# Uncertainty Quantification in Numerical Simulations of Biofluid Flows: Methods and Applications

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#### Abstract

Biofluid flows within the human body are often characterized by intricate geometries, variable material properties, and complex boundary conditions. These factors introduce considerable uncertainties into numerical simulations, requiring robust strategies to analyze and quantify possible variations in predicted flow parameters. While deterministic simulations have provided significant insights into physiological processes, recent efforts have increasingly emphasized the importance of incorporating uncertainty to improve predictive accuracy and guide clinical decision-making. This discussion offers a structured examination of how different methods can capture variability in transport phenomena, fluid-structure interactions, and boundary conditions, while ensuring consistency and computational efficiency. Special attention is paid to how stochastic parameterization in hemodynamics can help refine the quantification of flow rates, pressure gradients, and wall shear stresses under uncertain or imprecise data constraints. The overall goal is to highlight approaches that enhance confidence in simulation outcomes, thereby bolstering clinical relevance and translation to patient-specific scenarios. By integrating rigorous mathematical tools, advanced modeling techniques, and scalable computational strategies, this work demonstrates a pathway to more robust and physiologically realistic biofluid flow simulations. The subsequent sections focus on conceptual foundations, practical formulations, solution methodologies, and interpretive guidelines, leading to new avenues for precision medicine and improved understanding of critical flow phenomena.

### 1 Introduction

Biological systems exhibit diverse and often highly sensitive flow phenomena, driven by complex interactions between fluids, soft tissues, and biochemical processes [1]. In many applications related to cardiovascular research and other biofluid settings, the accurate representation of these flows requires that one account for geometric complexities, heterogeneous material properties, and uncertain boundary conditions. The challenge, therefore, lies in devising computational strategies that can systematically incorporate variabilities from experimental measurements, parameter uncertainties, and modeling assumptions [2]. Achieving robust simulation capabilities demands a unifying framework that can reconcile deterministic descriptions with a broader set of probabilistic or stochastic formulations.

Central to the motivation for systematically examining uncertainty in biofluid flows is the recognition that purely deterministic simulations might lead to overconfident predictions [3]. Such overconfidence arises when computational models neglect known or unknown variations in geometrical, physical, or physiological conditions. To illustrate, consider a set of vessel networks embedded in a patient-specific geometry, where vessel diameters, boundary inlets, and fluid rheological properties are not precisely known [4]. Traditional deterministic approaches will yield a single trajectory of solution fields, potentially overlooking significant fluctuations that arise from small but critical deviations in input parameters. These fluctuations can manifest in vector expressions such as (u, v, w)for velocity fields, which vary in time and space and become more pronounced when uncertain tissue properties and complex boundary conditions converge [5]. Ultimately, a more comprehensive approach is required, one that acknowledges each parameter's potential influence on the final numerical results.

It is often informative to express uncertain parameters within a set  $\Omega$ , where each element  $\omega \in \Omega$  represents a different realization of the model inputs [6]. Within this probabilistic context, the objective is often to compute

integrals of the form

$$\mathbb{E}[f(\omega)] = \int_{\Omega} f(\omega) \, dP(\omega),$$

where  $f(\omega)$  might correspond to a scalar or vector quantity derived from the simulation and P is a probability measure on  $\Omega$  [7]. When dealing with three-dimensional blood flow governed by the Navier-Stokes equations, one might have uncertain boundaries  $\partial \Omega(\omega)$ , uncertain viscosity values  $\mu(\omega)$ , or unknown external forcing terms  $g(\omega)$ . In each scenario, we seek to understand the distributional characteristics of critical quantities, such as the pressure  $p(\omega)$ , velocity vector fields  $\mathbf{u}(\omega)$ , or wall shear stress magnitudes.

