

DeepGOPlus: Improving protein function prediction from sequence

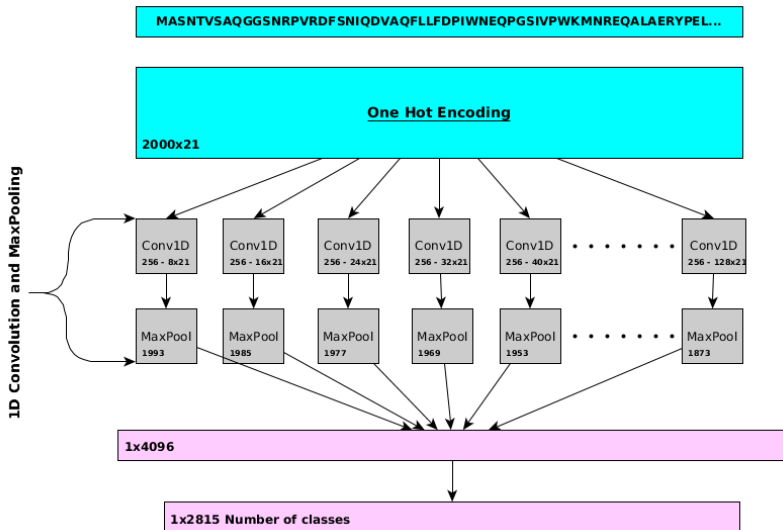
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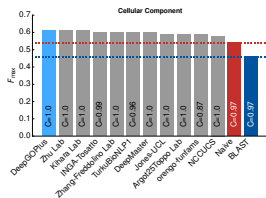
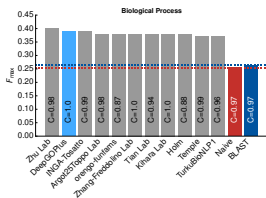
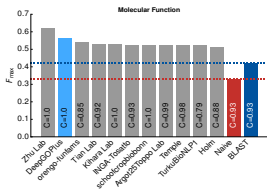
Bio-Ontologies Research Group, 2019



Deep Learning Model



Results



Annotate 50 proteins per second.

DeepGOPlus Protein Function prediction.

DeepGOPlus is a novel method for predicting protein functions based on protein sequence. It uses deep convolutional neural networks to learn sequence features and combines predictions with sequence similarity based predictions.

The tool only needs protein sequence as an input. The source code of the model is available on [GitHub repository](#)

The [REST API](#) is available for submitting sequences programmatically.

The number of sequences in one query should not exceed 1000!

Our previous function predictor [DeepGO](#) is available for running from command line.

Examples:

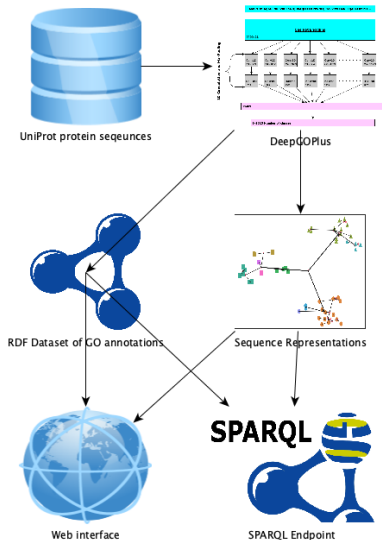
- [AAKB1 \(P80386\)](#) - FASTA
- [PPP2R5D \(Q14738\)](#) - Raw sequence

Data

DeepGOPlus by [BORG](#).

KAUST

Biohackathon



- UniProtKB/SwissProt - 550K proteins
- UniProtKB/Trembl - 167M proteins

Thanks !

<http://deepgoplus.bio2vec.net>

<https://github.com/bio-ontology-research-group/deepgoplus/>