Influence of Mesh Resolution on Atrial Electrophysiological Simulations

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Abstract

Computational simulations are powerful tools to investigate complex biological and physical systems, but their reliability critically depends on the spatial resolution of the underlying meshes. Choosing an appropriate resolution requires balancing the desired accuracy with the computational resources available.

In this work, the impact of mesh resolution on the evaluation of clinically relevant biomarkers in electrophysiological simulations was analyzed. As a case study, a volumetric model of the left atrium was remeshed at five spatial resolutions (0.2, 0.25, 0.3, 0.4 and 0.5 mm). Two pacing protocols were applied, and three biomarkers were measured representing main propagation and excitation properties. Richardson extrapolation was employed to approximate reference values corresponding to infinitely refined meshes, enabling the quantification of relative errors.

Results reveal that propagation-related metrics strongly depend on resolution (>20% error in coarse meshes, <5% in fine ones), while excitability and repolarization metrics are robust (<1.2% error in all cases). This approach demonstrates how convergence studies can guide mesh selection in computational modeling across a wide range of simulation-based applications.

1. Introduction

Electrophysiological simulations are a valuable tool to investigate atrial arrhythmic mechanisms. This is particularly relevant in the atria, which are anatomically complex, structurally heterogeneous, and highly sensitive to modelling assumptions. However, the choice of spatial resolution remains a critical challenge, as it directly affects the trade-off between numerical accuracy and computational performance. Grid convergence analysis provides a systematic approach to determine a resolution that ensures robust results without incurring unnecessary computational cost [1].

To achieve reliable simulations, it is necessary to establish the required level of anatomical and numerical detail for each specific application. The required spatial resolution for atrial simulations may vary depending on multiple factors, such as the biomarkers to be measured, the conduction velocity of the tissue, the type of signal being simulated, or the specific conditions of the protocol. In this context, an appropriate balance must be struck between model complexity and efficiency, avoiding the risks of oversimplification on one side and excessive resolution on the other [1].

The aim of this study is to evaluate the influence of mesh resolution when measured three electrophysiological biomarkers under two stimulation protocols. To this end, a patient-specific left atrial (LA) model was simulated at five resolutions, and Richardson extrapolation was used to quantify the relative errors.

2. Methods

2.1. Model Construction

Endocardial and epicardial left atrial surfaces were segmented from the CT scan of a patient referred for persistent atrial fibrillation (AF), within a prospective study conducted at the Hospital Universitario Puerta del Mar (Cádiz, Spain).

Following the methodology of the mesh convergence study in [2], five volumetric tetrahedral meshes were generated with edge lengths ranging from 0.5 mm to 0.2 mm, using a constant refinement ratio of 1.25 between successive meshes. The resulting meshes ranged from approximately 180k to over 2 million elements, from coarse to highly refined meshes. Finer resolutions could not be explored due to computational constraints. Table 1 summarizes the mean and standard deviation of edge lengths (in mm), as well as the number of vertices and tetrahedra for each mesh.

Table 1. Main characteristics of the atrial meshes.

Mesh	Mean (mm)	Std (mm)	Num. vertex	Num. tetra.
h1	0.2058	0.0291	2.128.809	12.929.411
h2	0.2493	0.0377	1.164.662	7.011.863
h3	0.3368	0.0449	534.631	3.027.247
h4	0.3931	0.0377	356.847	1.880.299
h5	0.4988	0.0540	183.080	911.834

2.2. Stimulation Configuration

Simulations were performed using a GPU-based biophysical solver with a fixed time step of 0.01 ms [3]. The Koivumäki atrial cellular model [4] was implemented with 100% electrical remodeling, corresponding to a chronic AF phenotype, this included the modifications indicated on [5]. The stimulation protocol consisted in three stimuli for sinus rhythm (SR) applied at a basic cycle length of 700 ms, reproducing the patient's clinical rhythm. Followed by a triple extra-stimulus protocol (3-Extra), which consisted of pacing intervals close to the effective atrial refractory period [6]. These three premature stimuli were delivered at progressively shorter coupling intervals, in the specific case of this patient they were 260, 240, and 230 ms.

Stimulation locations are shown in Figure 1 (up). SR pacing was applied over the Bachmann bundle (blue dot), while the 3-Extra protocol was delivered close to the left atrial appendage (orange dot). The total pacing sequence lasted 2130 ms, but simulations were extended to 3500 ms to ensure that no spurious reentrant activity or rotors persisted after stimulation. Figure 1 (middle) illustrates an example of a simulated action potential signal over the first 2.5 s, with SR stimulation (blue) and the 3-Extra protocol (orange) highlighted. For the analysis, the second SR stimulus and the third 3-Extra stimulus were selected, as these segments allowed complete repolarization and avoided overlap between protocols. These segments were used to calculate the biomarkers for the convergence study. An example is shown in Figure 1 (down), where the Local Activation Time (LAT) maps are represented for each selection.

