arrayMagic: two-colour DNA array quality control and preprocessing

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arrayMagic is a software package which facilitates the analysis of two colour DNA microarray data. The package is written in R (http://www.r-project.org) and integrates into Bioconductor (http://www.bioconductor.org). The automated analysis pipeline comprises data loading, normalisation and quality diagnostics. The pipeline is flexbile and can be adjusted for specific needs.

The package takes advantage of the S4 class mechanism. The normalised data, as well as their annotation is stored in the class exprSetRG, an extension of the class exprSet of the library Biobase which accounts for the specific requirements of two colour microarray data and integrates well in the existing Bioconductor framework. Eventually, it will be merged into the new eSet class of Biobase.

Several quality diagnostic plots are generated on the fly and allow to assess the hybridisation quality and to discard low quality hybridisations from further analysis. Different normalisation methods are offered to remove systematic variations like hybridisation and dye effects. The pipeline supports to process microarray data at high throughput.