Shiny App for Histone Post-translational Modifications Data Visualization

This Shiny application provides an interactive platform for **loading, filtering, visualizing, and downloading data**.
It is designed to help researchers process peptide-level tables exported from skyline and generate common exploratory plots such as PCA, heatmaps, and barplots.

✨ Features

- **Upload Data**
  - Import table from Skyline
- **Data Filtering**
  - Select or exclude unmodified peptides.
  - Choose samples or peptides of interest interactively.
- **Visualization**
  - **PCA plot** for dimensionality reduction and sample clustering.
  - **Heatmap** for peptide intensity patterns.
  - **Barplots** for selected peptides.
- **Download**
  - Export filtered tables in wide format.

🚀 Quick Start

1. **Open the `app.R` in RStudio.**

   Make sure `app.R` and `functions.R`, `ui.R`, and `server.R` are in the same directory.

2. **Load required packages.**

   In the R console, run:

   ```
   source("functions.R")
   depends_check()
   ```

3. **Run the app**

   Click the **Run App** button in the top-right corner of Rstudio.

👥 Authors

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