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FASTERp: A Feature Array Search Tool for Estimating Resemblance of Protein Sequences

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FASTERp: A Feature Array Search Tool for Estimating Resemblance of Protein Sequences

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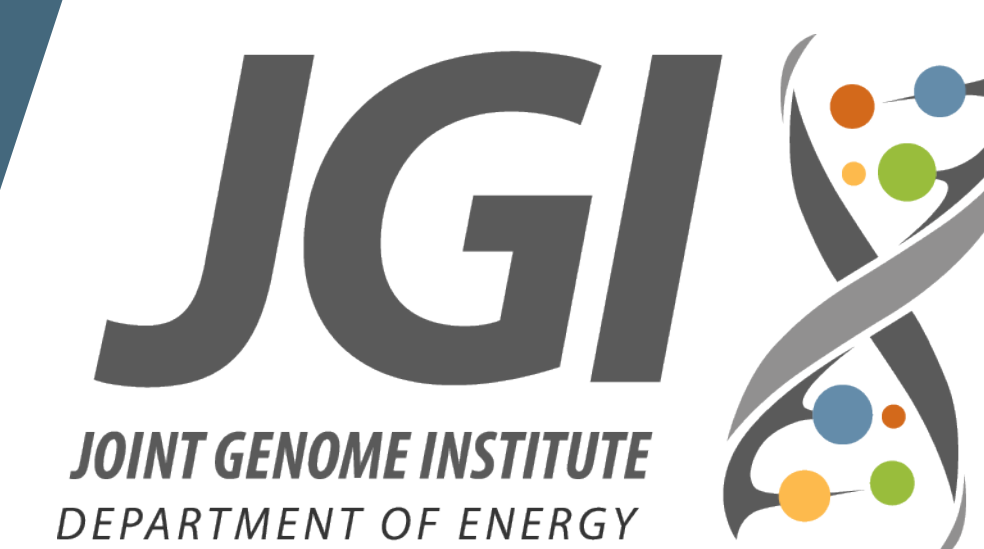
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FASTERp: A Feature Array Search Tool for Estimating Resemblance of protein sequences

Derek N. Macklin, Rob Egan, Zhong Wang
The Joint Genome Institute, Walnut Creek, CA, 94598



How can we efficiently perform homology search against billions of protein sequences?

