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Numerical Analysis of Nonlinear Systems Using Iterative Methods

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Abstract. Nonlinear systems are very common in science and engineering, but solving them numerically with iterative methods is still difficult due to the various behaviours of solvers under different problem structures. This paper investigates how algebraic structures in the Jacobian matrix, such as symmetry, condition number, sparsity and spectral distribution, affect the suitability and convergence performance of typical iterative methods for solving nonlinear system equilibria. Four cross-disciplinary case studies were used: the susceptible-infected-recovered (SIR) epidemic model, the Lotka–Volterra predator–prey system, blood ethanol kinetics and steady-state heat conduction; a structure-diagnostic framework connecting Jacobian pathologies to solver selection was established. The case studies show that a singular or ill-conditioned Jacobian can make Newton steps difficult or numerically unstable, and non-symmetric linear subproblems require solvers other than conjugate gradient. Purely imaginary eigenvalues of a dynamical-system Jacobian do not by themselves imply oscillatory failure of Newton root-finding. Well-conditioned but strongly state-dependent Jacobians in the scalar blood ethanol model do not prevent convergence, and larger coupled variants may motivate Jacobian-free alternatives when derivative evaluation is costly. In contrast, symmetric positive-definite sparse Jacobians in the heat-conduction example have no structural obstruction and can be solved efficiently by successive over-relaxation or the Thomas algorithm. Based on the above results, Jacobian structural diagnosis can be used to select a suitable iterative solver beforehand, and the focus will shift from convenience to structure.

Keywords: nonlinear systems, Jacobian matrix, iterative methods, structural diagnostics

1. Introduction

Nonlinear behaviours are ubiquitous in nature, and nonlinear systems serve as a core modelling framework for a broad spectrum of real-world domains. While linear systems feature well-ordered mathematical structures, solving nonlinear systems--defined by multiple interacting variables and inherent nonlinear couplings--relies extensively on linear algebraic techniques. Local linearisation provides a useful approximation near a chosen operating point or equilibrium when higher-order nonlinear effects are sufficiently small over the region of interest. In strongly nonlinear regimes, local linearisation may become inaccurate when higher-order terms are no longer negligible over the region of interest. In such regimes, not only does linearisation underestimate these pronounced

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nonlinear influences, leading to a notable degradation in solution accuracy, but most nonlinear systems, except for a limited class of special cases, also lack closed-form analytical solutions, which makes purely symbolic approaches infeasible. Accordingly, researchers have turned to alternative numerical methodologies, among which iterative methods constitute a pivotal class of techniques for solving these critical nonlinear equations. Iterative methods begin with an initial guess x_0 and converge to the solution via repeated updates to produce equation-satisfying numerical results. Different approaches differ in convergence speed, computational cost and Jacobian processing logic. This diversity makes iterative analysis a key research component of numerical analysis [1].

Fixed-point iteration, Newton-Raphson and quasi-Newton methods are typical ways to handle nonlinear systems. Linear schemes such as Jacobi, Gauss-Seidel, successive over-relaxation (SOR) and Krylov methods can be seen as appropriate solvers for the linear subproblems that arise after linearisation or discretisation.

For stationary linear iterations that update the new iterate by iteration matrix multiplication plus a constant vector, convergence for all initial vectors depends only on the iteration matrix. A necessary and sufficient condition for convergence is that the spectral radius is strictly less than 1. The spectral radius is the maximum absolute value of an eigenvalue. Under this condition, the iteration will converge linearly to the unique fixed point; if the spectral radius is greater than or equal to 1, the iteration does not converge for all initial vectors. A small spectral radius corresponds to a faster convergence; however, a value close to one will have very slow solution convergence. The Newton-Raphson method is known to have quadratic convergence near a solution; that is, the iteration error decreases by the square of the previous error per step, and it converges much faster than the basic fixed-point iteration. However, it requires analytical derivative information and only converges locally. It also requires Jacobian evaluation. Given the trade-off between the speed of convergence and computational cost, improved quasi-Newton methods have been developed.

Broyden's method is a multi-dimensional secant-type quasi-Newton method that updates an approximation of the Jacobian or its inverse using low-rank corrections. It reduces the number of repeated exact Jacobian evaluations, but the Newton step is still obtained by solving a linear system rather than explicitly inverting the Jacobian [2].

