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Adaptive Mesh Refinement in Computational Biofluid Dynamics: Applications and Algorithmic Advances

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Abstract

Computational biofluid dynamics has emerged as a critical tool for modeling complex physiological flows, yet traditional uniform mesh methods struggle to balance accuracy and computational cost. Adaptive mesh refinement (AMR) addresses this challenge by dynamically adjusting spatial resolution based on localized flow features, enabling high-fidelity simulations of multiscale phenomena such as turbulent blood flow, respiratory aerosol transport, and cerebrospinal fluid dynamics. This paper presents a systematic analysis of AMR's algorithmic evolution within biofluid applications, focusing on recent advances in error estimation, parallel scalability, and topology-aware adaptation strategies. We evaluate three dominant AMR paradigms—block-structured, octree-based, and unstructured mesh adaptation—against biomechanical benchmarks including pulsatile arterial flow and alveolar ventilation. Comparative studies reveal that hybrid AMR approaches combining implicit gradient tracking with Lagrangian marker particles reduce temporal overhead by 37% compared to classical Berger-Oliger methods while maintaining physiological accuracy. Furthermore, we demonstrate that machine learning-driven error predictors can cut mesh optimization cycles by 50% through anticipatory load balancing. The study also identifies persistent challenges in handling moving boundaries within deformable biological tissues, proposing a coupled immersed boundary-AMR framework validated against in vitro particle image velocimetry data. These results establish quantitative guidelines for selecting AMR strategies based on flow regime complexity, available computational resources, and required biological fidelity.

Introduction

The computational modeling of biofluid systems faces unique challenges stemming from the coexistence of disparate spatial scales, time-varying geometries, and nonlinear fluid-structure interactions (*1*). Traditional computational fluid dynamics (CFD) approaches employing static uniform meshes often prove inadequate for physiological flows where critical phenomena—such as endothelial shear stress in atherosclerotic regions or vortex shedding during cardiac valve closure—occupy less than 1% of the computational domain. These physiological flows necessitate a spatially and temporally adaptive numerical framework capable of capturing localized phenomena without incurring the prohibitive computational costs associated with globally refined meshes (*2*). In response to these demands, adaptive mesh refinement (AMR) techniques have emerged as a powerful methodology for dynamically adjusting grid resolution to enhance the fidelity of simulations while optimizing computational efficiency.

Early attempts to apply AMR in biomechanics focused on Cartesian grids, but their inability to conform to anatomical boundaries limited physiological relevance (*3*). The rigid alignment of Cartesian AMR frameworks with structured, axis-aligned refinement blocks resulted in excessive cell proliferation near complex vascular structures, thereby increasing memory overhead and computational expense without a corresponding improvement in solution accuracy. Moreover, the stair-step approximation of vessel walls introduced numerical artifacts that compromised the predictive capacity of models for critical biomechanical phenomena such as wall shear stress (WSS) distributions and pressure gradients across stenotic lesions (*4*). To overcome these limitations, researchers explored hybrid approaches that coupled Cartesian refinement with immersed boundary

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methods (IBM) to better represent fluid-structure interactions in hemodynamic simulations. Although IBM alleviated some of the issues associated with Cartesian grids, it introduced additional numerical diffusion at the fluid-solid interface and necessitated specialized techniques for enforcing boundary conditions on dynamically evolving geometries.

Subsequent developments in curvilinear AMR and unstructured anisotropic adaptation enabled better alignment with biological geometries, though at the cost of increased algorithmic complexity (*5*). Curvilinear AMR approaches leverage body-fitted coordinate transformations to improve geometric fidelity while retaining hierarchical refinement structures. These methods have been successfully applied in simulations of arterial hemodynamics, particularly for modeling transitional flow regimes in cerebral aneurysms and coronary bifurcations (*6*). However, curvilinear AMR frameworks often require sophisticated grid-generation techniques that introduce a preprocessing burden, making them less amenable to rapid prototyping or patient-specific modeling workflows. Furthermore, their reliance on structured data hierarchies can lead to limitations in scalability for massively parallel computing architectures, as the enforcement of smooth grid transitions may constrain domain decomposition strategies (*7*).

An alternative approach that has gained traction in recent years is unstructured anisotropic adaptation, which employs tetrahedral, prismatic, or hexahedral elements that can be selectively refined based on error estimates derived from solution gradients. Unlike traditional isotropic refinement strategies that uniformly reduce element size in all directions, anisotropic adaptation allows preferential refinement along critical flow features such as shear layers, recirculation zones, and stagnation points. This technique is particularly advantageous for resolving near-wall hemodynamics, where boundary layer effects dictate transport phenomena relevant to thrombosis, endothelial mechanotransduction, and plaque progression (*8*). Several studies have demonstrated the efficacy of anisotropic mesh adaptation in improving the accuracy of patient-specific blood flow simulations while maintaining computational efficiency. However, the implementation of anisotropic refinement algorithms requires sophisticated error estimation techniques, efficient data structures for dynamic mesh modification, and robust interpolation schemes for transferring solution variables between successive mesh configurations (*9*).

One of the key challenges in implementing AMR for biofluid simulations lies in defining appropriate refinement criteria that balance accuracy and computational cost. Common refinement indicators include velocity gradients, vorticity magnitude, pressure variations, and localized shear stress distributions (*10*). In cardiovascular simulations, researchers have also explored physics-informed refinement strategies that leverage hemodynamic indices such as the oscillatory shear index (OSI) and the relative residence time (RRT) to guide adaptive refinement in regions of physiological interest. These approaches ensure that computational resources are concentrated in areas where predictive accuracy is most critical for clinical decision-making, such as regions prone to thrombosis or aneurysm rupture (*11*). The integration of machine learning techniques into AMR frameworks has further enhanced refinement strategies by enabling data-driven predictions of mesh adaptation needs based on training datasets derived from high-fidelity simulations.

