Visual guide to install Fragman

1. Installation steps on Mac

2. Installation steps on Windows

The *Fragman* package is designed for Fragment analysis and automatic scoring of biparental populations (such as F1, F2, BC types) and populations for diversity studies. The program is designed to read files with FSA extension (which stands for FASTA-type file and contains lectures for DNA fragments) and extract the DNA intensities from the channels/colors where they are located, based on ABI machine platforms to perform sizing and allele scoring. Both platforms are supported and in this document we show a visual guide for installing the *Fragman* package

1. Installation steps on Mac

   a) With R studio opened you should be able to see the menu on the top of your Mac, something like this:
b) Select on the top menu the “Tools” tab and “Install packages…”

![Image of RStudio interface with the Tools menu highlighted]

![Image of Install Packages dialog with Fragman selected]

c) A new dialog window should come up which contains all possible names for the packages contained on CRAN (Comprehensive R Archive Network). Type the name *Fragman* as shown below:

![Image of Install Packages dialog with Fragman selected]

*Fragman*
d) You should be able to see in the console if the program was installed successfully as shown below:

![Console output showing successful installation](image)

```
library(Fragman)
```

You should see the `library(Fragman)` command executed in the console.

e) The package should be installed successfully and now you can create a script or write in the console “library(Fragman)” which basically will load the package in your session. Please use the help page to familiarize with the functions, just type “?Fragman”

![Help package](image)

In the help package you will find a great example showing how easy can be the use of the program, I am copying the example provided in the help page (?Fragman):
# LOAD YOUR DATA#

### you would use:###
my.plants <- storing.inds(folder)### where folder is the path where your samples are, i.e. "~/Documents"### here we just load our example data?my.plants
data(my.plants)
my.plants <- my.plants[1:2]

### MATCH YOU LADDER ###

### create a vector indicating the sizes of your ladder###
my.ladder <- c(120, 125, 129, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375)### match your ladder to the peaks and attach the information### to the R environment using the function:
ladder.info.attach(stored=my.plants, ladder=my.ladder)

### CREATE A PANEL ###

### you may use overview2 or overview to create you customized panel using:###
### here we select the channel 3 (yellow) by setting 'cols=3'### and providing the samples and ladder
overview2(my.inds=my.plants, cols = 3, ladder=my.ladder, init.thresh=5000)### you could also click on the peaks you think are real### by using the 'locator' function and press 'Esc' when you're done:
# my.panel <- locator(type="p", pch=20, col="red")$x### so you can click over the peaks and get the sizes### in base pairs stored in a vector named my.panel### Instead of doing that I will use the suggested peaks by### the program using overview2, which provides a vector with### expected DNA sizes to be used in the next step for scoring### we'll do it in the 160-190 bp region
my.panel <- overview2(my.inds=my.plants, cols = 3, ladder=my.ladder, init.thresh=7000, xlim=c(160,190)); my.panel

### SCORE YOUR SAMPLES ###
a <- score.easy (my.inds=my.plants, cols = 3, panel=my.panel, ladder=my.ladder, electro=FALSE)### extract your peaks in a data.frame
final.results <- get.scores(a)
final.results

For additional help or tutorials refer to our website:
http://cggl.horticulture.wisc.edu/software/
2. Installation steps on Windows

a) With R studio opened you should be able to see the menu on the top of your PC, something like this:

![R Studio Menu](image1)

b) Select on the top menu the “Tools” tab and “Install packages…”

![Install Packages Menu](image2)
c) A new dialog window should come up which contains all possible names for the packages contained on CRAN (Comprehensive R Archive Network). Type the name *Fragman* as shown below:

![Installation dialog window](image)

You should be able to see in the console if the program was installed successfully as shown below:

```
> install.packages("Fragman")
_installing package into 'C:/users/zalapab/documents/R/win-library/3.1'
(as 'lib' is unspecified)
trying URL 'http://cran.rstudio.com/bin/windows/contrib/3.1/Fragman_1.6.1.zip'
Content type 'application/zip' length 1606637 bytes (1.6 MB)
opened URL downloaded 1.6 MB
package 'Fragman' successfully unpacked and MD5 sums checked
```

The downloaded binary packages are in
```
C:\users\zalapab\appdata\local\temp\tmp0oEiQGuw\downloaded_packages
```
e) The package should be installed successfully and now you can create a script or write in the console “library(Fragman)” which basically will load the package in your session. Please use the help page to familiarize with the functions, just type “?Fragman”

In the help page for the package you will find a great example showing how easy can be the use of the program, I am copying the example provided in the help page (?Fragman):

```
### you would use:
# my.plants <- storing.inds(folder)
### where folder is the path where your samples are, i.e. "~/Documents"
### here we just load our example data
?my.plants
data(my.plants)
my.plants <- my.plants[1:2]
```
### MATCH YOU LADDER ###

### create a vector indicating the sizes of your ladder
my.ladder <- c(120, 125, 129, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375)

### match your ladder to the peaks and attach the information
### to the R environment using the function:
ladder.info.attach(stored=my.plants, ladder=my.ladder)

### CREATE A PANEL ###

### you may use overview2 or overview to create you customized panel using:
### here we select the channel 3 (yellow) by setting 'cols=3'
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overview2(my.inds=my.plants, cols = 3, ladder=my.ladder, init.thresh=5000)

### you could also click on the peaks you think are real
### by using the 'locator' function and press 'Esc' when you're done:
# my.panel <- locator(type="p", pch=20, col="red")$x
### so you can click over the peaks and get the sizes
### in base pairs stored in a vector named my.panel

### Instead of doing that I will use the suggested peaks by
### the program using overview2, which provides a vector with
### expected DNA sizes to be used in the next step for scoring
### we'll do it in the 160-190 bp region
my.panel <- overview2(my.inds=my.plants, cols = 3,
                      ladder=my.ladder, init.thresh=7000, xlim=c(160,190)); my.panel

### SCORE YOUR SAMPLES ###

### extract your peaks in a data.frame
final.results <- get.scores(a)
final.results

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