

ERRATUM

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Erratum to: Improving protein order-disorder classification using charge-hydrophathy plots

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During the production of our manuscript [1], an incorrect Figure 1 was put in place of the one we submitted, and we erred in not appropriately informing the production staff of this mistake. The corrected figure and the text describing this figure, as well as the figure legend, are present herein.

As stated in our manuscript [1], “The C-H plots generated using scale SVM parameters scale, Kyte-Doolittle hydrophathy scale, and Guy hydrophathy scale for whole protein prediction are shown in Figure 1. Figure 1A, which is derived by SVM parameters scale, shows many fewer misclassified disordered proteins on the ordered side, compared to Figure 1B and 1C.”

As further stated in reference [1]: “Figure 1. Charge-Hydrophathy plots. In (A) the IDP-Hydrophathy scale was used, in (B) the Guy (1985) Hydrophathy scale was used, and in (C) the Kyte-Doolittle (1981) hydrophathy scale was used. Red circles indicate disordered proteins, blue circles indicate structured proteins. For these plots, each scale was normalized to be in the interval of 0 to 1. The Guy’s scale is multiplied by -1 prior to normalization to conform to the energy rule set by Kyte-Doolittle scale. In (A) the function describing the boundary is: $\langle \text{charge} \rangle = 3.31 \langle \text{hydrophathy} \rangle - 0.97$. In (B) the function describing the boundary is: $\langle \text{charge} \rangle = 2.32 \langle \text{hydrophathy} \rangle - 0.93$. In (C), the function describing the boundary is $\langle \text{charge} \rangle = 1.35 \langle \text{hydrophathy} \rangle - 0.49$.”

For more details, the reader is referred to the published manuscript [1].

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1. Huang F, Oldfield CJ, Xue B, Hsu WL, Meng J, Liu X, Shen L, Romero P, Uversky VN, Dunker AK. IDP hydrophathy: A new hydrophathy scale that improves disorder prediction. *BMC Bioinformatics*. 2014;15 Suppl 17:54.

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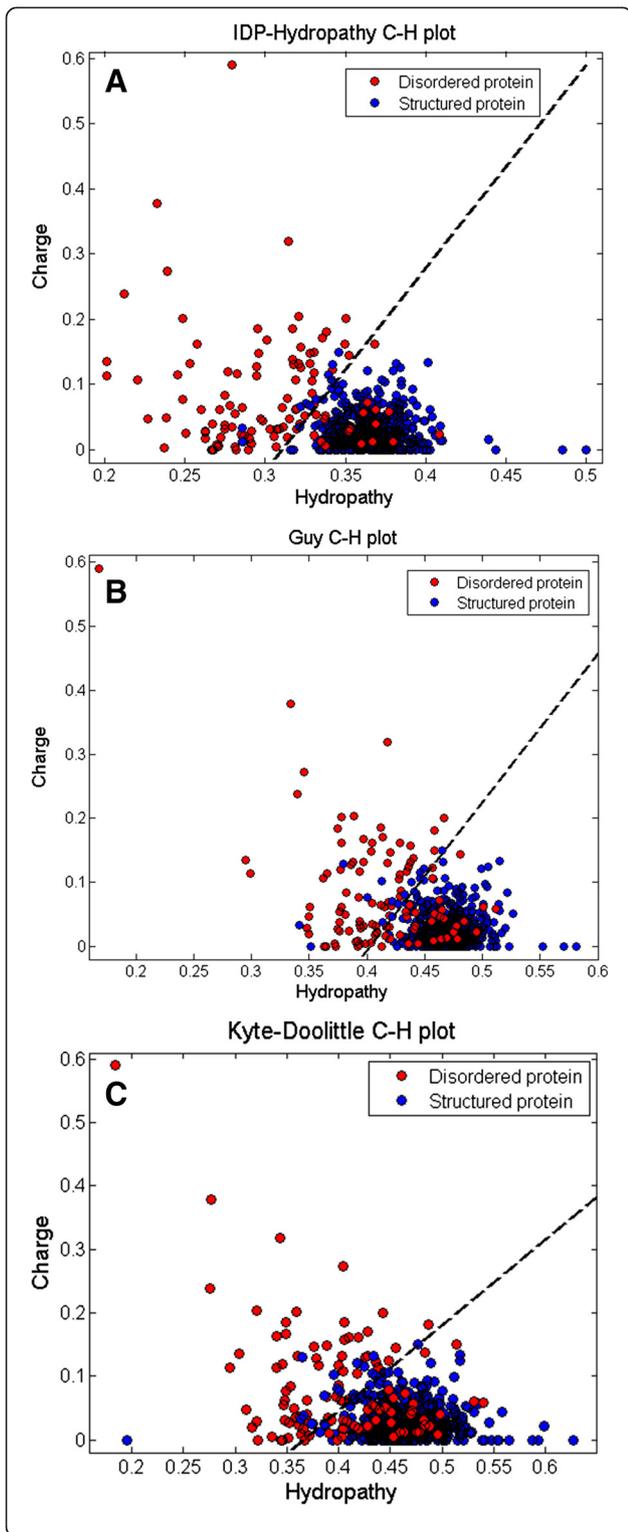


Figure 1. Charge-Hydropathy plots. In (A) the IDP-Hydropathy scale was used, in (B) the Guy (1985) Hydropathy scale was used, and in (C) the Kyte-Doolittle (1981) hydropathy scale was used. Red circles indicate disordered proteins, blue circles indicate structured proteins. For these plots, each scale was normalized to be in the interval of 0 to 1. The Guy's scale is multiplied by -1 prior to normalization to conform to the energy rule set by Kyte-Doolittle scale. In (A) the function describing the boundary is: $\langle \text{charge} \rangle = 3.31 \langle \text{hydropathy} \rangle - 0.97$. In (B) the function describing the boundary is: $\langle \text{charge} \rangle = 2.32 \langle \text{hydropathy} \rangle - 0.93$. In (C), the function describing the boundary is: $\langle \text{charge} \rangle = 1.35 \langle \text{hydropathy} \rangle - 0.49$.