CPStools: a package for analyzing chloroplast genome sequences

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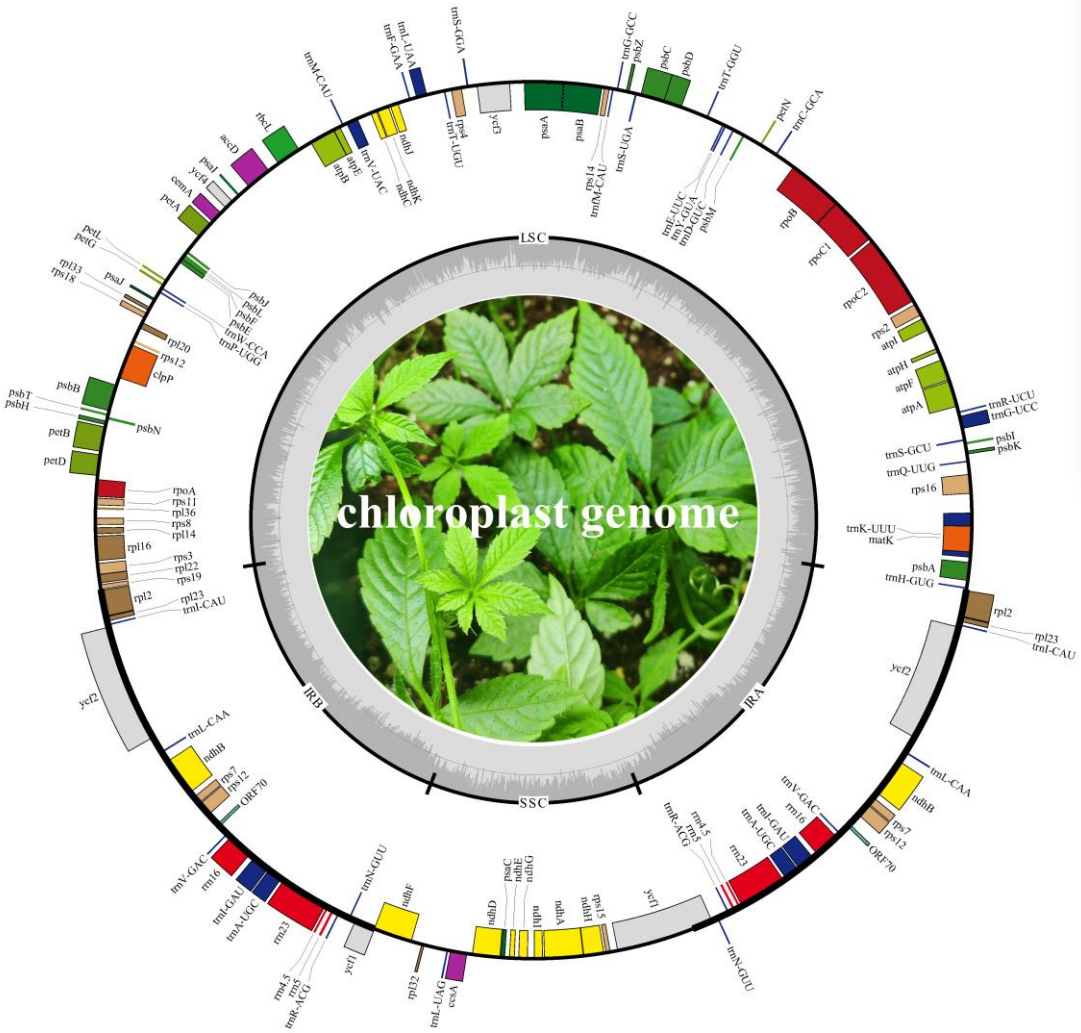
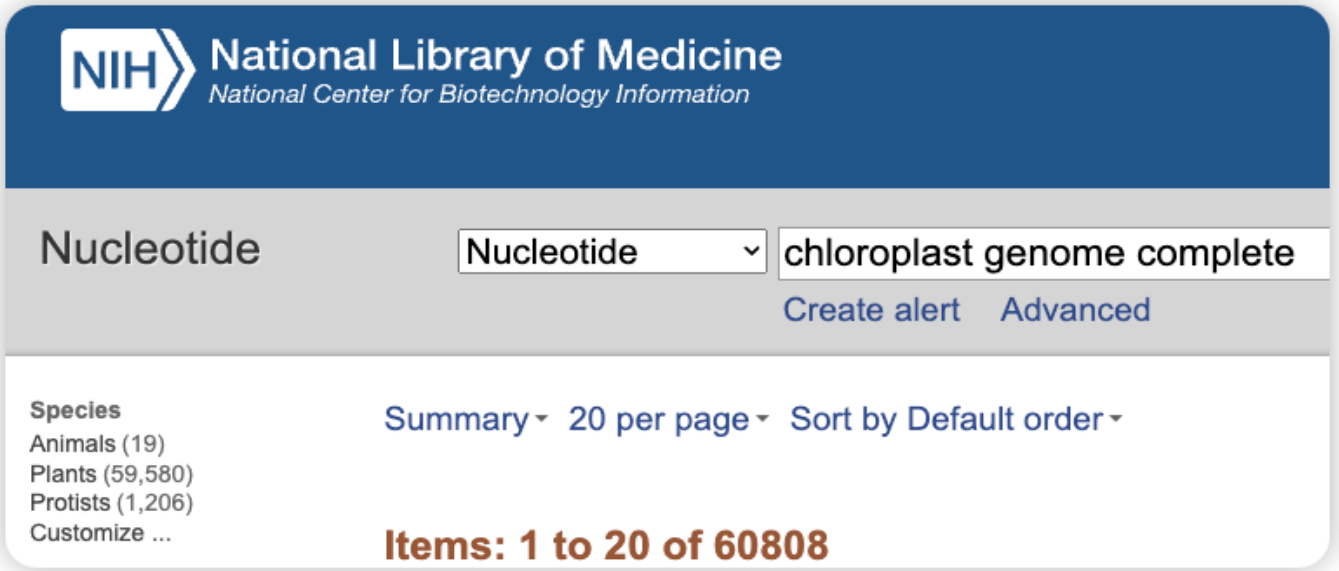
Background

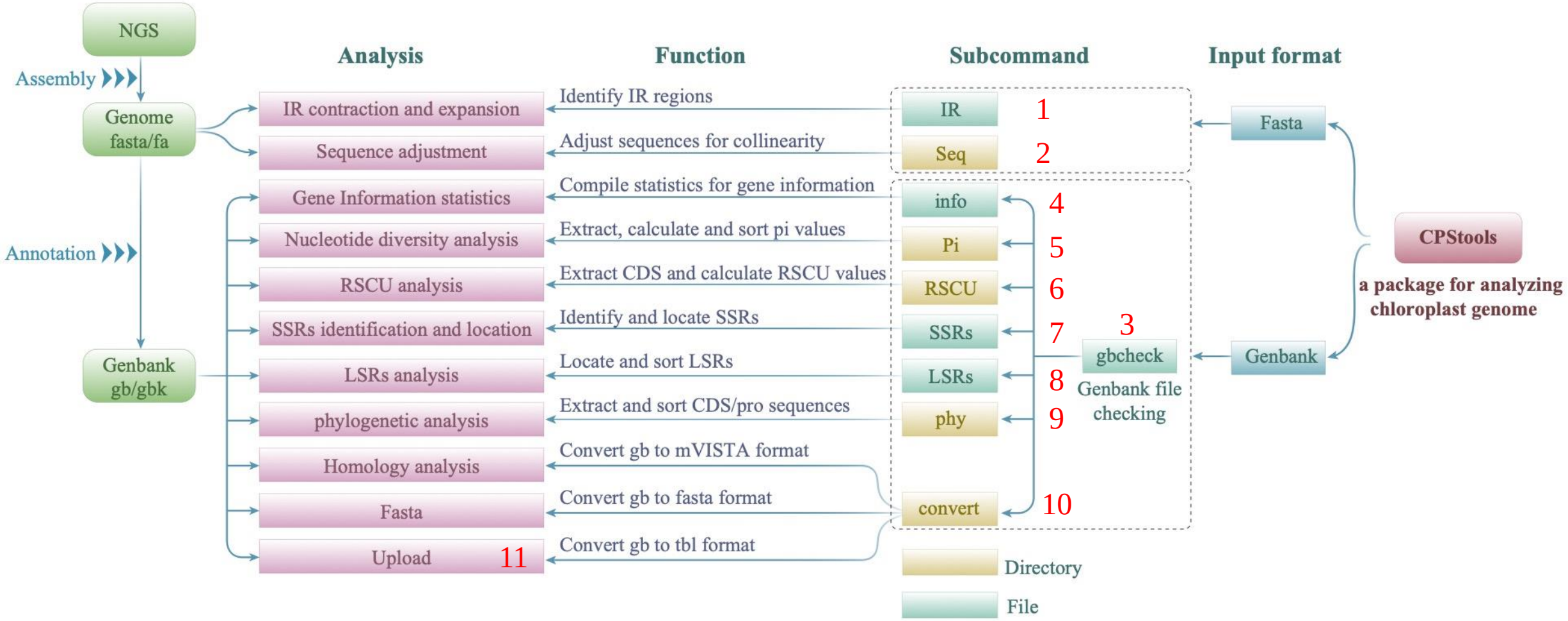




With the development of high-throughput sequencing technology, an increasing number of plant chloroplast genomes have been sequenced. To date, nearly 60,000 chloroplast genome sequences have been deposited in NCBI. However, aside from assembly, annotation, and IR boundary analysis, there is currently no dedicated software available for other types of chloroplast genome data analysis and visualization.

