



Mapping Biomedical Applications onto GPU Platforms

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Fluid-Structure Interactions

- Collaboration between GWU (Balaras), UMD (Solares, Wu), and University of Chicago (Dubey).
- Goal: Development of high performance algorithms applicable to fluid-structure interactions in viscous incompressible flows.
- Example application: interactions between the red blood cells and plasma
- Critical Components: Poisson equation solver combined with a multigrid algorithm. Multi-dimensional FFTs and several types of matrix computations

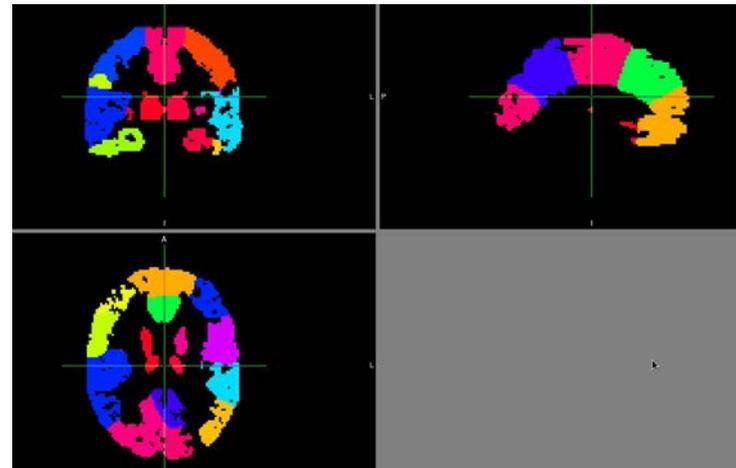
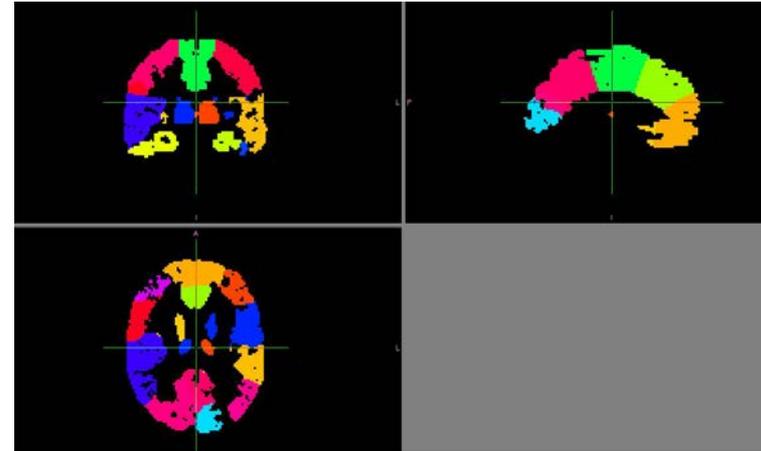
Data-Driven Understanding of Brain Disorders



- Collaboration between the University of Maryland (Varshney and JaJa) and the University of Maryland at Baltimore (Gullapalli, Herskovits, etc.)
- Understanding of brain connectivity differences between subjects with brain disorders and normal subjects using diffusion MRI.
- Dynamics of functional brain connectivity using resting state fMRI, for subjects with moderate TBI.

Connectivity Matrix

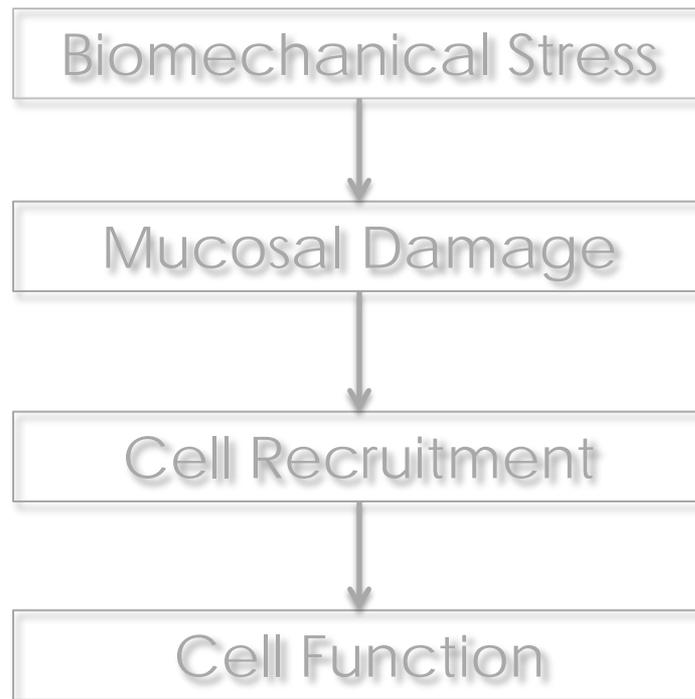
- Diffusion MRI images with 64 diffusion frames with resolution $128 \times 128 \times 52$.
- Probabilistic Tractography
- Number of entries in the sparse connectivity matrix: 100,000,000-200,000,000.
- Number of voxels in ROI: 100,000-200,000.



