Minutes: EDA-EMERGE Specialized Course 7:

"Special course on theory and practice of gene arrays"

Venue:	Institute for Environmental Research, RWTH Aachen University, Aachen, Germany
Organizer:	Dr. Knut Erik Tollefsen (NIVA)
Date:	29.10.2014
Time:	9h00 – 16h30

Course description:

The SC7 was a 1-day EDA-EMERGE training course on Toxicogenomics, with special emphasis on the use of gene arrays. The course was organized as a balance between theoretical and practical exercises and included the use of various molecular tools (genomics, transcriptomics, proteomics and metabolomics) to assist (eco)toxicological studies and provide more detailed description and practical exercises in the use of transcriptomics (Gene expression analysis). The course also provided insight into the basics on how to design and perform gene expression studies, how to perform the transcriptomics analysis (gene expression arrays), how to run biostatistics and bioinformatics, how to ensure successful interpretation of data and reporting the data in peer-review journals. The introduction into these topics were given by lectures from international-level experts, which have been combined with on-site discussions and supporting reading material (4 scientific papers) provided by the lecturers.

AGENDA

Wednesday, 29.10.2014			
Time	**Title**	**Content**	**Lecturer**
9:00-10:00	Introduction to Toxicogenomics	Introduction to (eco)tox, Challenges, different OMICS, how that may facilitate resolve research issues/Challenges.	Knut Erik Tollefsen
10:00-11:00	Transcriptomics – theory and practice	Molecular biology/Toxicology, different approaches, experimental designs, experiments, sample preparation, Gene expression analysis	Knut Erik Tollefsen
11:00-12:00	Biostatistics and bioinformatics	Introduction to biostatistics (normalisation, Statistical testing, False-discovery correction, Differential expression), Functional enrichment analysis (GO etc.), Biological/Toxicity pathways (KEGG, IPA, interaction networks)	Leonie K. Nüßer
12:00-13:00	Lunch		
13:00-15:00	Practical exercise using gene expression (microarray) data	Perform analysis of a sample data set	Knut Erik Tollefsen
15:00-15:30	Data Interpretation (how to make the most out of your data)	Developing the optimal analysis strategy from raw data to final results.	Knut Erik Tollefsen
15:30-16:00	Reporting of data (MIAME compliance, data repositories)	How to report (e.g. MIAME compliance etc.) and share (data repositories) and mine existing data.	Anthony Bolger
16:00-16:30	Summary and evaluation of course	Short summary, feedback.	Thomas-Benjamin Seiler

Course content

In detail the statistic course covered the following topics:

- Introduction to Toxicogenomics
    - Pollution and Effect assessment
    - Hazard and risk assessment
    - Biomarkers and Adverse Outcome Pathways
    - Toxicogenomics (OMICS)
    - Systems toxicology
    - Case study: nanoparticle toxicity to fish
- Transcriptomics – Theory & Practice
    - Transcriptomics - theory
    - DNA/RNA microarrays
    - Experimental design
    - Sample preparation
    - RNA extraction & isolation
    - Microarray analysis
    - Data normalisation
- Statistics and bioinformatics
    - Microarray data analysis pipeline
    - Differential expression
    - Hypothesis testing
    - Statistical testing
    - Functional enrichment analysis
    - Pathway analysis
    - Protein-protein interactions
    - Examples/case studies
- Practical session: microarray data analysis using Babelomics
    - Introduction to Babelomics
    - Uploading data from Gene expression Omnibus
    - Normalising data
    - Editing data files and pre-processing
    - Differential expression
    - Functional gene and gene set analysis
    - Pathway visualisation

    - Graphical functions
- Data interpretation: “How to get the most out of your microarray data”
    - Data analysis pipeline
    - Experimental design
    - Identifying differentially expressed genes
    - Functional enrichment analysis
    - Pathway analysis
    - Integrating your data
    - Verifying the performance of gene arrays
- Data Repositories
    - Rationale for why using data repositories
    - Which repositories exist
    - MIAME compliance
    - Data Retrieval from repositories
    - Repositories for RNA-sequencing data
    - Other repositories

This amounted to a minimum total academic involvement of 15 hours and equivalent to 0.5 ECTS points for the participants.