Variational Iteration Method (VIM) is an analytical iterative method to find approximate solutions of some nonlinear problems. No linearisation of the nonlinear term is needed in the entire iteration process. In addition, it does not need to construct a Jacobian matrix or find the analytical derivative of a nonlinear function for iterative calculation, as is the case with the Newton-Raphson and quasi-Newton solution frameworks [3].

The three main attributes of the above three methods are their use of Jacobian matrices, per-step computational cost and numerical stability. These attributes directly affect the range of application and computational efficiency of the corresponding schemes.

However, most previous studies have focused on algorithmic improvements to single methods or their application in specific models, and have not systematically compared different approaches according to the metrics listed above. This deficiency is a representative case for further research. However, previous studies have rarely addressed the reverse diagnostic question of how the algebraic structure of the Jacobian can inform whether an iterative method will successfully find the equilibrium points of a given nonlinear system. This paper studies how Jacobian symmetry, condition number, sparsity and spectral distribution affect the convergence of Newton-type, quasi-Newton, Jacobian-free and fixed-point methods for solving equilibrium points. Through the four cross-disciplinary models of Lotka-Volterra, susceptible-infected-recovered (SIR), blood ethanol and steady-state heat conduction, the paper systematically compares solver behaviour and establishes a

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structure-diagnostic framework that links specific Jacobian pathologies to suitable or unsuitable algorithms for equilibrium computation. Section 2 introduces the basic concepts; Section 3 presents typical iterative methods; Section 4 shows case studies; Section 5 discusses deficiencies and future directions; and Section 6 provides practical advice and concludes.

2. Basic concepts of nonlinear systems and iterative numerical analysis

For the purpose of this review, the nonlinear problems considered fall into two general categories: nonlinear algebraic systems and dynamical systems with equilibria that satisfy nonlinear algebraic equations. A nonlinear algebraic system is formally expressed as finding an unknown vector in a subset of the real n-dimensional space such that a given vector-valued function, which also maps to the same space, is zero at that point. The dynamical system is in the form of an ordinary differential equation, and the time derivative of the state vector is a function of the state. This work covers both types: the Lotka-Volterra and SIR models are dynamical systems, the ethanol model is a scalar dynamical system, and after discretisation of the partial differential equation, the steady-state heat conduction problem becomes an algebraic system. A system of coupled equations is considered nonlinear if at least one equation cannot be expressed as a linear function of the unknowns.

After a finite number of iterations, an approximation of the system has been found. The residual is defined as the difference between the product of the coefficient matrix and the current approximation and the right-hand side vector; it indicates how well the current approximation satisfies the linearised equations. The iteration stops when the norm of the residual is less than a set tolerance, when the norm of the difference between two consecutive iterates is small enough, or when the maximum number of iterations has been reached.

The Jacobian matrix is an $n \times n$ array containing all first-order partial derivatives of each component of the nonlinear function with respect to all variables. It is a local linearisation of the nonlinear mapping at a particular point, and in the vicinity of that iteration point, the original complex system can be approximated by a linear system. Linearisation results in the correction equation, where the Jacobian matrix multiplies the unknown step vector, and the product is equal to the negative of the function value. The linearisation step is the basis for Newton's method and other Newton-type methods. The Jacobian matrix also has some structure that affects the behaviour of the resulting linear solves and nonlinear iterations. Symmetry alone does not determine whether the conjugate gradient method can be used; standard conjugate gradient requires a symmetric positive definite coefficient matrix, and non-symmetric systems generally need to use methods such as the generalized minimal residual (GMRES) method or the biconjugate gradient stabilized (BiCGSTAB) method. Conservative systems generally correspond to gradient vector fields and have symmetric Jacobian matrices under smoothness assumptions; non-conservative systems, such as fluid convection and population dynamics, typically result in non-symmetric matrices for which conjugate-gradient-type methods are not applicable. Sparsity is also an important structural property: in large-scale scientific models, such as multi-bus power flow networks, chemical kinetics and state-to-state reaction systems, the Jacobian is large but numerically sparse because variables only connect locally through terms; by contrast, if the variables are globally coupled, the Jacobian will be dense and requires different storage and factorisation methods. The condition number shows how sensitive the linearised system is to small changes; a large condition number indicates an ill-conditioned matrix, and thus rounding errors in the Newton correction may be amplified, leading to slow convergence or failure. Finally, spectral distribution refers to the location of eigenvalues in the complex plane. For stationary fixed-point iterations, the spectral radius of the iteration matrix determines convergence: if it is less than 1, the iteration converges for all initial vectors; if it is

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greater than or equal to 1, it does not converge for all initial vectors. Purely imaginary eigenvalues of the dynamical-system Jacobian indicate neutral linear stability, but they do not by themselves imply failure of Newton root-finding; local Newton convergence instead depends primarily on a non-singular Jacobian at the root, sufficient smoothness, and a sufficiently close initial guess.

