Package ‘RcwlPipelines’

April 15, 2020

Title Bioinformatics pipelines based on Rcwl

Version 1.2.0

Description A collection of Bioinformatics tools and pipelines based on R and the Common Workflow Language.

Depends R (>= 3.6), Rcwl, BiocFileCache

Imports dplyr, rappdirs, jsonlite, methods, utils, tximport

License GPL-2

Encoding UTF-8

Suggests testthat, knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

RoxygenNote 6.1.1

biocViews Software, WorkflowStep, Alignment, Preprocessing, QualityControl, DNASeq, RNASeq, DataImport, ImmunoOncology

SystemRequirements nodejs

Collate 'RcwlPipelines-package.R' 'cwlTools.R' 'doc_pipelines.R' 'doc_tools.R' 'tl_tabix_index.R' 'tl_bgzip.R' 'tl_ReadBackedPhasing.R' 'tl_SortVcf.R' 'tl_CombineVariants.R' 'tl_RenameSampleInVcf.R' 'tl_bcfview.R' 'pl_phaseVcf.R' 'tl_vcf_expression_annotator.R' 'tl_kallisto_quant.R' 'pl_vcfExpression.R' 'tl_vcf_readcount_annotator.R' 'tl_bam_readcount.R' 'tl_vt_decompose.R' 'pl_vcfCoverage.R' 'tl_vep.R' 'pl_AnnPhaseVcf.R' 'tl_samtools_stats.R' 'tl_samtools_flagstat.R' 'tl_samtools_index.R' 'tl_ApplyBQSR.R' 'tl_BaseRecalibrator.R' 'pl_BaseRecal.R' 'tl_runWDL.R' 'tl_mvOut.R' 'pl_GAlign.R' 'tl_PoN.R' 'tl_GenomicsDB.R' 'pl_GPoN.R' 'tl_FilterOBias.R' 'tl_ColSeqArtifact.R' 'tl_FilterMutectCalls.R' 'tl_CalculateContamination.R' 'tl_GetPileupSummaries.R' 'tl_Mutect2.R' 'pl_Mutect2PL.R' 'tl_geneBody_coverage.R' 'tl_read_distribution.R' 'tl_genePredToBed.R' 'tl_gtfToGenePred.R' 'pl_RSeQC.R' 'tl_neusomatic_postprocess.R' 'tl_neusomatic_call.R' 'tl_neusomatic_preprocess.R' 'pl_neusomatic.R' 'tl_SomaticSeq_Wrapper.R' 'tl_VarScan2_somaticFilter.R' 'tl_VarScan2_processSomatic.R' 'tl_VarScan2_somatic.R' 'tl_samtools_mpileup.R' 'pl_VarScan2Somatic.R' 'tl_LoFreq.R' 'tl_VarDict.R' 'tl_SomaticSniper.R' 'tl_strelka.R' 'tl_manta.R'

'pl_mantaStrelka.R' 'tl_MuSE.R' 'pl_SomaticCallers.R'
'tl_markdup.R' 'tl_mergeBam.R' 'pl_mergeBamDup.R'
'tl_sortBam.R' 'tl_sam2bam.R' 'tl_bwa.R' 'pl_bwaAlign.R'
'pl_alignMerge.R' 'pl_bwaMMRecal.R' 'pl_bwaMRecal.R'
'pl_hapCall.R' 'pl_jdCall.R' 'tl_miRDeep2.R' 'tl_miRMapper.R'
'pl_miRDeep2PL.R' 'tl_featureCounts.R' 'tl_STAR.R'
'tl_fastqc.R' 'pl_rnaseq_Sf.R' 'tl_BedToIntervalList.R'
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'tl_salmon_quant.R' 'tl_starFusion.R'

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R topics documented:

`alignMerge` *DNASeq alignment, merge and markduplicates*

Description

The DNASeq pipeline to run bwa alignment, merge and mark duplicates.

Usage

```
alignMerge
```

Format

A ‘cwlStepParam‘ object.

bwaAlign to align fastqs with bwa and sort with samtools

mergeBamDup to merge BAMs from different flowcells and then mark duplicates with picard

Source

`https://hubentu.github.io/others/Rcwl_DNASeq_Align.html`

`annovar` *annovar*

Description

annovar

Usage

```
annovar
```

Format

An object of class `cwlParam` of length 1.

