Background
Together with the firm establishment of microarray technology in systems biology research and the accumulation of microarray experiments in public repositories, an extensive set of bioinformatics procedures has been developed to deal with the data, including quality control (QC) and processing of signals as well as interpretation of study outcome. This holds especially for Affymetrix gene expression chips. In contrast to this, there is currently a lack of a standardised, accessible, and user-friendly open-source software tool. On one hand, Affymetrix and other companies provide many integrated commercial and closed source software tools. On the other hand, many public contributions are available from the scientific community, but lack of an environment that bundles all available functionality compromises accessibility for non-expert users. This even leads to a tendency among researchers to not adopt available methods and perform suboptimal analyses.

Methods
One of the largest collections of public bioinformatics contributions in the microarray field is the Bioconductor repository, to be used conjointly with the open-source statistical scripting language R. We automated methods available from several libraries within this repository, extended with home-built functionality, in a workflow performing QC, pre-processing, statistical analysis, and pathway analysis of Affymetrix expression sets.

Results
We implemented a complete workflow that can be accessed using the user-friendly interface provided at www.arrayanalysis.org. The site offers user guides, technical documentation, example datasets and explanation of the output. We also provide open source R wrapper functions for running the modules locally. The QC step generates about twenty images assessing sample, hybridisation and overall signal quality, signal comparability and biases diagnostics, and array correlation. The pre-processing step includes gene re-annotation and proposes several normalisation methods. The statistics module computes the expression changes of genes between experimental groups of choice and their significance. The pathway module provides lists of the most affected cellular processes and visualisation of the data on those based on PathVisio [www.pathvisio.org] functionality. Availability of the integrated workflow facilitates implementation of current standards, and introduction of new standards in the future. It assists newcomers to the field in processing their microarray datasets. For experienced data analysts, it facilitates running all the established functionality in one go.

Conclusions
We provide the scientific community with an easy-accessible, open-source and extensively documented workflow for the QC, processing, and interpretation of Affymetrix expression datasets. Availability of such a method enhances the application and standardisation of up-to-date microarray data analysis.