class: Workflow

cwlVersion: v1.0

Header

id: workflowpractice1

label: workflowPractice1

$namespaces:

sbg: 'https://www.sevenbridges.com/'

inputs:

- id: fasta\_file

type: File

label: reference genome file

- id: known\_sites\_dir

type: Directory

outputs:

- id: output\_file

outputSource:

- call\_structural\_variants/output\_file

type: File

steps:

- id: download\_file

in: []

out:

- id: output\_1

- id: standard\_error

- id: standard\_output

run: ./download\_file.cwl

- id: trim\_fastq

in:

- id: fastq\_file\_1

source: download\_file/output\_1

- id: fastq\_file\_2

source: download\_file/output\_1

out:

- id: output\_1

- id: output\_2

- id: standard\_error

- id: standard\_output

run: ./trim\_fastq.cwl

- id: align\_fastq

in:

- id: fasta\_file

source: fasta\_file

- id: fastq\_file\_1

source: trim\_fastq/output\_1

- id: fastq\_file\_2

source: trim\_fastq/output\_2

out:

- id: output\_file

- id: standard\_error

- id: standard\_output

run: ./align\_fastq.cwl

- id: sort\_bam

in:

- id: bam\_file

source: align\_fastq/output\_file

out:

- id: output\_file\_1

- id: standard\_error

- id: standard\_output

run: ./sort\_bam.cwl

- id: mark\_dups\_bam

in:

- id: bam\_file

source: sort\_bam/output\_file\_1

out:

- id: output\_file\_1

- id: standard\_error

- id: standard\_output

run: ./mark\_dups\_bam.cwl

'sbg:x': 625.3289794921875

'sbg:y': -258.46295166015625

- id: calculate\_bqsr\_bam

in:

- id: bam\_file

source: mark\_dups\_bam/output\_file\_1

- id: fasta\_file

source: fasta\_file

- id: known\_sites\_dir

source: known\_sites\_dir

out:

- id: output\_file

- id: standard\_error

- id: standard\_output

run: ./calculate\_bqsr\_bam.cwl

'sbg:x': 784.34765625

'sbg:y': -137.17684936523438

- id: apply\_bqsr\_bam

in:

- id: bam\_file

source: mark\_dups\_bam/output\_file\_1

- id: bqsr\_table\_file

source: calculate\_bqsr\_bam/output\_file

- id: fasta\_file

source: fasta\_file

out:

- id: output\_file\_1

- id: standard\_error

- id: standard\_output

run: ./apply\_bqsr\_bam.cwl

'sbg:x': 1107.366943359375

'sbg:y': -75.92033386230469

- id: call\_small\_variants

in:

- id: fasta\_file

source: fasta\_file

- id: normal\_bam\_file

source: apply\_bqsr\_bam/output\_file\_1

- id: tumor\_bam\_file

source: apply\_bqsr\_bam/output\_file\_1

out:

- id: standard\_error

- id: standard\_output

run: ./call\_small\_variants.cwl

'sbg:x': 1584.1502685546875

'sbg:y': -60.4754753112793

- id: call\_structural\_variants

in:

- id: fasta\_file

source: fasta\_file

- id: normal\_bam\_file

source: apply\_bqsr\_bam/output\_file\_1

- id: tumor\_bam\_file

source: apply\_bqsr\_bam/output\_file\_1

out:

- id: output\_file

- id: standard\_error

- id: standard\_output

run: ./call\_structural\_variants.cwl

hints:

- {}

requirements: []

'sbg:toolAuthor': Stephen Piccolo