This enables also scientists not familiar with molecular biological methods to implement NGS and/or array experiments in their projects.

- Defined DNA fragmentation using Covaris Technology.
- Quality control and quantification: analyses of DNA, RNA, and protein using the 2100 Bioanalyzer/Tape Station 4200 microfluidics-based platforms (Agilent); quantification using the NanoDrop technology and Quantus (Promega).
- Amplification, fragmentation and labelling technologies for array applications (source, material quantity, chip and detection specific).
- DNA/RNA sample preparation for NGS - i.a. library Prep.
- Array Hybridization.
- NGS-Sequencing using the NextSeq500. When required the use of a MiSeq platform is also possible.
- Consulting in bioinformatics terms.
- Microarray-data analysis.
- Basic data analysis workflows for various NGS applications.
- Advanced bioinformatics support tailored to project specific needs.
- Development of analysis pipelines of emerging applications on request.
- Easy access to analysis results or online services through our web interface and time limited storage of sequence data.
- Recording of NGS- and MA-experiments and submission of results to GEO (Gene expression omnibus)

Technical Equipment

The Genomics Facility has access to following devices:

DNA & RNA Isolation
- Maxwell RSC (Promega)

Quantification of DNA & RNA
- Nanodrop ND-1000 (Thermo Scientific)
- Quantus (Promega)

Fragmentation of DNA & RNA
- Covaris M220

Quality Control of DNA & RNA & Protein
- Tape Station 4200 (Agilent)
- Bioanalyzer (Agilent)

PCR Amplification
- 7300 Real Time PCR System (Applied Biosystems)
- Gene Amp PCR 9700 (Applied Biosystems)
- PTC-200 (Pelletier Thermal Cycler, MJ Research)

Array Equipment
- GeneChip Hybridization Oven 645 (Affymetrix)
- GeneChip Fluidics Station 450 (2 x) (Affymetrix)
- GeneChip Scanner 3000 7G (Affymetrix)

NGS Equipment
- NextSeq500 (Illumina)

Data analysis & Storage
- RECT Rack Server RS-8685MR8 (Coreto)

(grey: equipment not directly belongs to the Genomics Facility)

Prof. Dr. Ingo Kurth
genomicsfacility@ukaachen.de
Tel.: +49 241 80 89684

Dr. Ali T. Abdallah
Bioinformatics
ali.abdallah@rwth-aachen.de
Tel: +49 241 80 35296

IZKF Interdisziplinäres Zentrum für Klinische Forschung | RWTH AACHEN UNIVERSITY

Core Facilities – Technologies, equipment and expertise for ambitious research goals

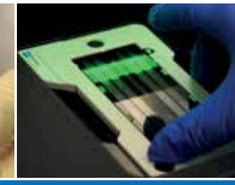
The IZKF provides valuable resources for a cost effective and high-quality research environment by operating:

- Brain Imaging Facility
- Genomics Facility
- Immunohistochemistry Facility and Confocal Microscopy Facility
- Proteomics Facility
- Transgenic Service
- Two-Photon Imaging Facility
- Flow Cytometry Facility

Multiple technologies and state-of-the-art equipment are available for all researchers of the Faculty of Medicine. Experienced technology experts provide services at any stage of the research process, including experimental design, method development, sample work-up and data interpretation on a partial cost recovery basis.

Karen De Bruyne, M.A.
IZKF Scientific Coordinating Office
Pauwelsstraße 30 I D-52074 Aachen
Elevator D5 I 4th floor I room 44
+49 (241) 80 80034 I izkf@ukaachen.de

Thinking the Future
Zukunft denken



Genomics Facility

Genome-Wide Analyses

Next Generation Sequencing

Microarrays

Bioinformatics

Univ.-Prof. Dr. med. Ingo Kurth (temporary)
Genomics Facility
elevator D3 I 3rd florr I corridor 43 I room 7
Pauwelsstrasse 30, 52074 Aachen
Tel.: +49 241 80 89684
genomicsfacility@ukaachen.de
www.genomicsfacility.rwth-aachen.de

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Why use Genomics Facility and how to use it to your advantage?

The mission of the Genomics Facility is to carry out and support internationally outstanding research on Next Generation Sequencing (NGS) and Micro Arrays (MA), which are meanwhile indispensable core technologies in the modern biological and medical sciences. The Genomics Facility endeavors to bundle the research performance within this area to enable researchers access to full NGS/MA workflows from experimental design to advanced interpretation and data integration. Different applications have different requirements, so researchers need to carefully weigh their options when making the choice to switch to a new technology or platform. Regardless of which technology they choose, the Genomics Facility can provide support for both platforms.

Why use Array Technology and how to use it to your advantage?

