Canu

output filename prefix → canu -p **canu** -d **out_dir** -fast genomeSize=5m stopOnLowCoverage=0

output directory name

faster read overlapping (recommended in release notes for genomes <1 Gbp in size)

true size of the reference genome

prevents premature termination in cases of suboptimal input reads

```
canu -p canu -d out_dir -fast genomeSize=5m stopOnLowCoverage=0
  useGrid=false minThreads=16 maxThreads=16 maxMemory=120 -nanopore-raw reads.fastq.gz
```

these four options tailor Canu to the computational environment

input read type (changed to -pacbio-raw for PacBio reads)

input read filename

Flye

output directory name

enable recovery of small plasmids

enable uneven coverage mode

true size of the reference genome

CPU threads to use

input read type (changed to --pacbio-raw for PacBio reads)

input read filename

```
flye -o out_dir --plasmids --meta --genome-size 5m --threads 16 --nano-raw reads.fastq.gz
```

Miniasm

input read filename

CPU threads to use

```
miniasm_and_minipolish.sh reads.fastq.gz 16
```

NECAT

contains read filename, genome size and thread count

```
necat.pl bridge config.txt
```

Raven

output graph filename

CPU threads to use

input read filename

```
raven --graphical-fragment-assembly graph.gfa --threads 16 reads.fastq.gz
```

Redbean

output filename prefix

true size of the reference genome

CPU threads to use

assembly preset (changed to rs for PacBio reads)

input read filename

```
wtdbg2.pl -o dbg -g 5m -t 16 -x ont reads.fastq.gz
```

Shasta

input read filename

the output directory name

CPU threads to use

```
seqtk seq -A reads.fastq.gz > reads.fasta
shasta --input reads.fasta --assemblyDirectory out_dir --threads 16
```