Installing farms - Factor Analysis for Robust Microarray Summarization

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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