CORRECTION
State of the art: refinement of multiple sequence alignments
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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 alignment).

Table 1 Impact on alignment quality following refinement.

| BAiBASE reference alignments | ClustalW | Dialign | Mafft |
|-----------------------------|---------|---------|-------|
|                             | Default | RASCAL | RF    | REFINER | Default | RASCAL | RF | REFINER | Default | RASCAL | RF | REFINER |
| Reference 1                 | 0.65    | 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  | 0.78    | 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   | 0.66 | 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    | 0.73    | 0.70   | 0.77 |
| Reference 5                 | 0.65    | 0.67   | 0.66  | 0.68    | 0.67    | 0.65   | 0.64 | 0.76    | 0.73    | 0.72   | 0.76 |
| Average                     | 0.682   | 0.694  | 0.69  | 0.704   | 0.690   | 0.682  | 0.692| 0.760   | 0.740   | 0.738  | 0.766|
| Increment (%)               | 0.000   | 1.760  | 1.173 | 3.226   | 0.000   | 1.770  | 0.590| 2.065   | 0.000   | -2.632 | -2.895|

| BAiBASE 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    | 0.70   | 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 | 0.83    | 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   | 0.64 |
| Reference 4                 | 0.71    | 0.72   | 0.68  | 0.74    | 0.77    | 0.75   | 0.71 | 0.77    | 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    | 0.69   | 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|
| Increment (%)               | 0.000   | 0.838  | -1.397| 2.514   | 0.000   | -1.823 | -3.906| 0.260   | 0.000   | 1.420  | 2.273|

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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.

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References

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