In-Situ Visualization for 3D Agent-Based Vocal Fold Inflammation and Repair Simulation

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Overview

• Problem:
  • Voice is one of our main forms of communication
  • Voice disorders afflict 1/13 Americans annually

• Overall Goal:
  • Development of a scalable computational model to simulate and visualize the vocal fold inflammation and healing processes at the cellular level.

• Main Contributions:
  • Novel scalable and efficient Agent-Based Modeling procedures to simulate the vocal fold at the cellular level on heterogeneous platforms.
  • Adaptive visualization techniques so as to enable in-situ visualization at almost no cost.
Outline

• **Introduction** – Vocal Fold Inflammation and Repair
• **Introduction** – Agent-Based Modeling (ABM)
• **Methods** – Simulation and Visualization Scheduling
• **Methods** – Visualized Data Reduction
• **Results**
• **Conclusion**
• **Future Work**
Outline

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Introduction – Vocal Fold Inflammation and Repair

- **Biomechanical Stress**
  - Force applied on tissue. Talking, shouting etc.

- **Mucosal Damage**
  - Damage in the “skin” layer of the vocal fold

- **Cell Recruitment**
  - Attracting cells such as platelets, neutrophils, and macrophages to the wound site

- **Cells Function**
  - Each cell performs its duty. One or more of the following:
    - Secrete chemical (IL-1, MMP-8 etc.) to attract, excite or inhibit other cells
    - Deposit ECM protein (collagen, elastin etc.) to heal damaged tissue
    - Clean up cell debris
Introduction – Vocal Fold Inflammation and Repair

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Image from: https://wiki.uiowa.edu/download/attachments/39001206/nodules%20op%205.png?api=v2
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Response to voice therapy treatments
- Voice rest
- Resonant voice
- Spontaneous speech
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What is Agent-based Modeling (ABM)?

- Powerful, widely-used approach to quantitatively simulate a system defined by a set of autonomous agents that operate and interact in discrete time steps.
Why use Agent-based Modeling (ABM)?

• Ability to capture complex interactions and multi-directional causality at the microscale level

• Has been successfully used in many domains such as biology, ecology, social sciences, economics, network theory, and business.

• Allows us to incorporate our current understanding of cellular processes that take place during inflammation and healing of damaged tissues.

• Has been partially validated on a small scale using empirical data related to vocal fold inflammation.
How is Agent-based Modeling (ABM) used?

- **Tissue area of interest** (ABMs term: World)
- **Slices of tissue** (ABMs term: Patches)
- **Components of tissue (ECM)** such as Collagen, Elastin, Hyaluronic Acid
- **Chemical Levels** (ABMs term: Patches Attributes)
How is Agent-based Modeling (ABM) used?

- Fibroblast (Cell) (ABMs term: Agents)
- Neutrophil (Cell) (ABMs term: Agents)
- Macrophage (Cell) (ABMs term: Agents)
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How is Agent-based Modeling (ABM) used?

Cytokine Secretion
How is Agent-based Modeling (ABM) used?

Cytokine Diffusion
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Methods – Simulation and Visualization Scheduling
Methods – Simulation and Visualization Scheduling

- seedCells()
- cellFunction()
- ECMFunction()
- ECMFragment()
- ABM_prep_and_transfer_data()
- DiffuseChem_0()
- DiffuseChem_1()
- DiffuseChem_n()
- ABM_kernel_0()
- ABM_kernel_1()
- ABM_kernel_n()

Program states for next iteration

$N_{GPU} = 1$
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## Problem Scale

<table>
<thead>
<tr>
<th>Item</th>
<th>Unit</th>
<th>Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>World</td>
<td>patches x patches</td>
<td>1390 x 1006 x 110</td>
</tr>
<tr>
<td>Patch Dimension</td>
<td>μm x μm x μm</td>
<td>15 x 15 x 15</td>
</tr>
<tr>
<td>Total Number of Patches</td>
<td>unit</td>
<td>154 million</td>
</tr>
<tr>
<td>ECM Data</td>
<td>types data points</td>
<td>3 461 millions</td>
</tr>
<tr>
<td>Chemical Data</td>
<td>types data points</td>
<td>8 1.2 billions</td>
</tr>
<tr>
<td>Simulated Area</td>
<td>mm x mm x mm</td>
<td>20.85 x 15.09 x 1.65</td>
</tr>
<tr>
<td>Simulated Time Step</td>
<td>minutes</td>
<td>30</td>
</tr>
</tbody>
</table>

**Initial number of**

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td>Neutrophils</td>
<td>cells</td>
<td>1.72 millions</td>
</tr>
<tr>
<td>Macrophages</td>
<td>cells</td>
<td>0.97 millions</td>
</tr>
<tr>
<td>Fibroblasts</td>
<td>cells</td>
<td>12.20 millions</td>
</tr>
</tbody>
</table>
Methods – Visualized Data Reduction

• Constant Sampling
Methods – Visualized Data Reduction

• Adaptive Sampling
  • Lower resolution in low-activity areas
  • Enhance resolution in high-activity areas
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Results

Execution Time Per Iteration
(30-minute Tick)

- Executed on GPU
- Executed on CPU

<table>
<thead>
<tr>
<th>GPU 0</th>
<th>GPU 1</th>
<th>CPUs 0 - 27</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Diffusion</td>
<td>Visualization</td>
<td>Cell</td>
</tr>
</tbody>
</table>

- $t(s)$
- 6.2 seconds/iteration
In Situ Visualization – VirtualGL and TurboVNC
Macrophages
Neutrophils
Fibroblasts

TNF

Aggregated Stats

Initial Damage (patches): 25%
Current Damage (patches): 36%
Percent Healed (%): 39.0

Chemical Concentration
0.00
0.25
0.50
0.75
1.00

Damages
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Conclusion

• **Adaptive sampling** scheme for data reduction with no compromise on resolution

• **CPU-GPUs task scheduling** technique to mask visualization cost

• **In situ VF ABM simulation suite** capable of:
  • Processing 17 million biological cells
  • Processing 1.2 billion chemical data points
  • Collecting and display aggregated stats

  in **real-time** (under 7 seconds per 30-minute iteration).
Future Work

• Better cell migration visualization using volume rendering
• Iso-surface for cytokine gradient visualization
• ECM visualization
• Activity-level-aware data reduction
Questions?