### AM 205: lecture 25

- Last time: SOR, multigrid
- ► Today: Multigrid, Krylov subspace methods

## Krylov Subspace Methods

We now give an overview of the role of Krylov<sup>1</sup> subspace methods in Scientific Computing

Given a matrix A and vector b, a Krylov sequence is the set of vectors

$$\{b, Ab, A^2b, A^3b, \ldots\}$$

The corresponding Krylov subspaces are the spaces spanned by successive groups of these vectors

$$\mathcal{K}_m(A, b) \equiv \operatorname{span}\{b, Ab, A^2b, \dots, A^{m-1}b\}$$

<sup>&</sup>lt;sup>1</sup>Aleksey Krylov, 1863–1945, wrote a paper on this idea in 1931

## Krylov Subspace Methods

Krylov subspaces are the basis for iterative methods for eigenvalue problems (and also for solving linear systems)

An important advantage: Krylov methods do not deal directly with A, but rather with matrix–vector products involving A

This is particularly helpful when A is large and sparse, since matrix–vector multiplications are relatively cheap

Also, Krylov sequence is closely related to power iteration, hence not surprising it is useful for solving eigenproblems

We define a matrix as being in Hessenberg form in the following way:

- ▶ A is called upper-Hessenberg if  $a_{ij} = 0$  for all i > j + 1
- ▶ *A* is called lower-Hessenberg if  $a_{ij} = 0$  for all j > i + 1

The Arnoldi iteration is a Krylov subspace iterative method that reduces A to upper-Hessenberg form

As we'll see, we can then use this simpler form to approximate some eigenvalues of  $\boldsymbol{A}$ 

For  $A \in \mathbb{C}^{n \times n}$ , we want to compute  $A = QHQ^*$ , where H is upper Hessenberg and Q is unitary (i.e.  $QQ^* = I$ )

However, we suppose that n is huge! Hence we do not try to compute the full factorization

Instead, let us consider just the first  $m \ll n$  columns of the factorization AQ = QH

Therefore, on the left-hand side, we only need the matrix  $Q_m \in \mathbb{C}^{n \times m}$ :

$$Q_m = \left| egin{array}{c|c} q_1 & q_2 & \dots & q_m \end{array} 
ight|$$

On the right-hand side, we only need the first m columns of H

More specifically, due to upper-Hessenberg structure, we only need  $\widetilde{H}_m$ , which is the  $(m+1) \times m$  upper-left section of H:

$$\widetilde{H}_{m} = \begin{bmatrix} h_{11} & \cdots & h_{1m} \\ h_{21} & h_{22} & & & \vdots \\ & \ddots & \ddots & \vdots \\ & & h_{m,m-1} & h_{mm} \\ & & & h_{m+1,m} \end{bmatrix}$$

 $\widetilde{H}_m$  only interacts with the first m+1 columns of Q, hence we have

$$AQ_m = Q_{m+1}\widetilde{H}_m$$

$$\begin{bmatrix} & & \\ & A & \end{bmatrix} \begin{bmatrix} & & \\ q_1 & \cdots & q_m \end{bmatrix} = \begin{bmatrix} & & \\ q_1 & \cdots & q_{m+1} \end{bmatrix} \begin{bmatrix} h_{11} & \cdots & h_{1m} \\ h_{21} & \cdots & h_{2m} \\ & \ddots & \vdots \\ & & h_{m+1,m} \end{bmatrix}$$

The  $m^{\rm th}$  column can be written as

$$Aq_m = h_{1m}q_1 + \cdots + h_{mm}q_m + h_{m+1,m}q_{m+1}$$

Or, equivalently

$$q_{m+1} = (Aq_m - h_{1m}q_1 - \cdots - h_{mm}q_m)/h_{m+1,m}$$

Arnoldi iteration is just the Gram-Schmidt method that constructs the  $h_{ij}$  and the (orthonormal) vectors  $q_j$ , j = 1, 2, ...