In cardiovascular modeling, for instance, obtaining robust estimates of flow patterns around stenotic segments or within complex bifurcations is central to predicting hemodynamic stresses and potential pathophysiological conditions [8]. Variations in vessel morphology, the presence of plaque deposits, local tissue elasticity, and patientspecific flow rates require careful treatment of uncertainty. The interplay between fluid and structure introduces additional levels of intricacy, especially if one aims to solve fluid-structure interaction equations in the presence of unknown elastic properties of vessel walls or uncertain external loads [9]. The partial differential equations that govern such systems can become a family of parameterized PDEs,

$$\mathcal{N}(\mathbf{u};\omega) = 0$$

where  $\mathcal{N}$  encapsulates a combination of linear, nonlinear, and time-dependent operators subject to random parameters. The complexity becomes even more pronounced if the fluid is non-Newtonian or if the boundary layer phenomena around small features demand refined meshes, as well as advanced numerical techniques for stabilizing the solution process. [10]

Handling these high-fidelity simulations in a deterministic setting is already challenging due to computational costs. Extending them to stochastic or uncertain frameworks raises the question of how to systematically approximate integrals over high-dimensional input spaces [11]. Techniques such as polynomial chaos expansion, stochastic Galerkin methods, or multi-level Monte Carlo approaches provide avenues to approximate integrals over random inputs. These methods typically represent uncertain parameters  $\xi \in \mathbb{R}^d$  by employing basis functions that capture the statistical variation in a low-rank or hierarchical manner. By exploiting orthogonality relationships, one can project solution fields onto a carefully chosen subspace, thereby enabling a more compact representation of the quantity of interest. [12]

The broader rationale for pursuing these strategies in biofluid flow simulations is to facilitate quantitative risk assessment, personalized therapeutic planning, and more reliable predictive modeling. In the context of vascular graft design, for example, reliability-based design optimization might require evaluating the probability of exceeding critical thresholds of wall shear stress under uncertain operating conditions **17z**, [13]. Similarly, in microfluidic devices for drug delivery, capturing variability in flow patterns could guide device geometry optimization to achieve robust performance across a range of physiological states.

The subsequent sections present a multi-layer perspective on uncertainty in biofluid simulations, focusing first on how to represent uncertain information in ways that are consistent with physiological reality [14]. The discussion then turns to numerical methods, addressing how high-dimensional integration and parameter sampling can be performed effectively within large-scale simulations. Further consideration is devoted to algorithmic strategies that balance accuracy and computational burden [15]. Finally, practical aspects will be considered, showcasing how these methods can be integrated with existing simulation pipelines to deliver meaningful predictions for clinicians and researchers.

## 2 Probabilistic and Non-Probabilistic Approaches for Uncertainty Representation

Uncertainty in biofluid simulations can be categorized along two principal axes: probabilistic methods that model inputs via well-defined probability distributions, and non-probabilistic methods that encode variability through sets or intervals [16]. Within the probabilistic category, one might consider parametric distributions for vessel diameters, fluid viscosities, or boundary inflow rates, introducing an appropriate measure on  $\Omega$ . Conversely, nonprobabilistic approaches such as interval analysis, fuzzy sets, or epistemic uncertainty modeling eschew explicit probability definitions, opting instead to bracket unknowns within permissible bounds or membership functions. [17]

In the probabilistic framework, each uncertain parameter can be mapped from a reference space  $\Gamma \subset \mathbb{R}^m$ onto a physical domain via a transformation  $\Xi : \Gamma \to \Omega$ . For example, one might define random variables  $\xi = (\xi_1, \xi_2, \ldots, \xi_m)$  with probability density function  $\rho(\xi)$ . The realization  $\omega = \Xi(\xi)$  can then characterize different configurations of vessel geometry or fluid properties [18]. When linear transformations suffice, one can express each parameter as  $\omega_i = \mu_i + \sigma_i \xi_i$ , where  $\mu_i$  is a mean value and  $\sigma_i$  is a standard deviation. In more complex scenarios involving correlated variables or data-driven distributions, one might rely on covariance matrices or kernel density estimates to capture intricate relationships among input parameters. [19]

