Unmatched Projector/Backprojector Pairs and Algebraic Iterative Reconstruction

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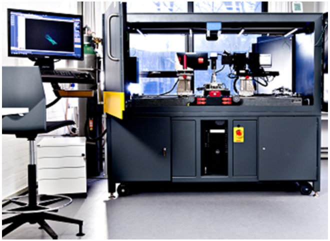
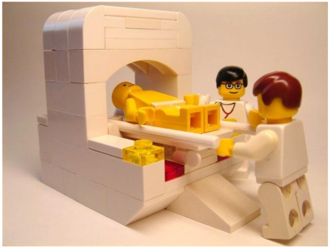
Joint work with Ken Hayami and Keiichi Morikuni
initiated last spring during a much too short visit funded by JSPS

1. What are unmatched projector pairs?
2. Fixing non-convergence of standard methods.
3. Alternative: use preconditioned GMRES.

Parallel-Beam X-Ray CT

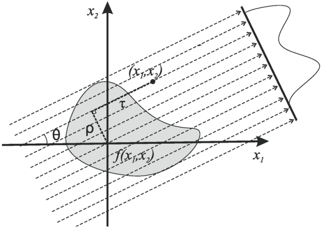


Lab scanner



Medical scanner

Synchrotron



Radon transform

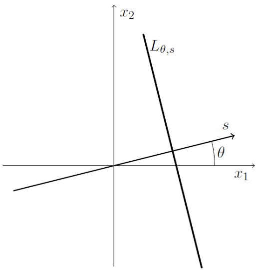
Forward and Back Projections

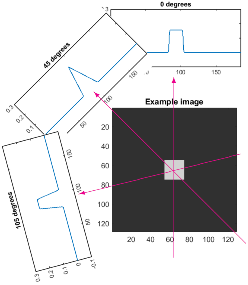
Forward projection models the physics via the Radon transform $\mathcal{R}$: integration of the image f along lines $L_{\theta,s}$

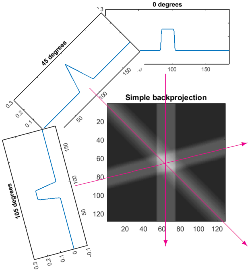
$$g(\theta, s) = \mathcal{R}[f](\theta, s) = \int_{L_{\theta,s}} f(x_1, x_2)\, d\ell \ .$$

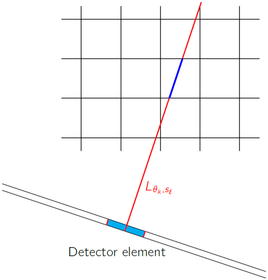
Back projection $\mathcal{B}$, a mathematical abstraction, smears g back along $L_{\theta,s}$

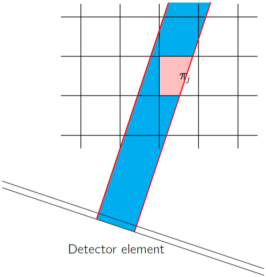
$$\mathcal{B}[g](x_1, x_2) = \int_0^{2\pi} g(\theta, x_1 \cos\theta + x_2 \sin\theta)\, d\theta = \text{adjoint}(\mathcal{R}) \ .$$

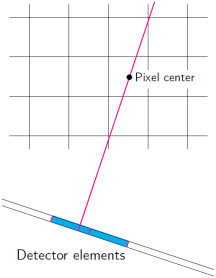












Forward line model	Forward strip model	Back projection model
Variant: Joseph model	More physically correct	Everyone uses this
Suited for GPUs	Not suited for GPUs	Suited for GPUs

$$\mathcal{B}[g](x_1, x_2) \approx \sum_k g(\theta_k, x_1 \cos\theta_k + x_2 \sin\theta_k) = \text{sum over proj. angles.}$$

Interpolate measured g-values to obtain $g(\theta_k, x_1 \cos\theta_k + x_2 \sin\theta_k)$.

Unmatched Projectors in **Matrix-Free** Methods

Multiplication with $A \leftrightsquigarrow$ action of forward projector.

Multiplication with $B \leftrightsquigarrow$ action of back projector.

Currently there is no pair of projection models such that $B = A^T$.

- ☺ Not a problem when we use B in filtered back projection.
- ☹ When A is not stored then we must use B for A^T.

Example: solve $\min_x \|A\,x - b\|_2$ with the **steepest descent** method

$$x^{k+1} = x^{(k)} + \omega\, A^T(b - A\,x^k) \quad -> \quad x^{k+1} = x^{(k)} + \omega\, B\,(b - A\,x^k)\ .$$

Convergence Analysis for Unmatched Pairs

We consider the simple **BA Iteration**

$$\boxed{x^{k+1} = x^k + \omega\, B\,(b - A\,x^k)\ , \qquad \omega > 0}$$

Generally not related to solving a minimization problem!

