Ciphe Infinity

AN INTERACTIVE GUIDE

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Introduction

"Ciphe Infinity" is a R-Shiny web-based tool that serves for the purpose of running "infinity Flow" analysis for cell-surface markers quantification in an intuitive way that doesn't require any prior coding knowledge.

It's based on the original package ("infintyFlow") for running the analysis and ("ggplot2") and ("complexHeatmap") for visualizing the results.

This tool is available for the moment on the GoT's dev server of CIPHE (soon should be implemented in the prod server).

Purpose of the guide

"Ciphe Infinity" is in the early stages of release, this guide is mainly directed towards the other members of the team in order to provide some feedback over some stuffs that they may not find intuitive or understandable enough inside the UI.

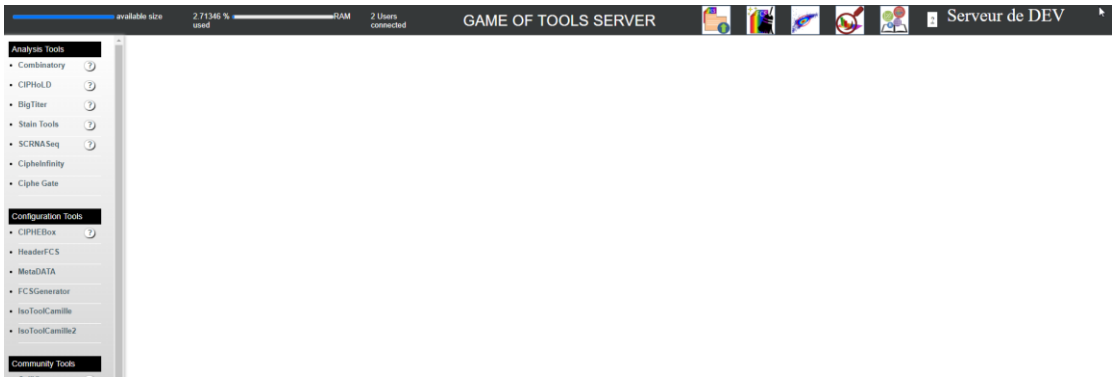
Guide

CONNECTING TO THE TOOL

As mentioned in the introduction, the tool is currently available (As of 13/5/2022) in the dev server of GoT (10.71.1.6).

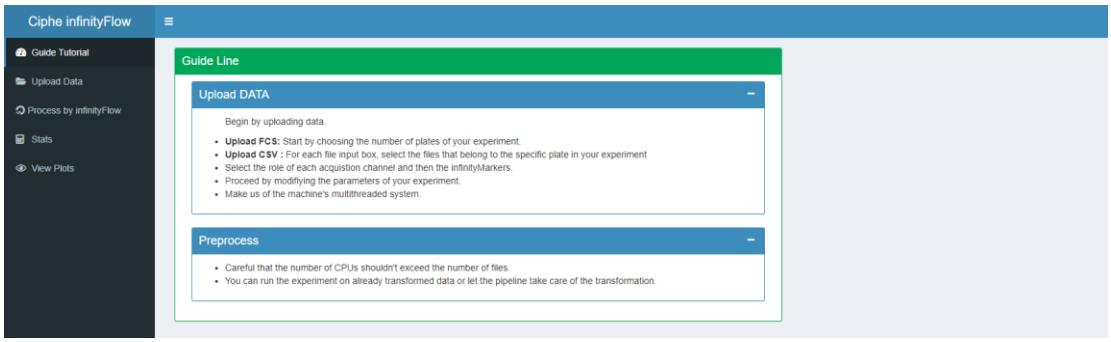
Use the following credentials: hluche1/hluche1

After successfully connecting to the server, the main page should look like this.



Click on “Ciphe Infinity” on the left in order to access tool.

