Keratoconus Growth Model: : A 10-Year Case Study

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Abstract:
Keratoconus (KC) is a bilateral disease characterized by asymmetrical steepening and thinning of the cornea, caused by a loss of its mechanical properties. A model capable of reproducing KC progression could be crucial for predicting disease's evolution. In this work, we apply a previously developed KC growth model [1] to evaluate its accuracy against patient-specific data.
Topographical data from a 10-year follow-up of a keratoconic patient were retrieved. A patient-specific finite element corneal model was constructed. An intraocular pressure of 15 mmHg was applied to the posterior surface and the corneal base was fixed. A heterogeneous HGO material model was used.
To model the growth a multiplicative decomposition of the deformation gradient F into a growth component F_g and an elastic component F_e was performed: $F = F_e·F_g$.
To initiate the growth process, the material properties of a localized pathological area progressively degraded over time until reaching 50% of their initial value both in the corneal thickness and radial direction. When strains increase locally, the growth process begins and Fg is updated according to the law:

$$F_g^{(t+1)} = F_g^t + K^+ \left(\frac{F_{g \max} - F_g^t}{F_{g \max} - 1} \right)^\gamma \cdot dt$$

where $F_{g max}=1.1$ is a growth limit introduced to avoid unlimited growth, constants $K^+=0.5$ and $γ=1$ module the growth velocity and dt is the time increment. Model's parameters were adjusted to properly reproduce the disease's progression with respect to clinical data.
The KC progression simulated by the model was compared with patient's disease progression in terms of pachymetric thinning (i.e. thickness thinning throughout time). A mean error of 0.3% and a maximum error of 1.1% were obtained with respect to clinical data. In the corneal model at the end of the simulated 10 years, a small bulge is visible, replicating the pathological cornea. The proposed formulation is capable of capturing disease's evolution.

[1] Fantaci et al, Comput Biol Med, 180, 2024