➢ **INSTALLING**

1) **Download** the latest zip available for your operating system

2) **Copy** all the files in the zip to any location

3) Install the free software **Mono** .NET framework with GTK# support. You can download the framework for GNU/Linux, Mac OS X or Windows from here:

   http://www.go-mono.com/mono-downloads/download.html

   If you use Ubuntu you can simply install the package "mono-runtime" instead.

➢ **EXECUTING**

1) Specific launchers are provided for the different platforms:

   a) **GNU/Linux**: just click on **PAnalyzer.exe** or execute **PAnalyzer.sh** from a console, which will automatically install the mono runtime if not detected

   b) **Mac OS X**: just click on the **PAnalyzer** application

   c) **Windows**: click on **PAnalyzer.bat** to run the application using Mono or directly on **PAnalyzer.exe** if you prefer using the Microsoft .NET runtime

2) Click **Open** and select one or more (multirun sample) protein files from the open dialog. You can download some samples from here:

   https://code.google.com/p/ehu-bio/downloads/list

3) Click **Execute** and select between the preferences (if applicable).

4) **Browse** the results in the Summary, Peptides and Proteins tabs.

5) **Save** the protein detection list to a file. A *.html and a *.csv output files are always generated and a *.mzid output file is only generated if the data came from another *.mzid input file.

➢ **DOCUMENTATION**

See file **PAnalyzer-BMC-Bioinformatics-2012.pdf**.