Bioconductor's nnNorm package

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1 Overview

The `nnNorm` package provides utilities to detect and correct for spatial bias with two color DNA microarrays (or paired single channel data). The normalization implemented in `nnNorm` package is based on neural networks models. Functionality to compare the distributions of the normalized log ratios is also provided. For the simpler case when only intensity normalization is desired (univariate distortion color model, similar to print tip loess normalization), we provide functionality to plot the bias estimate against the level of intensity for every print tip group.

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)
> 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)
> 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.