LMAS WORKFLOW

Input

--fastq

default path:
*"data/fastq/*_{1,2}*"*

--reference

default path:
"data/reference/.fasta"*

--md
default path:
"data/.md"*
Optional

Assembly

Assembler 1

Assembler 2

Assembler 3

Assembler 4

Assembler 5

...

Assembler *n*

Global Assessment

Read Mapping
minimap2

Global Metrics

Table Metrics
Original assembly: Number of contigs, Number of
basepairs, Maximum contig size, N*x*, Percentage of
mapped reads, Number of "N" basepairs
Contigs over minimum lenght: Number of contigs,
Number of basepairs, N*x*, Misassembled contigs,
Number of "N" basepairs

Plot Metrics
Contig size distribution, Gap size distribution,
Misassembled contigs

Parameters:
--minLength (default: 1000 bp)
--mapped_reads_threshold (default: 75%)
--n_target (default: 50%)

Filter Assembly

bbTools

parameters: --minLength (default: 1000 bp)

Per Reference Assessment

Assembly Mapping
minimap2

Reference Metrics

Table Metrics
LSA, Multiplicity, Validity, Parsimony, Identity, Lowest Identity, Breadth of Coverage,
Aligned Contigs, Misassembled Contigs, Lx, NAx, NGx, Aligned Basepairs, Number of "N" Basepairs

Plot Metrics
Genome fragmentation, Lx metric, NAx metric, NGx metric, PLS metric, Gaps, SNPs

Parameters:
--l_target (default: 90%)
--n_target (default: 50%)

Interactive Report