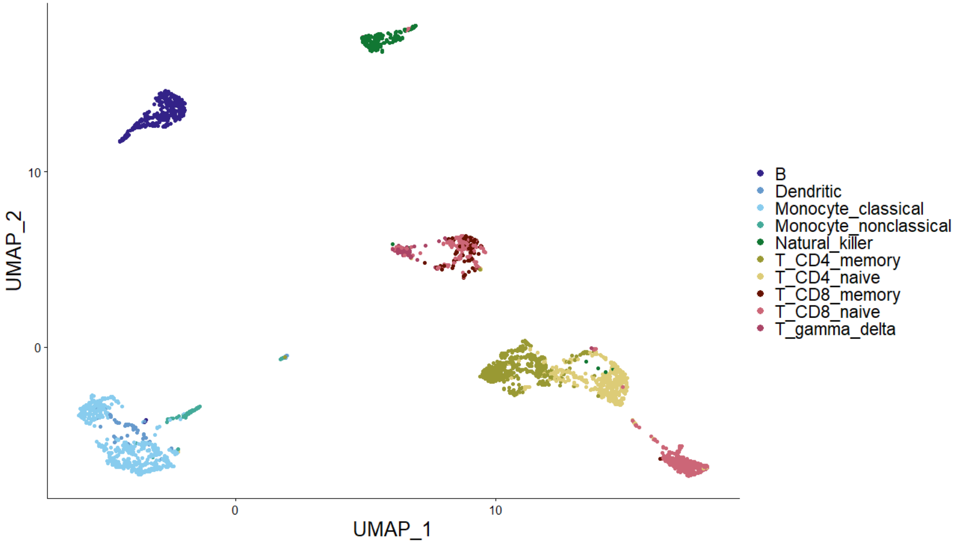
Color Palette:

● Built-in Palette ○ Custom Palette

Select: 12-color Tol (CBF)

- Automatically generated UMAP/tSNE
- Control over dot size and opacity
- Built-in palette (or custom ones) to change cluster colors easily

Data analysis in R using Seurat



```
# Normalizing the data
pbmc <- NormalizeData(pbmc, normalization.method = "LogNormalize", scale.factor = 10000)

# Identification of highly variable features
pbmc <- FindVariableFeatures(pbmc, selection.method = "vst", nfeatures = 2000)

# Scaling the data
all.genes <- rownames(pbmc)
pbmc <- ScaleData(pbmc, features = all.genes)

# Perform linear dimensional reduction
pbmc <- RunPCA(pbmc, features = VariableFeatures(object = pbmc))

# Cluster the cells
pbmc <- FindNeighbors(pbmc, dims = 1:20)
pbmc <- FindClusters(pbmc, resolution = 0.5)

# Run non-linear dimensional reduction
pbmc <- RunUMAP(pbmc, dims = 1:10)
DimPlot(pbmc, reduction = "umap", pt.size = 1.3, cols = c(ptol_pal()(12)))
```

Sample Tags (and assigning sample name)

Data analysis using the
BD Cellismo™ Data Visualization Tool

Graph Type: Dim. Reduction Scatter

Options:

Coordinates: UMAP

Color By: Bioproduct Expression / Bioproduct Set Expression / Cell Annotation

Annotation: Molecule Count (PROT) / Molecule Count (RNA) / Ribosomal % (RNA) / Sample_Tag / Sample_Tag_Name / SampleTag01_hs_Read_Count

Style:

Dot size 7

Opacity 1

Color Palette:

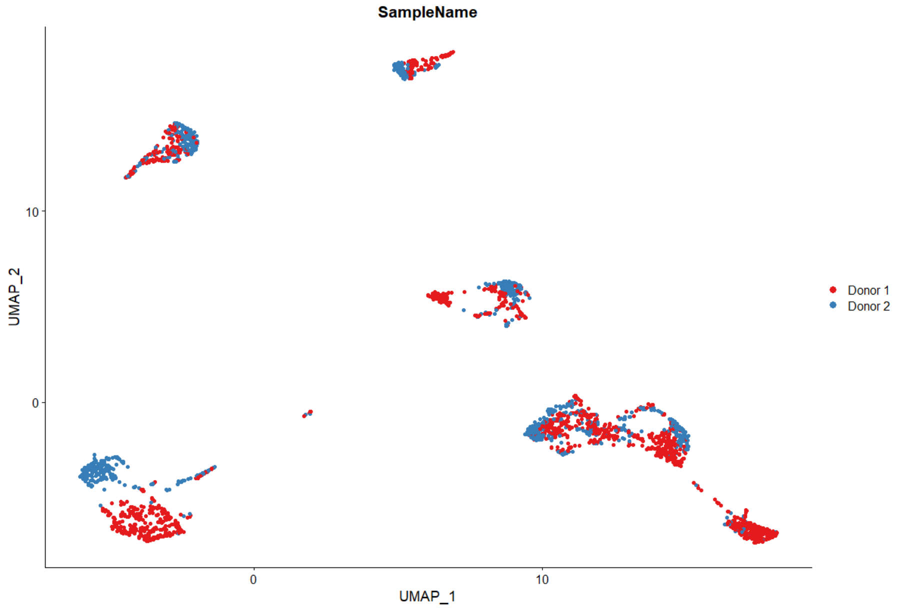
● Built-in Palette ○ Custom Palette

Select: 9-color Set1

Sample_Tag_Name - UMAP

- Assigning names to sample tags and removing the cells with multiple sample tags (multiplets) or no sample tags (undetermined)

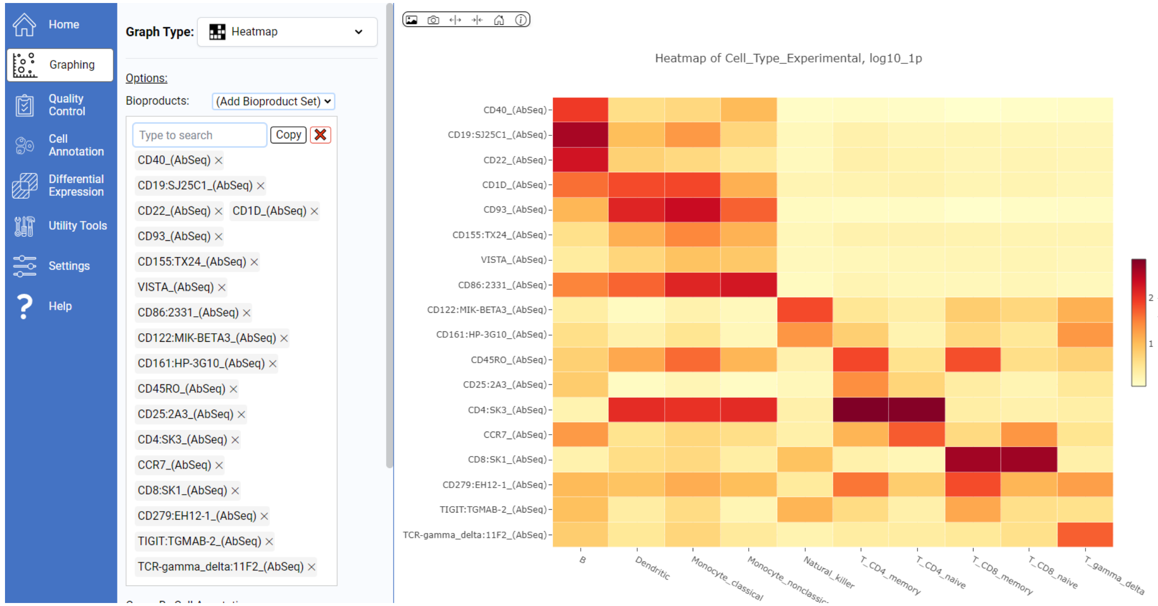
Data analysis in R using Seurat



```
## Sample Tags

# removing the cells with multiple sample tags (multiplets)
# or no sample tags (undetermined)
Idents(pbmc) <- pbmc@meta.data$Sample_Tag
pbmc <- subset(pbmc, cells = names(Idents(pbmc)[Idents(pbmc) %in% c("SampleTag01_hs",  "SampleTag02_hs")]))

# Assigning names to samples
SampleName <- c()
SampleName[which(colnames(pbmc@assays$RNA) %in% names(Idents(pbmc))[which(Idents(pbmc) %in% c("SampleTag01_hs"))])] <- "Donor 1"
SampleName[which(colnames(pbmc@assays$RNA) %in% names(Idents(pbmc))[which(Idents(pbmc) %in% c("SampleTag02_hs"))])] <- "Donor 2"
pbmc[["SampleName"]] <- SampleName

# Visualization of samples on the UMAP
DimPlot(pbmc, reduction = "umap", group.by = "SampleName",pt.size = 1.3, cols= brewer.pal(9,"Set1"))
```

