

PROJECT 1: FAST ITERATIVE SOLVERS

BRIEF SUMMARY REPORT

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POINTS OF INVESTIGATION:

Note: The questions are directly taken from the assignment pdf given in moodle

Question : For the full GMRES method: How many Krylov vectors do you need to solve the problem with and without preconditioning

Answer: Without Pre Conditioning, it takes at least 490 vectors to get the relative residue convergence under 10^{-8} , with a runtime of 3.88 seconds. In the plot below is representative of convergence achieved.

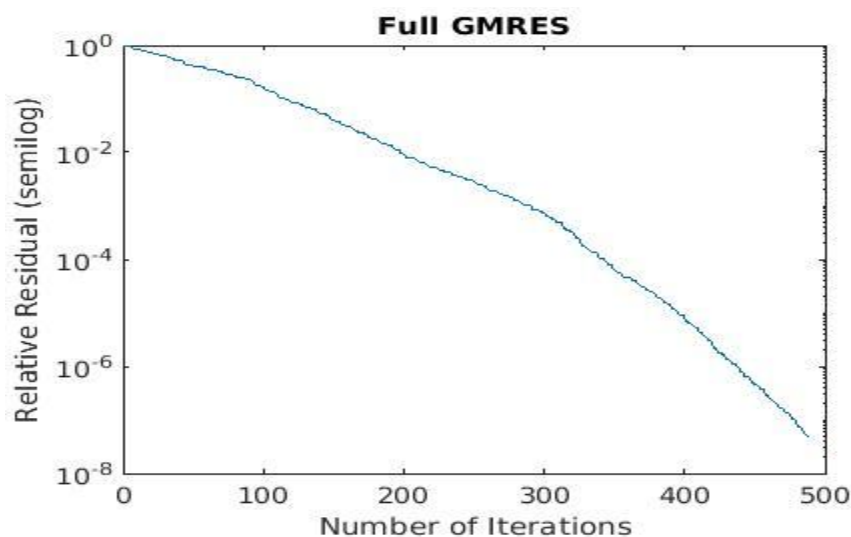


Fig1a: Full GMRES without preconditioning with 490 Krylov vectors, convergence plot with number iterations v/s log(relative residual)

Although after preconditioning the code should converge faster than non-preconditioned case, in my implementation the jacobi and gauss seidel let preconditioning method converged slower as shown below.

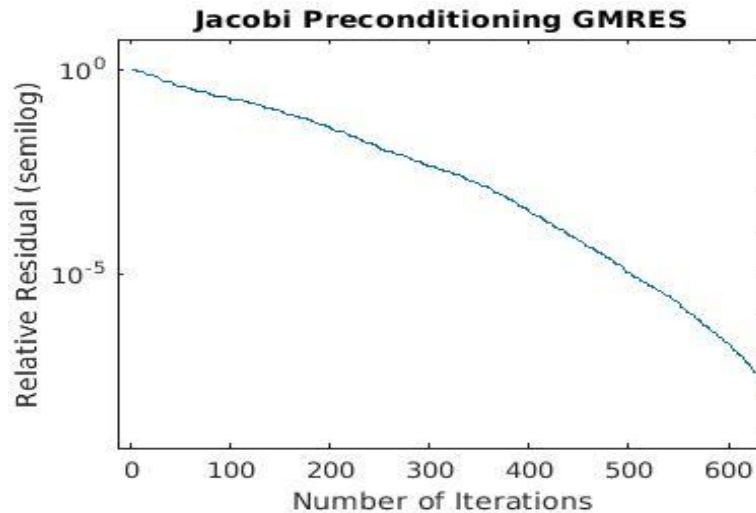


Fig1b: Full GMRES with Jacobi preconditioning with 580 Krylov vectors, convergence plot with number iterations v/s log(relative residual)

Question : For the restarted GMRES method: In an effort to try and find a good restart parameter, try $m=10$, $m=30$, $m=50$, $m=100$, and compare the runtime for these runs to full GMRES. Is restarted faster than full GMRES for some, or all values of m ? What factors other than runtime may provide motivation to use restart, as opposed to full GMRES

