

Package ‘RcwlPipelines’

October 16, 2019

Title Bioinformatics pipelines based on Rcwl

Version 1.0.11

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

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_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_bcfview.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_VarScan2_somaticFilter.R' 'tl_VarScan2_processSomatic.R' 'tl_VarScan2_somatic.R' 'tl_samtools_mpileup.R' 'pl_VarScan2Somatic.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_strelka.R' 'tl_manta.R' 'pl_mantaStrelka.R' 'tl_neusomatic_postprocess.R' 'tl_neusomatic_call.R' 'tl_neusomatic_preprocess.R' 'pl_neusomatic.R' 'tl_featureCounts.R' 'tl_STAR.R' 'tl_fastqc.R' 'pl_rnaseq_Sf.R' 'tl_Funcotator.R' 'tl_LoFreq.R' 'tl_MuSE.R' 'tl_SomaticSniper.R' 'tl_VarDict.R' 'tl_VarScan2.R' 'tl_bgzip.R' 'tl_blastn.R' 'tl_bowtie2.R' 'tl_bowtie2_build.R'

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 'tl_salmon_index.R' 'tl_salmon_quant.R' 'tl_starFusion.R'
 'tl_tabix_index.R'

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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

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.

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

Description

bgzip

bgzip

Usage

bgzip

bgzip

FormatAn object of class `cwlParam` of length 1.

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

Description

blastn

Usage

blastn

FormatAn object of class `cwlParam` of length 1.

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

Description

bowtie2

Usage

bowtie2

FormatAn object of class `cwlParam` of length 1.

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

Description

bowtie2-build

Usage

bowtie2_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.

ColSeqArtifact

gatk CollectSequencingArtifactMetrics

Description

gatk CollectSequencingArtifactMetrics

Usage

ColSeqArtifact

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()
```

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

Description

fastqc

Usage

fastqc

FormatAn object of class `cwlParam` of length 1.

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

Description

featureCounts

Usage

featureCounts

FormatAn object of class `cwlParam` of length 1.

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

Description

gatk FilterMutectCalls

Usage

FilterMutectCalls

FormatAn 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	<i>geneBody_coverage.py</i>
-------------------	-----------------------------

Description

geneBody_coverage.py

Usage

geneBody_coverage

Format

An object of class `cwlParam` of length 1.

genePredToBed	<i>genePredToBed</i>
---------------	----------------------

Description

genePredToBed

Usage

genePredToBed

Format

An object of class `cwlParam` of length 1.

GenomicsDB	<i>gatk GenomicsDBImport</i>
------------	------------------------------

Description

gatk GenomicsDBImport

Usage

GenomicsDB

Format

An object of class `cwlParam` of length 1.

GetPileupSummaries	<i>gatk GetPileupSummaries</i>
--------------------	--------------------------------

Description

gatk GetPileupSummaries

Usage

GetPileupSummaries

Format

An object of class `cwlParam` of length 1.

GPoN	<i>GATK4: create a panel of normals</i>
------	---

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	<i>gtfToGenePred</i>
---------------	----------------------

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

lancet *lancet*

Description

lancet

Usage

lancet

Format

An object of class `awlParam` of length 1.

LoFreq *LoFreq*

Description

LoFreq

Usage

LoFreq

Format

An object of class `awlParam` of length 1.

makeblastdb *makeblastdb*

Description

makeblastdb

Usage

makeblastdb

Format

An object of class `awlParam` of length 1.

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

Description

manta

manta

Usage

manta

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

multiqc	<i>multiqc</i>
---------	----------------

Description

multiqc

Usage

multiqc

FormatAn object of class `awlParam` of length 1.

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

Description

MuSE

MuSE

Usage

MuSE

MuSE

FormatAn object of class `awlParam` of length 1.

Mutect2	<i>gatk Mutect2</i>
---------	---------------------

Description

gatk Mutect2

Usage

Mutect2

FormatAn object of class `awlParam` 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	<i>neusomatic caller</i>
------------	--------------------------

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>

polysolver	<i>polysolver</i>
------------	-------------------

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.

RcwlPipelines	<i>RcwlPipelines</i>
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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

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

Description

read_distribution.py

Usage

read_distribution

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>
--------	---------------------

Description

java: runWDL

Usage

runWDL

Format

An object of class `awlParam` of length 1.

salmon_index	<i>salmon index</i>
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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>
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Description

samtools view

Usage

sam2bam

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.

SomaticSniper	<i>SomaticSniper</i>
---------------	----------------------

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.

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

Description

STAR

Usage

STAR

Format

An object of class cw1Param of length 1.

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

Description

STAR-Fusion

Usage

starFusion

Format

An object of class cw1Param of length 1.

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

Description

strelka

strelka

Usage

strelka

strelka

Format

An object of class cw1Param of length 1.

tabix_index	<i>tabix index</i>
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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 *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.

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