Once the uncertain inputs have been established, computational tasks typically revolve around evaluating moments or probability-based criteria of the solution fields. For the velocity field  $\mathbf{u}(x;\omega)$ , one may be interested in  $\mathbb{E}[\mathbf{u}(x;\omega)]$  or  $\operatorname{Var}[\mathbf{u}(x;\omega)]$ . Such calculations often entail integrals of the form [20]

$$\mathbb{E}[\mathbf{u}](x) = \int_{\Gamma} \mathbf{u}(x; \Xi(\xi)) \,\rho(\xi) \,d\xi,$$

which can be intractable for direct numerical quadrature over high-dimensional domains. This challenge gives rise to specialized approximation schemes, including stochastic collocation methods that sample the parameter space at carefully chosen quadrature nodes or use sparse grids to mitigate the curse of dimensionality. [21]

Alternatively, polynomial chaos expansions (PCE) seek to represent a random field by a series expansion in orthonormal polynomials  $\{\Phi_j(\xi)\}_{j=0}^{\infty}$ . Then one writes

$$\mathbf{u}(x;\omega) \approx \sum_{j=0}^{p} \mathbf{u}_{j}(x) \, \Phi_{j}(\xi),$$

where  $\mathbf{u}_j(x)$  are deterministic coefficients to be determined. For input parameters following Gaussian distributions, Hermite polynomials emerge as a natural choice, though alternative polynomial families (e.g., Legendre, Laguerre) can be used depending on the parameter distributions [22]. By projecting the governing equations onto this polynomial basis, one can derive a coupled system of deterministic equations for the coefficients  $\{\mathbf{u}_j\}$ , although the resulting system dimension grows with the order p and the number of parameters m.

Non-probabilistic methods, on the other hand, are useful in scenarios where limited data make it challenging to assign accurate probability distributions. Interval analysis defines bounds  $[\alpha_i, \beta_i]$  for each uncertain parameter, ensuring that any instance of the parameter falls within that range [23]. This approach yields guaranteed enclosures for solution outputs but may produce overly conservative bounds if the intervals are broad. Fuzzy set theory introduces membership functions that describe degrees of possibility for different parameter values [24]. Then one can perform level-cut analyses to propagate uncertainty through the computational domain, ultimately constructing a family of fuzzy outputs. Similarly, evidence theory or Dempster-Shafer theory can be employed to handle epistemic uncertainty. [25]

In biofluid contexts, the choice between probabilistic and non-probabilistic methods often hinges on data availability and the underlying purpose of the simulation. When ample data exist to infer distributional properties—e.g., from large cohorts of patient-specific flow measurements—probabilistic approaches can provide fine-grained insights into the likelihood of different hemodynamic states [26]. When data are scarce or highly qualitative, non-probabilistic strategies may prove more suitable by acknowledging that the precise probability structure is unknown. Such flexibility can be particularly valuable when modeling emergent or poorly characterized phenomena, for instance in cases of complex microcirculation or rare pathologies where the parameter space is only partially understood. [27]

Regardless of the selected representation, the crucial aspect is consistency. The introduction of uncertainties should align with the known physical or physiological constraints of the system [28]. If vessel elasticity has a plausible range, one should ensure the modeling framework never explores elasticity values outside that range. Even for more exotic or uncertain phenomena, such as non-Newtonian behavior in microvessels, the sets or distributions chosen should reflect some prior understanding of valid parameter regimes [29]. In sum, the thorough definition of random or uncertain inputs lays the foundation for subsequent numerical procedures aimed at quantifying their impact on flow fields and associated physiological indicators.

## 3 Advanced Computational Methods for Large-Scale Biofluid Simulations

High-fidelity simulations in biofluid mechanics often require solving three-dimensional, time-dependent Navier-Stokes equations over geometrically complex domains [30]. Adding uncertainty compounds the computational burden, as the solution must be evaluated repeatedly for multiple realizations or expansions of the random input space. Consequently, advanced numerical methods have been developed to ensure that the computational effort remains tractable, even as model fidelity and the dimensionality of the uncertain parameters increase. [31]

