Introduction to Tensor Decomposition Methods

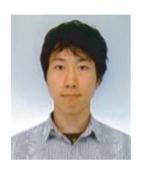
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The University of Tokyo

Includes joint work with Kohei Hayashi, Taiji Suzuki, and Hisashi Kashima

Who are we?



Ryota Tomioka
Ph.D. from University of Tokyo (2008)
Machine Learning, Kernel methods, Matrix and
Tensor decomposition methods

Conferences: NIPS, ICML, IBIS etc.



Intro to tensor decomposition (low-rank)



Kohei Hayashi Ph.D. from NAIST (2012) Machine Learning, Data-mining, Tensor models

Conferences: ICDM, ICML, IBIS etc.



Non low-rank matrix/tensor completion

Where are we from?







THE INSTITUTE OF MEDICAL SCIENCE
THE UNIVERSITY OF TOKYO







St Graduate School of Information Science and Technology
The University of Tokyo
Dept.of Computer Science

Yamanishi & Kashima Lab.

Laboratory of DNA Information
Analysis
Laboratory of Sequence Analysis
Miyano & Shibuya Lab.

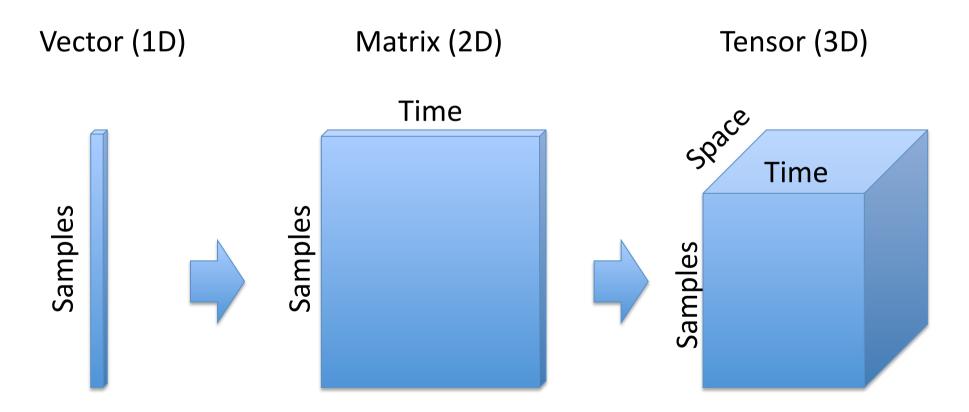


Tensor?

- Two ways to look at it:
 - As a representation of objects
 - As a representation of relations

Tensor represents objects

Can be regarded as generalization of matrices



More dimensions: multiple features, conditions, etc.

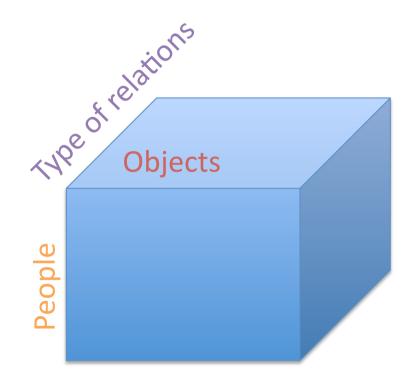
Is this a matrix (tensor)?

Images

Not obvious if a given data is *naturally* a tensor or not. We should ask whether tensor representation *helps* or not.

——Tensor is a special matrix, matrix is a special vector

Another view: tensor represents relations



Examples:

- John likes Starwars
- Steve is the CEO of Microsoft
- Drug A binds to protein B

Typical questions

Missing data imputation

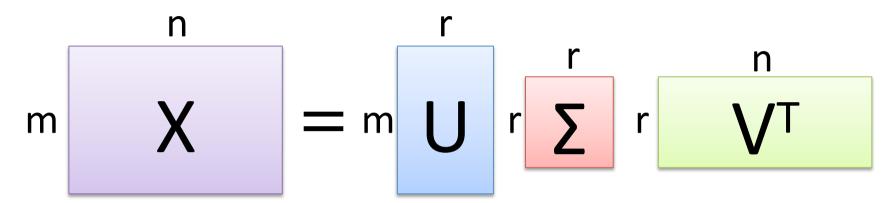
(📦 Hayashi-san's talk)

- Some sensors broken.
- Predict the relation between objects (drug-target interaction, recommendation, etc.)
- Uncover latent low-dimensional structure
 - Multi-linear generalization of singular value decomposition
 - What are the hidden components?



