

LATENT SEMANTIC ANALYSIS FOR FINDING RELEVANT BIOMEDICAL LITERATURE



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OVERVIEW

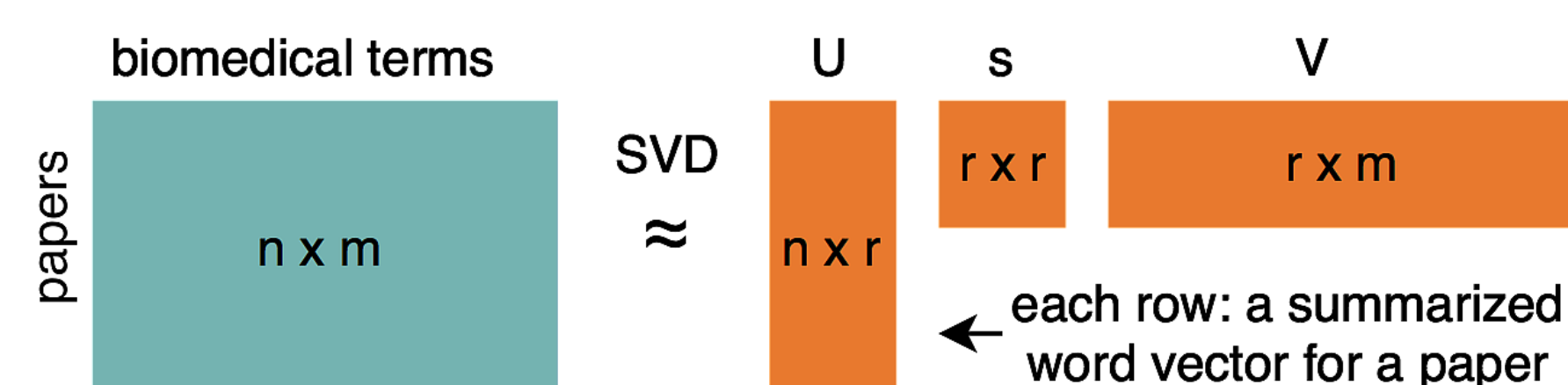
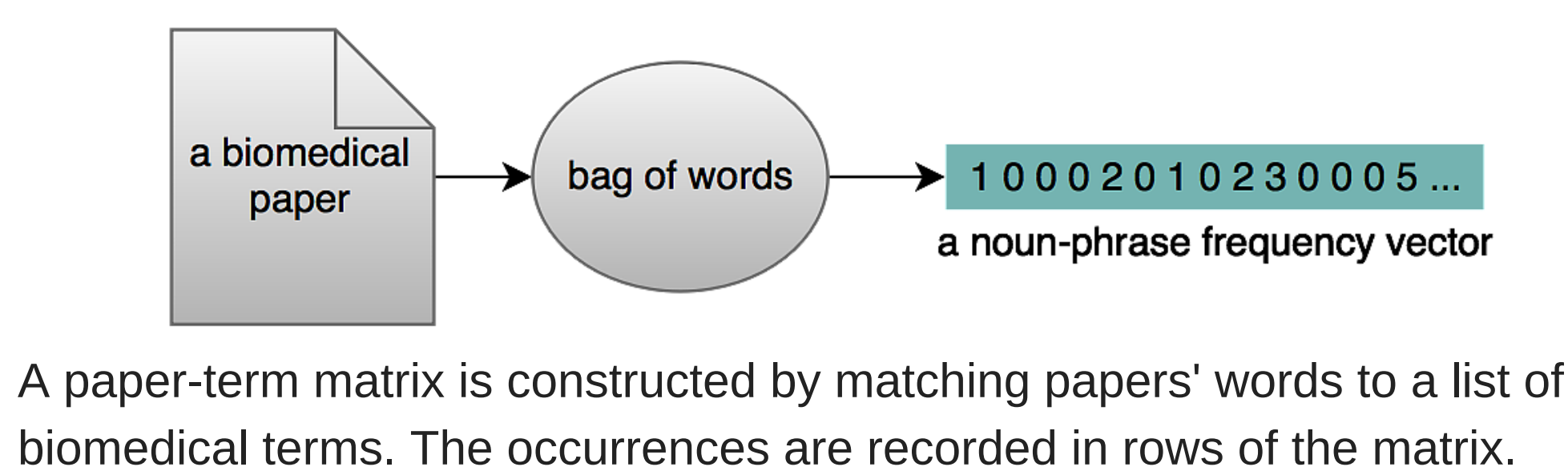
There are ~25 million records in the PubMed database. This astounding number makes it difficult for scientists to find publications relevant to their work, and the pace of biomedical research is increasing. Hence, finding better ways to retrieve relevant scientific papers is important. In this study, we look at how to use latent semantic analysis (LSA)—an application of singular value decomposition (SVD)—on finding relationships in a set of documents and terms to retrieve similar biomedical papers.

