

Table of Contents

Supplement S1 Methods Supplement - Datasets and Computational Methods

1. Gold standard datasets for classification
2. Biological data sources for human protein interaction prediction
3. The random forest classifier
4. Performance evaluation

Supplement S2 Results Supplement - Computational Results

1. Performance comparison – AUC scores
2. Performance comparison between the ‘Receptor’ protein interaction prediction task and the ‘General’ human protein interaction prediction task
3. Performance comparison between two settings of gold standard negatives
4. Performance comparison between two settings of gold standard positive for EGFR to investigate “homology effect”
5. Feature importance
6. Generating the receptor interactome and statistical significance analysis
7. Overlap and comparison to existing databases

Supplement S3 Methods Supplement - Experimental Methods

1. Materials
2. Transfection
3. Protein gels and western blots
4. In-vivo interaction studies of EGFR-TGF- β 1
5. In-vitro interaction studies of EGFR-TGF- β 1
6. Expression and purification of EGFR domains
7. Expression of GFP tagged dynamin-2
8. siRNA Downregulation of Hck

Supplement S4 Analysis Supplement - Visualization of Receptor Interactome

1. About the visualization
2. Number of nodes or edges in selected sub graphs of the receptor interactome
3. Visualization of the receptor interactome – predicted and known
4. The subgraphs related to receptors and ligands – predicted and known
5. The subgraphs connected to EGFR – predicted and known

Supplement S5 Web Server HMRI (Human Membrane Receptor Interactome)

1. Check the query protein
2. Search interaction partners for the query protein
3. Search interaction pairs among the set of input proteins
4. Check the predicted interaction score and related feature vector for a pair of input proteins
5. An example output from HMRI

Supplement S6 Results Supplement – the Predicted Receptor Interactome

This list of predicted receptor interaction pairs would be shared in EXCEL format when the paper is accepted. The statistical significance p-value would be included as well.

Supplementary Website <http://www.cs.cmu.edu/~qyj/HMRI>

This supplementary website provides file downloads of the predicted interaction scores for all human membrane receptors. The software implementation (including source code) of the proposed computational system could be downloaded here as well.