`AnnPhaseVcf` *AnnPhaseVcf*

Description

AnnPhaseVcf

Usage

```
AnnPhaseVcf
```

Format

A ‘cwlStepParam‘ object.

steps:

VCFvep annotate VCF with VEP

VCFcoverage add reads counts to VCF

VCFexpression add expression data to VCF

phaseVcf combine germline and somatic variant and phase

Source

https://pvactools.readthedocs.io/en/latest/pvacseq/input_file_prep.html

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`bam_readcount` *bam_readcount*

Description

bam_readcount

Usage

```
bam_readcount
```

Format

An object of class `cwlParam` of length 1.

`BaseRecal` *Base quality recalibration*

Description

Base quality recalibration

Usage

```
BaseRecal
```

Format

A ‘cwlStepParam‘ object.

BaseRecalibrator Detect systematic errors in base quality scores

ApplyBQSR Apply base quality score recalibration

samtools_index samtools index

samtools_flagstat samtools flagstat

samtools_stats samtools stats

Source

https://software.broadinstitute.org/gatk/best-practices/workflow?id=11165

`bcfview` *bcftools view*

Description

bcftools view

Usage

```
bcfview
```

Format

An object of class `cwlParam` of length 1.

`BedToIntervalList` *Picard BedToIntervalList*

Description

Picard BedToIntervalList

Usage

```
BedToIntervalList
```

Format

An object of class `cwlParam` of length 1.

`bgzip` *bgzip*

Description

bgzip

bgzip

Usage

```
bgzip
```

```
bgzip
```

Format

An object of class `cwlParam` of length 1.

`blastn` *blastn*

Description

blastn

Usage

```
blastn
```

Format

An object of class `cwlParam` of length 1.

`bowtie2` *bowtie2*

Description

bowtie2

Usage

```
bowtie2
```

Format

An object of class `cwlParam` of length 1.

`bowtie2_build` *bowtie2-build*

Description

bowtie2-build

Usage

```
bowtie2_build
```

Format

An object of class `cwlParam` of length 1.

`bowtie_build` *bowtie-build*

Description

bowtie-build

Usage

```
bowtie_build
```

Format

An object of class `cwlParam` of length 1.

`bwa` *bwa mem*

Description

bwa mem

Usage

```
bwa
```

Format

An object of class `cwlParam` of length 1.

`bwaAlign` *bwaAlign*

Description

bwa alignment

Usage

```
bwaAlign
```

Format

A ‘cwlStepParam‘ object.

bwa to align fastqs with bwa

sam2bam samtools view sam to bam format

sortBam sort Bam file by samtools sort

idxBam index Bam by samtools index

`bwaMMRecal` *DNASeq alignment, merge, markduplicates and recalibration*

Description

The DNASeq pipeline to run bwa alignment, merge, mark duplicates and recalibration.

Usage

```
bwaMMRecal
```

Format

A ‘cwlStepParam‘ object.

bwaAlign to align fastqs with bwa and sort with samtools

mergeBamDup to merge BAMs from different flowcells and then mark duplicates with picard

BaseRecal Base quality recalibration

Source

`https://hubentu.github.io/others/Rcwl_DNASeq_Align.html`

`bwaMRecal` *DNASeq alignment, markduplicates and recalibration*

Description

The DNASeq pipeline to run bwa alignment, mark duplicates and recalibration.

Usage

```
bwaMRecal
```

Format

A ‘cwlStepParam‘ object.

bwaAlign to align fastqs with bwa and sort with samtools

markdup to mark duplicates with picard

BaseRecal Base quality recalibration

Source

`https://hubentu.github.io/others/Rcwl_DNASeq_Align.html`

`bwa_index` *bwa index*

Description

bwa index

Usage

```
bwa_index
```

Format

An object of class `cwlParam` of length 1.

`CalculateContamination` *gatk CalculateContamination*

Description

gatk CalculateContamination

Usage

```
CalculateContamination
```

Format

An object of class `cwlParam` of length 1.

`cnvkit_batch` *cnvkit batch*

Description

cnvkit batch

Usage

```
cnvkit_batch
```

Format

An object of class `cwlParam` of length 1.

`ColSeqArtifact` *gatk CollectSequencingArtifactMetrics*

Description

gatk CollectSequencingArtifactMetrics

Usage

```
ColSeqArtifact
```

Format

An object of class `cwlParam` of length 1.

