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Vall d'Hebron
Institut de Recerca
Unitat de Recerca de
Reumatologia



INSTITUTO NACIONAL
DE BIOINFORMÁTICA



CEGEN



Centro Nacional de Genotipado

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3rd. Course on Genome-Wide Association Studies

A course aiming to provide an update on the increasingly popular Whole Genome Scan approach to perform association studies. A wide perspective of the field will be provided, with lectures covering from technological and design issues to new data analysis and interpretation strategies.

Pre-registration can be made at <http://www.cegen.org> and will be open until May the 21st.

Barcelona,
May the 31st and June the 1st 2010

Universitat Pompeu Fabra



Doctor Aiguader 88, 08003 Barcelona

09:00-09:15. *Welcome.* Arcadi Navarro.

09:15-10:30. *Introduction. Linking Genotypes and Phenotypes. Diseases as a phenotype: the mendelian to complex spectrum. How do we know that a disease has a genetic component?.* Arcadi Navarro. *Room 61.102-104*

10:30-11:00. *Design and Analysis of Association studies and Genome-Wide Association Studies (GWAS).* Arcadi Navarro. *Room 61.102-104*

11:00-11:30. Coffee break

11:30-12:30. *Basic design issues in a GWAS.* Carlos Morcillo. *Room 61.102-104*

12:30-14:00. *The Welcome Trust Case Control Consortium and other recent GWAS.* Carlos Morcillo. *Room 61.102-104*

14:00-15:00. Lunch

15:00-16:30. [Hands-on session]. *Association Analysis: P-link, GWASpi.* Hafid Laayouni & Fernando Muñiz. *Room 61.303*

16:30-18:00. [Hands-on session] *Association Analysis: P-link, GWASpi.* Hafid Laayouni & Fernando Muñiz. *Room 61.303*

09:00-10:00. *The multiple testing problem and Interactions: how do parts relate to the whole?.*

Arcadi Navarro / Francesc Calafell. *Room 61.102-104*

10:00-11:00. *The problem of the missing heritability.* Arcadi Navarro / Francesc Calafell. *Room 61.102-104*

11:00-11:30. Coffee break

11:30-12:30. *Structural Variation in the Genome. Copy Number Variants and WGAS.* Elodie Gazave. *Room 61.102-104*

12:30-13:30. *CNstream: A method for the identification and genotyping of copy number polymorphisms using Illumina microarrays.* Arnald Alonso. *Room 61.102-104*

13:30-14:00. *Where to now? GWAS and Next Generation sequences.* Arcadi Navarro. *Room 61.102-104*

14:00-15:00. Lunch

15:00-16:30. [Hands-on session] *Association Analysis: P-link, GWASpi.* Hafid Laayouni & Fernando Muñiz. *Room 61.303*

16:30-18:00. [Hands-on session] *Copy Number Variants and WGAS, a practical approach.* Elodie Gazave. *Room 61.303*