

nf-core/ scrnaseq

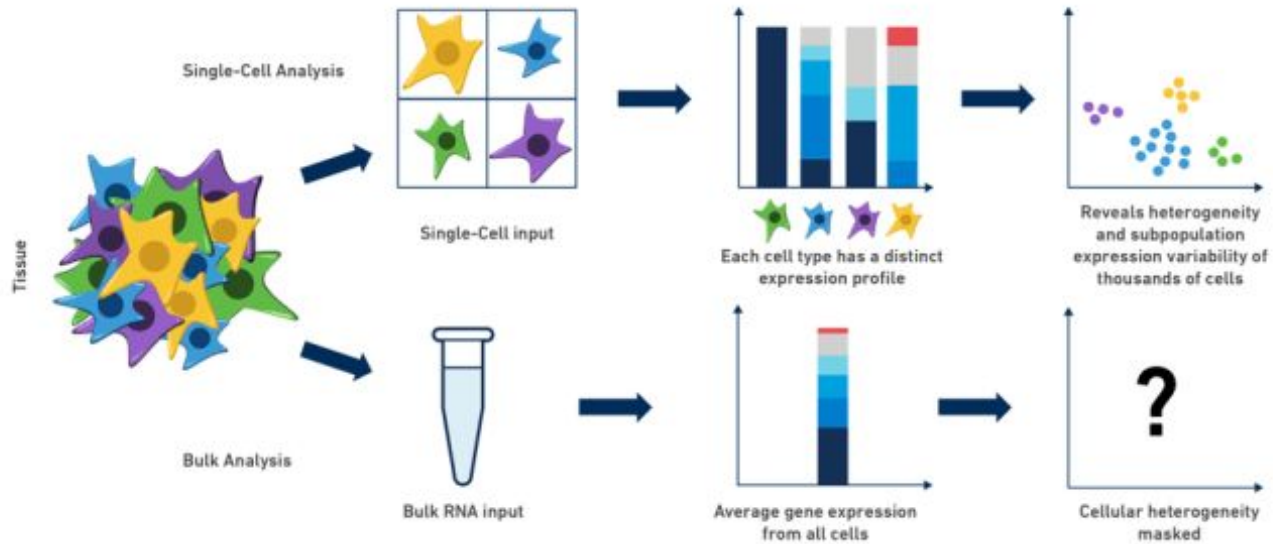
Chris Hakkaart - Seqera

nf-core/scrnaseq

nf-core/scrnaseq is a bioinformatics best-practice analysis pipeline for processing 10x Genomics single-cell RNA-seq data.

This is a community effort in building a pipeline capable to support:

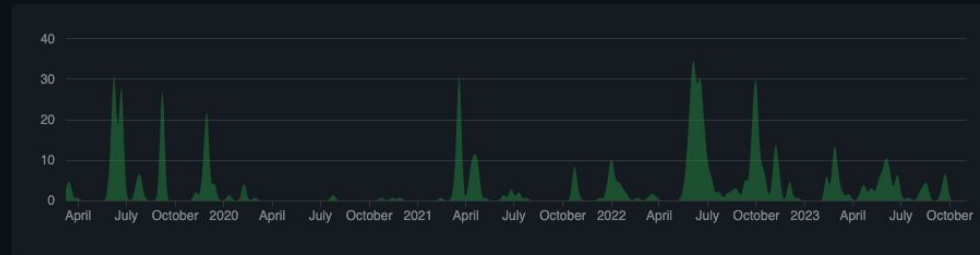
- Alevin-Fry + AlevinQC
- STARSolo
- Kallisto + BUSTools
- Cellranger
- UniverSC



Mar 10, 2019 – Nov 3, 2023

Contributions: Commits ▾

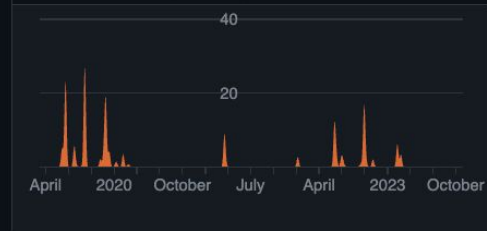
Contributions to master, excluding merge commits