Inflammatory Responses and Wound Healing in Vocal Fold

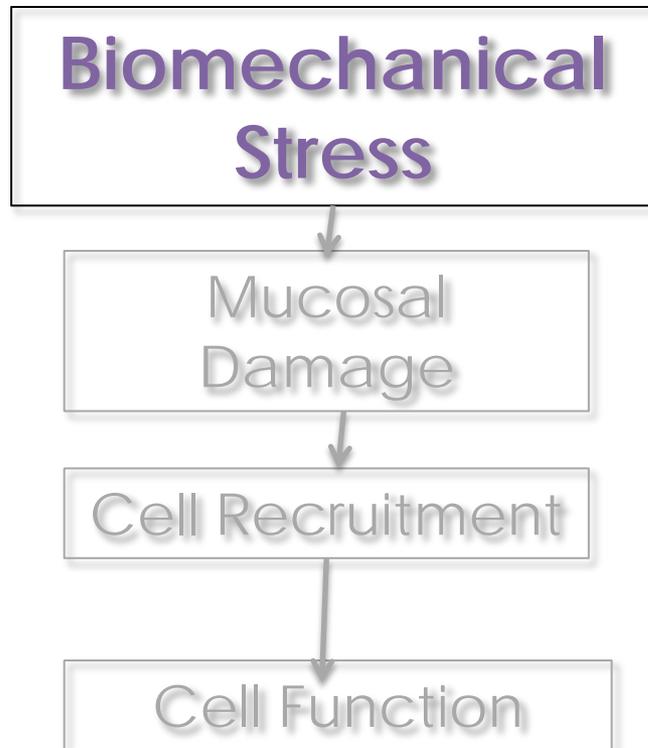
N. Seekhao

Collaborators: N. Li, C. Shung, L. Mongeau
(McGill U.)





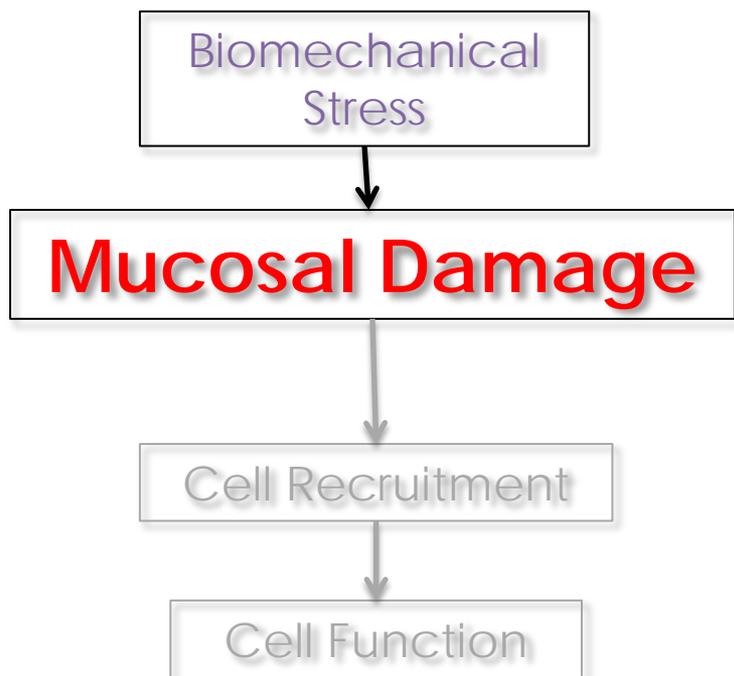
Inflammatory Responses & Wound Healing in Vocal Fold



