



International Agency for Research on Cancer

Centre International de Recherche sur le Cancer

IARC SUMMER SCHOOL IN CANCER EPIDEMIOLOGY - 2008

2008 schedule

Regular modules repeated every year

2 June - 6 June

Cancer Registration

9 June - 20 June

Introduction to Cancer Epidemiology

A specialised module

23 June - 27 June

Methodological Issues in the Design and Analysis of Gene and Environment Studies

Two regular modules will be held from 2 to 20 June 2008, the first module lasts one week and the second module two weeks.

1. Cancer Registration (*one week, 2-6 June*) is a basic element of cancer control, making possible the rational use of resources as well as the identification of areas in need of research. In many parts of the world, cancer registries provide the only source of information on the size, nature and evolution of the local cancer problem.

The course covers all relevant aspects of data collection, coding and analysis:

- sources of information, case-finding and methods of data abstraction;
- classification of tumours and coding according to ICD and ICD-O;
- quality control, measures of comparability, standard definitions according to IACR;
- data analysis and reporting.

Training in the implementation of all registry functions by means of the IARC CANREG4 software is an integral part of this program.

2. Introduction to Cancer Epidemiology (*two weeks, 9-20 June*)

- introduction to biostatistics
- measures of occurrence and association
- descriptive epidemiological studies in cancer surveillance and research.
- standardization
- cross-sectional, cohort and case-control studies
- bias and confounding
- interaction
- topics in cancer epidemiology
- cancer prevention

3. A specialised module will be held from 23 to 27 June:

Methodological Issues in the Design and Analysis of Gene and Environment Studies (*one week*)

Course Directors: Paolo Boffetta and Jon Wakefield

Overview: The availability of rapid and cheap molecular genotyping, and large population-based case-control and cohort studies allow the possibility for understanding complex disease processes. However, the large dimensionality of the covariate (gene and environment) space provides challenges in each of the design, analysis, and interpretation of gene-environment studies.

Background: genetics/molecular biology/genotyping platforms.

Genetic data only: Genotyping errors. Hardy-Weinberg testing. Single point analyses. Genetic models. Multipoint analyses. Multiple hypothesis-testing. Population stratification. Missing data. Design: sample sizes, tagging SNPs/haplotypes, enriched cases, sex chromosome.

Gene-gene/Gene-environment: Meaning of interaction statistical vs biological. Types of interaction. Case only studies.

Speakers:

- Jon Wakefield (Departments of Statistics and Biostatistics, University of Washington, Gene-Environment Epidemiology Group, IARC)

- Clare Weinberg (Biostatistics Branch, National Institute of Environmental Health Sciences, USA)
- David Balding (Imperial College, London)
- George Davey Smith (University of Bristol, UK)
- Nat Rothman (National Cancer Institute, USA)

FURTHER INFORMATION AND APPLICATION FORMS FROM:

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