Lecture 4: Restarted GMRES + Preconditioning

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Outline:

- GMRES recap
- Restarted GMRES
- Preconditioning
 - Introduction
 - Left versus right preconditioning
 - How to choose an appropriate preconditioner
 - Examples

GMRES Recap

In the last lecture, we used GMRES to solve Ax = b.

- It minimises the residual norm $||r^{(m)}|| = ||b Ax^{(m)}||$.
- Using the Arnoldi decomposition $AV_m = V_{m+1}\bar{H}_m$,

$$||r^{(m)}|| = ||\beta e_1 - \bar{H}_m y_m||.$$

 So the *n*-dimensional minimisation reduces to the *m*-dimensional least squares problem:

$$\min \|\beta e_1 - \bar{H}_m y_m\| \text{ over } y_m \in \mathbb{R}^m.$$

- That is, to "solve" $\bar{H}_m y_m = \beta e_1 \rightarrow y_m = \bar{H}_m \setminus (\beta e_1)$.
- Our approximate solution $x^{(m)} = V_m y_m \in \mathcal{K}_m(A, b)$.

GMRES Recap

The following inequality determines the convergence rate of GMRES

$$\frac{\|r^{(m)}\|}{\|b\|} \leq \operatorname{cond}(X) \inf_{\tilde{p}_m \in P_m} \sup_{z \in \sigma(A)} |\tilde{p}_m(z)|,$$

where $\tilde{p}_m(z) = 1 - z \, q_{m-1}(z)$ is a polynomial of degree m with constant coefficient 1 ($\tilde{p}_m(0) = 1$), and $A = X \, \text{diag}(\lambda_i) \, X^{-1}$.

 We see that small eigenvalues are not desirable and clustering of eigenvalues is desirable.

- Recall that GMRES builds an orthonormal basis $[v_1, v_2, ..., v_m]$ for the Krylov subspace \mathcal{K}_m , growing by one vector at each iteration.
- Each basis vector v_i is of dimension n: the size of the full problem.
- Hence storage cost for V_m is O(mn), which for large m is easily the dominant storage cost (much more memory than a typical sparse matrix with O(n) nonzeros).
- Furthermore, a typical sparse-matrix vector product requires O(n) operations: using each entry of A once.
- Whereas the cost of <u>orthogalising</u> the next Krylov basis vector against all the previous is O(m), and there are O(m) iterations: $O(m^2)$ work.
- For large *m* this can be the dominant runtime cost.

- So for reasons of storage limitations, or of runtime considerations, there may be an upper limit on the feasible size m.
- It is quite possible that GMRES cannot converge within limited *m* iterations.
- One idea is to use <u>restarting</u>: simply take m iterations, compute $x^{(m)}$ as usual, and use this as the initial guess for a new cycle of GMRES.
- Continuing this process, restarting every m iterations, is called Restarted GMRES, denoted GMRES(m).

How to set up initial guess in GMRES?

- Standard GMRES finds $x^{(m)} \in \mathcal{K}_m(A,b)$, effectively taking $x^{(0)} = 0$.
- If an initial guess is available, one can instead use the affine space $x^{(m)} \in x^{(0)} + \mathcal{K}_m(A, b)$.
- Let $r^{(0)} = b Ax^{(0)}$ and set $x = x^{(0)} + \delta x$, with δx to be determined.

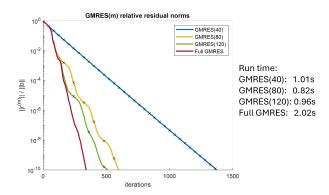
$$Ax = b \Rightarrow A(x^{(0)} + \delta x) = b$$

 $A\delta x = b - Ax^{(0)} \Rightarrow A\delta x = r^{(0)}$

- So run GMRES on this new problem $A\delta x = r^{(0)}$, calculating $\delta x^{(m)} \in \mathcal{K}_m(A, r^{(0)})$ and hence $x^{(m)} = x^{(0)} + \delta x^{(m)}$.
- In the next cycle of GMRES, use this $x^{(m)}$ as the initial guess.

