

Found perl:

```
/shared/ibfstor1/software/miniconda/envs/canu-2.1.1/bin/perl
perl: warning: Setting locale failed.
perl: warning: Please check that your locale settings:
    LANGUAGE = (unset),
    LC_ALL = (unset),
    LC_CTYPE = "UTF-8",
    LANG = "en_US.UTF-8"
are supported and installed on your system.
perl: warning: Falling back to a fallback locale ("en_US.UTF-8").
This is perl 5, version 32, subversion 0 (v5.32.0) built for
x86_64-linux-thread-multi
```

Found java:

```
/shared/ibfstor1/software/miniconda/envs/canu-2.1.1/bin/java
openjdk version "11.0.9.1-internal" 2020-11-04
```

Found canu:

```
/shared/ibfstor1/software/miniconda/envs/canu-2.1.1/bin/canu
perl: warning: Setting locale failed.
perl: warning: Please check that your locale settings:
    LANGUAGE = (unset),
    LC_ALL = (unset),
    LC_CTYPE = "UTF-8",
    LANG = "en_US.UTF-8"
are supported and installed on your system.
perl: warning: Falling back to a fallback locale ("en_US.UTF-8").
canu branch HEAD +0 changes (r10117
5638f7d9a5379373310ab62c28aa0cdbd864722d)
```

```
perl: warning: Setting locale failed.
perl: warning: Please check that your locale settings:
    LANGUAGE = (unset),
    LC_ALL = (unset),
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-- canu branch HEAD +0 changes (r10117
5638f7d9a5379373310ab62c28aa0cdbd864722d)
```

-- CITATIONS

```
-- For 'standard' assemblies of PacBio or Nanopore reads:
-- Koren S, Walenz BP, Berlin K, Miller JR, Phillippy AM.
-- Canu: scalable and accurate long-read assembly via adaptive k-mer
weighting and repeat separation.
-- Genome Res. 2017 May;27(5):722-736.
-- http://doi.org/10.1101/gr.215087.116
```

```
--  
-- Read and contig alignments during correction and consensus use:  
-- Šošić M, Šikić M.  
-- Edlib: a C/C ++ library for fast, exact sequence alignment using  
edit distance.  
-- Bioinformatics. 2017 May 1;33(9):1394–1395.  
-- http://doi.org/10.1093/bioinformatics/btw753  
--  
-- Overlaps are generated using:  
-- Berlin K, et al.  
-- Assembling large genomes with single-molecule sequencing and  
locality-sensitive hashing.  
-- Nat Biotechnol. 2015 Jun;33(6):623–30.  
-- http://doi.org/10.1038/nbt.3238  
--  
-- Myers EW, et al.  
-- A Whole-Genome Assembly of Drosophila.  
-- Science. 2000 Mar 24;287(5461):2196–204.  
-- http://doi.org/10.1126/science.287.5461.2196  
--  
-- Corrected read consensus sequences are generated using an algorithm  
derived from FALCON-sense:  
-- Chin CS, et al.  
-- Phased diploid genome assembly with single-molecule real-time  
sequencing.  
-- Nat Methods. 2016 Dec;13(12):1050–1054.  
-- http://doi.org/10.1038/nmeth.4035  
--  
-- Contig consensus sequences are generated using an algorithm derived  
from pbdagcon:  
-- Chin CS, et al.  
-- Nonhybrid, finished microbial genome assemblies from long-read  
SMRT sequencing data.  
-- Nat Methods. 2013 Jun;10(6):563–9  
-- http://doi.org/10.1038/nmeth.2474  
--  
-- CONFIGURE CANU  
--  
-- Detected Java(TM) Runtime Environment '11.0.9.1-internal' (from  
'java') without -d64 support.  
-- Detected gnuplot version '5.4 patchlevel 1' (from 'gnuplot') and  
image format 'png'.  
-- Detected 56 CPUs and 252 gigabytes of memory.  
-- Detected Slurm with 'sinfo' binary in /usr/bin/sinfo.  
-- Detected Slurm with task IDs up to 10000 allowed.  
--  
-- Found 16 hosts with 254 cores and 1993 GB memory under Slurm  
control.  
-- Found 2 hosts with 38 cores and 241 GB memory under Slurm  
control.
```

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-- Found 12 hosts with 30 cores and 115 GB memory under Slurm control.
-- Found 1 host with 124 cores and 3013 GB memory under Slurm control.
-- Found 3 hosts with 62 cores and 493 GB memory under Slurm control.
-- Found 65 hosts with 54 cores and 241 GB memory under Slurm control.

```

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--
--
-- (tag)Threads
-- (tag)Memory |
-- (tag) | algorithm
-- -----|-----
-- Grid: meryl 7.000 GB 2 CPUs (k-mer counting)
-- Grid: hap 7.000 GB 2 CPUs (read-to-haplotype
assignment)
-- Grid: cormhap 6.000 GB 2 CPUs (overlap detection with mhap)
-- Grid: obtovl 4.000 GB 2 CPUs (overlap detection)
-- Grid: utgovl 4.000 GB 2 CPUs (overlap detection)
-- Grid: cor 8.000 GB 4 CPUs (read correction)
-- Grid: ovb 4.000 GB 1 CPU (overlap store bucketizer)
-- Grid: ovs 8.000 GB 1 CPU (overlap store sorting)
-- Grid: red 8.000 GB 2 CPUs (read error detection)
-- Grid: oea 8.000 GB 1 CPU (overlap error adjustment)
-- Grid: bat 16.000 GB 4 CPUs (contig construction with
bogart)
-- Grid: cns -.--- GB 4 CPUs (consensus)

```

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-- In '398.seqStore', found Nanopore reads:

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-- Nanopore: 1

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```

-- Raw: 1

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-- Generating assembly '398' in '/shared/ifbstor1/projects/
clostridium_nanopore/Nano_Nadim/datatrimCANU_ALL3':

```

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-- - only correct raw reads.

```

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-- Parameters:

```

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-- genomeSize 4700000

```

```

-- Overlap Generation Limits:

```

```

-- corOvlErrorRate 0.3200 ( 32.00%)

```

```

-- obtOvlErrorRate 0.1200 ( 12.00%)

```

```

-- utgOvlErrorRate 0.1200 ( 12.00%)

```

```

-- Overlap Processing Limits:

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```

-- corErrorRate 0.5000 ( 50.00%)

```

```

-- obtErrorRate 0.1200 ( 12.00%)

```

```

-- utgErrorRate 0.1200 ( 12.00%)

```

```
--   cnsErrorRate    0.2000 ( 20.00%)
--
--
-- BEGIN CORRECTION
--
--
-- OVERLAPPER (mhap) (correction) complete, not rewriting scripts.
--
--
-- Mhap overlap jobs failed, tried 2 times, giving up.
--   job correction/1-overlapper/results/000003.ovb FAILED.
--   job correction/1-overlapper/results/000005.ovb FAILED.
--
```

ABORT:

ABORT: canu branch HEAD +0 changes (r10117
5638f7d9a5379373310ab62c28aa0cdbd864722d)

ABORT: Don't panic, but a mostly harmless error occurred and Canu
stopped.

ABORT: Try restarting. If that doesn't work, ask for help.

ABORT: