I'll create a markdown table explaining the STRING database columns, focusing especially on how the combined score is computed.

STRING Database Column Explanations

Column	Description
neighborhood	Score based on genomic proximity of genes across multiple species; indicates potential operons or co-regulated gene clusters
fusion	Score reflecting evidence of gene fusion events across species; suggests functional relationship
cooccurrence	Score based on phylogenetic profiles (presence/absence patterns across species)
coexpression	Score derived from correlated gene expression patterns across multiple experiments
experimental	Score from direct protein-protein interaction data (Y2H, co-IP, etc.)
database	Score from curated pathway databases and expert knowledge bases
textmining	Score from automated text analysis of scientific literature co-mentions
combined_score	Integrated confidence score (0-1000) combining all evidence types

Combined Score Calculation

The combined score in STRING uses a probabilistic approach based on naive Bayesian methods:

$$S = 1 - \prod_i (1 - S_i)$$

Where:

- S is the combined score
- S_i represents each individual evidence score (normalized between 0 and 1)
- $\prod$ is the product operator

This approach:

1. Treats each evidence channel as independent
2. Ensures that multiple weak signals can still produce a strong combined score
3. Prevents any single evidence type from dominating the final score

The final score is then calibrated against a gold standard of known interactions to ensure that the combined score reflects the probability that the interaction is biologically meaningful.