Example:

```
A = gallery('poisson', 100); b = rand(size(A,1),1);
tol = 1e-10; maxit = 1500;
m = 40; % restart every 40 iterations; and try m = 80 and 120
[x,flag,relres,iter,resvec] = gmres(A,b,m,tol,floor(maxit/m));
```



In summary,

- Restarted GMRES keeps the memory requirements bounded.
- It also limits the orthgonalisation costs.
- But there are serious consequences:
 - We lose optimality across cycles: the residual is only minimised within each cycle.
 - Whatever progress had been made in localising troublesome eigenvalues is lost; the cycle starts over from scratch, albeit with a (hopefully) improved initial guess.
 - The rate of convergence may seriously deteriorate compared to full GMRES.

Preconditioning: Introduction

- In the last lecture,
 - we saw that the eigenvalue distribution plays a significant role in the convergence of GMRES,
 - in a few examples we were able to vastly improve the convergence rate by shifting the spectrum, so that instead of solving Ax = b we were solving $(A + \sigma I)x = b$ for some shift σ .
- This, it has to be said, is cheating. But the idea is intriguing.
- What if we could find a way to alter the spectrum, in our favour, such that the solution was unchanged?
- This is exactly the goal of preconditioning!

Preconditioning: Introduction

- The basic idea of preconditioning is to find a matrix M which approximates A in some sense ($M \approx A$), and whose inverse is computationally efficient to apply.
- Reformulate our problem

$$Ax = b \qquad (1)$$

by multiplying by M^{-1} on both sides:

$$M^{-1} A x = M^{-1} b$$
 (2)

- Now the convergence will depend on the properties of $M^{-1}A$ instead of those of A.
- If we've chosen our preconditioner M wisely, the matrix $M^{-1}A$ will have a much more favourable spectrum (e.g. removal of small eigenvalues, clustering of eigenvalues), and (2) may be solved much more rapidly than (1).

How to choose an appropriate preconditioner

Preconditioned system:

$$M^{-1} A x = M^{-1} b$$
 (2)

- For the idea of preconditioning to be useful, we need to be able to compute the operation represented by M^{-1} efficiently.
- If M very closely approximates A, then $M^{-1}A \approx A^{-1}A$ is almost the identity I, but applying the preconditioner may be as hard as solving the original problem, and nothing has been gained.
- If M = I, then the preconditioned system (2) is the same as the original problem, so applying the preconditioner accomplishes nothing.
- So we need a matrix M that strike a balance between these two extremes.
- The matrix M has to somehow be effective at improving the spectrum of $M^{-1}A$, but not such that the expense of calculating $M^{-1}v$ is too costly.

Left versus right preconditioning

- The approach we've described so far is known as left preconditioning, since we multiply by the preconditioner on the left.
- Alternatively we can multiply on the right, to implement right preconditioning:

$$A M^{-1} M x = b$$

let u = Mx and solve

$$A M^{-1} u = b,$$
 (3)

then compute $x = M^{-1} u$.

Left versus right preconditioning

The difference between these two approaches is more than cosmetic.

• When preconditioning on the left, the residual vector, whose norm is monitored for convergence in GMRES, is

$$r_{\text{left}}^{(m)} = M^{-1} b - M^{-1} A x^{(m)} = M^{-1} (b - A x^{(m)}) = M^{-1} r^{(m)}$$

where $r^{(m)}$ is the ordinary residual vector (i.e. without preconditioning).

• If M^{-1} is quite close to A^{-1} (in its effect on $r^{(m)}$), then the left-preconditioned residual approximates the error $e^{(m)}$:

$$\varepsilon^{(m)} = x - x^{(m)} = A^{-1} b - x^{(m)} = A^{-1} (b - A x^{(m)})$$
$$= A^{-1} r^{(m)} \approx M^{-1} r^{(m)} = r_{\text{left}}^{(m)}.$$

• However, if M^{-1} is not very much like A^{-1} , then it may not be clear what the left preconditioned residual really represents.

Left versus right preconditioning

 On the other hand, with right preconditioning, the residual is unaffected:

$$r_{\text{right}}^{(m)} = b - (A M^{-1}) u^{(m)} = b - A M^{-1} M x^{(m)} = b - A x^{(m)} = r^{(m)}.$$

- Hence, the residual norm $\|r_{\text{right}}^{(m)}\|$ can be monitored during the GMRES iterations with full confidence that it represents the true, unpreconditioned, residual norm.
- Note: MATLAB's inbuilt gmres function implements left preconditioning.

