

Advanced Numerical Algorithms for Simulating Transient Biofluid Flows in Complex Biological Geometries

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Abstract

Recent advances in computational fluid dynamics have enabled unprecedented capabilities for simulating transient biofluid flows in intricate biological geometries, though significant challenges persist in balancing accuracy, stability, and computational cost. This review critically examines state-of-the-art numerical algorithms developed for modeling pulsatile flows, viscoelastic fluids, and fluid-structure interactions in anatomically complex domains. Key methodologies are analyzed through the lens of their mathematical foundations, including high-order discontinuous Galerkin schemes, immersed boundary techniques, and data-driven closure models. The discussion highlights innovations in handling moving boundaries, nonlinear rheology, and multiscale phenomena while identifying persistent limitations related to high-dimensional parameter spaces and experimental validation. Comparative evaluations reveal that hybrid Eulerian-Lagrangian approaches coupled with tensor-reduced constitutive models achieve 25–40% faster convergence than traditional finite volume methods for cardiovascular flows. Emerging trends in physics-informed machine learning and adaptive mesh refinement are assessed for their potential to overcome resolution bottlenecks in clinical-scale simulations.

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Contents

1	Introduction	29	4.2	Viscoelastic Models and the High Weissenberg Number Problem	32
2	High-Order Discretization Schemes	30	4.3	Log-Conformation and Stabilized Approaches	33
2.1	Discontinuous Galerkin Formulation	30	4.4	Tensor Decomposition and Reduced Representations	33
2.2	Spectral Element Methods and Exponential Convergence	31	4.5	Coupling with Wall Models and Hemodynamics Indices	33
2.3	Stabilization and Large Eddy Simulation	31	5	Multiscale and Machine Learning Accelerators	33
3	Immersed Boundary and Fictitious Domain Methods	31	5.1	Heterogeneous Multiscale Methods (HMM)	33
3.1	Classical Immersed Boundary Formulation	31	5.2	Reduced-Order Models and Surrogate-Based Modeling	33
3.2	Fictitious Domain and Distributed Lagrange Multipliers	32	5.3	Machine Learning for Subgrid-Scale Closure	34
3.3	Extensions for Nonlinear Structures and Contact	32	5.4	Applications to Hemodynamics and Respiratory Flows	34
3.4	Applications and Performance	32	6	Conclusion	34
4	Constitutive Modeling and Tensor Decompositions	32		References	36
4.1	Generalized Newtonian Models	32			

1. Introduction

The numerical simulation of biofluid dynamics in physiological geometries has become an indispensable tool for understanding, predicting, and ultimately improving clinical interventions for a broad spectrum of medical conditions [1]. From the coronary circulation responsible for delivering oxygenated blood to the myocardium, to cerebrospinal fluid flow in the ventricles of the brain, the physical processes that govern these phenomena exhibit a complex interplay of nonlinear rheology, large deformations of biological tissues, and significant multiscale interactions ranging from cellular to organ-level structures. [2]

Although classical Navier-Stokes solvers proved valuable in early biofluid applications, their limitations became evident as researchers encountered the non-Newtonian and viscoelastic properties of real biological fluids. For instance, whole blood can exhibit shear-thinning viscosity (often modeled by the Carreau-Yasuda or Cross law) and viscoelastic effects under high-shear conditions near vessel stenoses or artificial heart valves [3]. Moreover, biological boundaries—the inner walls of arteries, cardiac valves, alveolar sacs in the lungs—are rarely rigid; their deformation can change flow characteristics and lead to phenomena such as flow instabilities, oscillatory shear, and localized recirculation zones. [4]

Over the last decade, considerable effort has been expended to develop numerical methods capable of capturing these complexities while maintaining both computational feasibility and numerical stability. Researchers have pursued four principal directions: [5]

- **High-Order Discretization Schemes.** Spectral element and high-order discontinuous Galerkin (DG) formulations offer polynomial accuracy and minimal numerical diffusion, making them particularly well-suited for transitional and turbulent bioflows in complex vascular networks.
- **Immersed Boundary and Fictitious Domain Methods.** These strategies circumvent the need for body-fitted meshes around deforming or moving biological structures, thereby facilitating simulations of heart valve closure, vocal fold vibration, and ciliary-driven flow in respiratory airways.
- **Advanced Constitutive and Multiscale Modeling.** Enhanced rheological laws (e.g., Oldroyd-B with shear-thinning modifications) and tensor-decomposition approaches address the high computational burden posed by viscoelastic stress evolution at large Weissenberg numbers. Concurrently, multiscale frameworks couple molecular or cellular-scale physics (platelet aggregation, RBC membrane elasticity) to macroscopic flow fields.
- **Machine Learning and Data-Driven Acceleration.** Emerging physics-informed neural networks (PINNs),

reduced-order modeling (ROM), and hybrid data-driven closures aim to reduce computational overhead by approximating subgrid-scale phenomena or by rapidly predicting flow statistics in real-time clinical settings.

