UNIL | Université de Lausanne
Faculté de biologie et de médecine

Cardiovascular and Metabolism PhD Program

Mini-Symposium

"Bioinformatics for Personalised Health"

Organizer: Rory Johnson, Laboratory for Genomics of Long noncoding RNA and Disease, University and University Hospital of Bern

When: 14 May 2018 from 8:30 – 12:30
Where: CHUV Lausanne, main building BH08, Auditorium Yersin

PROGRAM

8:30 – 9:00	**Welcome coffee**
9:00 - 9:15	**Welcome** **Rory Johnson, Laboratory for Genomics of Long noncoding RNA and Disease, University and University Hospital of Bern**
9:15 - 10:00	**John Doench, Broad Institute of MIT and Harvard, Cambridge, MA** *Genetic Screens with CRISPR technology: A New Hope in functional genomics*
10:00 - 10:45	**Christina Kiel, University College Dublin, Dublin , Ireland** *Integrative and quantitative analysis of disease networks and implications for personalized medicine*
10:45 – 11:00	**Coffee Break**
11.00 - 11:45	**Simon Furney, RCSI Royal College of Surgeons in Ireland, Dublin, Ireland.** *Genomic Oncology approaches for Personalised Medicine*
11.45 - 12.30	**Thomas Derrien, Institute of Genetics and Development of Rennes, France** *Facilitating long non-coding RNAs (lncRNAs) annotation using FEELnc and its application to the dog transcriptome*
12.30 – 14.00	**Lunch**
14:00 – 16:00	**Afternoon workshops for PhD students with symposium speakers**

This mini-symposium will be accredited by the Association of Cantonal Veterinarians (SCAV), section Lausanne, as a half day of continuing education.

The meeting is free of charge, but for organization purposes please register by filling the form here prior to April 30, 2018. A maximum of 120 participants can be accommodated.
The UNIL doctoral school attributes 1.0 ECTS for PhD students who present a signed participation form for the mini-symposium (0.25 ECTS morning session, 0.75 ECTS afternoon session).
For additional information, please contact Dr. Ulrike Toepel (Ulrike.toepel@unil.ch)

Co-organized by UNIL | Université de Lausanne Faculté de biologie et de médecine CHUV

Talk abstracts

John Doench

Broad Institute of MIT and Harvard, Cambridge MA, U.S.A.

Genetic Screens with CRISPR technology: A New Hope in functional genomics

Characterizing the function of genes, and understanding how gene dysfunction leads to disease states, remains a fundamental challenge in biology. CRISPR technology represents the most promising approach yet for perturbing cells and measuring phenotypic outcomes. Here I will discuss the development of CRISPR-based tools and their application to diverse biological systems.

Christina Kiel

University College Dublin, Dublin, Ireland.

Integrative and quantitative analysis of disease networks and implications for personalized medicine

Network-based approaches are powerful to get a comprehensive understanding of the molecular basis underlying diseases and to investigate how genetic defects spread along the network. Within those approaches, my work focuses on the quantitative and 3D structural aspects of protein interaction networks. In my talk I will compare disease networks of monogenic diseases, with those of age-related complex diseases and cancer. I will show examples of how network-centric analyses provide quantitative and mechanistic insights into Retinitis pigmentosa and glycogen-storage diseases (as examples for monogenic diseases) and BRAF signalling networks (in cancer). I will further discuss why the classical gene-network centric approach fails for complex and age-related diseases and how they may be tackled in the future.

Simon Furney
RCSI Royal College of Surgeons in Ireland, Dublin, Ireland.

Genomic Oncology approaches for Personalised Medicine

The overarching theme of my presentation will be the inference of mechanisms of tumour development and evolution from oncogenomic data. I will present data on tumourigenesis in melanoma, breast cancer and colorectal cancer. In addition, I will show how different combinations of genomic oncology approaches including study design, next generation sequencing technologies, bioinformatic analysis, rodent models and in vitro experiments can aid personalised cancer medicine.

Thomas Derrien
Institute of Genetics and Development of Rennes, France

Facilitating long non-coding RNAs (lncRNAs) annotation using FEELnc and its application to the dog transcriptome

Whole transcriptome sequencing (RNA-seq) has become a standard for cataloguing and monitoring RNA populations. One of the main bottlenecks consists in correctly identifying the different classes of RNAs among the plethora of reconstructed transcripts, particularly those that will be translated (mRNAs) from the class of long non-coding RNAs (lncRNAs). Here, I will present FEELnc (FlExible Extraction of LncRNAs), an alignment-free program that accurately annotates lncRNAs based on a Random Forest model. FEElnc, freely available at https://github.com/tderrien/FEELnc, moves beyond conventional coding potential classifiers by providing a standardized and complete solution for annotating lncRNAs. Finally, I will develop the use of FEELnc to characterize lncRNAs in the domestic dogs (*Canis lupus familiaris*) and to pinpoint lncRNAs involved in diseases.