Installing farms - Factor Analysis for Robust Microarray Summarization

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Contents

1 Introduction

The *farms* package provides a new summarization algorithm called FARMS - Factor Analysis for Robust Microarray Summarization. The summarization method is based on a factor analysis model for which a Bayesian Maximum a Posteriori method optimizes the model parameters under the assumption of Gaussian measurement noise Hochreiter et al. (2006). Thereafter, the RNA concentration is estimated from the model.

Note: If you use this package please cite Hochreiter et al. (2006). This package is only free for non-commercial users. Non-academic users **MUST** have a valid license.

2 Requirements

To install the *farms* package successfully, the following basic requirements have to be covered:

- a running R version > 1.9
- installed Bioconductor package *affy*

3 Installation

Assuming you downloaded the *farms* package to a directory named "/path/to/".

3.1 For Linux:

To install it type

```
sudo R CMD INSTALL /path/to/farms_1.0.0.tar.gz
```

in your shell and press **Enter**. Please note that if you do not have **root** rights, you may ask your system administrator for help. The following example shows the expected installation output:

```
mnemonic:~> sudo R CMD INSTALL farms_1.0.0.tar.gz
* Installing *source* package 'farms' ...
** R
** inst
** help
 >>> Building/Updating help pages for package 'farms'
     Formats: text html latex example
  exp.farms                         text    html    latex   example
  generateExprVal.method.farms      text    html    latex   example
  l.farms                           text    html    latex   example
  q.farms                           text    html    latex   example
** building package indices ...
* DONE (farms)
mnemonic:~>
```

3.2 For Windows:

You can install the pre-compiled packages from a local .zip file by using install.packages in R:

```
install.packages("/path/to/farms.zip",repos=NULL)
```

There is further a menu item on the Packages menu, which provides a point-and-click interface for package installation.

4 Working with R and *farms*

As usual, first you have to load the library.

```
> library(farms)
```

```
Loading required package: affy
Loading required package: Biobase

Welcome to Bioconductor

        Vignettes contain introductory material.
        To view, simply type 'openVignette()' or start with 'help(Biobase)'.
        For details on reading vignettes, see the openVignette help page.
```

Further assistance with *farms* is provided by the vignette "Using farms", you can access the vignette through the method `openVignette()`:

```
> openVignette()
Please select (by number) a vignette

 1:  Using farms
 2:  affy primer
 3:  affy: Built-in Processing Methods
 4:  affy: Custom Processing Methods (HowTo)
 5:  affy: Automatic downloading of cdfenvs (HowTo):
 6:  affy: Import Methods (HowTo)
 7:  Biobase Primer
 8:  Howto Bioconductor
 9:  HowTo  HowTo
10:  eSet metadata structures
11:  esApply Introduction
12:  eSet metadata structures

Selection:
```

Enjoy!

References

Sepp Hochreiter, Djork-Arne Clevert, and Klaus Obermayer. A new summarization method for affymetrix probe level data. *Bioinformatics*, page btl033, 2006. doi: 10.1093/bioinformatics/btl033. URL http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btl033v1.