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On adaptative GMRES(m) in the PETSc package

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The Restarted Generalized Minimal Residual method (GMRES(m)) is a standard method for solving non-symmetric indefinite large linear systems of equations of the form Ax = b [1, 2]. It has the limitation that if the restating parameter m is not adequately chosen can present either a slow convergence or stagnation [3]. This problem has been faced in several previous works [4–6]. However, to be useful for solving practical engineering and simulation problems, it is necessary to have the method in a computationally appropriate platform, allowing the simultaneous implementation in parallel and distributed architectures, and the implementation of several preconditioners. This work introduces a PETSc (Portable, Extensible Toolkit for Scientific Computation) routine that enforces the adaptation in the restarted parameter of the restarted-GMRES method of the solver in the PETSc.

The routine starts from a default value for m = 30. This value is systematically decreased, evaluating at each cycle of the GMRES(m) the rate of convergence. This process continues until either a stagnation or a critical slowing down in the convergence is detected. A possible strategy to overcome this problem consists in modifying the restart parameter. A control updating law is presented at Algorithm 1 below [3, 6], where the input are: m_{j-1} last value of m, $m_{initial}$: last initial value of m, m_{min} the minimum value of m, m_{max} the maximum value of m, m_{step} : value by which $m_{initial}$ is incremented when $m < m_{min}$ or m_j is decremented when $m > m_{max}$, r_q is the last q residuals, $r_{j-1}, r_{j-2}, \dots, r_{j-q}$, and the output is m_j the restart parameter used in $GMRES(m), m_{initial}$ for iteration j.

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Algorithm 1 PD Control Rule for Restart Parameter m

1.	if $j > 3$, then
2.	$m_{j} = m_{j-1} + \left[(\alpha) \frac{\ r_{j-1}\ }{\ r_{j-2}\ } + (\gamma) \frac{\ r_{j-1}\ - \ r_{j-3}\ }{2\ r_{j-2}\ } \right]$
3.	else if $j > 2$, then $m_j = m_{j-1} + \left[(\alpha) \frac{\ r_{j-1}\ }{\ r_{j-2}\ } \right]$
4.	$else m_j = m_{initial} \ end \ if$
5.	if $m_j < m_{initial}$, then $m_{initial} = m_{initial} + m_{step}$, $m_j = m_{initial}$ end if
6.	if $m_j > m_{max}$, then $m_j = m_j - m_{step}$ end if
7.	return m_j , $m_{initial}$ for the next iteration.

This technique allows having a dynamic *m*, saving computational time and memory requirements when the dimension of the Krylov subspace can be decreased or increased but in a controlled way. The package (with the implemented algorithm) was evaluated using numerical examples and compared with the existing Matlab implementation. The results showed that the proposed implementation in PETSc is able to emulate the results up to the compared dimensions, in terms of the behavior of the residual as a function of the number of iterations, with better computational performance.

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