



EMERALD



Enhancing microarray data quality

The European Union FP6 Coordination Action (CA) EMERALD aims to establish and disseminate quality metrics (QM), microarray standards and best laboratory practices throughout the European microarray community. This will allow microarray data production to take full advantage of QA/QC, thereby significantly enhancing the quality of microarray data and setting a precedent for other array-based technologies. Data quality and meta data (documentation) are key to all microarray data generation and analysis, to ensure that maximum information can be extracted from the data. The need to reanalyse and reproduce data spawned a 'grassroots movement', now the MGED Society, that established guidelines for experiment description (MIAME) and a structured data exchange model (MAGE-ML). MGED initiatives have been predominantly focused on data context, and its scope has only recently been extended to included data content. Quality and integrity of microarray data compendia (e.g. in ArrayExpress) are major determinants for information and extraction model building. High quality data will constitute one of the pillars of systems biology. This CA is designed to structure and amalgamate ongoing efforts across the European community, in close association with MGED and the ERCC.

Recent updates on workshops

4th EMBO Conference: From Functional Genomics to Systems Biology

EMERALD will organize a workshop in collaboration with the 4th EMBO Conference: From Functional Genomics to Systems Biology, to discuss and illustrate the importance of (microarray) data quality for systems biology.

Presentations will highlight efforts on the implementation of quality metrics, the production of benchmark datasets and checklists to archive experimental metadata to facilitate data analysis and integration.

The workshop will take place at EMBL in Heidelberg, Germany, at Tuesday November 18, 13:00 – 17:00.

More information about the meeting and the EMERALD workshop can be found at this page:

http://www-db.embl.de/jss/EmblGroupsOrg/conf_82

Confirmed speakers in our session are:

John Quackenbush, Dana-Farber, Harvard, US.

Chris F Taylor, EBI, UK.

Misha Kapushesky, EBI, UK.

Audrey Kauffmann, EBI, UK.

Wolfgang Huber, EBI, UK.

CAMDA2008

EMERALD will organize a workshop at CAMDA 2008, to discuss the importance of (microarray) data quality. Presentations will highlight efforts on the implementation of quality metrics, the production of benchmark datasets and the development of ontologies. Specific topics are: "Quality metrics and their performance on public data repositories"; "Data quality and data mining"; "Data quality and evidence code/score" and "Review of QM and protocols from ArrayExpress".

The workshop will take place at Boku University in Vienna, Austria, on the 5th of December.

More information about the meeting and the EMERALD workshop can be found at this page:

<http://camda.bioinfo.cipf.es/>

Confirmed speakers in our session are:

Ernst Witt, University of Groningen, NL

Walter Liggett, NIST, US.

Participate in

EMERALD QC web survey

The goal of this survey is to gain insight into procedures, platforms, and needs of the microarray users community. The focus is both on commercial GeneChip arrays and all sources of cDNA and oligonucleotide microarrays. The survey is geared to gather information anonymously from academic, pharmaceutical, and commercial laboratories, which use microarray technologies routinely. The survey is now open and can be found on our web page: www.microarray.quality.org

or directly at: <http://kvass.itea.ntnu.no/eval/login.do?externalid=2021-14551abbr>

The results of the survey will be made freely available to the microarray community, through our web page, following analysis of the data. We appreciate your participation in this study.

New version this autumn

A Tool for Quality Assessment

We are developing a new Bioconductor package, named `arrayQualityMetrics`, that provides a HTML report with diagnostic plots for one or dual color microarray data. The quality report contains the evaluation of the individual array quality, the existence of spatial effects, the reproducibility of the experiments, the homogeneity between the experiments, the GC content effects, the mapping of the reporters, and the evaluation of the biological signal to noise ratio. This report can be used as a first step of the microarray analysis or to compare the efficiency of different methods of normalisation. The most recent version, available this autumn, will provide an overview table added, identifying arrays identified as having a potential problem or as being an outlier.

People responsible are Audrey Kauffmann and Wolfgang Huber at EBI, Hinxton, UK.

More information about the `arrayQualityMetrics` can be found at our web page: www.microarray-quality.org or at the Bioconductor web page: <http://bioconductor.org/packages/2.1/bioc/html/arrayQualityMetrics.html>

Sign up for future issues of the EMERALD Newsletter at our web page:
www.microarray-quality.org

New database for methods

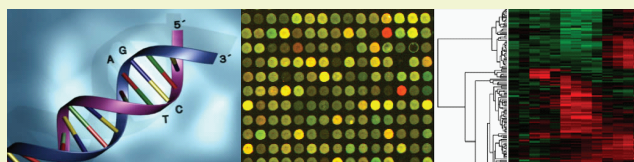
The Molecular Methods Database (MolMeth)

MolMeth is a structured database that provides free access to methods used in molecular biology and molecular medicine, and it allows the user to print user-friendly manuals. A unique accession number is assigned by the database which permanently identifies the protocol submitted. Each method includes a short description of the method and a list of the required reagents and equipments. The methods also include a detailed step-by-step protocol that the user can download as a pdf, print or view on the screen. Submitted methods and contributions are subject to manual curation.

One key aspect of the database is that new methods can be created that are combinations of methods already available in MolMeth. Thereby, methods available in the database can be reused in different combinations. We also link reagents to the suppliers and aim to link to databases with chemical and structural information (e.g. PubChem). MolMeth, methods that have been published in scientific journals will also be cross-linked to PubMed.

The Molecular Methods Database (MolMeth) is currently being developed to provide the research community with a reliable source of methods and protocols used in molecular biology and molecular medicine.

The beta version of the database can be found through this web page: <http://beta.molmeth.org/> and will later move to <http://www.molmeth.org/>.



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