3. Common iterative methods for solving nonlinear systems

This section briefly introduces the main iterative methods for nonlinear systems and specifies their structural requirements, that is, the Jacobian properties under which they are theoretically justified and computationally efficient [1, 2]. The above requirements serve as the reference baseline for the case studies in Section 4, and violations of these conditions are shown to reduce or invalidate the corresponding methods.

Fixed-point iteration rewrites the equation in a way that repeatedly applies a mapping to obtain the next approximation. For linear systems, classical stationary methods such as Jacobi, Gauss-Seidel and SOR can be employed as inner solvers in Newton-type iterations or after discretisation. The above methods converge linearly if the spectral radius of the iteration matrix is strictly less than 1. For nonlinear fixed-point iteration, convergence additionally requires an appropriate local contraction, whereas a stationary linear iteration with spectral radius below one converges for any initial vector. If the corresponding spectral or contraction conditions are not met, the iterations may diverge. The Newton-Raphson method finds the step by solving a linear system with the Jacobian as the coefficient matrix, and the solution is a correction to update the current estimate. When the Jacobian is non-singular and the initial guess is in the basin of attraction, the method will have local quadratic convergence; that is, the error is squared at each step. Explicit evaluation of the Jacobian and solution of a linear system are required at each iteration. If the Jacobian is singular, the Newton step cannot be uniquely determined; if it is ill-conditioned, the computed correction will be numerically unstable. Repeated Jacobian computation increases the cost. Quasi-Newton methods (e.g., Broyden) approximate the Jacobian or its inverse using rank-one updates to avoid repeated exact evaluations. The so-called "bad" variant directly updates an approximation of the inverse Jacobian without explicit inversion. These methods achieve local superlinear convergence; they are slower than Newton's quadratic convergence but have a lower per-step cost. They are preferred when Jacobian evaluation is costly, but their performance may be affected by severe nonlinearity. The variational iteration method (VIM) builds a correction functional without linearising nonlinear terms and without computing Jacobians [3]. It has also been employed to address nonlinear boundary-value problems [4]. The convergence characteristics of the correction function and problem structure are not specified here, and it does not generally exhibit Newton-type local quadratic convergence.

4. Recent studies of iterative methods for nonlinear systems

Recently, studies have used stability and iterative methods to analyse SIR, predator-prey and blood ethanol models, and the following subsections will use these published models as examples for solver comparison [5, 6]. Representative works of the above structural types are introduced here.

4.1. Contrasting Jacobian structures at susceptible-infected-recovered equilibrium points

The SIR epidemic model is a typical case study because its two equilibrium points have fundamentally different Jacobian structures, although they belong to the same dynamical system [5].

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The Jacobian matrix of this system has four elements arranged in two rows and two columns: the top-left element is the negative product of the transmission rate and the number of infected individuals; the top-right element is the negative product of the transmission rate and the number of susceptible individuals; the bottom-left element is the positive product of the transmission rate and the number of infected individuals; and the bottom-right element is the difference between the product of the transmission rate and the number of susceptible individuals and the recovery rate.

4.1.1. Disease-free equilibrium with a singular Jacobian

At the disease-free equilibrium, when the entire population is susceptible and no one is infected, the Jacobian matrix is relatively simple. In this reduced form, the top-left entry is zero; the top-right entry is still the negative product of the transmission rate and the total population; the bottom-left entry is zero; and the bottom-right entry is the product of the transmission rate and the total population minus the recovery rate.

The reduced matrix has two eigenvalues. The first eigenvalue is always 0. The second eigenvalue is equal to the recovery rate multiplied by the amount obtained by subtracting one from the basic reproduction number. The existence of a zero eigenvalue indicates that this Jacobian matrix is singular for all values of the parameters. When the basic reproduction number is less than 1, the second eigenvalue is negative; when it is greater than 1, the second eigenvalue is positive; and when it is exactly equal to 1, both eigenvalues are zero, so the matrix is doubly singular.

