script for the video

Hi, my name is Jiaxin Hu and I am glad to present our paper "Learning Multiple Network via Supervised Tensor Decomposition".

The motivation of our paper is two-folded. First, the scientific studies such as neuroimaging and social network analysis often collect the tensor observations with side information. And second, the tensor observation may consist of non-Gaussian measurements such as binary and count data. Figure 1 gives us an exmaple in the brain connectivity network study. The left hand side is the tensor observation composed by the binary adjacency matrices from n individuals. And the right hand side is the feature matrix contains the individual side information including the their age, gender, and other features. Our goal is to identify the structural variation in the data tensor affected by side information.

To achieve our goal, we propose our supervised tensor decomposition model. We let Y denote the order K tensor observation, let X_i s denote the feature matrices contain the side information for each mode, and let the multiplication symbol subscript by i denote the tensor-by-matrix product on the i-th mode. Our model is presented in the equation (1). On the right hand side, the f is the known link functin depending on the data type in Y, C is an unknown full rank core tensor, and M_i s are unknown factor matrices consisting of orthonormal columns.

Figure 2 illustrates our model for an order-3 tensor. The left hand side is the mean of the data tensor. And in the right hand side, the three colored matrices X_1, X_2 X3 are feature matrices. The white tensor C and white matrices M1 M2 M3 in the dashed rectangle is the tensor decomposition under the supervision of the side information. The features X_i s affect the distriubtion of tensor entries through the matrix product X_i M_i. And the factor matrices M_is not only reduce the demision in the tensor decomposition but also reduce the dimension of the feature matrices. We call M_i s as the dimension reduction matrices and call the matrix products X_i M_i as "supervised tensor factors" or "sufficient features". The core tensor C collects the interaction effects between the sufficient features.

The unknown parameters consist of K+1 blocks: C, M_1, ...,M_K. To estimate the unknown parameters, we first propose a likelihood based estimator which satisfies the euqation (2) and then we further propose an alternating optimization algorithm which updates one block of parameters at a time to solve the estimator (2). Figure 3 shows the likelihood trajectories when we apply our algorithm to normal data tensor with different settings. We can see that our algorithm converges quickly in few iterations and the objective values at convergent points are close to or larger than the value at true parameters. This implies that our algorithm can give us high quality estimations.

We also find statistical guarantees for our estimator. Under mild technical assumtpions, with high probability, we have inequality (3) which is an upper bound for the angle distance between the column spaces of the true Mi and the estimated Mi. We also have the inequality (4) which is an upper bound for the frobenius norm between the true supervised tensor decomposition and the estimated decomposition.

Last, we apply our method to the brain connectivity networks from the Human Connectome Project. Figure 4 shows the top brain edges with large effects. Red edges represent positive effects and the blue edges represent negative effects.

Subfigure a shows the global connectivity pattern. We can see the nodes within each hemisphere are more densely connected with each other. Subfigure b shows the female effect to the connection. We can see that the Female brains display higher inter-hemispheric connectivity. Subfigure c and d show the effects from age 22 and age 31 respectively. We can find that several edges in frontal-pole region have declined connections in the group of Age 31+.

Our results are in agreement with other neuroscience studies. This implies our method is able to highlight the brain connection variation with biological meanings.

More information about our data and codes are available in our R package. Thank you for watching!