Heatmap: average expression for BD® AbSeq Protein Markers

Data analysis using the BD Cellismo™ Data Visualization Tool



Graph Type: Heatmap

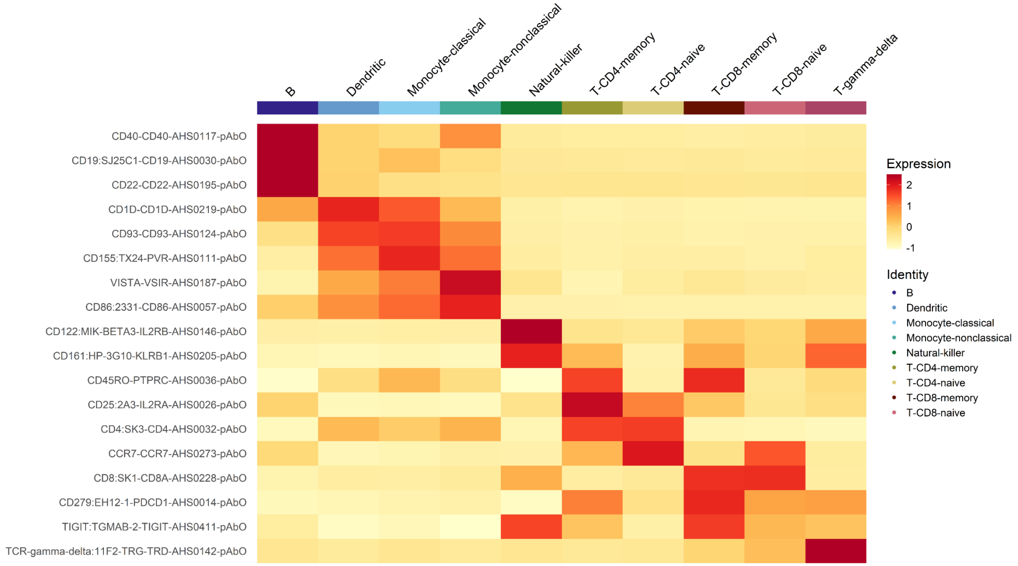
Options:

Bioproducts: (Add Bioproduct Set)

Type to search

- CD40_(AbSeq) ×
- CD19:SJ25C1_(AbSeq) ×
- CD22_(AbSeq) ×
- CD1D_(AbSeq) ×
- CD93_(AbSeq) ×
- CD155:TX24_(AbSeq) ×
- VISTA_(AbSeq) ×
- CD86:2331_(AbSeq) ×
- CD122:MIK-BETA3_(AbSeq) ×
- CD161:HP-3G10_(AbSeq) ×
- CD45RO_(AbSeq) ×
- CD25:2A3_(AbSeq) ×
- CD4:SK3_(AbSeq) ×
- CCR7_(AbSeq) ×
- CD8:SK1_(AbSeq) ×
- CD279:EH12-1_(AbSeq) ×
- TIGIT:TGMAB-2_(AbSeq) ×
- TCR-gamma_delta:11F2_(AbSeq) ×

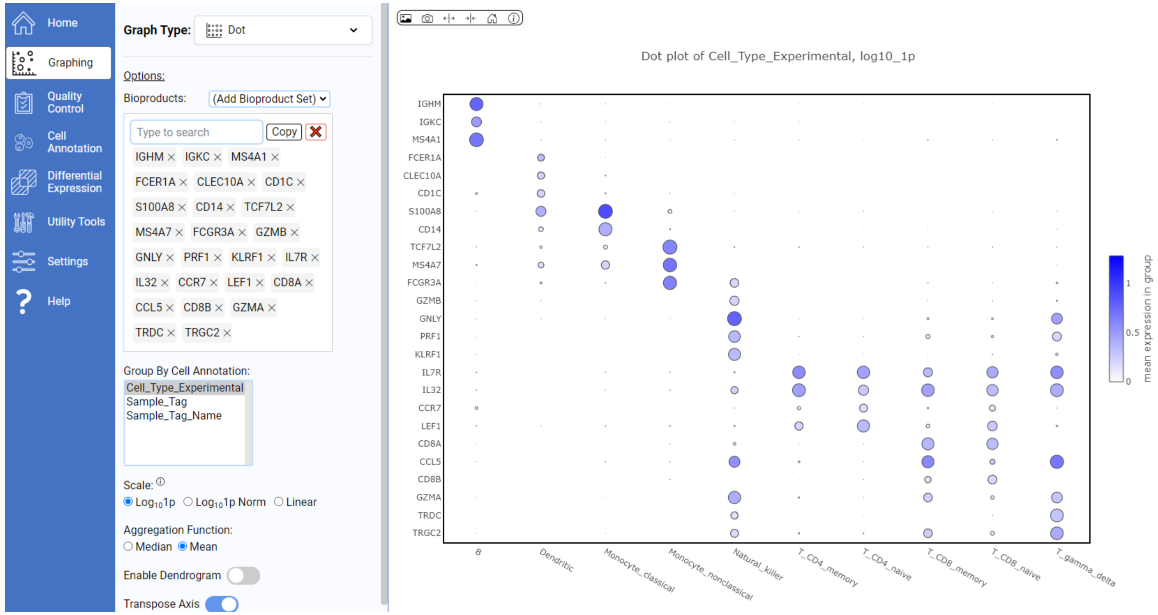
Data analysis in R using Seurat



```r
DefaultAssay(pbmc) <- "ADT"
avgexpabseq = AverageExpression(pbmc, return.seurat = T)
mapal <- colorRampPalette(RColorBrewer::brewer.pal(8, "YlOrRd"))(256)
DoHeatmap(avgexpabseq, group.bar.height = 0.03, group.bar = TRUE, group.colors  = c(ptol_pal()(12)),
          features = abseq, size = 5, hjust = 0, vjust = 0, angle = 45,
          combine = TRUE, draw.lines = FALSE) + scale_fill_gradientn(colours = (mapal)) & theme(text= element_text(size = 15))
```

Dotplot: average gene expression for biomarkers (RNA)

Data analysis using the
BD Cellismo™ Data Visualization Tool



Graph Type: Dot

Options:

Bioproducts: (Add Bioproduct Set)

Type to search

IGHM × IGKC × MS4A1 ×
FCER1A × CLEC10A × CD1C ×
S100A8 × CD14 × TCF7L2 ×
MS4A7 × FCGR3A × GZMB ×
GNLY × PRF1 × KLRF1 × IL7R ×
IL32 × CCR7 × LEF1 × CD8A ×
CCL5 × CD8B × GZMA ×
TRDC × TRGC2 ×

Group By Cell Annotation:

Cell_Type_Experimental
Sample_Tag
Sample_Tag_Name

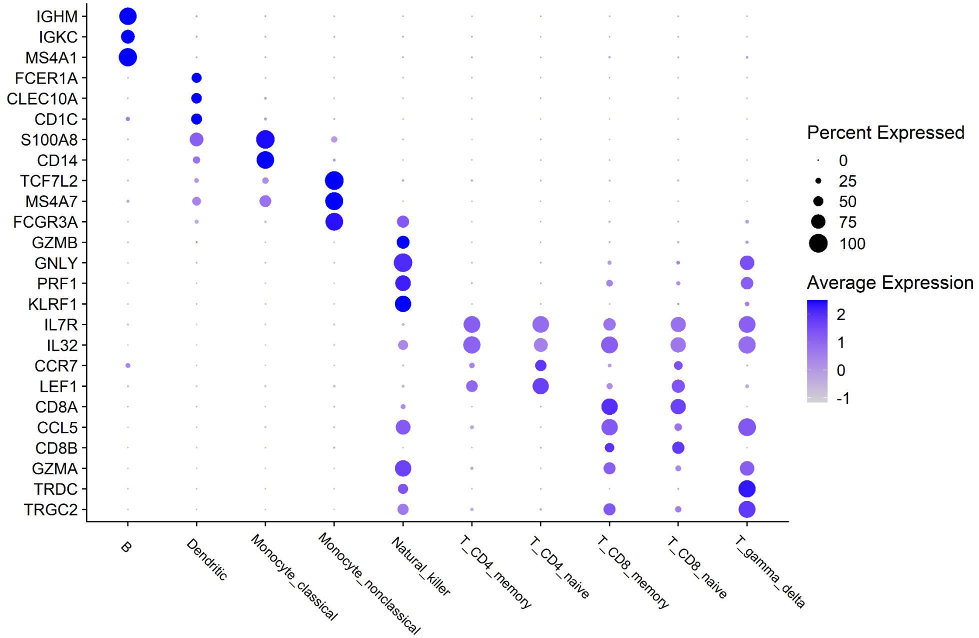
Scale:
● Log_{10}1p ○ Log_{10}1p Norm ○ Linear

Aggregation Function:
○ Median ● Mean

Enable Dendrogram ○

Transpose Axis ●

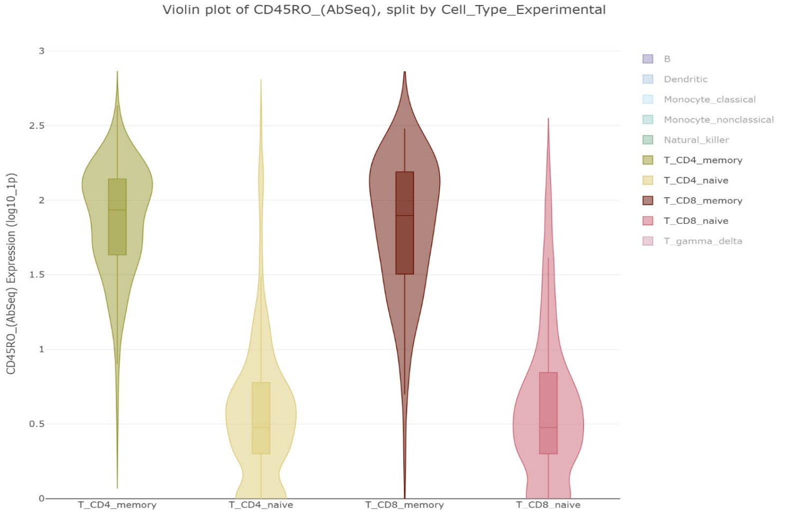
Data analysis in R
using Seurat

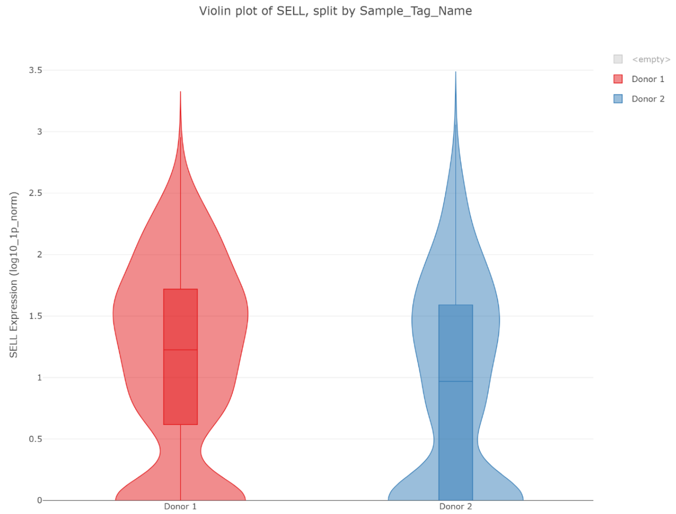


```
genes <- c("IGHM", "IGKC", "MS4A1", "FCER1A", "CLEC10A", "CD1C", "S100A8", "CD14", "TCF7L2", "MS4A7", "FCGR3A",
"GZMB", "GNLY", "PRF1", "KLRF1", "IL7R", "IL32", "CCR7", "LEF1", "CD8A", "CCL5", "CD8B", "GZMA","TRDC", "TRGC2")

DotPlot(pbmc, features = genes, dot.scale=6, assay = "RNA") + theme(axis.text.x = element_text(size = 10, angle = -45,hjust = 0.1)) + coord_flip()
```