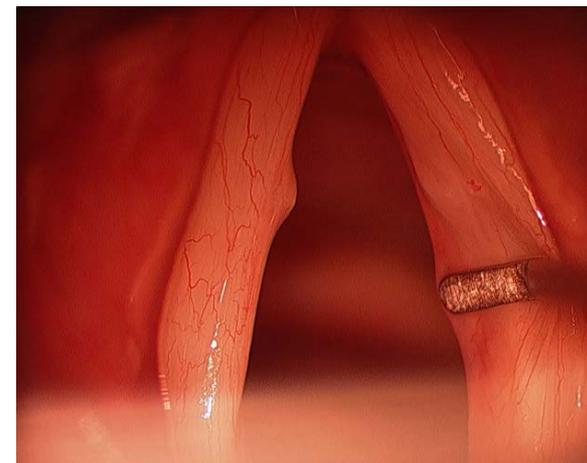
Force applied on tissue. Talking, shouting etc.



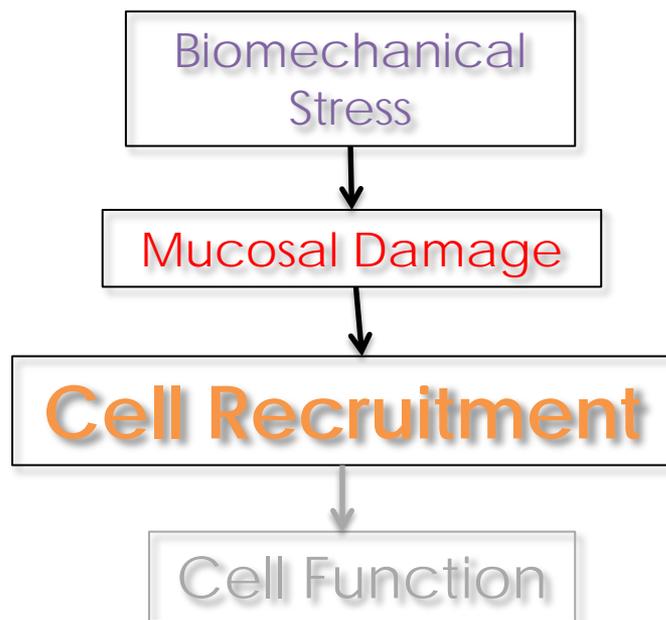
Inflammatory Responses & Wound Healing in Vocal Fold



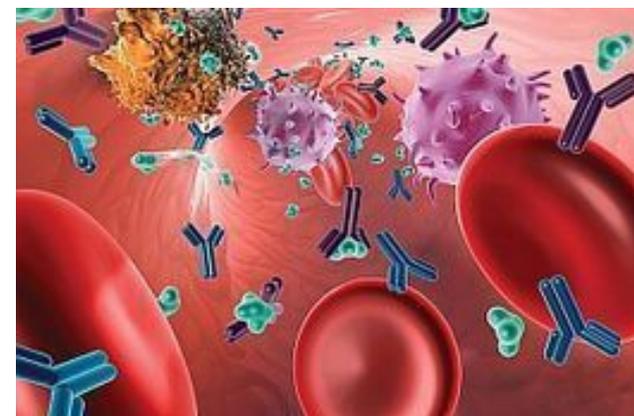
Damage in the tissue of the vocal fold



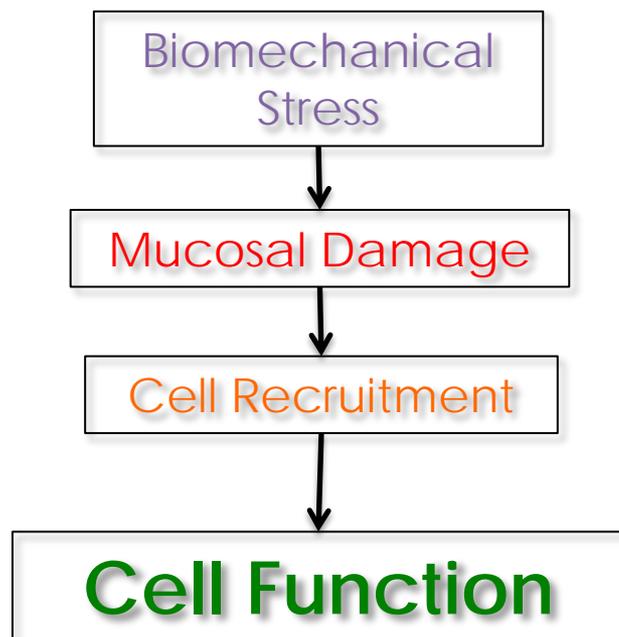
Inflammatory Responses & Wound Healing in Vocal Fold



