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On the knotty effect of a single parameter on cardiac muscle simulations

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Cardiac tissue organ-on-a-chip [1] are appealing tools for investigations on drug safety and efficacy. Particularly, stem-cell derived tissues recapitulate many patient-specific features typical of the *in-vivo* conditions, thus improving the assay personalization.

In-silico replicas of these *in-vitro* cardiac models [2] may provide insights on the drug design but the computational effort, due to the finite element discretization [3], limits their utility.

To overcome this issue, isogeometric analysis has been employed in simulations of *in-vivo* tissues [4] and consequently it seems an effective technique also for the analysis of stem-cell derived tissue. Despite the premise, the reduced tissue conductivity shifts the effort from the computation of the diffusive term of the monodomain equation to the reactive part, limiting the advantages provided by isogeometric analysis with respect to standard finite elements. Moreover, the accuracy on the ion concentrations slightly decrease as the spline order is elevated, leading to unexpected considerations in the choice of the basis functions.

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