

Corrigendum

HH-MOTiF: *de novo* detection of short linear motifs in proteins by Hidden Markov Model comparisons

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The authors wish to make the following correction to their article.

In the Supplementary Information, the following equation is incorrect:

Regex generation and evaluation: The p-value of a regex with highly or moderately conserved columns C_{cons} and cumulative frequencies $freq_j$ of amino acids in the input dataset listed in the column j is calculated according to the formula:

$$p = \frac{\sum_{i=1}^{N_{corr}} \left(1 - \left(1 - \prod_{j=1}^{C_{cons}} freq_j \right)^M \right)}{N_{corr}}$$

This formula is the averaged version of the Šidák correction formula (1). N_{corr} is the effective number of non-homologous proteins for a given motif tree.

The correct equation is provided below and has been corrected in the published article:

Regex generation and evaluation: The p-value of a regex with highly or moderately conserved columns C_{cons} and cumulative frequencies $freq_j$ of amino acids in the input dataset listed in the column j is calculated according to the formula:

$$p = \frac{\sum_{i=1}^{N_{tree}} \left(1 - \left(1 - \prod_{j=1}^{C_{cons}} freq_j \right)^M \right)}{N_{tree}}$$

This formula is the averaged version of the Šidák correction formula (1). N_{tree} is the number of proteins a given motif tree locates to.

1. Wright, S.P. (1992) Adjusted P-values for simultaneous inference. *Biometrics*, 48, 1005–1013.

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