



collectmultiplemetrics

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Run a GPU-accelerated version of GATK's CollectMultipleMetrics.

This tool applies an accelerated version of the GATK CollectMultipleMetrics for assessing BAM file metrics such as alignment success, quality score distributions, GC bias, and sequencing artifacts. This functions as a 'meta-metrics' tool that can run any combination of the available metrics tools in GATK to perform an overall assessment of how well a sequencing run has been performed. The available metrics tools (PROGRAMs) can be found in the reference section below.

Quick Start

```
# This command assumes all the inputs are in INPUT_DIR and all the outputs go to OUTPUT_DIR. docker run --rm --gpus all --volume INPUT_DIR:/workdir --volume OUTPUT_DIR:/outputdir \ --workdir /workdir \ nvc.io/nvidia/clara/clara-parabricks:4.3.1-1 \ pbrun collectmultiplemetrics \ --ref /workdir/${REFERENCE_FILE} \ --bam /workdir/${INPUT_BAM} \ --out-qc-metrics-dir /outputdir/${OUTPUT_DIR} \ --gen-all-metrics
```

Compatible GATK4 Command

The command below is the GATK4 counterpart of the Parabricks command above. The output from this command will be identical to the output from the above command.

```
$ gatk CollectMultipleMetrics \ --REFERENCE_SEQUENCE <INPUT_DIR>/${REFERENCE_FILE} \ -I <INPUT_DIR>/${INPUT_BAM} \ -O <OUTPUT_DIR>/${OUTPUT_DIR} \ --PROGRAM CollectAlignmentSummaryMetrics \ --PROGRAM CollectInsertSizeMetrics \ --PROGRAM QualityScoreDistribution \ --PROGRAM MeanQualityByCycle \ --PROGRAM CollectBaseDistributionByCycle \ --PROGRAM CollectGcBiasMetrics \ --PROGRAM CollectSequencingArtifactMetrics \ --PROGRAM CollectQualityYieldMetrics
```

collectmultiplemetrics Reference

Run collectmultiplemetrics on a BAM file to generate files for multiple classes of metrics.

Input/Output file options

--ref REF

Path to the reference file. (default: None)

Option is required.

--bam BAM

Path to the BAM file. (default: None)

Option is required.

--out-qc-metrics-dir OUT_QC_METRICS_DIR

Output Directory to store results of each analysis.

(default: None)

Option is required.

Tool Options:

--gen-all-metrics

Generate QC for every analysis. (default: None)

--gen-alignment

Generate QC for alignment summary metric. (default: None)

--gen-quality-score

Generate QC for quality score distribution metric. (default: None)

--gen-insert-size

Generate QC for insert size metric. (default: None)

--gen-mean-quality-by-cycle

Generate QC for mean quality by cycle metric. (default: None)

--gen-base-distribution-by-cycle

Generate QC for base distribution by cycle metric. (default: None)

--gen-gc-bias

Prefix name used to generate detail and summary files for gc bias metric. (default: None)

--gen-seq-artifact

Generate QC for sequencing artifact metric. (default: None)

--gen-quality-yield

Generate QC for quality yield metric. (default: None)

Performance Options:

--bam-decompressor-threads BAM_DECOMPRESSOR_THREADS

Number of threads for BAM decompression. (default: 3)

Common options:

--logfile LOGFILE

Path to the log file. If not specified, messages will only be written to the standard error output. (default: None)

--tmp-dir TMP_DIR

Full path to the directory where temporary files will be stored.

--with-petogene-dir WITH_PETAGENE_DIR

Full path to the PetaGene installation directory. By default, this should have been installed at /opt/petogene. Use of this option also requires that the PetaLink library has been preloaded by setting the LD_PRELOAD environment variable. Optionally set the PETASUITE_REFPATH and PGCLOUD_CREDPATH environment variables that are used for data and credentials (default: None)

--keep-tmp

Do not delete the directory storing temporary files after completion.

--no-seccomp-override

Do not override seccomp options for docker (default: None).

--version

View compatible software versions.

GPU options:

--num-gpus NUM_GPUS

Number of GPUs to use for a run. GPUs 0..(NUM_GPUS-1) will be used.

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