

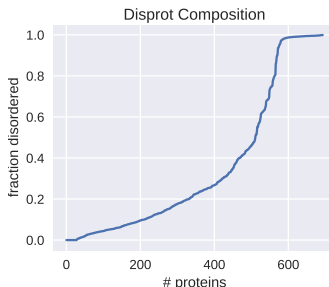
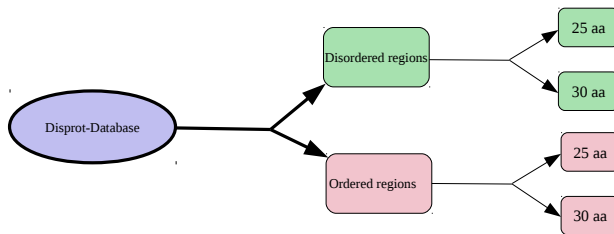
Prediction of Disordered Protein Regions

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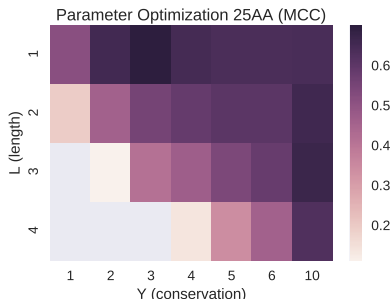
2016-06-16

We extracted fragments from Disprot.



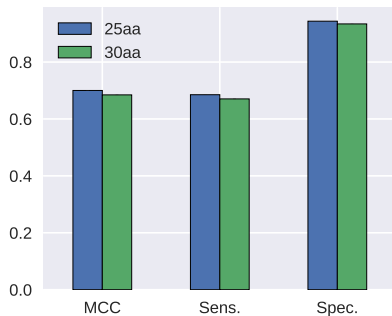
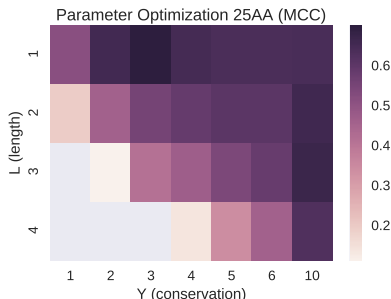
We performed a parameter optimization on the profile kernel.

Optimal combination: $L = 1$, $Y = 3$:

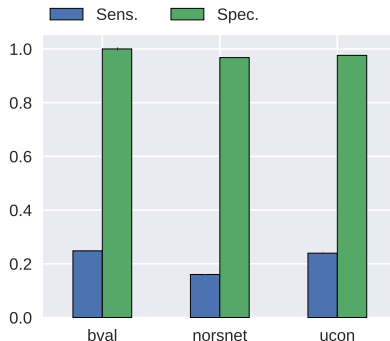
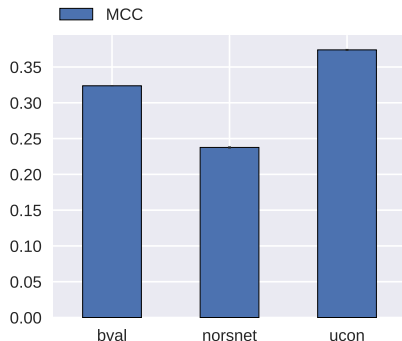


We performed a parameter optimization on the profile kernel.

Optimal combination: $L = 1$, $Y = 3$:



We tested our method against other approaches.



Is the amino acid composition driving disorder?