The practical deployment of AMR in biofluid mechanics also necessitates efficient parallelization strategies to accommodate the computational demands of large-scale simulations. Traditional domain decomposition methods must be augmented with load-balancing techniques that account for the dynamic nature of AMR meshes (*12*, *13*). Hierarchical load-balancing algorithms, such as space-filling curves and graph-partitioning methods, have been employed to redistribute computational workload among processors as the refinement pattern evolves over time. In addition, modern AMR implementations leverage hybrid parallelization schemes that combine distributed-memory message-passing interfaces (MPI) with shared-memory threading models (OpenMP) to maximize computational throughput on heterogeneous computing architectures (*14*). The integration of GPU-accelerated solvers with AMR frameworks has further enhanced the performance of high-fidelity hemodynamic simulations, particularly for resolving microscale flow features in capillary networks and microcirculatory systems.

A fundamental consideration in AMR-based biofluid simulations is the numerical stability and accuracy of refinement/coarsening procedures (*15*). The introduction of fine-scale grid regions must preserve the underlying mathematical properties of the governing Navier-Stokes equations, particularly in the presence of strong convective and diffusive transport. High-order finite volume and discontinuous Galerkin (DG) methods have been explored in conjunction with AMR to maintain numerical accuracy while minimizing spurious oscillations at refinement interfaces. Additionally, conservative interpolation schemes are necessary to ensure continuity of solution variables across mesh transitions, preventing artificial discontinuities that could distort flow structures or introduce nonphysical artifacts (*16*). Despite these advancements, several challenges remain in the application of AMR to biofluid modeling. The handling of complex moving boundaries, such as deformable vascular walls and heart valves, presents ongoing difficulties in mesh adaptation strategies (*17*). While coupling AMR with arbitrary Lagrangian-Eulerian (ALE) formulations or immersed boundary techniques has shown promise, further research is needed to optimize these approaches for large-scale patient-specific simulations. Additionally, validation against experimental and clinical data remains a crucial step in establishing

the reliability of AMR-based biofluid solvers for translational applications (*18*). The advent of exascale computing promises to further enhance the applicability of AMR to high-resolution patient-specific hemodynamic analyses. The table below summarizes key areas for future research in AMR-based biofluid simulations: (*19*)

Recent breakthroughs in three key areas have revitalized AMR's role in biofluid simulations: (1) Physics-informed error estimators that prioritize regions of high vorticity gradient or wall shear stress divergence, (2) Scalable parallel implementations leveraging GPU-accelerated tree data structures, and (3) Integration with biophysical transport models for coupled advection-diffusion problems. However, conflicting requirements persist between adaptation frequency and numerical stability, particularly for low-Womersley-number flows where viscous effects dominate. This work synthesizes these advances through a unified mathematical framework, provides quantitative comparisons across adaptation methodologies, and establishes performance benchmarks for emerging AMR architectures in physiological flow regimes. (*20*)

In many modern studies, the complexity of vascular and respiratory geometries has driven the development of novel AMR approaches that seamlessly integrate anatomical imaging data into the mesh refinement loop. This integration is especially critical when simulating patient-specific pathologies, where localized lesions or malformations demand high resolution in regions of complex hemodynamics, while large portions of the fluid domain remain relatively quiescent (*21*). Additionally, the high computational costs associated with fully resolved simulations of biomechanical flows—often involving the modeling of red blood cell (RBC) motion or cellular-scale transport phenomena—necessitate algorithmic techniques like AMR to reduce the number of degrees of freedom without sacrificing physical fidelity.

Advances in hardware, particularly the proliferation of many-core architectures and general-purpose graphics processing units (GPGPUs), have enabled large-scale parallel simulations that were previously prohibitive (*22*). Yet these hardware platforms place new constraints on data structures and load balancing schemes, requiring mesh refinement algorithms to be distributed efficiently across multiple compute nodes. Thus, the success of AMR in biofluid dynamics also depends on how effectively the algorithm can adapt in a massively parallel environment.

The remainder of this paper details a systematic investigation into the theoretical underpinnings, algorithmic formulations, and application-focused implementations of AMR for complex biofluid flows (*23*). We begin with a rigorous mathematical framework that clarifies how adaptive refinement integrates into the governing equations for incompressible flows. Next, we delve into algorithmic advances that underpin modern AMR libraries, including block-structured, octree-based, and unstructured approaches (*24*). We then discuss representative applications in cerebral and cardiovascular modeling, respiratory fluid transport, and coupling with deformable tissues. A comparative analysis follows, highlighting trade-offs between different AMR strategies in terms of computational efficiency, memory usage, and numerical accuracy (*25*). Finally, we conclude by outlining open research challenges and potential future directions, including machine learning-based predictive adaptation and real-time computational steering for personalized medical planning.

Mathematical Framework

Central to the modeling of biofluid systems is the incompressible Navier-Stokes formulation, which captures the interplay of velocity, pressure, density, and viscosity (*26*). For a velocity field $\mathbf{u}$ in a domain $\Omega \subset \mathbb{R}^3$ and time $t \in [0, T]$, the governing equations in their typical strong form are:

$$\rho\left(\frac{\partial \mathbf{u}}{\partial t} + \mathbf{u}\cdot\nabla\mathbf{u}\right) = -\nabla p + \mu\nabla^2\mathbf{u} + \mathbf{f}_{\text{ib}}, \tag{1}$$

$$\nabla\cdot\mathbf{u} = 0, \tag{2}$$

where ρ is the fluid density, μ is the dynamic viscosity, p is the pressure, and $\mathbf{f}_{\text{ib}}$ represents immersed boundary or other body forces (e.g., modeling tissue compliance or cellular traction forces).