BACKGROUND

Many frameworks that retrieve related articles require information that is not always available, such as full text, MeSH headings, and citations.

For example, PubMed identifies a number of related articles using the manually assigned MeSH headings. As a result, their method is not scalable.

SVD is a matrix factorization method that decomposes a matrix into a set of uncorrelated components. As used in PCA, it identifies dimensions on which the data exhibits the most variance and represents the simplified and salient structures underlying the data.



SVD decomposes the matrix into three matrices. Rows in U are summarized word vectors, which are used to measure distances between papers.

SVD has been widely applied in recommendation systems such recommenders for movies and products.

We want to use SVD to recommend similar articles because it can generalize the patterns in a large corpus of text and thus address some problems, such as term independence, synonymy, and noise, in other retrieval methods. For example, two papers using different synonyms describing the same topic would be seemed as dissimilar by a naive method, but SVD would identify them as similar by recognizing that those vocabularies often occur together in other papers.

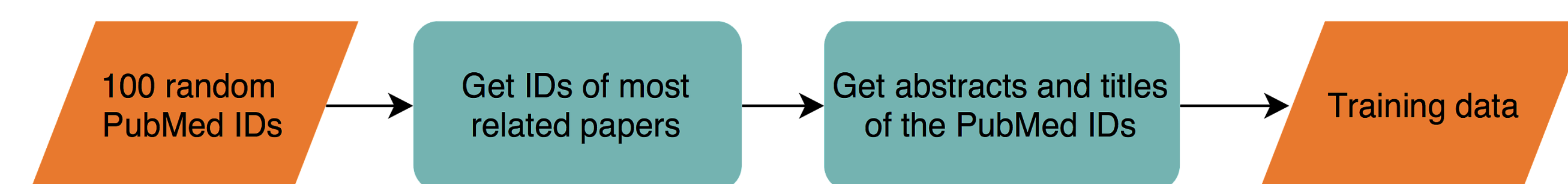
There are parameters to optimize when performing SVD, such as the matrix type and the distance function. This study explore different combination of parameters for finding related biomedical literature.

CONCLUSION

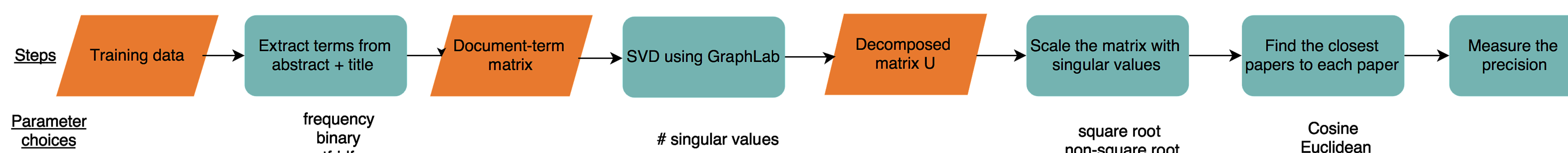
We demonstrated that SVD, a machine learning method, can generalize concepts in biomedical literature and thus find similar papers. After using different parameters of SVD to retrieve related biomedical papers that are suggested by PubMed, we found that **using a term frequency-inverse document frequency (TF-IDF) matrix in combination with cosine distance yields the best precision**. The next step is to investigate how SVD would perform on a much larger corpus (*i.e.* millions of papers).