It is a *fixed-point iteration* whose convergence depends on the product $B\,A$. Any fixed point x^* satisfies the *unmatched normal equations*

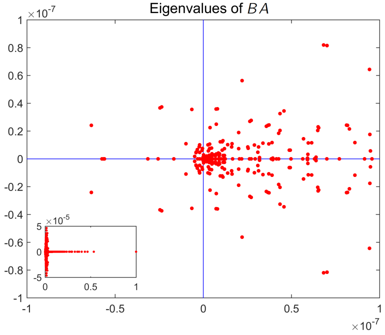
$$\boxed{B\,A\,x^* = B\,b}$$

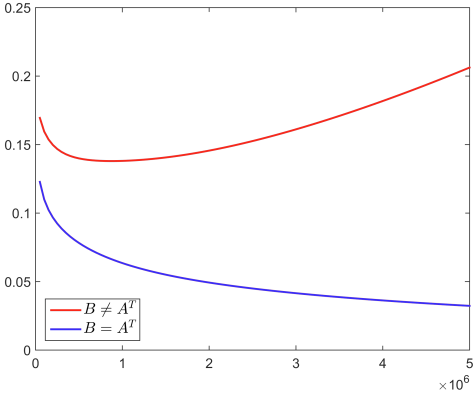
Shi, Wei, Zhang (2011); Elfving, H (2018)

The **BA Iteration** converges to a solution of $B\,A\,x = B\,b$ if and only if

$$0 < \omega < \frac{2\,\mathrm{Re}\,\lambda_j}{|\lambda_j|^2} \quad \text{and} \quad \mathrm{Re}\,\lambda_j > 0, \qquad \{\lambda_j\} = \mathtt{eig}(B\,A)\ .$$

Unmatched pair from *ASTRA* software package, image has 64 × 64 pixels, 90 proj. angles, 60 detector elements, no noise, $\min \mathrm{Re}\, \lambda_j = -6.4 \cdot 10^{-8}$.





No convergence when $B \neq A^T$ ☹

The Shifted BA Iteration (Suggested by Tommy Elfving)

We define the **Shifted BA Iteration**

$$\boxed{x^{k+1} = (1 - \alpha\,\omega)\,x^k + \omega\,B\,(b - A\,x^k)\ , \qquad \omega > 0}$$

This is equivalent to applying the BA Iteration with the substitutions

$$A \to \begin{bmatrix} A \\ \sqrt{\alpha}\,I \end{bmatrix}, \qquad B \to \left[\,B\,,\ \sqrt{\alpha}\,I\,\right]\ , \qquad b \to \begin{bmatrix} b \\ 0 \end{bmatrix}.$$

NB: we introduce the shift $\alpha\,\omega$ to fix convergence – not to regularize.

Dong, H, Hochstenbach, Riis (2019)

The Shifted BA Iteration converges to a fixed point if and only if

$$0 < \omega < 2\,\frac{\mathrm{Re}\,\lambda_j + \alpha}{|\lambda_j|^2 + \alpha\,(\alpha + 2\,\mathrm{Re}\,\lambda_j)} \qquad \text{and} \qquad \mathrm{Re}\,\lambda_j + \alpha > 0\ .$$

Just choose α large enough that $\mathrm{Re}\,\lambda_j + \alpha > 0$ for all j.

Numerical Results – Divergence and Convergence

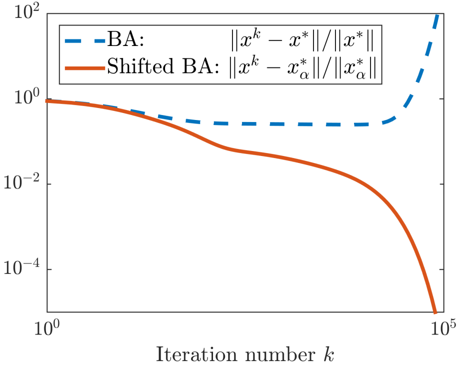
Both A and B are from the GPU-version of the *ASTRA* toolbox.

Image has 128×128 pixels, 90 proj. angles, 80 detector pixels, no noise.

$\rho(BA) = 1.76 \cdot 10^4$

$\alpha = 1.85$

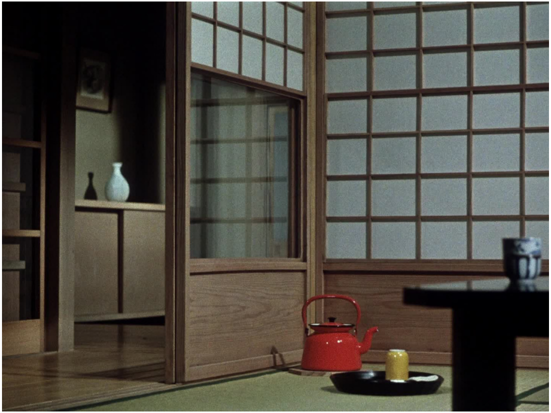
$\min \lambda_j$ determine by Krylov-Schur method



The BA Iteration diverges from $x^* = (BA)^{-1}Bb$.

