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Predicting Potential Protein Therapeutic Candidates from the Gut Microbiome

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Abstract : Microbes that reside inside the mammalian GI tract, commonly referred to as the gut microbiome, have been shown to have therapeutic effects in animal models of disease. We hypothesize that specific proteins produced by these microbes are responsible for this activity and may be used directly as therapeutics. To speed up the discovery of these key proteins from the big-data metagenomics, we have applied machine learning techniques. Using amino acid sequences of known epitopes and their corresponding binding partners, protein interaction descriptors (PID) were calculated, making a positive interaction set. A negative interaction dataset was calculated using sequences of proteins known not to interact with these same binding partners. Using Random Forest and positive and negative PID, a machine learning model was trained and used to predict interacting versus non-interacting proteins. Furthermore, the continuous variable, cosine similarity in the interaction descriptors was used to rank bacterial therapeutic candidates. Laboratory binding assays were conducted to test the candidates for their potential as therapeutics. Results from binding assays reveal the accuracy of the machine learning prediction and are subsequently used to further improve the model.

Keywords : protein-interactions, machine-learning, metagenomics, microbiome
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