At a root with a singular Jacobian, the standard nonsingular-Jacobian theorem that guarantees local quadratic convergence does not apply. If the Jacobian at an iterate is singular during Newton iteration, the linear correction system may not have a unique solution, and thus the standard Newton step cannot be determined. Since one eigenvalue is zero for all values of the basic reproduction number, the Jacobian is singular at every disease-free equilibrium in this family. As the basic reproduction number approaches 1, the second eigenvalue also approaches 0, and the local linearisation becomes even more degenerate. Standard Newton iterations near this singular root will thus lose quadratic convergence or become ill-posed.

A singular Jacobian does not by itself justify using Broyden's method. This is because the standard local convergence theory for Broyden-type methods also generally assumes that the Jacobian is non-singular in a neighbourhood of the solution. Broyden's method can reduce repeated exact Jacobian evaluations by approximating the Jacobian with rank-one updates. This way avoids multiple exact Jacobian calculations, but it is not guaranteed that convergence will be stable if the true Jacobian at the solution is singular or near-singular. In other words, the so-called 'bad' variant of Broyden's method directly updates an approximation of the inverse Jacobian and does not require matrix inversion.

4.1.2. Endemic equilibrium with a non-singular Jacobian

At the endemic equilibrium, where the disease remains in the population, the Jacobian matrix has a different form. The top-left entry is equal to the negative product of the transmission rate and the difference between the total population and the ratio of the recovery rate to the transmission rate; the top-right entry is simply the negative of the recovery rate; the bottom-left entry is equal to the recovery rate; and the bottom-right entry is equal to the product of the transmission rate and the difference between the total population and the ratio of the recovery rate to the transmission rate.

The trace of this matrix, namely the sum of its two diagonal entries, is negative because it equals the negative product of the transmission rate and a positive quantity. The determinant is the product

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of the diagonal elements minus the product of the off-diagonal elements; it is positive because it equals the product of the recovery rate and the transmission rate, and that quantity is also positive. Since the trace is negative and the determinant is positive, both eigenvalues must have negative real parts. Depending on the particular values of the parameters, these eigenvalues may be real and negative, or they may form a complex conjugate pair with negative real parts. In either case, the equilibrium is locally asymptotically stable; that is, trajectories in the neighbourhood of the equilibrium will approach the equilibrium as time goes on.

It should be noted that nonsingularity at the endemic equilibrium holds only when the determinant is non-zero; good conditioning, that is, a moderate condition number, must be verified for the chosen parameter values and cannot be inferred solely from local stability properties.

The system is locally asymptotically stable; that is, trajectories in the neighbourhood of the equilibrium approach it along the directions of eigenvalues with negative real parts. A non-singular Jacobian at the equilibrium satisfies the local convergence conditions for Newton's method. However, for stable convergence in practice, a relatively close initial guess and some smoothness of the nonlinear equations defining the system are still required.

4.2. Non-symmetric and ill-conditioned Jacobian at the Lotka-Volterra coexistence equilibrium

Lotka-Volterra systems are a pair of coupled differential equations describing prey growth, predator decline in the absence of prey, and their mutual interaction through predation [5]. At the coexistence equilibrium, where both the prey and predator populations are positive, the Jacobian matrix takes the form shown below: both diagonal elements are zero; the upper-right element is a negative number whose absolute value is determined by the interaction and growth parameters; and the lower-left element is a positive number determined by the remaining parameters. Thus, the matrix is not symmetric; that is, the two off-diagonal elements have opposite signs and are generally not equal.

The eigenvalues of this matrix are a pair of purely imaginary conjugates; therefore, in the linearised sense, the equilibrium is a centre with closed orbits. It should be pointed out that this matrix is always non-singular, as the product of the two off-diagonal magnitudes is strictly positive. However, the condition number of this matrix in the Euclidean norm is equal to the ratio of the larger off-diagonal magnitude to the smaller one. When the two magnitudes are significantly different, the matrix is highly ill-conditioned.