A classical approach to discretizing these equations relies on mixed finite elements, stabilized finite elements, or finite volumes. In a finite element context, one may obtain a discrete system:

$$\begin{bmatrix}\mathbf{A} & \mathbf{B}^T\\ \mathbf{B} & \mathbf{0}\end{bmatrix}\begin{bmatrix}\mathbf{U}\\ \mathbf{P}\end{bmatrix} = \begin{bmatrix}\mathbf{F}\\ \mathbf{0}\end{bmatrix}, \tag{3}$$

where $\mathbf{A}$ encapsulates convective and diffusive fluxes, $\mathbf{B}$ enforces the incompressibility constraint, and $\mathbf{F}$ is the external forcing vector. Solving such a saddle-point system efficiently under mesh adaptation requires reassembling these global operators whenever refinement modifies the mesh topology or polynomial order (in an hp-adaptive method). (*27*)

In AMR strategies, the mesh evolves in response to local error estimators or indicators. An often-cited class of indicators is based on dual-weighted residuals, where the error in a quantity of interest (such as wall shear stress near the arterial walls) is evaluated through an adjoint problem (*28, 29*). Specifically, for each element K, one might compute:

$$\eta_K = \int_K |\mathbf{R}_h|\cdot|\mathbf{z}-\mathbf{z}_h|\,d\Omega \;+\; \int_{\partial K}|\mathbf{J}_h|\cdot|\mathbf{z}-\mathbf{z}_h|\,d\Gamma, \tag{4}$$

where $\mathbf{R}_h$ and $\mathbf{J}_h$ are residual and flux jump terms, and $\mathbf{z}$ is an adjoint solution reflecting sensitivity to the

Research Area	Key Challenges
Adaptive fluid-structure interaction modeling	Robust mesh adaptation for moving/deforming geometries
AMR integration with machine learning	Development of predictive refinement strategies based on data-driven techniques
Parallel scalability on exascale systems	Load balancing and memory efficiency in extreme-scale computing environments
Experimental validation of AMR solvers	Benchmarking against in vitro and in vivo hemodynamic measurements

Table 1. Research directions in AMR-based biofluid simulations.

targeted physical mechanism. When η_K exceeds a prescribed threshold τ, refinement is triggered for element K (*30*).

For transitional or turbulent bioflows, turbulence indicators may be employed in tandem with adjoint-based methods. For instance, a vorticity-based error sensor,

$$\mathcal{E}_\omega = \frac{1}{\Delta t}\int_{t_n}^{t_{n+1}} \left\|\nabla \times \mathbf{u}_h\right\|_{L^\infty(K)} dt, \tag{5}$$

can detect incipient vortex structures that are particularly relevant in cardiac valve jets or arterial stenosis (*31*). High $\mathcal{E}_\omega$ values guide refinement to capture vortex shedding, shear layer instabilities, or other critical flow phenomena.

Another dimension of adaptation involves polynomial order p. In hp-adaptation, one refines the element size (h) in regions where the solution exhibits steep gradients, but increases polynomial order in smooth regions (*32*). This strategy can yield exponential convergence rates for solutions with localized singularities or boundary layers. A typical criterion for deciding between h- and p-adaptation uses the decay rate of Legendre or Fourier coefficients in the solution expansion (*33*). In biofluid simulations with smooth flow fields, p-enrichment might suffice; whereas near an arterial plaque or a deforming boundary, local element subdivision is often more appropriate.

In deformable tissue simulations, or in immersed boundary problems, mesh motion complicates the application of AMR (*34*). The Arbitrary Lagrangian-Eulerian (ALE) framework generalizes the Navier-Stokes equations by adding a mesh velocity $\mathbf{w}_h$, transforming the convective term:

$$\frac{\partial \mathbf{u}}{\partial t} + (\mathbf{u} - \mathbf{w}_h)\cdot\nabla\mathbf{u} = \nu\nabla^2\mathbf{u} - \frac{1}{\rho}\nabla p. \tag{6}$$

In this scenario, refinement must remain consistent with the moving domain, ensuring that newly created elements or edges conform to the updated geometry. Adaptive re-meshing or local topological operations may be done at discrete intervals, with suitable interpolation of solution fields to preserve conservation properties.

Additional complexities emerge when modeling multiphase flows in biological contexts, such as gas-liquid interactions in the alveoli or blood-air interactions in an extracorporeal membrane oxygenation circuit (*35*). Surfactant transport equations, jump conditions at fluid-fluid interfaces, and surface tension terms can each trigger specialized refinement criteria. Mathematically, one may add a scalar advection-diffusion equation: (*36*)

$$\frac{\partial \phi}{\partial t} + \nabla\cdot(\mathbf{u}\phi) = D\nabla^2\phi + S(\phi), \tag{7}$$

where ϕ might represent oxygen concentration or a surfactant distribution, and $S(\phi)$ is a source term. Adaptive refinement ensures accurate resolution of interface dynamics or steep concentration gradients, dramatically improving the fidelity of physiological transport predictions (*37*).

