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P0469: TOGGLE-3: A Framework to Build Quickly Pipelines and to Perform Large-Scale NGS Analysis

POSTER

Dear biologist, have you ever dreamed of using the whole power of those numerous NGS tools that your bioinformatician colleagues uses through this awful list of command lines ?

Dear bioinformatician, have you ever wished for a really quick way of designing a new NGS pipeline without having to retype again dozens of code lines to readapt your scripts or starting from scratch ?

So, be happy ! TOGGLE is for you !

With TOGGLE (TOolbox for Generic nGs anaLysEs), you can create your own pipeline through an easy and user-friendly approach. Indeed, TOGGLE integrate a large set of NGS softwares and utilities to easily design pipelines able to handle hundreds of samples. The pipelines can start from Fastq (plain or compressed), SAM, BAM or VCF (plain or compressed) files, with parallel (by sample) and global analyses (by multi samples). Moreover, TOGGLE offers an easy way to configure your pipeline with a single configuration file:

- Organizing the different steps of workflow,
- Setting the parameters for the different softwares,
- Managing storage space through compressing/deleting intermediate data,
- Determining the way the jobs are managed (serial or parallel jobs through scheduler SGE, SLURM and LSF).

TOGGLE can work on your laptop, on a single machine server as well as on a HPC system, as a local instance or in a Docker machine. The only limit will be your available space on the storage system, not the amount of samples to be treated or the number of steps. TOGGLE was used on different organisms, from a single sample to more than one hundred at a time, in RNAseq, DNAREseq/SNP discovery and GBS analyses.

List of bioinformatics tools included:

- Cleaning and Quality checking : FastQC, CutAdapt, fastxTrimmer
- Assembly : TransAbyss, Trinity, TGI-CL
- Mapping : BWA (aln/sampe and mem), TopHat
- SAM/BAM management : picardTools, SAMtools, GATK
- SNP calling/cleaning/annotation : SAMtools, GATK, VarScan, snpEff
- ReadCount : HTseq-count
- Structural Variations : BreakDancer, Pindel

Web site: <https://github.com/SouthGreenPlatform/TOGGLE>

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