Singular Value Decomposition

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Goal: Another matrix decomposition (SVD) for low-rank matrix approximation

cf. Eigen decomposition
$$A = Q \ Q^{T}$$
QR decomposition
$$A = Q \ Q$$

See note on "least square fit" & Numerical Recipes Sec. 2.6





Rank of a Matrix

• $N \times M$ matrix A as a mapping: $R^M \to R^N$

$$M \quad \begin{bmatrix} x \\ x \end{bmatrix} \quad x (\in \mathbb{R}^M) \xrightarrow{A} b = Ax (\in \mathbb{R}^N) \quad \begin{bmatrix} b \\ b \end{bmatrix} \quad N$$

- Range of A: Vector space $\{b = Ax | \forall x\}$
- Rank of A: Number, m, of linearly-independent vectors in the range, i.e., how many linearly-independent N-element vectors are there in the range, such that

$$b = A^{\forall} x = \sum_{v=1}^{m} c_v |v\rangle$$

Low Rank Approximations of a Matrix

• Rank-1 approximation: $NM \rightarrow N + M$

$$N \left[\begin{array}{c} N \times M \\ N \times 1 & 1 \times M \end{array} \right]$$

$$|u\rangle\langle v|\forall x\rangle \propto |u\rangle$$

$$|u\rangle\langle v|\forall x\rangle \propto |u\rangle$$

• Rank-2 approximation: $NM \rightarrow 2(N + M)$

$$\left[\begin{array}{c} \psi \\ \end{array} \right] \cong \left[u_1 \right] w_1 \left[\begin{array}{c} v_1 \\ \end{array} \right] + \left[u_2 \right] w_2 \left[\begin{array}{c} v_2 \\ \end{array} \right]$$

• Rank-m ($m \ll N, M$) approximation: $NM \rightarrow m(N + M)$

$$\left[\begin{array}{c} \psi \\ \end{array} \right] \cong \sum_{v=1}^{m} \left[u_{v} \right] w_{v} \left[\begin{array}{c} v_{v} \\ \end{array} \right]$$

Singular Value Decomposition

- Problem: Optimal approximation of an $N\times M$ matrix ψ of rank-m ($m\ll N$)?

• Theorem: An
$$N \times M$$
 matrix ψ (assume $N \ge M$) can be decomposed as
$$\psi = UDV^T = \sum_{v=1}^M U_{iv} d_v V_{jv} = \sum_{v=1}^M u_i^{(v)} d_v v_j^{(v)}$$

where $U \in \mathbb{R}^N \times \mathbb{R}^M$ & $V \in \mathbb{R}^M \times \mathbb{R}^M$ are column orthogonal & D is diagonal

$$\mathbf{M} \qquad U^T U = V^T V = I_M$$

$$\mathbf{N} \begin{bmatrix} \psi \end{bmatrix} = \begin{bmatrix} U & \mathbf{M} \\ U & \mathbf{M} \end{bmatrix} \begin{bmatrix} \mathbf{M} \\ \mathbf{M} \\ \mathbf{M} \end{bmatrix} \begin{bmatrix} \mathbf{V}^T \\ \mathbf{M} \\ \mathbf{M} \end{bmatrix}$$

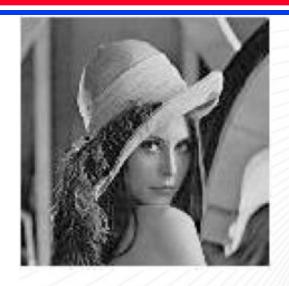
• Theorem: Sort the SVD diagonal elements in descending order, $d_1 \ge d_2 \ge ... \ge$ $d_M \ge 0$, & retain the first m terms $\psi^{(m)} = \sum_{i=1}^{m} u^{(v)} d_v v^{(v)T}$

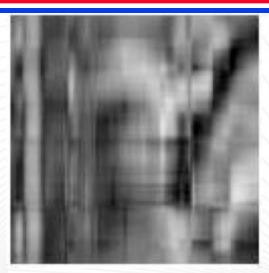
which is optimal among ∀rank-*m* matrices in the 2-norm sense with the error

$$\min_{rank(A)=m} ||A - \psi||_2 = ||\psi^{(m)} - \psi||_2 = d_{m+1}$$

Use the program!