The Shifted BA Iteration converges to fixed point $x^*_\alpha = (BA + \alpha I)^{-1}Bb$.

A Quiet Moment Before the Next Topic



Alternative: Just Solve the Unmatched Normal Equations

Instead of fixing an algorithm designed for solving another problem, just solve the unmatched normal equations in one of the forms

$$\boxed{B\,A\,x = B\,b} \qquad \text{or} \qquad \boxed{A\,B y = b\ , \quad x = B\,y}$$

The left- or right-preconditioned GMRES method for (A, b) immediately presents itself as a good choice with B as the preconditioner.

<u>BA-GMES</u> solves $B\,A\,x = B\,b$ with B as a left preconditioner.

<u>AB-GMES</u> solves $A\,B y = b\ ,\ x = B\,y$ with B as a right preconditioner.

Advantage: no need for relaxation parameter or shift parameter.

Convergence Analysis for Preconditioned GMRES

Hayami, Yin, Ito (2010)

AB-GMRES: $\min_x \|A\,x - b\|_2 = \min_z \|b - A\,B\,z\|_2$ holds for all b if and only if $\mathrm{range}(A\,B) = \mathrm{range}(A)$.

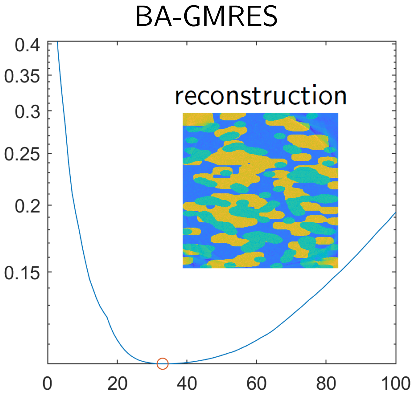
BA-GMRES: The problems $\min_x \|A\,x - b\|_2$ and $\min_x \|B\,A\,x - B\,b\|_2$ are equivalent for all b if and only if $\mathrm{range}(B^T B\,A) = \mathrm{range}(A)$.

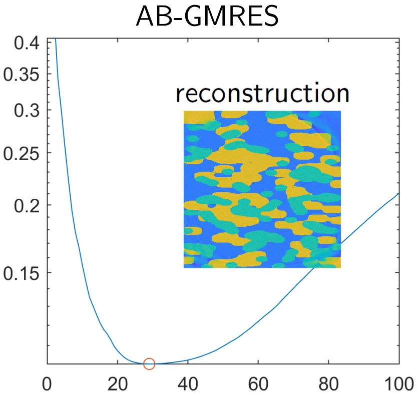
These results tells us that, under the stated assumptions, both methods converge to a solution to the least squares problem

$$\min_x \|A\,x - b\|_2 \ .$$

Unfortunately, the conditions are difficult (impossible?) to check in a given X-ray CT problem.

Image has 420×420 pixels, 600 projection angles, 420 detector pixels.

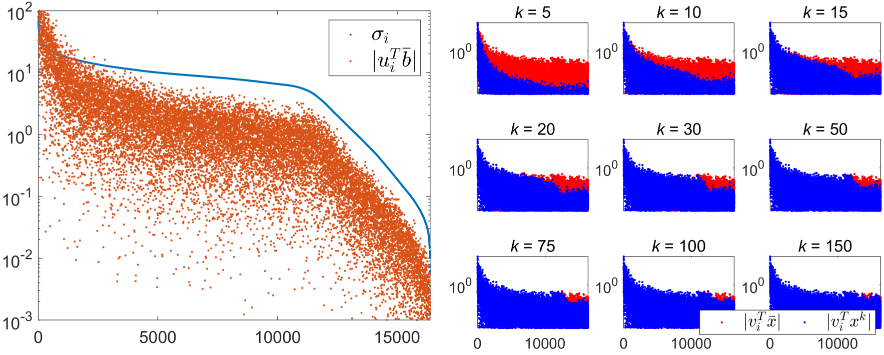




- Semi-convergence is evident for both methods (next slide ↬).
- Same minimum reconstruction error $\|x^k - \bar{x}\|_2 / \|\bar{x}\|_2 \approx 0.10$ for both.
- Slightly fewer iterations for AB-GMRES in this example.