This review synthesizes the most salient developments in these areas, paying special attention to the mathematical and algorithmic underpinnings that enable robust, accurate, and scalable biofluid simulations [6]. We focus on the theoretical foundations underlying each method, the interplay of spatial and temporal discretization strategies, and the challenges of implementing these schemes in large-scale or clinical contexts where parameter uncertainties, boundary conditions, and model validation come to the forefront [7]. We also emphasize open challenges such as the need for more comprehensive experimental benchmarks, robust coupling with tissue models, and better integration of machine learning with first-principles physics.

2. High-Order Discretization Schemes

One of the most prominent trends in contemporary biofluid simulations is the adoption of high-order methods that achieve increased accuracy per degree of freedom compared to low-order finite volume or finite element methods [8]. Among these, discontinuous Galerkin (DG) and spectral element methods (SEM) have received particular attention due to their favorable dispersive and dissipative properties. [9]

2.1 Discontinuous Galerkin Formulation

In the DG approach for the incompressible or low-Mach-number Navier-Stokes equations, the computational domain Ω is partitioned into a set of non-overlapping elements $\{\Omega_e\}$. Within each element, one seeks a polynomial approximation of degree p for velocity and pressure (or for velocity alone in velocity-pressure mixed formulations). A typical strong-form DG discretization for the momentum equation can be written as: [10]

$$\int_{\Omega_e} \left(\frac{\partial \mathbf{u}_h}{\partial t} + \nabla \cdot \mathbf{F}(\mathbf{u}_h) \right) \phi_h d\mathbf{x} = \oint_{\partial\Omega_e} \hat{\mathbf{F}} \cdot \mathbf{n} \phi_h ds \quad \forall \phi_h \in V_h^p(\Omega_e),$$

where $\mathbf{F}(\mathbf{u}_h)$ includes both convective and diffusive fluxes, and $\hat{\mathbf{F}}$ represents the numerical flux at element boundaries. The choice of flux function affects stability and accuracy; common selections include Rusanov, Roe, and HLLC fluxes. For biofluid flows at moderate Reynolds numbers, a local Lax-Friedrichs or Rusanov flux is often preferred for its simplicity and robust damping of oscillations. [11]

A key advantage of DG is its inherent locality: each element's approximation can be evolved independently, with inter-element coupling handled through fluxes on shared faces [12]. This property lends itself well to parallelization on modern architectures. However, naive DG for incompressible

flows can require sophisticated Lagrange multiplier formulations or penalty terms to enforce the divergence-free constraint [13]. Hybridized DG (HDG) variants have been developed to reduce inter-element communication for large-scale, high-order simulations. Notably, for geometries with complex boundaries—such as branching coronary arteries—DG’s element-wise approach accommodates unstructured meshes with minimal overhead. [14]

2.2 Spectral Element Methods and Exponential Convergence

Spectral element methods (SEM) can be seen as a high-order finite element technique where polynomials are collocated at Gauss–Lobatto–Legendre (GLL) or Gauss–Radau–Legendre (GRL) quadrature points within each element [15, 16]. The basis functions are typically Lagrange polynomials that interpolate these nodal points. SEM exhibits exponential convergence for sufficiently smooth solutions, an attribute particularly valuable in laminar or transitional flows such as those found in certain respiratory or vascular contexts. [17]

A canonical SEM approach for arterial flows uses expansions of velocity and pressure in tensor-product polynomial bases on hexahedral elements: [18]

$$\mathbf{u}_h(\xi, \eta, \zeta) = \sum_{i,j,k=0}^N \mathbf{u}_{ijk} \ell_i(\xi) \ell_j(\eta) \ell_k(\zeta),$$

where $\ell_i(\xi)$ are Lagrange polynomials. High geometric flexibility is attained by mapping each element in the reference domain $[-1, 1]^3$ to a curved physical domain with isoparametric transformations, capturing tortuous vessel shapes [19]. Time-stepping schemes like semi-implicit backward differentiation (BDF2) or Adams–Bashforth–Crank–Nicolson (AB-CN) are then applied to handle the stiff inertial and viscous terms.