One pathway is the stochastic Galerkin method, wherein the governing equations are transformed into a system of coupled deterministic equations. By introducing polynomial bases in the random space and employing a Galerkin projection, one obtains a tensor product approximation of the solution fields [32]. In the context of biofluid simulations, let  $\mathbf{u}(x,t;\omega)$  represent the velocity field and  $p(x,t;\omega)$  the pressure. Defining an appropriate set of orthonormal polynomials  $\{\Phi_k(\xi)\}$  based on the joint density of  $\xi \in \mathbb{R}^m$ , one writes:

$$\mathbf{u}(x,t;\omega) \approx \sum_{k=0}^{K} \mathbf{u}_k(x,t) \,\Phi_k(\xi(\omega)), \quad p(x,t;\omega) \approx \sum_{k=0}^{K} p_k(x,t) \,\Phi_k(\xi(\omega)).$$

Substituting into the Navier-Stokes equations and taking inner products against each polynomial basis function yields a large system of coupled partial differential equations for  $\{\mathbf{u}_k, p_k\}$ . Efficient iterative solvers are typically required, given the high dimensionality that ensues. Sparse block solvers, multigrid preconditioners, or Krylov subspace methods that leverage the block structure of the system are common [33], [34]. Though the stochastic Galerkin approach can yield spectral convergence rates when inputs conform to smooth distributions, it can also be sensitive to the curse of dimensionality if many uncertain parameters are considered.

Alternatively, the stochastic collocation method focuses on sampling the random space at a set of points chosen through advanced quadrature schemes, such as Smolyak sparse grids, tensor-product grids, or quasi-Monte Carlo point sets [35]. For each sample  $\xi_i$ , one solves a deterministic Navier-Stokes problem to obtain  $\mathbf{u}(x,t;\xi_i)$ . Interpolating across these sample solutions in the random domain allows approximation of expected values and other statistical measures. This approach can be easier to implement within existing deterministic solvers, as each realization is handled through a standard code, and the results are then post-processed [36]. It also offers a non-intrusive path, meaning it requires minimal modification to the underlying flow solver, aside from a driver that handles multiple parameter sets. The downside is that the number of samples can grow significantly with dimensionality, although sparse grid techniques mitigate this issue to some extent. [37]

For even larger parameter spaces, multi-level and multi-fidelity methods have emerged, seeking to exploit coarse or reduced-order models alongside high-fidelity solvers. The multi-level Monte Carlo method, for instance, systematically reduces variance in estimates of  $\mathbb{E}[\mathbf{u}]$  by partitioning the random sample among different levels of mesh refinement, so that computational effort is optimally allocated [38], [39]. In biofluid contexts, one might use a coarse solver for approximating certain boundary condition variations while reserving expensive, fine-mesh simulations for the most critical subsets of the parameter space [40]. Reduced-order modeling techniques, such as proper orthogonal decomposition, can further compress the dimension of the system by constructing low-dimensional bases for velocity and pressure fields. Then, one can solve a smaller system of ordinary differential equations for the expansion coefficients, significantly speeding up repeated evaluations needed in uncertainty propagation. [41]

In parallel with these stochastic methods, advanced mesh generation techniques are crucial for accurately capturing the fine geometric features often found in biological domains. Vascular networks can involve intricate branching patterns, and internal organ structures may exhibit undulating surfaces that challenge standard meshing algorithms [42]. Automated mesh adaptation can be particularly helpful, adjusting local element resolution based on solution features like velocity gradients or wall shear stresses. If uncertain geometric parameters are included in the random space, dynamic meshing strategies may be needed to accommodate morphological variations [43]. Such techniques can be combined with parametric geometry descriptions, enabling a smooth mapping from the parameter space to the computational domain [44], [45].