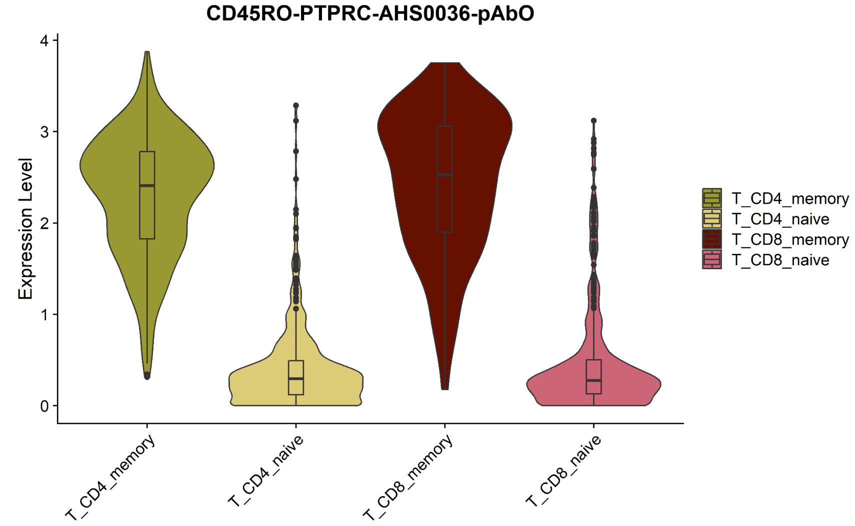
Violin plots

Data analysis using the BD Cellismo™ Data Visualization Tool

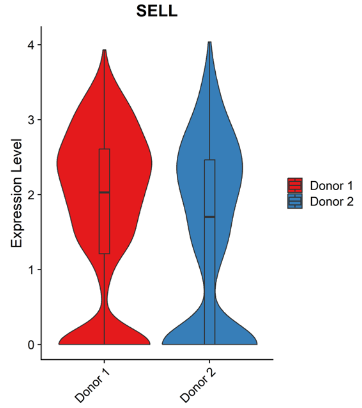




Data analysis in R using Seurat



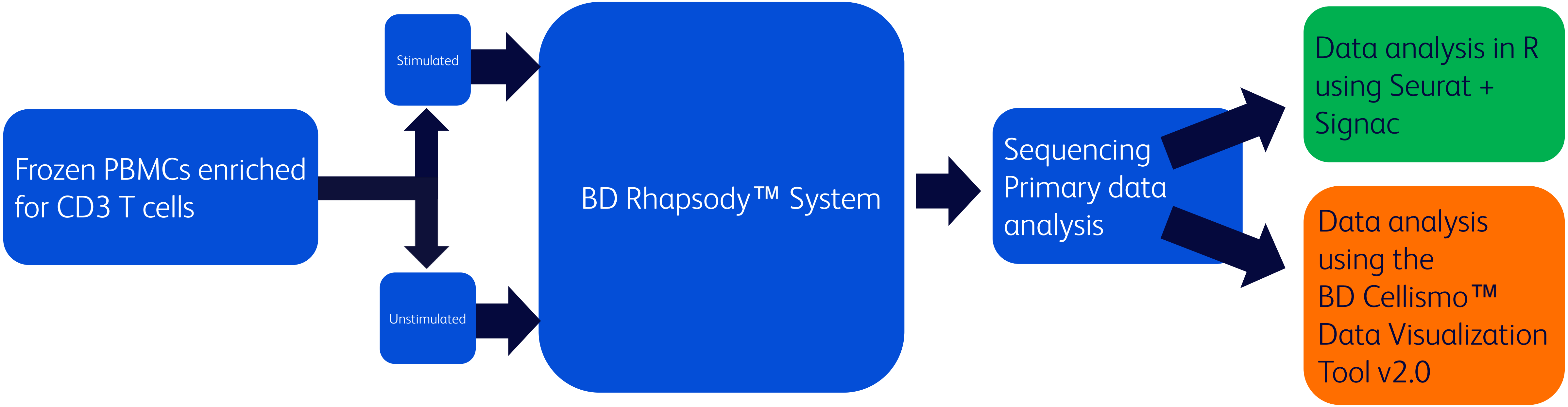
```
VlnPlot(pbmc, features = "CD45RO-PTPRC-AHS0036-pAbO", pt.size = 0, assay = "ADT", cols = c("#999933","#DDCC77", "#661100", "#CC6677"),
group.by = "Cell_Type_Experimental",idents = c("T_CD4_memory", "T_CD4_naive","T_CD8_memory", "T_CD8_naive")) + geom_boxplot(width=0.1)
```



```
VlnPlot(pbmc, features = "SELL", pt.size = 0, cols= brewer.pal(9,"Set1"), assay = "RNA") + geom_boxplot(width=0.1)
```

Performance v2.0

For ATAC-Seq data, generate the same visualization as R using the BD Cellismo™ Data Visualization Tool v2.0


Frozen PBMCs enriched for CD3 T cells

Stimulated

Unstimulated

BD Rhapsody™ System

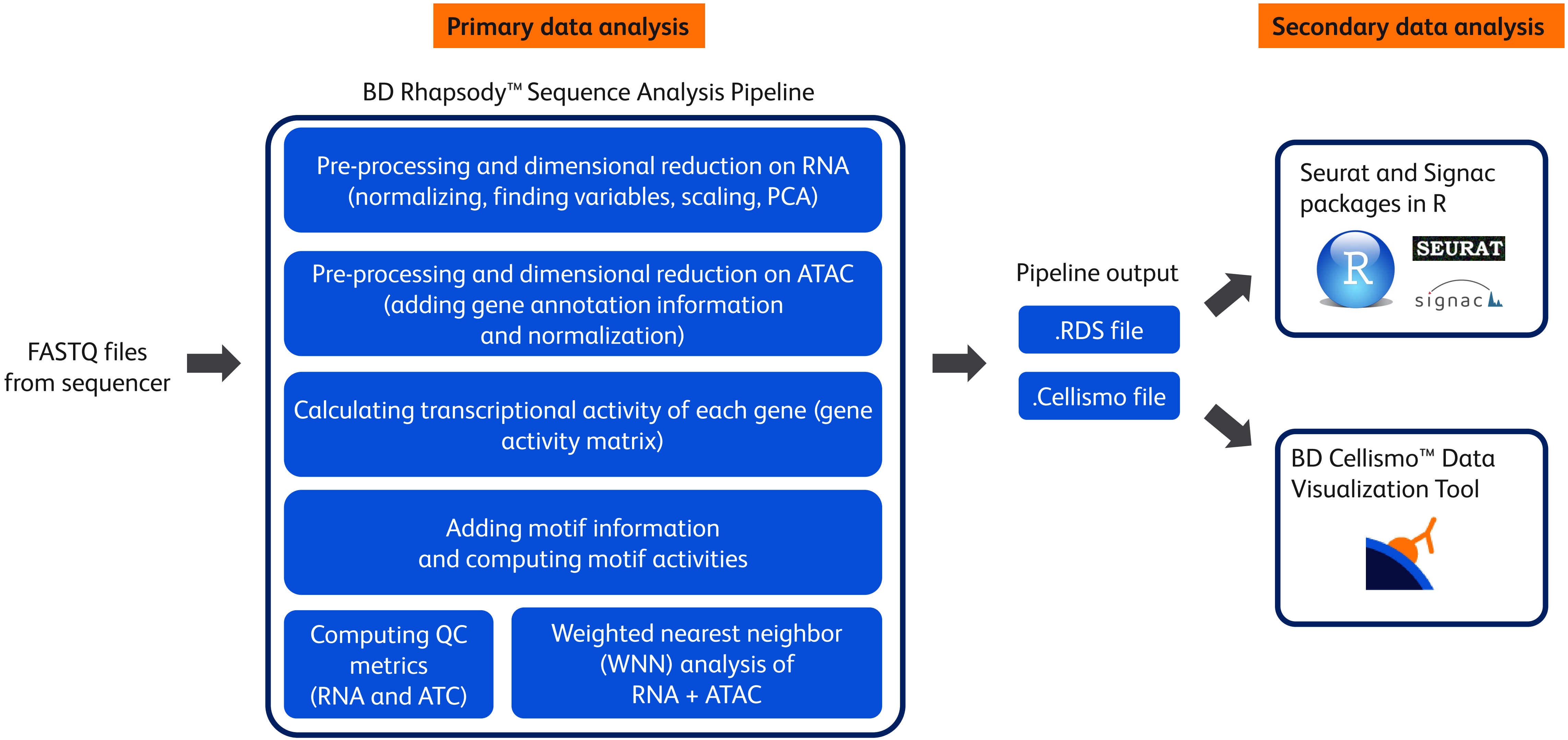
Sequencing Primary data analysis

Data analysis in R using Seurat + Signac

Data analysis using the BD Cellismo™ Data Visualization Tool v2.0

- BD Rhapsody™ Single-Cell Multiomic ATAC-Seq Assay

Data analysis workflow



Primary data analysis

Secondary data analysis

FASTQ files
from sequencer

BD Rhapsody™ Sequence Analysis Pipeline

- Pre-processing and dimensional reduction on RNA (normalizing, finding variables, scaling, PCA)
- Pre-processing and dimensional reduction on ATAC (adding gene annotation information and normalization)
- Calculating transcriptional activity of each gene (gene activity matrix)
- Adding motif information and computing motif activities
- Computing QC metrics (RNA and ATC)
- Weighted nearest neighbor (WNN) analysis of RNA + ATAC