Attracting cells such as platelets, neutrophils, and macrophages to the wound site



Inflammatory Responses & Wound Healing in Vocal Fold



Each cell perform 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



Agent-Based Modeling (ABM)



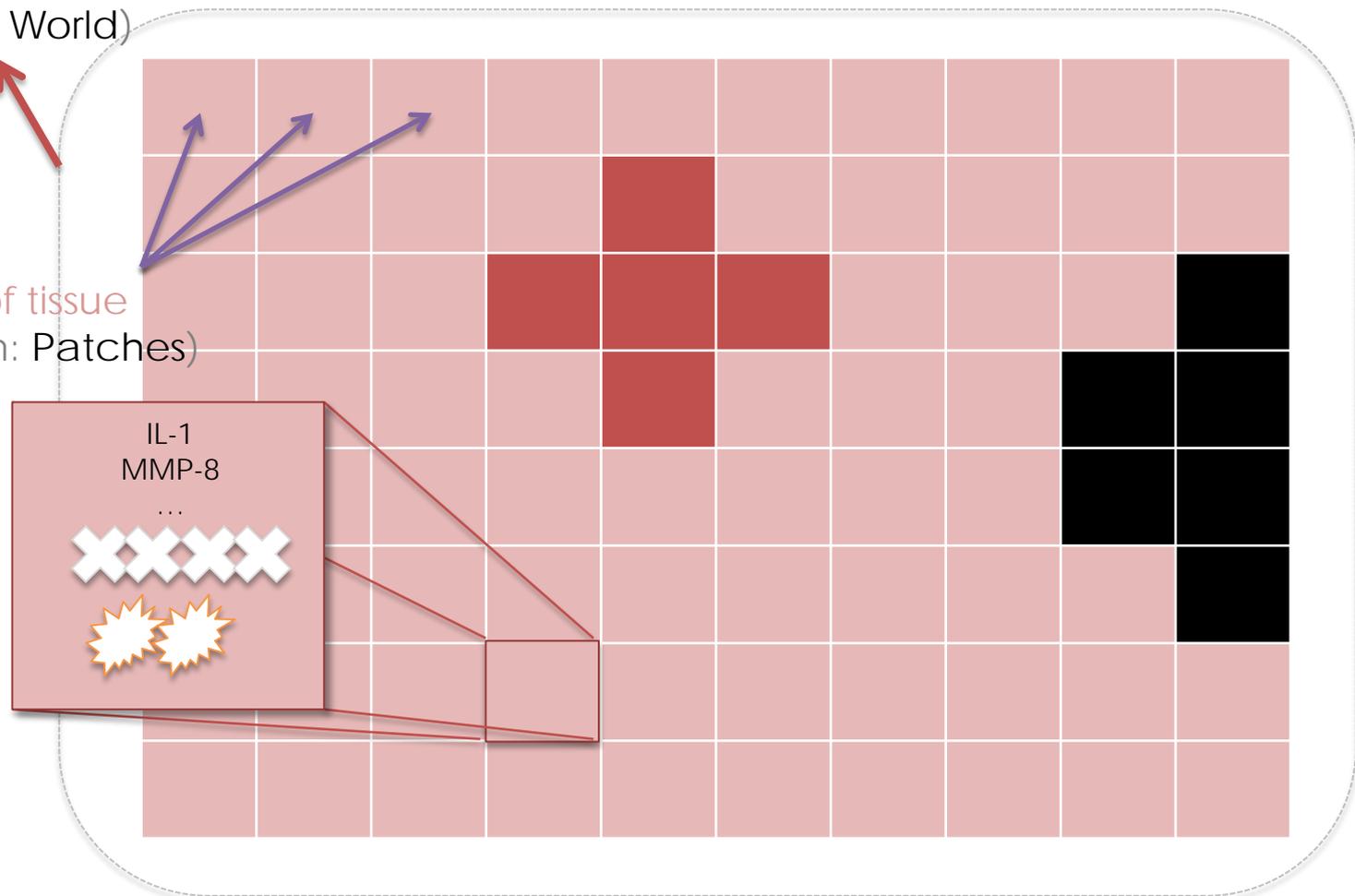
1. Bottom-up, rule-based, discrete-event and discrete-time computational model