Time discretization strategies that remain stable and accurate under random fluctuations in material properties or boundary conditions also play a role [46]. Implicit methods with adaptive time stepping can handle abrupt changes in fluid properties, while explicit methods may be more straightforward for parallelization. Balancing these design choices, one can tailor a numerical pipeline that accommodates both the fluid dynamic complexity and the computational overhead of uncertainty quantification. [47]

In many biofluid simulations, performance optimization is central to ensuring that multi-realization workflows are feasible. Domain decomposition strategies and high-performance computing platforms are typically employed to distribute the computational load [48]. Coupled with techniques like in-situ visualization or data compression, these strategies allow scientists to manage the voluminous output data that result from analyzing hundreds or thousands of parameter realizations. Ultimately, the aim is to produce robust and detailed uncertainty estimates for quantities of interest, such as flow rates through key arterial segments or pressure fields within anatomical cavities, without exceeding available computational resources. [49]

#### 4 Implementation Challenges, Validation, and Interpretive Strategies

Deploying uncertainty quantification methods for biofluid flow simulations involves numerous implementation challenges, ranging from algorithmic complexity to data validation. One critical barrier is the discrepancy between simplified models, often used in uncertainty propagation, and the actual complexity of living systems [50]. Even though advanced partial differential equations can represent fluid transport within anatomically accurate geometries, many assumptions—such as treating tissue as a purely elastic medium or blood as a continuum fluid without particulate behavior—may introduce modeling errors. Distinguishing between these model-form errors and genuine parameter uncertainties is essential for drawing valid conclusions. [51]

Another concern arises from the computational burden of high-fidelity simulations. Even with parallel computing resources, the cost of evaluating the Navier-Stokes equations for many realizations or expansions can be prohibitive [52]. Efficient load balancing and domain decomposition are crucial to make large-scale uncertainty studies viable. Practitioners often resort to surrogate models that approximate the full solver's response surface in the parameter space [53], [54]. These surrogates might employ Gaussian process regression, radial basis function interpolation, or machine learning architectures like neural networks. Once trained, the surrogate can rapidly estimate the desired quantities under new parameter configurations [55]. However, constructing accurate surrogates requires careful sampling of the parameter space, ensuring coverage of salient regions without excessive computational expense. Techniques like active learning or adaptive sampling can automate the selection of new sample points that improve surrogate fidelity. [56]

Verification and validation (V&V) procedures provide a further layer of complexity. Verification ensures that the numerical methods are implemented correctly: finite element or finite volume discretizations must converge appropriately, time integration must maintain stability, and the uncertainty propagation algorithm must reflect the intended mathematical framework [57]. Validation, on the other hand, compares simulation outputs to experimental or clinical data, establishing the reliability of the entire modeling pipeline. For biofluid flows, in vitro experiments with patient-specific phantoms or *in vivo* measurements using techniques such as Doppler ultrasound, MRI, or particle image velocimetry can serve as reference data. Matching simulation results across a range of flow conditions under varying boundary states helps confirm whether the modeled uncertainties align with observed variability [58]. These validation efforts may also guide refinement of the input distributions or intervals, revealing if initial assumptions about parameter ranges were too narrow or too broad.

Interpretation of uncertainty results poses another layer of difficulty [59]. Clinicians or biomedical researchers may require actionable insights, such as the probability of exceeding a critical shear stress threshold within certain arterial regions, or confidence intervals for flow partitioning at bifurcations. Communicating these outputs effectively demands careful visualization and summarization [60]. From an operational standpoint, one might calculate distribution functions or confidence bands for velocity profiles, or produce color-coded maps highlighting regions of high variance. The challenge is to do so in a manner that is both scientifically accurate and easily interpretable by non-specialists in computational fluid dynamics. [61]

Additionally, the choice of metrics for uncertainty quantification is not always straightforward. While global measures like mean and variance can offer an initial overview, more sophisticated indicators—such as higherorder moments, skewness, kurtosis, or tail probabilities—may be critical when extreme events have severe clinical consequences [62]. In the study of aneurysms, for instance, the potential for rupture might hinge on low-probability, high-stress events. As a result, one must look beyond expected values to evaluate the probabilities of rare but catastrophic outcomes [63]. Techniques like importance sampling or rare-event simulation can be integrated into the computational framework, further expanding the complexity of the analysis.