SVD for Image Compression







Original Image

5 Iterations

10 Iterations

D. Richards & A. Abrahamsen





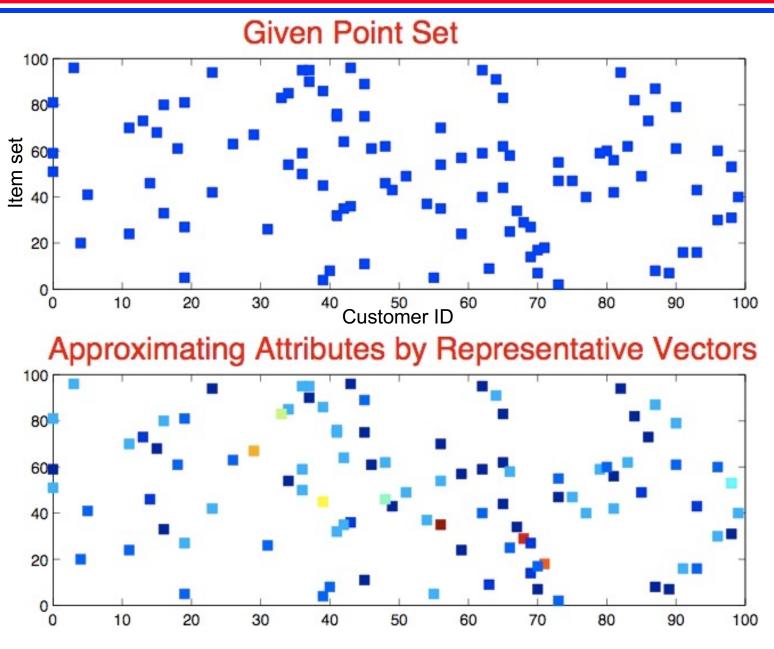


20 Iterations

60 Iterations

100 Iterations

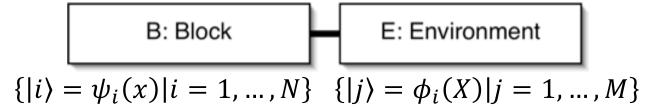
SVD in Data Mining



N. Ramakrishnan & A. Y. Grama

Reduced Density Matrix

Quantum system coupled to an environment



∀Quantum state of block + environment

$$|\psi\rangle = \sum_{i=1}^{N} \sum_{j=1}^{M} \psi_{ij} |i\rangle |j\rangle$$
 or $\Psi(x,X) = \sum_{i=1}^{N} \sum_{j=1}^{M} \psi_{ij} \psi_i(x) \phi_j(X)$

Reduced density matrix

Low-Rank Approx. to Reduced Density Matrix

$$\psi \cong \psi^{(m)} = \sum_{v=1}^{m} u^{(v)} d_{v} v^{(v)T} \qquad \psi_{ij}^{(m)} = \sum_{v=1}^{m} u_{i}^{(v)} d_{v} v_{j}^{(v)}$$

$$\rho = \psi \psi^{T} \cong \psi^{(m)} \psi^{(m)T} = \sum_{v=1}^{m} \sum_{v'=1}^{m} u^{(v)} d_{v} \left(v^{(v)T} v^{(v')} \right) d_{v'} u^{(v')T}$$

$$= \sum_{v=1}^{m} \sum_{v'=1}^{m} u^{(v)} d_{v} \left(\delta_{vv'} \right) d_{v'} u^{(v')T} = \sum_{v=1}^{m} u^{(v)} d_{v}^{2} u^{(v)T} \equiv \rho^{(m)}$$

$$\rho_{ii'}^{(m)} = \sum_{v=1}^{m} u_{i}^{(v)} d_{v}^{2} u_{i'}^{(v)}$$

- Density matrix renormalization group = systematic procedure to accurately obtain a quantum ground state:
 - 1. Incrementally add environment to a block
 - 2. Solve the global (= block + environment) ground state
 - 3. Construct a low-rank approx. to represent the block with reduced d.o.f.

S. R. White, *Phys. Rev. B* **48**, 10345 ('93); G. K.-L. Chan & S. Sharma, *Annu. Rev. Phys. Chem.* **62**, 465 ('11) (Eqs. 3-10)

More SVD in quantum chemistry

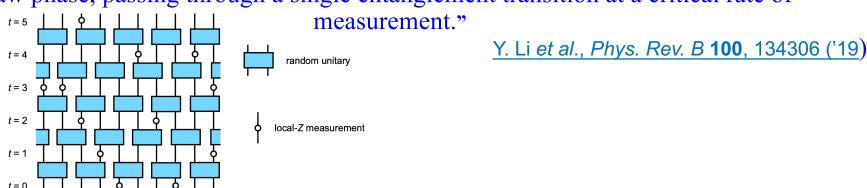
J. F. Gonthier & M. Head-Gordon, J. Chem. Phys. 147, 144110 ('17)

Entanglement Entropy & Quantum Computing

- Entanglement entropy: A measure of quantum entanglement between two subsystems. If a state describing two subsystems A and B is a *separable* state $|\Psi_{AB}\rangle = |\varphi_A\rangle|\varphi_B\rangle$ (*i.e.*, tensor product), then the reduced density matrix $\rho_A = \text{Tr}_B|\Psi_{AB}\rangle\langle\Psi_{AB}| = |\varphi_A\rangle\langle\varphi_A|$ is a *pure state*. Thus, the entropy of the state is zero. A reduced density matrix having a non-zero entropy is therefore a signal of the existence of entanglement in the system.
- Area law: A quantum state satisfies an *area law* if the leading term of the entanglement entropy grows at most proportionally with the *boundary* between the two partitions. Area laws are remarkably common for ground states of local *gapped* quantum many-body systems. *It greatly reduces the complexity of quantum many-body systems. The density matrix renormalization group and matrix product states, for example, implicitly rely on such area laws.*https://en.wikipedia.org/wiki/Entropy of entanglement