apeltzer

237 commits 6,358 ++ 3,822 --

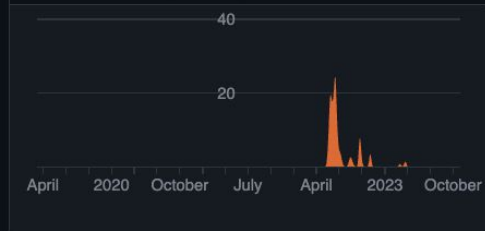
#1



fmalmeida

140 commits 2,663 ++ 1,985 --

#2



grst

70 commits 2,432 ++ 2,894 --

#3

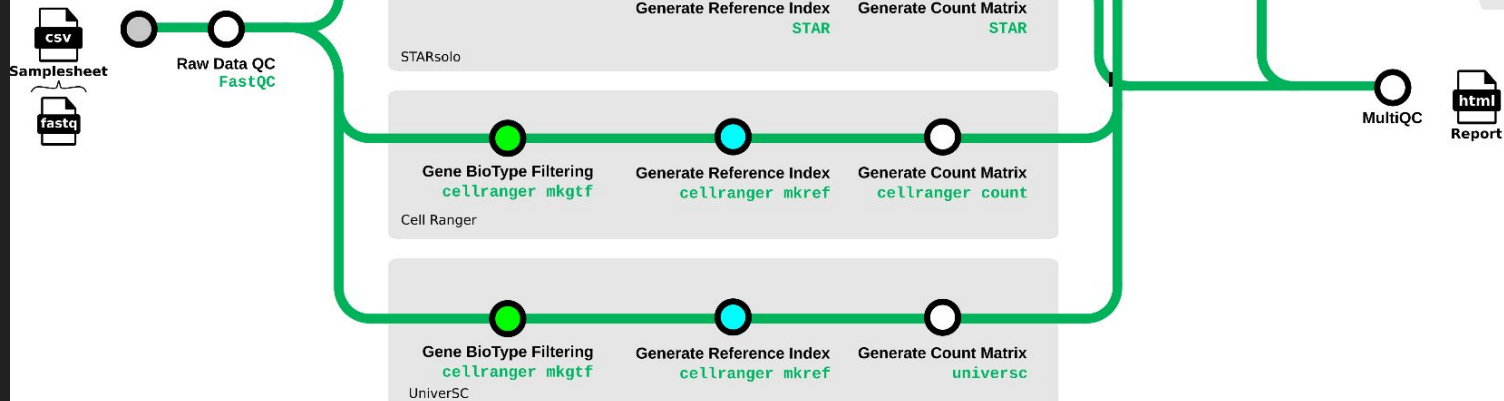


olgabot

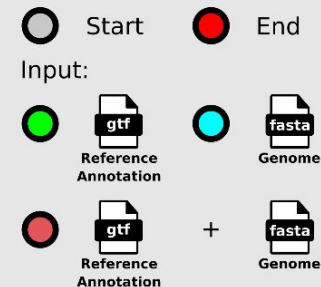
63 commits 1,475,507 ++ 1,475,093 --

#4





Legend



```
nextflow run nf-core/scrnaseq \  
  -profile test,docker \  
  --outdir results
```

```
params {
    config_profile_name      = 'Test profile'
    config_profile_description = 'Minimal test dataset to check pipeline function'

    max_cpus    = 2
    max_memory  = '6.GB'
    max_time    = '6.h'

    input      = 'samplesheet-2-0.csv'

    fasta      = 'GRCm38.p6.genome.chr19.fa'
    gtf        = 'gencode.vM19.annotation.chr19.gtf'
    aligner    = 'star'
    protocol   = '10XV2'

    validationSchemaIgnoreParams = 'genomes'
}

process {
    withName: '.*:CELLRANGER_COUNT' {
        maxForks = 1
    }
}
```

```
params {  
  config_profile_name      = 'Full Test profile'  
  config_profile_description = 'Full test dataset to check pipeline function'  
  
  input      = 'samplesheet_2.0_full.csv'  
  
  // Genome references  
  genome      = 'GRCh38'  
  aligner     = 'star'  
  protocol    = '10XV2'  
  
  validationSchemaIgnoreParams = 'genomes'  
}
```


“5000”

samplesheet.csv

sample	fastq_1	fastq_2	expected_cells	seq_center
Sample_X	Sample_X_S1_L1_R1.fastq.gz	Sample_X_S1_L1_R2.fastq.gz	“5000”	"Site 1"
Sample_Y	Sample_Y_S1_L1_R1.fastq.gz	Sample_Y_S1_L1_R2.fastq.gz	“5000”	"Site 2"
Sample_Y	Sample_Y_S1_L2_R1.fastq.gz	Sample_Y_S1_L2_R2.fastq.gz	“5000”	"Site 3"

```
$ nextflow run scrnaseq/ -profile test,docker --outdir results
N E X T F L O W ~ version 23.10.0
Launching `scrnaseq/main.nf` [ecstatic_miescher] DSL2 - revision: bd078e3da5
executor > local (14)
[e9/3dc2c1] process > NFCORE_SCRNASEQ:SCRNASEQ:INPUT_CHECK:SAMPLESHEET_CHECK (samplesheet-2-0.csv) [100%] 1 of 1 ✓
[42/930a0d] process > NFCORE_SCRNASEQ:SCRNASEQ:FASTQC_CHECK:FASTQC (Sample_Y) [100%] 2 of 2 ✓
[cc/df9dca] process > NFCORE_SCRNASEQ:SCRNASEQ:GTF_GENE_FILTER (GRCm38.p6.genome.chr19.fa) [100%] 1 of 1 ✓
[81/d73a70] process > NFCORE_SCRNASEQ:SCRNASEQ:STARSOLO:STAR_GENOMEGENERATE (GRCm38.p6.genome.chr19.fa) [100%] 1 of 1 ✓
[8c/2c18e3] process > NFCORE_SCRNASEQ:SCRNASEQ:STARSOLO:STAR_ALIGN (Sample_Y) [100%] 2 of 2 ✓
[0b/1ca671] process > NFCORE_SCRNASEQ:SCRNASEQ:MTX_CONVERSION:MTX_TO_H5AD (Sample_X) [100%] 2 of 2 ✓
[cb/8a97ee] process > NFCORE_SCRNASEQ:SCRNASEQ:MTX_CONVERSION:CONCAT_H5AD [100%] 1 of 1 ✓
[ae/e8c1c4] process > NFCORE_SCRNASEQ:SCRNASEQ:MTX_CONVERSION:MTX_TO_SEURAT (Sample_Y) [100%] 2 of 2 ✓
[b9/35129b] process > NFCORE_SCRNASEQ:SCRNASEQ:CUSTOM_DUMPSOFTWAREVERSIONS (1) [100%] 1 of 1 ✓
[ef/2862c4] process > NFCORE_SCRNASEQ:SCRNASEQ:MULTIQC [100%] 1 of 1 ✓
-[nf-core/scrnaseq] Pipeline completed successfully-
Completed at: 30-Oct-2023 12:20:43
Duration : 7m 17s
CPU hours : 0.3
Succeeded : 14
```