METHODS

1. Generating training data using Entrez.Bio:
A python library for querying NCBI databases.



2. Finding the best parameters for SVD by evaluating the precisions of different combinations of parameters.

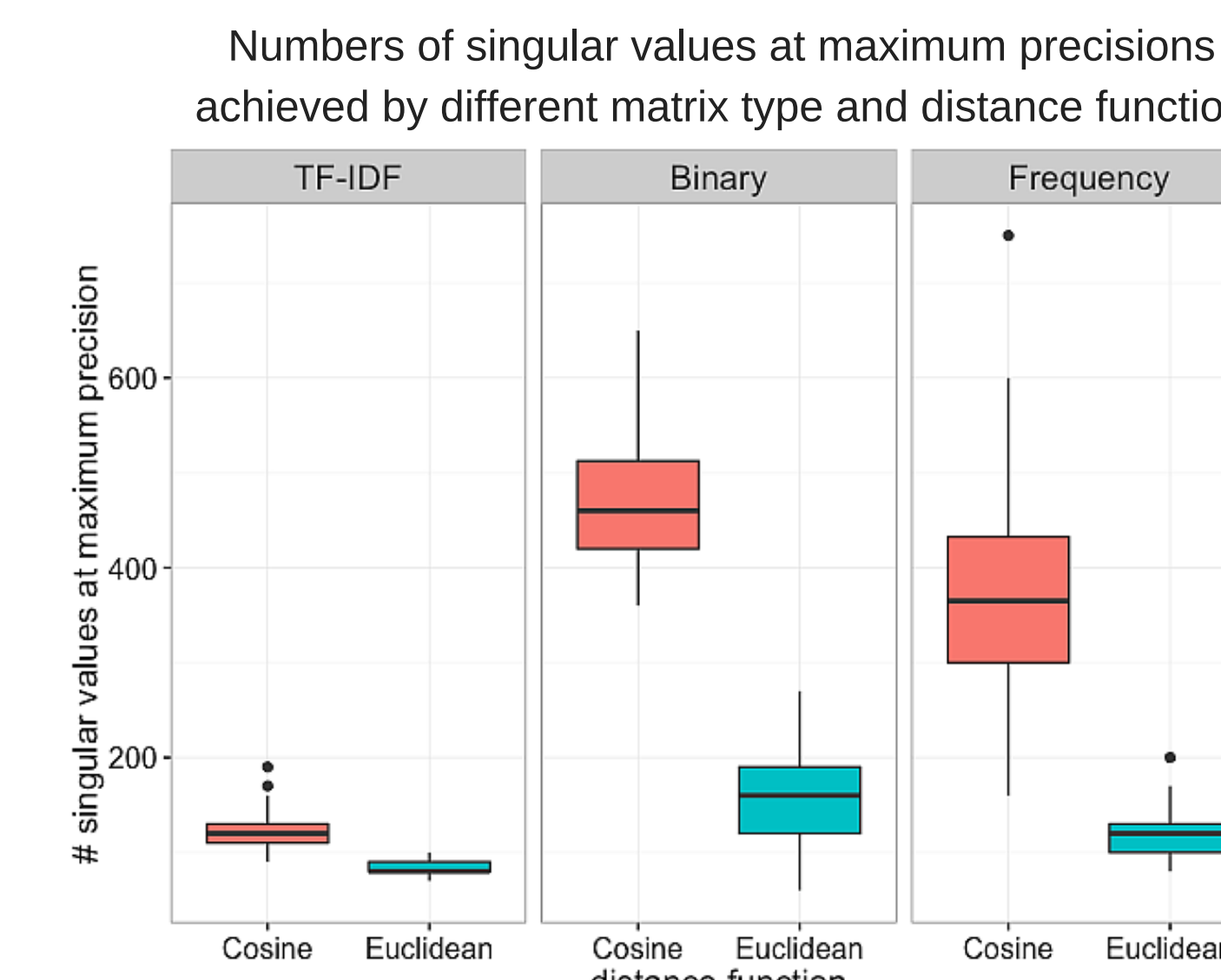
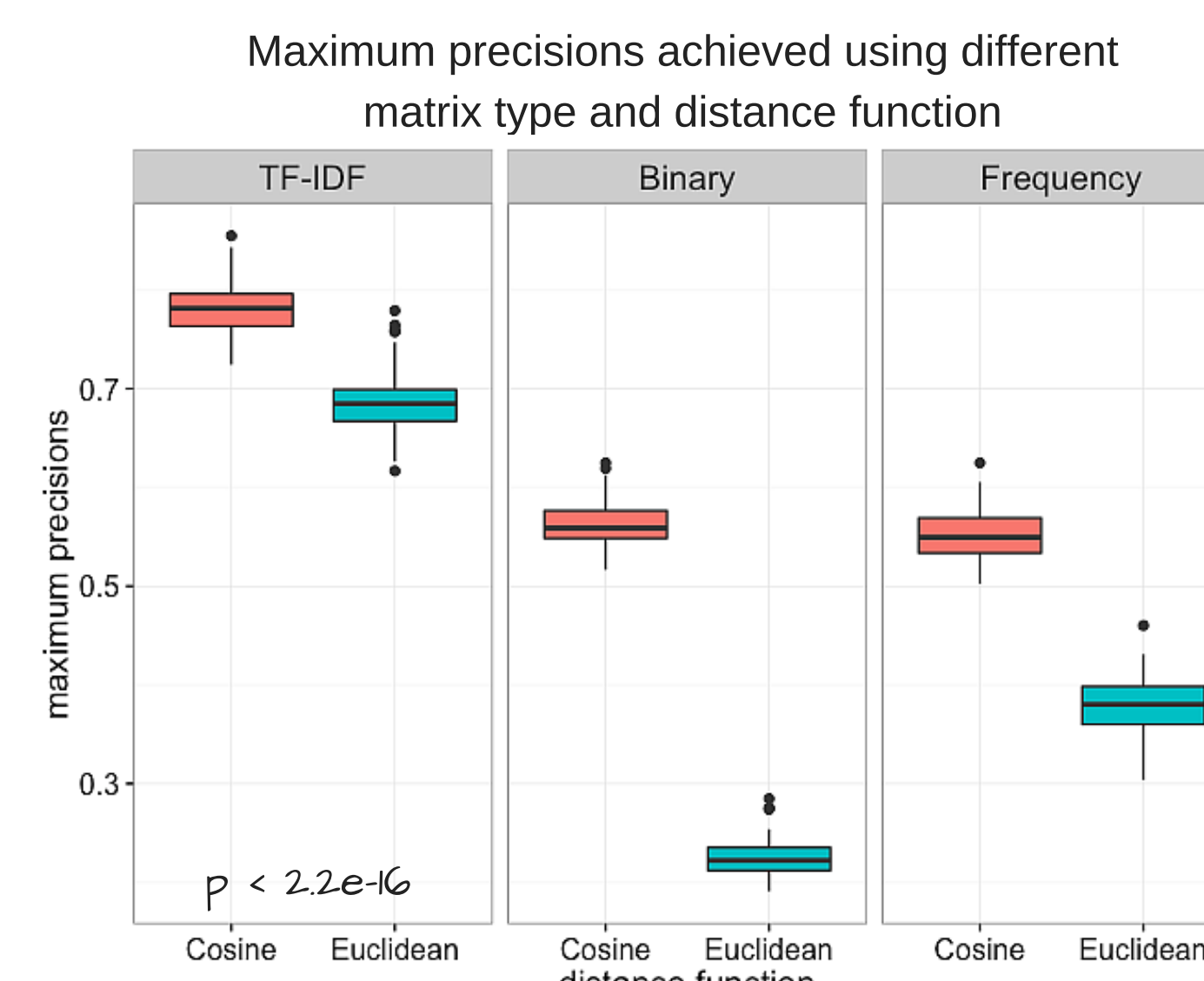