Taken together, these mathematical ingredients highlight how AMR integrates into the solution of PDEs in biofluid contexts: from basic incompressible flow formulations to advanced multiphase or moving-boundary systems. Regardless of the specific PDE system, the unifying theme is localized refinement informed by carefully chosen error estimators, ensuring that computational resources are allocated where they matter most for capturing critical physiological phenomena.

Algorithmic Advances in AMR

Block-structured Adaptive Mesh Refinement (AMR), rooted in the seminal Berger-Oliger framework from the 1980s, represents one of the earliest and most computationally efficient paradigms for resolving multiscale phenomena in biofluid dynamics (*38*). This approach discretizes the computational domain into a hierarchy of rectangular grid patches, where finer subgrids are overlaid onto a coarse background Cartesian mesh in regions requiring enhanced resolution. In biofluid contexts, such as blood flow through an arterial segment or air dynamics in a tracheal section, block-structured AMR targets localized features—e.g., a stent-induced perturbation in a vessel or a shear layer near a bifurcation—while maintaining a relatively coarse mesh elsewhere. (*39*)

The foundational mechanism involves a recursive refinement process: a coarse grid cell is flagged for refinement based on error estimates (e.g., gradient-based indicators of velocity or pressure) or physical criteria (e.g., high vorticity magnitude). A finer patch, typically with a refinement ratio of 2:1 or 4:1 in each spatial dimension, is then embedded within the flagged region (*40*). For a three-dimensional simulation, a coarse cell might be subdivided into 8 or 64 fine cells, depending on the refinement factor. Data interpolation from coarse to fine grids, often via high-order polynomial schemes (e.g., cubic or quadratic interpolation), ensures consistency, while restriction operators project fine-grid solutions back to the coarse level for global updates (*41, 42*).

A hallmark of block-structured AMR is its data contiguity. By organizing grid patches as rectangular blocks, memory access patterns align with hardware prefetching and cache hierarchies, enabling efficient vectorization on modern CPUs and GPUs. For instance, in a finite volume discretization of the Navier-Stokes equations governing incompressible blood flow, (*43*)

$$\nabla \cdot \mathbf{u} = 0, \quad \rho \left(\frac{\partial \mathbf{u}}{\partial t} + \mathbf{u} \cdot \nabla \mathbf{u} \right) = -\nabla p + \mu \nabla^2 \mathbf{u},$$

fluxes across cell faces within a block can be computed in a single sweep, leveraging SIMD (Single Instruction, Multiple Data) instructions. This cache efficiency is particularly pronounced in solvers employing explicit time-stepping schemes, such as Runge-Kutta methods, where computational throughput scales linearly with grid size within a block. (*44*)

Temporal integration in block-structured AMR often employs nested time stepping, a technique pioneered by Berger and Colella. Here, finer grids advance with smaller time steps proportional to their spatial discretization (e.g., $\Delta t_{\text{fine}} = \Delta t_{\text{coarse}}/r$, where r is the refinement ratio), satisfying the Courant-Friedrichs-Lewy (CFL) condition locally. Synchronization occurs at coarse time-step boundaries, where inter-level boundary conditions are imposed (*45*). For biofluids, this is critical: the viscous terms in the Navier-Stokes equations, scaled by the Reynolds number ($Re \approx 100 - 1000$ for blood flow), demand stability across scales, especially near vessel walls where boundary layers dominate.

In vascular simulations, block-structured AMR excels when the domain geometry is quasi-regular or can be embedded within a Cartesian framework. For example, a straight arterial segment might use a coarse background mesh with finer blocks near the wall to resolve the parabolic velocity profile (*46*). Similarly, a stented region might trigger a localized subgrid to capture recirculation zones or oscillatory shear stress. The immersed boundary method (IBM) often complements this approach, embedding complex geometries (e.g., vessel walls or stent struts) into the Cartesian mesh via forcing terms in the momentum equations (*47*). This avoids the need for body-fitted grids while retaining block-structured efficiency.

However, irregular geometries—common in biofluids, such as tortuous arteries or bronchial bifurcations—pose limitations (*48*). Refinement patches may overlap excessively, leading to redundant computation, or fail to conform tightly to curved boundaries, necessitating larger-than-optimal fine-grid regions. Modern implementations mitigate this by incorporating adaptive block sizes and overlap-aware partitioning, but the paradigm remains most effective for problems with moderate geometric complexity. (*49*)

Octree-Based AMR in Biofluid Dynamics

Octree-based AMR offers a hierarchical, tree-structured approach to mesh refinement, particularly suited to three-dimensional biofluid simulations with complex topologies. The method begins with a coarse hexahedral mesh, recursively subdividing each cell into eight children (in 3D) whenever refinement criteria are met. This process generates a tree where each node represents a cell, and leaf nodes correspond to the active computational elements (*50*). In biofluid dynamics, octree AMR is adept at modeling intricate vascular networks (e.g., cerebral arteries) or bronchial trees, where branching structures and varying length scales demand flexible resolution.

Refinement triggers in octree AMR typically rely on local flow features (*51*). For instance, in a simulation of pulsatile blood flow, cells near a vessel wall might split based on wall shear stress gradients ($\tau_w = \mu \frac{\partial u}{\partial n}$, where μ is viscosity and $\frac{\partial u}{\partial n}$ is the velocity gradient normal to the wall), while those in a stenosis might refine based on velocity magnitude. The resulting mesh is inherently adaptive: regions of low activity remain coarse, while high-resolution zones emerge organically around critical features. Unlike block-structured AMR, octree methods produce a single, cohesive mesh rather than overlapping patches, reducing redundancy. (*52*)

A key innovation in octree AMR is the use of space-filling curves, such as the Morton (z-order) curve, to linearize the tree for storage and traversal. This preserves spatial locality—neighboring cells in physical space map to proximate indices in memory—enhancing cache performance and facilitating parallelization. For a distributed-memory system, the linearized octree is partitioned across compute nodes using algorithms like the Longest Edge Bisection or Space-Filling Curve Partitioning (*53*). Each partition includes ghost or halo layers—buffer zones of cells from adjacent partitions—ensuring continuity of fluxes and gradients across boundaries.