In certain contexts, the solution space may be subjected to constraints or additional modeling layers [64]. For fluid-structure interaction problems, one must solve coupled equations linking the displacement of the vessel wall or tissue domain to the fluid flow, resulting in random fields for both the fluid and structural variables. This coupling can magnify uncertainties, especially if material properties such as Young's modulus and Poisson's ratio are also random [65], [66]. Even if the fluid solver is robust, the structural solver might demand specialized element formulations to accommodate large deformations or near-incompressibility. Propagating uncertainty through both the fluid and structure equations requires a careful partitioning of random variables, such that correlated effects (e.g., stiffer tissue influencing velocity profiles) are accurately captured. [67]

The presence of multiple scales compounds the modeling effort. For instance, microcirculation networks involve vessel diameters ranging from centimeters down to tens of micrometers, each with its own regime of flow behavior and uncertainty [68]. In such situations, computational homogenization or multi-scale coupling strategies might be invoked to bridge from large vessels to capillary beds. Ensuring that uncertainties at smaller scales are consistently represented at larger scales, and vice versa, demands a coherent framework for multi-scale modeling under uncertainty. [69]

Summarizing these multi-faceted challenges clarifies that the successful implementation of uncertainty quantification in biofluid simulations rests on synergy between advanced numerical algorithms, high-performance computing resources, robust validation campaigns, and clear interpretive strategies. In some respects, the inherent complexity of human physiology acts as both a motivator and a barrier: it motivates the need for sophisticated tools, yet it complicates efforts to ensure models truly capture the full breadth of physiological variation [70]. Nonetheless, as computational power continues to grow and mathematical techniques become more refined, there is a growing capacity to integrate uncertainty into biofluid models at unprecedented levels of detail.

#### 5 Practical Insights and Future Perspectives

Embedding uncertainty quantification into biofluid flow simulations offers a wide spectrum of potential benefits, from refining surgical planning to enhancing the reliability of implant designs [71]. In practice, several considerations can guide the selection of appropriate methods and the interpretation of outcomes. The first is the distinction between aleatory and epistemic sources of uncertainty [72]. Aleatory uncertainty arises from inherent variability—such as fluctuations in heart rate or natural variations in vessel morphology across a population—whereas epistemic uncertainty stems from limited knowledge or incomplete data. Some frameworks unify these concepts within a single mathematical representation, but in many practical cases, it is helpful to treat them distinctly to identify which aspects of the simulation can be reduced through better experiments or improved modeling. [73]

A second consideration involves the data assimilation and parameter estimation phases that often precede uncertainty quantification. Clinical measurements, such as phase-contrast MRI data on velocity fields, can feed into an inverse problem where unknown parameters are estimated by minimizing a misfit function subject to the fluid dynamics constraints [74]. Combining such data-driven calibration with uncertainty representations transforms the inverse problem into a Bayesian framework, where one updates prior distributions to posterior distributions via a likelihood function. For example, if  $\theta$  represents uncertain geometric or material parameters, one seeks

#### $p(\boldsymbol{\theta} \mid \text{data}) \propto p(\text{data} \mid \boldsymbol{\theta}) p(\boldsymbol{\theta}),$

where  $p(\theta)$  is the prior,  $p(\text{data} | \theta)$  is the likelihood of observing the data given the parameters, and  $p(\theta | \text{data})$  is the posterior. This posterior distribution then becomes the foundation for subsequent uncertainty propagation [75]. Stochastic sampling algorithms such as Markov chain Monte Carlo or variational inference can be employed, though their application to high-dimensional PDE-constrained problems remains challenging.

Looking ahead, emerging computational hardware and algorithmic innovations promise to expand the reach of these methods [76]. Graphics processing units, tensor processing units, and heterogeneous computing architectures can significantly accelerate PDE solvers, polynomial chaos expansions, and large-scale sampling. On the algorithmic front, new dimension-reduction strategies aimed at high-dimensional uncertainty spaces continue to evolve [77]. For instance, active subspace methods identify lower-dimensional directions in parameter space along which the model output is most sensitive, thereby reducing the effective dimensionality of the problem.

