

multiPrime2-GUI.exe: Designing degenerate primers for maximum coverage with minimal degeneracy.

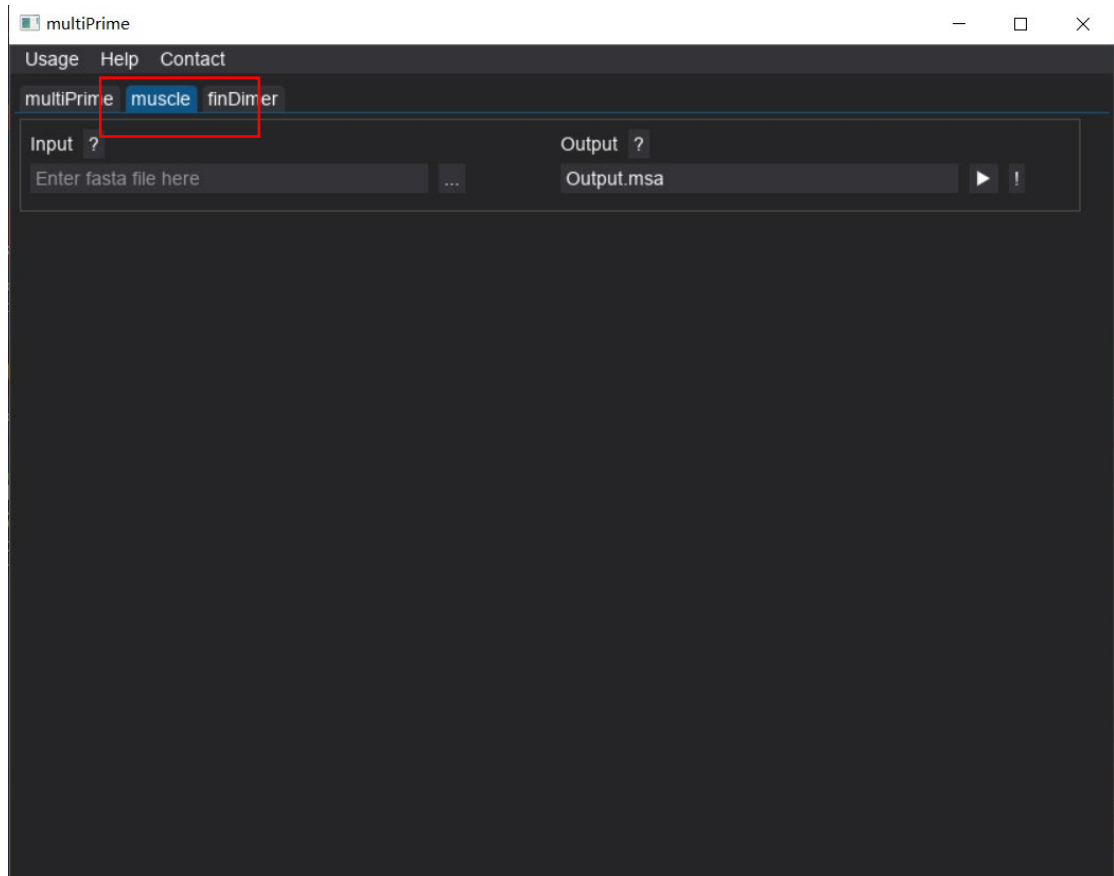
Welcome to multiPrime2-GUI.exe! MultiPrime2 is a user-friendly and one-step tool for designing degenerate primer pairs. It integrates degenerate primer design theory with mismatch handling, resulting in improved accuracy and specificity in detecting broad spectrum sequences. It outperformed conventional programs in terms of run time, primer number, and primer coverage. In the Method, the 'multiPrime1' approach represents a local optimum solution, resembling the core primer design module of multiPrime, available at <https://github.com/joybio/multiPrime>. In contrast, the 'multiPrime2' Method stands as a global optimum solution, capable of achieving maximum primer coverage with minimal degeneracy.

How to Use multiPrime2-GUI.exe

To utilize multiPrime-core.exe effectively, follow these steps:

1. **Input Data:** Prepare your input data in a msa format (multiple alignment file). If you're unsure about the meaning of a parameter, simply click the question mark symbol (?), and it will provide you with an explanation.

If you don't have multiple alignment file, you can run muscle in the muscle window.




2. **General Settings:** Customize Options to Suit Your Preferences

In the use multiPrime2-GUI application, we understand the importance of flexibility in tailoring the tool to your specific needs. As such, all the available options can be easily configured according to your preferences. You have the freedom to set them as you see fit. Empower yourself with complete control over the tool's behavior, allowing for seamless integration into your research and analysis workflows.

multiPrime

Usage Help Contact

multiPrime muscle finDimer



Input ?

Enter Multiple alignment file here

Primer length ? 18 - + Indel Filter ? F

Single candidate primer ?

DPrime.tmp

Primer pairs ?