Tucker decomposition (HOSVD) / CP decomposition

Recap: Singular value decomposition

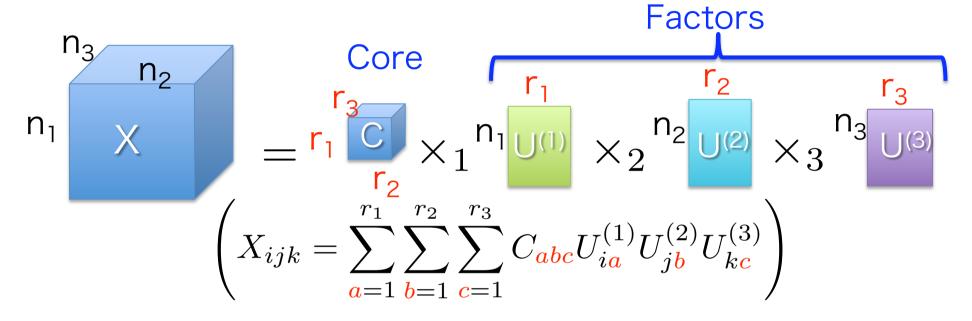


where U, V: Orthogonal ($U^{T}U=I$, $V^{T}V=I$)

 σ_{j} : jth largest singular value r: rank (number of non-zero singular values)

- Note: r <= min(m,n)
- Can be computed efficiently even for very large matrices (see Mark Tygert's pca.m)

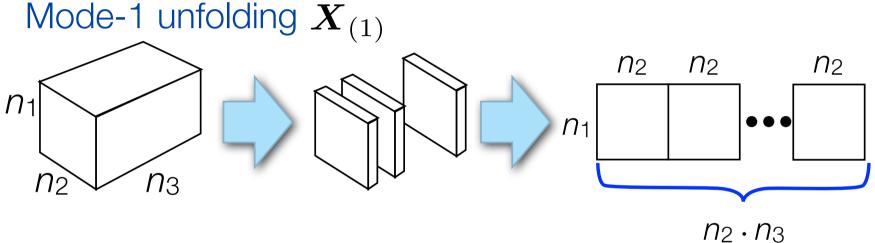
Tucker decomposition [Tucker 66]



- rank is defined for each mode (dimension)
- core is not diagonal!
- Orthogonal ambiguity

Computing Tucker decomposition

1. Unfolding (matricization)

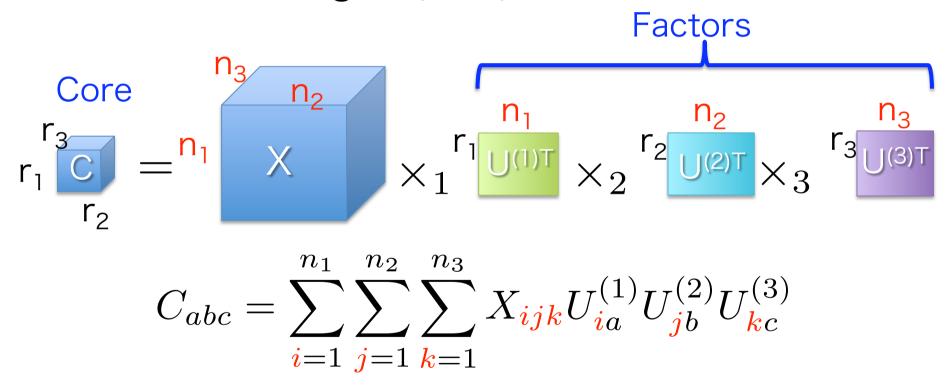


2. Compute SVD

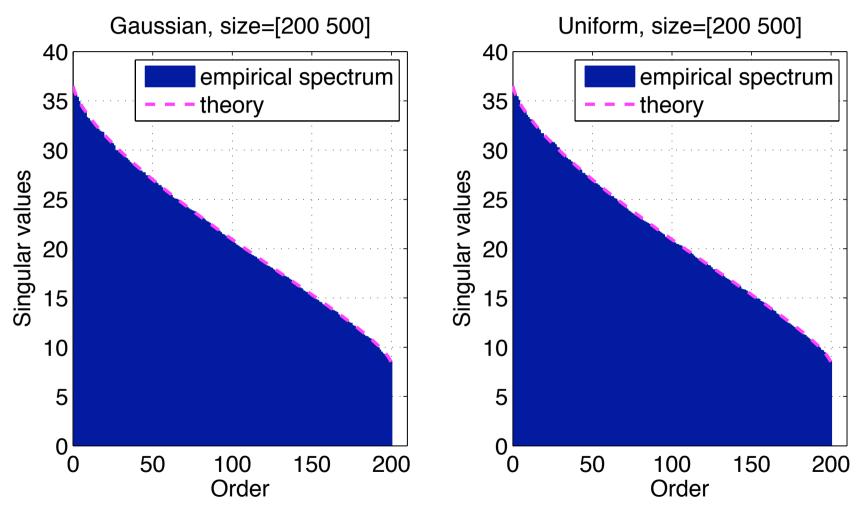
3. Repeat for every mode.