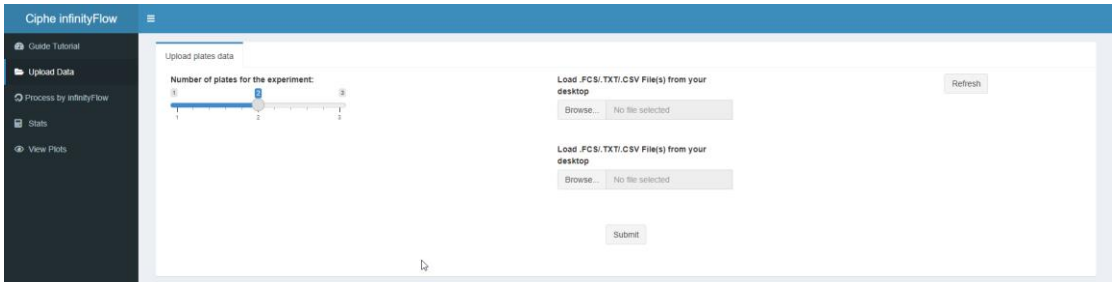
NAVIGATION



Feel free to read the gentle intro that indicates the general use and steps of the tool.

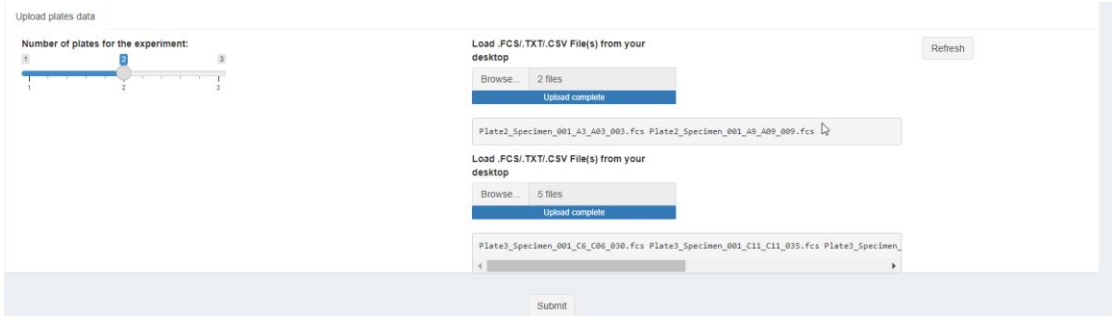
Now moving to the next tab “Upload Data”.

UPLOADING DATA



Currently there is only one possibility for uploading files. (Soon to be implemented a shinyDirChoose that allows for direct server-side files selections, if files are saved in the analysis server.)

The user should choose how many plates are there in his experiment, in our example we will use an an experiment of two plates with 5 files in total.

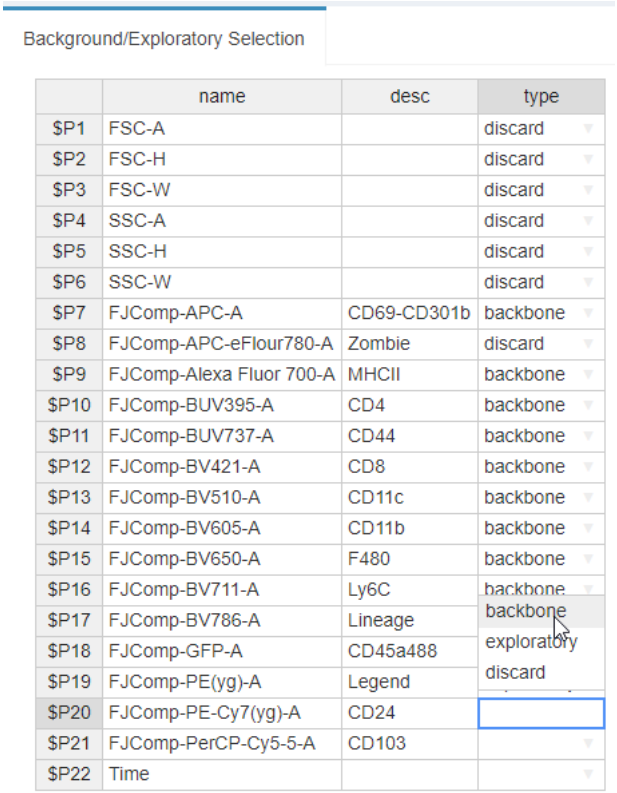


Submitting data will generate a new tab that will allow for user selection of grouping of columns of acquisition under three labels: Discarded (not used in analysis), Backbone (over which the ML model will run the analysis) and Exploratory (which will be used to infer the values of expression for the markers).

