BD Cellismo™

Data Visualization Tool

More actionable insights. No coding required

BD

Contents

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 datasets with ease

User friendly: No cost of adoption; no coding required

Features

- 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

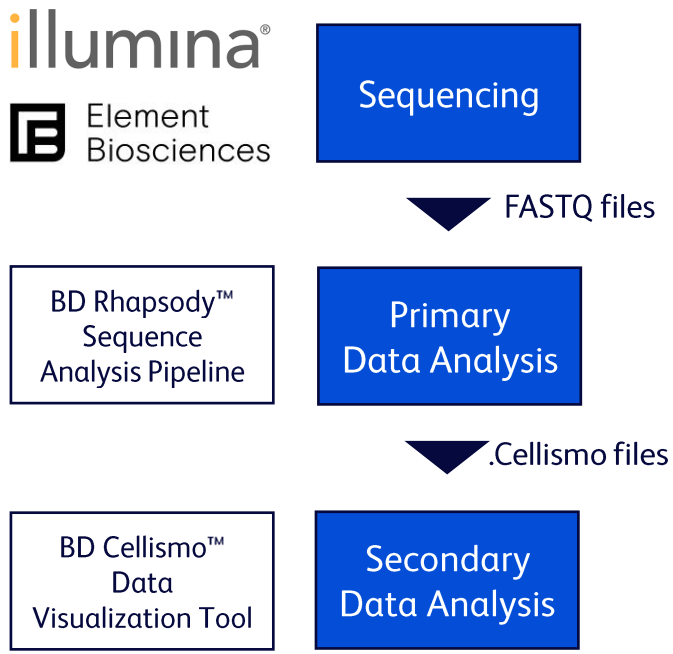
How to access the BD Cellismo™ Data Visualization Tool

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

- (Preferred) .Cellismo output file from the BD Rhapsody™ Sequence Analysis Pipeline.
  - Contains the expression data for all modalities (RNA and AbSeq)
  - Contains any cell annotations that are created by the pipeline (e.g., Sample Multiplexing Tag, Immune Cell Type).
- Alternative inputs formats:
  - Market exchange (MEX)
  - H5AD/H5MU
- Windows:
  - Windows 10 or later (64-bit)
- MacOS:
  - MacOS 11 (Big Sur) or later
  - Intel or Apple silicon chip
- RAM :
  - 8 GB RAM minimum
  - 16 GB RAM for 200,000 cells
  - 64 GB RAM for 1M cells



Pricing: Free!

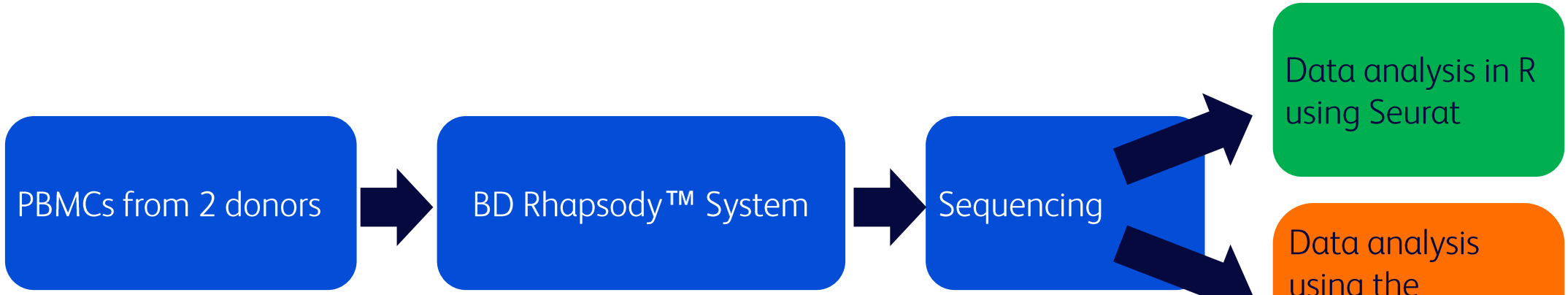
- The BD Cellismo™ Data Visualization Tool is offered free of charge

