

# Package: MuPETFlow (via r-universe)

September 25, 2026

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

**Version** 0.1.2

**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.

**License** GPL (>= 3)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

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

**Suggests** knitr, flowCore, rmarkdown

**VignetteBuilder** knitr

**Config/pak/sysreqs** cmake make libicu-dev libuv1-dev zlib1g-dev

**Repository** <https://cintiag.r-universe.dev>

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**RemoteUrl** <https://github.com/cintiag/mupetflow>

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`runMuPETFlow`*Run the MuPETFlow app*

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## 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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