Package ‘MuPETFlow’

July 21, 2025

Title Multiple Ploidy Estimation Tool for all Species Compatible with Flow Cytometry

Version 0.1.1

Description A graphical user interface tool to estimate ploidy from DNA cells stained with fluorescent dyes and analyzed by flow cytometry, following the methodology of Gómez-Muñoz and Fischer (2024) <doi:10.1101/2024.01.24.577056>. Features include multiple file uploading and configuration, peak fluorescence intensity detection, histogram visualizations, peak error curation, ploidy and genome size calculations, and easy results export.

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Encoding UTF-8

Date/Publication 2025-01-15 19:40:19 UTC

RoxygenNote 7.3.2

Imports BiocManager, dplyr, DT, ggplot2, ggrepel, gridExtra, markdown, shiny, shinythemes, tidyr, zoo

Suggests knitr, flowCore, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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`runMuPETFlow` *Run the MuPETFlow app*

Description

This function launches the Shiny app included in MuPETFlow. Once the application is launched, you can either:

1. Load your experimental data.
2. Run an in-app example by clicking the 'Example' button.

Usage

```
runMuPETFlow()
```

Details

After launching the app, you can follow the app flow, which is divided into three tabs: **Peaks**, **Regression** and **Summary**. Below is a general description of the options available in each tab:

Peaks:

- **Select a sample (optional):** Allows visual exploration of individual samples if desired.
- **Adjust smoothing (optional):** Adjusts the histogram curve for noisy samples.
- **Adjust window width (optional):** Defines the interval where the app will look for peaks.
- **Select minimum cell count to call a peak (optional):** Useful for samples with a low number of events.
- **Select maximum number of peaks to plot (optional):** Useful for samples with heterogeneous populations where more peaks are present.

Regression:

- **Select type of analysis:** Choose between "Ploidy" or "Genome size" analysis.
- **Select number of standards:** A minimum of two different standards is required, but more are recommended.
- **Select standard samples and values:** This is the ploidy or genome size of your standards.

Summary:

- **Results preview:** Creates a compiled figure with histograms for all samples.
- **Save plot:** Saves the histograms in either PNG or TIFF format with customizable size and quality. Optionally, you can control the grid layout.
- **Save table:** Exports the parameters used and the estimated ploidy or genome size as a CSV file.

Value

No return value, called for side effects.

Examples

```
if (interactive()) {
  # Example: Check that the function exists and runs
  runMuPETFlow()
} else {
  message("This is a Shiny app wrapper. Run interactively to use.")
}
```

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