Course Overview: practical information & project overview

Surf64 – 25 June, 2018

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Practical Information

- Internet Access: see WiFi set up email or `eduroam` connection
- Course documents and information on Github:

  `https://github.com/benoit-liquet/XP_Practice_SURF64`

  .
- Social Dinner on Wednesday at l'Avant Scène
- Teaching organisation:
  - Supervision: tutors, lecturers, and during morning presentation
  - Organisation: group presentation, technical lectures, group work
- Expected outcomes:
  - Day 1: Data preparation, exploration and analytical plan
  - Day2: Performing the main analyses
  - Day 3: Sensitivity/Stability analyses and interpretation
  - Day 4: Network models and/or OMICs integration
  - Day 5: Results finalisation and presentation

EXPOsOMICS data: 4 projects

- Design: $\sim$ 150 healthy participants wearing a real-time exposure monitoring device for 24 hours in three occasions
- Exposure data:
  - Three main exposure assayed: $PM_{2.5}$, Ultra-Fine Particles (UFP), and NO_2
  - Measured exposure: $PM_{2.5}$, and NO_2
  - Modelled exposure (averaged for one year prior to the session)
- Biosample: blood collected after each session
  - Targeted proteomics: 13 inflammatory markers (Luminex assay)
  - Transcriptomics: Agilent microarray (30k mRNA transcripts)
  - Metabolomics: Mass Spectrometry (5 to 10K features)
  - Epigenomics: Illumina 450K assay

Projects 1 & 2: Omics response to air Pollution

- Aim: Explore the OMICs response to long term exposure to air pollution at multiple molecular level
- Specific Aims:
  - Identify from each of the OMICs platform, molecular signatures of exposures
  - Investigate multivariate responses to environmental exposures
  - Account for the repeated measurement design
  - Functionally interpret results from profiling analyses
  - Assess heterogeneity across countries
  - Assess the relationship across signals detected at different molecular levels
- Groups:

Group 1: UFP	Group 2: $PM_{2.5}$
Julie Guibon	Julian Krauskopf
Sei Harada	Ayano Takeuchi
Gao He	Simon Tiendrebeogo

Project 3: Assessing OMICs stability

- Aim: Evaluate if OMICs profile vary in time, and what are the potential drivers of these changes
- Specific Aims:
  - Identify sets of OMICs signals that are stable in time
  - Identify sets of OMICs signals that vary in time
  - Explore the rate at which OMICs levels change
  - Interpret the involved (metabolic) pathways and possible mechanisms
  - Evaluate if these changes are related to exposures / exposure changes
  - Investigate the link between stable and variable signals across OMIC platforms
- Group:

  Binbin Xu

  Sebastien Coube

  Nikita Shvestov

Project 4: Identify a multi-OMICs inflammasomestability

- Aim: Identify OMICS markers related to inflammation as measured by targeted proteins
- Specific Aims:
  - Identify from each OMICs platforms, signatures of each of the 13 inflammatory markers
  - Investigate the 13 inflammatory markers as a measure of inflammation
  - Combine the metabolomic and methylation data
  - Explore the contribution/role of each set of OMICs markers in inflammation
  - Assess the functional relevance of the identified markers
  - Evaluate the stability/reproducibility of the findings.
- Group:

  Su Kang

  Yusef Badi

  Alexei Novolaca

Project 5: Identification of drug resistance in Lymphomas

- Data: gene expression data (Affymetrix Human Genome U133 Plus 2.0 Array, GPL570 in GEO) consisting in a total of 54,675 probes from GEO and it consists in individuals with both subtypes of DLBCL along with its response to the treatment with R-CHOP.
- Aims: explore drug response mechanisms common to different lymphoma subtypes. Data includes several studies from two different subtypes of lymphoma. The main question is to explore whether there are common mechanisms (genes) involved in the resistance to the response of the lymphoma. In this regard, it is not clear whether the common mechanisms involve only common genes or also similar expression levels.
- Group:

  Camilo Broc

  Soufiane Djebbar

  Maitena Tellaetxe