

6th Intercanceropole Bioinformatics Workshop

Cancer Genomics and Data Integration

8-9th April 2013 - STRASBOURG

Program

● Monday April 8th ●

14:30-14:45 Introduction – Pierre Oudet, Scientific director, CGE, Strasbourg

14:45-15:45 Opening conference
Jean-François Deleuze, Head, National Centre of Genotyping
François Artiguenave Bio-Informatique director, CNG/CEA, Saclay
Genomics perspective and data integration

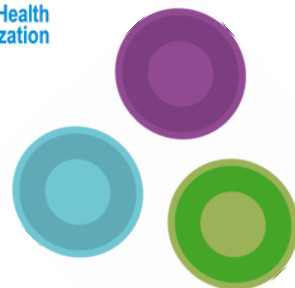
15:45-16:35 - **SESSION 1: Environmental exposure and mutation profiling**
Moderator: James McKay, GCS/IARC, Lyon

15:45-16:15 Magali Olivier and Jiri Zavadil, Molecular Mechanisms and Biomarkers Group, International Agency for Research on Cancer (IARC), Lyon
Integrated Analysis of Genetic Alterations and Transcriptomic Dysregulation in Upper Urinary Tract Carcinomas.

16:15-16:35 **Sophie Blein**, PhD student, Cancer Research Center, Lyon
Factors associated with oxidative stress and cancer risk in the Breast and Prostate Cancer Cohort Consortium (BPC3)

16:35-17:05 **Coffee break (Poster session)**

17:05-18:05 **Pascal Sempé** IBM Research, **Xavier Mary** IBM Software Group
From Research to bedside : turning data into insights



18:05-19:15 - SESSION 2: Stem cells, tumor heterogeneity and metastasis

Moderator: Jean Imbert, Scientific Director,
Plateforme IBiSA TGML; TAGC UMR_S 1090; Inserm,
Marseille

18:05-18:35 Lucy Yates, Sanger Institute, London

Single and Multi-Sampling Approaches to Exploring Evolving Heterogeneity in Cancers

18:35-18:55 Magali Michaut, Postdoc, Netherlands Cancer Institute Amsterdam

Pathway mutation status predicts chemotherapy response in triple negative breast cancer

18:55-19:15 Sarah Lennon, PhD student, Laboratoire de spectrométrie de masse bio-organique, Strasbourg

Membrane proteomics to search for specific glioblastoma cancer stem cells biomarkers.

● **Tuesday April 9th** ●

08:00-09:40 - SESSION 4: Data integration, constrain in data mining, new perspective

Moderator: Olivier Poch, Laboratory of Bioinformatics and Integrative Genomic, IGBMC, Illkirch

08:00-08:30 Philippe Hupé, Head, Biostatistics and data analysis, Curie Institute, Paris

Data integration of omics experiments in cancer research

08:30-09:00 Jean-François Gibrat, Head, Mathematics, Informatics and Genome Unit, Bioinformatics French Institute, INRA, Jouy-en Josas,

The French Bioinformatics Institute: a national infrastructure in Bioinformatics

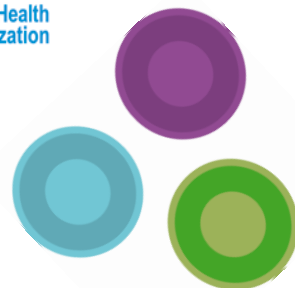
09:00-09:20 Petr Nazarov, biostatistician research worker, CRP-Sante, Luxembourg

Pipeline for an integrative analysis of interplay between microRNAs, transcription factors, and target genes using microarray data

09:20-09:40 Vincent Walter, Laboratory of Bioinformatics and Integrative Genomic, IGBMC, Illkirch

GEPETTO : Framework for gene prioritization

09:40-10:10 Coffee break (Poster session)



● **Tuesday April 9th** ●

10:10-11:10

● Conference ●

Roland Eils, Head, Dept. Theoretical Bioinformatics,
DKFZ (German Cancer Research Center) Heidelberg,
Germany

Lessons learnt from massive cancer genome sequencing

11:10-12:30 - SESSION 3: Disregulated cancer transcriptome

Moderator: Irwin Davidson, IGBMC, Department of Transcription,
Illkirch

11:10-11:40 **Evelyne Friederich**, Research Director, CNRS on leave coordinator of
Research Unit Life Sciences Research Unit-FSTC University of
Luxembourg

No title available

11:40-12:10 **Wolfgang Raffelsberger**, Laboratory of Bioinformatics and Integrative
Genomic, IGBMC, Illkirch

Tumor progression model from transcriptome view

12:10-12:30 **Arnaud Muller**, Bioinformatician, CRP-Sante Engineer Luxembourg
*Integrative Analysis Of Non-Small Cell Lung Cancer Combining RNA-seq
and Microarrays Experiments.*

12:30-14:00

Cocktail lunch (Poster session)

14:00-15:10 - SESSION 5: High throughput screening for targeted therapies

Moderator: Siamak Bahram

14:00-14:30 **Didier Rognan**, Head, Drug Bioinformatics Group, Laboratory for
Molecular Pharmacochimistry, Illkirch

High-throughput virtual screening of compound libraries

14:30-14:50 **Sarah Cianferani**, Chercheur, CNRS, Strasbourg

*Proteomics for cancer biomarker discovery : where do we stay in
finding a needle in a haystack?*

14:50-15:10 **Nicodème Paul**, Head of Bioinformatics, GENOMAX NGS platform,
INSERM UMR_S 1109, School of Medicine, Strasbourg

*Automated pipeline for mutation discovery using family-based exome
sequencing on the SOLiD platform*

15:10-15:20

Conclusion –

15:20 sharp:

End of meeting