Nextflow workflow report
[cranky_torricelli]

Workflow execution completed successfully!

Run times
05-Nov-2019 08:06:30 - 07-Nov-2019 20:21:36 (duration: 2d 12h 15m 6s)

Nextflow command
nextflow /home/rpetit3/repos/bactopia/main.nf --accessions ../lactobacillus-accessions.txt --datasets /home/rpetit3/datasets --species lactobacillus --coverage 100 --cpus 4 -profile slurm --min_genome_size 1000000 --max_genome_size 4200000

CPU-Hours 3'052.4 (0% failed)
Launch directory /home/rpetit3/projects/lactobacillus/bactopia
Work directory /home/rpetit3/projects/lactobacillus/bactopia/work
Project directory /home/rpetit3/repos/bactopia
Script name main.nf
Script ID b763323ed48f19eda2aff0c1a481f11
Workflow session 90a3fb3c-b891-4c5a-a6b5-5c6159277170
Workflow profile slurm
Nextflow version version 19.10.0, build 5170 (21-10-2019 15:07 UTC)

Resource Usage
These plots give an overview of the distribution of resource usage for each process.

CPU

CPU Usage

file:///Users/timothyread/Downloads-supplementary-data-3-nextflow-report.html
Number of bytes read

(tasks table omitted because the dataset is too big)

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