2.3. Biomarkers and Extrapolation

From each simulation, three electrophysiological biomarkers were extracted to allow comparison across mesh resolutions. As a propagation metric, LAT98 was computed, defined as the local activation time at the 98th percentile. The upper 2% LATs were not considered to avoid artifacts on the measure. Excitability was assessed using the mean APA (action potential amplitude), calculated as the difference between the maximum transmembrane voltage during the action potential and the resting membrane potential (RMP). Finally, as a stimulus-related metric, APD90 was selected, representing the duration of the action potential measured at 90% repolarization. APA and APD90 were measured for each simulation node and then averaged.

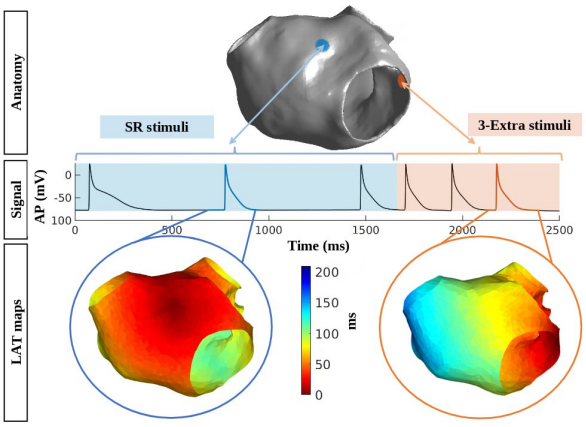

Figure 1. (Up) anatomical structure of LA with locations of stimulation marked, blue for SR and orange for 3-Extra. (Middle) example of AP signal, with blue highlight on SR stimuli and orange on 3-Extra. (Down) LAT maps for the SR and 3-Extra selected segments.

Convergence analysis was performed using Richardson extrapolation, following the methodology described in [7]. This approach requires the analysis of three meshes with a constant grid refinement ratio r>1.1. For this study, r=1.25 was selected to achieve resolutions comparable to those used in previous works. Given the five available mesh generated, three mesh subgroups were defined: fine (h1–h3), medium (h2–h4) and coarse (h3–h5). For each group of three consecutive meshes, the simplified Richardson formulation [7] was applied to calculate the order of convergence (p), the extrapolated value (f_extrap), the convergence ratio (R), and the Grid Convergence Index (GCI). The extrapolation obtained from the fine subgroup (h1–h3) was considered the most accurate approximation to the theoretical infinitely fine mesh, and was therefore used as the reference value for calculating relative errors.

3. Results

For each of the three biomarkers, convergence plots were obtained across the five mesh resolutions simulated. In the convergence graphs shown in Figure 2 the x-axis represents the mesh resolution, with the coarsest discretization (0.5 mm) on the right and the finest simulated resolution (0.2 mm) on the left. Each of the five dots corresponds to the value of the biomarker measured from the simulation at the given resolution.

Following the procedure described in Section 2.3, the

meshes were grouped into three subsets to apply Richardson extrapolation. The yellow markers represent the value of the biomarker measured at the simulations performed in the three coarsest meshes, with the extrapolated value as a yellow dashed line. Similarly, the medium-resolution subset is shown in red, with its extrapolated value as a red dashed line, and the fine subset in blue, with the extrapolated value shown as a blue dashed line. The fine-subset extrapolation was taken as the reference, representing the closest estimation in the limit of an infinitely refined mesh.

Relative errors were then computed by comparing the biomarker values obtained from each mesh with respect to this fine extrapolated reference. These errors quantify the accuracy achieved at each resolution and allow assessing the impact of mesh refinement on the reliability of the simulations. Results for each pacing protocol will be explained separatelly.

3.1. Results for Sinus Rhythm Protocol

Left column of Figure 2, shows the convergence plots for the three biomarkers analyzed under the SR protocol. For LAT98, relative errors clearly decrease with mesh refinement. The fine extrapolation value was 83.83 ms, which was taken as the reference to compute relative errors. Comparing this value with the measurements obtained at each mesh resolution allows to calculate relative errors. The coarsest mesh (0.5 mm) yielded a LAT98 of 101.76 ms, that comparing with the extrapolation corresponds to a relative error of 21.38%, while the finest mesh (0.2 mm) provided a value of 88 ms, leading to a relative error of 4.97%. For APA, a similar trend was observed, although in this case all measured values ranged between 102.88 and 104.02 mV, while the fine extrapolation was 104.06 mV. Relative errors were already minimal across all mesh resolutions, never exceeding 1.2%. Finally, for APD90, measured values ranged from 89.33 to 89.67 ms, compared with a fine extrapolation of 89.85 ms, resulting in relative errors consistently below 0.6%. Although the convergence plot displays some oscillatory behavior, the differences are negligible, and the metric can be considered converged.