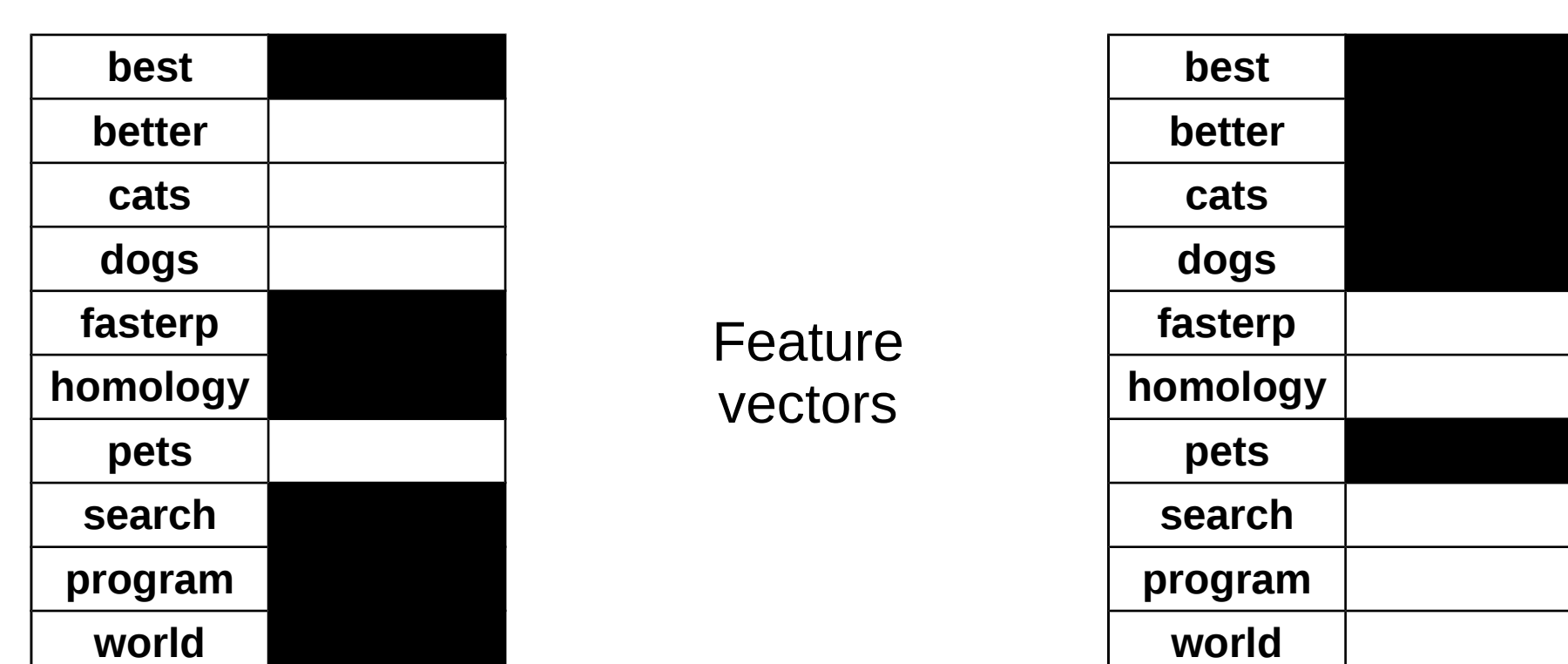
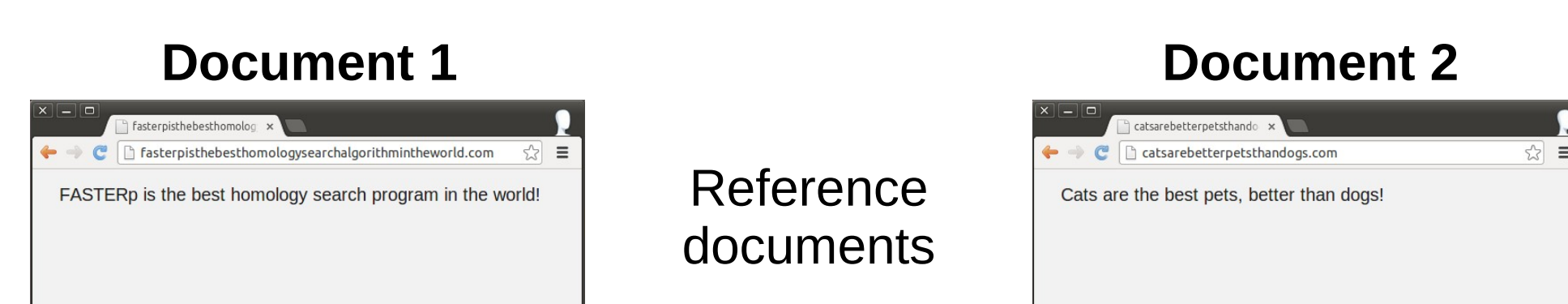
HYPOTHESIS

We can represent protein sequences as feature vectors and rapidly compute vector similarity.

