Decoupling Dominant Z-eigenvectors of Tensor Kronecker Products

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We present a new extremal Z-eigenvector theorem for the Kronecker products of tensors which shows that the dominant eigenvector of $\underline{\boldsymbol{B}} \otimes \underline{\boldsymbol{A}}$ decouples to the dominant eigenvectors of $\underline{\boldsymbol{B}}$ and $\underline{\boldsymbol{A}}$, a surprising generalization of the matrix counterpart. Formally, we show [1]

> Let $\underline{\boldsymbol{A}}$ be a symmetric, k-mode, m-dimensional tensor and $\underline{\boldsymbol{B}}$ be a symmetric, k-mode, n-dimensional tensor. Suppose that $(\lambda_A^*, \mathbf{u}^*)$ and $(\lambda_B^*, \mathbf{v}^*)$ are any dominant tensor Z-eigenvalues and vectors of $\underline{\boldsymbol{A}}$ and $\underline{\boldsymbol{B}}$, respectively. Then $(\lambda_A^* \lambda_B^*, \mathbf{v}^* \otimes \mathbf{u}^*)$ is a dominant eigenpair of $\underline{\boldsymbol{B}} \otimes \underline{\boldsymbol{A}}$.

Decoupling the tensor Kronecker product gives us a new foothold to facilitate the use of *motifs* – small repeating subgraphs – in network alignment algorithms. We explore how this new theorem impacts TAME [2], an unsupervised method for network alignment – which is used to identify protein ortholog candidates from protein interaction data. The key to TAME was a tensor that encoded the presence of motifs among groups of nodes, and the algorithm sought to use the eigenvector of the Kronecker product of two such tensors to indicate how the original networks ought to align. Our new algorithms $\Lambda-$TAME & LowRankTAME outperform the original TAME when aligning the LVGNA [3] protein interaction networks, both running orders of magnitude faster and matching, at the minimum, as many triangles motifs as TAME.

Specifically, the decoupling allows our new $\Lambda-$TAME to use the power iterations of $\underline{\boldsymbol{T}}_A$ and $\underline{\boldsymbol{T}}_B$ independently to access useful information on a possible dominant eigenspace. This moves the computational bottleneck from computing iterations with the Kronecker product of tensors, as in TAME, to the step of producing an alignment from the possible eigeninformation. This means that $\Lambda-$TAME runs two orders of magnitude faster than TAME on the largest problems tested and aligns more triangles. When finding the maximum matching is infeasible, searching over the quadratic pairs of vectors computed in any step of the power iterations, is a simple algorithm that runs 3 orders of magnitude faster than TAME in exchange for a modest reduction in triangles matched.

The theory allows further improvements to the computations. Note that the above dominant eigenvector result strongly suggests that iterates of a power method applied to a

Kronecker product of tensors should have low-rank structure (when viewed as a matrix). We show how to use low-rank structure within the iterates of TAME itself, in concert with a tensor-generalized mixed product property [4, Thm 3.1], to produce a method that uses low-rank structure when appropriate. Thus, even without changing the underlying iteration, we show how to improve the computation TAME's iterates. In our experiments we see that we can run an order of magnitude faster than TAME, producing the same iterates with less susceptibility to numerical imprecision and opening the door to low-rank matching strategies.

We hope that our work will encourage a wider dissemination of these techniques, revealing the seemingly daunting runtime costs of tensor Kronecker products as nothing more than a paper tiger.

References

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