Answer: To answer this question, restart -gmres algorithm is run for different number of Krylov vectors, to compare and analyze the table below is shown

Krylov vectors(m)	10	30	50	100
Elapsed Time (in seconds)	N/A	5.91	5.77	6.77
Number of times the gmres function is called	100,000+	210	51	16
Cumulative iterations	N/A	6300	2550	1600

Table1: For different number of Krylov vectors, run-time, number of function calls, and cumulative iterations is tabulated

As shown in the table, the restarted Gmres the **runtime is more than** the full Gmres method with 490 Krylov vectors which takes 3.88 seconds as shown in answer to question one, the main reason could be because of less function calls. Further, the convergence plots is shown below

Further from table1, it can be observed that for very less Krylov vectors (ex $m= 10$), the solution do not converge, but as the number Krylov vectors increase the number of function calls are decreased, this is because using more Krylov vectors results in better starting approximation for

gmres, thus the solution will converge in less number of iterations. But the increase in runtime is observed because of the increase in size of matrix storage of orthonormal basis

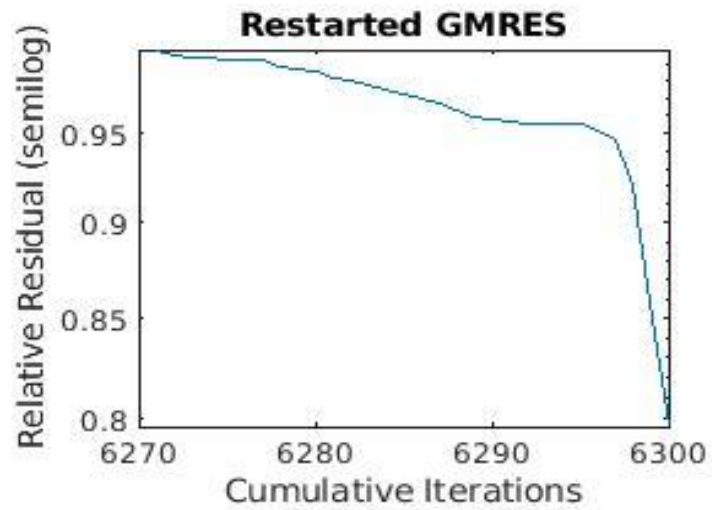


Fig2: Restarted GMRES without preconditioning with 30 Krylov vectors, convergence plot with cumulative iterations v/s $\log(\text{relative residual})$

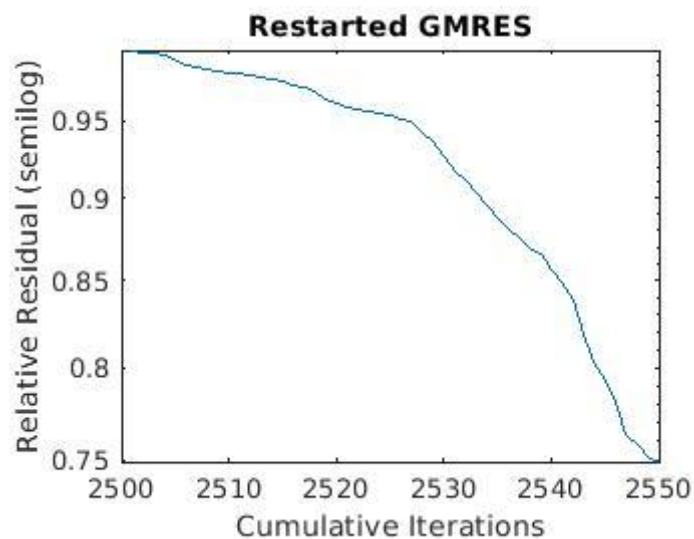


Fig3: Restarted GMRES without preconditioning with 50 Krylov vectors, convergence plot with cumulative iterations v/s $\log(\text{relative residual})$