RELATED WORK

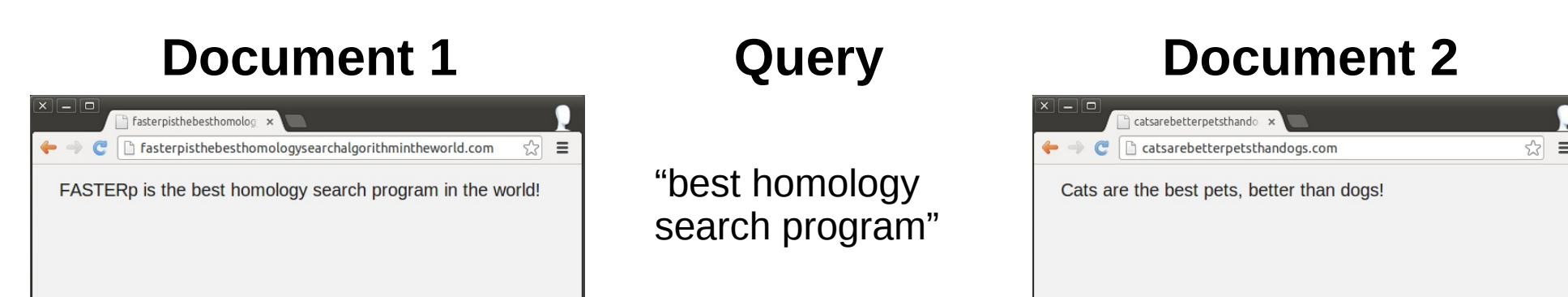
Search engines query against trillions of URLs

They represent documents as a feature vector using a "bag of words" model



Geometrical representation

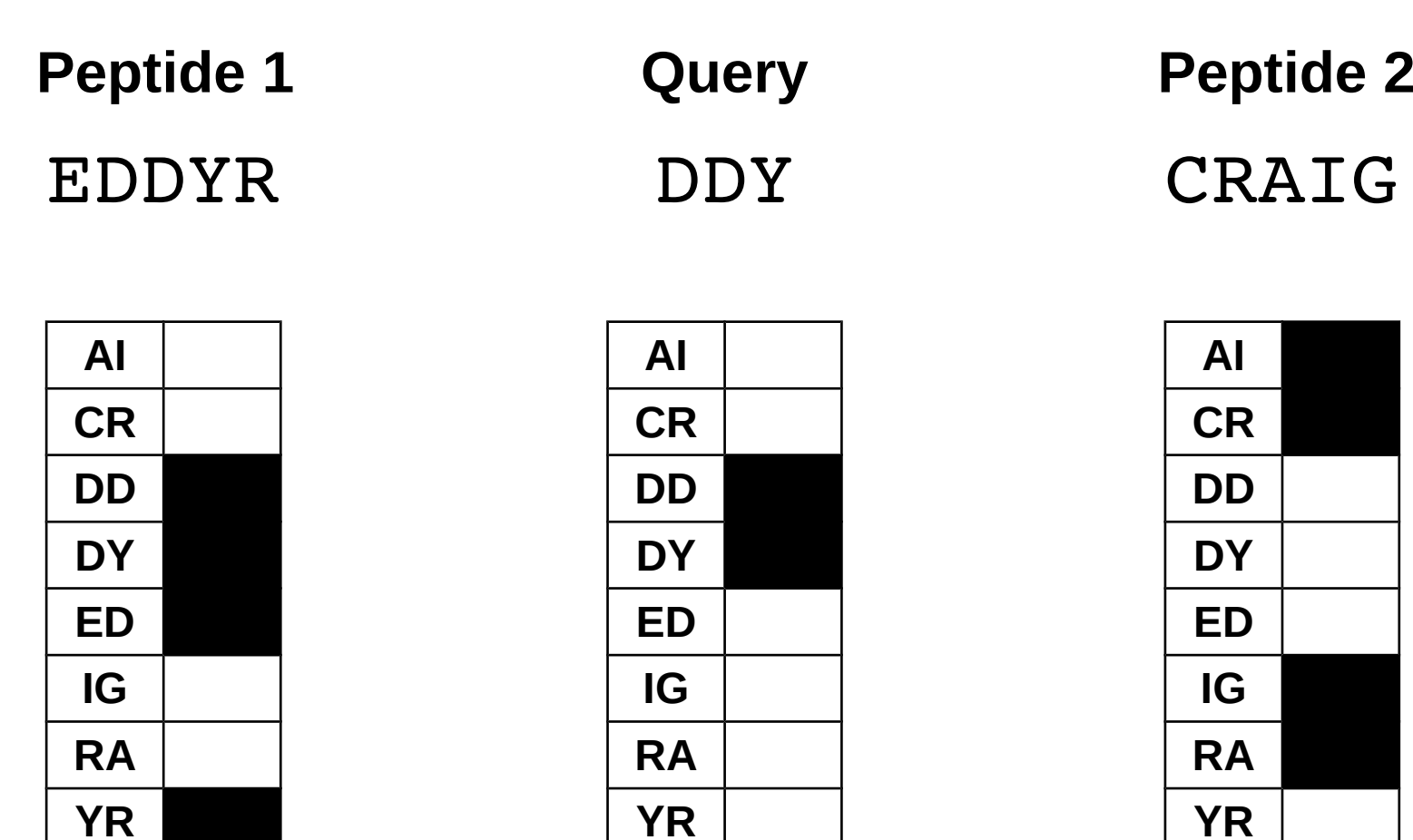
Similarity of feature vectors can be rapidly computed to find documents matching query



