

Instrurama 2003 (VAKBEURS VAN 2 tot 4 APRIL IN BRUSSELS EXPO)

Symposium ingericht door Sectie Analytische KVCV: Do 3 april 2003

ism UDIAS (M. Panis: m.panis@udias.be)

Samenvatting huidige informatie (stand 22/1/03)

Voormiddagssessie:

“The Environment – A Challenge for Instrumental Analysis”

Sprekers 1-4

Namiddagssessie:

“Analysis in the Biotech Era”

Sprekers 5-7

Spreker 1:

Carine Vanoeteren

Milieucoördinator
Milieubeheer Monitoring en Advies
Bayer Antwerpen NV
carine.vanoeteren.cv@bayant.bayer.be
tel 03 540.39.51

“Influence of Quality and Environmental Management Systems on the Laboratory”

Both systems have a severe impact on the instrumentation and organisation of a laboratory. Documentation, training, method validation and corrective and preventive actions play an important role in the management of the modern laboratory.

Spreker 2:

Christine Declerck

Sales Manager Analytical
ABB Automation
christine.declerck@be.abb.com
tel 0032 475 29 06 07

“ON – LINE EMISSION MONITORING”

The measurement of emissions is becoming more and more important for a lot of companies, as the regulatory standards become stricter.

We will explain during the presentation :

- when do we talk about continuous monitoring?
- Official requirements
- Some available techniques
- Data acquisition
- Reference measurement and approval by official laboratory

Spreker 3:

Tom Van de Wiele and Willy Verstraete

LabMET, Centre of Environmental Sanitation, University Ghent
<http://labmet.rug.ac.be>
Laboratory for Microbial Ecology and Technology (LabMET)
Faculty for agricultural and appl. biological engineering
University Ghent
tel 09 264.59.76
info@kelma.com / willy.verstraete@rug.ac.be

“The use of on-line respiration measurements to quantify the biodegradation, the need for oxygen and the toxicity”

The aerobic bioconversion processes are very important in waters, soils and

wastes. They are brought about by a variety of micro-organisms and relate to the breakdown of hydrocarbons (oils, greases, ..), carbohydrates, proteins, lignines, ... Hence, by monitoring the oxygen uptake, one can obtain vital information about these processes and also about the organisms bringing them about.

Numerous technologies have been developed to monitor the oxygen uptake in various environmental and technical conditions. A brief review will be given. However, a most interesting instrumental approach consists of the so-called RODTOX apparatus. By means of this instrument, one can determine the amount of rapidly biodegradable material present in a sample such as wastewater. One can also determine the extent and the kinetics of the nitrification processes occurring in activated sludge. Moreover, any type of toxicity, imposed on the microbial community and reflected in the respiration dynamics, can be registered. Hence, by the RODTOX approach, one can collect on-line data and feed them to an ICT - configuration for further use and implementation.

Examples of application of environmental respirometry will be provided.

Spreker 4:

F. David, B. Tienpont and P. Sandra

Research Institute for Chromatography, Kennedyapark 20, 8500 Kortrijk
frank.david@richrom.com

"Automated Systems for the Determination of Trace Contaminants in Water Samples"

The analysis of classical organic pollutants, such as polyaromatic hydrocarbons, PCBs and organochlorine pesticides in water samples is well established. Currently more and more attention is paid to new classes of organic pollutants such as endocrine disruptors, flame retardants, organotin compounds, odour contaminants etc. The detection limits that have to be reached for the determination of these compounds is 10 to 100 times lower than the detection limits and norms for the classical organic pollutants.

In this presentation some new and automated systems are presented that can be used for the determination of the new classes of pollutants at ultra-trace levels. The systems are based on (selective) extraction, followed by thermal desorption - GC-MS or liquid desorption - LC-MS. Several examples are shown how these systems can be used for real life applications.

Spreker 5:

Eddy L. Esmans, F.Lemière, W.Van Dongen, C.Borges, J.Embrecchts, B.Van den Driessche

University of Antwerp
Nucleoside Research & Mass spectrometry Unit
Groenenborgerlaan 171
B-2020 Antwerp, Belgium
Eddy.Esmans@ua.ac.be

"Analysis of nucleosides and nucleotides in biochemical samples by miniaturized LC- ESMS/MS"

Nucleosides and nucleotides are biomolecules which play an important role in a lot of biochemical processes. Examples will be given of the analysis of nucleosides, nucleotides and DNA-adducts by miniaturized LC-MS.