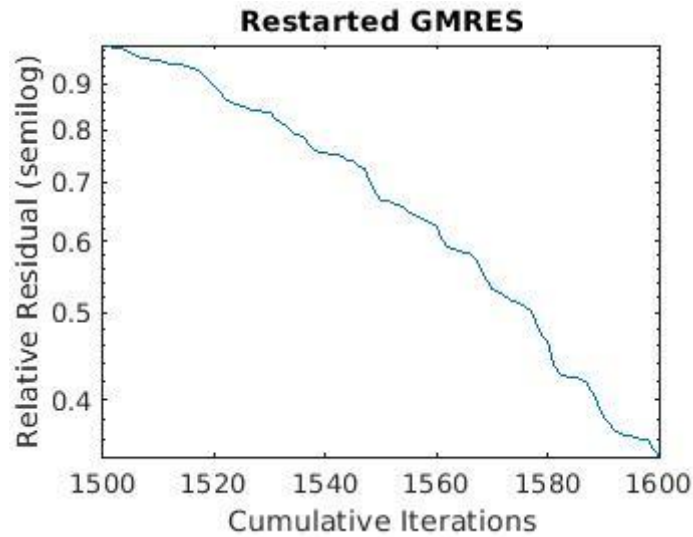


Fig4: Restarted GMRES without preconditioning with 100 Krylov vectors, convergence plot with cumulative iterations v/s log(relative residual)

Question : Plot both the error in A-norm, i.e. $\|e\|_A = p(Ae, e)$, and the residual in standard 2-Norm, i.e. $\|r\|_2 = p(r, r)$ against the iteration index on a semi-log scale. Compare qualitatively the difference in convergence behavior. (i.e. the difference between the two norms). Is there an explanation for what you observe?

Answer: Elapsed time=130 seconds

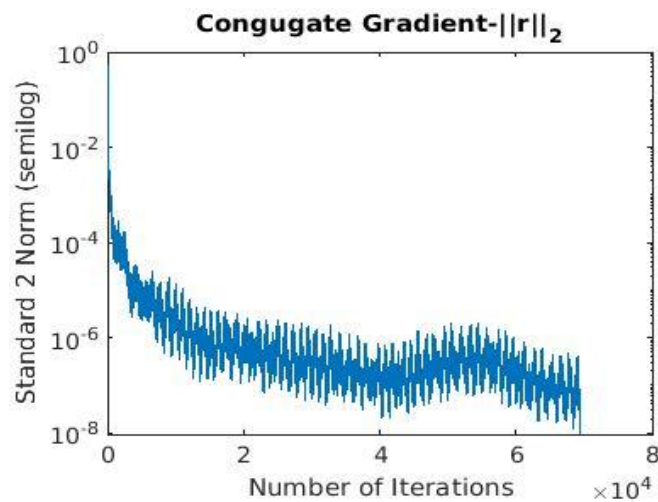


Fig5: Conjugate Gradient Norm Plot with standard norm

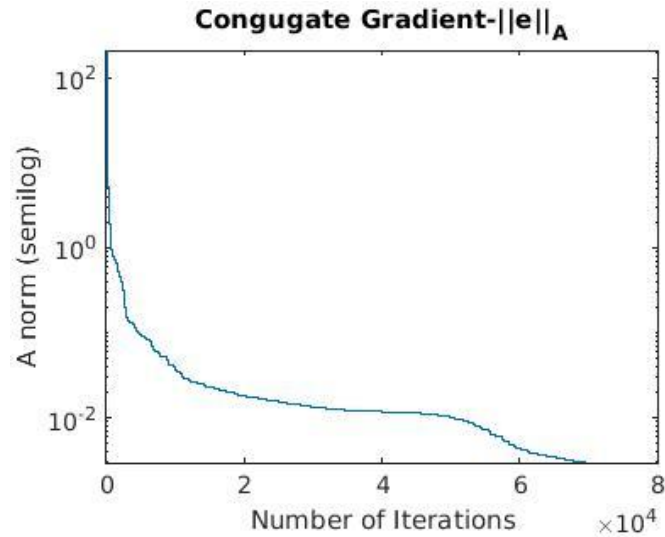


Fig6: Conjugate Gradient Norm Plot with standard norm

From the above graphs we can see that, the convergence obtained from A-norm is much better than the residual L2 norm, the reason is the the normal norm is calculated using the usual difference is error has effects from other components which gives the oscillations, but the A norm will have other residual norms dot product zero i.e $(r_{m+1}, r_k) = 0$.