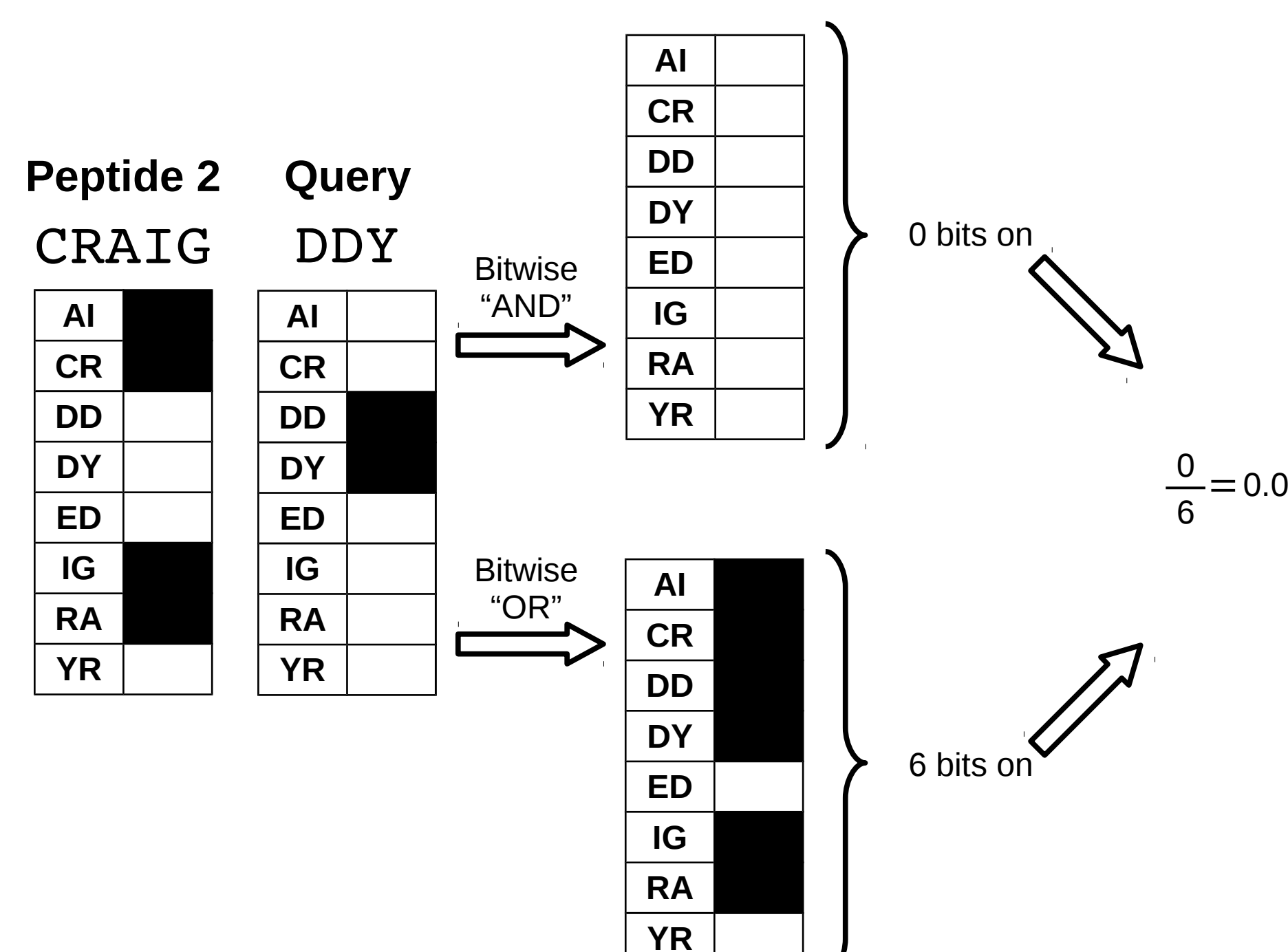