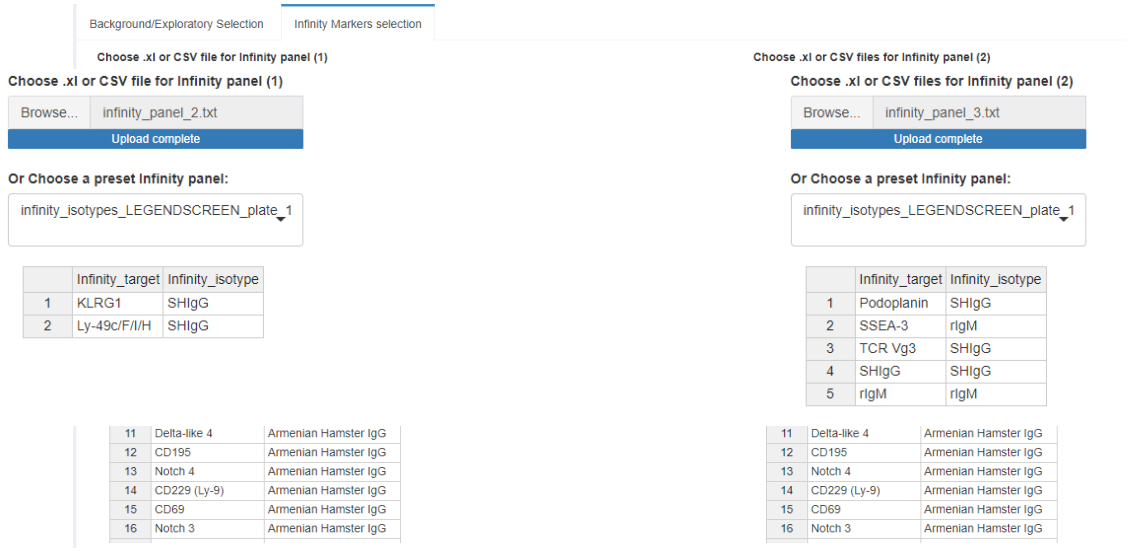
Background/Exploratory Selection

	name	desc	type
$P1	FSC-A		
$P2	FSC-H		
$P3	FSC-W		
$P4	SSC-A		
$P5	SSC-H		
$P6	SSC-W		
$P7	FJComp-APC-A	CD69-CD301b	
$P8	FJComp-APC-eFlour780-A	Zombie	
$P9	FJComp-Alexa Fluor 700-A	MHCII	
$P10	FJComp-BUV395-A	CD4	
$P11	FJComp-BUV737-A	CD44	
$P12	FJComp-BV421-A	CD8	
$P13	FJComp-BV510-A	CD11c	
$P14	FJComp-BV605-A	CD11b	
$P15	FJComp-BV650-A	F480	
$P16	FJComp-BV711-A	Ly6C	
$P17	FJComp-BV786-A	Lineage	
$P18	FJComp-GFP-A	CD45a488	
$P19	FJComp-PE(yg)-A	Legend	
$P20	FJComp-PE-Cy7(yg)-A	CD24	
$P21	FJComp-PerCP-Cy5-5-A	CD103	
$P22	Time		

Confirm Background Exploratory Selection

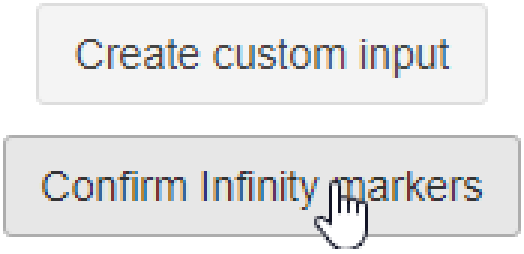


After validating our selection, another table will also show up to choose the labels and isotypes of the studied markers in the experiment. Initially, preset LEGENDScreen plates will be shown to make the selection easier for the user(with the possibility to add new presets for later use).