`CombineVariants` *CombineVariants*

Description

CombineVariants

Usage

```
CombineVariants
```

Format

An object of class `cwlParam` of length 1.

`cutadapt` *cutadapt*

Description

cutadapt

Usage

```
cutadapt
```

Format

An object of class `cwlParam` of length 1.

`cwlTools` *cwlTools*

Description

To generate a file cache object for CWL tools in the package.

Usage

```
cwlTools(cachePath = "Rcwl", ...)
```

Arguments

`cachePath`	The cache path of the BiocFileCache object.
`...`	options from ‘bfcadd‘.

Value

A BiocFileCache object for existing CWL tools.

Examples

```
tools <- cwlTools()
```

`DepthOfCoverage` *Picard DepthOfCoverage*

Description

Picard DepthOfCoverage

Usage

```
DepthOfCoverage
```

Format

An object of class `cwlParam` of length 1.

`fastqc` *fastqc*

Description

fastqc

Usage

```
fastqc
```

Format

An object of class `cwlParam` of length 1.

`featureCounts` *featureCounts*

Description

featureCounts

Usage

```
featureCounts
```

Format

An object of class `cwlParam` of length 1.

`FilterMutectCalls` *gatk FilterMutectCalls*

Description

gatk FilterMutectCalls

Usage

```
FilterMutectCalls
```

Format

An object of class `cwlParam` of length 1.

`FilterOBias` *gatk FilterByOrientationBias*

Description

gatk FilterByOrientationBias

Usage

```
FilterOBias
```

Format

An object of class `cwlParam` of length 1.

`Funcotator` *gatk Funcotator*

Description

gatk Funcotator

Usage

```
Funcotator
```

Format

An object of class `cwlParam` of length 1.

`GAlign` *GATK alignment pipeline*

Description

Workflows for processing high-throughput sequencing data for variant discovery with GATK4 and related tools. Two workflows from github, seq-format-conversion (last update: 7/13/2018) and gatk4-data-processing (last update: 8/1/2018) were cloned to the package.

Usage

```
GAlign
```

Format

A ‘cwlStepParam‘ object.

fq2ubam To covert fastq to ubam with read group information

align To run BWA alignment and BAM BaseRecalibration.

Source

https://github.com/gatk-workflows/seq-format-conversion

https://github.com/gatk-workflows/gatk4-data-processing

https://hubentu.github.io/others/Rcwl_GATK4.html

`geneBody_coverage` *geneBody_coverage.py*

Description

geneBody_coverage.py

Usage

```
geneBody_coverage
```

Format

An object of class `cwlParam` of length 1.

`genePredToBed` *genePredToBed*

Description

genePredToBed

Usage

```
genePredToBed
```

Format

An object of class `cwlParam` of length 1.

`GenomicsDB` *gatk GenomicsDBImport*

Description

gatk GenomicsDBImport

Usage

```
GenomicsDB
```

Format

An object of class `cwlParam` of length 1.

`GetPileupSummaries` *gatk GetPileupSummaries*

Description

gatk GetPileupSummaries

Usage

```
GetPileupSummaries
```

Format

An object of class `cwlParam` of length 1.

`GPoN` *GATK4: create a panel of normals*

Description

The Panel of Normals Workflow

Usage

```
GPoN
```

Format

A ‘cwlStepParam‘ object.

GPoN The best practice pipeline to create a panel of normals.

Source

https://software.broadinstitute.org/gatk/documentation/article?id=24057

`gtfToGenePred` *gtfToGenePred*

Description

gtfToGenePred

Usage

```
gtfToGenePred
```

Format

An object of class `cwlParam` of length 1.

`hapCall` *GATK haplotypecaller pipeline*

Description

The workflow runs HaplotypeCaller from GATK4 in GVCF mode on a single sample according to the GATK Best Practices (June 2016), scattered across intervals. The workflow from github, gatk4-germline-snps-indels (last update: 7/23/2018) was cloned to this package.

Usage

```
hapCall
```

Format

A ‘cwlStepParam‘ object.

HC HaplotypeCaller from GATK4

Source

https://github.com/gatk-workflows/gatk4-germline-snps-indels

https://hubentu.github.io/others/Rcwl_GATK4.html

`hisat2_align` *hisat2*

Description

hisat2

Usage

```
hisat2_align
```

Format

An object of class `cwlParam` of length 1.