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

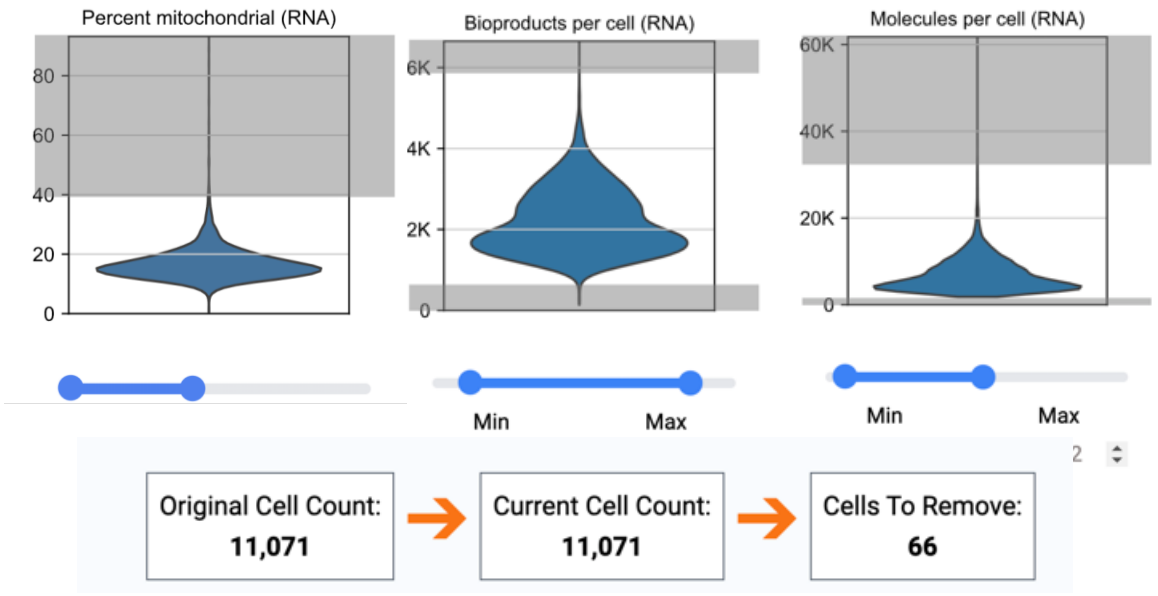
Generate the same data visualization as Seurat using the BD Cellismo™ Data Visualization Tool



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

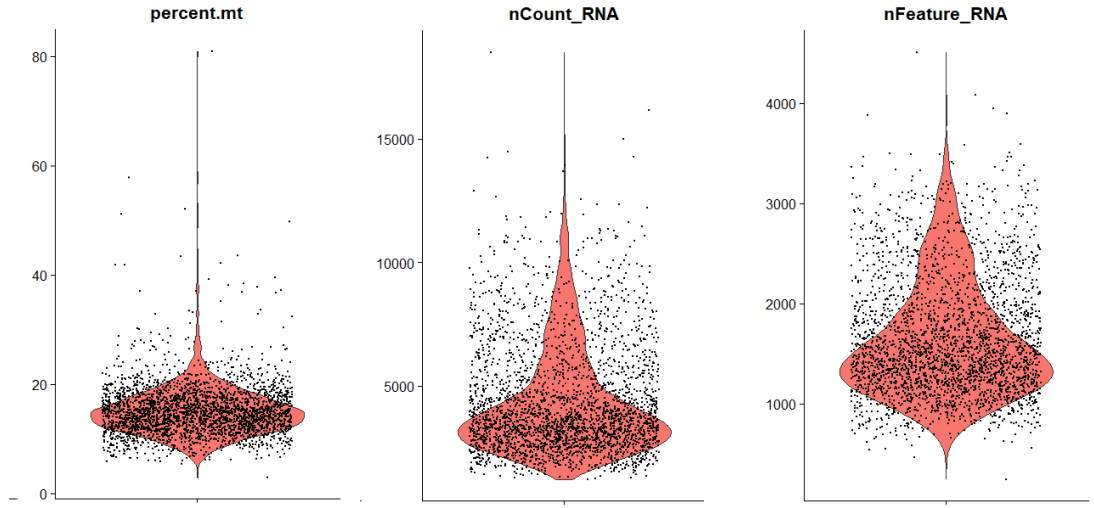
Quality control and filtering out low quality cells