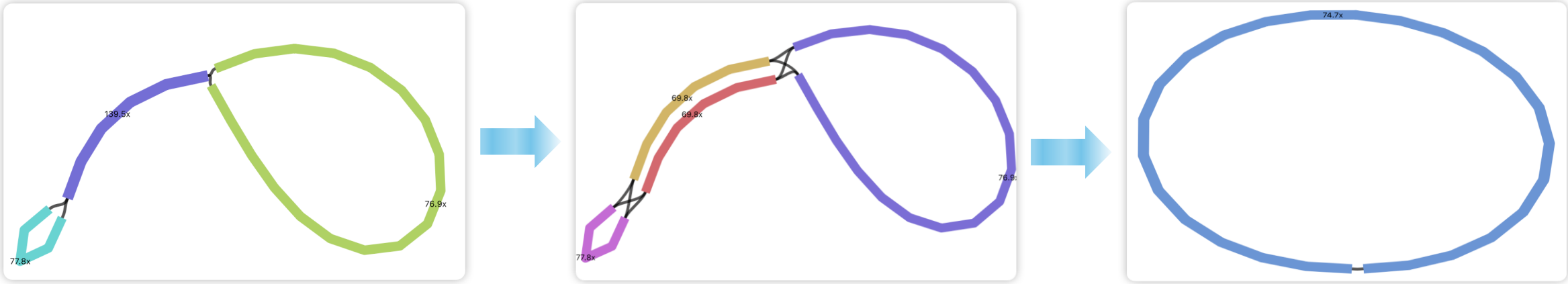
Highlights

The workflow of CPStools

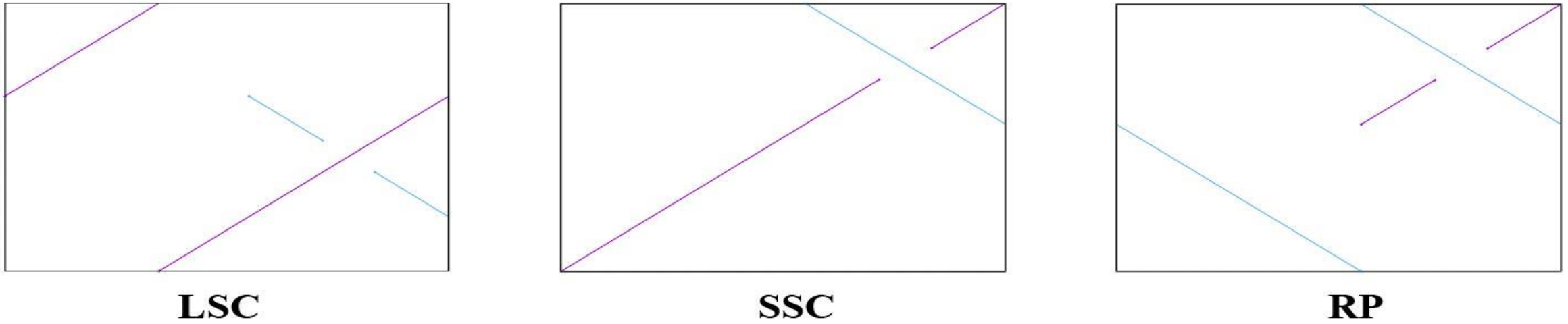


Core Function

Decatenation



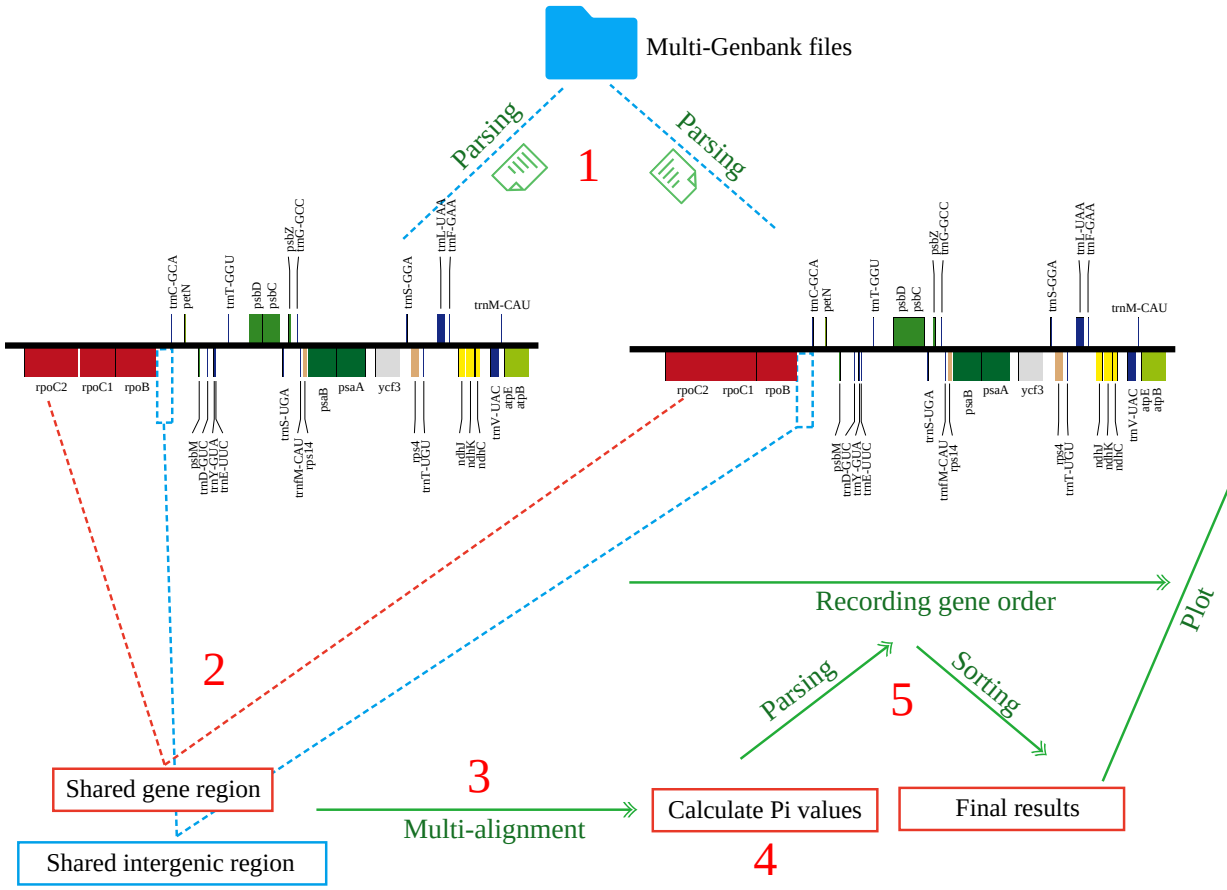
Collinearity

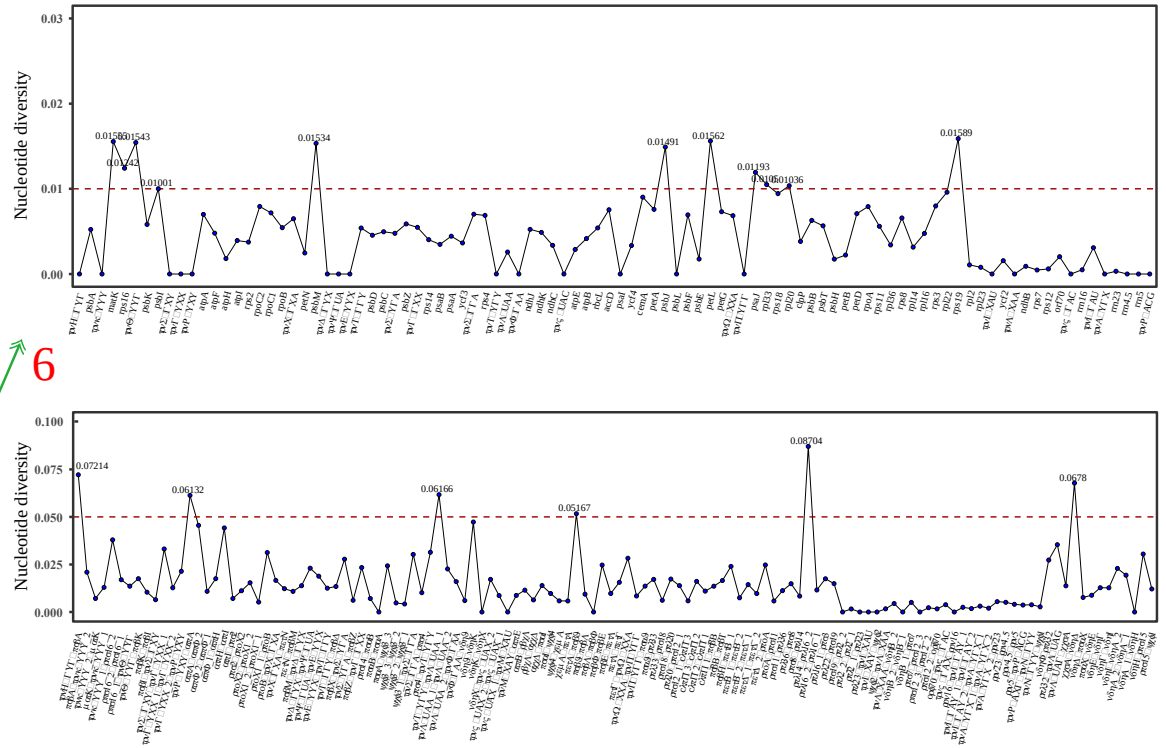