Pipeline output

- .RDS file
- .Cellismo file

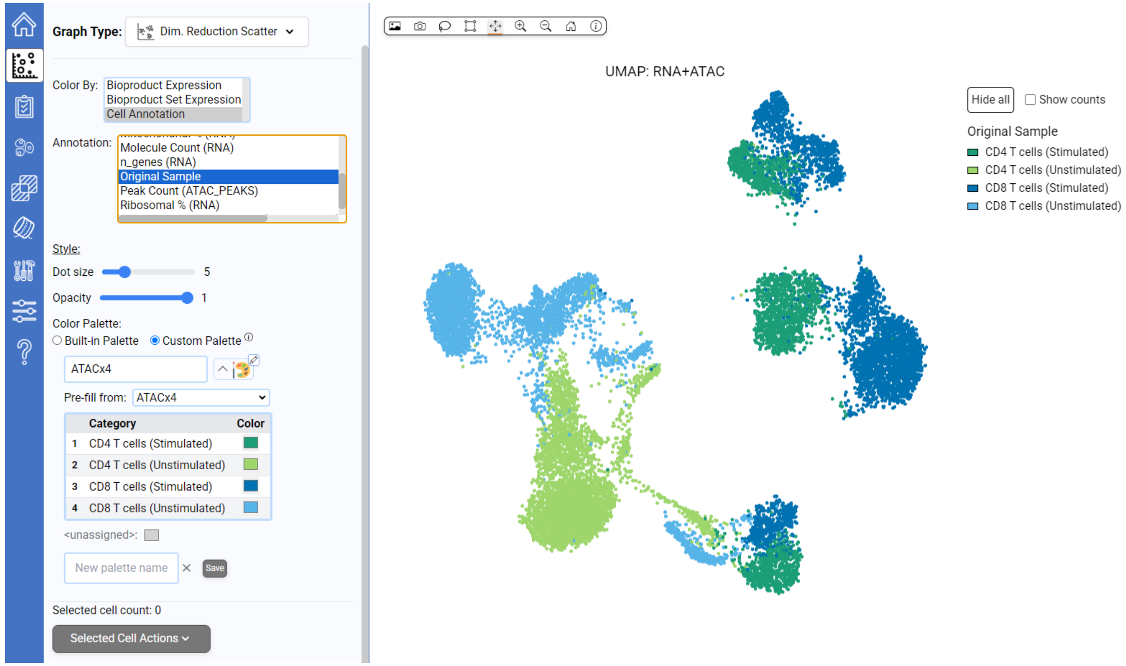
Seurat and Signac packages in R

BD Cellismo™ Data Visualization Tool

Dimensionality reduction (UMAP/t-SNE)

Data analysis in R using Seurat + Signac

Data analysis using the
BD Cellismo™ Data Visualization Tool v2.0



Color By: Bioproduct Expression / Bioproduct Set Expression / Cell Annotation

Annotation: Molecule Count (RNA) / n_genes (RNA) / Original Sample / Peak Count (ATAC_PEAKS) / Ribosomal % (RNA)

Style:

Dot size 5

Opacity 1

Color Palette:
○ Built-in Palette ● Custom Palette

ATACx4

Pre-fill from: ATACx4

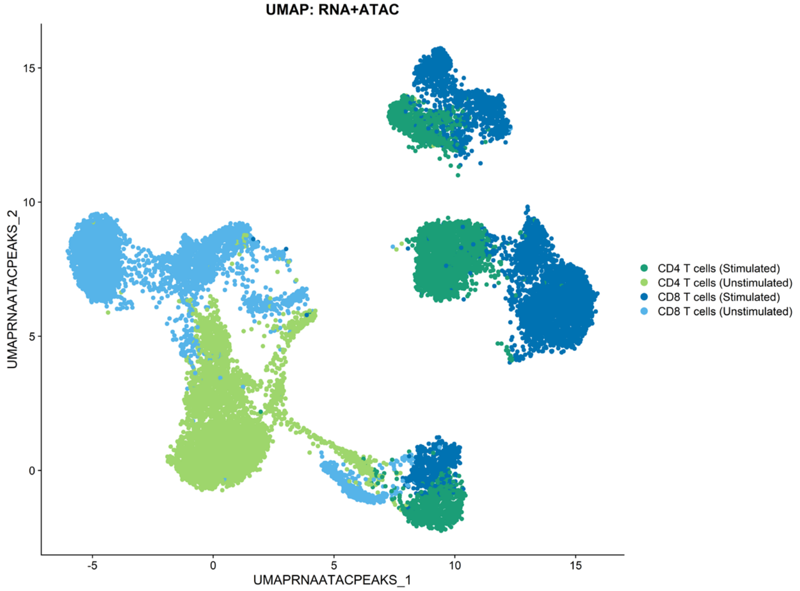
	Category	Color
1	CD4 T cells (Stimulated)	🟩
2	CD4 T cells (Unstimulated)	🟩
3	CD8 T cells (Stimulated)	🟦
4	CD8 T cells (Unstimulated)	🟦

<unassigned>:

New palette name × Save

Selected cell count: 0

Interactive customization of colors, dot size, displayed annotations, and selected modalities for dimensionality reduction

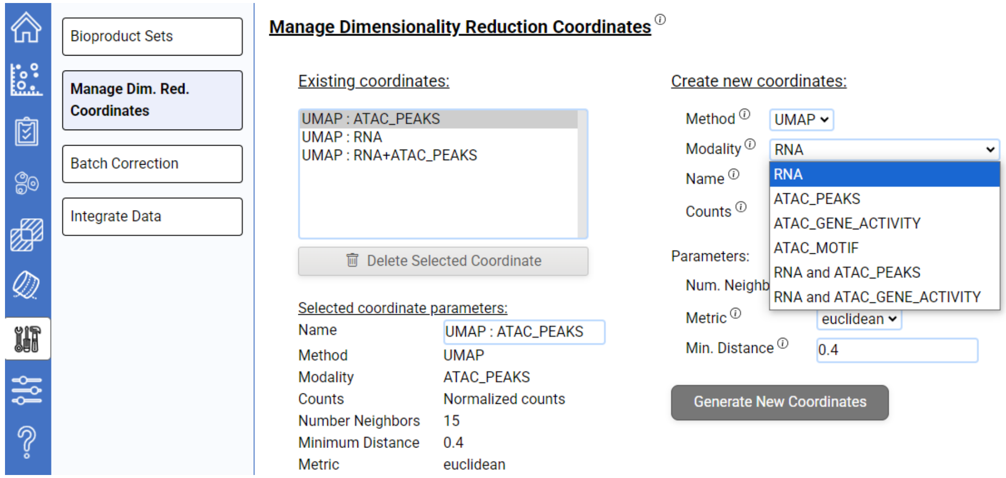


Code in R:

```
# RNA analysis
DefaultAssay(Seurat_object) <- "RNA"
Seurat_object <- SCTransform(Seurat_object, verbose = FALSE) %>% RunPCA() %>%
                 RunUMAP(dims = 1:50, reduction.name = 'umap.rna', reduction.key = 'rnaUMAP_')

# ATAC analysis
DefaultAssay(Seurat_object) <- "peaks"
Seurat_object <- RunTFIDF(Seurat_object)
Seurat_object <- FindTopFeatures(Seurat_object, min.cutoff = 'q0')
Seurat_object <- RunSVD(Seurat_object)
Seurat_object <- RunUMAP(Seurat_object, reduction = 'lsi', dims = 2:50, reduction.name = "umap.atac", reduction.key = "atacUMAP_")

# WNN graph, representing a weighted combination of RNA and ATAC-seq modalities.
Seurat_object <- FindMultiModalNeighbors(Seurat_object, reduction.list = list("pca", "lsi"), dims.list = list(1:50, 2:50))
Seurat_object <- RunUMAP(Seurat_object, nn.name = "weighted.nn", reduction.name = "UMAP.RNA.ATAC_PEAKS", reduction.key = "wnnUMAP_")
Seurat_object <- FindClusters(Seurat_object, graph.name = "wsnn", algorithm = 3, verbose = FALSE, resolution = 0.3)

DimPlot(my_seurat_object, reduction = 'UMAP.RNA.ATAC_PEAKS', group.by = "Original Sample",
       cols = c(col4s,col4us,col8s,col8us), pt.size = 1.5) + ggtitle("UMAP: RNA+ATAC")
```

UMAP /t-SNE visualization across modalities: RNA, ATAC and RNA+ATAC

Data analysis using the
BD Cellismo™ Data Visualization Tool v2.0



Manage Dimensionality Reduction Coordinates

Existing coordinates:

UMAP : ATAC_PEAKS
UMAP : RNA
UMAP : RNA+ATAC_PEAKS

Selected coordinate parameters:

Name	UMAP : ATAC_PEAKS
Method	UMAP
Modality	ATAC_PEAKS
Counts	Normalized counts
Number Neighbors	15
Minimum Distance	0.4
Metric	euclidean

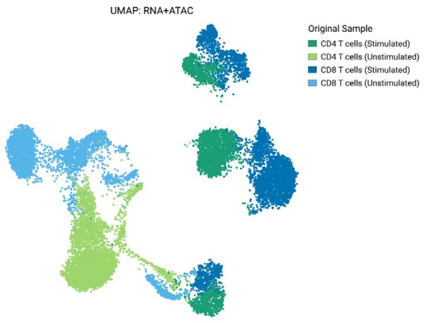
Create new coordinates:

