# Article information:

Assembly of chromosome-scale contigs by efficiently resolving repetitive sequences with long reads - PMC  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6877557/>

# Article summary:

1. HERA is a genome assembly method that resolves repeats efficiently by constructing a connection graph from an overlap graph.

2. HERA was tested on the genomes of rice, maize, human, and Tartary buckwheat with single-molecule sequencing and mapping data.

3. HERA can be used to fill gaps and fix errors in reference genomes, resulting in dramatically improved, highly contiguous genome assemblies with newly assembled gene sequences.

# 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 “Assembly of chromosome-scale contigs by efficiently resolving repetitive sequences with long reads” is a reliable source of information about the HERA genome assembly method. The article provides detailed information about the method and its application to various complex eukaryotic genomes such as rice, maize, human, and Tartary buckwheat. The authors provide evidence for their claims by citing previous studies and providing results from their own experiments. Furthermore, the authors discuss potential risks associated with using the HERA method such as incomplete gene sequences or mispositioned contigs on chromosomes.

The article does not present any one-sided reporting or unsupported claims; instead it provides a balanced view of both the advantages and disadvantages of using the HERA method for genome assembly. Additionally, all claims made are supported by evidence from previous studies or results from experiments conducted by the authors themselves. The article also does not contain any promotional content or partiality towards any particular method or technology; instead it provides an unbiased overview of different methods available for genome assembly and their respective advantages and disadvantages.

In conclusion, this article is a reliable source of information about the HERA genome assembly method due to its balanced view of different methods available for genome assembly as well as its support for all claims made through evidence from previous studies or results from experiments conducted by the authors themselves.

# Topics for further research:

* Genome assembly methods
* Chromosome-scale contigs
* Resolving repetitive sequences
* Long read sequencing
* Eukaryotic genome assembly
* Genome assembly risks

# Report location:

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