

*Supplement to:*

**MoMo: Discovery of statistically significant post-translational modification motifs**

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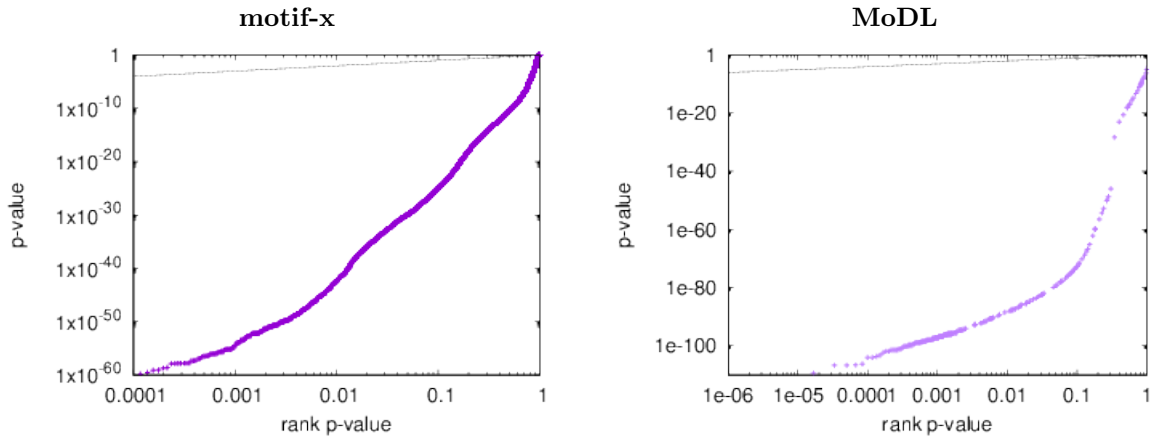


Figure 1: **Inaccuracy of MoMo  $p$ -values when background peptides are from the proteome.** The two panels show empirical assessments (Q-Q plots) of the statistical accuracy of the  $p$ -values reported by MoMo’s improved implementations of motif-x (left panel) and MoDL (right panel), respectively, when the background peptides are from the *Plasmodium falciparum* proteome. The modified peptides are shuffled versions of the peptides in [1] Supplemental Data 2 pr8b00062.si\_003.xlsx. MoMo parameters are `--db-background --score-threshold 0.001`. The sorted adjusted  $p$ -values ( $Y = 1 - (1 - p_i)^n$ , where  $p_i$  is the unadjusted  $p$ -value and  $n$  is the number of independent tests), are plotted against the rank  $p$ -values ( $X = 1/(r_i + 1)$ ), where  $r_i$  is the rank of the  $p$ -value), for 10,000 shuffled input datasets, where shuffling conserves the central residue.



Figure 2: Motifs reported by motif-x\* when run with and without the `-harvard` switch on the 3875 peptides in the Supplemental Data 2 file from Pease *et al.* [1]. As noted in the paper, the set of motifs found by motif-x\* when the `-harvard` switch is given is identical to those found by the original motif-x algorithm.

## References

- [1] Pease, B. N., Huttlin, E. L., Jedrychowski, M. P., Dorin-Semblat, D., Sebastiani, D., Segarra, D. T., Roberts, B. F., Chakrabarti, R., Doerig, C., Gygi, S. P., and Chakrabarti, D. (2018). Characterization of *Plasmodium falciparum* Atypical Kinase Pfk7 Dependent Phosphoproteome. *Journal of Proteome Research*, **17**, 2112–2123.