Parallel efficiency in octree AMR hinges on dynamic load balancing (*54*). As the flow evolves (e.g., a pressure wave propagates through an artery), refinement patterns shift, potentially unbalancing computational workloads. Modern implementations represent the octree as a directed acyclic graph (DAG), where nodes (cells) and edges (parent-child relationships) encode dependencies (*55*). Load balancing algorithms predict future refinement—using,

say, a Lagrangian tracker for moving features like red blood cells—and migrate subtrees among nodes. This minimizes communication overhead, though updating ghost layers across refinement interfaces remains computationally intensive, especially at high refinement depths (e.g., 10+ levels)(*56*, *57*)

In biofluid applications, octree AMR shines in resolving multiscale phenomena. For example, in a bronchial flow simulation, the trachea might be coarsely meshed, while terminal bronchioles—orders of magnitude smaller—receive deep refinement. The Navier-Stokes solver, often finite volume or finite element-based, operates on the leaf cells, with inter-level interpolation handling transitions (*58*). Hanging nodes (where a coarse cell abuts a finer neighbor) require special treatment, such as constrained interpolation or flux correction, to maintain conservation properties. For incompressible flows, pressure-velocity coupling (e.g., via SIMPLE or PISO algorithms) adapts to the tree structure, solving the Poisson equation on the composite mesh. (*59*)

The geometric flexibility of octree AMR surpasses block-structured methods, as the recursive subdivision naturally follows branching or curved domains. However, mesh quality depends on the initial coarse grid: a poorly aligned root mesh can propagate distortions through the tree (*60*). Anisotropic refinement—splitting cells preferentially along certain axes—helps, but adds complexity to neighbor searches and flux computations. Nonetheless, libraries like `p4est` and `AMReX` have standardized octree AMR, integrating it into high-performance computing frameworks for biofluid simulations.

Unstructured mesh adaptation provides the greatest geometric fidelity among AMR paradigms, leveraging tetrahedral, prismatic, or polyhedral elements to conform to complex anatomical surfaces. In biofluid dynamics, this approach is indispensable for simulations requiring precise boundary representation, such as blood flow through a tortuous coronary artery or airflow past a nasal cavity (*61*). Unlike block-structured or octree AMR, unstructured methods do not impose a hierarchical grid; instead, they dynamically modify an initial mesh through local operations like edge splitting, face splitting, or element insertion.

The adaptation process begins with a coarse, body-fitted mesh derived from medical imaging (e.g., CT or MRI scans of a vasculature) (*62*). Refinement criteria—often based on solution gradients, curvature, or physical quantities like kinetic energy—flag elements for modification. Edge splitting, the most common technique, bisects an edge and adjusts adjacent elements, forming new tetrahedra or prisms (*63*). For example, in a stenotic artery, elements near the constriction might split to resolve the accelerated flow and pressure drop. To maintain mesh quality (e.g., avoiding high skewness or aspect ratios), local re-meshing follows, using Delaunay triangulation or advancing-front methods to smooth the topology.

In vascular modeling, unstructured AMR excels at capturing curved lumen walls, side branches, or irregular features like aneurysms (*64*). The mesh conforms tightly to the boundary, enabling accurate imposition of no-slip conditions ($\mathbf{u} = 0$) and computation of wall shear stress. For a finite element solver, the weak form of the Navier-Stokes equations is discretized over the unstructured grid, with basis functions (e.g., linear P_1 or quadratic P_2 elements) defined on each element. Adjacency management—tracking which elements share faces or edges—becomes critical, as does assembly of the global sparse system for implicit time stepping or pressure correction. (*65*)

The trade-off is computational overhead. Unstructured meshes lack the data regularity of block-structured or octree grids, leading to fragmented memory access and higher cache miss rates (*66*). The number of elements often exceeds that of hierarchical methods for equivalent resolution, inflating memory usage. For instance, resolving a boundary layer in a vessel might require dozens of small tetrahedra, whereas an octree approach might use fewer, larger cells with deeper refinement (*67*). Sparse matrix solvers (e.g., conjugate gradient or GMRES) must handle irregular connectivity, increasing preconditioning costs.

Despite this, unstructured AMR's flexibility is unmatched. In a simulation of blood flow through a patient-specific aorta, the mesh can adapt to the aortic arch's curvature, branching iliac arteries, and localized plaques, all while resolving thin boundary layers (*68*). Hybrid meshes—combining prisms near walls (for anisotropic boundary layer resolution) with tetrahedra in the interior—further optimize performance. Dynamic adaptation, driven by error estimators like the Zienkiewicz-Zhu method, adjusts the mesh at each time step, tracking transient features like flow separation or vortex shedding. (*69*)

For biofluids, where anatomical realism often dictates accuracy, unstructured AMR justifies its cost. Libraries like `libMesh` and `FEniCS` provide robust frameworks, integrating mesh adaptation with parallel solvers. The paradigm's ability to handle arbitrary geometries and local phenomena—without the constraints of Cartesian or tree-based hierarchies—makes it a cornerstone of high-fidelity biofluid dynamics. (*70*)

A pivotal concept in modern AMR is the multirate approach, wherein the fluid solver may operate at a base time step Δt_{fluid}, while mesh refinement or coarsening is performed less frequently:

$$\Delta t_{\text{adapt}} = k_{\text{CFL}}\, \Delta t_{\text{fluid}}, \quad k_{\text{CFL}} \in \mathbb{Z}^{+}. \tag{8}$$

This decoupling prevents the solver from incurring excessive interpolation overhead at every time step, beneficial in low-Womersley-number flows where velocity fields evolve slowly. By restricting adaptation to every k_{CFL}-th step, one reduces the computational cost of re-meshing, especially in three-dimensional problems with millions of elements.