The preferential use of MAs clearly depends on the aims of the study. To conduct profiling to get an idea which known genes and pathways might be involved in a biological response (to treatment, to disease, to cell development, etc.) MAs are the perfect option. The Genomics Facility provides more than a decade of experience with both operating MAs and data analyzing for which a general consensus has emerged on the major methods for processing the data. Despite NGS advancements, MAs remain popular because expression arrays are still cheaper and easier when processing large numbers of samples. Arrays suffer from fundamental 'design bias' - they only return results from those regions for which probes have been designed. Consequently, arrays are only as good as the databases from which they are designed, which, however, doesn´t matter for mouse and man.

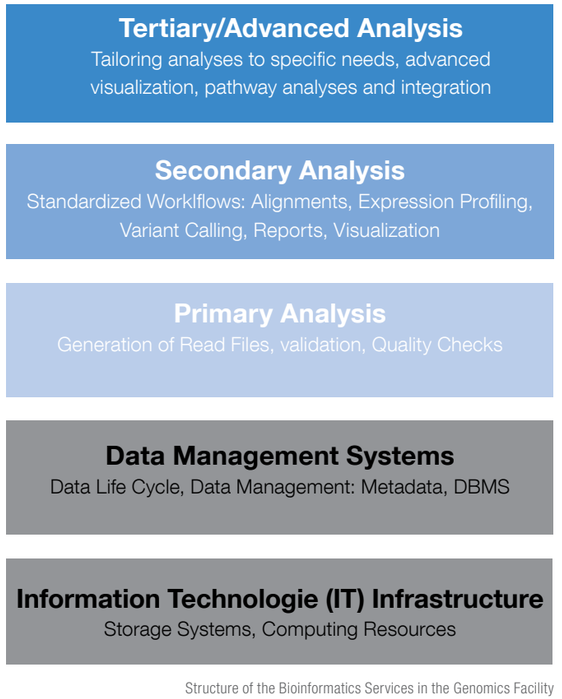
Why use NGS and how to use it to your advantage?

A swift transition has beenseen from MA to NGS in a number of applications e. g. ChIP, as ChIP is less demanding in terms of what is needed from the sequencing platforms - only a small number of short reads are required. Conversely, the various RNA-Seq methods cover all aspects of the transcriptome. NGS can be used to analyze all kind of DNA and RNA samples and is a popular tool in functional genomics. NGS-based approaches have several advantages including:

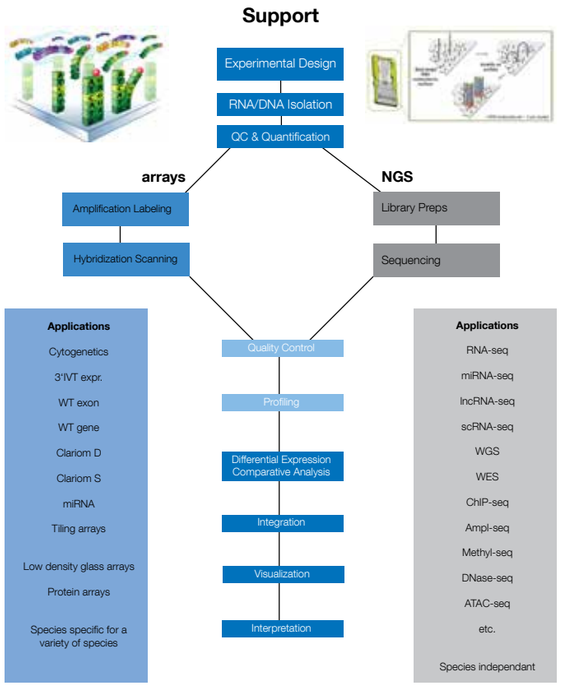
- a priori knowledge of the genome or genomic features is not required;
- it offers single-nucleotide resolution, making it possible to detect related genes (or features), alternatively spliced transcripts, noncoding RNAs, allelic gene variants and single nucleotide polymorphisms;
- higher dynamic range of signal;
- requires less DNA/RNA as input

Why use Bioinformatics and how to use it to your advantage?

The lag between the development of data analysis tools and the speed with which the NGS technology is advancing is creating a data bottleneck for many scientists – also known as the big data issue. We implement „state of the art" bioinformatics solutions to settle the big data problem, reduce analyses times and speed up biological research. We offer up-to-date and standardized data analysis workflows embedded in a generic, extendable bioinformatics environment and supply with our advanced bioinformatics support and downstream analysis. By archiving sequenced data, storing analyses results and metadata in our databases, we ensure high level of reproducibility and allow for fast and parameterized reanalysis.



Structure of the Bioinformatics Services in the Genomics Facility



What services do we offer?

We are able to facilitate researchers' access to the promising NGS-/array methods, which enable them to achieve their scientific goals more efficiently.

This includes :

- Technical and experimental consulting
- Sample preparation: from cell culture, tissue, and blood; sample preparation in accordance with favourite standard procedures (total RNA, mRNA, miRNA, DNA, protein). RT-qPCR based experiments.