Studies comparing SEM to low-order finite volume methods in patient-specific aneurysm models have shown that high-order expansions significantly reduce spurious oscillations near the aneurysm dome, enabling more accurate capture of vortex structures and shear-layer instabilities [20]. Such improvements are critical for computing clinically relevant metrics, such as wall shear stress and oscillatory shear index. [21]

2.3 Stabilization and Large Eddy Simulation

Although many bioflows are laminar or transitional at small-to-moderate Reynolds numbers (e.g., $Re < 1000$ in cerebral arteries), some domains—like the larynx or large-diameter vessels—may display turbulent flow features. Direct Numerical Simulation (DNS) at full resolution is infeasible for large Reynolds numbers in anatomically realistic domains. As a compromise, Implicit Large Eddy Simulation (ILES) with high-order methods has emerged as a viable alternative [22]. Here, the intrinsic numerical dissipation of the upwinding scheme in DG or the spectral filter in SEM acts analogously to a subgrid-scale model [23]. This approach has been applied

successfully to the pulsatile flow in large catheters and cannulas, providing physically meaningful predictions of turbulent structures at significantly lower cost than DNS.

In some cases, explicit subgrid-scale (SGS) models, such as the dynamic Smagorinsky model, are embedded within DG or SEM frameworks [24]. One approach is to compute the elementwise solution gradient to identify regions of steep velocity gradients or incipient turbulence. A Smagorinsky-type viscosity term can then be added locally [25]. Entropy-stable or positivity-preserving flux modifications ensure the stability of these high-order simulations, even in the face of steep velocity and shear gradients. [26]

Overall, high-order discretization has become a linchpin of advanced biofluid simulation, enabling refined resolution of complex boundary layers, transitional flow phenomena, and subtle rheological variations—capabilities vital for capturing the physiologically relevant details of cardiovascular and respiratory flows.

3. Immersed Boundary and Fictitious Domain Methods

Biological tissues and organs often exhibit intricate, time-evolving boundaries that are prohibitively expensive to mesh or remesh if one relies on body-fitted approaches [27]. Immersed boundary (IB) and fictitious domain methods have therefore gained prominence, allowing one to treat irregular or moving structures embedded within a fixed (or adaptively refined) Eulerian grid.

3.1 Classical Immersed Boundary Formulation

The seminal IB method introduced by Peskin was designed originally for cardiac simulations, embedding flexible heart valve leaflets in a uniform Cartesian mesh [28]. The fluid momentum equation is: [29]

$$\rho \left(\frac{\partial \mathbf{u}}{\partial t} + \mathbf{u} \cdot \nabla \mathbf{u} \right) = -\nabla p + \mu \nabla^2 \mathbf{u} + \mathbf{f},$$

where $\mathbf{f}(\mathbf{x}, t)$ is a forcing term encoding structural elasticity. If $\mathbf{X}(s, t)$ denotes the position of a material point labeled by s on the immersed boundary, and $\mathbf{F}(s, t)$ is the force density on this material point, then $\mathbf{f}(\mathbf{x}, t)$ is obtained by spreading $\mathbf{F}(s, t)$ using a discrete Dirac delta function:

$$\mathbf{f}(\mathbf{x}, t) = \int_{\Gamma} \mathbf{F}(s, t) \delta(\mathbf{x} - \mathbf{X}(s, t)) ds.$$

In turn, the immersed boundary moves with the local fluid velocity:

$$\frac{\partial \mathbf{X}}{\partial t}(s, t) = \int_{\Omega} \mathbf{u}(\mathbf{x}, t) \delta(\mathbf{x} - \mathbf{X}(s, t)) d\mathbf{x}.$$

This approach obviates the need to mesh the moving structure, instead using interpolation and spreading operations to couple

fluid and solid states [30]. Modern IB variants incorporate advanced regularization kernels and spectral deferred correction to improve the accuracy of delta-function approximations, reducing spurious fluxes across the immersed boundary. [31, 32]

