ChIP-seq analysis

How to set up infrastructure for ChIP-seq analysis using the Biostars Handbook 2nd edition according to Ming Tangs Guide.

Setting up the folder structure

Go to the directory for ChIP-seq with your analysis

```
cd ~/work/ChIP-seq_<analysis-name>
mkdir {data,results,scripts,software}
mkdir -p results/{bams,peaks,fastqc,motifs}
cd data
```

Download data

Get the annotation list from the sra run selector

`IDs.txt`

Prefetch and convert files to fastq

Go into the ~/work/ChIP-seq__/data

```
time parallel -j 10 'prefetch {}' :::: IDs.txt
```

```
time parallel -j 10 'fasterq-dump {}/{}/sra --split-files --threads 6 :::: IDs.txt
```