Inter-Species Pathway Perturbation Prediction via Data Driven Detection of Functional Homology

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Supplemental Material

Figure S1: Team performance as a function of the number of stimuli that human pathways are perturbed by in the training data set.

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	TN	\mathbf{FP}	Specificity
$Team 49_{alt1}$	1820	0	1.000
$Team 111_alt1$	1811	9	0.995
Team 50	1799	21	0.988
Team 105	1797	23	0.987
Team 49	1737	83	0.954
Team 133	1735	85	0.953
$Team 133_alt1$	1734	86	0.953
Team 131	1566	254	0.860
Team 52	1362	458	0.748
Team 111	9	1811	0.005

Table S2: Specificity on the 70 pathways that are not perturbed in the human test stimuli.

Correlation Analysis of gene pairs

In this subsection we show how our response-ortholog pairs are correlated between rat and human in the training data, as well as the test data. For reference, we also show the correlations of sequence-based orthologs (HGNC).

The following plots summarize the spearman correlations of inter-species gene pairs. To calculate these correlations, we used the normalized ranks, which we derived from the moderated t-values as returned by LIMMA (see main method section Team49).



Figure S2: Example pairs for the Team49 method. The left column shows gene ranking in training stimuli, while the right column shows gene ranking in test stimuli. The gene pairs shown have the 75th, 80th, 90th, 95th and 99th percentile correlation in the training data.



Figure S3: Example pairs for the Team133_alt1 method. The left column shows gene ranking in training stimuli, while the right column shows gene ranking in test stimuli. The gene pairs shown have the 75th, 80th, 90th, 95th and 99th percentile correlation in the training data.



Figure S4: Example pairs for the sequence-based ortholog pairs (HGNC). The left column shows gene ranking in training stimuli, while the right column shows gene ranking in test stimuli. The gene pairs shown have the 75th, 80th, 90th, 95th and 99th percentile correlation in the training data.

Response-ortholog pair correlation: Team49



Response-ortholog pair correlation: Team133_alt1



Sequence-based ortholog pair correlation



Figure S5: Gene pair correlation in training data vs test data. In all cases the correlation was significant (p < 0.0001).