Tutorial on PlantPathoPPI

This tutorial provides a step-by-step guide on predicting protein-protein interactions (PPI) between plant and pathogen proteins using PlantPathoPPI.

Upon visiting the PlantPathoPPI homepage, users can initiate the prediction process by clicking the “Prediction” button, as shown in Figure 1.

Welcome to PlantPathoPPI!

Protein-protein interactions play a critical role in deciding whether a plant's encounter with a pathogen results in disease or not.Thus, an in-depth understanding of plant-pathogen interactions is required for the breeding of disease-resistant crops and the improvement of agricultural productivity. In view of this, PlantPathoPPI, a machine learning based classifier has been developed to facilitate the task of predicting protein-protein interaction (PPI) between plant and pathogen protein based on their amino acid sequence.

Click on "Start Prediction" or go to "Prediction" tab to start the prediction. Provide the protein sequence pairs of plant and pathogen in their respective input box and then click "Submit". Result is provided in tabular format. Positive and negative interactions are represented as "1" and "0" respectively, in the "Prediction" column of the result. PlantPathoPPI also provides probability score of each prediction, i.e., the probability of interaction or no interaction. As obvious, the sum of these two probabilities will be equal to 1.

Figure 1: Homepage of PlantPathoPPI.

Providing Input Sequences

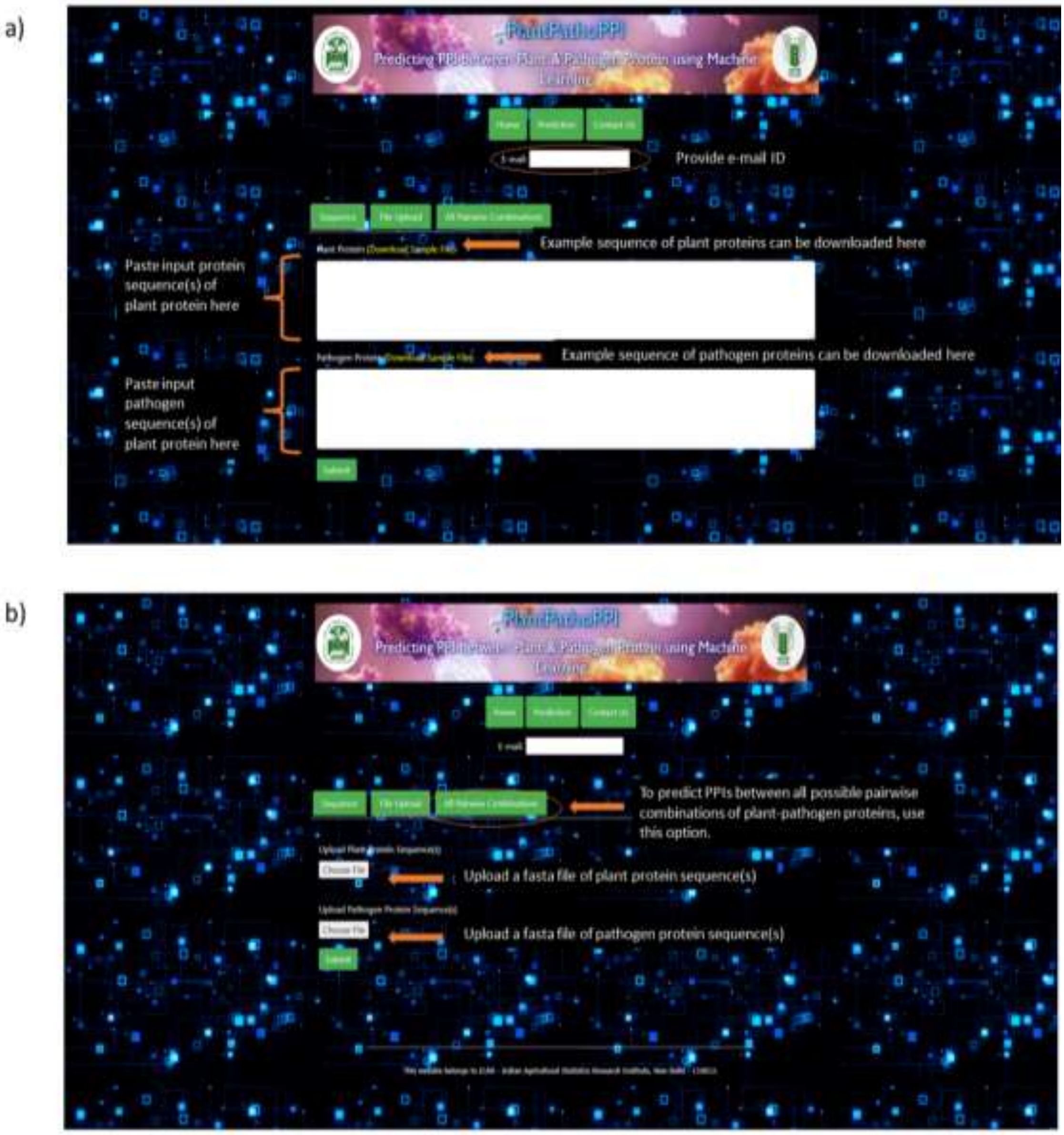
Users can input protein sequences in two ways:

