starfusion

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Identifies candidate fusion transcripts.

This tool performs fusion calling for RNA-Seq samples, utilizing the STAR-Fusion algorithm. This requires input of a genome resource library, in accordance with the original STAR-Fusion tool, and outputs candidate fusion transcripts.

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 \ nvcr.io/nvidia/clara/clara-
parabricks:4.3.1-1 \ pbrun starfusion \ --chimeric-junction
/workdir/${CHIMERIC_JUNCTION_INPUT} \ --genome-lib-dir
/workdir/${PATH_TO_GENOME_LIBRARY}/ \ --output-dir
/outputdir/${PATH_TO_OUTPUT_DIRECTORY}/
```

Compatible CPU Command

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

```
$ ./STAR-Fusion \ --chimeric_junction <INPUT_DIR>/${CHIMERIC_JUNCTION_INPUT} \
--genome_lib_dir <INPUT_DIR>/${PATH_TO_GENOME_LIBRARY} \ --output_dir
<OUTPUT_DIR>/${PATH_TO_OUTPUT_DIRECTORY}
```

starfusion Reference

Identify candidate fusion transcripts supported by Illumina reads.

Input/Output file options

--chimeric-junction CHIMERIC_JUNCTION

Path to the Chimeric.out.junction file produced by STAR. (default: None)

Option is required.

--genome-lib-dir GENOME_LIB_DIR

Path to a genome resource library directory. For more information, visit https://github.com/STAR-Fusion/STAR-Fusion/wiki/installing-star-fusion#data-resources-required. (default: None)

Option is required.

--output-dir OUTPUT_DIR

Path to the directory that will contain all of the generated files. (default: None)

Option is required.

Tool Options:

--out-prefix OUT_PREFIX

Prefix filename for output data. (default: None)

Performance Options:

--num-threads NUM_THREADS

Number of threads for worker. (default: 4)

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-petagene-dir WITH_PETAGENE_DIR

Full path to the PetaGene installation directory. By default, this should have been installed at /opt/petagene. 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.