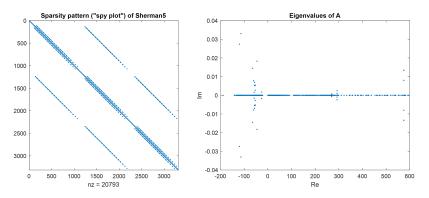
Classical Preconditioners

- Jacobi
- Gauss-Seidel
- Symmetric Gauss-Seidel
- Incomplete LU

To illustrate the effect of these preconditioners, we will consider a matrix from a problem in oil reservoir simulation. This is the matrix Sherman5 taken from the Matrix Market, an online repository of test matrices.

Classical Preconditioners

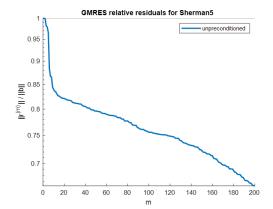
Sherman5: size 3312×3312 ; real non-symmetric matrix



- The real parts of eigenvalues range from -200 to 600 with no clustering.
- There are some small eigenvalues in magnitude.

Classical Preconditioners

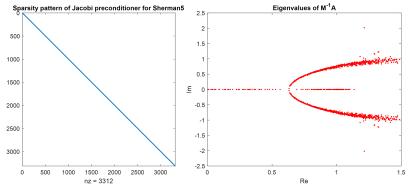
Solve the unpreconditioned system: set tolerance of 10^{-10} in relative norm with the maximum number of iterations 200. Use MATLAB's builtin function gmres.



• There's really nothing much happening here; the residual norm has barely budged in 200 iterations. We need preconditioners!

Classical Preconditioners: Jacobi

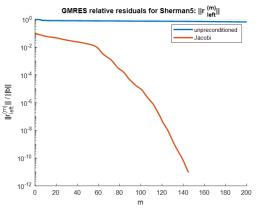
Solve the preconditioned system $M^{-1}Ax = M^{-1}b$ with the Jacobi preconditioner: $M = \operatorname{diag}(A)$. Cheap to apply.



- There are no longer any eigenvalues in the left half-plane.
- The range of magnitudes has also been greatly reduced, and there is a hint of clustering around unity.
- Some small magnitude eigenvalues evidently remain.

Classical Preconditioners: Jacobi

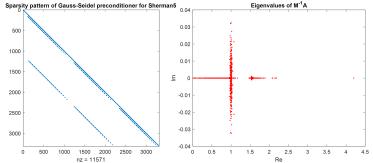
Let's check out the performance of the Jacobi preconditioner.



- The Jacobi preconditioned GMRES converges to the desired tolerance in 145 iterations.
- If it can be this effective, how much better could we get by choosing something a little more elaborate?

Classical Preconditioners: Gauss-Seidel

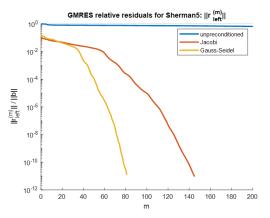
Solve the preconditioned system $M^{-1} A x = M^{-1} b$ with the Gauss-Seidel preconditioner: M = tril(A), which uses the entire lower triangular portion of A as M.



- We can see a definite clustering of eigenvalues around unity, and again the negative eigenvalues are all gone. There are a couple of small eigenvalues still hanging around.
- This looks like a better distribution than we had for Jacobi, so we might expect convergence to be improved again.

Classical Preconditioners: Gauss-Seidel

Let's check out the performance of the Gauss-Seidel preconditioner.



• By including more information about *A* in our preconditioner *M*, the convergence has been improved again.

Classical Preconditioners: Symmetric Gauss-Seidel

Solve the preconditioned system $M^{-1}Ax = M^{-1}b$ with the symmetric Gauss-Seidel preconditioner:

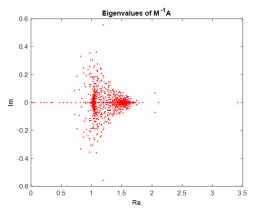
$$M = M_1 M_2$$

with $M_1 = tril(A)$ and $M_2 = triu(A)./(diag(A))$.

- It brings in the upper triangular portion of A as well, through the product $M = M_1 M_2$, where M_1 is the lower triangular portion and M_2 is the upper triangular portion scaled by the diagonal (to avoid "double-counting" the diagonal).
- The product $M = M_1 M_2$ has a similar sparsity pattern to A.
- Importantly, this product is never computed explicitly. Whenever the algorithm calls for the product $w = (M_1 M_2)^{-1} A v$ for some vector v, it is computed entirely through matrix-vector operations: $w = M_2^{-1} (M_1^{-1} (A v))$, i.e., $M_2 \setminus (M_1 \setminus (A v))$.