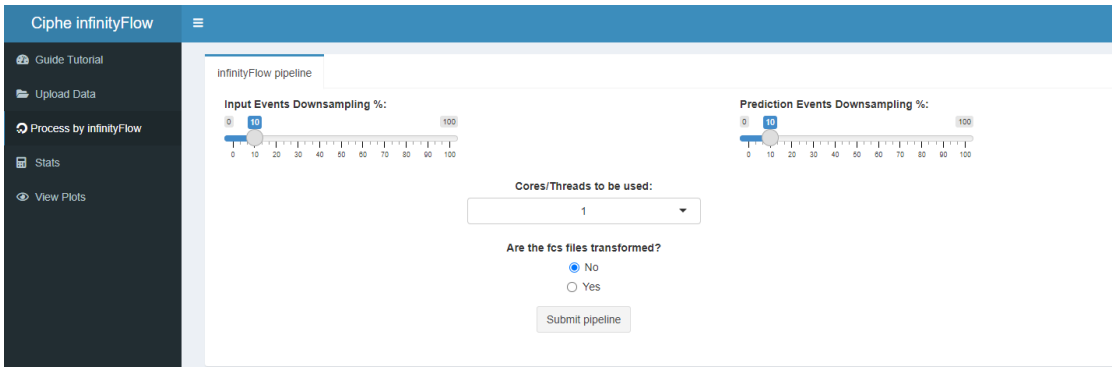
Alternatively, the user can upload his CSV file (like the case in this example). Or also by pressing “Create custom input” an empty table will be initialized which will be then customized.

Press “Confirm Infinity markers” to proceed.

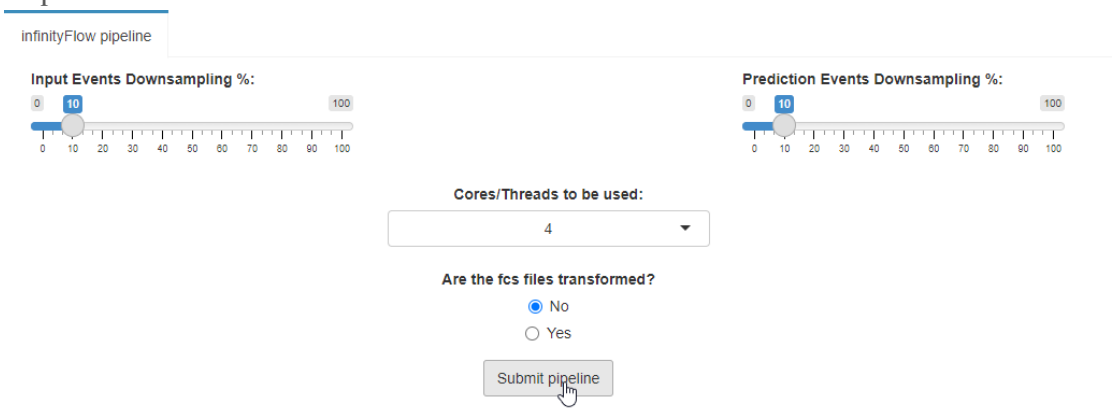


PROCESS BY INFINITYFLOW

After successfully uploading all the necessary input for the pipelines, the last step consists of specifying the parameters that will be used for the pipeline run.

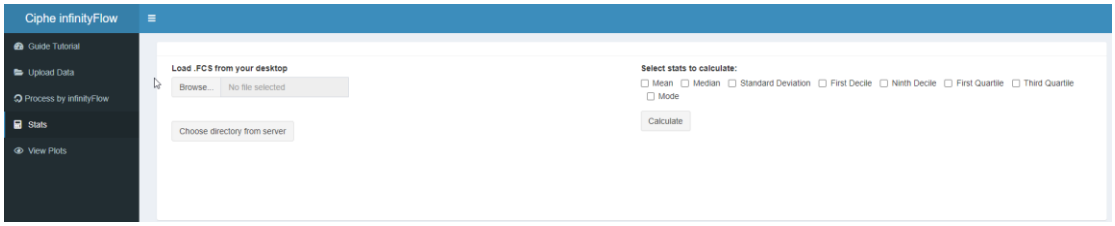


Based on the average number of events per file, the % of sampling will be applied to all the input files. Moreover, the user has the possibility to opt for multithreaded analysis (<!> the number of cpu's that shouldn't be higher than the number of files chosen), also if the files are already transformed, the user can choose to skip the transformation step.