- ✓ Paste the sequences directly into the respective text boxes.
- ✓ Upload sequences in FASTA format.

Additionally, users can:

- ✓ Provide pre-defined protein pairs for interaction prediction.

- ✓ Input a variable number of plant and pathogen proteins and generate all possible pairwise combinations for analysis (Figure 2).



Provide e-mail ID

Example sequence of plant proteins can be downloaded here

Paste input protein sequence(s) of plant protein here

Example sequence of pathogen proteins can be downloaded here

Paste input pathogen sequence(s) of plant protein here

To predict PPIs between all possible pairwise combinations of plant-pathogen proteins, use this option.

Upload a fasta file of plant protein sequence(s)

Upload a fasta file of pathogen protein sequence(s)

Figure 2: View of the prediction tab. a) Option to paste the sequence(s) in respective tab. b) Option to upload the sequence(s) in fasta format.

Viewing and Interpreting Results

Predictions are displayed in a tabular format and can be downloaded for further analysis (Figure 3).

Prediction outcomes:

- ✓ 1 → Positive interaction predicted.
- ✓ 0 → No interaction predicted.

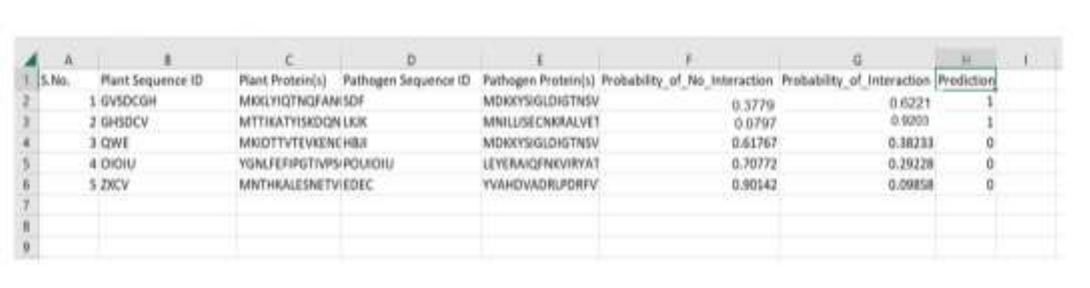
Each prediction includes an interaction probability score.

Figure 3: Result view.

In the given example, the result shows that the probability of interaction between the first two given protein pairs is 100%. ‘1’ in the ‘Prediction’ column means that the model predicted positive interaction. Whereas, the bottom three pairs have a higher probability of not interacting and hence the final prediction was in favor of negative interaction or no interaction represented by ‘0’.

Downloading and Analyzing Results

Users can download results for offline analysis. The downloaded results can be viewed in Excel or any spreadsheet tool (Figure 4).



S.No.	Plant Sequence ID	Plant Protein(s)	Pathogen Sequence ID	Pathogen Protein(s)	Probability_of_No_Interaction	Probability_of_Interaction	Prediction
1	GVSDCGH	MKKLYIQTNQFAN	SDF	MDKKYSIGLDIGTNSV	0.3779	0.6221	1
2	GHSDCV	MTTIKATYISKDQN	LKJK	MNILLISECNKRALVET	0.0797	0.9203	1
3	QWE	MKIDTTVTEVKENC	HBJI	MDKKYSIGLDIGTNSV	0.61767	0.38233	0
4	OIOIU	YGNLFEFIPGTIVPS	POUIOIU	LEYERAIQFNKVIRYAT	0.70772	0.29228	0
5	ZXCV	MNTHKALESNETVI	EDEC	YVAHDVADRLPDRFV	0.90142	0.09858	0

Figure 4: Snapshot of the downloaded result.