RESULTS

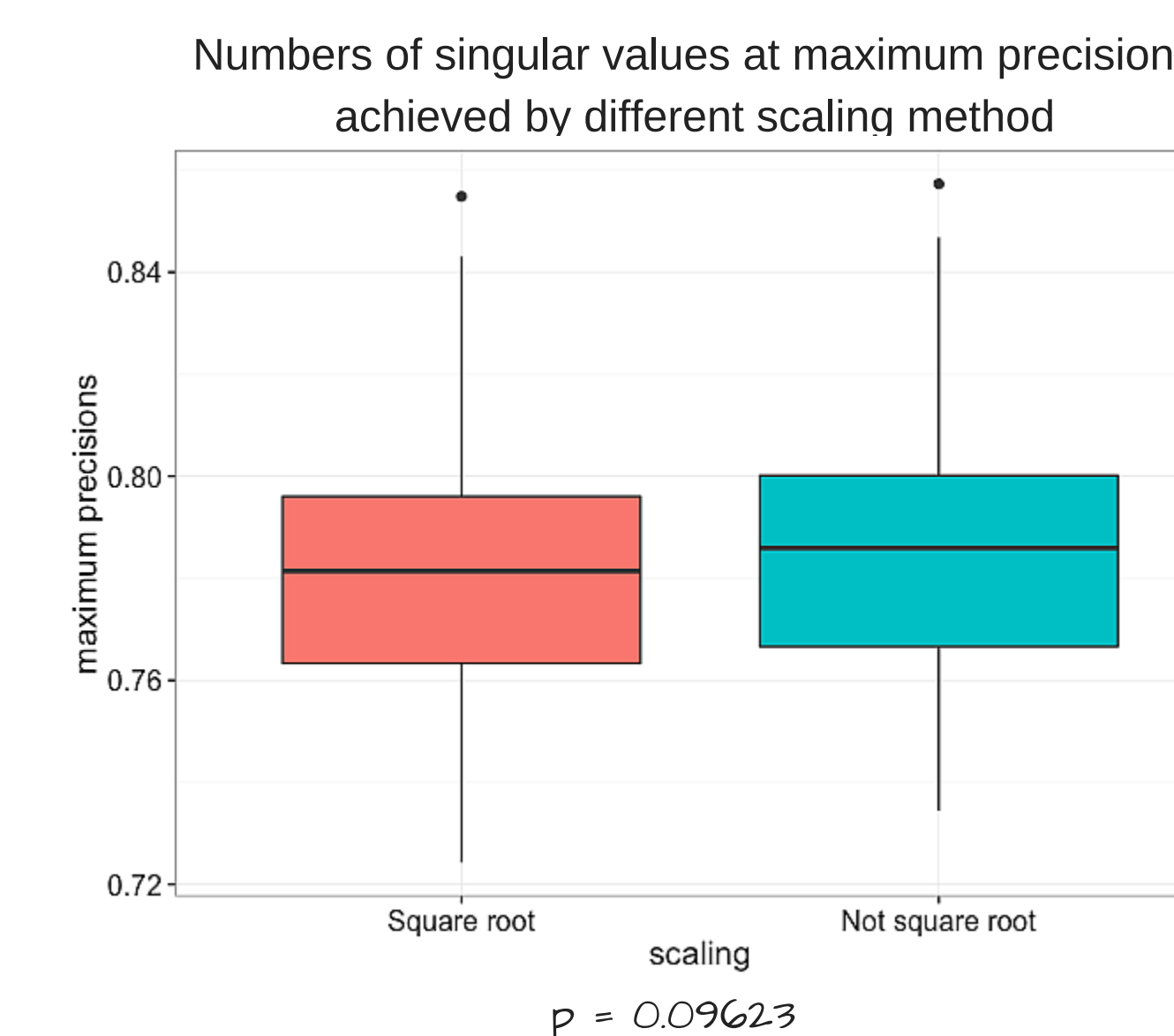
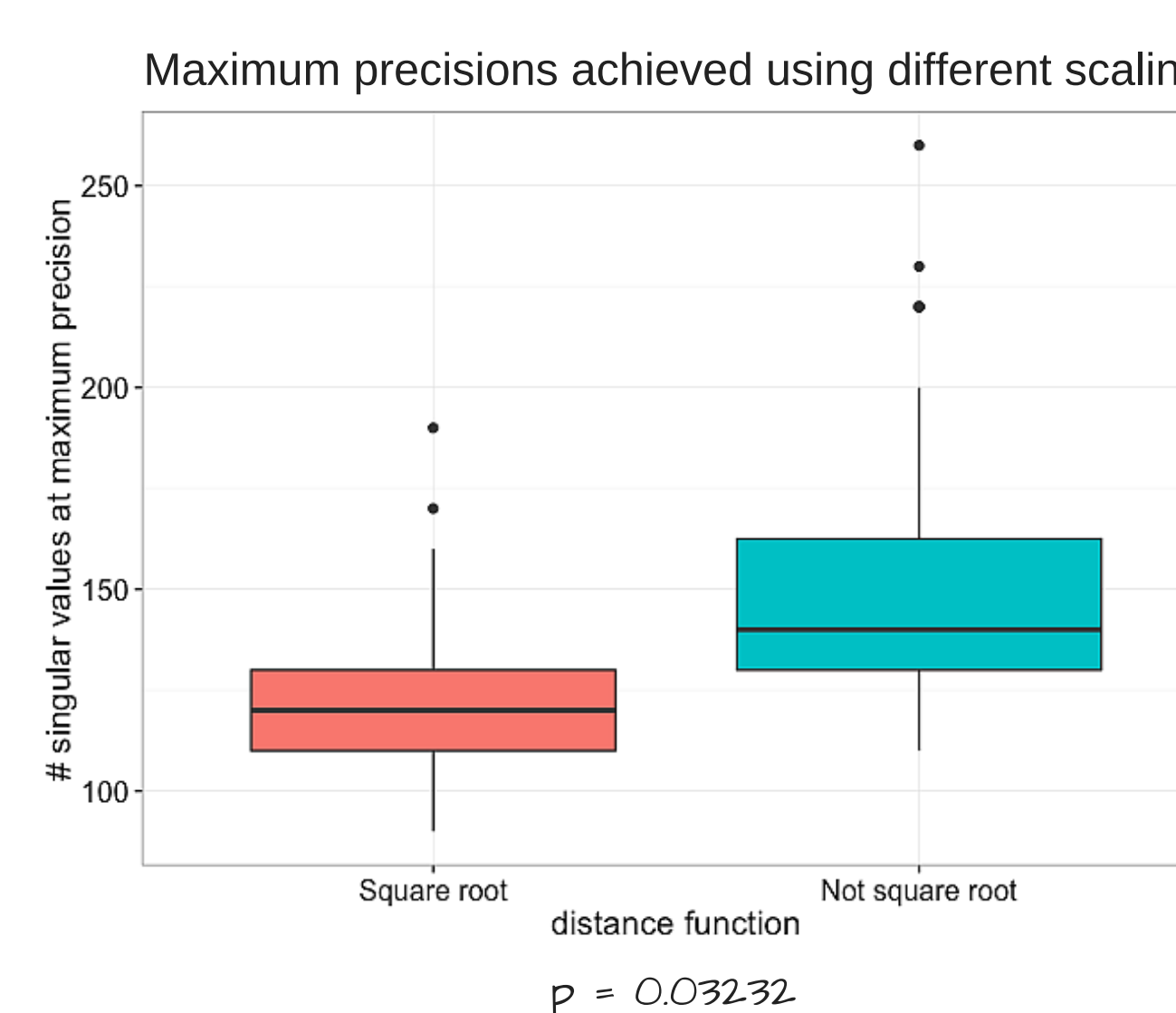
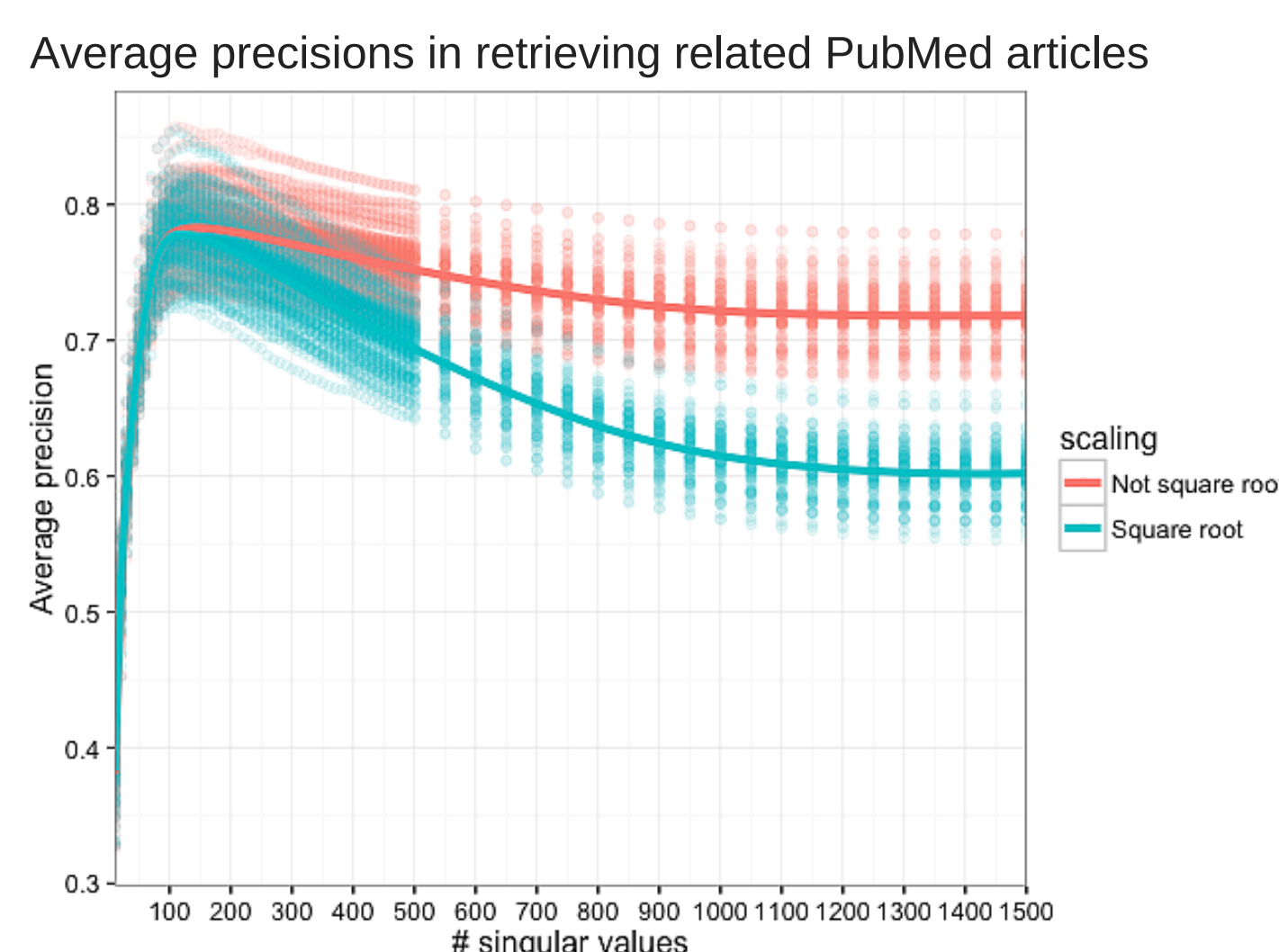
1. TF-IDF and cosine distance function work best



The curves peak and then taper. This indicates that after a number of singular values, SVD has generalized enough concepts to make the best prediction before the inclusion of noise starts to affect the precision.



2. Scale the matrix with singular values might result in higher precisions



ACKNOWLEDGMENTS

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RELATED WORKS

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