01_demonstration

pooja

2025-06-18

01 Demonstration - Plotting a Histogram from a seurat object

```r
plot_celltype_distribution_by_sample <- function(seurat_obj,
                                                  sample_col = "samples",
                                                  celltype_col = "cell_annotation",
                                                  title = "Cell Type Distribution by Treatment",
                                                  colors = NULL,
                                                  save_path = NULL) {
  library(ggplot2)
  library(dplyr)
  library(RColorBrewer)

  # Step 1: Count cells per sample and celltype
  celltype_counts <- seurat_obj@meta.data %>%
    dplyr::group_by(.data[[sample_col]], .data[[celltype_col]]) %>%
    dplyr::summarise(count = dplyr::n(), .groups = "drop") %>%
    dplyr::rename(samples = 1, celltype = 2)

  # Step 2: Normalize to get percentages
  celltype_percent <- celltype_counts %>%
    dplyr::group_by(samples) %>%
    dplyr::mutate(percentage = count / sum(count) * 100)

  # Step 3: Define color palette
  if (is.null(colors)) {
    n_types <- length(unique(celltype_percent$celltype))
    colors <- colorRampPalette(brewer.pal(8, "Pastel1"))(n_types)
  }

  # Step 4: Create bar plot
  p <- ggplot(celltype_percent, aes(x = samples, y = percentage, fill = celltype)) +
    geom_bar(stat = "identity", width = 0.75) +
    scale_fill_manual(values = colors) +
    labs(
      title = title,
      x = "Cytokine Treatment",
      y = "Cell Type Percentage",
      fill = "Cell Type"
    ) +
    theme_minimal(base_size = 14) +
```

```r
    theme(
      plot.title = element_text(hjust = 0.5, face = "bold", size = 16, color = "#6a51a3"),
      axis.text.x = element_text(angle = 45, hjust = 1, size = 12, color = "#4d4d4d"),
      axis.text.y = element_text(size = 12),
      legend.position = "right",
      legend.title = element_text(face = "bold"),
      panel.grid.major.y = element_line(color = "gray90")
    )

  # Step 5: Optionally save
  if (!is.null(save_path)) {
    ggsave(save_path, plot = p, width = 10, height = 6)
  }

  return(p)
}
```

```r
load("data/oIL9R_annotated.RData")
```

```r
# Use Barbie palette if desired
barbie_colors <- c(
  "#ff69b4", "#ffb6c1", "#ffc0cb", "#dda0dd", "#db7093",
  "#f8c8dc", "#e75480", "#d8bfd8", "#ff82ab", "#da70d6"
)

# Call function
plot_celltype_distribution_by_sample(
  seurat_obj = oIL9R_main,
  sample_col = "samples",
  celltype_col = "cell_annotation",
  title = "IL-9 Signaling:Cluster-Level Impact",
  colors = barbie_colors,
  save_path = "preliminary/special_clusterdistribution.png"
)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

IL−9 Signaling:Cluster−Level Impact