Introduction to practical sessions

Céline Keime
keime@igbmc.fr

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

  - Data available in GalaxEast
    - Shared Data → Data Libraries → NGS data analysis training → RNAseq

Introduction to the datasets

- **ChIP-seq dataset**

  - Illumina GAIIx sequencer

  - Single-end reads

  - 1 sample per line

Sample name	Read length
Mitf	54
Control	54
H3K4me3	40
polII	40

  - Data available in GalaxEast

    - Shared Data → Data Libraries → NGS data analysis training → ChIPseq