

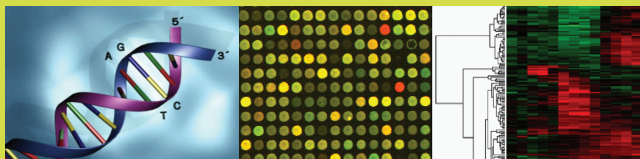
## Project management

The project is managed by a project board which has representatives of the eight partners:

- Martin Kuiper** Flanders Institute for Biotechnology, VIB, Gent, Belgium and Norwegian University of Science and Technology, NTNU, Norway.
- Arne K. Sandvik** Norwegian University of Science and Technology, NTNU, Norway.
- Alvis Brazma** European Bioinformatics Institute, EBI, United Kingdom.
- Carole Foy** LGC, United Kingdom.
- Joaquin Dopazo** Centro de Investigacion Principe Felipe, Spain.
- Laszlo Puskas** Biological Research Center of the Hungarian Academy of Sciences, Hungary.
- Heinz Schimmel** Institute for Reference Materials and Measurements, Belgium.
- Ulf Landegren** Uppsala University, Sweden.

The project management is assisted by a scientific advisory board:

- Frank Holstege** Utrecht University, Netherlands.
- Helen Causton** Imperial College London, United Kingdom.
- Rafael Irrizarry** Johns Hopkins University, United States.
- Joerg Hoheisel** German Cancer Research Center, DKFZ, Germany.
- Astrid Lægread** Norwegian University of Science and Technology, Norway.
- Marc Salit** National Institute of Standards and Technology, NIST, United States.



## EMERALD

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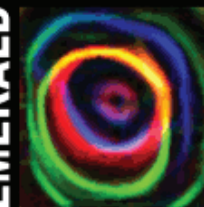
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EMERALD



European Project on  
Standards and Standardisation  
of Microarray Technology and  
Data Analysis

## Project objectives

This European Union Framework Program 6 Coordination Action (CA) will serve to establish and disseminate quality metrics (QM), microarray standards and best laboratory practices throughout the European microarray community. This will allow microarray data production governed by QA/QC, significantly enhancing the quality of microarray data and setting a precedent for other array-based technologies. Over the last 15 years microarray technology has proved the method of choice for capturing molecular biological data in a massively parallel fashion. 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. Very early in the development of microarray-based transcript profiling the microarray community has realised the importance of structured documentation accompanying microarray

## www.microarray-quality.org

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 predominantly been focused on data context, and 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 extraction model building and high quality data will be one of the pillars of systems biology. This CA is designed to structure and amalgamate ongoing efforts across Europe, in close association with MGED and the ERCC.

## Coordination and dissemination activities

Coordination activities are defined in six main areas relevant for microarray analysis: Development of quality metrics, ontology for data description, implementation of standards and best practices, selection of standards that are candidates for European Reference Materials, impact on data information content, and dissemination of QA/QC principles to novel experimental high-throughput techniques for the different -omics domains. These activities are made up of six work packages (WP).

## 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, identify 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](http://www.microarray-quality.org) or at the Bioconductor web page: <http://bioconductor.org/packages/2.1/bioc/html/arrayQualityMetrics.html>

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## Normalisation and Transformation ontology (NTO)

The diversity in microarray experiment designs and applications requires that a large number of pre-processing approaches are available. In order to facilitate unambiguous and consistent descriptions of experimental data transformation the development of a 'normalisation and transformation ontology' (NTO) has been undertaken. This provides a means to conceptualize and classify the approaches used, describe relationships between these concepts and store these in a machine readable form. Such a representation can offer a useful checking mechanism to ensure that data is correctly modelled as well as a more powerful querying mechanism. The NTO has been developed as part of the Ontology for Biomedical Investigations (OBI), a large, multi-national, collaborative community development project. A Beta version of the ontology is now available from [http://obi-ontology.org/page/Main\\_Page](http://obi-ontology.org/page/Main_Page).

People responsible: Helen Parkinson and James Malone (EBI).

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](http://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.

## EMERALD workshops

- WS7:** Data quality and Systems Biology (in collaboration with the 4th EMBO Conference: From Functional Genomics to Systems Biology, 15-18 November 2008, Heidelberg, Germany).
- WS8:** Data quality Control and Transformation workshop (in collaboration with the 8th international conference for the Critical Assessment of Microarray Data Analysis CAMDA, 4-6, December, Vienna, Austria, 2008).
- WS9:** Towards federal standards (planned Spring 2009).
- WS10:** Implications for new technologies (planned Spring 2009).
- WS11:** Dissemination of results to larger community (planned Autumn 2009).

## Web pages relevant for the project

**EMERALD** ([www.microarray-quality.org](http://www.microarray-quality.org))

**Microarray Gene Expression Data (MGED) Society** ([www.mged.org](http://www.mged.org))  
**National Institute of Standards and Technology (NIST)** ([www.nist.gov/](http://www.nist.gov/))

**External RNA Control Consortium (ERCC)**

([www.cstl.nist.gov/biotech/Cell&TissueMeasurements/GeneExpression/ERCC.htm](http://www.cstl.nist.gov/biotech/Cell&TissueMeasurements/GeneExpression/ERCC.htm))

**MicroArray Quality Control (MAQC) project**

([www.fda.gov/nctr/science/centers/toxicoinformatics/maqc/](http://www.fda.gov/nctr/science/centers/toxicoinformatics/maqc/))