Method: UMAP
Modality: RNA
RNA
ATAC_PEAKS
ATAC_GENE_ACTIVITY
ATAC_MOTIF
RNA and ATAC_PEAKS
RNA and ATAC_GENE_ACTIVITY
Name
Counts

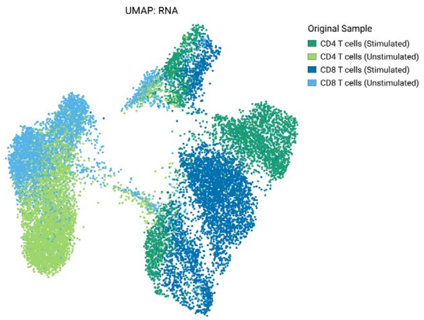
Parameters:

Num. Neighb
Metric: euclidean
Min. Distance: 0.4

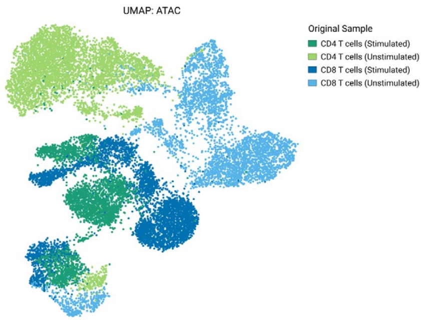
RNA + ATAC



RNA



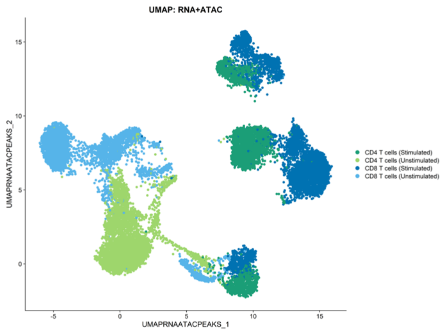
ATAC



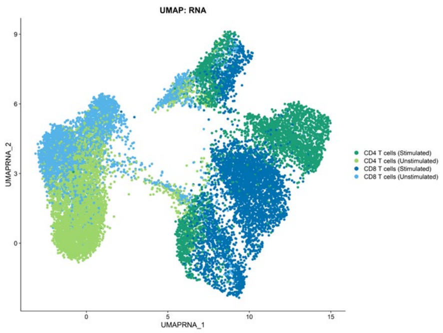
Manage dimensionality reduction by choosing either RNA data, ATAC data, or a combination of both modalities.

Data analysis in R using Seurat + Signac

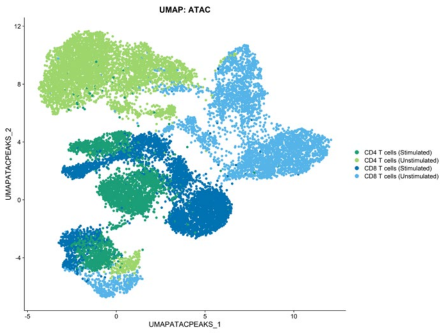
RNA + ATAC



RNA

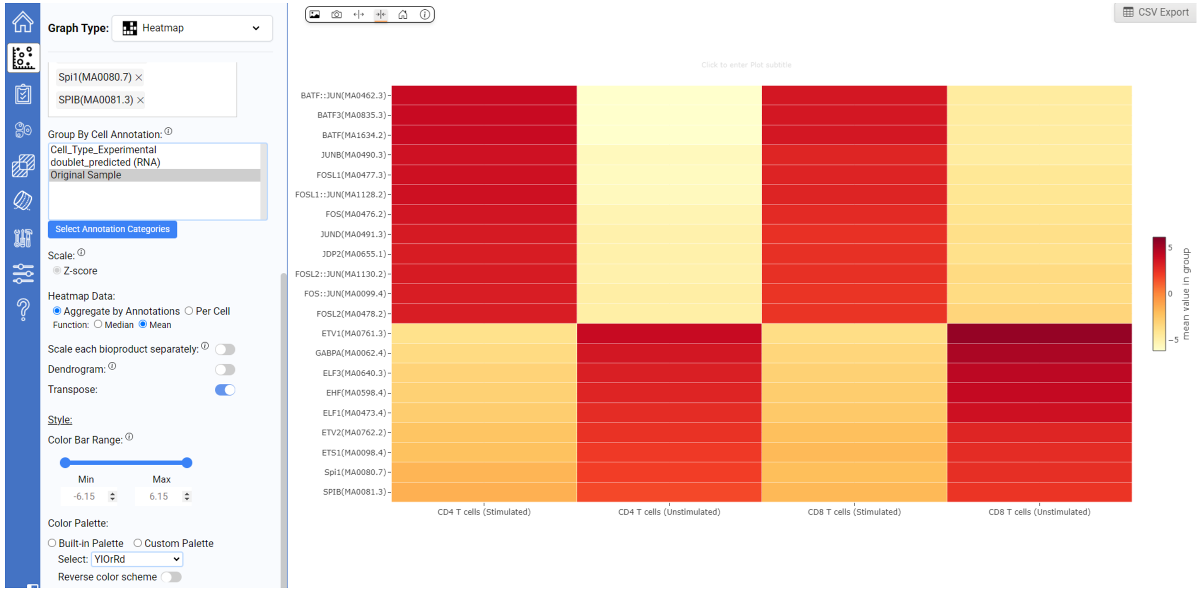


ATAC



Transcription factor activity

Data analysis using the BD Cellismo™ Data Visualization Tool v2.0


Graph Type: Heatmap

Spi1(MA0080.7) ×
SPIB(MA0081.3) ×

Group By Cell Annotation:
Cell_Type_Experimental
doublet_predicted (RNA)
Original Sample

Scale: ● Z-score

Heatmap Data: ● Aggregate by Annotations ○ Per Cell
Function: ○ Median ● Mean

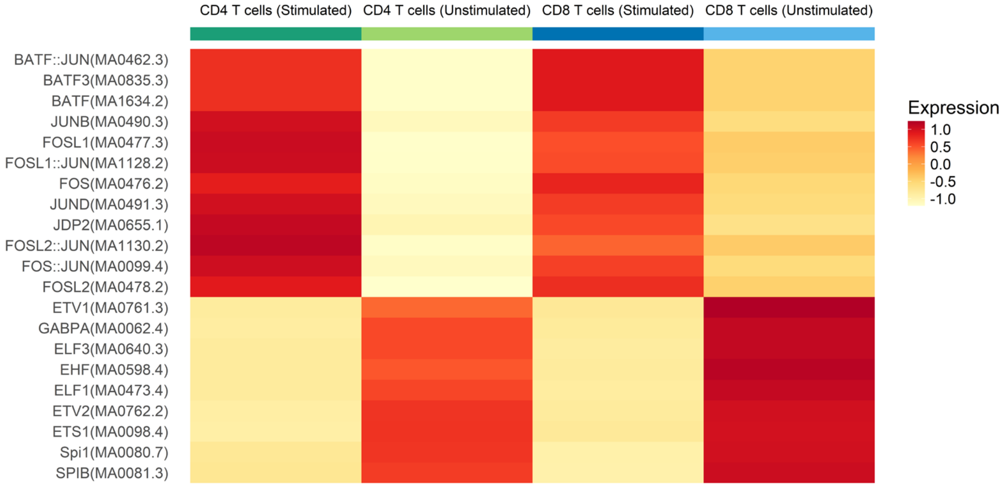
Scale each bioproduct separately: ○
Dendrogram: ○
Transpose: ●