`hisat2_build` *hisat2-build*

Description

hisat2-build

Usage

```
hisat2_build
```

Format

An object of class `cwlParam` of length 1.

`htseq` *htseq-count*

Description

htseq-count

Usage

```
htseq
```

Format

An object of class `cwlParam` of length 1.

`jdCall` *GATK joint discovery pipeline*

Description

The joint discovery and VQSR filtering portion of the GATK Best Practices (June 2016) for germline SNP and Indel discovery in human whole-genome sequencing (WGS) and exome sequencing data.

Usage

```
jdCall
```

Format

A ‘cwlStepParam‘ object.

JD variant joint genotyping

Source

https://github.com/gatk-workflows/gatk4-germline-snps-indels

https://hubentu.github.io/others/Rcwl_GATK4.html

`kallisto_index` *Kallisto index*

Description

Kallisto index

Usage

```
kallisto_index
```

Format

An object of class `cwlParam` of length 1.

`kallisto_quant` *Kallisto quant*

Description

Kallisto quant

Usage

```
kallisto_quant
```

Format

An object of class `cwlParam` of length 1.

`lancet` *lancet*

Description

lancet

Usage

```
lancet
```

Format

An object of class `cwlParam` of length 1.

`LoFreq` *LoFreq*

Description

LoFreq

Usage

```
LoFreq
```

Format

An object of class `cwlParam` of length 1.

`makeblastdb` *makeblastdb*

Description

makeblastdb

Usage

```
makeblastdb
```

Format

An object of class `cwlParam` of length 1.

`manta` *manta*

Description

manta

Usage

```
manta
```

Format

An object of class `cwlParam` of length 1.

`mantaStrelka` *strelka somatic caller*

Description

Strelka2 Somatic caller pipeline.

Usage

```
mantaStrelka
```

Format

A ‘cwlStepParam‘ object.

steps:

manta Call candidate small indels

strelka somatic calling by strelka2

Source

https://github.com/Illumina/strelka

`markdup` *picard MarkDuplicates*

Description

picard MarkDuplicates

Usage

```
markdup
```

Format

An object of class `cwlParam` of length 1.

`mergeBam` *picard MergeSamFiles*

Description

picard MergeSamFiles

Usage

```
mergeBam
```

Format

An object of class `cwlParam` of length 1.

`mergeBamDup` *mergeBamDup*

Description

merge Bam files and mark duplicates

Usage

```
mergeBamDup
```

Format

A ‘cwlStepParam‘ object.

mergeBam picard merge Bam files

markdup picard mark duplicated alignments

samtools_index index Bam by samtools index

samtools_flagstat samtools flagstat

`miRDeep2` *miRDeep2*

Description

miRDeep2

Usage

```
miRDeep2
```

Format

An object of class `cwlParam` of length 1.

`miRDeep2PL` *miRDeep2*

Description

miRDeep2

Usage

```
miRDeep2PL
```

Format

A ‘cwlStepParam‘ object.

steps:

miRMapper run mapple.pl

miRDeep2 run mirdeep2.pl

Source

https://github.com/rajewsky-lab/mirdeep2

`miRMapper` *miRDeep2 mapper*

Description

miRDeep2 mapper

Usage

```
miRMapper
```

Format

An object of class `cwlParam` of length 1.

`multiqc` *multiqc*

Description

multiqc

Usage

```
multiqc
```

Format

An object of class `cwlParam` of length 1.

`MuSE` *MuSE*

Description

MuSE

Usage

```
MuSE
```

Format

An object of class `cwlParam` of length 1.

`Mutect2` *gatk Mutect2*

Description

gatk Mutect2

Usage

```
Mutect2
```

Format

An object of class `cwlParam` of length 1.

`Mutect2PL` *GATK4: Mutect2*

Description

Somatic short variant discovery (SNVs + Indels)

Usage

```
Mutect2PL
```

Format

A ‘cwlStepParam‘ object.

Mutect2PL The best practice pipeline to Identify somatic short variants (SNVs and Indels).

Source

`https://software.broadinstitute.org/gatk/best-practices/workflow?id=11146`

`mvOut` *Rscript: mvOut*

Description

Rscript: mvOut

Usage

```
mvOut
```

Format

An object of class `cwlParam` of length 1.

`neusomatic` *neusomatic caller*

Description

neusomatic caller pipeline with ensemble mode.