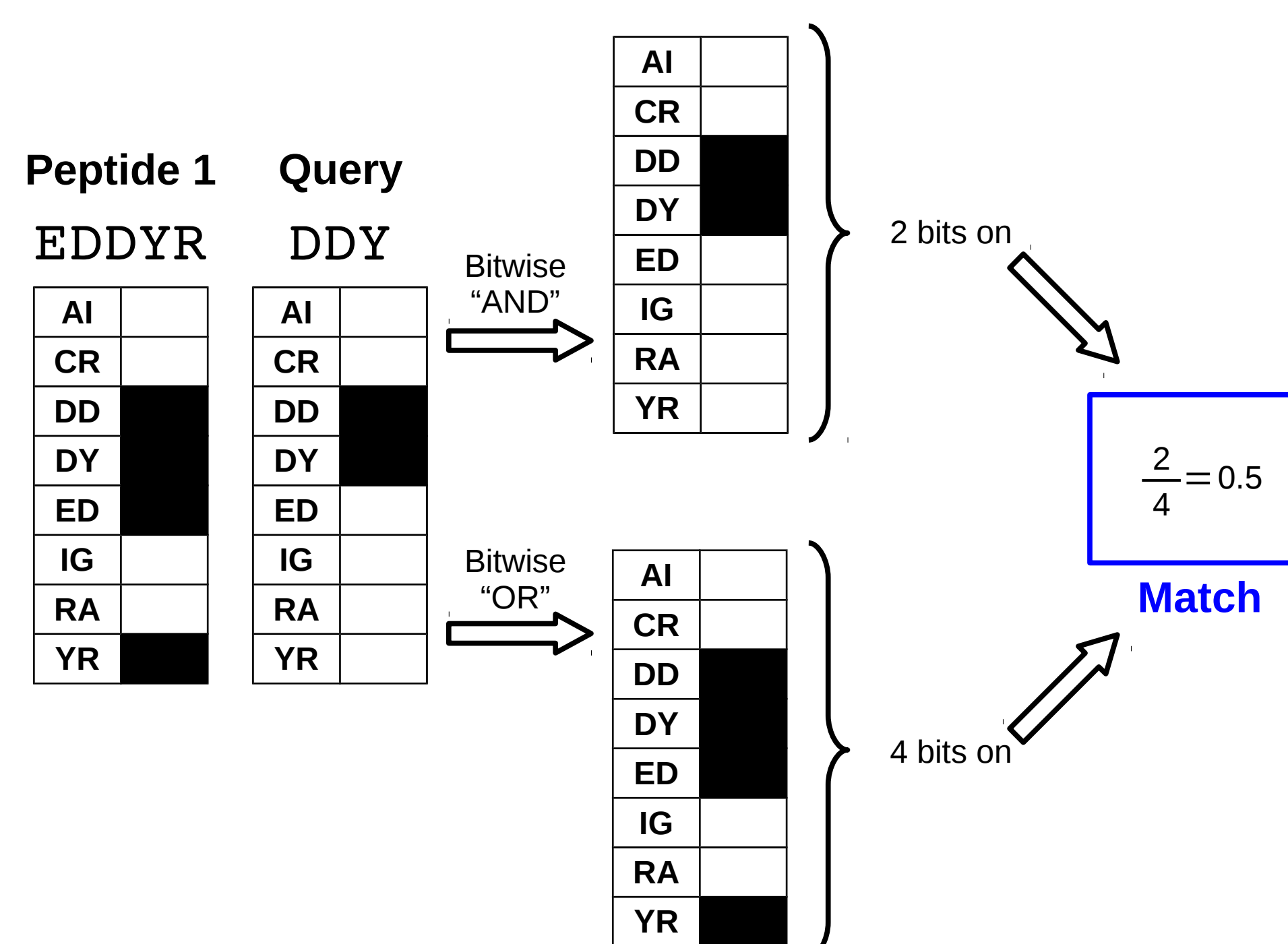
Match

