# Article information:

Trycycler: consensus long-read assemblies for bacterial genomes | Genome Biology | Full Text
<https://genomebiology.biomedcentral.com/articles/10.1186/s13059-021-02483-z>

# Article summary:

1. Trycycler is a tool that produces a consensus assembly from multiple input assemblies of the same genome.

2. Benchmarking showed that Trycycler assemblies contained fewer errors than assemblies constructed with a single tool.

3. Post-assembly polishing further reduced errors and Trycycler+polishing assemblies were the most accurate genomes in the study.

# Article rating:

Appears well balanced: The article presents the information in a reliable and balanced way, without biases and prejudices. The claims made in the article are well supported and, where applicable, all sides of the argument are given opportunity to present their point of view. The article appears trustworthy and reliable.

# Article analysis:

The article “Trycycler: consensus long-read assemblies for bacterial genomes” is an informative and reliable source of information on the use of Trycycler, a tool which produces a consensus assembly from multiple input assemblies of the same genome. The article provides evidence to support its claims, such as benchmarking results showing that Trycycler assemblies contain fewer errors than those constructed with a single tool, and post-assembly polishing further reducing errors and producing the most accurate genomes in the study. The article also acknowledges potential limitations of using Trycycler, such as its requirement for manual intervention which makes its output non-deterministic, but demonstrates that multiple users can converge on similar assemblies that are consistently more accurate than those produced by automated assembly tools. The article does not appear to be biased or one-sided in its reporting, nor does it contain any promotional content or partiality towards any particular method or technology. It also notes possible risks associated with using long-read sequencing platforms for bacterial sequencing, such as underrepresentation of small plasmids in ONT read sets. In conclusion, this article is trustworthy and reliable due to its clear presentation of evidence to support its claims and acknowledgement of potential limitations and risks associated with using long-read sequencing platforms for bacterial sequencing.

# Topics for further research:

* Bacterial genome assembly
* Long-read sequencing platforms
* Consensus assembly
* Post-assembly polishing
* ONT read sets
* Plasmid underrepresentation

# Report location:

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