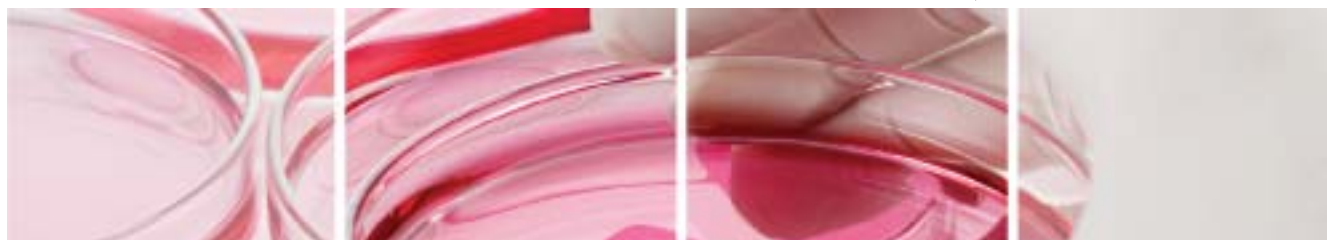


Support Opportunity



Dedicated R&D genomics support

- Custom (multistrain) microarray design
- Advanced microarray technology support
- Advanced bioinformatics
- Genomics consultancy

MAD-IBU | Genomics

2011

Background

In life-science experimentation microarray technology has become an important tool in genome and gene-expression studies. However, nearly all array experiments are unique due to differences in experiment design, experimental procedure, level of completeness of the data and cellular responses. Also methods with which array studies are analyzed are topic of much bioinformatics research. Therefore state-of-the-art genomics experiments are subject to change and the approach and analysis must be highly flexible.

The Microarray Department & Integrative Bioinformatics Unit (MAD-IBU) of the University of Amsterdam is the only Dutch semi-commercial microarray service and support provider, and has a 11 year successful track record including over 70 (collaborative) scientific publications.

The Technology

Next to the standard microarray platforms: Affymetrix (GeneChip and GeneTitan), Agilent and NimbleGen as well as standard bioinformatics such as DataQC and analysis pipelines, we offer dedicated, advanced microarray applications such as:

- Consultancy for sophisticated design for experimentation.
- Optimization of RNA isolation i.e. sample preparation protocols.
- Custom microarray design and data management for multistrain prokaryote studies.
- Custom microarray design and data management for eukaryotic organisms based on next generation sequencing data.
- Proprietary spike-ins (patent pending) applications.
- Sensitive microRNA analysis.
- Advanced and dedicated bioinformatics analysis.
- High-performance/Cloud computing for complex transcriptomics studies.
- Ample opportunity for transcriptomics contract research.

Applications

Microarray technology and next-generation sequencing can be employed in basically any research set up that involves living cells. Also, non-model organisms are now suited for advanced genomics experimentation.

Supporter Providers

Dr. Timo M. Breit, molecular biologist, PI of MAD-IBU, t.m.breit@uva.nl

Dr. Mark de Jong, biochemist, CSO of MAD, h.m.dejong@uva.nl

Dr. Martijs Jonker, bioinformatician, CSO of IBU, m.j.jonker@uva.nl

Key publications

1. Bruning O, Rodenburg W, Radonic T, Aeilko, Zwinderman AH, de Vries A, Breit TM, de Jong M. RNA isolation for transcriptomics of Human and Mouse small skin biopsies BMC Research Notes accepted
2. Smits NJP, Pronk TE, Bruning O, Wittink FRA, Breit TM, van Strijp JAG, Fluit AC, Boel CHE Operon structure of *Staphylococcus aureus*. Nucleic Acids Res. 2010 Jun; 38(10):3263-74.
3. Jonker MJ, Bruning O, van Iterson M, Schaap MM, van der Hoeven TV, Vrieling H, Beems RB, de Vries A, van Steeg H, Breit TM, Luijten M. Finding transcriptomics biomarkers for in vivo identification 1 of (non-)genotoxic carcinogens using wild-type and Xpa/p53 mutant mouse models. Carcinogenesis 2009 Oct;30(10):1805-12.