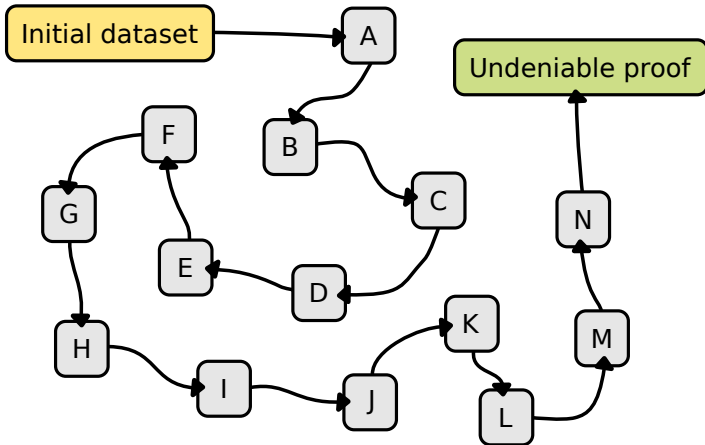


# Workflow management with GNU Guix

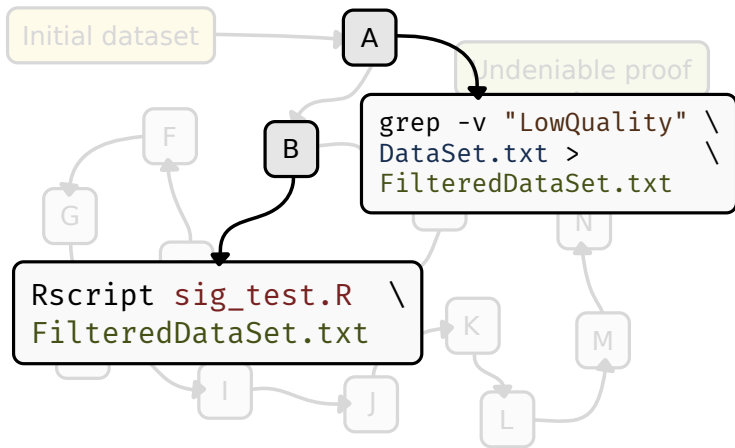
Roel Janssen

February 5, 2017

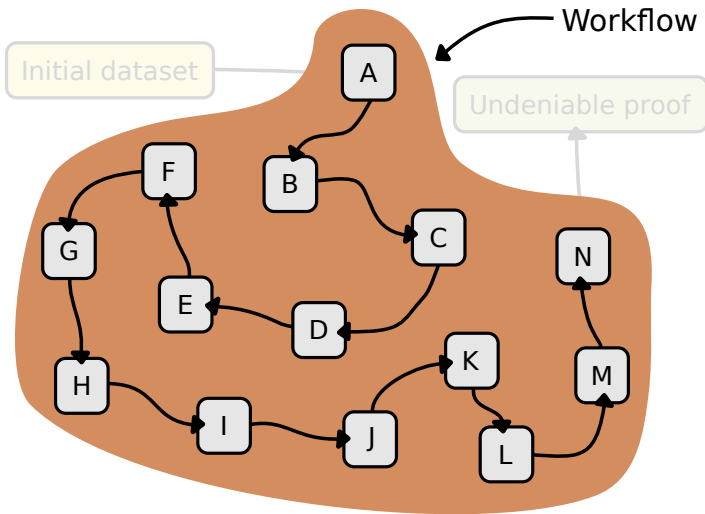
# Data analysis



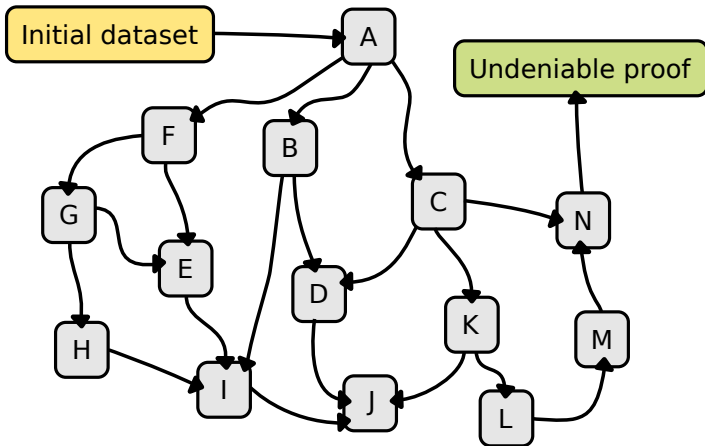
# Processes



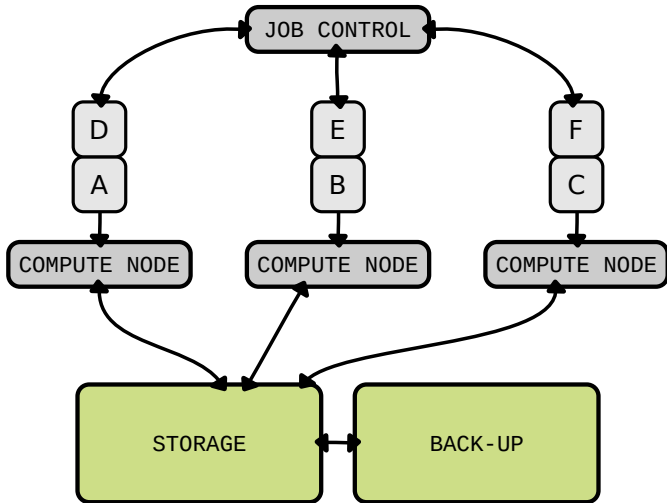
# The workflow



## Parallel steps



# Executing on a computer cluster



## Process record type

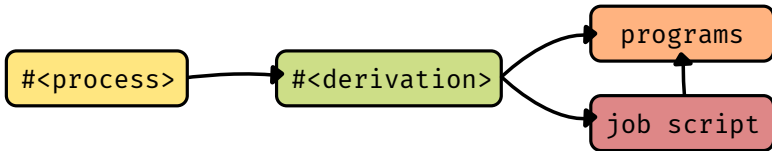
```
(define quality-control
  (process
    (name "quality-control")
    (version "1.0")
    (package-inputs '(("fastqc" ,fastqc-0.11.4)))
    (data-inputs '("/path/to/sample_R1_001.fastq.gz"))
    (output-path "/path/to/rnaseq-out")
    (run-time (complexity (space (* 1024 1024))
                          (time 60)))
    (procedure #~(begin (map (lambda (sample)
                              (system* (string-append
                                         "$@"(assoc-ref package-inputs "fastqc")
                                         "/bin/fastqc") sample "-o" #$output-path)
                              #'#$data-inputs))))
    (synopsis "Report read quality of FastQ files")
    (description "...")))
```

## Workflow record type

```
(define rnaseq-workflow
  (workflow
    (name "rnaseq-workflow")
    (version "1.0")
    (input "/path/to/input/files")
    (output "/path/to/output")
    (processes
      '(,quality-control
        ,align-reads
        ,add-read-groups
        ,sort-and-index))
    (restrictions
      '((,add-read-groups ,align-reads)
        (,sort-and-index ,add-read-groups)))
    (synopsis "RNA sequencing workflow")
    (description "...")))
```



## How it works



# Get started

- Tutorial:  
<https://gwl.roelj.com>
- Source code:  
<https://git.roelj.com/guix/guix-wl>
- Questions:  
[roel@gnu.org](mailto:roel@gnu.org)

# Acknowledgements

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- GNU Guile contributors