Generalized Power Method for Sparse Principal Component Analysis

Peter Richtárik

CORE/INMA – Catholic University of Louvain – Belgium



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1. Outline

- Sparse PCA
- Optimization reformulations
- Algorithm and complexity analysis
- Numerical experiments

2. Sparse PCA (sPCA)

- Input: Matrix $A = [a_1, \ldots, a_n] \in \mathbf{R}^{p \times n}, \quad p \le n$
- Goal: Find unit-norm vector $z^* \in \mathbf{R}^n$ which simultaneously
 - 1. maximizes variance $z^T A^T A z$
 - 2. is sparse

If sparsity is **not** required, z^* is the **dominant right singular vector** of A:

$$\max_{z^T z \le 1} z^T A^T A z = \lambda_{\max}(A^T A) = (\sigma_{\max}(A))^2.$$

Extracting more components: Discussion above is about the **single-unit case** (m = 1). Often more components (sparse dominant singular directions) are needed: **block case** (m > 1).

Applications: gene expression, finance, data visualization, signal processing, vision, ...

3. Our approach to sPCA

- 1. Formulate sPCA as an optimization problem with sparsityinducing penalty (ℓ_1 or ℓ_0) controlled by a single parameter
- 2. Reformulate to get problem of a suitable form:
 - suitable for analysis
 - suitable for computation
- 3. "Solve" reformulation using a simple gradient scheme
- 4. Recover solution of the original problem

Will illustrate steps 1) and 2) and 4) on the single-unit ℓ_1 penalized case and then jump to general analysis of step 3).

4. Three observations about the ℓ_1 penalty

Notation: $||z||_1 = \sum_i |z_i|$.

Penalty formulation of single-unit sPCA:

$$\phi_{\ell_1}(\gamma) \stackrel{\text{def}}{=} \max_{z^T z \le 1} \sqrt{z^T A^T A z} - \gamma \|z\|_1.$$
(1)

Observations:

1. $\gamma = 0 \Rightarrow$ no reason to expect zero coordinates in z^* 2. $\gamma \ge ||a_{i^*}||_2 \stackrel{\text{def}}{=} \max_i ||a_i||$, then $z^* = 0$. Indeed, since

$$\max_{z \neq 0} \frac{\|Az\|_2}{\|z\|_1} = \max_{z \neq 0} \frac{\|\sum_i z_i a_i\|_2}{\|z\|_1}$$
$$\leq \max_{z \neq 0} \frac{\sum_i |z_i| \|a_i\|_2}{\sum_i |z_i|} = \max_i \|a_i\|_2.$$

3. In fact, $\gamma \geq \|a_i\|_2 \Rightarrow z_i^*(\gamma) = 0$ for all i

5. Reformulation

Note that:

$$\phi_{\ell_1}(\gamma) = \max_{z \in \mathcal{B}^n} \|Az\|_2 - \gamma \|z\|_1 = \max_{z \in \mathcal{B}^n} \max_{x \in \mathcal{B}^p} x^T A z - \gamma \|z\|_1$$
$$= \max_{x \in \mathcal{B}^p} \max_{z \in \mathcal{B}^n} \sum_{i=1}^n z_i(a_i^T x) - \gamma |z_i|.$$

For fixed x, the inner max-problem has the closed-form solution

$$z_i = \operatorname{sign}(a_i^T x)[|a_i^T x| - \gamma]_+, \qquad z^* = z/||z||_2.$$

Hence to solve (1), we only need to solve this reformulation:

$$\phi_{\ell_1}^2(\gamma) = \max_{\substack{x \in \mathbf{R}^p \\ x^T x = 1}} \sum_{i=1}^n [|a_i^T x| - \gamma]_+^2,$$
(2)

Note: The objective function of (2) is convex and smooth and the feasible region is in \mathbb{R}^p instead of \mathbb{R}^n ($p \ll n$).