BA-GMRES: SVD Analysis, Small System $23\,040 \times 16\,384$

Right-hand side: $\bar{b} = A\,\bar{x}$ $\bar{x}$ = ground truth   no noise.



- Left plot is typical for X-ray CT problems; no rank deficiency.
- As k increases we capture more SVD components in x^k.
- At $k = 30$ we already capture the first 11 000 SVD components.
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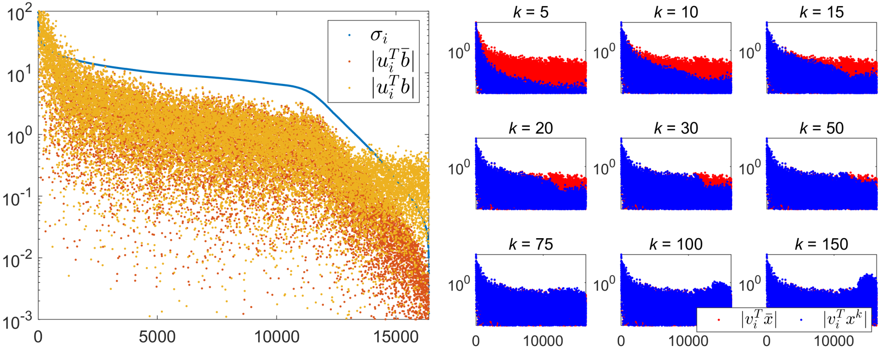
BA-GMRES: SVD Analysis – Now With Noisy Data

Right-hand side: $b = A\,\bar{x} + e \qquad \bar{x}$ = ground truth $\qquad e$ = noise.



- Left plot is typical for X-ray CT problems; no rank deficiency.
- As k increases we capture more SVD components in x^k.
- At $k = 30$ we already capture the first 11 000 SVD components.
- Eventually we include noisy SVD components = **semi-convergence**.
- We obtain the best reconstruction after $k \approx 50$ iterations.

Discussion (Technical Details $\rightarrow$ Forthcoming Paper)

Assumptions

- $A\,x = b$ comes from discretization of an inverse problem.
- The noise-free solution is dominated by the principal SVD components $\rightarrow$ we have already seen this.

Hence it is important to use an iterative method that initially captures the principal right singular vectors $v_1, v_2, \ldots$ of A.

Semi-convergence: at later iterations the noise dominates (also saw this).

BA-GMRES

1. If $B = A^T$ then it is natural to use CLGS whose semi-convergence has been established in many previous works.
2. If $B \approx A^T$ then (hopefully) the left and right singular vectors of $B\,A$ resemble those of $A^T A$ – we cannot prove this.
3. Then BA-GMRES exhibits semi-convergence, cf. Gazzola & Novati.

Computational Insight

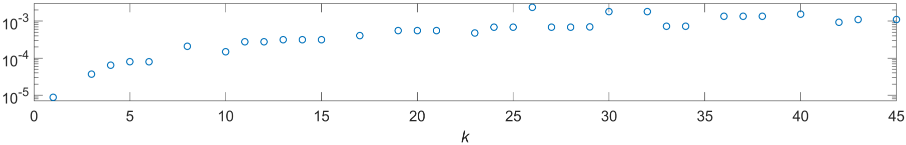
Compare the subspaces defined from the principal singular vectors:

$$\mathcal{V}_A^{(k)} = \mathrm{range}(V_A(:,1{:}k)) \qquad A^T A = V_A \Sigma^2 V_A^T$$

$$\mathcal{V}_{BA}^{(k)} = \mathrm{range}(V_{BA}(:,1:k)) \qquad BA = U_{BA} \Sigma_{BA} V_{BA}^T$$

Distance between the two subspaces:

$$\mathrm{dist}(\mathcal{V}_A^{(k)}, \mathcal{W}_{BA}^{(k)}) \equiv \big\| V_A(:,1{:}k) V_A(:,1{:}k)^T - V_{BA}(:,1:k) V_{BA}(:,1:k)^T \big\|_2 \,.$$



Conclusion: the two subspaces remain close as k increaes.

Hence, BA-GMRES captures the (approximate) SVD components in the desired order and exhibits semi-convergence.

Conclusion

Facts

- Unmatched projector pairs are here to stay – because computational efficiency is very important for large-scale problems.
- Some CT scientists claim that unmatched pairs give better results.

Need efficient iterative reconstruction methods for unmatched pairs

- Use a standard method that ignores the mismatch
  $\rightarrow$ hope for the best.
- Modify a standard method, e.g., as in the Shifted BA Iteration
  $\rightarrow$ but this requires an estimate of the leftmost eigenvalue.
- Use a method that solves the unmatched normal equations
  $\rightarrow$ AB-GMRES and BA-GMRES are the choices here.

Next step: convince the CT community to use the latter methods.