Usage

```
neusomatic
```

Format

A ‘cwlStepParam‘ object.

steps:

preprocess Preprocess step in call mode

call Call variants

postprocess Postprocess step (resolve long INDEL sequences, report vcf)

Source

https://github.com/bioinform/neusomatic

`phaseVcf` *phase VCF*

Description

phase VCF

Usage

```
phaseVcf
```

Format

A ‘cwlStepParam‘ object.

steps:

CombineVariants combine germline and somatic variant

ReadBackedPhasing Phasing using GATK ReadBackedPhasing

Source

https://pvactools.readthedocs.io/en/latest/pvacseq/input_file_prep/proximal_vcf.html

`polysolver` *polysolver*

Description

polysolver

Usage

```
polysolver
```

Format

An object of class `cwlParam` of length 1.

`PoN` *gatk CreateSomaticPanelOfNormals*

Description

gatk CreateSomaticPanelOfNormals

Usage

```
PoN
```

Format

An object of class `cwlParam` of length 1.

`pvacseq` *pvacseq*

Description

pvacseq

Usage

```
pvacseq
```

Format

An object of class `cwlParam` of length 1.

`RcwlPipelines` *RcwlPipelines*

Description

A package for a collection of Rcwl pipelines. Currently four pipeplines have been collected in the package.

Details

rnaseq_Sf, **multiqc**: RNASeq alignment, QC and quantification pipeline

alignMerge: DNASeq alignment

GAlign, **hapCall**, **jdCall**: GATK4 pipeline for Germline calling

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`ReadBackedPhasing` *ReadBackedPhasing*

Description

ReadBackedPhasing

Usage

```
ReadBackedPhasing
```

Format

An object of class `cwlParam` of length 1.

`read_distribution` *read_distribution.py*

Description

read_distribution.py

Usage

```
read_distribution
```

Format

An object of class `cwlParam` of length 1.

`RenameSampleInVcf` *Picard RenameSampleInVcf*

Description

Picard RenameSampleInVcf

Usage

```
RenameSampleInVcf
```

Format

An object of class `cwlParam` of length 1.

`rnaseq_Sf` *RNASeq pipeline with STAR and featureCounts*

Description

RNASeq pipeline by STAR and featureCounts.

Usage

```
rnaseq_Sf
```

Format

A ‘cwlStepParam‘ object.

An RNASeq alignment and quantification pipeline built by ‘Rcwl‘, which contains steps:

fastqc The reads QC step by fastQC

STAR The alignment step by STAR

samtools_index Index bam file by samtools

samtools_flagstat Flag stat by samtools

featureCounts Gene level quantification by featureCounts

RSeQC QC for RNASeq alignments by RSeQC

Source

https://hubentu.github.io/others/Rcwl_RNASeq.html

`RSeQC` *RNASeq quality control by RSeQC*

Description

RNASeq pipeline by STAR and featureCounts.

Usage

```
RSeQC
```

Format

A ‘cwlStepParam‘ object.

An RNASeq QC pipeline by RSeQC which contains steps:

gtfToGenePred GTF to GenePred format

genePredToBed GenePred format to Bed format

read_distribution Reads distribution over genome feature

geneBody_coverage Reads coverage over gene body

Source

http://rseqc.sourceforge.net/

`runWDL` *java: runWDL*

Description

java: runWDL

Usage

```
runWDL
```

Format

An object of class `cwlParam` of length 1.

`salmon_index` *salmon index*

Description

salmon index

Usage

```
salmon_index
```

Format

An object of class `cwlParam` of length 1.

`salmon_quant` *salmon quant*

Description

salmon quant

Usage

```
salmon_quant
```

Format

An object of class `cwlParam` of length 1.

`sam2bam` *samtools view*

Description

samtools view

Usage

```
sam2bam
```

Format

An object of class `cwlParam` of length 1.

`SamToFastq` *picard SamToFastq*

Description

picard SamToFastq

Usage

```
SamToFastq
```

Format

An object of class `cwlParam` of length 1.

`samtools_flagstat` *samtools flagstat*

Description

samtools flagstat

Usage

```
samtools_flagstat
```

Format

An object of class `cwlParam` of length 1.

`samtools_index` *samtools index*

Description

samtools index

Usage

```
samtools_index
```

Format

An object of class `cwlParam` of length 1.

`samtools_mpileup` *samtools_mpileup*

Description

samtools_mpileup

Usage

```
samtools_mpileup
```

Format

An object of class `cwlParam` of length 1.

