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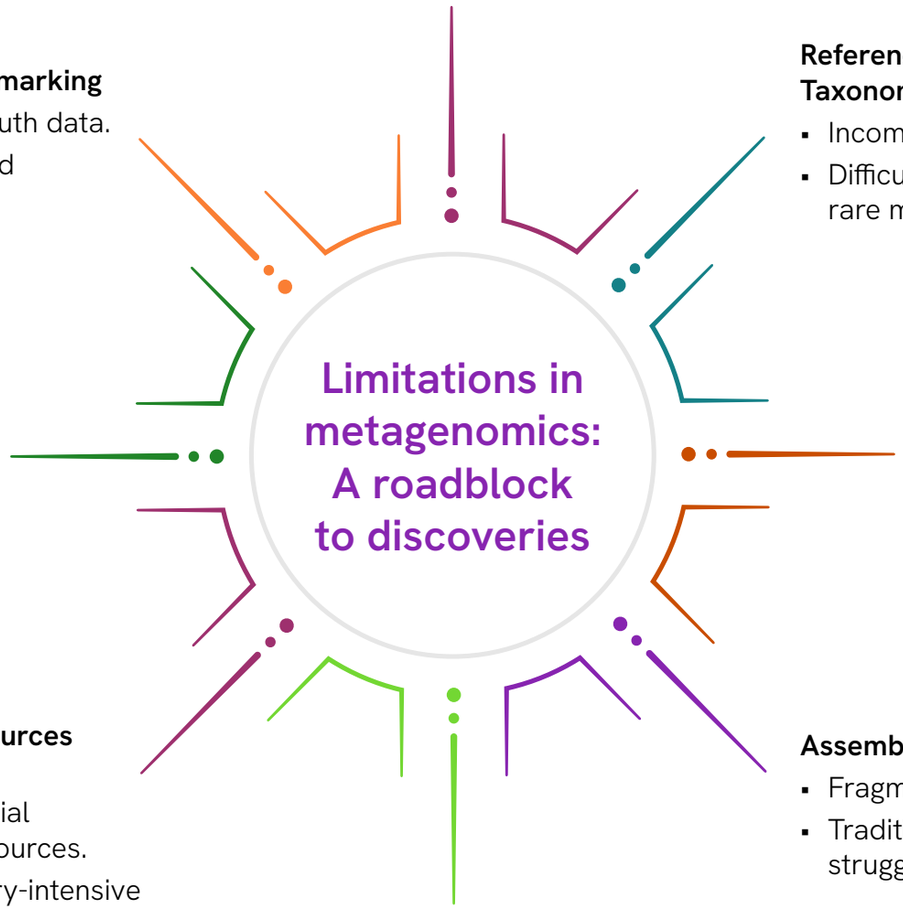
# Limitations in metagenomics: A roadblock to discoveries



### Data Overload and Complexity

- Millions of short DNA sequences.
- Specialized tools needed for efficient analysis.

### Reference Databases and Taxonomic Classification

- Incomplete and biased databases.
- Difficulty in identifying novel or rare microbes.

### Functional Annotation and Pathway Prediction

- Challenges in predicting gene functions and metabolic pathways.
- Need for more sophisticated algorithms.

### Assembly Challenges

- Fragmented sequences.
- Traditional assemblers struggle with diversity.

### Sample Heterogeneity and Bias

- Unique biases in different environments.
- Contamination from host DNA or reagents.

### Computational Resources and Scalability

- Demands substantial computational resources.
- Tools often memory-intensive and time-consuming.

### Integration with Other Omics Data

- Essential for a holistic understanding.
- Lack of tools for seamless integration.

### Verification and Benchmarking

- Absence of ground truth data.
- Need for standardized benchmarks.

### Conclusion

Metagenomics holds immense promise for unraveling microbial life mysteries, but addressing tool limitations is crucial.

### Revvity Solutions

Cutting-edge tools for microbial sample processing and analysis. Democratizing microbiome analysis for all.

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