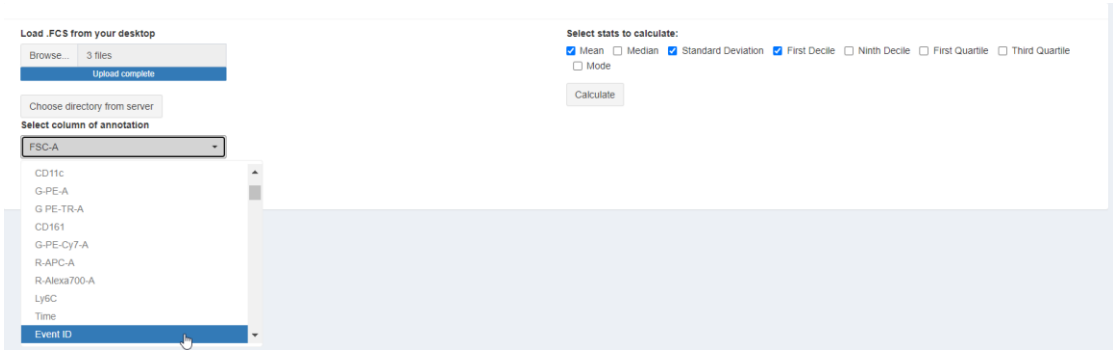


GENERATION OF STATISTICS

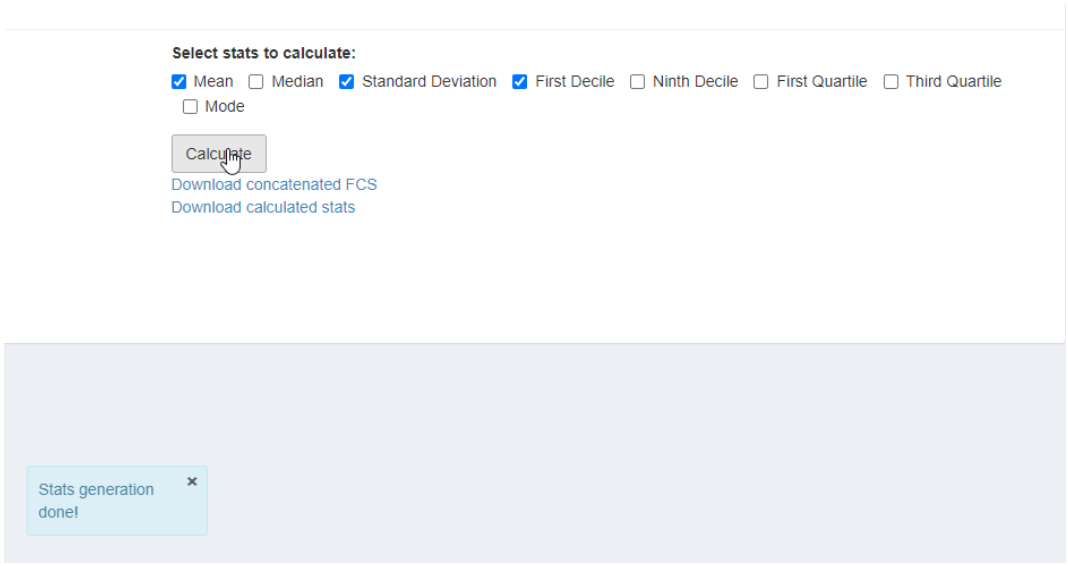
The user can choose to generate statistics for FCS files uploaded from their local PC or from the server he is working on.



There are different choices of statistics. This tool offers the flexibility of being used with files that are from tools outside the pipeline.

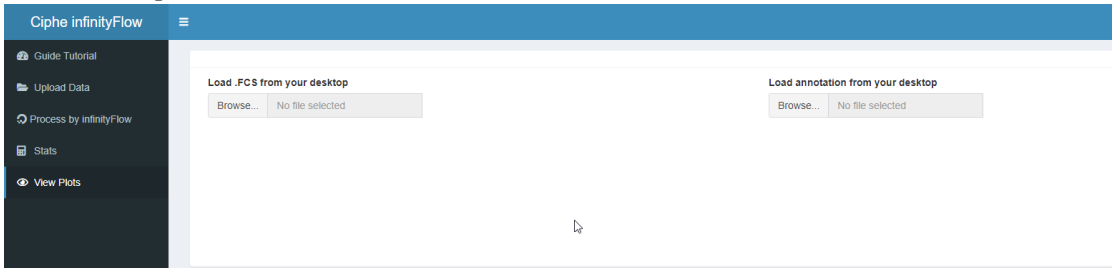


When the calculation is done, the files can be downloaded alongside the concatenated sampled FCS files resulting from the selection.

