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).

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.

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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.