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AGENT-BASED FUNCTIONAL 3-DIMENSIONAL BLADDER MODEL: INITIAL APPROACH

Aims of Study

Agent-based models have been used to understand systems consisting of distributed elements, such as the national electrical grid and the internet [1,2]. To the best of our knowledge, agent-based models have not yet been used to model biological systems. The goal of this project was to develop a functional 3-dimensional bladder model using an agent-based modeling approach.

Methods

In agent-based modeling, each agent represents an elemental unit, in this case a small piece of bladder tissue or a drop of urine. Agents are given characteristics and rules and then operate to follow them. Two types of agents were used to represent voiding, one defining the bladder wall and the other defining urine. The bladder was defined as a solid with the ability to contract during voiding according to basic properties of contracting smooth muscle [3]. The urine agents, characterizing a fluid, were used to fill the bladder prior to the start of voiding using a raster method.
The bladder shape was obtained from a high resolution pelvic floor magnetic resonance image (MRI) performed on an asymptomatic nulliparous 23 y/o female. The scan had 107 slices obtained by 2 series of T_2–weighted axial images with a slice thickness of 3.0mm (General Electric 1.5 Tesla magnet). The slices from both series were interleaved to obtain a slice gap of 1.5mm. The digitized scans were imported into MIMCS (Materialise) and the bladder was manually segmented. A polygonal 3-D model was created (CTM, Materialise) and imported to Geomagics (Raindrops) for polygon reduction and surface smoothing. A hole the size of the urethra (diameter 13.6mm) was also defined and exported to the agent-based model, to allow an exit for urine during voiding.
The density of points needed in the agent-based program was investigated by exporting several different bladder models with 4,000 - 400,000 uniformly distributed points. Each point in the bladder model was used to form a bladder agent in the agent-based model. The greater the number of agents, the greater the accuracy of the agent-based model and the greater the computation time needed. Therefore, a sensitivity analysis was performed to determine which bladder model provided the greatest accuracy (as measured by the fewest number of urine leaks outside the urethra).

Results

With increasing number of points there were fewer leaks (Figures 1 and 2) and most of the urine exited via the urethra. The bladder model with the fewest points, 4,350, leaked 91.42% of the urine agents outside the urethra. Bladder models with more than 11,680 points, leaked less than 1% of the urine agents (Figure 3), although there were some fluctuations. The bladder model with 17,155 points seemed to be optimal since it had a low percent of leakage with relatively few points, requiring few computer calculations.

A. B.

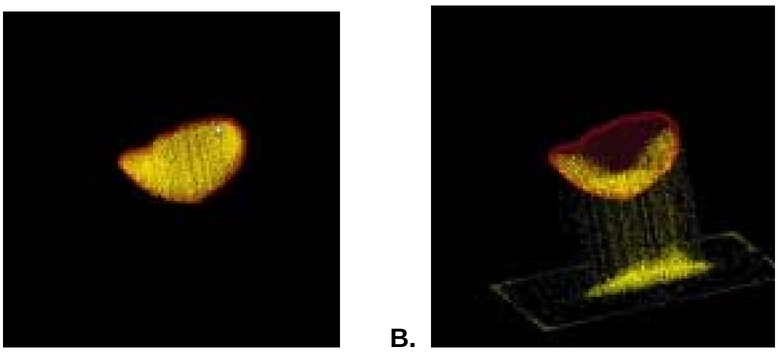
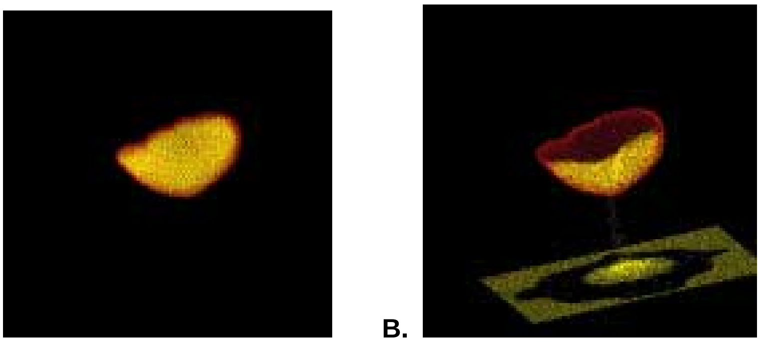


Figure 1: A. Agent model with 4,350 points before emptying. **B.** Agent model 50% empty and with 91.42% leakage of agents. Note that the exit hole (urethra) is not visible since this is an anterior view and it is on the posterior side of the bladder.



A. B.

Figure 2: A. Agent based model with 17,155 points before emptying. **B.** Agent model 50% empty and with 0.79% leakage of points.

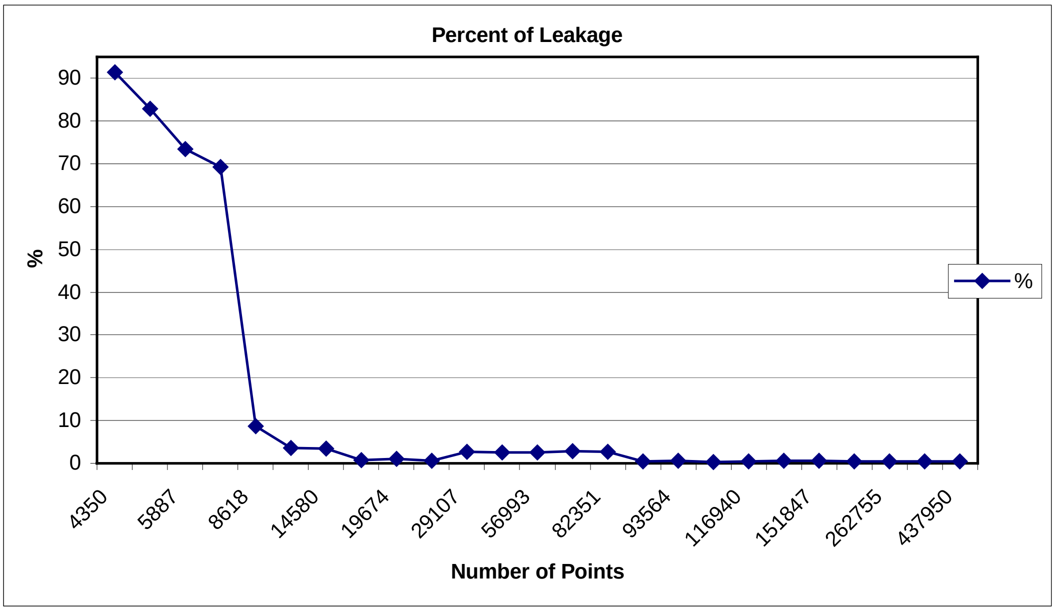


Figure 3: Percentage of leakage of urine agents as a function of number of bladder agents in model.

Conclusions

The agent-based bladder model was able to void through the urethra with a reasonable number of bladder agents. Future models will improve the accuracy and biomechanical representation of the voiding bladder, as well as include pathological properties.

The urethra in our model came from an MRI scan during continence. In contrast, during voiding, the urethral diameter is 2.3 mm-5mm [4], smaller than the urethra modeled here. Future models will include a hole the size of the urethral lumen during voiding.

As far as we know, this project represents the first attempt to use agent-based modeling in biology. This modeling technique has potential for creating functional models of a variety of organs and tissues and could improve our understanding of human physiology.

Works Cited

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