


Paris Workshop on Molecular and Statistical Genomic Epidemiology



Ateliers de formation N° 136

Inserm

Institut national
de la santé et de la recherche médicale

Organisateurs / Organizers:

Ivo Gut (Centre National de Génotypage, Évry, France)
Mark Lathrop (Centre National de Génotypage, France)
Dan Weeks (University of Pittsburgh, USA)

Méthodologie pour l'étude de la variation génomique

Phase I - Le point sur...

2-3 mai 2002 - La Roche-Posay

Objectifs

L'objectif de cet atelier est de fournir une introduction aux développements méthodologiques récents pour la caractérisation et l'analyse de variants génétiques, en particulier les *single nucleotide polymorphisms* (SNPs). Les technologies « clés » pour le génotypage de grande échelle, et les avancées récentes dans les méthodes statistiques pour l'analyse de déséquilibre de liaison et d'association entre marqueurs et phénotypes seront exposés. Les outils bio-informatiques pour l'identification de variants génétiques, et la manière de planifier une étude en génétique humaine seront discutés.

Methods for the elucidation of genomic variation

Phase I - Critical assessment

2-3 May 2002 - La Roche-Posay

Aims

The workshop aims to provide an introduction to recent methodological developments for the characterization and analysis of DNA variants, particularly single nucleotide polymorphisms (SNPs). Key technologies for large-scale genotyping will be reviewed, and recent advances in statistical methods for the analysis of linkage disequilibrium and disease association data will be introduced. The use of bioinformatics tools for identifying genetic variants and issues related to design of studies in human genetics will be discussed.

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Sponsored by:



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EU Integrated Projects MolTools and MolPage



The European Commission
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Directorate F - Health Research



Centre National de Génotypage

Introduction to Methodology

Sunday 8th May – Tuesday 10th May 2005

Advanced Statistical Methods

Wednesday 11th May 2005

Organisers: Ivo Glynne Gut (Fr), Mark Lathrop (Fr), Dan Weeks (USA)

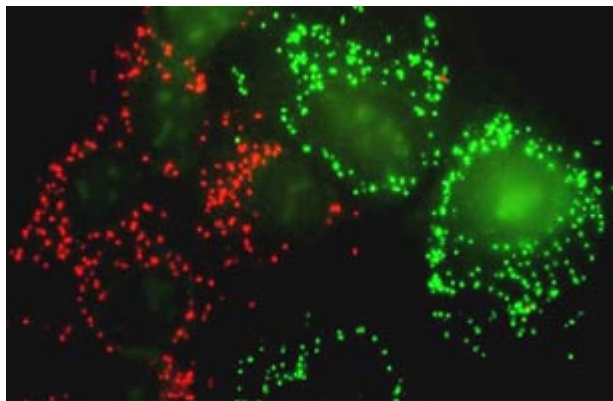
Venue: Maison de la Chimie, Paris, France

Programme: High density linkage disequilibrium (LD) mapping with single nucleotide polymorphisms (SNPs) is now possible on a genome-wide basis with technologies that permit characterisation of several hundred thousand polymorphisms simultaneously. This approach promises to lead to rapid advances in identifying the genetic factors underlying multifactorial traits in humans. Moreover, genetic approaches can be coupled with other methods of analysis (e.g. gene expression, DNA methylation, proteins and metabolites) to provide a powerful combined approach to detection and validation of biomarkers of diseases. The purpose of this workshop is to introduce researchers to new methodologies that underpin these studies, particularly in the context of on-going research funded by the EU under the auspices of the MolTools and MolPage Integrated Projects. New methodologies for genetic and biomarker studies will be presented by researchers at the forefront of their development. The interactive session on "Advanced Statistical Methods" is intended for a specialised audience interested in problems associated with theoretical and applied statistics to address interpretation.

Moltools

- New molecular tools will give us the opportunity to identify all molecules encoded in our genomes, even at the single-molecule level, and to do this in individual patient samples.
- The EU FP6 project MolTools aims to promote the development and implementations of such tools by bringing together leading European groups in the area of molecular technology development.

In situ genotyping individual DNA molecules by target-primed rolling circle amplification of padlock probes



Molpage

- Epidemiologists, clinical trialists and experimental scientists are confronted with a wealth of potential opportunities for molecular phenotyping large numbers of biological samples obtained from cohorts, patients or animal models.
- The challenge now is to ensure that these tools are developed to permit high-throughput analyses of significant numbers of samples, cohort protocols are in place for sample collection and storage, and that systems are in place to capture, warehouse and analyse the range of biological data that will emerge from these studies.

DNA Methylation Detection Using the Bisulphite Method