`SomaticCallers` *Combined Somatic Mutation Callers*

Description

Combined caller pipelines with neosomatic ensemble mode.

Usage

```
SomaticCallers
```

Format

A ‘cwlStepParam‘ object.

steps:

Mutect2PL mutect2 pipeline

MuSE MuSE

manta strelka2 strelka2 with manta

SomaticSniper SomaticSniper

VarDict VarDict

LoFreq LoFreq

VarScan2 VarScan2 pipeline

neusomatic neusomatic ensemble mode

Source

https://github.com/bioinform/neusomatic

`SomaticSniper` *SomaticSniper*

Description

SomaticSniper

Usage

```
SomaticSniper
```

Format

An object of class `cwlParam` of length 1.

`sortBam` *samtools sort*

Description

samtools sort

Usage

```
sortBam
```

Format

An object of class `cwlParam` of length 1.

`SortVcf` *Picard SortVcf*

Description

Picard SortVcf

Usage

```
SortVcf
```

Format

An object of class `cwlParam` of length 1.

`STAR` *STAR*

Description

STAR

Usage

```
STAR
```

Format

An object of class `cwlParam` of length 1.

`starFusion` *STAR-Fusion*

Description

STAR-Fusion

Usage

```
starFusion
```

Format

An object of class `cwlParam` of length 1.

`strelka` *strelka*

Description

strelka

Usage

```
strelka
```

Format

An object of class `cwlParam` of length 1.

`tabix_index` *tabix index*

Description

tabix index

tabix_index

Usage

```
tabix_index

tabix_index
```

Format

An object of class `cwlParam` of length 1.

`VarDict` *VarDict*

Description

VarDict

VarDict

Usage

```
VarDict

VarDict
```

Format

An object of class `cwlParam` of length 1.

`VarScan2Somatic` *VarScan2 somatic caller*

Description

VarScan2 Somatic caller pipeline.

Usage

```
VarScan2Somatic
```

Format

A ‘cwlStepParam‘ object.

VarScan2 Somatic caller pipeline, which contains steps:

mpileup mpileup by samtools

somatic somatic calling by VarScan2 somatic

processSomatic processSomatic by VarScan2

somaticFilter Filter by VarScan2

Source

http://varscan.sourceforge.net

`VarScan2_processSomatic`
VarScan2_processSomatic

Description

VarScan2_processSomatic

Usage

```
VarScan2_processSomatic
```

Format

An object of class `cwlParam` of length 1.

`VarScan2_somatic` *VarScan2_somatic*

Description

VarScan2_somatic

Usage

```
VarScan2_somatic
```

Format

An object of class `cwlParam` of length 1.

`VarScan2_somaticFilter` *VarScan2_somaticFilter*

Description

VarScan2_somaticFilter

Usage

```
VarScan2_somaticFilter
```

Format

An object of class `cwlParam` of length 1.

`vcfCoverage` *vcfCoverage*

Description

vcfCoverage

Usage

```
vcfCoverage
```

Format

A ‘cwlStepParam‘ object.

steps:

decompose vt decompose

readcount bam-readcount

readcount_annotator_snv add snv counts

readcount_annotator_indel add indel counts

Source

https://pvactools.readthedocs.io/en/latest/pvacseq/input_file_prep/readcounts.html

---

`vcfExpression` *vcfExpression*

Description

vcfExpression

Usage

```
vcfExpression
```

Format

A ‘cwlStepParam‘ object.

steps:

kallistoQuant transcript quantification using kallisto quant

cleanExp R function to clean results from kallisto

vcf_expression_annotator add expression to vcf

Source

https://pvactools.readthedocs.io/en/latest/pvacseq/input_file_prep/expression.html

---

`vcf_expression_annotator` *vcf_expression_annotator*

Description

vcf_expression_annotator

Usage

```
vcf_expression_annotator
```

Format

An object of class `cwlParam` of length 1.

`vcf_readcount_annotator` *vcf_readcount_annotator*

Description

vcf_readcount_annotator

Usage

```
vcf_readcount_annotator
```

Format

An object of class `cwlParam` of length 1.

`vep` *vep*

Description

vep

Usage

```
vep
```

Format

An object of class `cwlParam` of length 1.

`vt_decompose` *vt decompose*

Description

vt decompose

Usage

```
vt_decompose
```

Format

An object of class `cwlParam` of length 1.

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