

Package ‘RcwlPipelines’

November 21, 2019

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

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alignMerge	<i>DNaseq alignment, merge and markduplicates</i>
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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	<i>annovar</i>
---------	----------------

Description

annovar

Usage

annovar

Format

An object of class `cwlParam` of length 1.

AnnPhaseVcf	<i>AnnPhaseVcf</i>
-------------	--------------------

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

bam_readcount	<i>bam_readcount</i>
---------------	----------------------

Description

bam_readcount

Usage

bam_readcount

Format

An object of class `cwlParam` of length 1.

BaseRecal	<i>Base quality recalibration</i>
-----------	-----------------------------------

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	<i>bcftools view</i>
---------	----------------------

Description

bcftools view

Usage

bcfview

Format

An object of class cwlParam of length 1.

BedToIntervalList	<i>Picard BedToIntervalList</i>
-------------------	---------------------------------

Description

Picard BedToIntervalList

Usage

BedToIntervalList

Format

An object of class cwlParam of length 1.

bgzip	<i>bgzip</i>
-------	--------------

Description

bgzip

bgzip

Usage

bgzip

bgzip

Format

An object of class cwlParam of length 1.

blastn	<i>blastn</i>
--------	---------------

Description

blastn

Usage

blastn

Format

An object of class `awlParam` of length 1.

bowtie2	<i>bowtie2</i>
---------	----------------

Description

bowtie2

Usage

bowtie2

Format

An object of class `awlParam` of length 1.

bowtie2_build	<i>bowtie2-build</i>
---------------	----------------------

Description

bowtie2-build

Usage

bowtie2_build

Format

An object of class `awlParam` of length 1.

bowtie_build	<i>bowtie-build</i>
--------------	---------------------

Description

bowtie-build

Usage

bowtie_build

Format

An object of class `cwlParam` of length 1.

bwa	<i>bwa mem</i>
-----	----------------

Description

bwa mem

Usage

bwa

Format

An object of class `cwlParam` of length 1.

bwaAlign	<i>bwaAlign</i>
----------	-----------------

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	<i>gatk CollectSequencingArtifactMetrics</i>
----------------	--

Description

gatk CollectSequencingArtifactMetrics

Usage

ColSeqArtifact

Format

An object of class `cwlParam` of length 1.

CombineVariants	<i>CombineVariants</i>
-----------------	------------------------

Description

CombineVariants

Usage

CombineVariants

Format

An object of class `cwlParam` of length 1.

cutadapt	<i>cutadapt</i>
----------	-----------------

Description

cutadapt

Usage

cutadapt

Format

An object of class `cwlParam` of length 1.

cwlTools	<i>cwlTools</i>
----------	-----------------

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	<i>Picard DepthOfCoverage</i>
-----------------	-------------------------------

Description

Picard DepthOfCoverage

Usage

```
DepthOfCoverage
```

Format

An object of class cwlParam of length 1.

fastqc	<i>fastqc</i>
--------	---------------

Description

fastqc

Usage

fastqc

Format

An object of class `cwlParam` of length 1.

featureCounts	<i>featureCounts</i>
---------------	----------------------

Description

featureCounts

Usage

featureCounts

Format

An object of class `cwlParam` of length 1.

FilterMutectCalls	<i>gatk FilterMutectCalls</i>
-------------------	-------------------------------

Description

gatk FilterMutectCalls

Usage

FilterMutectCalls

Format

An object of class `cwlParam` of length 1.

FilterOBias	<i>gatk FilterByOrientationBias</i>
-------------	-------------------------------------

Description

gatk FilterByOrientationBias

Usage

FilterOBias

Format

An object of class cwlParam of length 1.

Funcotator	<i>gatk Funcotator</i>
------------	------------------------

Description

gatk Funcotator

Usage

Funcotator

Format

An object of class cwlParam of length 1.