6. Single-unit sPCA via ℓ_0 penalty

Similar story as in the ℓ_1 case, so only briefly:

Notation: $||z||_0 = Card\{i : z_i \neq 0\}.$

Penalty formulation:

$$\phi_{\ell_0}(\gamma) \stackrel{\text{def}}{=} \max_{z^T z \le 1} z^T A^T A z - \gamma \|z\|_0, \tag{3}$$

To solve (3), first solve this reformulation:

$$\phi_{\ell_1}(\gamma) = \max_{\substack{x \in \mathbf{R}^p \\ x^T x = 1}} \sum_{i=1}^n [(a_i^T x)^2 - \gamma]_+,$$
(4)

and then set

$$z_i = [\operatorname{sign}((a_i^T x)^2 - \gamma)]_+ a_i^T x, \qquad z^* = z/||z||_2.$$

7. Maximizing convex functions

Problems (2) and (4) (and their block generalizations) are of the form

$$f^* = \max_{x \in \mathcal{Q}} f(x), \tag{P}$$

where

- E is a finite-dimensional vector space,
- $f: \mathbf{E} \to \mathbf{R}$ is a convex function,
- $\mathcal{Q} \subset E$ is compact.

In particular,

- Q = unit Euclidean sphere in \mathbf{R}^p / Single-unit case (m = 1)
- Q = **Stiefel manifold** in $\mathbb{R}^{p \times m}$, i.e. the set of $p \times m$ matrices with orthonormal columns / Block case (m > 1)

How to solve (P)?

8. Gradient algorithm

We solve (P) using this simple gradient method:

- 1. Input: Initial iterate $x_0 \in Q$
- 2. For $k \ge 0$ repeat
 - $x_{k+1} \in \operatorname{Arg\,max}\{f(x_k) + \langle f'(x_k), y x_k \rangle \mid y \in \mathcal{Q}\}$ • $k \leftarrow k+1$

This algorithm generalizes the **power method** for computing the largest eigenvalue of a symmetric positive definite matrix C:

$$f(x) = \frac{1}{2}x^T C x \quad \to \quad x_{k+1} = \frac{C x_k}{\|C x_k\|_2}.$$

Hence "Generalized Power Method" (GPower).

9. Iteration complexity: basic result

At any point $x \in Q$ we introduce a measure for the first-order optimality conditions:

$$\Delta(x) \stackrel{\text{def}}{=} \max_{y \in \mathcal{Q}} \langle f'(x), y - x \rangle.$$

Clearly, $\Delta(x) \ge 0$ and it vanishes only at the points where the gradient f'(x) belongs to the normal cone to $\operatorname{Conv}(\mathcal{Q})$ at x.

Denote
$$\Delta_k \stackrel{\text{def}}{=} \min_{0 \le i \le k} \Delta(x_i).$$

Theorem Let sequence $\{x_k\}_{k=0}^{\infty}$ be generated by GPower as applied to a convex function f. Then the sequence $\{f(x_k)\}_{k=0}^{\infty}$ is monotonically increasing and $\lim_{k\to\infty} \Delta(x_k) = 0$. Moreover,

$$\Delta_k \le \frac{f^* - f(x_0)}{k+1}.$$
(5)

10. Strong convexity of functions and sets

Function f is strongly convex if there exists a constant $\sigma_f > 0$ such that for any $x, y \in \mathbf{E}$

$$f(y) \ge f(x) + \langle f'(x), y - x \rangle + \frac{\sigma_f}{2} ||y - x||^2.$$

The set $\operatorname{Conv}(\mathcal{Q})$ is strongly convex if there exists a constant $\sigma_{\mathcal{Q}} > 0$ such that for any $x, y \in \operatorname{Conv}(\mathcal{Q})$ and $\alpha \in [0, 1]$ the following inclusion holds:

$$\alpha x + (1-\alpha)y + \frac{\sigma_{\mathcal{Q}}}{2}\alpha(1-\alpha)\|x-y\|^2 \cdot \mathcal{S} \subset \operatorname{Conv}(\mathcal{Q}).$$

Theorem If $f : \mathbf{E} \to \mathbf{R}$ is nonnegative, has $\sigma_f > 0$ and f' is L_f -Lipschitz, then for any $\omega > 0$, the level set

$$\mathcal{Q}_{\omega} \stackrel{\mathsf{def}}{=} \{ x \mid f(x) \le \omega \}$$

is strongly convex with parameter $\sigma_{Q_{\omega}} = \sigma_f / \sqrt{2\omega L_f}$.

