

API Documentation

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Contents

Contents	1
1 Script script-iReportMaker	2
1.1 Functions	2
1.2 Variables	3
2 Script script-iVARCall	4
2.1 Functions	4
2.2 Variables	5
3 Script script-iVCFmaker_SNP	6
3.1 Functions	6
3.2 Variables	6
4 Script script-iVCFmerge_SNP	7
4.1 Functions	7
4.2 Variables	7

1 Script script-iReportMaker

Make a PDF report from the log file generated by the VarCall workflow.

1.1 Functions

get_parser()

Parse arguments

Return Value

arguments list

(*type=parser object*)

texHeader(texFile)

Write the header of the LaTeX output file

Parameters

texFile: path of the output LaTeX file

(*type=string*)

writeVarCallCommand(lines, texFile)

Write the VarCall command in the LaTeX output file

Parameters

lines: lines of the log file

(*type=list*)

texFile: path of the output LaTeX file

(*type=string*)

extractReadStatistics(lines)

Extract reads statistics from the log file lines.

Parameters

lines: lines of the log file

(*type=list*)

Return Value

dictionnary with sample name in key and for value an other dictionnary with the number of reads before and after trimming, the number of reads mapped and properly paired, and the deep and breadth coverage.

(*type=dictionnary*)

workdir()

Find working directory and transformed it for write in latex file

Return Value

working directory transformed

(type=string)

version()

Find all version of all tools used by VarCall

Return Value

dictionnary with program name as key and version as value.

(type=dictionnary)

main()**1.2 Variables**

Name	Description
<code>--doc--</code>	Value: ...
<code>--package--</code>	Value: None

2 Script script-iVARCall

Do the SNP calling from several FASTQ files

Requires:

- BWA
- samtools
- picard-tools
- Trimmomatic
- GATK
- SnpSift
- BAMmaker, iVCFmaker_SNP, iVCFmerge_SNP, VCFfilter, VCFtoMATRIX and VCFto-FASTA in \$PATH

Paired-end reads must be named as "prefix_R1.XXXX" and "prefix_R2.XXXX". Example : E1_R1.fq and E1_R2.fq

2.1 Functions

get_parser()

Parse arguments

Return Value

arguments list

(*type=parser object*)

checkPE(*readsList*)

checks all paired-end reads and reordering them

Parameters

readsList: list of reads given by the argument parser

(*type=list*)

Return Value

read list

(*type=list*)

checkFiles(*fileList*)

Check if all file of a list exist

Parameters

fileList: list file pathway

(*type=list*)

commandLaunched (<i>Arguments</i> , <i>logFile</i>)
Print VarCall command in log file
Parameters
Arguments: list of arguments (<i>type=parser object</i>)
logFile: log file (<i>type=string</i>)

main ()

2.2 Variables

Name	Description
__doc__	Value: ...
__package__	Value: None
accept2dyear	Value: 1
altzone	Value: -7200
daylight	Value: 1
timezone	Value: -3600
tzname	Value: ('CET', 'CEST')

3 Script *script-iVCFmaker_SNP*

Requires: GATK

3.1 Functions

get_parser()

Parse arguments

Return Value

arguments list

(*type=parser object*)

exec_commands(*cmds, nbThreads*)

Exec commands in parallel in multiple process (as much as we have CPU)

@param *cmds*: list of commands

@type *cmds*: list

@param *nbThreads*: number of threads to use

@type *nbThreads*: integer

main()

3.2 Variables

Name	Description
<code>--doc--</code>	Value: ...
<code>--package--</code>	Value: None

4 Script script-iVCFmerge_SNP

Requires:

- bgzip
- tabix
- merge-vcf

4.1 Functions

get_parser()

Parse arguments

Return Value

arguments list

(*type=parser object*)

exec_commands(*cmds, nbThreads*)

Exec commands in parallel in multiple process (as much as we have CPU)

@param *cmds*: list of commands

@type *cmds*: list

@param *nbThreads*: number of threads to use

@type *nbThreads*: integer

main()

4.2 Variables

Name	Description
<code>__doc__</code>	Value: ...
<code>__package__</code>	Value: None

Index

- script-iReportMaker (*script*), 2–3
 - script-iReportMaker.extractReadStatistics (*function*), 2
 - script-iReportMaker.get_parser (*function*), 2
 - script-iReportMaker.main (*function*), 3
 - script-iReportMaker.texHeader (*function*), 2
 - script-iReportMaker.version (*function*), 3
 - script-iReportMaker.workdir (*function*), 2
 - script-iReportMaker.writeVarCallCommand (*function*), 2
- script-iVARCall (*script*), 4–5
 - script-iVARCall.checkFiles (*function*), 4
 - script-iVARCall.checkPE (*function*), 4
 - script-iVARCall.commandLaunched (*function*), 4
 - script-iVARCall.get_parser (*function*), 4
 - script-iVARCall.main (*function*), 5
- script-iVCFmaker_SNP (*script*), 6
 - script-iVCFmaker_SNP.exec_commands (*function*), 6
 - script-iVCFmaker_SNP.get_parser (*function*), 6
 - script-iVCFmaker_SNP.main (*function*), 6
- script-iVCFmerge_SNP (*script*), 7
 - script-iVCFmerge_SNP.exec_commands (*function*), 7
 - script-iVCFmerge_SNP.get_parser (*function*), 7
 - script-iVCFmerge_SNP.main (*function*), 7