

# R for cytometry - citrus

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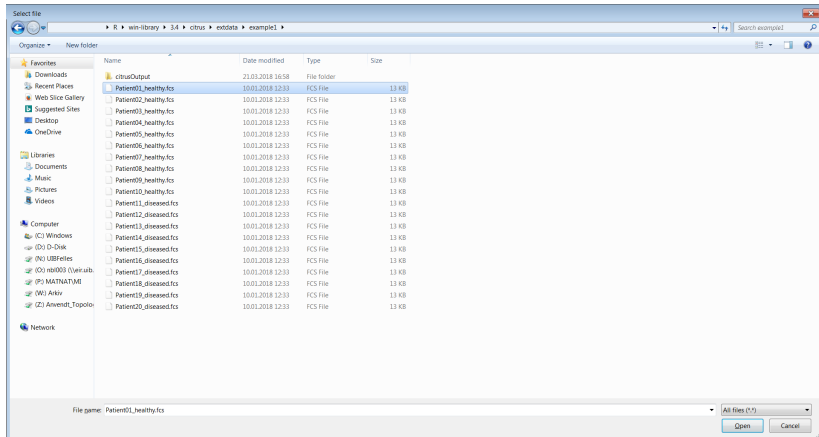
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# Citrus

Tutorial

# Start Citrus GUI

```
require(citrus)  
citrus.launchUI()
```



The screenshot shows the Citrus UI v0.8 web application in a browser window. The browser's address bar shows the URL 127.0.0.1:7707. The application has a top navigation bar with tabs: Sample Group Setup, Clustering Setup, Cluster Characterization, Association Model Configuration, and Run!.

### Citrus Runtime Summary:

Working Directory:  
C:\Users\mb003R\win-library\3.4\citrus\extdata\example1

Groups Summary:

- Group 1 Samples: 0
- Group 2 Samples: 0

Condition Summary:

- Default Condition

Clustering Summary:

- Events sampled per file: 1000
- Clustering Parameters: **None Selected**
- Transform Parameters: None Selected

Cluster Characterization Summary:

- Minimum Cluster Size: 5%
- Computed Cluster Features:
  - Cluster Abundances

Class Summary:

- Cross Validation Folds: **None**
- Two-Class Models: **None**

Sample Summary:

File	Group
Patient01_healthy.fcs	
Patient02_healthy.fcs	
Patient03_healthy.fcs	
Patient04_healthy.fcs	
Patient05_healthy.fcs	

Number Of Sample Groups: 2

Group 1

Group 1 samples

- Patient01\_healthy.fcs
- Patient02\_healthy.fcs
- Patient03\_healthy.fcs
- Patient04\_healthy.fcs

Group 2

Group 2 samples

- Patient01\_healthy.fcs
- Patient02\_healthy.fcs
- Patient03\_healthy.fcs
- Patient04\_healthy.fcs

## Generated script

```
# Use this line to limit the number of  
# threads used by clustering  
# Rclusterpp.setThreads(1);  
options("mc.cores"=1);  
  
# What analysis to perform?  
family = "classification"  
  
# Set data and output directories  
dataDirectory =  
  "C:/R/win-library/3.4/citrus/extdata/example1"  
outputDirectory = file.path(dataDirectory,"citrusOutput")
```

## Generated script

```
# Specify columns to use  
clusteringColumns = c("Red","Blue")  
medianColumns=c()  
  
transformColumns = c()  
transformCofactor = 5  
  
scaleColumns = c()
```

## Generated script

```
# Specify parameters
minimumClusterSizePercent = 0.05
modelTypes = c("pamr")
fileSampleSize = 1000
nFolds = 1
featureType = c("abundances")

# List files
fileList = data.frame(
  defaultCondition=c("Patient01_healthy.fcs","Patient02_healthy.fcs",
labels = as.factor(c("healthy","healthy","healthy","healthy"))
```



## Generated script

```
# Run citrus
```

```
results = citrus.full(  
    fileList=fileList,  
    labels=labels,  
    clusteringColumns=clusteringColumns,  
    dataDirectory=dataDirectory,  
    outputDirectory=outputDirectory,  
    family=family,  
    modelTypes=modelTypes,  
    nFolds=nFolds,  
    fileSampleSize=fileSampleSize,  
    featureType=featureType,  
    minimumClusterSizePercent=minimumClusterSizePer  
    transformColumns=transformColumns,  
    transformCofactor=transformCofactor,  
    scaleColumns=scaleColumns,  
    medianColumns=medianColumns  
)
```

## Generated script

```
# plot results  
plot(results, outputDirectory)
```