DPrime.out

Reset setting

Setting

Options 1

Degenerate number ? 4 - +

Degeneracy ? 10 - +

Mismatch number ? 1

Entropy ? 3.600 - +

GC ? 0.2,0.7

Options 2

Product size ? 200,500

Primer coverage ? 0.600 - +

Positions ? 1,2,-1

Process ? 5 - +

Hairpin ? 4 - +

Options 3

DPrime_adaptor ? TCTTTCCTACACGACGCTCTTCCGATCT,TCTTTCCC

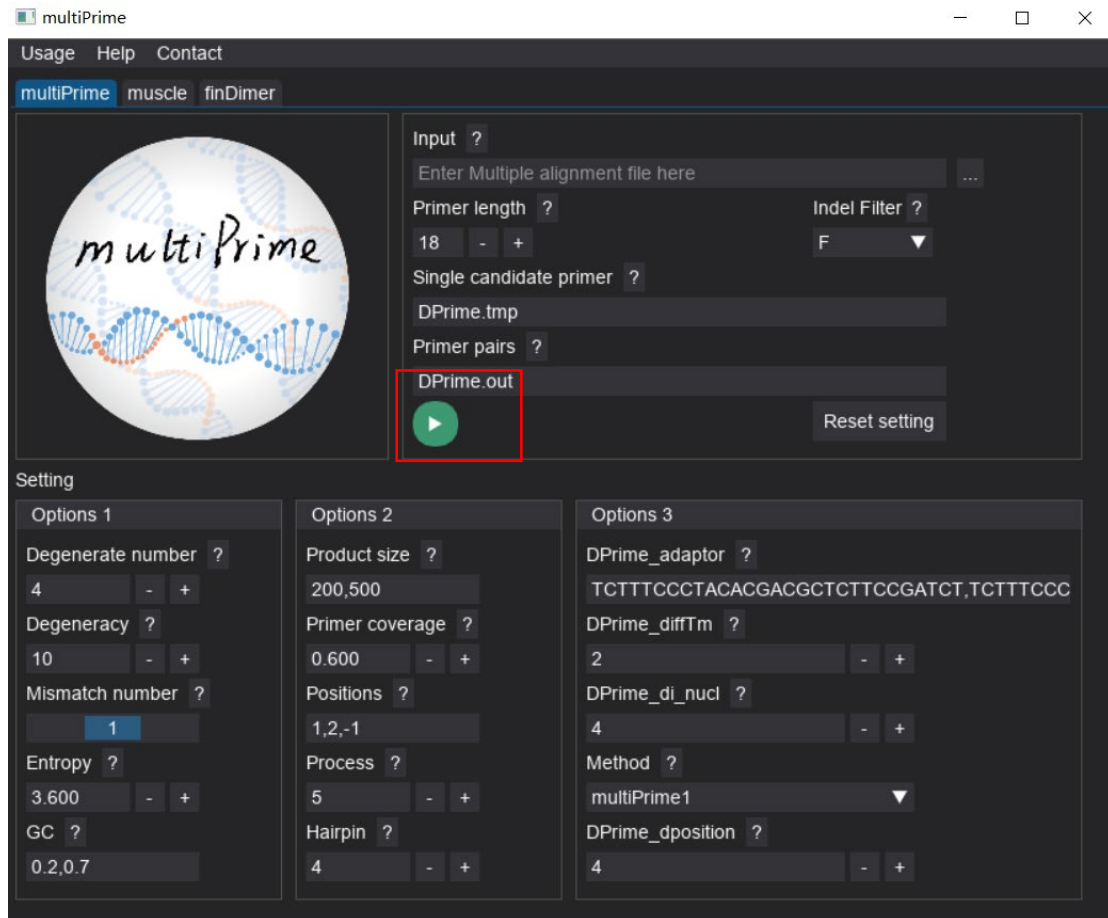
DPrime_diffTm ? 2 - +

DPrime_di_nucl ? 4 - +

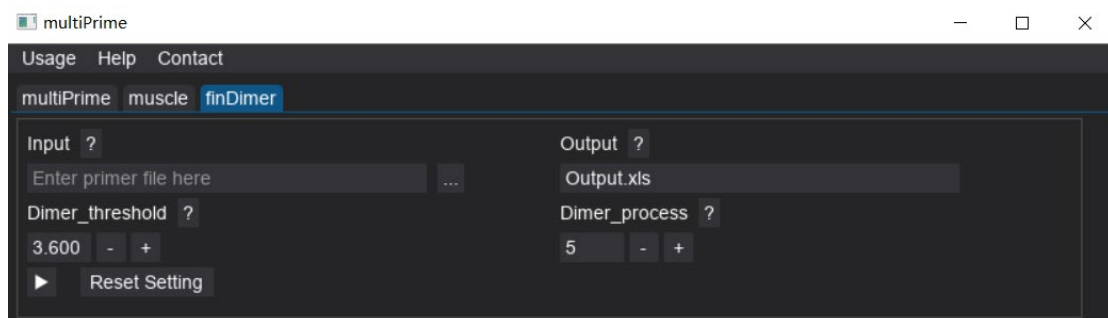
Method ? multiPrime1

DPrime_dposition ? 4 - +

3. **Primer Pair Generation:** Run multiPrime2-GUI.exe on your input data to initiate the primer pair design module. The tool will use its mismatch-tolerant approach to generate highly specific and effective degenerate primer pairs.



4. **Analyze Results:** Once the primer design step is complete, carefully review the results, including the generated primer pairs, PCR product lengths, melting temperatures, and other relevant factors.
5. **Dimer examination:** We have also integrated a dimer examination tool into the multiPrime2-GUI.exe. This tool accepts FASTA files and provides the capability to assess the potential for dimer formation within the FASTA sequences.



System Requirements

- Operating System: Windows
- CPU: NA
- RAM: NA
- Disk Space: NA

Dependencies

Please ensure you have the following dependencies installed on your system before using

multiPrime-core.exe:

- NA

Installation and Execution

- NA

Support and Contact

If you encounter any issues, have questions, or need further assistance, please don't hesitate to contact me at [yang_junbo_hi@126.com] or [1806389316@pku.edu.cn]. We value your feedback and are committed to enhancing the multiPrime pipeline for a better user experience.

Acknowledgments

We would like to express our gratitude to all contributors and developers who have made the multiPrime pipeline possible. Your dedication and support have been invaluable in creating this powerful tool for the scientific community.

License

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Thank you for choosing multiPrime2-GUI! We hope this tool proves to be an invaluable asset in your target sequence detection endeavors using tNGS. Happy sequencing!