Bioconductor's nnNorm package

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1 Overview

The `nnNorm` package contains mainly a function for intensity and spatial normalization of cDNA two color data, or paired single channel data, based on neural networks fitting. Functionality to compare the distributions of the normalized log ratios is also provided. For the simpler case when only intensity normalization is performed (univariate distortion color model), we provide functionality to plot the bias estimates against the level of intensity for each print tip group on the slide.

This document provides only a basic introduction to the `nnNorm` package. A more extended description is available in the nnNormGuide.pdf document. For a detailed description of the principles and algorithmic implemented by this package consult Tarca and Cooke (2005).

We demonstrate the functionality of this package using the swirl data set from the `marray` package. To load the swirl dataset in a object called `swirl` of type `marrayRaw` we use the following lines:

```
> library(marray)

Loading required package: limma

> data(swirl)
```

Now we perform normalization with the method `maNormNN` available in the `nnNorm` package. This function returns a `marrayNorm` object (containing the normalized log ratios).

```
> library(nnNorm)

Loading required package: nnet

> swirl_n <- maNormNN(swirl[, 1:2])

Processing array 1 of 2
****************
Processing array 2 of 2
****************
```

If data is available in a RGList or MAList object (see `limma` package) they can be easily converted to a `marrayRaw` object using functionality of the library `convert`. For more details on the `nnNorm` package Please consult nnNormGuide.pdf.

References

A. L. Tarca and J. E. K. Cooke. A robust neural networks approach for spatial and intensity-dependent normalization of cdna microarray data. *Bioinformatics*, 21(11):2674–2683, 2005.