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