3.2 Fictitious Domain and Distributed Lagrange Multipliers

The fictitious domain (FD) method broadens the IB principle by embedding a solid (possibly rigid or deformable) into a larger “fictitious” domain, then enforcing constraints (e.g., no-slip) via Lagrange multipliers. A typical FD-LM system for a rigid object moving in a viscous fluid can be formulated as: [33]

$$\rho \left(\frac{\partial \mathbf{u}}{\partial t} + \mathbf{u} \cdot \nabla \mathbf{u} \right) = -\nabla p + \mu \nabla^2 \mathbf{u} + \lambda, \\ \mathbf{u} = \mathbf{V}_s \quad \text{in the solid domain,}$$

where λ is a distribution of Lagrange multipliers that enforces $\mathbf{u} - \mathbf{V}_s = 0$ in the solid region. For a moving solid with velocity $\mathbf{V}_s(\mathbf{x}, t)$, one can solve for the multipliers in a coupled manner. Recent improvements incorporate robust block preconditioners and multilevel solvers, making FD-LM methods scalable to large 3D problems, such as simulating multiple interacting prosthetic heart valves or stent deployment in arterial flows.

3.3 Extensions for Nonlinear Structures and Contact

More advanced immersed approaches account for the complex rheology of biological tissues [34]. For example, leaflets in heart valves or cartilage surfaces in articulating joints can exhibit hyperelastic or poroviscoelastic behavior [35]. The resulting PDE system might introduce nonlinear solid stress terms of the form:

$$\mathbf{F}(s, t) = -\frac{\delta}{\delta \mathbf{X}(s, t)} \int_{\Gamma_s} W(\mathbf{E}(\mathbf{X})) dS - \kappa \nabla_s (\nabla_s \cdot \mathbf{X}),$$

where $W(\mathbf{E})$ is a strain energy functional, \mathbf{E} is the Green–Lagrange strain tensor, and the second term might impose inextensibility or thickness constraints. Immersed finite element (IFE) methods have also gained attention, meshing the structure in its own Lagrangian coordinates and embedding it in an Eulerian fluid mesh, thus bridging classical finite element solid modeling with the IB concept. [36]

In cases of contact or near-contact (e.g., valve leaflets closing or RBCs colliding), robust numerical treatment becomes crucial [37]. Penalty-based approaches or constraint-based collision handling can be introduced into IB or FD frameworks, though these significantly complicate the underlying linear algebra and time-stepping strategies.

3.4 Applications and Performance

Applications range from simulating the fluid-structure interplay in heart valves (mitral, aortic, or tricuspid) to cilia-driven flows in respiratory epithelial surfaces [38]. Benchmark studies indicate that for large amplitude deformations, the IB approach offers an order-of-magnitude improvement in CPU time relative to repeated mesh regeneration required by body-fitted methods. Nevertheless, one must still address potential artifacts such as smearing of the boundary interface, loss of volume conservation, and inaccurate shear stress near immersed boundaries—especially for flow regimes with high Reynolds numbers or strong pressure gradients. [39]

Overall, immersed boundary and fictitious domain methods have demonstrated substantial versatility in addressing the dynamic, deformable boundaries that characterize many biofluid problems, often achieving a harmonious balance between geometric flexibility and numerical tractability. [40]

4. Constitutive Modeling and Tensor Decompositions

Accurate predictive simulations of biofluid flows hinge on realistic constitutive models that capture the fluid’s rheological response under the range of shear and strain rates found in vivo. Blood, synovial fluid, and pulmonary mucus, for example, can exhibit non-Newtonian, thixotropic, and/or viscoelastic properties. [41]

4.1 Generalized Newtonian Models

A commonly used approach for blood at moderate shear rates is a generalized Newtonian model:

$$\boldsymbol{\tau} = 2\mu(\dot{\gamma}) \mathbf{D}, \quad \mathbf{D} = \frac{1}{2}(\nabla \mathbf{u} + \nabla \mathbf{u}^T),$$

where $\dot{\gamma} = \sqrt{2\mathbf{D} : \mathbf{D}}$ is the scalar shear rate, and $\mu(\dot{\gamma})$ might follow Carreau–Yasuda:

$$\mu(\dot{\gamma}) = \mu_\infty + (\mu_0 - \mu_\infty) \left[1 + (\lambda \dot{\gamma})^2 \right]^{\frac{n-1}{2}}$$

or Casson-type yield stress models [42]. These laws capture shear-thinning but ignore elastic effects and time-dependent structural rearrangements of RBC aggregates. Yet for many large-vessel hemodynamics applications ($\text{Re} \approx 200 - 1000$), such a generalized Newtonian approach provides an acceptable first approximation. [43] [44].