Data analysis using the BD Cellismo™ Data Visualization Tool



- 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

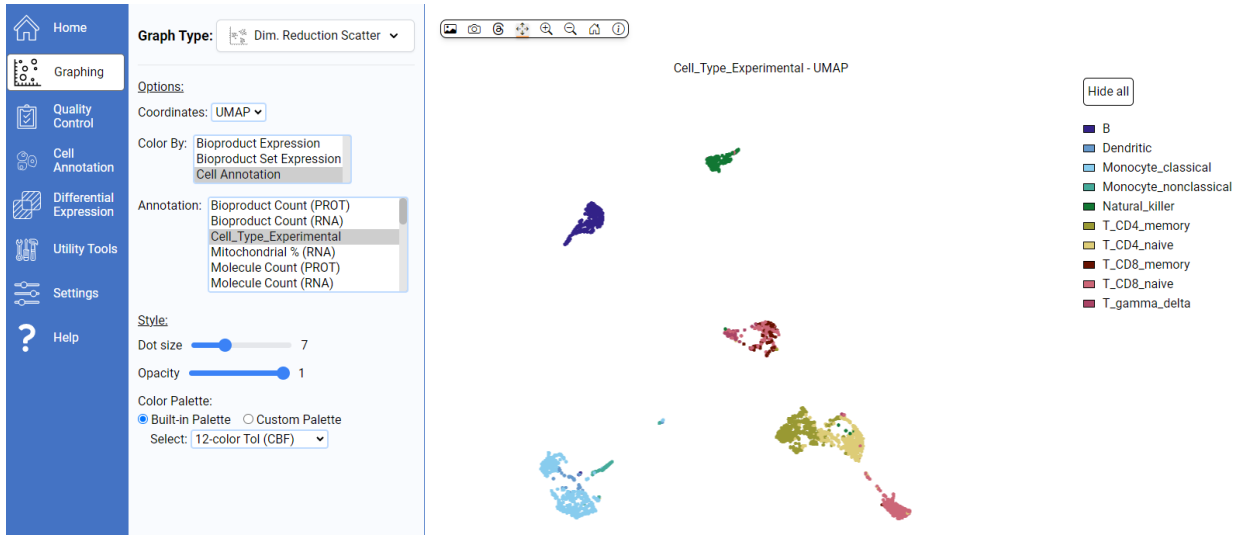
Data analysis in R using Seurat




```
# 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)
```

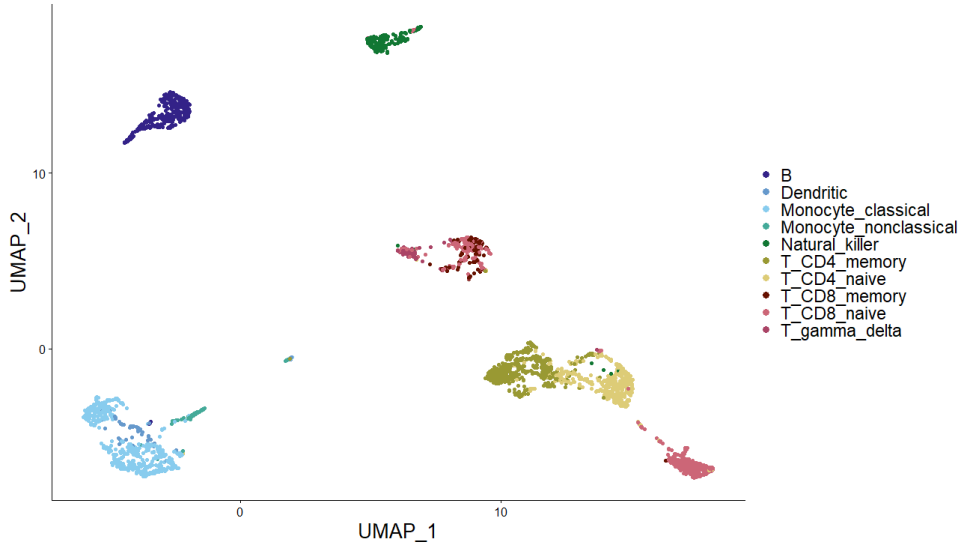
Dimensional reduction (UMAP/tSNE)