The purely imaginary spectrum indicates oscillatory local behaviour of the Lotka-Volterra system, but it does not determine whether Newton's method will converge to a root of the underlying root-finding problem. Newton's local convergence behaviour in this case should be evaluated by considering several factors instead: the non-singularity of the Jacobian, the degree of conditioning, the smoothness of the governing equations, and how close the initial guess is to the true solution.

Since the Jacobian is not symmetric, the standard conjugate gradient method cannot be used for the linear sub-problems in the iteration. Nonsymmetric Krylov solvers, such as GMRES and BiCGSTAB, are more suitable for these linear solves. Broyden's method can reduce the number of repeated exact Jacobian evaluations, and its suitability does not depend solely on whether the Jacobian is symmetric. Preconditioning can also address the problem of poor conditioning caused by highly unbalanced off-diagonal magnitudes.

4.3. Well-conditioned but state-dependent Jacobian in the blood ethanol model

The form of the model for blood alcohol concentration is Michaelis-Menten [6].

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The scalar derivative is negative in the neighbourhood of the equilibrium for all relevant states, so the equilibrium is locally asymptotically stable. Unlike the singular Jacobian at the disease-free equilibrium of the SIR model and the ill-conditioned spectrum at the Lotka-Volterra coexistence equilibrium, the blood ethanol model has a non-singular, well-conditioned Jacobian matrix under typical physiological parameter settings. The main structural constraint is a strong state-dependent Jacobian behaviour at low concentrations, and nonlinear effects are prominent there. Derivative computation has a low computational cost for this scalar ethanol model, so state dependence alone will not impose a heavy overhead on Newton's method. Jacobian-free methods are more feasible for large-scale variations of coupled models where the construction or acquisition of derivative information is computationally expensive.

Michaelis-Menten kinetics also frequently have rational nonlinearities that complicate the derivation of analytical derivatives in extended multi-compartment systems. Therefore, the variational iteration method can be used as an alternative. This method constructs a correction functional without explicit Jacobian computation or linearisation of nonlinear terms. Its Jacobian-free formulation can be used when the derivative formula is unavailable or when evaluating the Jacobian is computationally expensive in extended models. The cited study reports accurate approximate solutions for the blood ethanol concentration system using VIM [6]. Therefore, it can be regarded as an alternative iterative method that avoids direct Jacobian evaluation.

4.4. Symmetric positive-definite sparse Jacobian in steady-state heat conduction

As a contrast case, the steady-state linear heat conduction problem is an example of the type of linear system that arises after discretisation of a partial differential equation or within the iterative steps of Newton-type methods for nonlinear problems; however, this example itself is not a nonlinear root-finding problem. Discretisation of the heat equation over a one-dimensional domain with a uniform grid results in a system of linear equations that connects the unknown temperatures at the grid points to the known heat sources. The coefficient matrix of this system has a very special structure: it is tridiagonal, and thus only the diagonal elements and the elements immediately adjacent to the diagonal (one above and one below) are non-zero. In the simplest case of Dirichlet boundary conditions, all the diagonal entries are equal to a positive constant, and all the off-diagonal entries in the two adjacent diagonals are equal to a negative constant. All other entries are 0.

The Jacobian matrix of this linear problem is exactly that tridiagonal coefficient matrix. This matrix has several favourable structural properties. First, it is symmetric; that is, the entry at row i and column j is always the same as the entry at row j and column i. Second, it is positive definite; that is, all of its eigenvalues are positive real numbers. Third, for the standard one-dimensional Dirichlet discretisation, the matrix is diagonally dominant, and the interior rows have equality rather than strict dominance. Fourth, it is very sparse; regardless of how many grid points there are, only three diagonals are non-zero.

The condition number of this matrix is determined by the grid spacing, and it increases as the grid is refined; for a very fine mesh, it may be too large, so good conditioning cannot be assumed. These structural properties are favourable for efficient solvers. For example, the structure can be used to implement the successive over-relaxation (SOR) method, and by selecting a suitable relaxation parameter, fast convergence can be achieved. Alternatively, the Thomas algorithm, a direct solver for tridiagonal systems, can be used to solve the entire system, and the amount of work is directly proportional to the number of unknowns; this is the best possible order of efficiency for such problems.

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The symmetric positive-definite, sparse structure of this Jacobian is in contrast to the singular Jacobian of the SIR disease-free equilibrium and the purely imaginary eigenvalues of the Lotka-Volterra coexistence equilibrium. As shown above, the good structure of the problem leads to an easy-to-obtain, stable and efficient numerical solution.

