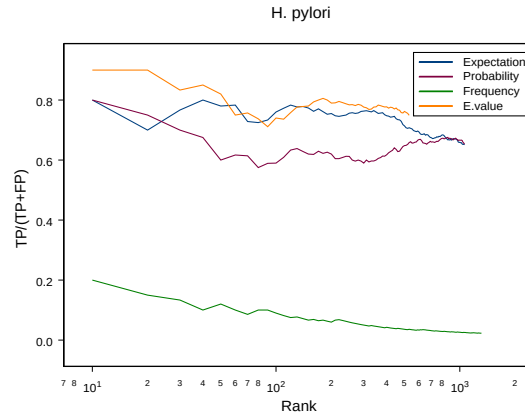


Figure S3



The relationship between rank and true positive rate ($TP/(TP+FP)$) compared to the domain interactions from *H. pylori* for predicted domain interactions from *H. pylori* based on four score functions. “Expectation” ranks domain pairs according to the expected number of occurrences of domain pairs in protein interactions; “Probability” ranks domain pairs according to the estimated probability of interactions from the MLE method; “Frequency” ranks domain pairs according to the number of protein interactions having domain pair; “E-value” ranks domain pairs according to the E-value defined in Riley et al. [1].

References

- [1] Riley, R., Lee, C., Sabatti, C. and Eisenberg, D. (2005) Inferring protein domain interactions from databases of interacting proteins. *Genome Bio.*, **6**(10), R89.