Data analysis using the BD Cellismo™ Data Visualization Tool



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

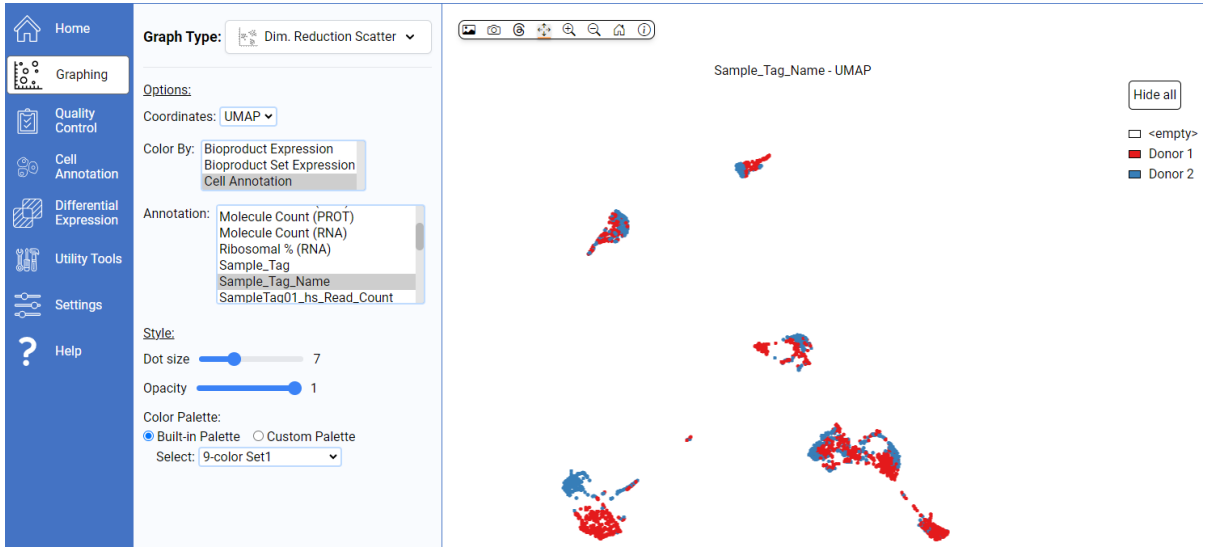
Data analysis in R using Seurat




```
# 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)))
```

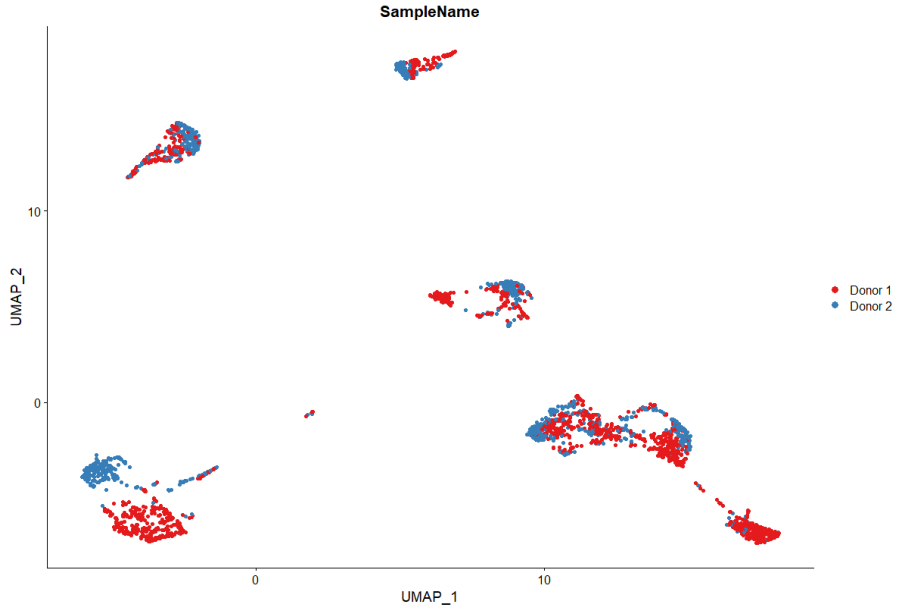
Sample Tags (and assigning sample name)