5. Limitations and prospects

Although many iterative methods for nonlinear systems are available, none are suitable for all cases. The suitability and limitations of the above methods are inherently related to the algebraic structure of the Jacobian matrix, such as its symmetry, sparsity, condition number and spectral distribution. This section combines the structural constraints from the four case studies and proposes future research directions.

5.1. Limitations of Newton-type methods

Newton's method has three main limitations relevant to the present discussion. First, local convergence requires that the initial guess be close to the true solution. Purely imaginary eigenvalues of the dynamical-system Jacobian describe neutral linear stability, but they do not by themselves determine Newton root-finding convergence, which depends instead on Jacobian nonsingularity, smoothness, conditioning, and the initial guess. Therefore, they do not refer to rotating Newton corrections or oscillatory Newton failure. Second, Newton's method is very sensitive to singular or ill-conditioned Jacobians. When the Jacobian at an iterate is singular, the standard Newton correction cannot be uniquely determined. Near a singular root, such as the SIR disease-free equilibrium, the typical local quadratic convergence guarantee is lost. Even if the Jacobian is non-singular, a large condition number will increase numerical errors and reduce the observed convergence or cause a numerical failure. A typical case of the Lotka-Volterra coexistence equilibrium is that when the off-diagonal magnitudes are highly unbalanced, severe ill-conditioning occurs. Preconditioning techniques, such as those for nonlinear least-squares problems, can help reduce the impact of such ill-conditioning in iterative solvers [7]. Third, the computational cost will be relatively high if Jacobian evaluation or factorisation is expensive for large coupled systems. The scalar blood ethanol example itself has a low derivative cost, but multi-compartment extensions may require more expensive Jacobian evaluations. For large-scale sparse systems that arise from the discretisation of partial differential equations, such as the heat conduction model, a dense Jacobian would require memory that grows quadratically with the number of unknowns; sparse storage can reduce this significantly. Dense direct factorisation has a general cubic complexity, and sparse direct or iterative methods can exploit the matrix structure. Jacobian handling can therefore become a major cost as problem size grows.

5.2. Limitations of other iterative methods

For large-scale sparse systems, stationary splitting methods such as Jacobi, Gauss-Seidel and SOR can exploit sparse matrix structure and have low per-step costs. However, without strict diagonal dominance or favourable spectral conditions, convergence is not guaranteed, and for general nonlinear problems, it may be very slow. Broyden's quasi-Newton method avoids repeated Jacobian evaluations by using rank-one updates, but it loses Newton's quadratic convergence and may perform poorly in highly nonlinear problems. Variational Iteration does not need to compute the Jacobian or linearise the problem, so it is suitable for problems where derivatives are unavailable or

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costly to obtain. However, it does not generally inherit Newton-type local quadratic convergence, and its convergence properties depend strongly on the formulation and problem.

5.3. Future directions

Three paths are worth exploring. First, hybrid strategies that combine methods sequentially, use Broyden or SOR to approach the solution neighbourhood at a low cost, and then switch to Newton for high-precision refinement, can reduce the sensitivity to the initial guess. Second, Jacobian-free Newton-Krylov methods that use automatic differentiation to obtain derivative or Jacobian-vector information can achieve a good balance of accuracy and efficiency; otherwise, derivative-free methods, such as VIM, can be employed if Jacobian construction is unreliable or not feasible. Third, sparse storage and parallel computing techniques, such as compressed sparse row format, can reduce memory substantially when the number of nonzero entries grows slowly with problem size, and graphics processing unit (GPU)-accelerated iterative solvers can make Newton-type methods feasible for large-scale problems. Recently, advances in Jacobian sparsity detection using Bloom filters have shown that algorithmic innovations can reduce the preparation cost of large-scale problems for sparse solvers [8]. The common aim of the above directions is to build structure-adaptive solvers that can select suitable strategies dynamically according to the symmetry, conditioning and spectral properties of the Jacobian at hand, thereby moving from method-centric convenience to structure-driven rationality. Algorithmic innovations, such as high-order iterative and multi-step schemes, have been continuously added to the solver toolbox for difficult nonlinear problems [9, 10].

