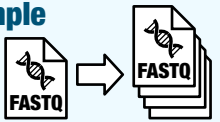
fully automated steps

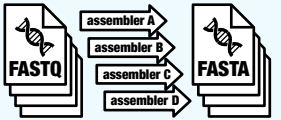
Autocycler subsample

Splits a long-read FASTQ into multiple subsampled files with minimal overlap.



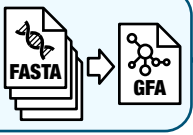
Generate input assemblies

Each subset is assembled with multiple tools to generate diverse assemblies of the same genome.



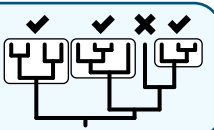
Autocycler compress

Losslessly compresses assemblies into a compacted De Bruijn graph that preserves all sequences.



Autocycler cluster

Contigs are clustered into putative replicons with automated QC.

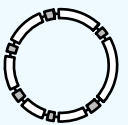


Autocycler trim

Trims excess sequence, including circular and hairpin overlaps.

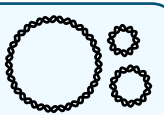
Autocycler resolve

Builds a consensus path from common anchors and most supported bridges.



Autocycler combine

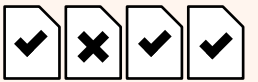
Merges all resolved sequences into a final consensus assembly.



optional steps

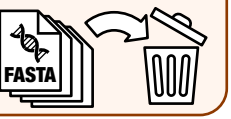
Curate input assemblies

Low-quality assemblies (e.g. failed to circularise) can be discarded before subsequent steps.



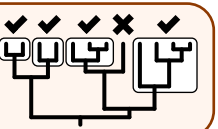
Delete input assemblies

Input assemblies are recoverable from the graph and can be safely deleted to save disk space.



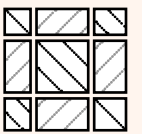
Curate clusters

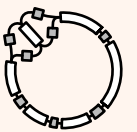
Users can adjust clustering by manually selecting valid groups.



Autocycler dotplot

Dotplots reveal overlap patterns before and after trimming to facilitate manual trimming.



Inspect resolution

Intermediate files reveal genomic heterogeneity and assembler disagreement.