Data analysis using the BD Cellismo™ Data Visualization Tool



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

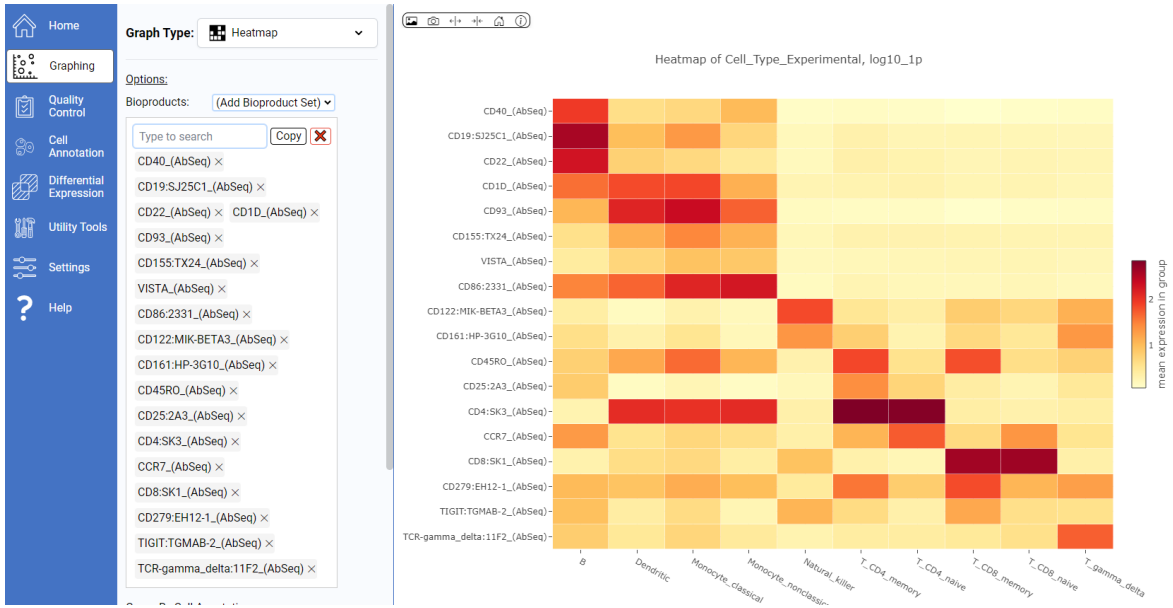
Data analysis in R using Seurat



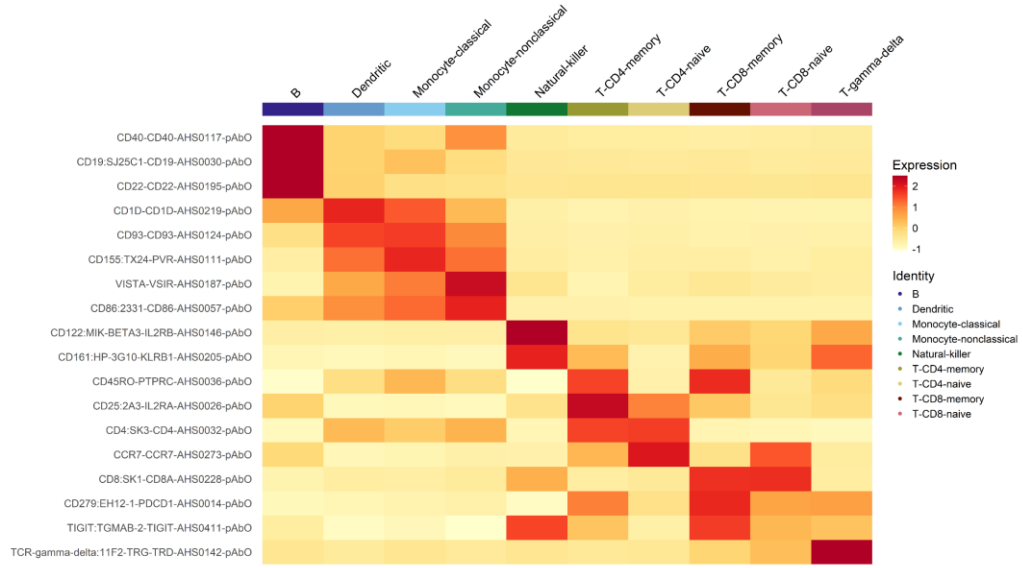

```
## Sample Tags

# 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



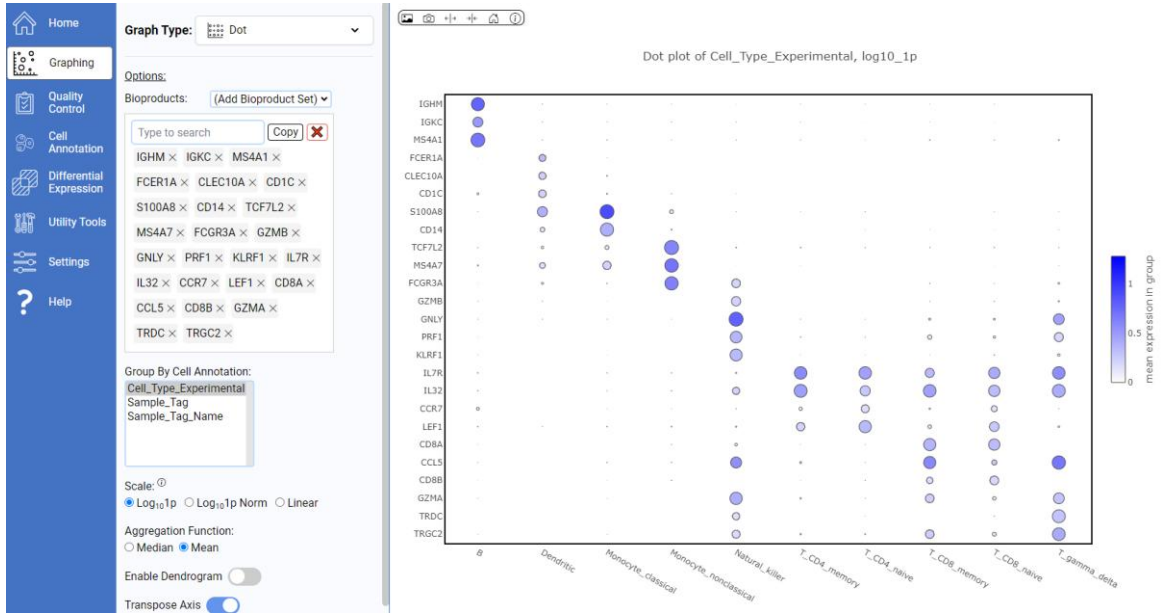
Data analysis in R using Seurat