Computing the core

• After obtaining U⁽¹⁾, U⁽²⁾, U⁽³⁾



Singular-values of random matrices: Marchenko-Pastur distribution



No similar result known for Tucker decomposition.

genes

4,329

13 time points

3 conditions

Full-rank Tucker decomposition

Mode-1 unfolding = $4,329 \times 39$

Mode-2 unfolding = $13 \times 12,987$

Mode-3 unfolding = $3 \times 56,277$

Note: maximum rank = 39x13x3

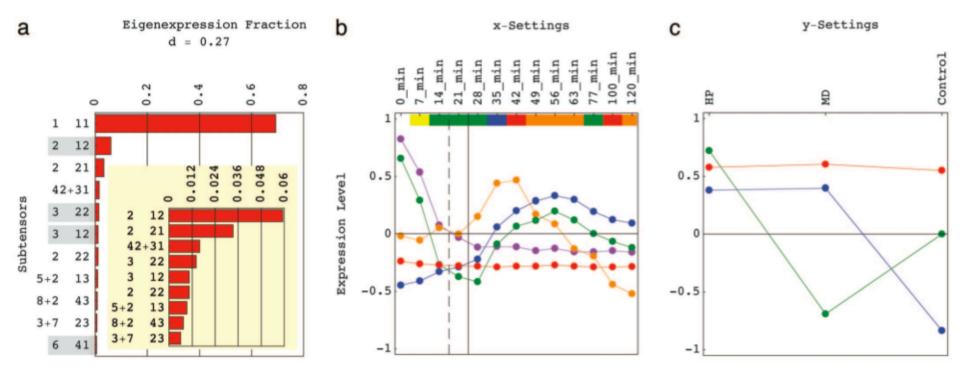
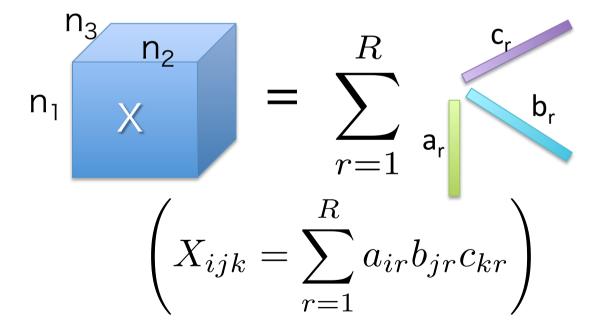


Fig. 1. Significant HOSVD subtensors, after rotation of the approximately degenerate subtensor spaces S(4, 2+3, 1), S(5+2, 1, 3), S(8+2, 4, 3), and S(3+7, 2, 3). (a) Bar chart of the fractions of the 11 most significant subtensors. The higher-order singular values corresponding to subtensors highlighted in gray are <0. The entropy of the data tensor is 0.27. (b) Line-joined graphs of the first (red), second (blue), third (green), and fourth (orange) x-eigengenes and the superposition of the second and third x-eigengenes (violet), which define the expression variation across time in these subtensors. The time points are color-coded according to their cell cycle classification in the control time course: M/G_1 (yellow), G_1 (green), $S(G_2)$ (red), and G_2/M (orange). The grid lines mark the dissipation of the response to α -factor in the control time course (dashed) and the start of exposure to either HP or MD, at \approx 20 and 25 min, respectively. (c) Line-joined graphs of the first y-eigengene (red), and the second (blue) and third (green) rotated y-eigengenes, which define the expression variation across the oxidative stress conditions.