Style:
Color Bar Range:
Min -6.15
Max 6.15

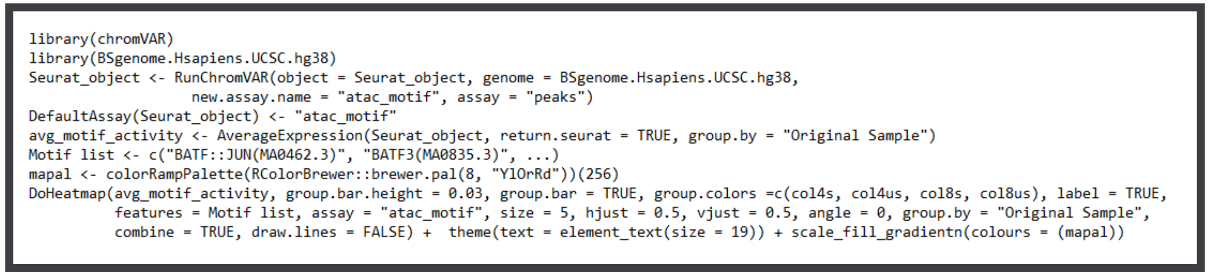
Color Palette:
○ Built-in Palette ○ Custom Palette
Select: YlOrRd
Reverse color scheme ○

- Flexible data computation and visualization options, including mean or median display, per-cell or aggregated display, and support for built-in or custom color palettes
- Differential analysis to identify up and down-regulated transcription factors for each sample or subset of interest
- Interactive environment for adjusting scale and adding or removing parameters

Data analysis in R using Seurat + Signac

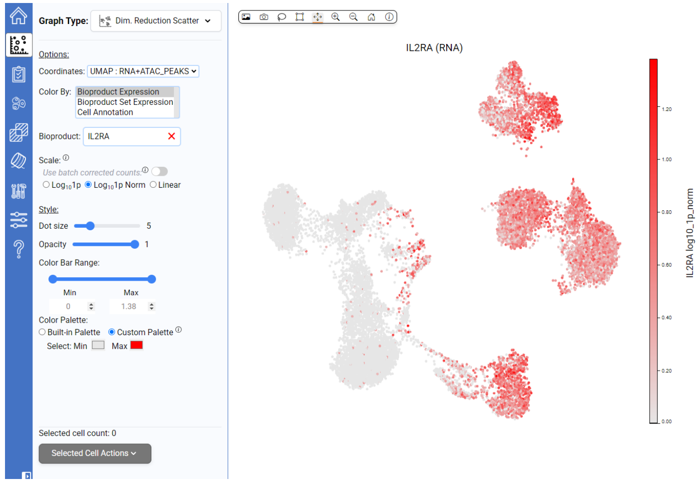


Code in R:


```
library(chromVAR)
library(BSgenome.Hsapiens.UCSC.hg38)
Seurat_object <- RunChromVAR(object = Seurat_object, genome = BSgenome.Hsapiens.UCSC.hg38,
                   new.assay.name = "atac_motif", assay = "peaks")
DefaultAssay(Seurat_object) <- "atac_motif"
avg_motif_activity <- AverageExpression(Seurat_object, return.seurat = TRUE, group.by = "Original Sample")
Motif list <- c("BATF::JUN(MA0462.3)", "BATF3(MA0835.3)", ...)
mapal <- colorRampPalette(RColorBrewer::brewer.pal(8, "YlOrRd"))(256)
DoHeatmap(avg_motif_activity, group.bar.height = 0.03, group.bar = TRUE, group.colors =c(col4s, col4us, col8s, col8us), label = TRUE,
          features = Motif list, assay = "atac_motif", size = 5, hjust = 0.5, vjust = 0.5, angle = 0, group.by = "Original Sample",
          combine = TRUE, draw.lines = FALSE) +  theme(text = element_text(size = 19)) + scale_fill_gradientn(colours = (mapal))
```

Gene activity and RNA expression

Data analysis using the
BD Cellismo™ Data Visualization Tool v2.0



Graph Type: Dim. Reduction Scatter

Options:

Coordinates: UMAP : RNA+ATAC_PEAKS

Color By: Bioproduct Expression

Bioproduct: IL2RA

Scale: ○ Log10 1p ● Log10 1p Norm ○ Linear

Style:

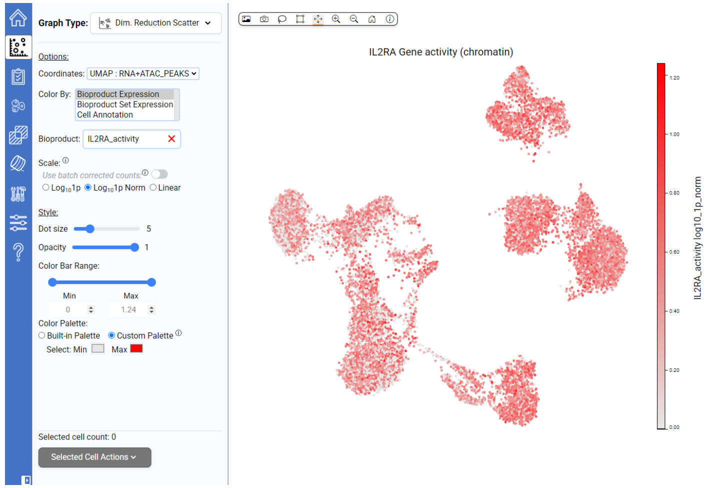
Dot size 5

Opacity 1

Color Bar Range: Min 0 Max 1.38

Color Palette: ○ Built-in Palette ● Custom Palette

Selected cell count: 0



Graph Type: Dim. Reduction Scatter

Options:

Coordinates: UMAP : RNA+ATAC_PEAKS

Color By: Bioproduct Expression

Bioproduct: IL2RA_activity

Scale: ○ Log10 1p ● Log10 1p Norm ○ Linear

Style:

Dot size 5

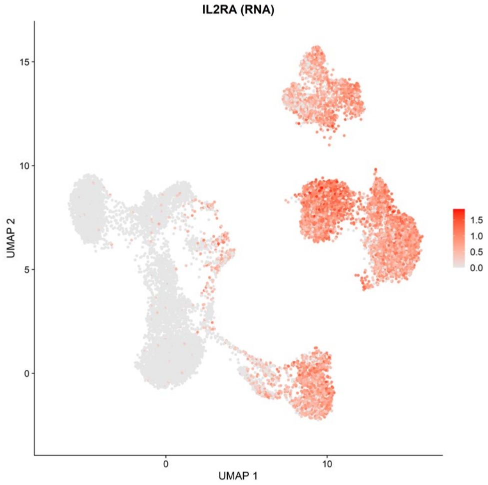
Opacity 1

Color Bar Range: Min 0 Max 1.24

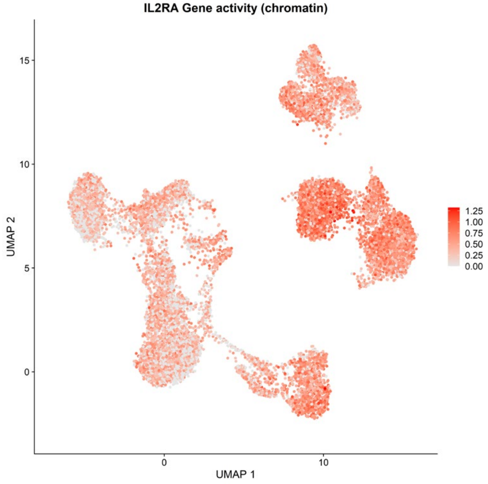
Color Palette: ○ Built-in Palette ● Custom Palette

