

scRNA-seq snakemake pipeline manual

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Introduction:

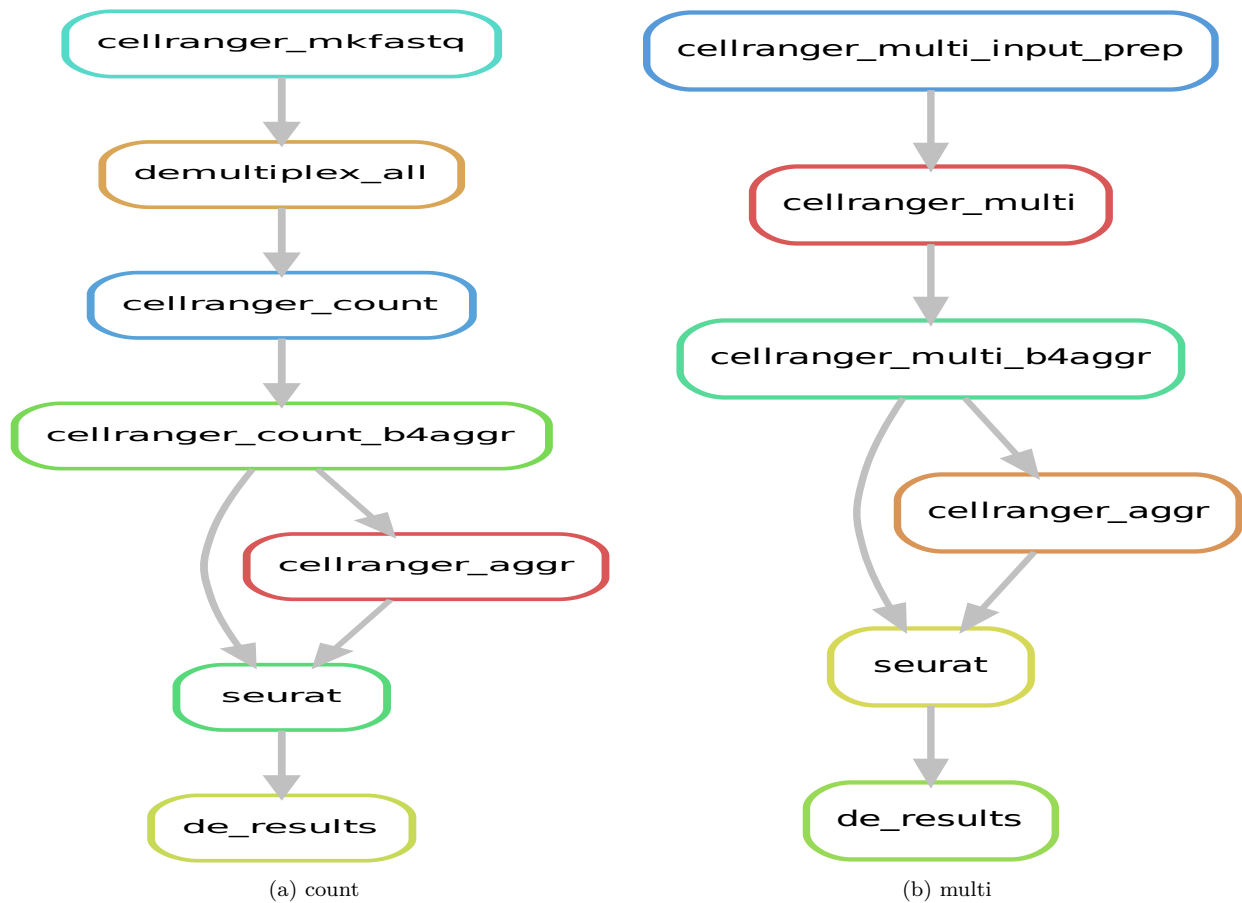


Figure 1: pipeline

The single-cell RNA pipeline can start from either bcl files with initial demultiplexing or already demultiplexed fastq files.

Based on the data format at the start

BCL files

Please prepare a csv file in one of the following formats:

[a] pipeline **count**: gene expression-only data

```
feature_type,run_bcl_path,iem_samplesheet,samplesheet_4_bcl,fastq_outdirectory,bcl_run_index
"Gene Expression",/path/bcl/folder1,False,/path/to/samplesheet/for/bcl/folder1,/path/to/fastq/output/dir
"Gene Expression",/path/bcl/folder2,True,/path/to/samplesheet/for/bcl/folder2,/path/to/fastq/output/dir
```

[b] pipeline **multi**: gene expression and VD(J) data

```
feature_type,run_bcl_path,iem_samplesheet,samplesheet_4_bcl,fastq_outdirectory,bcl_run_index
"Gene Expression",/path/bcl/folder1,False,/path/to/samplesheet/for/bcl/folder1,/path/to/fastq/output/dir
"VDJ-B",/path/bcl/folder2,False,/path/to/samplesheet/for/bcl/folder2,/path/to/fastq/output/vdj_bcell,run
"VDJ-T",/path/bcl/folder3,False,/path/to/samplesheet/for/bcl/folder3,/path/to/fastq/output/vdj_tcell,run
```

The bcl samplesheet (/path/to/samplesheet/for/bcl/folder1) can either be a simple samplesheet (iem_samplesheet **False**)

```
Lane,Sample,Index
1,test_sample_atac,SI-NA-A1
```

or

an Illumina Experiment Manager file (iem_samplesheet **True**)

```
[Header],,,,,,
IEMFileVersion,4,,,,,
Investigator Name,rjr,,,,,
Experiment Name,hiseq_test,,,,,
Date,8/15/16,,,,,
Workflow,GenerateFASTQ,,,,,
Application,HiSeq FASTQ Only,,,,,
Assay,TruSeq HT,,,,,
Description,hiseq sample sheet,,,,,
Chemistry,Default,,,,,
,,,,,
[Reads],,,,,,
26,,,,,
98,,,,,
,,,,,
[Settings],,,,,,
,,,,,
[Data],,,,,,
Lane,Sample_ID,Sample_Name,Sample_Plate,Sample_Well,I7_Index_ID,index,Sample_Project,Description
1,s1,test_sample,,,SI-P03-C9,SI-P03-C9,p1,
```

FASTQ files

Please prepare csv file with the following format:

```
fastq,sample,library_type
/path/to/sampl1_fastq_directory/,sample1,Gene Expression
/path/to/sampl2_fastq_directory/,sample2,Gene Expression
/path/to/sampl3_fastq_directory/,sample3,Gene Expression
/path/to/sampl4_fastq_directory/,sample4,Gene Expression
```