Module 9 ChipSeq Module Plan
NGS Bioinformatics - Remote classrooms

Module Title: Chip Seq

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➜ **Summary or objectives** – To understand the theory of chipseq experiments and the practice of basic chipseq analysis on a transfac (PAX5) binding profile

➜ **List of learning outcomes specific for this module**

Theory:
- Understand the basic epigenetics underlying Chip-Seq
- Understand typical signatures of the biology chipseq is used to detect
  - Transcription factors
  - Histone Modes
- Understand possible experimental technical issues and their signatures
- Appreciate how a peak-caller works, and what a motif is

Practical:
- generate an unspliced alignment by aligning raw sequencing data to the human genome usingBowtie2
- manipulate the SAM output in order to visualise the alignment in IGV
- based on the aligned reads, find immuno-enriched areas using the peak caller MACS2
- perform functional annotation and motif analysis on the predicted binding regions

➜ **Total number of hours:** 4 hours

➜ **Tools/software and resources**
- ◆ Software - should already be on image:
  - Bedtools
  - Bowtie2
  - IGV
  - MACS2
  - Meme
  - Samtools
  - Tomtom
  - UCSC Tools

- ◆ Description of datasets to be used (if known)

- ◆ Other resources, or readings

➔ **Overview of activities and exercises**

Chipseq practical Activity 1: Aligning PAX5 data to the genome
Chipseq practical Activity 2: Viewing alignments in IGV
Chipseq practical Activity 3: Finding enriched regions using MACS2
Chipseq practical Activity 4: using bedtools to annotated Peaks with genes
Chipseq practical Activity 5: PAX5 motif analysis using meme and tomtom

➔ **Assessment (s)**
MCQ will assess lecture understanding
Each practical activity has a write-up which the students can submit on completion.