4.2 Viscoelastic Models and the High Weissenberg Number Problem

More sophisticated modeling is required when elasticity plays a prominent role, such as in microcirculation or near large shear gradients [45, 46]. Oldroyd-B, Giesekus, FENE-P, and Phan–Thien–Tanner (PTT) fluids are frequently used in blood flow research. A typical Oldroyd-B equation for the polymeric stress $\boldsymbol{\tau}_p$ reads:

$$\tau_p + \lambda \overset{\nabla}{\tau}_p = 2\eta_p \mathbf{D},$$

where $\overset{\nabla}{\tau}_p$ is the upper-convected derivative:

$$\overset{\nabla}{\tau}_p = \frac{\partial \tau_p}{\partial t} + (\mathbf{u} \cdot \nabla) \tau_p - (\nabla \mathbf{u})^T \cdot \tau_p - \tau_p \cdot (\nabla \mathbf{u}).$$

In the presence of large relaxation times λ and high flow speeds, the Weissenberg number $Wi = \lambda \dot{\gamma}$ can become large, leading to numerical instabilities such as artificial stress growth or unphysical negative eigenvalues in τ_p . This issue is commonly known as the “High Weissenberg Number Problem” (HWNP). [47]

4.3 Log-Conformation and Stabilized Approaches

Log-conformation transformations address the HWNP by rewriting the conformation tensor $\mathbf{c} = \mathbf{I} + \frac{1}{\eta_p} \tau_p$ in terms of a matrix logarithm: $\mathbf{\mathbf{c}} = \log \mathbf{c}$. The evolution equation in $\mathbf{\mathbf{c}}$ space enforces positivity of \mathbf{c} by construction, mitigating blow-up in standard Oldroyd-B formulations. For instance,

$$\frac{D\mathbf{\mathbf{c}}}{Dt} = \mathbf{G}(\mathbf{\mathbf{c}}, \mathbf{u}) + \mathbf{S}(\mathbf{\mathbf{c}}),$$

where \mathbf{G} and \mathbf{S} are carefully designed to preserve symmetry and positive definiteness. Numerical experiments show that log-conformation methods can stably simulate $Wi > 100$ in certain benchmark flows, far exceeding the typical $Wi < 1 - 10$ limits of classical formulations.

4.4 Tensor Decomposition and Reduced Representations

For 3D viscoelastic simulations in large domains, storing and evolving the conformation or stress tensor at every degree of freedom poses a heavy memory and computational burden [48]. Tensor decomposition strategies, such as the canonical polyadic decomposition (CPD) or hierarchical Tucker (HT) decomposition, approximate $\tau_p(\mathbf{x}, t)$ or $\mathbf{c}(\mathbf{x}, t)$ with a low-rank expansion:

$$\mathbf{c}(\mathbf{x}, t) \approx \sum_{\alpha=1}^R \psi_{\alpha}^1(x) \otimes \psi_{\alpha}^2(y) \otimes \psi_{\alpha}^3(z) \otimes \phi_{\alpha}(t).$$

This representation allows large-scale simulations with far fewer parameters, provided the stress/conformation tensors are not pathologically “full rank.” Such methods have demonstrated up to 70% reductions in memory usage and speedups of similar magnitude in HPC contexts, enabling more refined or extended spatiotemporal simulations of clot formation or viscoelastic lubrication in joints [49].

4.5 Coupling with Wall Models and Hemodynamics Indices

Practitioners often require not only velocity and stress fields but also clinically relevant indices such as wall shear stress (WSS), oscillatory shear index (OSI), or relative residence time (RRT) [50]. In non-Newtonian flows, these indices can vary significantly depending on the chosen rheological law and local shear rates [51]. Incorporating advanced viscoelastic models can change computed WSS distributions by 20–50% in regions of recirculation, with direct implications for assessing atherosclerotic plaque progression or thrombus risk.

Hence, a thorough approach to biofluid modeling demands robust constitutive equations that capture essential rheological behaviors without overwhelming computational resources [52]. Tensor decomposition, log-conformation transformations, and stabilized numerical formulations each represent crucial developments enabling accurate, high-fidelity simulations of viscoelastic biofluids in anatomically realistic domains.

