Πρόγραμμα σεμιναρίων σε θέματα Βιοϊατρικής Πληροφορικής

Συνδιοργάνωση από:

το Τμήμα Μηχανικών Η/Υ και Πληροφορικής

και

το Διατμηματικό ΠΜΣ «Πληροφορική Επιστημών Ζωής»

20 και 24 Φεβρουαρίου 2015

Αίθουσα Π.200, Προκάτ, ΤΜΗΥΠ

ΠΡΟΓΡΑΜΜΑ

Παρασκευή, 20 Φεβρουαρίου 2015:

10:00 -10:45
From microarray data production (mice experiments) to functional gene representation, part 1 (45’)
NEHAR-BELAID Djamel, Immunologist

11:00 – 11:45
Transcriptome analysis: from raw data to signature, part 1 (45’)
DERIAN Nicolas, Bioinformatician

12:00 – 12:45
From microarray data production (mice experiments) to functional gene representation, part 1 (45’)
CHAARA Wahiba, Bioinformatician

Τρίτη, 24 Φεβρουαρίου 2015

10:00- 11:00
CFR 21 part 11 compliance for the computer scientist, (60’)
DRAKOS Ioannis, Computer and Software Engineer

11:15-11:45
From microarray data production (mice experiments) to functional gene representation, part 2 (30’)
NEHAR-BELAID Djamel, Immunologist

12:00-12:30

Transcriptome analysis: from raw data to signature, part 2 (30’)
DERIAN Nicolas, Bioinformatician

12:30-13:00
From microarray data production (mice experiments) to functional gene representation, part 2 (30’)
CHAARA Wahiba, Bioinformatician

Περισσότερες πληροφορίες για τις ομιλίες

Immune repertoire modelling using NGS data

Next-generation sequencing is one of the recent major technological advancements in biomedical data production. The amount of the produced gene sequencing data has been boosted by the introduction of the NGS techniques by at least three orders of magnitude making their management, processing, analysis and interpretation a challenging task.

A major application field for NGS is systems biology and a characteristic example of the added value of NGS in systems biology is the (more accurate) molecular characterization of the T-cell receptor (TCR) diversity. The NGS technology became a valuable asset to decipher the complexity of antigen-specific T-cell responses and to define the correlations of an adaptive immunity.

The seminar will be split in two parts. The first part will focus on the technological aspects of Next-Generation Sequencing and the challenges that arise with it. The second part will focus on the concept of the diversity of the immune system and how NGS data can be used to decipher its complexity.

CHAARA Wahiba <wahiba.chaara@upmc.fr>, Senior Bioinformatician, i3.

Transcriptome analysis: from raw data to signature

Transcriptomic analyses are widely used in systems biology to map the activity of the genome, mainly because the activity of a gene can be related to the amount of transcripts that it produces.

The seminar will be split in two sessions. The first session will focus on the definition of the biological objects and the technological aspects of what we call microarray. The second one will go through a step by step strategy of molecular signatures discovery, focusing on the independent component analysis (ICA) technique.

DERIAN Nicolas <nicolas.derian@upmc.fr>, Senior Bioinformatician, i3.

CFR 21 part 11 compliance for the computer scientist

Code of Federal Regulations (CFR) title 21 (rules of the Food and Drug Administration) part 11 (electronic records; electronic signatures) is the most commonly used regulatory protocol for digital management of Clinical Trials worldwide. In a US Foods and Drugs Administration (FDA) approved Clinical Trial, digital records stored in a CFR 21 part 11 compliant system are considered to be equivalent to paper records. The main aim of the protocol is to guarantee the Good Clinical Practices (GCP) and bioethics throughout the whole length of a Clinical Trial and the heaviest implementation weight resides in computer science. The seminar will focus on these issues from a computer science point of view.

DRAKOS Ioannis, <ioannis.drakos@upmc.fr>, Computer and Software Engineer, i3 and CEID

From microarray data production (mice experiments) to functional gene representation

Part I: Experiment steps required to produce reliable datasets

This part will focus on experiment design based on scientific hypothesis including tissue harvesting, RNA extraction and quality check of data.

Part II: A way to visualize and represent data

The second part will be devoted to gene set enrichment analysis using network-based graphical visualizations.

Djamel NEHAR-BELAID <nehar.djamel@gmail.com>, Immunologist, i3.

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