 2. Initial "World" and a collection of "agents."
 3. Interactions between agents and the world.
 - Agents migrate to area of injury
 - Remove dead cells and tissue debris
 - Remodel ECM to heal damaged tissue
 4. Stochastic moves
 5. Emergent behavior
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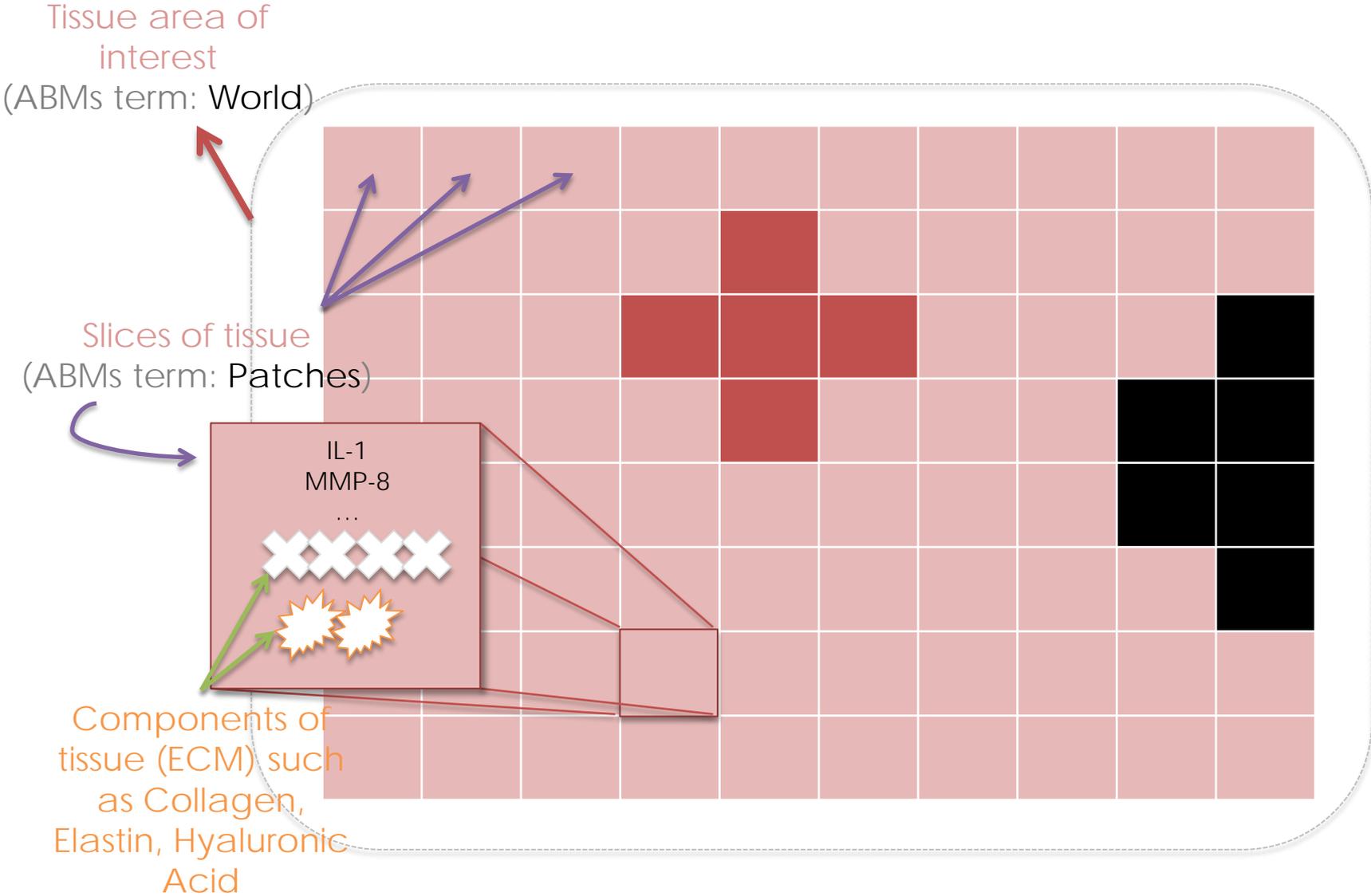
ABMs of Vocal Fold Wound Healing Process