Moreover, machine learning-based approaches to surrogate modeling and solution acceleration are rapidly gaining prominence [78]. Neural networks can serve as universal approximators, learning mappings from parameters to solution fields given sufficient training data. In biofluid contexts, specialized neural architectures, such as physics-informed neural networks, incorporate the Navier-Stokes equations directly into the loss function, aiming to produce solutions that are physically consistent for various parameter settings [79], [80]. While these methods are still an area of active research, they hold promise for tackling the computational bottleneck of large-scale uncertainty quantification.

On the application side, patient-specific modeling stands to gain the most from robust uncertainty frameworks [81]. By assimilating medical imaging data, laboratory measurements, and known physiological ranges, one can produce individualized simulations that provide probability distributions for key indicators such as pressure gradients, shear stress hotspots, or volumetric flow rates. These insights can help clinicians gauge the likelihood of complications, identify robust treatment strategies, or optimize device placements [82]. If integrated into clinical workflows, the ability to present uncertainties could lead to more informed medical decisions, balancing risk and potential benefits in areas like stent selection, aneurysm repair, or surgical graft design.

A parallel track of research involves addressing emergent phenomena in organs other than the cardiovascular system, such as cerebrospinal fluid dynamics in the brain or air flow in the lungs [83]. Each domain introduces unique challenges and uncertain parameters, whether it be tissue permeability in porous regions of the brain or dynamic boundary conditions in respiratory cycles. Nevertheless, the fundamental mathematical and computational principles are broadly transferable, suggesting that a unified uncertainty quantification framework could eventually address a range of biofluid problems. [84]

Collaboration between biomedical engineers, clinicians, mathematicians, and computational scientists is indispensable for making further progress. The complexity of modeling living systems under uncertainty demands multidisciplinary perspectives, combining detailed physiological knowledge with advanced numerical techniques [85]. As new imaging modalities and sensor technologies become available, the potential for high-fidelity data to inform and refine simulation models grows, potentially creating feedback loops between in silico predictions and real-world measurements. This convergence of data, modeling, and computation represents an exciting frontier in biofluid mechanics research. [86]

#### 6 Conclusion

Quantifying uncertainty in numerical simulations of biofluid flows is a multifaceted endeavor, encompassing considerations of model formulation, data acquisition, computational feasibility, and interpretive clarity. By extending beyond deterministic viewpoints, one gains access to more robust, and arguably more clinically relevant, insights into how parameters, boundary conditions, and tissue properties can vary [87]. This approach helps mitigate the risk of overconfident predictions and highlights regions or conditions where the system exhibits heightened sensitivity. As illustrated, representing unknowns through probability distributions, intervals, or fuzzy sets offers multiple avenues for capturing variability [88]. Each method—be it a polynomial chaos expansion, stochastic Galerkin technique, or sparse-grid collocation—strives to balance accuracy with computational practicality. Furthermore, advanced mesh adaptation, parallel computing, and surrogate modeling are integral to accommodating the high-dimensional nature of many biofluid problems. [89]

The inclusion of systematic verification and validation steps, combined with transparent reporting of uncertain inputs, can significantly enhance confidence in the predictions. When the framework is enriched by patient-specific data or real-time measurements, it sets the stage for powerful individualized modeling capabilities, ultimately contributing to improved clinical decision-making and device design [90], [91]. Nonetheless, numerous challenges remain. These include high computational costs, limited data for building probabilistic models, the intricacies of coupled fluid-structure interactions, and the difficulties of validating model predictions across complex physiological scenarios [92]. Future research will likely focus on refining dimensionality-reduction techniques, exploring hybrid physics-driven and data-driven approaches, and extending uncertainty quantification methodologies to encompass multi-scale phenomena that bridge molecular, cellular, and organ-level processes.

In conclusion, uncertainty quantification is not merely an additional step in computational biofluid analysis but rather an essential component for creating realistic, reliable, and interpretable models [93]. Its adoption broadens the potential for simulations to influence medical diagnostics, inform therapeutic interventions, and guide the design of new biomedical devices. As mathematical methods and computational resources continue to advance, the capacity to capture and analyze uncertainties in biofluid flows will deepen, offering a richer, more nuanced understanding of fundamental physiological processes and paving the way for transformative impacts in healthcare and biomedical research. [94]

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