## Supplementary Material

## How to integrate tools in a workflow without having a component

The following code shows how to use Kallisto (https://pachterlab.github.io/kallisto/) in a pipeline without having a component for it. In this example the index is created separately so the quantification step can be run inside a for-loop with several samples without unnecessarily recomputing the index.

val index = QuickBash(in=reference,

 script="kallisto index -i $out $in")

val quant = BashEvaluate(var1=index.out,

 var2=reads,

 script="kallisto quant -i @var1@ -o @folder1@ -b 100 --single @var2@")

## Comparison table between bioinformatics frameworks

Comparison of Anduril 2 to other workflow frameworks/engines specific for Bioinformatics or popular in the field. All of them are publicly available and are still maintained (have been updated at least once in 2018).

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Anduril 2 | Bpipe | Cromwell | Galaxy | Nextflow | Pegasus | Pypiper | Ruffus | Snakemake | Taverna | Toggle |
| Bioinfo.resources | 400+ | ✘ | ✘ | 500+ | ✘ | ✘ | 50+ | ✘ | 35+ | webservices | 120+ |
| Dynamic loops | ✔ | ✘ | not nested | ✘ | ✘ | ✔ | ✘ | ✔ | ✔ | ✘ | ✘ |
| GUI for pipeline construction | ✘ | ✘ | ✘ | ✔ | ✘ | ✔ | ✘ | ✘ | ✘ | ✔ | ✘ |
| Parallel-ization | ✔ | not automated | ✔ | ✔ | ✔ | ✔ | ✔ | ✔ | ✔ | ✔ | by sample |
| Programming knowledge | ✔ | ✘ | ✔ | ✘ | ✔ | ✔ | ✔ | ✔ | ✔ | ✘ | ✘ |
| Command line1 | ✔ | ✔ | ✔ | ✘ | ✔ | ✔ | ✔ | ✔ | ✔ | ✘ | ✔ |
| Workflow sharing2 | ✘ | ✘ | ✘ | ✔ | ✘ | ✔ | ✘ | ✘ | ✘ | ✔ | ✘ |
| Built-in cluster support | ✔ | ✔ | ✔ | ✔ | ✔ | ✔ | withLooper | ✘ | ✔ | ✔ | ✘ |
| Available as docker image | ✔ |  | ✔ | ✔ | ✔ | ✔ | ✘ | ✔ | ✔ | ✔ | ✘ |
| Set CPU requirements | ✔ | ✔ | ✔ | ✔ | ✔ | ✔ | ✘ | ✘ | ✔ | ✘ | ✘ |
| Registration needed | ✘ | ✘ | ✘ | ✔ | ✘ | ✘ | ✘ | ✘ | ✘ | ✘ | ✘ |
| Cloud support | ✘ | ✘ | ✔ | ✔ | ✔ | ✔ | ✘ | ✘ | ✔ | ✔ | ✘ |
| Years of development | 8+ | 5+ | 3+ | 8+ | 5+ | 11+ | 5+ | 8+ | 6+ | 12+ | 3+ |

1Execute command or software in the command line inside the pipeline

2Sharing workflows inside the framework with other users