METHODS

Use short kmers as features

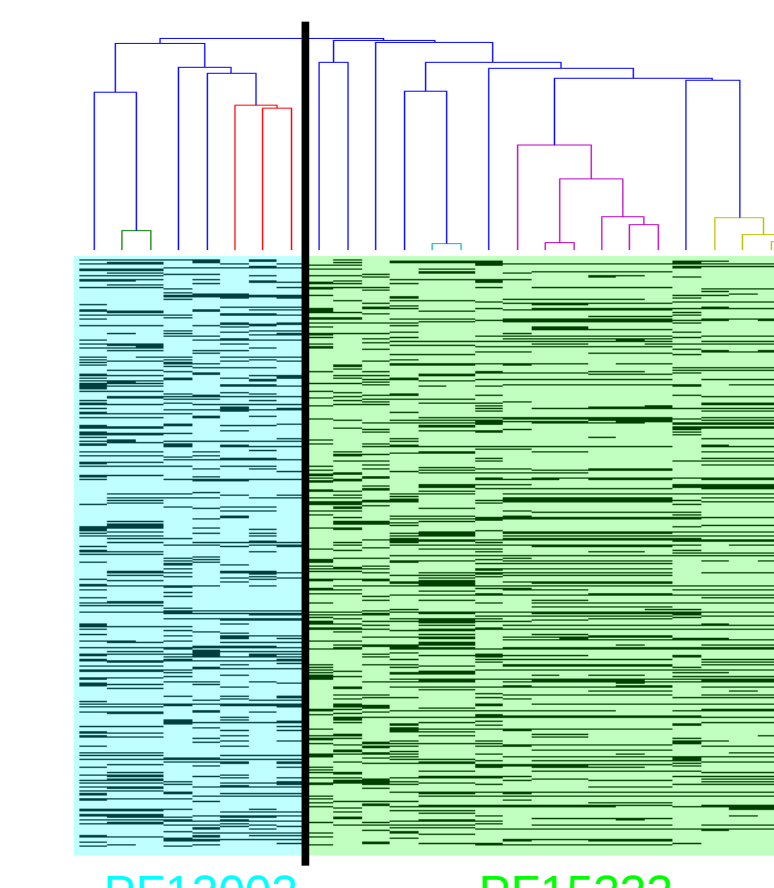


Compute similarity using the Tanimoto score

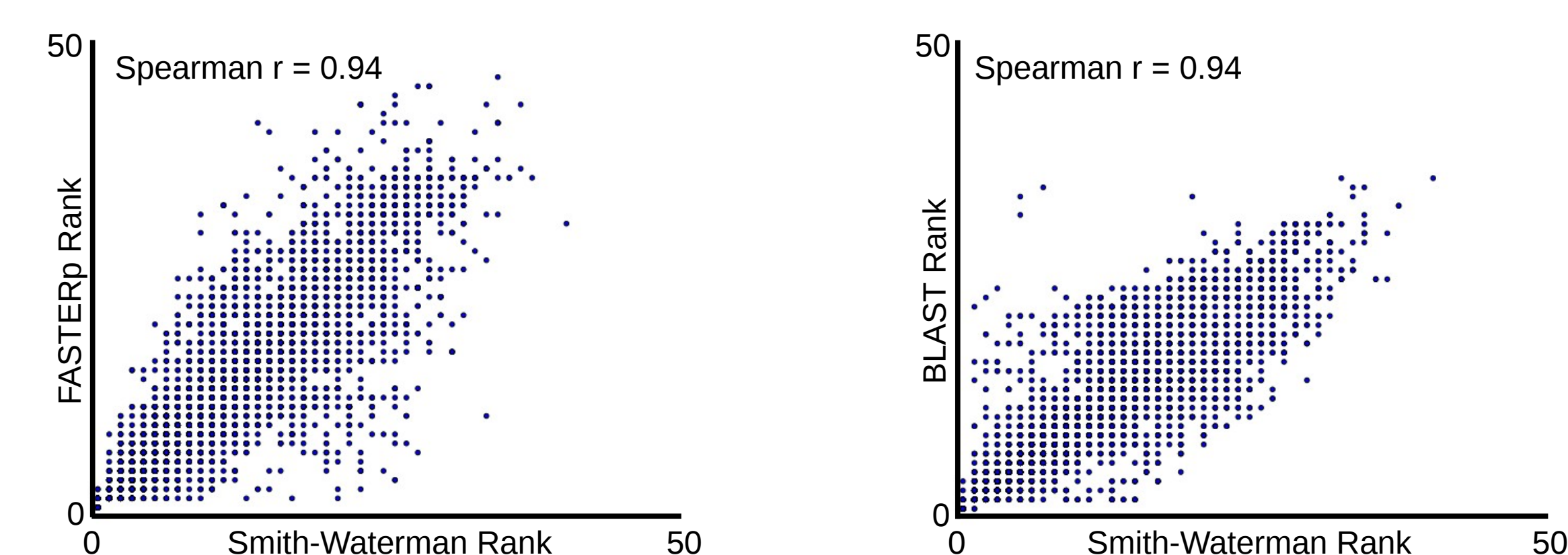


RESULTS

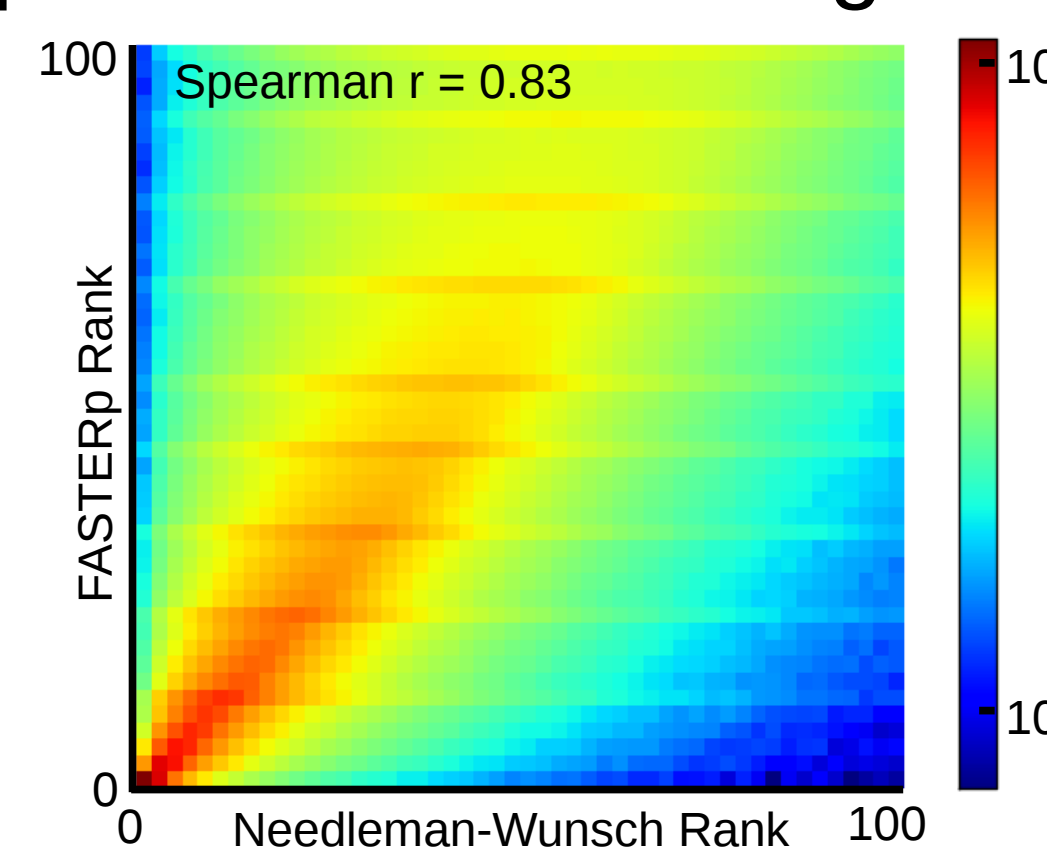