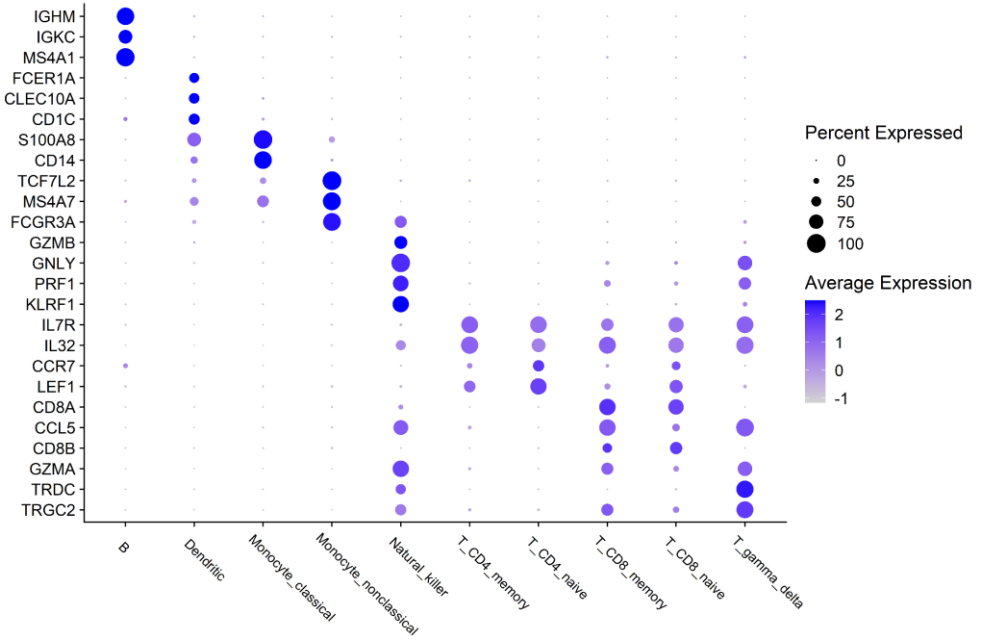

```
DefaultAssay(pbmc) <- "ADT"
avgexpabseq = AverageExpression(pbmc, return.seurat = T)
mapal <- colorRampPalette(RColorBrewer::brewer.pal(8, "YlOrRd"))(256)
DoHeatmap(avgexpabseq, group.bar.height = 0.03, group.bar = TRUE, group.colors  = c(ptol_pal()(12)),
          features = abseq, size = 5, hjust = 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