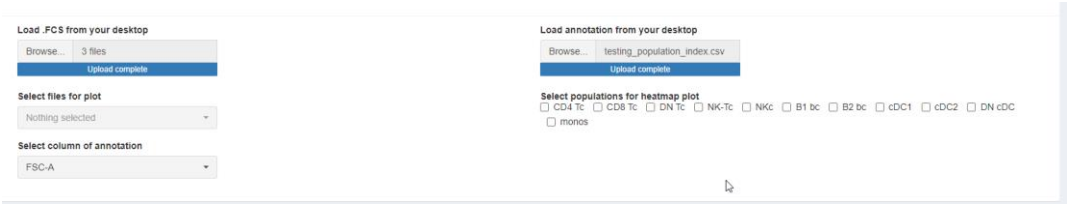


VISUALIZING PLOTS

Finally, Ciphe Infinity also offers the possibility of visualizing the data using UMAP and heatmap.



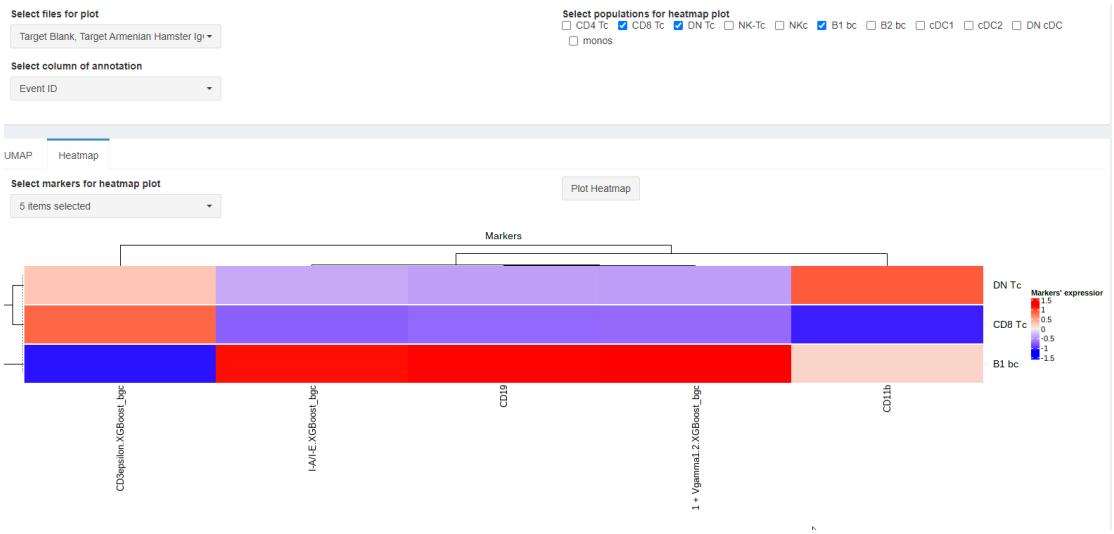
In this example, three FCS files where provided alongside a CSV indicating the annotation of the populations (generate by another tool, CIPHE Gate).



The annotation ID in this example is called “Event ID”, and as we can see we decide to plot a UMAP based on the values inferred to CD3epsilon.

Also for heatmaps, we can choose more than one column (marker). Two hierarchical clustering methods are applied on populations and markers.

We can choose to visualize all the populations, or a group of the populations annotated by selecting the buttons underneath the annotation file box.


Select files for plot
Target Blank, Target Armenian Hamster Ig
Select column of annotation
Event ID
Select populations for heatmap plot
CD4 Tc
CD8 Tc
DN Tc
NK-Tc
NKc
B1 bc
B2 bc
cDC1
cDC2
DN cDC
monos
UMAP
Heatmap
Select markers for heatmap plot
5 items selected
Plot Heatmap
Markers
DN Tc
CD8 Tc
B1 bc
Markers' expressior
1.5
1
0.5
0
-0.5
-1
-1.5
CD3epsilon.XGBoost_bgc
I-A/I-E.XGBoost_bgc
CD19
1 + Vgamma1.2.XGBoost_bgc
CD11b