

RMAGEML: integrating MAGE-ML format microarray data and Bioconductor

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The microarray gene expression markup language (MAGE-ML) is a widely used XML standard for describing and exchanging information about microarray experiments. It can describe microarray designs, microarray experiments designs, gene expression data and data analysis results. Bioconductor is an open source project that provides a framework for the statistical analysis of genomic data in R. These R packages provide a wide range of microarray data analysis tools. Up till now it was not possible to import data stored in MAGE-ML format in Bioconductor. Because of the importance of both MAGE-ML and Bioconductor in the field of microarray data analysis, this acute gap had to be filled. We describe RMAGEML, a new Bioconductor package that provides a link between MAGE-ML format microarray data and Bioconductor. The current version enables MAGEML-import to the limma and marray Bioconductor packages. RMAGEML is available at <http://www.bioconductor.org>