

High resolution classification of orthogroups by recursive dynamic Markov clustering

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Abstract

Key words: orthogroup, clustering

Table 1. File format support provided by each BuddySuite module for reading (R) and writing (W).

Format	SeqBuddy	AlignBuddy	PhyloBuddy
Clustal	R & W [†]	R & W	None
EMBL [‡]	R & W	R [†] & W	None

[†]All sequences must be the same length

[‡]Supports rich sequence annotation

Introduction

Methods

I used MAFFT (Kato and Standley, 2013), because it’s awesome.

Results

Discussion

Conclusions

Acknowledgments

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References

Kato, K. and Standley, D. M. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular biology and evolution*, 30(4): 772–780.