3.2. Results for 3-Extra Protocol

Similarly to the observations in Section 3.1, the right column of Figure 2 presents the convergence plots for the three biomarkers measured under the 3-Extra protocol. For LAT98, the difference between the measured values and the fine extrapolated reference (132.17 ms) decreases as the mesh resolution is refined, with measured values ranging from 152 ms for the coarsest mesh to 132 ms for the finest, yielding relative errors of 15% and nearly 0%, respectively. For mean APA, the extrapolated reference was 98.15 mV, while measured values ranged from 97.13 mV to 98.15 mV, with all relative errors remaining below 1.2%. Finally, for APD90, the fine extrapolation was 89.55 ms, with measured values spanning from 90.27 ms to 89.58 ms, resulting in relative errors consistently below 1%

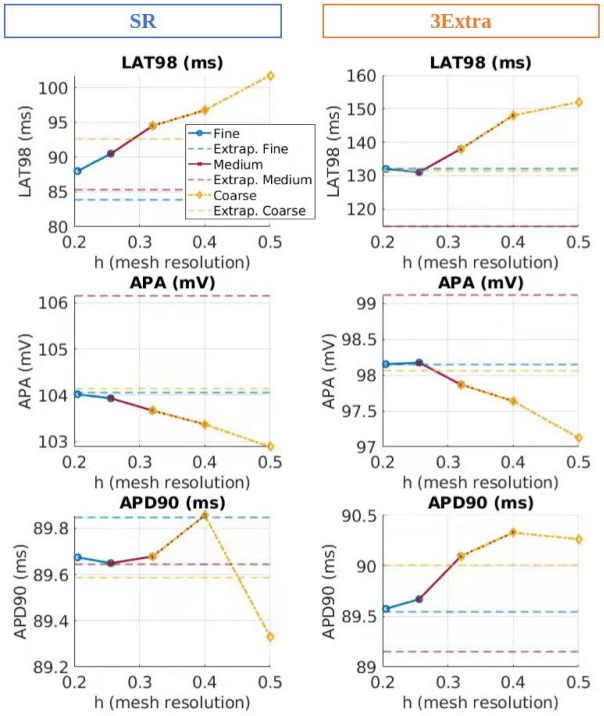

Figure 2. Convergence graphs for SR (left column) and 3-Extra (right column) simulations for each of the three biomarkers measured.

3.3. Relative Errors Summary

Table 2 shows the relative errors calculated for each biomarker measured across all simulated mesh resolutions: the white rows corresponds to the SR protocol, and the gray rows to the 3-Extra protocol. In both cases, a similar pattern is observed: the propagation metric (LAT98) exhibits the highest relative errors, which decrease progressively as the mesh resolution increases. In contrast, the other two metrics (mean APA and APD90) show consistently low errors, remaining below 1.2% across all resolutions, indicating little dependence to mesh refinement.

These measurements provide a practical tool to guide simulation design. For instance, when using the 3-Extra protocol, for propagation metrics such as LAT98 with a target error of approximately 10%, Table 2 indicates that a mesh resolution between 0.3 and 0.4 mm is sufficient to achieve the desired precision.

Table 2. Relative error (%) for each biomarker measured across different mesh resolutions (mm) during SR and 3-Extra stimulation.

	h1 (0.20)	h2 (0.25)	h3 (0.30)	h4 (0.40)	h5 (0.50)
LAT98 (SR)	4.97	7.95	12.72	15.42	21.38
LAT98 (3Extra)	0.13	0.88	4.41	11.98	15.00
APA (SR)	0.04	0.12	0.38	0.66	1.13
APA (3Extra)	0.00	0.02	0.29	0.52	1.05
APD90 (SR)	0.19	0.22	0.19	0.01	0.57
APD90 (3Extra)	0.03	0.14	0.61	0.87	0.80

3.4. Computational Cost Summary

Finally, to assess the computational cost, the simulation time and memory requirements were measured for 3.5 s of simulated activity on each mesh resolution with a sampling frequency of 2 kHz. Simulation time increased substantially with mesh refinement: the finest mesh required approximately 7 hours, whereas the coarsest mesh completed in about 30 minutes. Memory requirements showed even more pronounced differences. The simulation with the finest mesh demanded nearly 120 GB of memory, while all other simulations required less than 40 GB.

4. Discussion and Conclusion

This study aims to determine a mesh resolution that ensures reliable results while minimizing computational cost in terms of time and memory. To this end, three biomarkers were measured across five simulations performed with meshes of different spatial resolutions. The analysis shows that propagation metrics, such as LAT98, display a stronger dependence on mesh resolution, whereas APA and APD90 remain largely independent of the mesh used. This finding confirms that propagation is highly sensitive to spatial resolution, as the conduction of an electrical stimulus depends directly on the spatial arrangement of the nodes and numerical errors accumulate as the activation wavefront advances. In contrast, excitability metrics and stimulus related metrics are determined by local cellular dynamics and therefore show a much more robust behavior against spatial discretization.

The main limitations of this study are the use of a single LA model from one patient, the inability to simulate resolutions below 0.2 mm due to the high computational cost, the fact that arrhythmic conditions were not simulated and no fibrotic tissue were included. In addition, convergence studies should ideally be performed for each specific condition and biomarker, as the sensitivity to mesh resolution may vary.

In conclusion, mesh convergence studies provide a systematic approach to determine the appropriate spatial resolution for a given simulation, allowing informed decisions that balance accuracy with computational cost. This work offers a guidance for configuring future computational simulations, ensuring reliable results while optimizing resources.

Acknowledgments

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