LSC SSC RP

Core Function

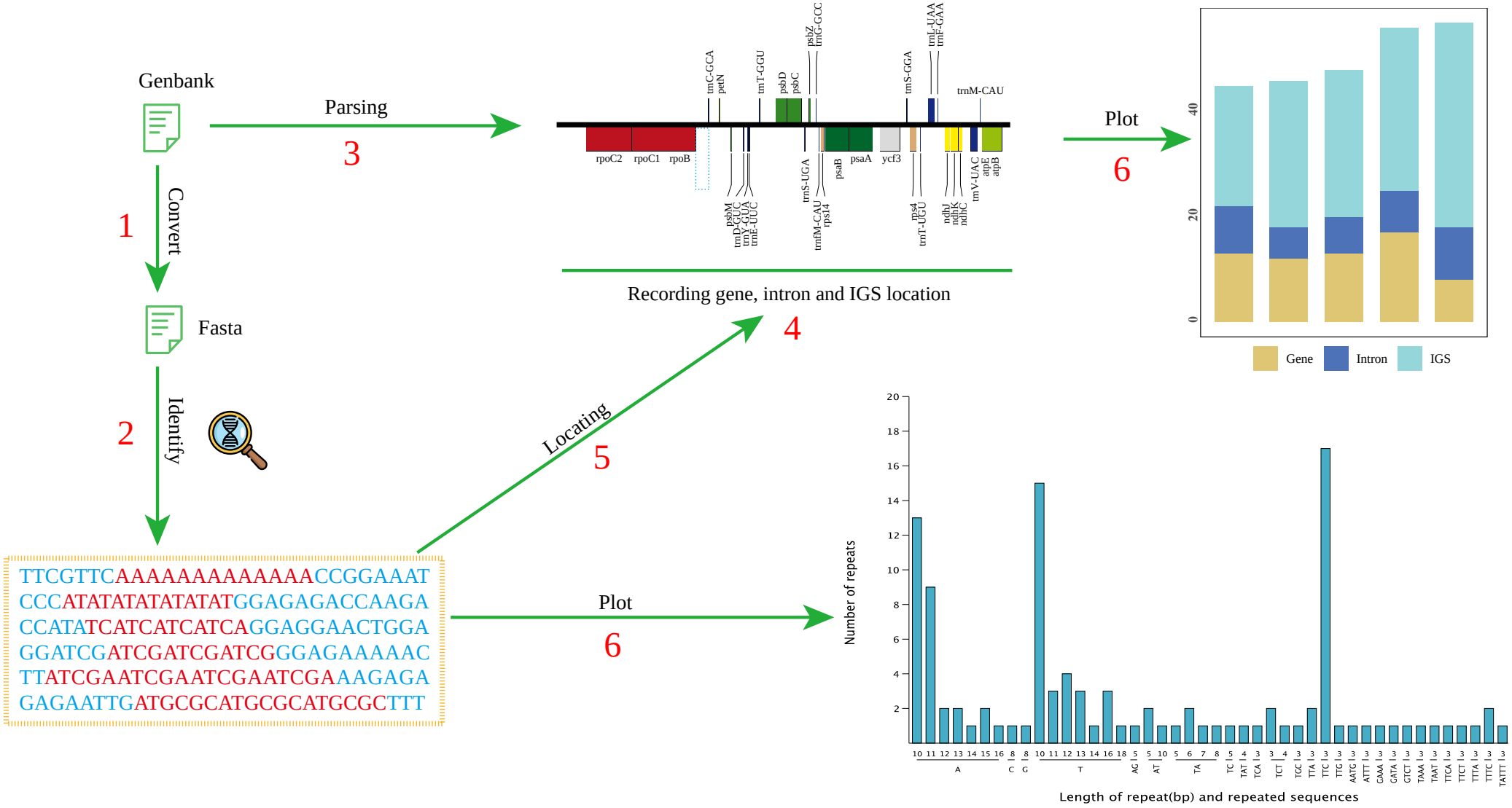
The workflow of Pi





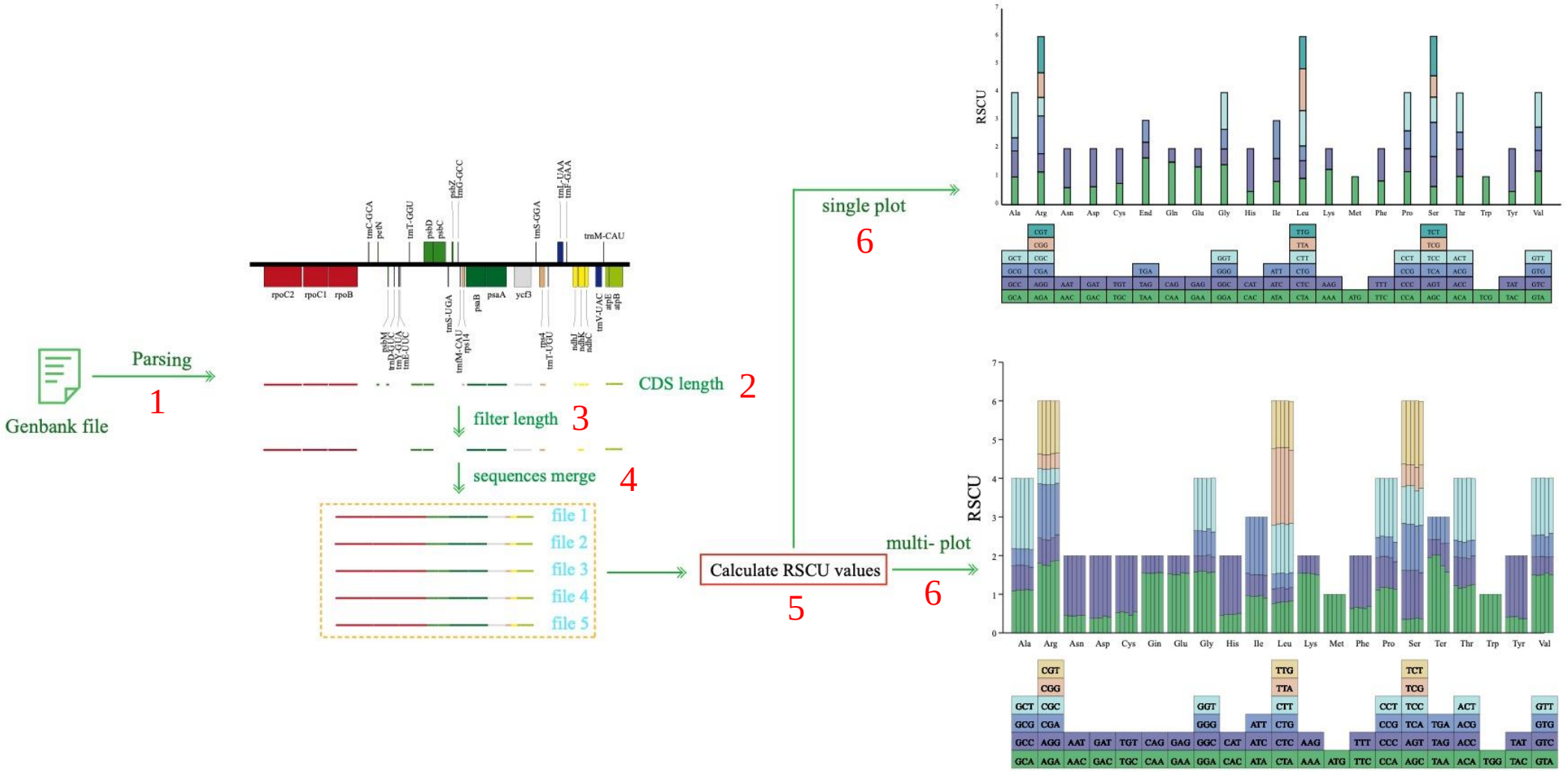
Core Function

The workflow of SSRs



Core Function

The workflow of RSCU



Conclusion

