

- « Classical » analysis
- Clusters analysis
- Optional step
- TODO → modifications to do
- RNA-seq data

## Pre-processing :

- Demultiplexing
- Quality reports
- Filtering of reads with bad IQF
- Filtering of PCR duplicates
- Extract Unique Molecular Identifier TODO
- Adapters trimming
- Size selection

For each sample

## Pre-processing :

- Pool all sequences / sample
- Pool all sequences over all samples

All sequences availables over all samples

## Mapping :

- Filtering of reads mapped to rRNA
- Mapping to reference genome
- Filtering of multi-reads
- Mapping output sorted & indexed

PCR duplicates removing TODO

Triplet-periodicity analysis TODO

Metagene analysis

P-site offsets analysis

Isoform-level estimation

Multi-mapped annotations clustering

Expression estimation considering :

- Longest CDS
- Splicing-isoform-level assessing
- Clusters

Differenretial analysis :

- Genes/Clusters translation
- Regulation level