Tissue area of interest
(ABMs term: World)

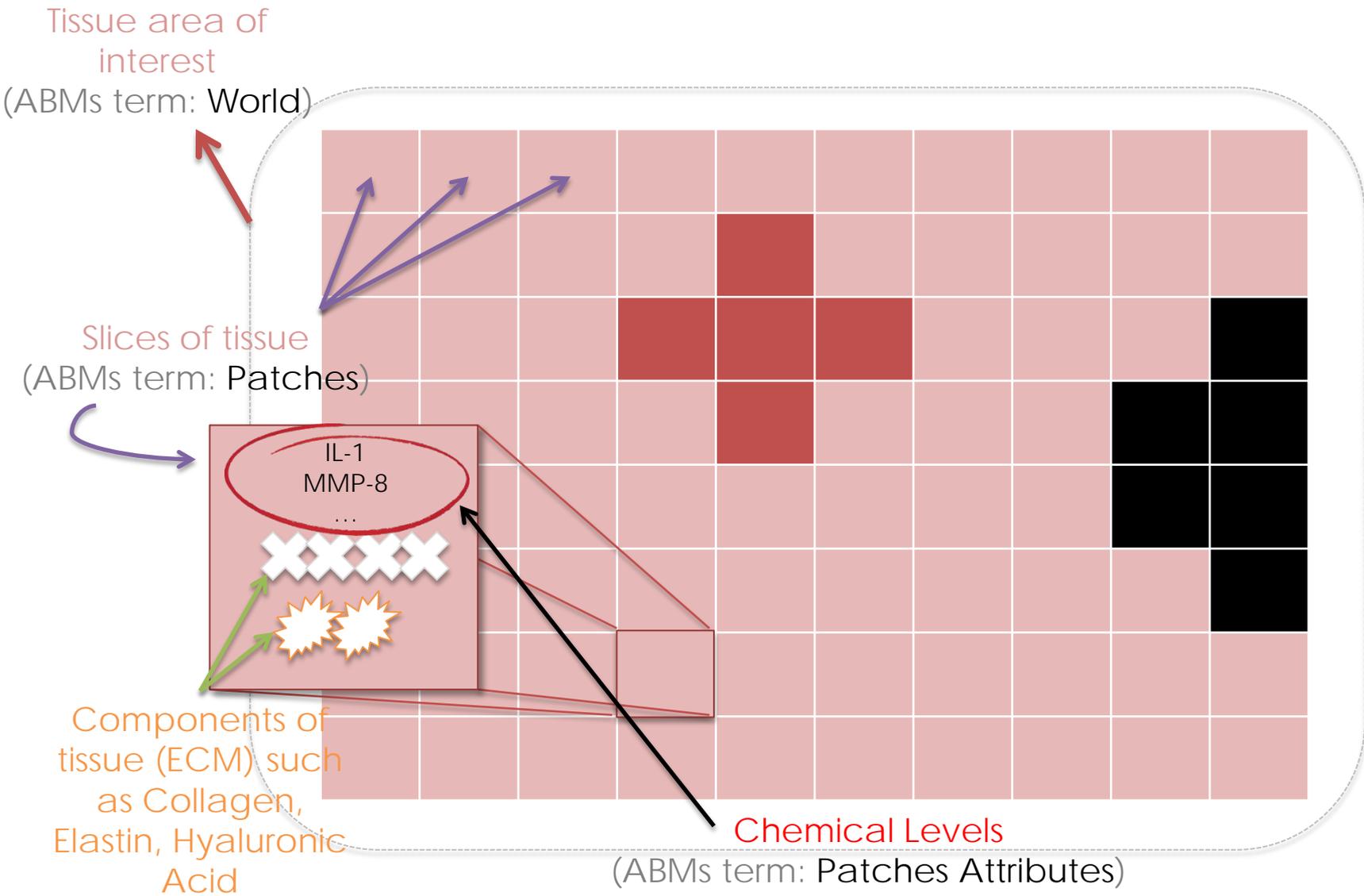
Slices of tissue
(ABMs term: Patches)