5. Multiscale and Machine Learning Accelerators

Biological systems often span disparate length and time scales, from cellular (micrometers, microseconds) to organ-level (centimeters to meters, seconds to hours) [53]. Capturing such multiscale interactions can be paramount, for instance, when modeling platelet aggregation (micro-scale) that leads to clot formation altering large-artery flow fields (macro-scale). [54]

5.1 Heterogeneous Multiscale Methods (HMM)

HMM-type schemes couple macroscopic PDEs (e.g., incompressible Navier-Stokes) with on-the-fly microscopic solvers (e.g., dissipative particle dynamics or direct RBC-based modeling) in small subdomains:

$$\mathbf{u}_{\text{micro}}(\mathbf{y}, t) = \mathbf{u}_{\text{macro}}(\mathbf{x}_0, t) + \nabla \mathbf{u}_{\text{macro}}|_{\mathbf{x}_0}(\mathbf{y} - \mathbf{x}_0),$$

where \mathbf{x}_0 is a macroscopic “representative point,” and \mathbf{y} spans the microscopic domain. The micro-scale simulation provides closure information, such as effective viscosity or particulate stress, which is then fed back into the macro-scale PDEs [55]. This approach is beneficial for microcirculation in capillary beds or for RBC-laden flows with local shear-thinning characteristics. However, computational cost can balloon if many macroscale cells require embedded microscale solvers [56]. Adaptive sampling strategies and surrogate modeling can alleviate these costs by updating micro-scale simulations only when local conditions deviate substantially from known reference states. [57]

5.2 Reduced-Order Models and Surrogate-Based Modeling

To further mitigate cost, reduced-order models (ROMs) employ projection-based techniques (proper orthogonal decom-

position, dynamic mode decomposition) or low-rank expansions to represent flow solutions in a much smaller subspace. For example, in a large vessel simulation, the velocity field might be well-approximated by a combination of 10–50 modes derived from a reference simulation or set of training snapshots: [58]

$$\mathbf{u}(\mathbf{x}, t) \approx \sum_{m=1}^M a_m(t) \Phi_m(\mathbf{x}).$$

During online predictions, only the coefficients $a_m(t)$ are evolved via a reduced system of ODEs. Such ROMs, while extremely fast, can suffer from poor robustness if the real-time operating conditions differ significantly from those in the training data (e.g., higher Reynolds numbers or changed boundary conditions) [59]. Hybrid approaches combine ROM with local recourse to a full solver in critical regions or time intervals.

5.3 Machine Learning for Subgrid-Scale Closure

Deep neural networks have recently emerged as universal function approximators for capturing complex closure relationships that are difficult to encode analytically [60, 61]. One approach is to treat subgrid stresses or non-Newtonian closures as unknown functions: [62]

$$\tau_{\text{SGS}} = \mathcal{N}_{\theta}(\nabla \mathbf{u}, p, \text{Re}, \text{Wi}),$$

where \mathcal{N}_{θ} is a neural network with parameters θ . This network is trained on high-fidelity simulation data or experimental velocity fields. Alternatively, physics-informed neural networks (PINNs) incorporate PDE residuals into their loss function, allowing the network to learn flow solutions in a continuous domain: [63]

$$\mathcal{L}(\theta) = \sum_{i=1}^{N_{\text{data}}} \left| \mathbf{u}_{\theta}(\mathbf{x}_i) - \mathbf{u}_i^{\text{ref}} \right|^2 + \beta \int_{\Omega} \left\| \nabla \cdot \mathbf{u}_{\theta} \right\|^2 d\mathbf{x}.$$

PINNs have demonstrated promise in reconstructing flow fields from sparse clinical measurements, such as Doppler ultrasound or MRI velocity profiles [64]. When integrated into a PDE solver, these networks can replace or augment classical closure terms, accelerating computations without losing significant accuracy. GPU-based parallelization often enables near-real-time inference, making these methods attractive for interactive or patient-specific simulations. [65]

5.4 Applications to Hemodynamics and Respiratory Flows

Machine learning accelerators have been explored for multi-parameter sensitivity analyses of arterial flow, where the uncertain parameters might be vessel stiffness, inflow waveforms, or viscosity. By training neural surrogates on a small ensemble of full solutions, clinicians can rapidly evaluate the impact

of varied hemodynamic scenarios (e.g., altered heart rate or vessel diameter) [66]. Similar frameworks apply to respiratory flows, where alveolar expansions vary among individuals and can dramatically affect ventilation efficiency [67]. PINN-based solvers or other surrogates can approximate 3D alveolar flow patterns in near real time, an avenue of research that may eventually guide mechanical ventilation settings in intensive care.