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1: choose b arbitrarily, then q_1 = b/\|b\|_2
2: for m = 1, 2, 3, \dots do
3: v = Aa_m
4: for j = 1, 2, ..., m do
5: h_{jm} = q_j^* v
6: v = v - h_{jm}q_j
7: end for
8: h_{m+1,m} = ||v||_2
9: q_{m+1} = v/h_{m+1}
10: end for
```

This is akin to the modified Gram-Schmidt method because the updated vector v is used in line 5 (vs. the "raw vector"  $Aq_m$ )

Also, we only need to evaluate  $Aq_m$  and perform some vector operations in each iteration

The Arnoldi iteration is useful because the  $q_j$  form orthonormal bases of the successive Krylov spaces

$$\mathcal{K}_m(A,b) = \operatorname{span}\{b,Ab,\ldots,A^{m-1}b\} = \operatorname{span}\{q_1,q_2,\ldots,q_m\}$$

We expect  $\mathcal{K}_m(A, b)$  to provide good information about the dominant eigenvalues/eigenvectors of A

Note that this looks similar to the QR algorithm, but the QR algorithm was based on QR factorization of

$$\left[\begin{array}{c|c}A^ke_1&A^ke_2&\dots&A^ke_n\end{array}\right]$$

Question: How do we find eigenvalues from the Arnoldi iteration?

Let  $H_m = Q_m^* A Q_m$  be the  $m \times m$  matrix obtained by removing the last row from  $\widetilde{H}_m$ 

Answer: At each step m, we compute the eigenvalues of the Hessenberg matrix  $H_m$  (via, say, the QR algorithm)<sup>2</sup>

This provides estimates for m eigenvalues/eigenvectors ( $m \ll n$ ) called Ritz values, Ritz vectors, respectively

Just as with the power method, the Ritz values will typically converge to extreme eigenvalues of the spectrum

<sup>&</sup>lt;sup>2</sup>This is how eigs in Python/Matlab works

We now examine why eigenvalues of  $H_m$  approximate extreme eigenvalues of A

Let  $^3$   $\mathbb{P}^m_{\mathrm{monic}}$  denote the monic polynomials of degree m

Theorem: The characteristic polynomial of  $H_m$  is the unique solution of the approximation problem: find  $p \in \mathbb{P}_{\text{monic}}^m$  such that

$$||p(A)b||_2 = \min$$

Proof: See Trefethen & Bau

 $<sup>^3</sup>$ Recall that a monic polynomial has coefficient of highest order term of 1

This theorem implies that Ritz values (i.e. eigenvalues of  $H_m$ ) are the roots of the optimal polynomial

$$p^* = \arg\min_{p \in \mathbb{P}_{\text{monic}}^m} \|p(A)b\|_2$$

Now, let's consider what  $p^*$  should look like in order to minimize  $\|p(A)b\|_2$ 

We can illustrate the important ideas with a simple case, suppose:

- ▶ A has only m ( $\ll$  n) distinct eigenvalues
- ▶  $b = \sum_{j=1}^{m} \alpha_j v_j$ , where  $v_j$  is an eigenvector corresponding to  $\lambda_j$

Then, for  $p \in \mathbb{P}_{\text{monic}}^m$ , we have

$$p(x) = c_0 + c_1 x + c_2 x^2 + \cdots + x^m$$

for some coefficients  $c_0, c_1, \ldots, c_{m-1}$ 

Applying this polynomial to a matrix A gives

$$p(A)b = (c_0 I + c_1 A + c_2 A^2 + \dots + A^m) b$$

$$= \sum_{j=1}^m \alpha_j (c_0 I + c_1 A + c_2 A^2 + \dots + A^m) v_j$$

$$= \sum_{j=1}^m \alpha_j (c_0 + c_1 \lambda_j + c_2 \lambda_j^2 + \dots + \lambda_j^m) v_j$$

$$= \sum_{j=1}^m \alpha_j p(\lambda_j) v_j$$

Then the polynomial  $p^* \in \mathbb{P}^m_{\text{monic}}$  with roots at  $\lambda_1, \lambda_2, \dots, \lambda_m$  minimizes  $\|p(A)b\|_2$ , since  $\|p^*(A)b\|_2 = 0$ 