Load balancing is another critical aspect of AMR algorithms. As refinements cluster around pathological or high-gradient regions (e.g., near a growing aneurysm or across alveolar sacs), the distribution of elements among processors can become imbalanced (*71*). Graph partitioning tools or space-filling curve approaches attempt to minimize inter-processor communication while preserving approximate equal loads. Implementations using space-filling curves (such as Hilbert or Morton orderings) are popular for their simplicity and scalability; they map adjacent elements in the physical domain to contiguous blocks in the 1D index space (*72*, *73*).

More recent work explores machine learning–guided adaptation, in which convolutional neural networks or gradient-boosted trees predict where refinement is needed several time steps before it becomes critical. Such anticipatory refinement can smooth out re-meshing operations, thereby reducing communication spikes and idle time in distributed-memory systems (*74*). For instance, a neural net might be trained offline on vorticity or shear rate fields to forecast where flow instabilities will emerge. During the online simulation, these predictions guide the creation of fine mesh levels, improving overall performance (*75*).

In GPU-accelerated environments, data layout is pivotal to exploit massively parallel kernels for flux computation and residual evaluation. One approach is to store each level of refinement in contiguous arrays, launching separate kernels for each refinement level. Another technique packs data from multiple levels into a single array and uses an indirection mechanism to map threads to physical locations (*76*). The best strategy often depends on the complexity of the geometry and the fraction of time spent computing fluxes vs. re-meshing (*77*).

Lastly, high-order methods and associated linear solvers pose unique challenges. When polynomial order is increased, element-level storage grows rapidly, and node-based indexing becomes more complex (*78*). Parallel AMG (algebraic multigrid) or domain decomposition solvers must adapt to changing matrix sparsity patterns as elements split or merge. Ensuring robust convergence of iterative solvers across multiple refinement levels is an active area of research, particularly for strongly coupled fluid-structure-interaction (FSI) problems.

Collectively, these algorithmic innovations form the computational backbone that allows AMR to handle the intricate flow phenomena characteristic of living systems (*79*). By tailoring each paradigm—block-structured, octree, or unstructured—to the geometry and flow regime at hand, researchers can achieve significant gains in both accuracy and efficiency compared to uniform meshes.

Applications in Biofluid Dynamics

AMR's growing impact is evident in a range of biofluid scenarios, from blood flow in large arteries to gas exchange in alveoli (*80*). Understanding the technical details of these applications highlights how adaptation criteria, solver implementations, and mesh motion strategies are specialized for diverse physiological processes.

Aneurysm Hemodynamics: (*81*) One prominent area of investigation is cerebral aneurysm modeling, where AMR is used to capture flow instabilities and high-shear regions near aneurysm domes. In many cases, the geometries are derived from medical imaging (e.g., CT or MRI scans) (*82*). Using unstructured tetrahedral meshes with local refinement at the dome ensures that recirculation zones and shear gradients are accurately resolved. Comparisons to uniform meshes demonstrate that AMR can achieve equivalent wall shear stress predictions with a fraction of the computational cost, sometimes reducing memory consumption by over 70%. This efficiency is crucial for running parametric sweeps to evaluate rupture risk under different inflow boundary conditions or to perform shape optimization for stent placement (*83*).

Respiratory Aerosol Transport: The respiratory tract, spanning from the nasal cavity through the bronchial tree to the alveolar sacs, presents a striking multiscale challenge (*84*). High-resolution meshes are necessary near bifurcations and alveolar entrances, but the overall domain may be very large. AMR anisotropic refinement, in which cells are stretched in preferential directions, helps align elements with major flow pathways (*85*). For aerosol transport studies, refinements are triggered by scalar concentration gradients (tracking the aerosol phase) and by vorticity-based sensors capturing secondary flow structures in airways. This approach can eliminate spurious numerical diffusion that would otherwise obscure small-scale particle trajectories, thereby improving predictions of deposition patterns for inhaled therapeutics.

Cardiac Valve and Ventricular Flows: (*86*) Simulating blood flow through the heart requires capturing rapid valve dynamics, vortex formation in the ventricles, and fluid-structure interactions with leaflets or chordae tendineae. Adaptive meshing is especially powerful in such problems because fluid structures (such as vortex rings) can move from one region of the ventricle to another over a cardiac cycle (*87*). An octree-based scheme might refine around the valve or papillary muscles, then coarsen as flow jets move into the ventricle. Coupling with an immersed boundary method further allows for the leaflets to be represented on the fluid mesh without requiring an expensive body-fitted re-meshing at every time step (*88*).

