



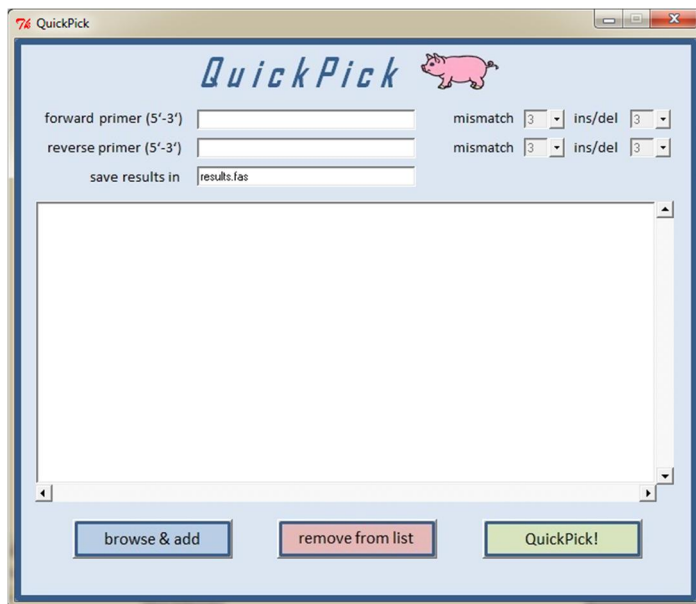
1. Usage

QuickPick is a handy tool to pick inserts from vector sequences. QuickPick will find inserts irrespective of ligation direction by searching primer sequences in sense and antisense orientation allowing up to five mismatches including insertions and deletions.

2. Requirements

QuickPick uses the SeqMap algorithm (Jiang and Wong 2008) for fast mismatch-tolerant primer detection. Therefore, seqmap.exe has to be copied into the QuickPick folder. SeqMap is freely available at <http://biogibbs.stanford.edu/~jiangh/SeqMap/>.

3. Implementation



QuickPick accepts .seq files as input, which contain pure sequence without annotation. Add files to the processing list by clicking "browse & add". Remove files from the processing list by selecting them and clicking "remove from list". Quote primer sequences (for the cloned insert) in the respective boxes and adjust maximum mismatch (incl. ins/del) and insertions/deletions (N's in input sequence will be treated as deletions). Enter the name of the file where your results will be saved. Start insert search by clicking the "QuickPick" button. The results file

will be saved in the QuickPick working directory. If one or both primer sequences could not be traced, the respective files will be listed in the progress window.

4. License

Anyone can use QuickPick free of charge for non-commercial use. For commercial use, please contact.

5. References

Hui Jiang and Wing Hung Wong (2008) SeqMap : mapping massive amount of oligonucleotides to the genome. *Bioinformatics* 24(20): 2395-2396.

Please report any bugs, trouble or suggestions for improvement to:

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