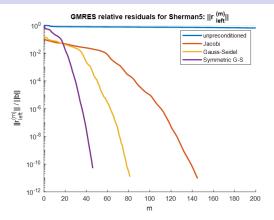
Classical Preconditioners: Symmetric Gauss-Seidel

Let's have a look at the eigenvalue spectrum for the symmetric Gauss-Seidel preconditioned matrix. Note that here we did compute the product $(M_1\,M_2)^{-1}\,A$, but this is just for the purposes of illustration.



• This may or may not look better than ordinary Gauss-Seidel to you, but certainly it's quite similar in its effect on the spectrum.

Classical Preconditioners: Symmetric Gauss-Seidel

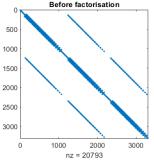


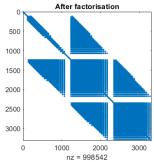
• Symmetric Gauss-Seidel does outperform ordinary Gauss-Seidel as a preconditioner for this problem.

- This is an example of a preconditioner that is often used in practice.
- The idea of incomplete LU is to compute an approximate factorisation for A, $A \approx LU$, where the LU factors are not the exact LU factors (which would be too expensive to work with) but inexact, sparse LU factors.

For comparison, let's first consider the full, exact LU factorisation of our matrix.

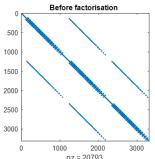
After factorisation

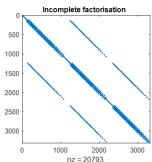




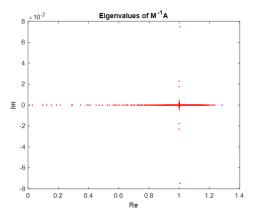
- Notice the large amount of fill-in generated by this factorisation.
- The number of nonzero entries in the factorised matrix has exploded: almost 50 times more nonzero entries after factorisation.
- The computational and memory costs associated with generating this factorisation quickly get out of control for larger matrices, making it impractical.

- Idea of incomplete LU (ILU): Drop entries from the factorisation to keep the matrix sparse.
- The computed LU factors are no longer exact, but in many cases they suffice as a preconditioner.
- The criteria for dropping entries can be simple, or more elaborate based on tolerances.
- Here we'll just look at ILU(0), which drops every single entry that would have otherwise filled in.



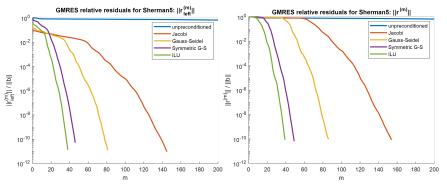


Let's check out the resulting spectrum.



- The clustering around unity looks very nice.
- There are still those couple of pesky small eigenvalues that none of our preconditioners has been able to properly deal with.

Let's check out the performance of ILU.



- ILU is the winner for today. It outperforms all our other preconditioners, yielding convergence in only 38 iterations.
- Note: the plot on the left is using $||r_{\text{left}}^{(m)}|| = ||M^{-1}r^{(m)}||$ which is from the preconditioned system; the plot on the right is using the true residual $||r^{(m)}||$.

Summary of Lectures 3 and 4

GMRES (Generalised Minimal Residual)

- Iterative Krylov subspace method for solving Ax = b.
- Finds the approximate solution $x^{(m)} \in \mathcal{K}_m(A, b)$ by minimising the residual norm $||r^{(m)}||$.
- Convergence rate depends on the properties of the matrix A: the cond(X) and the eigenvalue distribution of the matrix A.

Restarted GMRES (GMRES(m))

- Restarts after every *m* steps to control storage cost and run time.
- May have slow convergence or even stall

Preconditioning

- To improve the convergence for iterative methods.
- Left-preconditioned system: $M^{-1} A x = M^{-1} b$.
- Right-preconditioned system: $A M^{-1} u = b$, then $x = M^{-1} u$.
- Never form M^{-1} or $M^{-1}A$ explicitly; always compute the action of M^{-1} through $M^{-1}v$ (i.e., $M \setminus v$).