11. Refined analysis under strong convexity

Theorem

Let

- f be convex with strong convexity parameter $\sigma_f \ge 0$, and
- Conv(Q) be convex with strong convexity parameter $\sigma_Q \ge 0$. If $0 < \delta_f = \inf_{x \in Q} ||f'(x)||_*$ and either $\sigma_f > 0$ or $\sigma_Q > 0$, then

$$\sum_{k=0}^{N} \|x_{k+1} - x_k\|^2 \le \frac{2(f^* - f(x_0))}{\sigma_{\mathcal{Q}}\delta_f + \sigma_f}$$

Note: If f is *not* minimized on Q, then $\delta_f > 0$.

12. Computational experiments

We compare the following **Sparse PCA algorithms:**

| $GPower_{\ell_1}$ | Single-unit sparse PCA via ℓ_1 -penalty [1] |
|---------------------|---|
| $GPower_{\ell_0}$ | Single-unit sparse PCA via ℓ_0 -penalty [1] |
| $GPower_{\ell_1,m}$ | Block sparse PCA via ℓ_1 -penalty [1] |
| $GPower_{\ell_0,m}$ | Block sparse PCA via ℓ_0 -penalty [1] |
| SPCA | SPCA algorithm [2] |
| $Greedy^*$ | Greedy method [3] |
| $rSVD_{\ell_1}$ | Method [4] with ℓ_1 -penalty ("soft thresholding") |
| $rSVD_{\ell_0}$ | Method [4] with ℓ_0 -penalty ("hard thresholding") |

*Greedy slows down dramatically, compared to the other methods, if aimed at obtaining a component of higher cardinality.

Test Problems:

• Randomly generated

A =Gaussian with zero mean and unit variance

• Gene-expression data

13. Trade-off curves



Trade-off between **explained variance** and **cardinality**. The algorithms aggregate in two groups. The methods GPower_{ℓ_1} , GPower_{ℓ_0} , Greedy and rSVD_{ℓ_0} do better **(black solid lines)**, and SPCA and rSVD_{ℓ_1} do worse **(red dashed lines)**.

Based on 100 random test problems of size p = 100, n = 300.

14. Controlling sparsity with γ



Dependence of **cardinality** on the value of the **sparsity-inducing parameter** γ . The horizontal axis shows a normalized interval of reasonable values of γ . The vertical axis shows percentage of nonzero coefficients of the resulting sparse loading vector z^* .

Based on 100 random test problems of size p = 100, n = 300.

15. How does the trade-off evolve in time?



Evolution of the **explained variance** (solid lines and left axis) and **cardinality** (dashed lines and right axis) in time for the methods $GPower_{\ell_1}$ and $rSVD_{\ell_1}$.

Based on random test problem of size p = 250 and n = 2500.

16. Random data: speed

| Fixed n/p ratio: | | | | | | | |
|--------------------|---|------|------|------|--|--|--|
| $p \times n$ | $250 \times 2500 500 \times 5000 750 \times 7500 1000 \times 1000$ | | | | | | |
| $GPower_{\ell_1}$ | 0.85 | 2.61 | 3.89 | 5.32 | | | |
| $GPower_{\ell_0}$ | 0.46 | 1.21 | 2.41 | 2.93 | | | |
| SPCA | 2.77 | 14.0 | 41.0 | 81.6 | | | |
| $rSVD_{\ell_1}$ | 1.40 | 6.80 | 17.8 | 41.2 | | | |
| $rSVD_{\ell_0}$ | 1.33 | 6.20 | 15.4 | 36.3 | | | |