Question: Compare the true absolute residual $r := b - Ax$ with the residual of preconditioned system. Does the relative residual reduction depend on which residual you monitor?

Answer: The true absolute residual 'r' is calculated in the end, which will show the same nature/trend as the relative residual, but the residual that we monitor is based on choice, since both are of decreasing trend. Further, in this case the relative residual converge faster than than the absolute residual.

Question s:For full GMRES: check the orthogonally of the Krylov vectors, Plot the computed values of (v_1, v_k) against k on a semi-log scale.

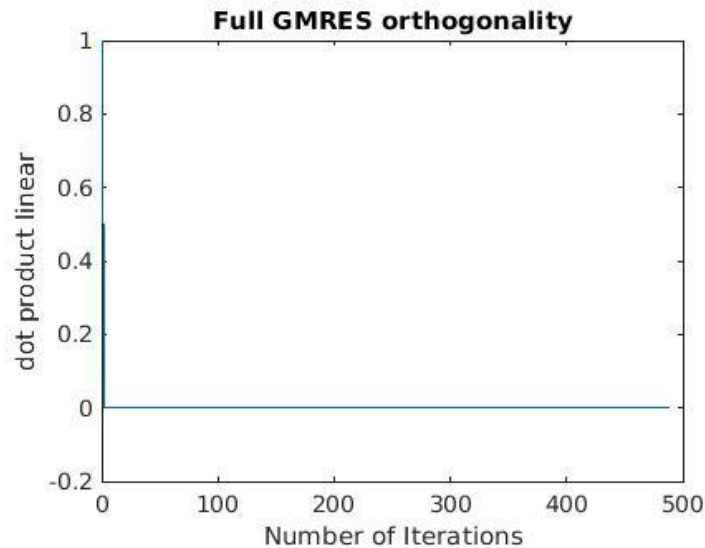


Fig7: Orthogonality Check in Linear Scale

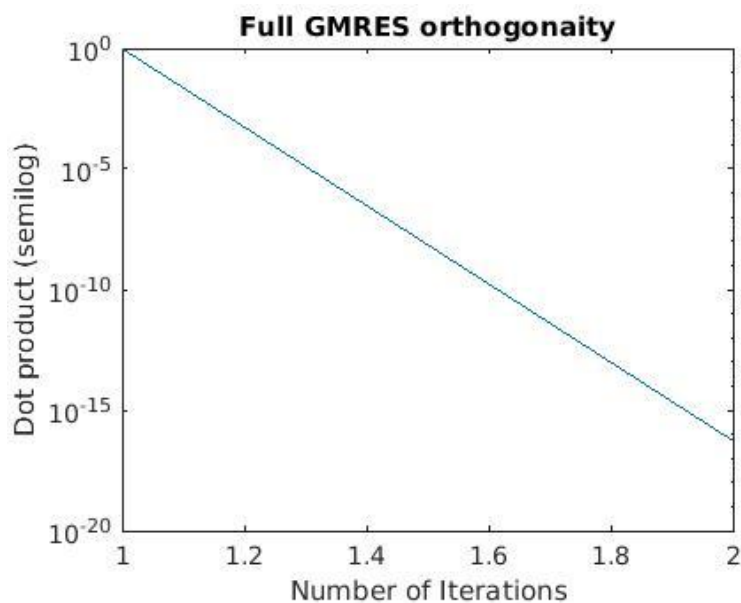


Fig8: Orthogonality Check in Semilog Scale

From the above two graphs it can be seen that, the dot product between the two vectors obtained from the Gram Schmidt orthogonalization are orthogonal, the first plot gives the dot product values in linear scale, the second plot is in semilog scale focused more closely in between the two iterations.