

Short installation guide: The HOOK - program

Step 1: Download the JAVA-package

The program runs on:

- Windows 32Bit including JRE
 - Windows 64Bit including JRE
 - Linux 32 Bit including Sun JRE
 - Linux 64 Bit including Sun JRE
- (the downloads includes the JAVA RUNNING ENVIRONMENT (JRE) which you need for proper running the program)
- Java Program only (suitable for all platforms) without JRE (see <http://java.sun.com>)

Step 2: Unzip the Package into a free directory.

Step 3: Copy the cel-file(s) you want to process into the subdirectory
_AffyDaten/CEL/....

Note: The program usually processes all cel-files one after another and it writes the results into the subdirectory (see step 5 below)

_Results/....

Step 4:For proper processing, two additional files providing information about the used chip-type must be available in the subdirectories

_AffyDaten/CDF/....

(for the *.CDF-file referring to the used chip-type)

_AffyDaten/ProbeSequences/....

(for the respective probe-sequence ASCII-file referring to the used chip-type)

Note: The program processes only *.cel-files of one chip-type at once. The CDF- and probe-sequence files are available, for example, from

<http://www.affymetrix.com/support/technical/index.affx>

Step 5: Configure your analysis:

Open the subdirectory

- *_General/....*

and edit the file **Configuration.txt** using, e.g., the standard-text editor:

- a) most of the entries are default settings of the parameters which are already set properly
- b) for assignments read the comments and/or use the example-settings deactivated by the leading comment-"#" in the respective line
- c) chip-type information

The names of the CDF-file and of the sequence-file (plus path) must be explicitly typed, e.g.,

CDF-File = "../_AffyDaten/CDF/HG-U133A_tag.CDF"

and

Sequence-File = "../_AffyDaten/ProbeSequences/HG-U133A_probe_tab.txt"

Note: A leading "#" deactivates the respective line

- d) By default, no information about the cel-files must be given: The program processes all cel-files in the respective directory one after another (see step 3), which however must belong to one and the same type specified in c).
Alternatively you can specify a single cel-file by substituting CEL-File = "" →
CEL-File =
"../_AffyDaten/CEL/12_13_02_U133A_Mer_Latin_Square_Expt9_R2.CEL", for example.
- e) Edit the parameter-settings if appropriate (see the comments)
- f) Important: Save your settings in **Configuration.txt!**

Step 6: Start the program

Double click on **run.bat** (WINDOWS) or **run.sh** (LINUX) in the root-directory.

Note: The program requires at least 768MB of physical memory. Alternatively one can adjust the **-Xmx768MB** switch in the run-file (edit and save).

Step 7: View the output files

The program generates a separate output-directory for each processed cel-file in the

- **_Results/....**-subfolder,

which contains the html-report, jpg-images, and ASCII-tables (e.g. of the expression measures).