- In this study, we introduced a user-friendly Python package specifically designed for chloroplast genome sequences -- CPStools.
- Currently, the package has developed 10 subcommands, covering 11 analysis functions for chloroplast genomes. The package will continue to be updated to meet the needs of users for standardized and personalized chloroplast genome data analysis.
- We have provided detailed video tutorials and problem explanations on Bilibili platform, and a comprehensive README document is also available on GitHub for reference.
- Bilibili website： https://www.bilibili.com/video/BV1fZ421K7nw/

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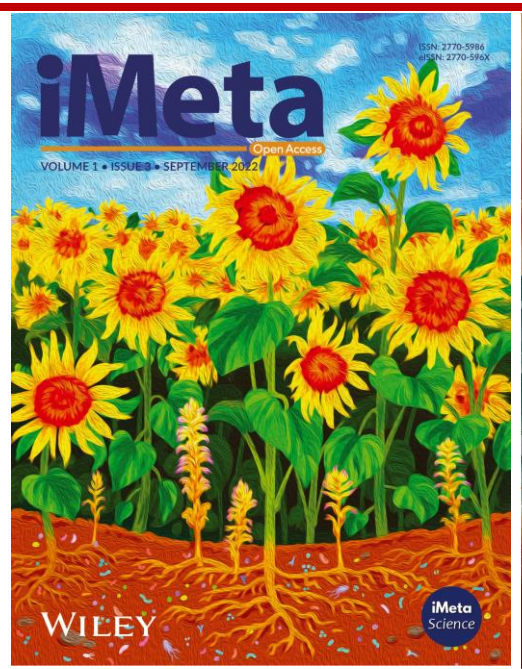

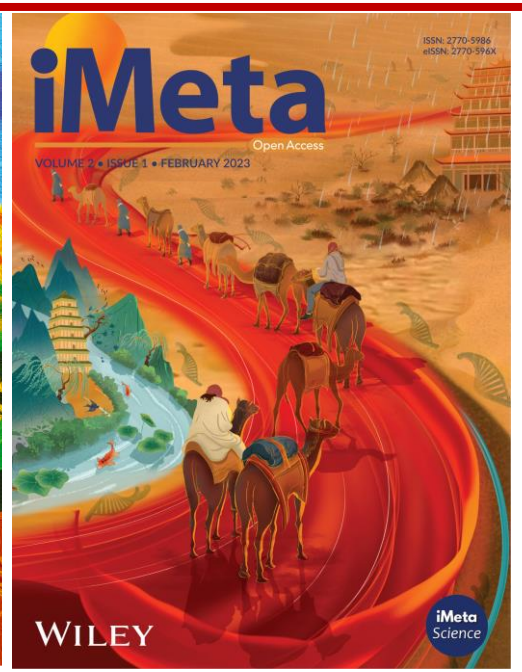

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