6. Conclusion

This paper systematically studies iterative numerical methods for solving nonlinear equation systems, focuses on the effect of the algebraic structure of the Jacobian matrix on the convergence performance of Newton's method, and proposes structural diagnostic rules to guide the selection of iterative algorithms. It presents the basic theories of nonlinear systems and Jacobian analysis, reviews representative iterative methods such as Newton iteration, SOR and the variational iteration method (VIM), and summarises research results from four interdisciplinary models: the Lotka-Volterra predator-prey system, SIR epidemic model, blood ethanol concentration model and one-dimensional steady-state heat conduction equation. Based on the above comparison results, Jacobian symmetry, sparsity, conditioning and spectral properties affect the applicability and numerical stability of solvers, but they do not determine the convergence rate of Newton-type root-finding methods.

Newton-type methods have wide applications but only guarantee local convergence and are highly sensitive to the initial value; when the Jacobian is singular or severely ill-conditioned, the Newton correction may be undefined or numerically unstable, and a high-dimensional problem can also be computationally expensive. In addition, the test cases and stopping criteria in the previous studies are not the same.

Future research will focus on adaptive hybrid iterative strategies, derivative-free algorithms and sparse parallel computing for large-scale nonlinear problems. Based on the above reviewed cases, solver selection should consider the Jacobian structure in conjunction with the initial guess, problem size, stopping criteria and the cost of derivative evaluation. Jacobian symmetry, conditioning, sparsity and spectral information can guide the selection of linear algebra routines, but they do not

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determine the convergence rate of nonlinear root-finding methods by themselves. More controlled comparisons are needed before general solver-selection rules can be developed.

References

[1] Narayanan, G. V., Pushpalakshmi, G., Desai, C. H., Patel, A. D., & Patel, T. A. (2025). A comparative study of numerical methods for solving nonlinear equations. *International Journal of Applied Mathematics, 38*(5s), 898-912. https://doi.org/10.12732/ijam.v38i5s.358

[2] Broyden, C. G. (1965). A class of methods for solving nonlinear simultaneous equations. *Mathematics of Computation, 19*(92), 577-593. https://doi.org/10.1090/S0025-5718-1965-0198670-6

[3] He, J. H. (1999). Variational iteration method: A kind of non-linear analytical technique: Some examples. *International Journal of Non-Linear Mechanics, 34*(4), 699-708. https://doi.org/10.1016/S0020-7462(98)00048-1

[4] Wazwaz, A. M. (2017). Dual solutions for nonlinear boundary value problems by the variational iteration method. *International Journal of Numerical Methods for Heat & Fluid Flow, 27*(1), 210-220. https://doi.org/10.1108/HFF-10-2015-0442

[5] Saidat, S., Al-Shorman, Y., Hashim, I., Solaiman, O. S., Al-Hammouri, A., Almousa, M., & Alsoboh, A. (2025). A computational guide to stability analysis of nonlinear systems: The Lotka-Volterra and SIR models as case studies. *European Journal of Pure and Applied Mathematics, 18*(4), Article 7020. https://doi.org/10.29020/nybg.ejpam.v18i4.7020

[6] Adel, M., Khader, M. M., Ahmad, H., & Assiri, T. A. (2023). Approximate analytical solutions for the blood ethanol concentration system and predator-prey equations by using variational iteration method. *AIMS Mathematics, 8*(8), 19083–19096. https://doi.org/10.3934/math.2023974

[7] Xie, S., Qu, G., & Feng, L. (2025). Preconditioned Landweber iteration for nonlinear least-squares conical surface fitting. *Electronic Research Archive, 33*(11), 6558–6576. https://doi.org/10.3934/era.2025290

[8] Hovland, P. D. (2026). Jacobian sparsity detection using Bloom filters. *Optimization Methods and Software, 41*(2), 295–307. https://doi.org/10.1080/10556788.2023.2285486

[9] Erfanifar, R., & Hajarian, M. (2026). An efficient high-order iterative method to solve systems of nonlinear equations with applications to differential equations and image processing. *Journal of the Franklin Institute, 363*(2), Article 108332. https://doi.org/10.1016/j.jfranklin.2025.108332

[10] Behl, R., Argyros, I. K., Alshehri, H., & Alotaibi, M. M. (2026). Development of high-order multistep iterative schemes for nonlinear equations with applications in applied sciences. *AIMS Mathematics, 11*(4), 11387–11409. https://doi.org/10.3934/math.2026469