

Speaker: Saharon Rosset, *Tel Aviv University*

Title: **Isotonic Modeling: Methodology and Applications**

Abstract:

In isotonic modeling, non parametric predictive models $\hat{y} = \hat{f}(x)$ are fitted to data, requiring only that $\hat{f}(x)$ is isotonic, i.e., monotone in all explanatory variables. The monotonicity assumption on the underlying data generation process is appropriate in many applications, for example in modeling gene-gene interactions in genetics. However, isotonic modeling has enjoyed limited interest as a tool for modern data modeling due to a combination of statistical (overfitting) difficulties and computational difficulties. I will first describe our Isotonic Recursive Partitioning (IRP) algorithm, which overcomes both difficulties in fitting isotonic regression (i.e, isotonic modeling with squared loss) to large data. IRP recursively partitions the covariate space to an increasing number of regions and at every iteration fits the best isotonic model to the current partition. At each iteration a linear program is solved, and the whole algorithm can be practically applied to datasets with tens of thousands of observations. Surprisingly, this greedy algorithm provably converges to the global isotonic regression solution, and we view the recursive partitioning process as a regularization path which allows overfitting control.

As time permits, I will discuss further methodological topics. First, generalization of IRP to non-squared loss situations, like Poisson regression, or using robust Huber's loss. Second, development of other practically useful and theoretically sound regularization approaches for isotonic modeling. In this context, we propose to use the range of model predictions as a regularization functional. This problem can be formulated as a lasso problem in the very high dimensional basis of upper-sets in the covariate space, and can be solved very efficiently using some properties I will describe.

Finally, I will review some "modern" applications of isotonic modeling, including isotonic stacking and modeling of gene-gene interactions in human disease.

This is joint work with Ronny Luss of IBM Research.