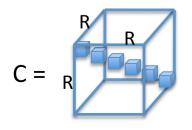
CP decomposition

 CP = CANDECOMP [Carroll & Chang 70] / PARAFAC [Harshman 70]



Special case of Tucker decomp. with diagonal core

minimal R is called the rank



Properties of CP decomposition

- Tensor rank is NP complete [Håstad 90]
 - computing the minimal decomposition is NP hard.
 - In practice, alternate least squares is used.
- CP is unique up to permutation and scaling if

$$k_{\mathbf{A}} + k_{\mathbf{B}} + k_{\mathbf{C}} \ge 2R + 2.$$

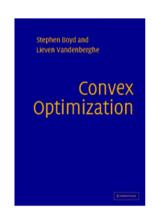
k-rank: maximum number s.t. any k columns of a given matrix is linearly independent.

Issues

- How do we deal with noise and missing data?
 - SVD cannot be used.
 - alternate least squares can over-fit.
- How do we choose the rank?
 - Tucker: three numbers r_1 , r_2 , r_3
 - CP: single number R

Our recent work: "Statistical Performance of Convex Tensor Decomposition"

 Formulate Tucker decomposition as a convex optimization problem



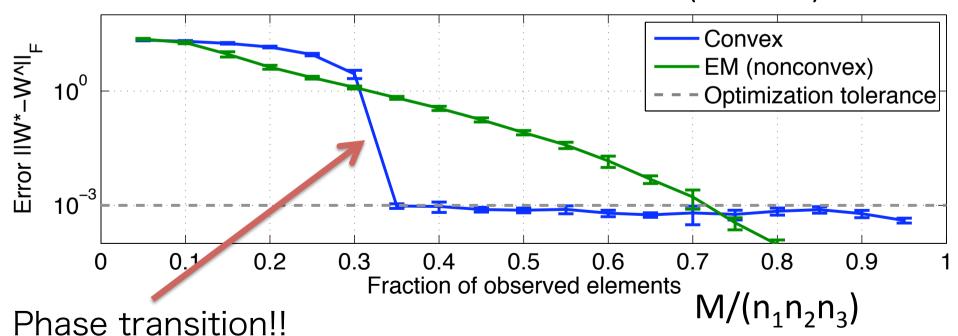
- Convex optimization is fast and reliable
- Instead of choosing ranks (r_1, r_2, r_3) choose the regularization constant λ (like in SVM)
- Statistical analysis of the performance

Empirical Performance

Tensor completion result [Tomioka+ 10]

min
$$\left\|\mathcal{W}
ight\|_{S_1}$$
 s.t. $\mathcal{W}_{ijk}=\mathcal{Y}_{ijk}$ $((ijk)\in\Omega)$

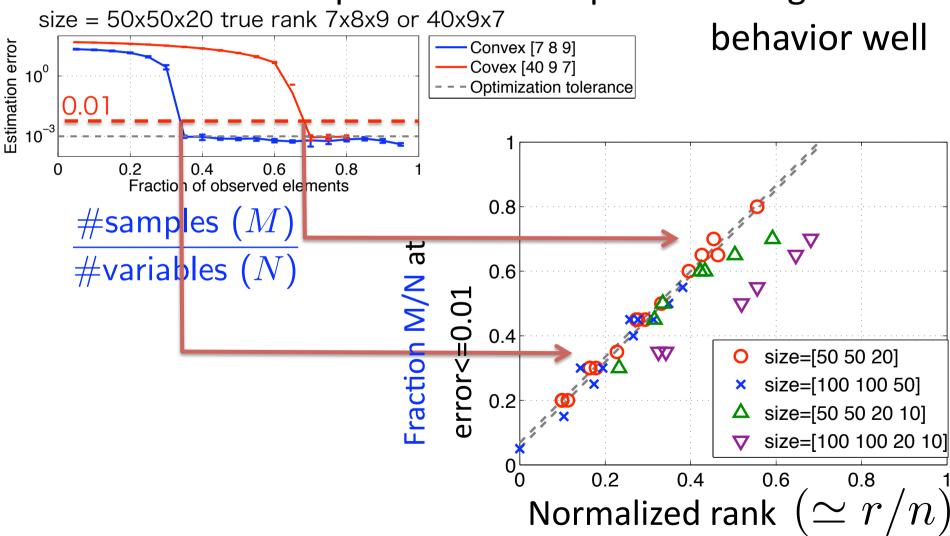
size=50x50x20, rank=7x8x9 (No noise)



Can we predict this theoretically?

Theoretical analysis

Normalized rank predicts the empirical scaling



Summary

- Two views for tensor data
 - as a representation of objects
 - as a representation of relations
- Two tensor decomposition methods
 - Tucker decomposition
 - CP decomposition
- Convex optimization based tensor decomposition with performance guarantee.

References

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 SIAM Review.
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