GAlign	<i>GATK alignment pipeline</i>
--------	--------------------------------

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	<i>GATK haplotypcaller pipeline</i>
---------	-------------------------------------

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	<i>hisat2</i>
--------------	---------------

Description

```
hisat2
```

Usage

```
hisat2_align
```

Format

An object of class cwlParam of length 1.

hisat2_build	<i>hisat2-build</i>
--------------	---------------------

Description

hisat2-build

Usage

hisat2_build

FormatAn object of class `cwlParam` of length 1.

htseq	<i>htseq-count</i>
-------	--------------------

Description

htseq-count

Usage

htseq

FormatAn object of class `cwlParam` of length 1.

jdCall	<i>GATK joint discovery pipeline</i>
--------	--------------------------------------

Description

The joint discovery and VQS 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

FormatA `'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	<i>Kallisto index</i>
----------------	-----------------------

Description

Kallisto index

Usage

kallisto_index

Format

An object of class `cwlParam` of length 1.

kallisto_quant	<i>Kallisto quant</i>
----------------	-----------------------

Description

Kallisto quant

Usage

kallisto_quant

Format

An object of class `cwlParam` of length 1.

lancet	<i>lancet</i>
--------	---------------

Description

lancet

Usage

lancet

Format

An object of class `cwlParam` of length 1.

LoFreq	<i>LoFreq</i>
--------	---------------

Description

LoFreq

Usage

LoFreq

FormatAn object of class `cwlParam` of length 1.

makeblastdb	<i>makeblastdb</i>
-------------	--------------------

Description

makeblastdb

Usage

makeblastdb

FormatAn object of class `cwlParam` of length 1.

manta	<i>manta</i>
-------	--------------

Description

manta

Usage

manta

FormatAn object of class `cwlParam` of length 1.

mantaStrelka	<i>strelka somatic caller</i>
--------------	-------------------------------

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	<i>picard MarkDuplicates</i>
---------	------------------------------

Description

picard MarkDuplicates

Usage

markdup

Format

An object of class cwlParam of length 1.

mergeBam	<i>picard MergeSamFiles</i>
----------	-----------------------------

Description

picard MergeSamFiles

Usage

mergeBam

Format

An object of class cwlParam of length 1.

mergeBamDup	<i>mergeBamDup</i>
-------------	--------------------

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	<i>miRDeep2</i>
----------	-----------------

Description

miRDeep2

Usage

miRDeep2

Format

An object of class cwlParam of length 1.

miRDeep2PL	<i>miRDeep2</i>
------------	-----------------

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	<i>miRDeep2 mapper</i>
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Description

miRDeep2 mapper

Usage

miRMapper

Format

An object of class cwlParam of length 1.

multiqc	<i>multiqc</i>
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Description

multiqc

Usage

multiqc

Format

An object of class cwlParam of length 1.

MuSE	<i>MuSE</i>
------	-------------

Description

MuSE

Usage

MuSE

Format

An object of class `cwlParam` of length 1.

Mutect2	<i>gatk Mutect2</i>
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Description

`gatk Mutect2`

Usage

Mutect2

Format

An object of class `cwlParam` of length 1.

Mutect2PL	<i>GATK4: Mutect2</i>
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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

FormatAn object of class `cwlParam` of length 1.

neusomatic

neusomatic caller

Description

neusomatic caller pipeline with ensemble mode.

Usage

neusomatic

FormatA ‘`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	<i>gatk CreateSomaticPanelOfNormals</i>
-----	---

Description

`gatk CreateSomaticPanelOfNormals`

Usage

PoN

Format

An object of class `cwlParam` of length 1.

<code>pvacseq</code>	<i>pvacseq</i>
----------------------	----------------

Description

`pvacseq`

Usage

`pvacseq`

Format

An object of class `cwlParam` of length 1.

RcwlPipelines	<i>RcwlPipelines</i>
---------------	----------------------

Description

A package for a collection of Rcwl pipelines. Currently four pipelines 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

ReadBackedPhasing	<i>ReadBackedPhasing</i>
-------------------	--------------------------

Description

ReadBackedPhasing

Usage

ReadBackedPhasing

Format

An object of class `cwlParam` of length 1.

read_distribution	<i>read_distribution.py</i>
-------------------	-----------------------------

Description

read_distribution.py

Usage

read_distribution

Format

An object of class `cwlParam` of length 1.