Hence, in this simple case the Arnoldi method finds  $p^*$  after m iterations

The Ritz values after m iterations are then exactly the m distinct eigenvalues of A

Suppose now that there are more than m distinct eigenvalues (as is generally the case in practice)

It is intuitive that in order to minimize  $||p(A)b||_2$ ,  $p^*$  should have roots close to the dominant eigenvalues of A

Also, we expect Ritz values to converge more rapidly for extreme eigenvalues that are well-separated from the rest of the spectrum

(We'll see a concrete example of this for a symmetric matrix A shortly)

Lanczos iteration is the Arnoldi iteration in the special case that A is hermitian

However, we obtain some significant computational savings in this special case

Let us suppose for simplicity that A is symmetric with real entries, and hence has real eigenvalues

Then  $H_m = Q_m^T A Q_m$  is also symmetric  $\implies$  Ritz values (i.e. eigenvalue estimates) are also real

Also, we can show that  $H_m$  is tridiagonal: Consider the ij entry of  $H_m$ ,  $h_{ij}=q_i^TAq_j$ 

Recall first that  $\{q_1,q_2,\ldots,q_j\}$  is an orthonormal basis for  $\mathcal{K}_j(A,b)$ 

Then we have  $Aq_j \in \mathcal{K}_{j+1}(A,b) = \operatorname{span}\{q_1,q_2,\ldots,q_{j+1}\}$ , and hence  $h_{ij} = q_i^T(Aq_j) = 0$  for i > j+1 since

$$q_i \perp \text{span}\{q_1, q_2, \dots, q_{j+1}\}, \text{ for } i > j+1$$

Also, since  $H_m$  is symmetric, we have  $h_{ij} = h_{ji} = q_j^T(Aq_i)$ , which implies  $h_{ij} = 0$  for j > i + 1, by the same reasoning as above

Since  $H_m$  is now tridiagonal, we shall write it as

$$T_{m} = \begin{bmatrix} \alpha_{1} & \beta_{1} & & & & \\ \beta_{1} & \alpha_{2} & \beta_{2} & & & & \\ & \beta_{2} & \alpha_{3} & \ddots & & & \\ & & \ddots & \ddots & \beta_{m-1} & \\ & & & \beta_{m-1} & \alpha_{m} \end{bmatrix}$$

The consequence of tridiagonality: Lanczos iteration is much cheaper than Arnoldi iteration!

The inner loop in Lanczos iteration only runs from m-1 to m, instead of 1 to m as in Arnoldi

This is due to the three-term recurrence at step m:

$$Aq_m = \beta_{m-1}q_{m-1} + \alpha_m q_m + \beta_m q_{m+1}$$

(This follows from our discussion of the Arnoldi case, with  $T_m$  replacing  $\widetilde{H}_m$ )

As before, we rearrange this to give

$$q_{m+1} = (Aq_m - \beta_{m-1}q_{m-1} - \alpha_m q_m)/\beta_m$$

#### Which leads to the Lanczos iteration

```
1: \beta_0 = 0, q_0 = 0

2: choose b arbitrarily, then q_1 = b/\|b\|_2

3: for m = 1, 2, 3, \dots do

4: v = Aq_m

5: \alpha_m = q_m^T v

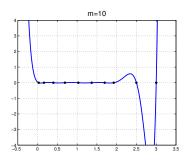
6: v = v - \beta_{m-1}q_{m-1} - \alpha_m q_m

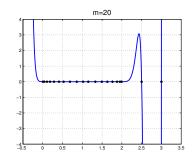
7: \beta_m = \|v\|_2

8: q_{m+1} = v/\beta_m

9: end for
```

Python demo: Lanczos iteration for a diagonal matrix





We can see that Lanczos minimizes  $||p(A)b||_2$ :

- p is uniformly small in the region of clustered eigenvalues
- roots of p match isolated eigenvalues very closely

Note that in general p will be very steep near isolated eigenvalues, hence convergence for isolated eigenvalues is rapid!