

# Research Statement

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## Background

- My research focuses on the analysis of large scale data sets, through embeddings of metric spaces, clustering, and statistical machine learning.
- The advent of the internet as well as the introduction of a variety of sensors and other data sources creates a glut of data which is not being analyzed. Developing new tools and methods to analyze data, and especially large scale data holds the potential to both unlock commercial value as well as provide new insights into complex problems.

## Current research

- My research focuses on the analysis of large scale data sets, through embeddings of metric spaces, clustering, and statistical machine learning.
- My research has contributed to developing a deeper understanding of the protein metric space. My earlier work on non-expansive hashing allowed deeper understanding of locality-preserving data structured and embeddings.

## Future research

- I am currently particularly interested in data visualization and in ways to be able to present to decision makers and stakeholders data in a way they can act upon. Tools and techniques for such visualization can support decision support across a wide variety of organizations.
- I am also interested in developing systems for automatic or semi-automatic extraction of knowledge from large databases, and specifically those generated by simulations.

## **Selected Publications and Outputs**

1. N. Linial and O. Sasson, “Non-Expansive Hashing”, *Combinatorica* 18 (1998) p. 121-132.
2. R. Krauthgramer and O. Sasson, “Property Testing of Data Dimensionality”, In 14th Symposium on Discrete Algorithms (SODA'03), p. 18-27, Jan. 2003.
3. O. Sasson, N. Linial, and M. Linial. “The metric space of proteins – comparative study of clustering algorithms”. In the proceedings of ISMB 2002, *Bioinformatics* 18(S1):S14-S21, 2002.
4. I. Kifer, O. Sasson, and M. Linial, “Predicting Fold Novelty based on ProtoNet Hierarchical Classification”, *Bioinformatics*, 21 (7), April 2005, p. 1020-1027.
5. O. Sasson, N. Kaplan, M. Linial, “Functional annotation prediction: All for one and one for all”, *Protein Science* 15 (2006), 1557-1562.