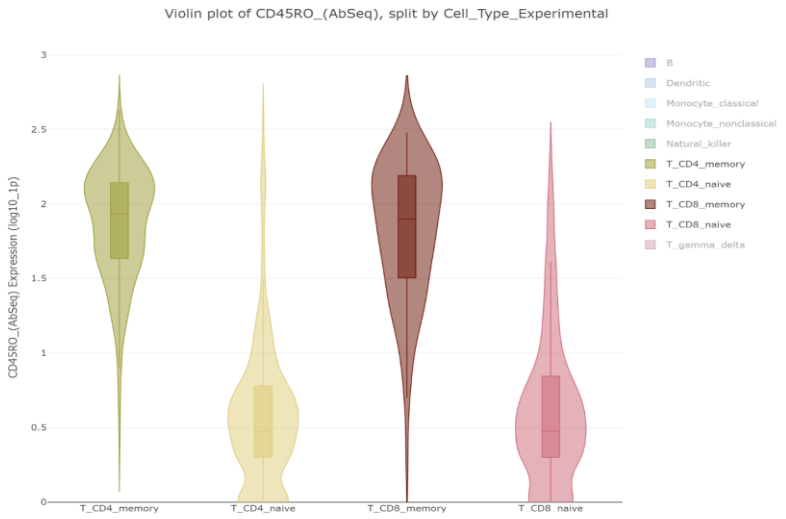
Data analysis in R using Seurat

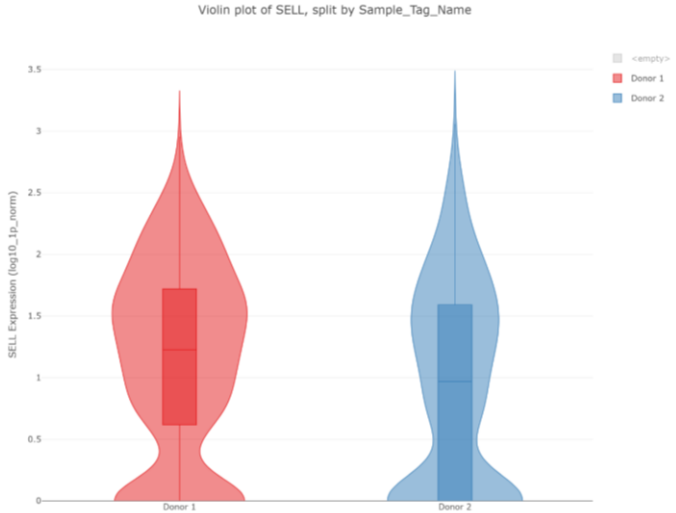



```
genes <- c("IGHM", "IGKC", "MS4A1", "FCER1A", "CLEC10A", "CD1C", "S100A8", "CD14", "TCF7L2", "MS4A7", "FCGR3A",
"GZMB", "GNLY", "PRF1", "KLRF1", "IL7R", "IL32", "CCR7", "LEF1", "CD8A", "CCL5", "CD8B", "GZMA","TRDC", "TRGC2")

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

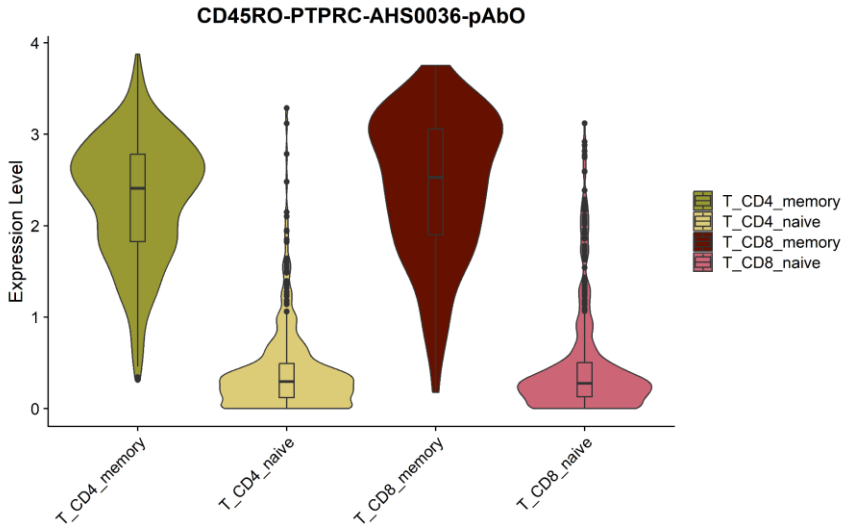
Violin plots

Data analysis using the BD Cellismo™ Data Visualization Tool

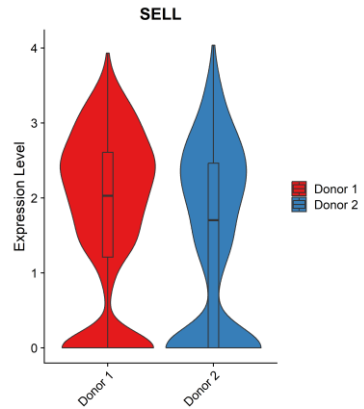




Data analysis in R using Seurat