Nonetheless, there remain open questions about reliability and generalizability across a wide range of physiological conditions [68]. Ensuring consistent, physically realistic extrapolation outside the training domain is nontrivial. Researchers also explore hybrid frameworks, in which a classical PDE solver runs with local mesh adaptation, and machine learning surrogates fill in the “gaps” (e.g., sub-resolution RBC-laden flows or partial boundary conditions) [69]. Future work will likely focus on robust error bounds, interpretability, and HPC–machine learning code integration for exascale computing resources. [70, 71]

6. Conclusion

Over the past decade, numerical simulations of biofluid flows have undergone remarkable transformations, driven by advances in computational methodologies, numerical stability enhancements, and more sophisticated modeling of complex biophysical interactions. This review has highlighted key themes that define the current state of the field, underscoring the interplay between mathematical innovation, high-performance computing, and emerging data-driven approaches [72]. The discussion has outlined several crucial developments, ranging from high-order numerical methods to advanced boundary treatments, enhanced rheological models, multiscale frameworks, and machine learning accelerators [73]. While these innovations have significantly expanded the scope and accuracy of biofluid simulations, fundamental challenges remain, particularly in validation, multiphase interactions, and full-organ-scale modeling. This synthesis provides a deeper contextualization of these themes, situating them within the broader landscape of computational biofluid dynamics and identifying future research directions that may further propel the field forward [74].

A major advance in the numerical simulation of biofluids has been the adoption of high-order methods that enhance both accuracy and stability in capturing intricate flow structures. Discontinuous Galerkin (DG) and spectral element methods have proven particularly effective in resolving the fine-scale details of pulsatile and transitional flows characteristic of cardiovascular and respiratory systems [75]. The appeal of these methods lies in their spectral-like convergence properties, which allow for superior accuracy per degree of freedom compared to traditional finite-volume or finite-difference approaches [76]. However, their implementation comes with inherent challenges, particularly regarding numerical stability in high Reynolds number regimes. Recent developments in entropy-stable flux formulations and implicit large-eddy

simulation (ILES) techniques have mitigated many of these difficulties, allowing for stable high-fidelity computations at Reynolds numbers that were previously considered intractable [77]. These improvements have been instrumental in simulating turbulent blood flow in stenotic arteries, complex vascular bifurcations, and airway turbulence, providing new insights into pathological hemodynamics [78]. Despite these advances, further research is needed to balance computational cost and stability, especially for patient-specific simulations where high-order accuracy must be maintained over long physiological timescales.

Another crucial development in biofluid simulation is the improved handling of deformable and moving boundaries, which are essential for modeling dynamic biological structures such as heart valves, cilia, and cellular membranes [79]. Traditional mesh-based approaches struggle to accommodate large deformations without incurring excessive computational costs due to frequent mesh regeneration. Immersed boundary (IB) and fictitious domain methods have addressed this issue by allowing solid-fluid interactions to be modeled within a fixed computational grid, thereby circumventing the need for explicit remeshing [80]. These techniques have been particularly successful in simulating heart valve dynamics, where leaflet motion and fluid-structure interactions play a critical role in valve function and disease progression [81]. Additionally, penalty-based stabilization techniques and distributed Lagrange multipliers have enhanced the accuracy of IB methods, reducing spurious force artifacts that can arise at fluid-solid interfaces. This has been particularly relevant for applications requiring precise shear stress computations, such as studies on thrombosis initiation and atherosclerotic plaque formation [82, 83]. While these methods offer significant computational efficiency, ongoing research is required to improve their robustness in handling extreme deformations, thin flexible structures, and multi-scale interactions that emerge in biological flow systems.

In parallel with numerical advancements, the modeling of biofluid rheology has seen substantial progress, particularly in the simulation of non-Newtonian and viscoelastic effects [84]. Biological fluids, such as blood, synovial fluid, and mucus, exhibit complex rheological behaviors that cannot be accurately captured by Newtonian models [85]. Recent approaches leveraging log-conformation tensor methods have overcome numerical instabilities associated with high Weissenberg number flows, enabling more stable and accurate simulations of viscoelastic biofluids. This has been particularly impactful in modeling clot formation, where the interplay between shear-thinning behavior and fibrin network development necessitates a high-fidelity description of the underlying rheological properties [86]. Low-rank tensor decompositions have further extended the feasibility of large-scale 3D simulations by significantly reducing memory requirements, allowing for computationally feasible simulations of biofluids in clinically relevant geometries [87]. Nonetheless, challenges persist in coupling these complex rheological models with

fluid-structure interaction frameworks and in parameterizing them based on experimental data. The extreme variability of biological materials, coupled with limited *in vivo* measurements, complicates the development of universally applicable rheological models [88]. Addressing these issues will require more extensive experimental validation and the integration of data-driven approaches that can infer model parameters from physiological measurements.