Fixed p, growing n:

| | | 1 0 | <u> </u> | |
|-------------------|-------------------|-------------------|-------------------|--------------------|
| $p \times n$ | 500×2000 | 500×4000 | 500×8000 | 500×16000 |
| $GPower_{\ell_1}$ | 0.97 | 1.96 | 4.30 | 8.43 |
| $GPower_{\ell_0}$ | 0.39 | 0.97 | 2.01 | 4.63 |
| SPCA | 7.37 | 11.4 | 22.4 | 44.6 |
| $rSVD_{\ell_1}$ | 2.56 | 5.27 | 11.3 | 26.8 |
| $rSVD_{\ell_0}$ | 2.30 | 4.70 | 10.3 | 23.8 |

17. Gene expression data: speed

| Data sets (breast cancer cohorts): | | | | |
|------------------------------------|---------------|-------------|-----------------------------|--|
| Study | Samples (p) | Genes (n) | Reference | |
| Vijver | 295 | 13319 | van de Vijver et al. [2002] | |
| Wang | 285 | 14913 | Wang et al. [2005] | |
| Naderi | 135 | 8278 | Naderi et al. [2006] | |
| JRH-2 | 101 | 14223 | Sotiriou et al. [2006] | |

| Speed (in seconds): | | | | | | |
|--------------------------|------|------|------|------|--|--|
| Vijver Wang Naderi JRH-2 | | | | | | |
| $GPower_{\ell_1}$ | 7.72 | 6.96 | 2.15 | 2.69 | | |
| $GPower_{\ell_0}$ | 3.80 | 4.07 | 1.33 | 1.73 | | |
| $GPower_{\ell_1,m}$ | 5.40 | 4.37 | 1.77 | 1.14 | | |
| $GPower_{\ell_0,m}$ | 5.61 | 7.21 | 2.25 | 1.47 | | |
| SPCA | 77.7 | 82.1 | 26.7 | 11.2 | | |
| $rSVD_{\ell_1}$ | 46.4 | 49.3 | 13.8 | 15.7 | | |
| $rSVD_{\ell_0}$ | 46.8 | 48.4 | 13.7 | 16.5 | | |

18. Gene expression data: content

PEI-values based on 536 cancer-related pathways:

| | Vijver | Wang | Naderi | JRH-2 |
|---------------------|--------|--------|--------|--------|
| PCA | 0.0728 | 0.0466 | 0.0149 | 0.0690 |
| $GPower_{\ell_1}$ | 0.1493 | 0.1026 | 0.0728 | 0.1250 |
| $GPower_{\ell_1}$ | 0.1250 | 0.1250 | 0.0672 | 0.1026 |
| $GPower_{\ell_1,m}$ | 0.1418 | 0.1250 | 0.1026 | 0.1381 |
| $GPower_{\ell_0,m}$ | 0.1362 | 0.1287 | 0.1007 | 0.1250 |
| SPCA | 0.1362 | 0.1007 | 0.0840 | 0.1007 |
| $rSVD_{\ell_1}$ | 0.1213 | 0.1175 | 0.0914 | 0.0914 |
| $rSVD_{\ell_0}$ | 0.1175 | 0.0970 | 0.0634 | 0.1063 |

Pathway Enrichment Index (PEI) measures the statistical significance of the overlap between two kinds of gene sets.

19. Summary

We have

- developed 4 reformulations (single unit/block $\times \ell_1/\ell_0$) of the sPCA problem which enabled us to
 - devise a very fast method (we work in dimension $p \ll n$ and use only gradients), and
 - analyze the **iteration complexity** of the method;
- analyzed a simple gradient method (Generalized Power Method) for maximizing convex functions on compact sets;
- applied GPower to 4 reformulations and ended-up with 4 algorithms for sPCA;
- tested our algorithms on random and gene expression data:
 - they outperform other methods significantly in speed (finish before some other algorithms initialize),
 - for the biological data, they produce slightly higher quality of solution in terms of PEI.

20. References

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