Feature vectors naturally cluster protein families



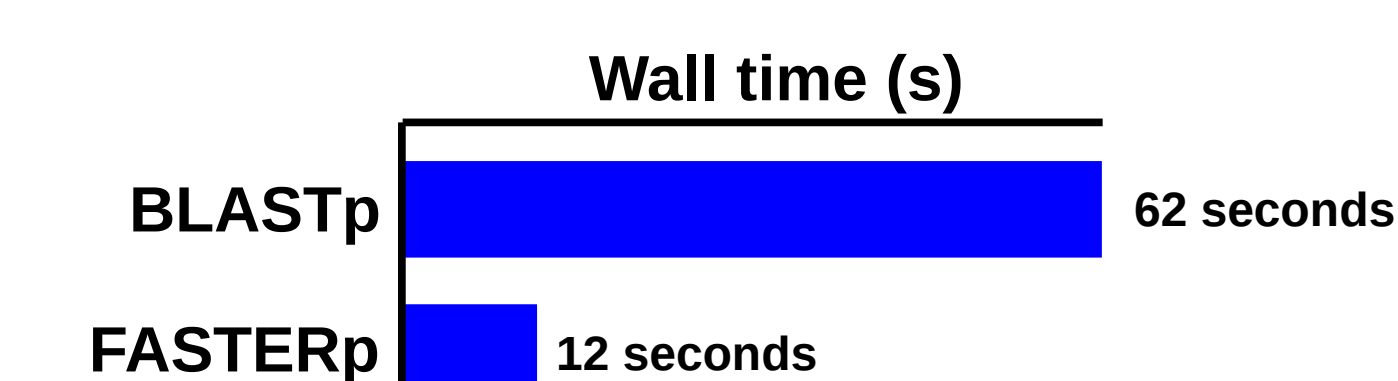
FASTERp comparable to BLAST on small data set



FASTERp performs well on larger data set



Unoptimized prototype already faster than BLAST



FUTURE WORK

Tune algorithm parameters to improve accuracy

Index database of feature vectors to reduce search time

Efficiently implement Tanimoto computations to reduce search time