Selected cell count: 0

Data analysis in R using
Seurat + Signac



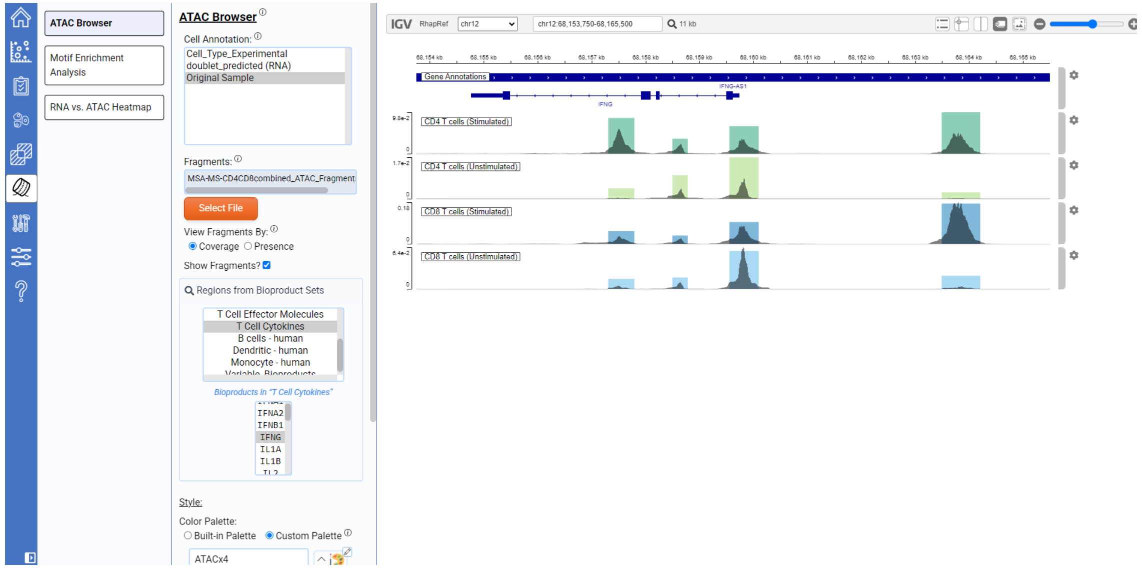
IL2RA
(RNA)



IL2RA
(Gene activity)

Visualization of genomic regions

Data analysis using the BD Cellismo™ Data Visualization Tool v2.0



ATAC Browser

Cell Annotation: Original Sample

Fragments: MSA-MS-CD4CD8combined_ATAC_Fragment

View Fragments By: ● Coverage ○ Presence

Show Fragments? ☑

Regions from Bioproduct Sets: T Cell Cytokines

Bioproducts in "T Cell Cytokines": IFNG

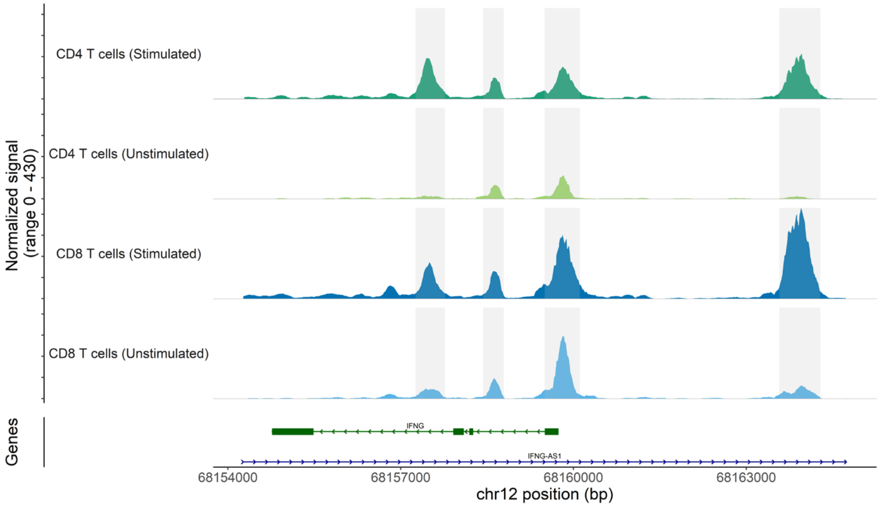
Color Palette: ○ Built-in Palette ● Custom Palette

ATACx4

IGV RhapRef chr12 chr12:68,153,750-68,165,500 11 kb

Easy-to-use Integrative Genomics Viewer (IGV) for exploring genomic regions.

Data analysis in R using Seurat + Signac



IFNG
Genomic region

Code in R:

```
ranges.show <- StringToGRanges(c("chr12-68159500-68160100", "chr12-68163500-68164200",
                                "chr12-68158450-68158800","chr12-68157300-68157800"))
CoveragePlot(Seurat_object, region = c("IFNG"), annotation = T, peaks = F, links = F, heights = 8,
             extend.upstream = 500, extend.downstream = 5000, group.by = "Original Sample",  window = 150, region.highlight = ranges.show)
             & scale_fill_manual(values= c(col4s, col4us, col8s, col8us)) & theme(text = element_text(size=16))
```

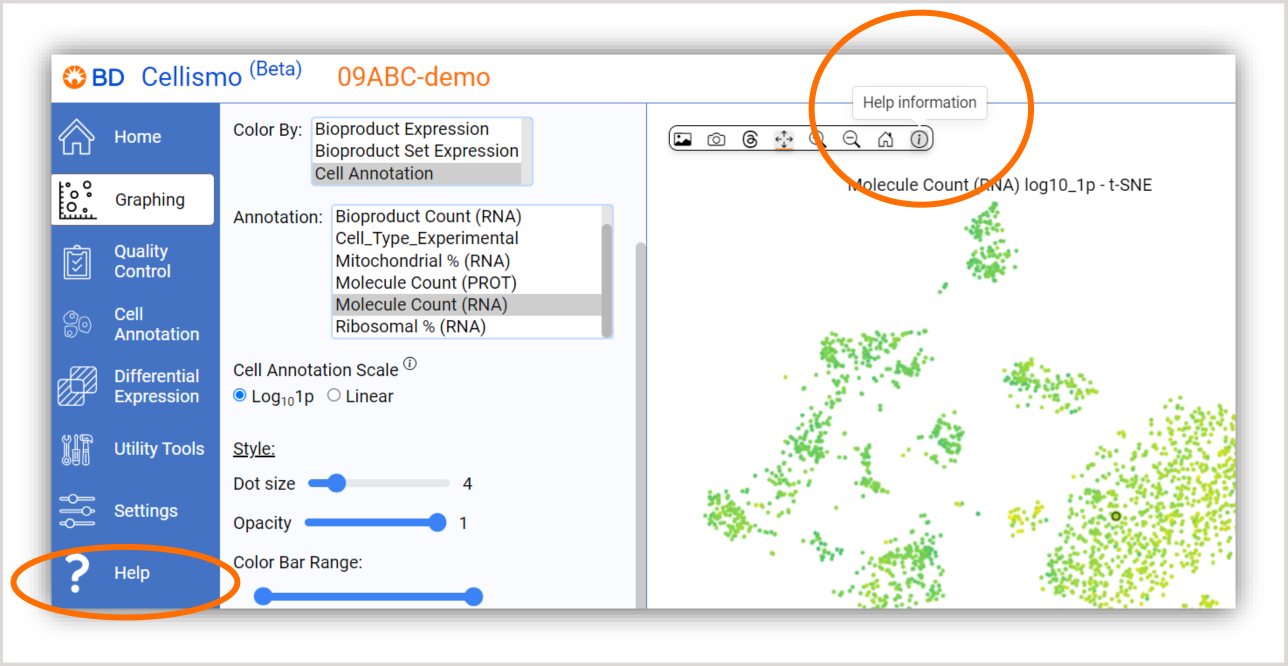
Support

Support resources

- Click on the information icon within the software for help

  ⓘ

- Access training videos on:
  - Scomix
  - BD Biosciences YouTube channel
- For any further questions, email us (emails also available in the Help section)
  - Europe: biox_support_emea@bd.com
  - China: bd-scm-bioinformatic@bd.com
  - USA: gmb-us-scm_bioinformatics@bd.com
  - Rest of the world: scomix@bd.com



Color By: Cell Annotation

Annotation: Molecule Count (RNA)

Cell Annotation Scale ● Log_{10}1p ○ Linear

Dot size 4

Opacity 1

Thank you