Measurement-driven entanglement transition in hybrid quantum circuits

"With increasing measurement rate, the volume law phase is unstable to a disentangled area law phase, passing through a single entanglement transition at a critical rate of

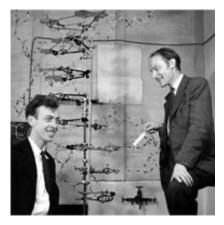


SVD for Rapid Genome Sequencing

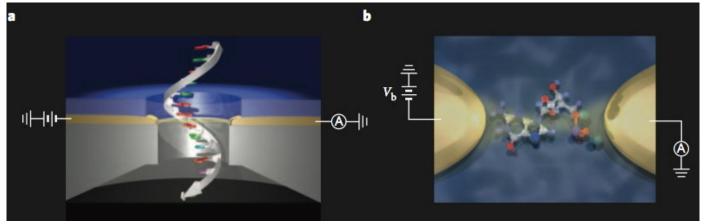
• \$10M Archon X prize for decoding 100 human genomes in 10 days & \$10K per genome (http://genomics.xprize.org): Preemptive attack on diseases



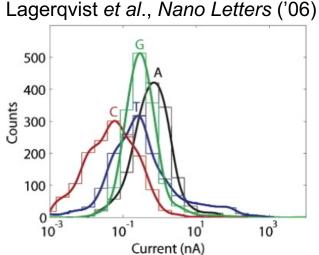




Quantum tunneling current for rapid DNA sequencing?



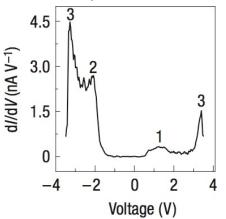
Tsutsui et al., Nature Nanotechnology ('10)



• Tunneling current alone cannot distinguish the 4 nucleotides (A, C, G, T)

Rapid DNA Sequencing via Data Mining

• Use tunneling current (I)-voltage (V) characteristic (or electronic density-ofstates) as the 'fingerprints' of the 4 nucleotides



0.20

0.18

0.16

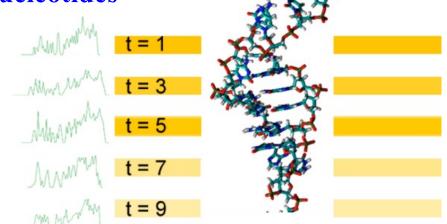
0.14

0.12

0.10

0.08

Shapir et al., Nature Materials ('08)



• Principal component analysis (PCA) & fuzzy c-means clustering clearly

distinguish the 4 nucleotides

Projection on first 2 PCs

Adenosine
Cytosine
AAA Guanine
0.12

C

O.10

O.08

O.06

O.06

O.06

O.07

O.08

O.08

O.09

-0.10

-0.08

-0.06

-0.04

Viterbi algorithm for even higher-accuracy sequencing

See <u>Henry's landmark discovery</u>

SVD vs. PCA (in Economics)

• SVD of N (number of companies) \times T (number of time points) of stock-price time series

$$\Xi^{T} = \bigcup_{T \times N} \sum_{N \times N} \mathbf{V}^{T}$$

Stock correlation matrix

$$\mathbf{C}_{N\times N} = \mathbf{\Xi} \quad \mathbf{\Xi}^{T}$$

$$N\times N = \mathbf{T} \quad T\times N$$

Principal component analysis (PCA):
 Eigen decomposition of the correlation matrix

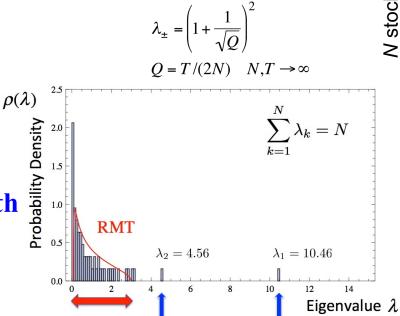
$$C = \Xi \Xi^{T}$$

$$= V \Sigma \widetilde{U^{T} U} \Sigma V^{T}$$

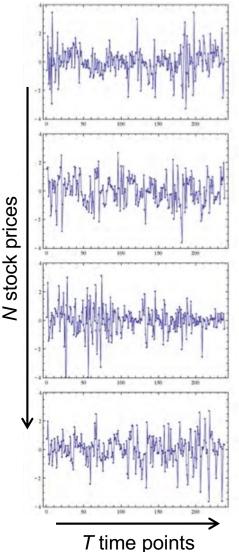
$$= V \Sigma^{2} V^{T}$$

• Compare the spectrum with that of random matrix theory (RMT) for judging statistical significance

Apply it in your area!



 $\rho_{\rm RMT} = \frac{Q}{2\pi} \frac{\sqrt{(\lambda_+ - \lambda)(\lambda - \lambda_-)}}{\lambda}$



Y. Kichikawa et al., Proc. Comp. Sci. **60**, 1836 ('15)