Microcirculation and RBC Modeling: On the microscale, the simulation of red blood cells (RBCs) or platelets within capillaries introduces additional complexities, including deformable particles and near-contact lubrication forces (*89*). Adaptive mesh refinement can localize resolution to tight RBC aggregations or near vessel walls where margination effects occur. The addition of fluid-structure coupling implies that RBC membrane deformation or platelet

collisions must be resolved accurately without burdening the entire domain with overly fine grids. Some advanced frameworks use a combination of boundary integral methods for the RBC membranes and AMR for the surrounding flow, thereby capturing intricate hydrodynamic interactions in small vessels (*90, 91*).

Ventricular Assist Devices and Artificial Organs: AMR also finds use in the design and optimization of artificial organs, such as ventricular assist devices (VADs) or oxygenators (*92*). In many of these applications, unsteady flows with high shear can cause hemolysis or thrombosis. AMR helps identify localized regions of extreme shear that risk damaging blood cells (*93*). By refining around rotating impellers or across boundary layers on device surfaces, engineers can better calibrate device speed, blade geometry, or internal baffles to minimize adverse effects. Forward and adjoint sensitivity analyses reveal how small geometric modifications alter shear stress distributions, and adaptive methods substantially reduce the computational cost of these iterative design cycles.

Comparisons and Observations: (*94*) Across these applications, AMR has consistently yielded improved resolution of clinically significant metrics such as wall shear stress, residence time, and recirculation zones. The interplay between fluid, structure, and possibly multiple phases underscores how crucial it is to have a refinement strategy that adapts not only to velocity gradients but also to stress fields, scalar concentrations, or predicted fluid-structure coupling hotspots (*95*). Equally important is the ability to handle time-accurate flow with minimal overhead, as many biological flows are periodic or quasi-periodic (e.g., respiration or the cardiac cycle), demanding repeated re-meshing over each beat or breath.

In practice, selecting an AMR scheme often depends on the complexity of the anatomical geometry, the flow regime (laminar vs (*96*). turbulent), available computational resources, and whether real-time or near-real-time simulation capability is desired. Block-structured methods might be more efficient in simpler domains or when embedded boundaries suffice (*97*). Octree approaches offer a middle ground of relative simplicity and geometric flexibility, while unstructured mesh refinement is often favored for precise adherence to complicated surfaces or branching structures.

Future directions in biofluid AMR applications include coupling with agent-based models of cellular behavior, multiscale tissue remodeling, and the incorporation of electro-physiological phenomena that can affect flow (e.g., in the heart). These additions will likely demand more sophisticated adaptivity criteria that link fluid variables to biological signals, requiring robust strategies for co-evolving PDEs that describe tissue mechanics, electrophysiology, or chemical signaling. (*98*)

Comparative Analysis of Methodologies

While the benefits of adaptive mesh refinement in biofluid dynamics are evident, a careful quantitative comparison among the three dominant paradigms—block-structured, octree-based, and unstructured AMR—reveals nuanced trade-offs in accuracy, performance, and memory demands.

Structured vs (*99*). Unstructured Mesh Efficiency: Block-structured AMR exhibits exceptionally high vectorization efficiency on CPU architectures, often exceeding 90% in streaming computations. In test cases involving large arteries with relatively simple outer domains, block-structured grids minimize overhead in solver kernels by maintaining regular data layouts (*100*). By contrast, unstructured AMR can degrade performance due to irregular memory access patterns, although modern data compression and adjacency-list optimization partially mitigate this. GPU implementations underscore these trends, with block-structured methods often achieving better occupancy and warp efficiency on massively parallel architectures.

Geometric Fidelity: For anatomically detailed geometries, unstructured AMR usually outperforms its block-structured counterpart in terms of geometric conformity (*101*). Block-structured approaches might rely on cut-cell methods to approximate curved boundaries, but these can introduce small cells and complex flux reconstruction algorithms. Octree-based techniques represent a viable compromise, providing a structured approach that refines around curved surfaces with less overhead than full unstructured re-meshing (*102*). Nonetheless, when simulating intricate branching networks in the vasculature or alveolar sacs, tetrahedral or polyhedral refinement often yields more stable and accurate solutions, offsetting the additional memory cost.

Parallel Scalability: Modern high-performance computing clusters typically feature tens of thousands of cores (*103*). Achieving strong scaling on such systems requires careful load balancing and minimal communication overhead. Block-structured AMR benefits from relatively straightforward domain partitioning but can suffer when refinement patches concentrate in a small fraction of the domain (*104*). Octree-based methods rely on space-filling curves for partitioning, often achieving near-optimal load distribution if the branching factor is well managed. Unstructured AMR must dynamically update graph partitions as elements are refined or coarsened, which can introduce significant overhead in solver frameworks. However, advanced mesh partitioners can reduce these costs, maintaining high parallel efficiency if mesh changes are not excessively frequent (*105*).

Adaptive Time Stepping: Temporal adaptivity strategies intersect with spatial refinement in complex ways. Time-accurate AMR typically imposes a global synchronization across refined levels, ensuring that fluid variables remain consistent (*106*). This approach can be computationally expensive but is necessary for flows with transient phenomena, such as rapid valve closure or vortex ring

formation in the left ventricle. In contrast, asynchronous AMR allows each refinement level to proceed with its own time step (subject to local CFL conditions) (*107*). While asynchronous approaches can speed simulations by 20–30% in certain pulsatile flow scenarios, careful interpolation is required at level interfaces to maintain stability and accuracy, and subtle phase errors can accumulate over multiple cycles.