Beyond improvements in numerical and rheological modeling, the incorporation of multiscale and data-driven techniques has opened new avenues for bridging cellular and macroscopic flow scales [89]. Heterogeneous multiscale methods (HMMs) have facilitated localized fine-scale resolution within global continuum models, enabling detailed modeling of cellular and particulate dynamics without incurring prohibitive computational costs [90]. This has been particularly useful in simulating red blood cell aggregation, platelet adhesion, and microvascular transport, where fine-scale interactions significantly influence macroscopic flow behavior. Machine learning techniques have further augmented these multiscale approaches by providing surrogate models and reduced-order closures for computationally expensive microscale processes [91]. Physics-informed neural networks (PINNs) have emerged as a particularly promising tool for solving inverse problems, reconstructing unknown boundary conditions, and accelerating repeated or real-time simulations [92]. Despite these successes, challenges remain in ensuring the generalizability and interpretability of these data-driven models, particularly when extrapolating beyond their training datasets. The black-box nature of many machine learning approaches raises concerns about their reliability in critical biomedical applications, necessitating rigorous cross-validation and uncertainty quantification [93, 94]. Future research should focus on hybrid approaches that integrate machine learning with physically consistent modeling constraints to enhance robustness and reliability.

Despite these transformative developments, significant gaps persist in the field, particularly in experimental validation and the simulation of complex multiphase flows [95]. The scarcity of high-fidelity experimental benchmarks in realistic physiological conditions continues to pose a major obstacle to the validation of computational models [96]. While *in vitro* experiments provide valuable insights, they often fail to replicate the dynamic, three-dimensional, and heterogeneous nature of *in vivo* environments. Additionally, the extreme biological variability in tissue properties, fluid composition, and physiological responses complicates the development of universally applicable models [97]. Addressing this challenge requires a concerted effort to develop standardized datasets, advanced imaging techniques, and *in situ* validation methodologies that can provide more comprehensive benchmarks for computational models.

Another major challenge is the simulation of multiphase and multi-component flows, which are ubiquitous in biological systems but remain only partially addressed in current

numerical frameworks [98]. Examples include air-mucus interactions in pulmonary flows, red blood cell and platelet coupling in hemodynamics, and lipid-protein emulsions in digestive processes [99]. Accurately capturing these interactions requires advanced interface tracking methods, adaptive meshing strategies, and efficient coupling of disparate physical models. While recent advances in phase-field methods and volume-of-fluid techniques have improved multiphase modeling, challenges remain in achieving accurate interfacial dynamics, resolving nano-scale interactions, and maintaining computational tractability at organ-level scales [100]. The complexity of these flows demands further integration of high-performance computing, exascale simulations, and advanced numerical techniques capable of handling extreme disparity in spatial and temporal scales [101].

Lastly, the ultimate frontier in biofluid simulations lies in the integration of fluid dynamics with structural mechanics, electrophysiology, and biochemical signaling to create holistic models of organ function. While fluid-structure interaction (FSI) models have successfully captured aspects of cardiac and vascular biomechanics, their coupling with electrophysiological and biochemical transport models remains relatively underdeveloped [102]. The interplay between hemodynamics, myocardial electrophysiology, and metabolic processes is crucial for understanding pathophysiological conditions such as arrhythmias, heart failure, and stroke. Similarly, in pulmonary systems, the interaction between airway fluid dynamics, epithelial transport, and immune responses plays a critical role in diseases such as cystic fibrosis and chronic obstructive pulmonary disease (COPD) [103]. Addressing these challenges will require the development of multi-physics solvers, adaptive coupling strategies, and efficient computational frameworks that can handle the immense complexity of fully coupled biological systems [104]. Numerical simulations of biofluid flows have made extraordinary progress in recent years, with advancements in high-order numerical methods, improved boundary treatments, sophisticated rheological models, and multiscale frameworks expanding the frontiers of biomedical fluid dynamics. Machine learning and data-driven techniques are further accelerating progress, offering new ways to overcome computational bottlenecks and handle uncertain physiological conditions [105]. However, critical challenges remain, particularly in experimental validation, multiphase modeling, and whole-organ simulations. The next decade will likely witness further integration of these computational techniques with high-performance computing, multi-physics modeling, and real-time clinical applications, ultimately driving more accurate, predictive, and patient-specific biofluid simulations. [106]

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