Spreker 6:

Paul Van Hummelen

Research Manager MicroArray Facility
VIB MicroArray Facility, MAF

UZ Gasthuisberg, Onderwijs en Navorsing
Herestraat 49
3000 Leuven
Belgium
tel: 32 (0)16 34 79 39
<http://www.microarrays.be>
<http://www.vib.be>

"BIOCHIPS"

With the human genome project reaching its completion scientists are looking for new ways to process the sequence data to functional knowledge of the genes in biological processes. During the last 5 years a new technique, DNA-MicroArrays-Chip, immersed that allows to studying gene expression on a large scale.

The DNA-MicroArray is an inverse hybridization based technology in which the molecular probes (array elements) are immobilized in 300 micron spots on glass microscope slides and the sample is fluorescent labeled and hybridized on the array elements. Samples exist out of RNA extracted from two different biological sources, as example, one from a breast tumor cells as the test sample and one from a normal breast cells as the reference sample. Each RNA sample will be reverse transcribed to DNA and simultaneously labeled with a fluorescent dye: test sample in red; reference sample in green. Both samples are hybridized on one DNA-MicroArray which will than be scanned with a confocal laser scanner.

Applications:

1. One can easily think about many different applications of DNA-MicroArrays. An obvious application is monitoring gene expression during cell differentiation in tissues, organs, embryos or cancer. The development and progression of cancer and the experimental reversal of tumorigenicity are accompanied by complex changes in patterns of gene expression. Using expression profiles, genes can be clustered in biochemical or cellular pathways. This will lead to better understanding of multi-geneic processes or transcriptional cascades. Clustering genes in known or unknown pathways may lead to the discovery of novel genes or (new) functions of already known genes.

2. With the same approach new drug targets can be identified by large-scale drug testing in In Vitro, In Vivo or Ex Vivo models resembling human diseases. The expression profiles can be translated in drug specific expression fingerprints. The fingerprint idea can also be used to monitor drug therapy. Based on expression changes due to drug treatment, chemotherapy can be tailored for each specific patient.

3. MicroArrays can also be used in genetic toxicology. Expression profiles can identify and classify mutagenic, carcinogenic or toxic agents. With carefully designed model systems a better and global view on the genetic consequences of exposure can be measured.

It is clear that MicroArrays offer the highest productivity of all gene expression tools in the genomics laboratory and show great promise in reducing the time and costs associated with basic research, or development of new diagnostic tests and drugs.

Spreker 7:

Marc Zabeau

Department of Plant Systems Biology
Ghent University, K.L. Ledeganckstraat 35, B-9000 GENT, Belgium
Vlaams Interuniversitair Instituut voor Biotechnologie (VIB)
Tel. + 32 (0)9.264.87.38 - Fax + 32 (0)9 220.33.59
marc.zabeau@skynet.be
<http://www.psb.rug.ac.be>

***"Novel developments in high throughput automated DNA analysis
by mass spectrometry.***

The sequencing complete genomes is the hallmark of the genomics paradigm shift, which is rapidly revolutionizing life science research. Concomitant with the rapid pace with which the genomes of various organisms are being sequenced, the need emerges for more performant high throughput automated platforms for DNA analysis. Indeed, the next challenge once the genome sequence of an organism is known is to inventorize the spectrum of sequence variations present in the genomes of individuals. In particular, the medical implications of the sequence variations in the human genome are rapidly being recognized, and a global effort is now underway to characterize the 20 to 30 million Single Nucleotide Substitutions (SNPs), prevalent in the human population. This gargantuan task is now becoming feasible thanks to the development of a new generation of high throughput DNA analysis platforms. Matrix Assisted Laser Desorption Ionisation (MALDI)-Time of Flight (TOF) mass spectrometry has proven to be an outstanding platform because of its short analysis times (seconds), high accuracy and sensitivity. The Flemish biotech start-up Methexis Genomics has developed a radically new technology for re-sequencing DNA, which is now being commercialised in a partnership with the San Diego based Sequenom Inc. The current platform is capable of sequencing a few million base pairs per day. Incremental improvements in the near future are opening the perspective to resequence the complete genome of an individual. These developments will undoubtedly have far reaching medical implications, resulting in what is now termed as "Personalized medicine".