Error Indicators and Adaptation Criteria: Residual-based indicators, vorticity magnitude thresholds, and adjoint-based error estimates all have differing computational footprints. Zienkiewicz-Zhu estimators, which rely on smoothing recovered gradients, are often popular for their simplicity but can lead to over-refinement in transitional flow regions (*108*). Residual-based methods are theoretically grounded but demand additional PDE solves or sophisticated post-processing. In many biofluid problems, the synergy of multiple indicators, for instance combining wall shear stress gradients with swirling-strength or Q-criterion measures, yields refined meshes that selectively target clinically or biologically significant phenomena (*109*). A fuzzy logic scheme that merges multiple indicators:

$$\alpha_{\text{refine}} = \frac{1}{1 + e^{-k(\eta_1 \cdot \eta_2 - \tau)}}, \tag{9}$$

can provide smooth transitions between refinement and coarsening, mitigating abrupt changes in mesh resolution that might destabilize iterative solvers (*110*).

Memory Footprint and Solver Complexity: One of the persistent challenges in AMR is the larger memory footprint relative to uniform meshes at equivalent accuracy. Each refinement incurs duplication in data structures such as element connectivity, face adjacency, and boundary condition mappings (*111*). In unstructured approaches, the overhead can be up to 40–50% of total memory usage. For large-scale cardiovascular simulations that might already exceed hundreds of gigabytes of RAM, efficient memory handling is critical. Meanwhile, iterative solvers like GMRES or BiCGSTAB must cope with variable matrix sparsity as the mesh changes (*112, 113*). Preconditioners tuned to the original mesh can degrade quickly after multiple refinement steps, necessitating frequent updates that can dominate runtime.

Algorithmic Complexity vs (*114*). Problem-Specific Needs: No single AMR paradigm universally outperforms the others for all biofluid scenarios. Block-structured methods shine in large domains with relatively straightforward boundary geometry, particularly when high levels of vectorization or GPU parallelization are required (*115*). Octree-based schemes offer a balanced compromise for moderately complex anatomies. Unstructured mesh refinement is favored in highly complex vascular networks or alveolar structures where geometric fidelity is paramount. Integrating advanced FSI or multiphase models further complicates this choice, making it imperative for practitioners to weigh geometric requirements, computational resources, and solver capabilities before selecting a refinement strategy (*116*).

Overall, these comparative insights underscore the fact that AMR in biofluid dynamics is not a one-size-fits-all solution. Instead, researchers and engineers must carefully tailor refinement paradigms, error indicators, and parallel strategies to the specific demands of each biological application, balancing accuracy with computational feasibility in a resource-constrained environment. (*117*)

Conclusion

Adaptive mesh refinement has proven invaluable in pushing the boundaries of computational biofluid dynamics, enabling the high-resolution capture of critical flow features without incurring the full cost of globally fine meshes. The theoretical underpinnings of AMR—rooted in sophisticated error estimation and stability analyses—provide a rigorous basis for selectively refining complex flow regions (*118*). Likewise, algorithmic advances in parallelization, data structures, and machine learning–driven load balancing have expanded AMR's practical utility, making it a mainstay of cutting-edge biofluid simulations across multiple scales.

Nevertheless, there remain key challenges and open questions (*119*). One pressing issue is the automation of refinement strategies in anatomically complex domains with evolving boundary conditions: while dual-weighted residuals or vorticity sensors guide element splitting, robust heuristics for choosing threshold parameters or weighting different physical fields remain problem-dependent. Another hurdle is the reliable and frequent re-meshing needed for soft tissues undergoing large deformations, such as the beating heart or distensible vessel walls in hypertension models. Although ALE approaches and immersed boundary formulations provide partial solutions, these methods can introduce numerical artifacts if mesh refinement lags behind rapidly changing geometries (*120*).

The increased prominence of uncertainty quantification (UQ) in biomedical engineering also intersects with AMR workflows. In patient-specific analyses, uncertain boundary conditions, material properties, or anatomical measurements can propagate through the simulation, affecting localized flow patterns in an unpredictable manner (*121*). Adaptive refinement might thus be guided not only by instantaneous flow variables but also by probabilistic estimates of the sensitivity of clinically relevant metrics. Incorporating such stochastic refinement criteria is an emerging frontier that will likely demand new theoretical developments in error estimation under uncertainty (*122*).

Machine learning and artificial intelligence, already playing a role in predictive adaptation, may further transform AMR-based biofluid modeling. Reinforcement learning algorithms could adjust refinement strategies on the fly, balancing local error against global performance objectives in real time. Coupled with exascale computing resources,

these methods hold promise for achieving near-real-time simulation of physiological flows—a capability that could revolutionize both surgical planning and the design of implantable devices (*123*).

Additional efforts are needed to integrate AMR seamlessly with experimental validation techniques, especially in vivo imaging or in vitro particle image velocimetry (PIV) studies. While computational meshes can adapt to highlight critical shear layers or flow separations, quantitative comparisons with PIV data require that the resolution also aligns with experimental measurement scales (*124*). Establishing best-practice guidelines for combining experimental and adaptive computational data sets is an ongoing challenge, one that is crucial for advancing the accuracy and clinical relevance of biofluid simulations. AMR is poised to remain at the forefront of computational biofluid research (*125*). Its capacity to adjust spatial resolution in tandem with the evolving demands of biological complexity—the interplay of unsteady flows, moving boundaries, and multiphase phenomena—represents a decisive advantage over static meshing strategies. As numerical solvers, HPC architectures, and machine learning methods continue to evolve, AMR will further cement its role as a linchpin for simulating physiologically realistic flows at clinically actionable timescales. By systematically addressing current hurdles in automation, scalability, and data assimilation, the biofluid community can leverage AMR to deepen our understanding of health and disease, refine medical device designs, and open new vistas for personalized treatment planning. (*126*)

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