

CORRECTION

Open Access

State of the art: refinement of multiple sequence alignments

Saikat Chakrabarti*, Christopher J Lanczycki, Anna R Panchenko, Teresa M Przytycka, Paul A Thiessen, Stephen H Bryant

Abstract

Correction to Chakrabarti S, Lanczycki CJ, Panchenko AR, Przytycka TM, Thiessen PA and Bryant SH: State of the art: refinement of multiple sequence alignments. BMC Bioinformatics 2006, 7:499.

Correction

After publication of [1] we have noticed an error in our manuscript. We have realized that there were some numbers incorrectly inserted within the Table 1 of the manuscript [1]. Corrected values are now provided In

Table 1, for six of the numbers that were entered incorrectly: the SP scores for References 1, 4 and 5 under Muscle reference alignment (REFINER refinement alignment) and, SP scores for References 2, 3 and 5 under T-Coffee reference alignment (Default refinement

Table 1 Impact on alignment quality following refinement.

BALiBASE reference alignments	ClustalW				Dialign				Mafft			
	Default	RASCAL	RF	REFINER	Default	RASCAL	RF	REFINER	Default	RASCAL	RF	REFINER
Reference 1	0.65	0.63	0.66	0.66	0.62	0.65	0.67	0.62	0.70	0.69	0.69	0.71
Reference 2	0.78	0.80	0.80	0.80	0.78	0.80	0.79	0.79	0.83	0.82	0.83	0.82
Reference 3	0.66	0.69	0.67	0.68	0.65	0.64	0.65	0.66	0.76	0.73	0.75	0.77
Reference 4	0.67	0.68	0.66	0.70	0.67	0.71	0.66	0.69	0.75	0.73	0.70	0.77
Reference 5	0.65	0.67	0.66	0.68	0.67	0.65	0.64	0.67	0.76	0.73	0.72	0.76
Average	0.682	0.694	0.69	0.704	0.678	0.690	0.682	0.692	0.760	0.740	0.738	0.766
Increment (%)	0	1.760	1.173	3.226	0.000	1.770	0.590	2.065	0.000	-2.632	-2.895	0.789
BALiBASE reference alignments	Muscle				Probcons				T-Coffee			
	Default	RASCAL	RF	REFINER	Default	RASCAL	RF	REFINER	Default	RASCAL	RF	REFINER
Reference 1	0.66	0.66	0.67	0.68	0.72	0.72	0.70	0.73	0.68	0.68	0.69	0.68
Reference 2	0.80	0.81	0.80	0.80	0.83	0.83	0.82	0.82	0.8	0.83	0.82	0.82
Reference 3	0.71	0.71	0.71	0.73	0.76	0.73	0.75	0.77	0.61	0.62	0.62	0.64
Reference 4	0.71	0.72	0.68	0.74	0.77	0.75	0.71	0.77	0.71	0.71	0.70	0.72
Reference 5	0.70	0.71	0.67	0.72	0.76	0.74	0.71	0.75	0.72	0.73	0.69	0.74
Average	0.716	0.722	0.706	0.734	0.768	0.754	0.738	0.77	0.704	0.714	0.704	0.720
Increment (%)	0.000	0.838	-1.397	2.514	0.000	-1.823	-3.906	0.260	0.000	1.420	0.000	2.273

* Correspondence: chakraba@mail.nih.gov

National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894, USA

alignment). However, this does not affect our original interpretation of the data presented in our original publication in any way. We regret any inconvenience that this inaccuracy might have caused.

Received: 10 November 2009

Accepted: 4 January 2010 Published: 4 January 2010

References

1. Chakrabarti S, Lanczycki CJ, Panchenko AR, Przytycka TM, Thiessen PA, Bryant SH: State of the art: refinement of multiple sequence alignments. *BMC Bioinformatics* 2006, 7:499.

doi:10.1186/1471-2105-11-3

Cite this article as: Chakrabarti et al.: State of the art: refinement of multiple sequence alignments. *BMC Bioinformatics* 2010 11:3.

Submit your next manuscript to BioMed Central
and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