RenameSampleInVcf	<i>Picard RenameSampleInVcf</i>
-------------------	---------------------------------

Description

Picard RenameSampleInVcf

Usage

RenameSampleInVcf

Format

An object of class `cwlParam` of length 1.

rnaseq_Sf	<i>RNASeq pipeline with STAR and featureCounts</i>
-----------	--

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	<i>RNASeq quality control by RSeQC</i>
-------	--

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	<i>java: runWDL</i>
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Description

java: runWDL

Usage

runWDL

Format

An object of class `awlParam` of length 1.

salmon_index	<i>salmon index</i>
--------------	---------------------

Description

salmon index

Usage

salmon_index

Format

An object of class `awlParam` of length 1.

salmon_quant	<i>salmon quant</i>
--------------	---------------------

Description

salmon quant

Usage

salmon_quant

Format

An object of class `awlParam` of length 1.

sam2bam	<i>samtools view</i>
---------	----------------------

Description

samtools view

Usage

sam2bam

Format

An object of class `cwlParam` of length 1.

SamToFastq	<i>picard SamToFastq</i>
------------	--------------------------

Description

picard SamToFastq

Usage

SamToFastq

Format

An object of class `cwlParam` of length 1.

samtools_flagstat	<i>samtools flagstat</i>
-------------------	--------------------------

Description

samtools flagstat

Usage

samtools_flagstat

Format

An object of class `cwlParam` of length 1.

samtools_index	<i>samtools index</i>
----------------	-----------------------

Description

samtools index

Usage

samtools_index

Format

An object of class `cwlParam` of length 1.

samtools_mpileup	<i>samtools_mpileup</i>
------------------	-------------------------

Description

samtools_mpileup

Usage

samtools_mpileup

Format

An object of class `cwlParam` of length 1.

SomaticCallers	<i>Combined Somatic Mutation Callers</i>
----------------	--

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	<i>SomaticSniper</i>
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Description

SomaticSniper

Usage

SomaticSniper

Format

An object of class cwlParam of length 1.

sortBam	<i>samtools sort</i>
---------	----------------------

Description

samtools sort

Usage

sortBam

Format

An object of class cwlParam of length 1.

SortVcf	<i>Picard SortVcf</i>
---------	-----------------------

Description

Picard SortVcf

Usage

SortVcf

Format

An object of class `cwlParam` of length 1.

STAR	<i>STAR</i>
------	-------------

Description

STAR

Usage

STAR

Format

An object of class `cwlParam` of length 1.

starFusion	<i>STAR-Fusion</i>
------------	--------------------

Description

STAR-Fusion

Usage

starFusion

Format

An object of class `cwlParam` of length 1.

strelka	<i>strelka</i>
---------	----------------

Description

strelka

Usage

strelka

Format

An object of class `cwlParam` of length 1.

tabix_index	<i>tabix index</i>
-------------	--------------------

Description

tabix index

tabix_index

Usage

tabix_index

tabix_index

Format

An object of class `cwlParam` of length 1.

VarDict	<i>VarDict</i>
---------	----------------

Description

VarDict

VarDict

Usage

VarDict

VarDict

Format

An object of class `cwlParam` of length 1.

VarScan2Somatic	<i>VarScan2 somatic caller</i>
-----------------	--------------------------------

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	<i>VarScan2_processSomatic</i>
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Description

VarScan2_processSomatic

Usage

VarScan2_processSomatic

Format

An object of class cwlParam of length 1.

VarScan2_somatic	<i>VarScan2_somatic</i>
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Description

VarScan2_somatic

Usage

VarScan2_somatic

Format

An object of class cwlParam of length 1.

VarScan2_somaticFilter	<i>VarScan2_somaticFilter</i>
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Description

VarScan2_somaticFilter

Usage

VarScan2_somaticFilter

Format

An object of class cwlParam of length 1.

vcfCoverage	<i>vcfCoverage</i>
-------------	--------------------

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	<i>vcfExpression</i>
---------------	----------------------

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	<i>vcf_expression_annotator</i>
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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 `ctlParam` of length 1.

vep *vep*

Description

vep

Usage

vep

Format

An object of class `ctlParam` of length 1.

vt_decompose *vt_decompose*

Description

vt_decompose

Usage

vt_decompose

Format

An object of class `ctlParam` of length 1.

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