```
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)
```

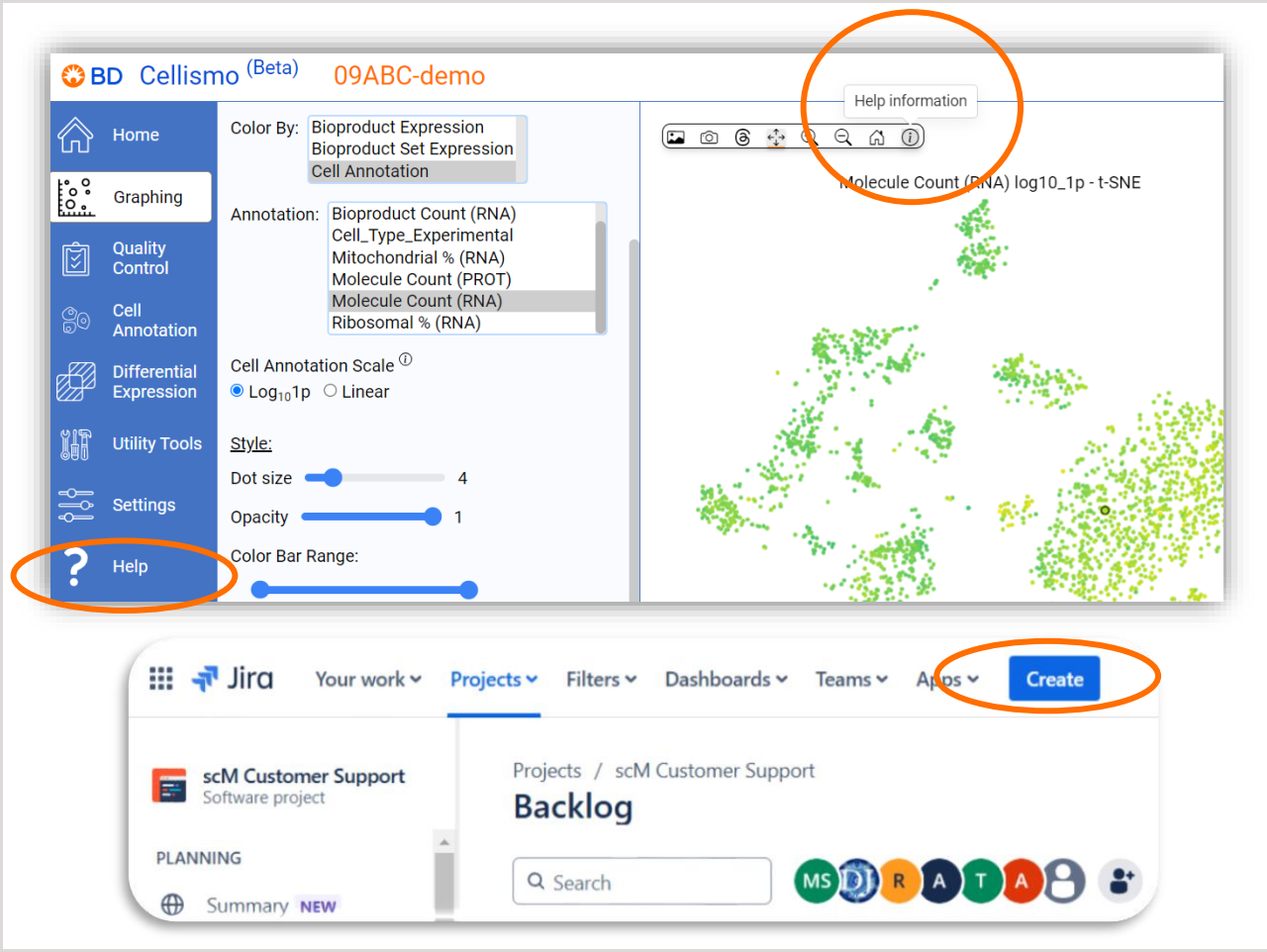



```
VlnPlot(pbmc, features = "SELL", pt.size = 0, cols= brewer.pal(9,"Set1"), assay = "RNA") + geom_boxplot(width=0.1)
```

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 (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
- If the first line of support does not resolve the issue, create a task on the JIRA board (FAS and Scomix only)



Thank you