Lite-SeqCNN: A Light-weight Deep CNN Architecture for Protein Function Prediction : Supplemental document S1

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S.I. ENSEMBLE BASED COMPARISON ANALYSIS FOR DATA2017, CAFA3, AND DATA2016 DATASETS

In this section, the prediction results produced by $Lite-SeqCNN^+$ trained on different segmented databases having segment sizes $\in (300, 400, 500)$ are shown in Figures S1(for Data2017), S2 (for CAFA3), and S3 (for Data2016). The results produce with segment sizes (300, 400, and 500) are very much similar to those obtained with the *Lite-SeqCNN$^+$* (with segment sizes taken as 200, 300, and 400).
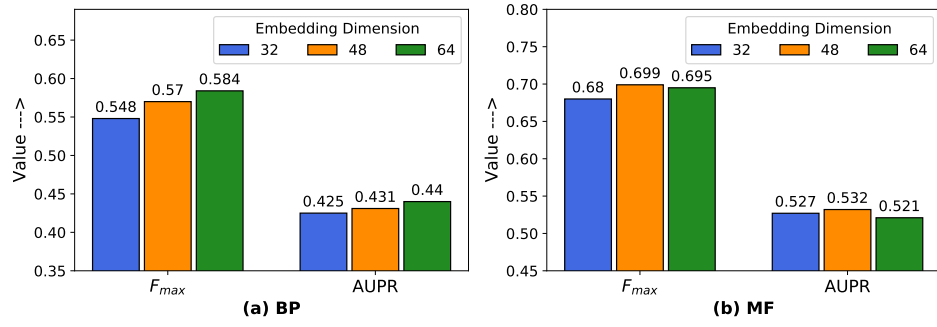
Fig. S1. Bar graph showing the change in values of the proposed ensemble model, *Lite-SeqCNN$^+$*, for F_{max} and AUPR on increasing the embedding dimension given as legend for Data2017 dataset.
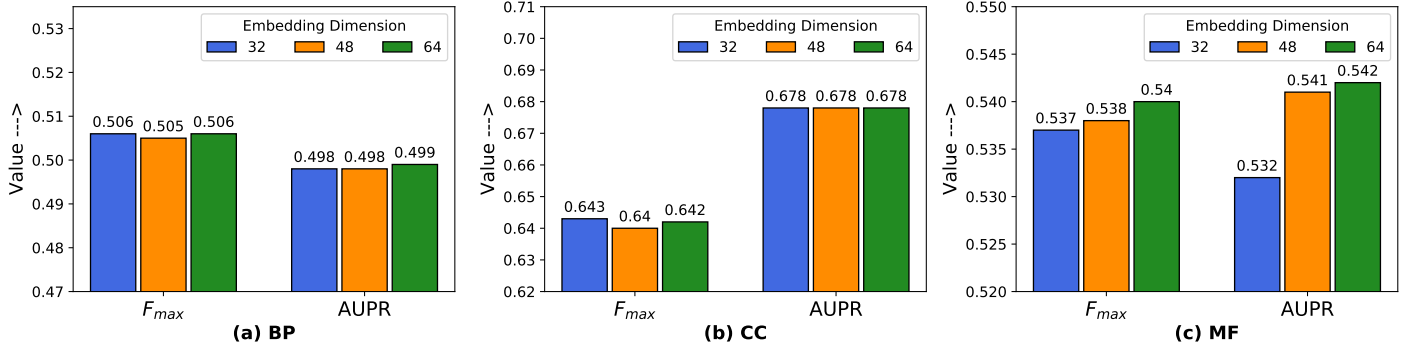

Fig. S2. Bar graph showing the change in values of the proposed ensemble model, *Lite-SeqCNN$^+$*, for F_{max} and AUPR on increasing the embedding dimension given as legend for CAFA3 dataset.
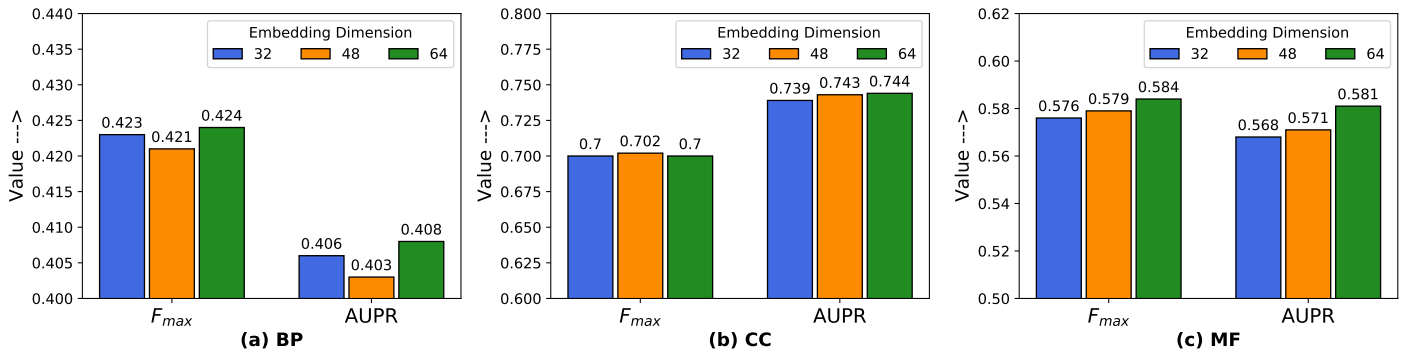

Fig. S3. Bar graph showing the change in values of the proposed ensemble model, *Lite-SeqCNN$^+$*, for F_{max} and AUPR on increasing the embedding dimension given as legend for Data2016 dataset.