Introduction to practical sessions

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Introduction to the biological question

- For all further practical sessions we will use data from Thomas Strub et al. (IGBMC, Davidson team)

- Main biological question
  - What is the role of MITF in melanoma ?
  - MITF = MIcrophthalmia Transcription Factor
  - Why study MITF ?
    - Essential for the survival of melanocytes
      Regulates multiple aspects of normal melanocyte function
    - Important role in regulating the proliferative and invasive properties of melanoma cells

Introduction to the datasets

- In order to have a comprehensive view of MITF role in human melanoma cells
  - Generation of a human melanoma cell line stably expressing HA-tagged MITF
  - ➔ **Anti-HA ChIP-Seq on the tagged and native cells**
  - Use of siRNAs to knockdown MITF expression in melanoma cells
  - ➔ 3’end RNA-Seq on RNA from siMITF and control cells

    Strub et al. Oncogene 2011
  - ➔ **mRNA-Seq on RNA from siMITF and control cells**

Introduction to the datasets

- mRNA-seq dataset
  - Illumina TruSeq stranded mRNAseq protocol
  - Illumina Hiseq2500 sequencer
  - Single-end 50bp
  - 4 samples per lane

Sample name	Condition
siLuc2	siLuc
siLuc3	siLuc
siMitf3	siMitf
siMitf4	siMitf

Introduction to the datasets

- ChIP-seq dataset
  - Illumina GAIIx sequencer
  - Single-end reads
  - 1 sample per line

Sample name	Read length (pb)
Mitf	54
Control	54
H3K4me3	40
polII	40

Data files available

- On your computer
- On Galaxy
  - “NGS data analysis training Strasbourg” history
    - All files needed for the training on Galaxy
  - “NGS data analysis training Strasbourg - RNAseq” and “NGS data analysis training Strasbourg - ChIPseq” histories
    - All datasets generated during the training
    - To be used only if you did not manage to perform an analysis step

RNAseq : https://usegalaxy.fr/u/celine/h/ngs-data-analysis-training-strasbourg---rnaseq
ChIPseq : https://usegalaxy.fr/u/stephanie/h/ngs-data-analysis-training-strasbourg---chipseq