ABMs of Vocal Fold Wound Healing Process

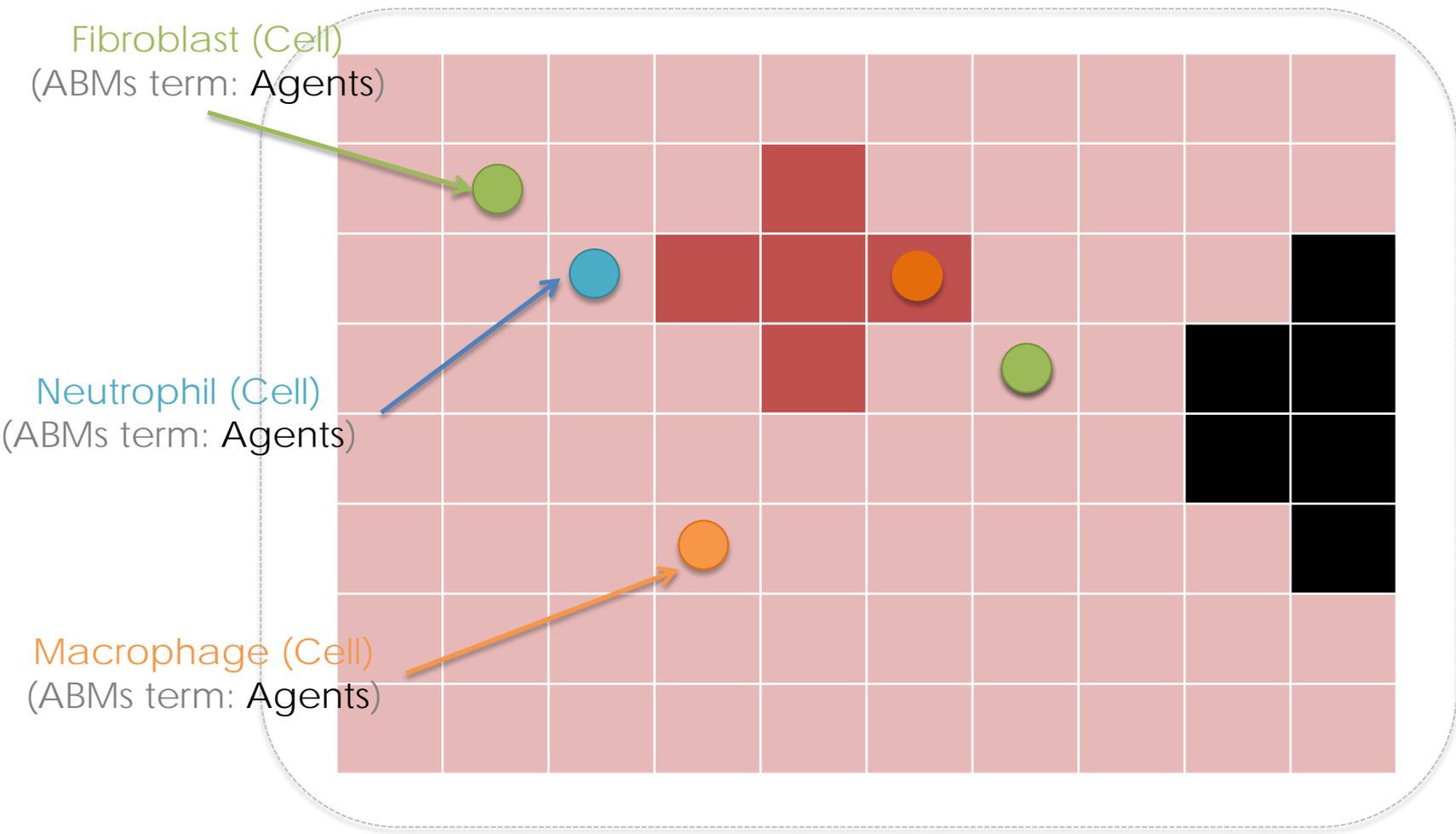


ABMs of Vocal Fold Wound Healing Process



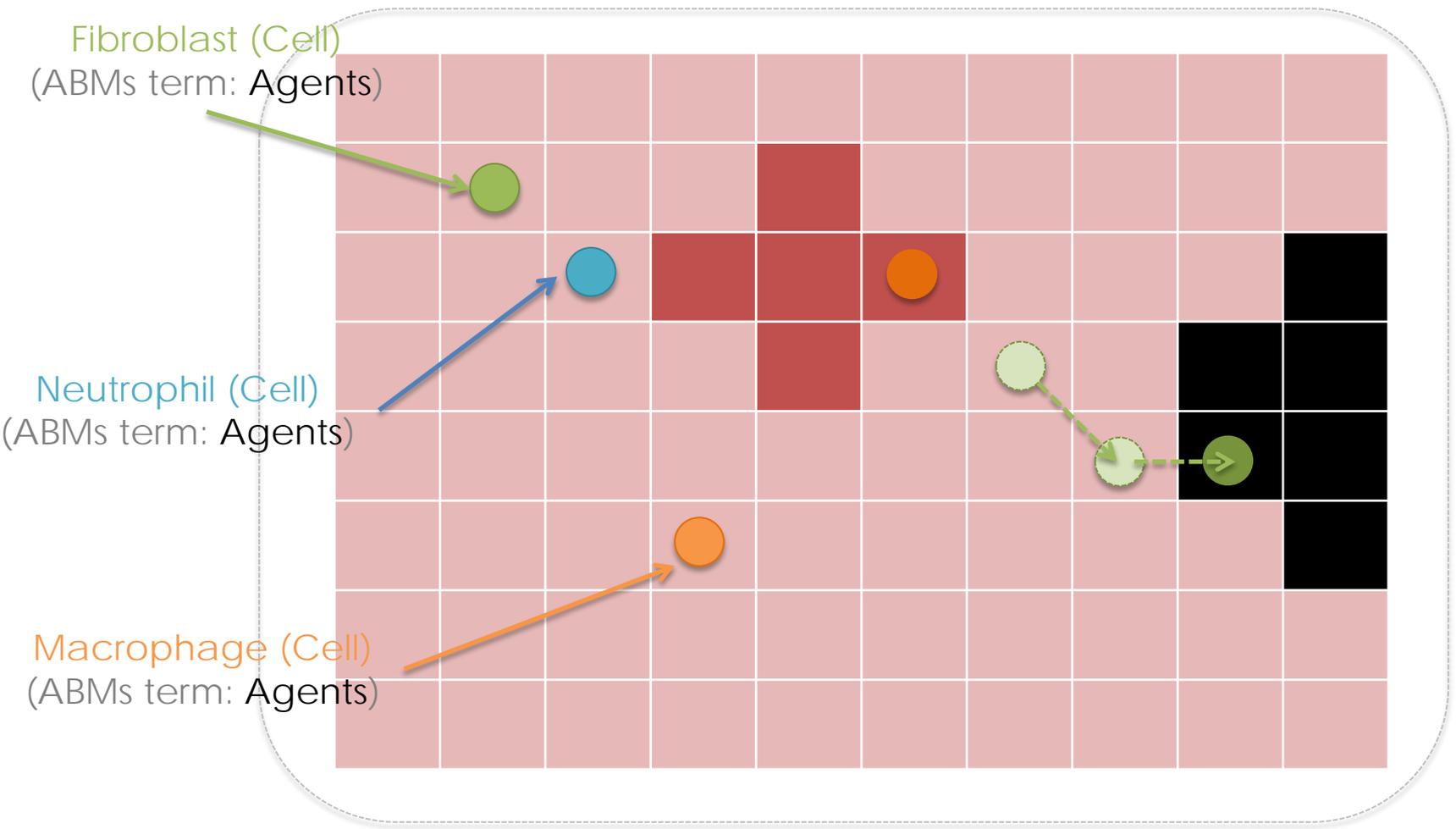


ABMs of Vocal Fold Wound Healing Process





ABMs of Vocal Fold Wound Healing Process





Problem Scale

| | Unit | Current Model | New Model | 3D |
|---------------------------|-------------------|---------------|---------------|-----------------------|
| World size | patches x patches | 120 x 240 | 1160 x 1660 | 1160 x 1660 x 100 |
| Patch size | mm x mm | 0.04 x 0.04 | 0.015 x 0.015 | 0.015 x 0.015 x 0.015 |
| Simulated area dimension | mm x mm | 4.8 x 9.6 | 17.4 x 24.9 | 17.4 x 24.9 x 1.5 |
| Number of Patches | | 28.8k | 1.9m | 192.56m |
| Simulated area size | mm ² | 46.08 | 433.26 | n/a |
| Simulated area volume | mm ³ | n/a | n/a | 649.89 |
| | | | | |
| Initial number of: | | | | |
| Neutrophils | cells | 100 | 182.4k | 18.24m |
| Macrophages | cells | 50 | 22.8k | 2.28m |
| Fibroblasts | cells | 50 | 22.8k | 2.28m |

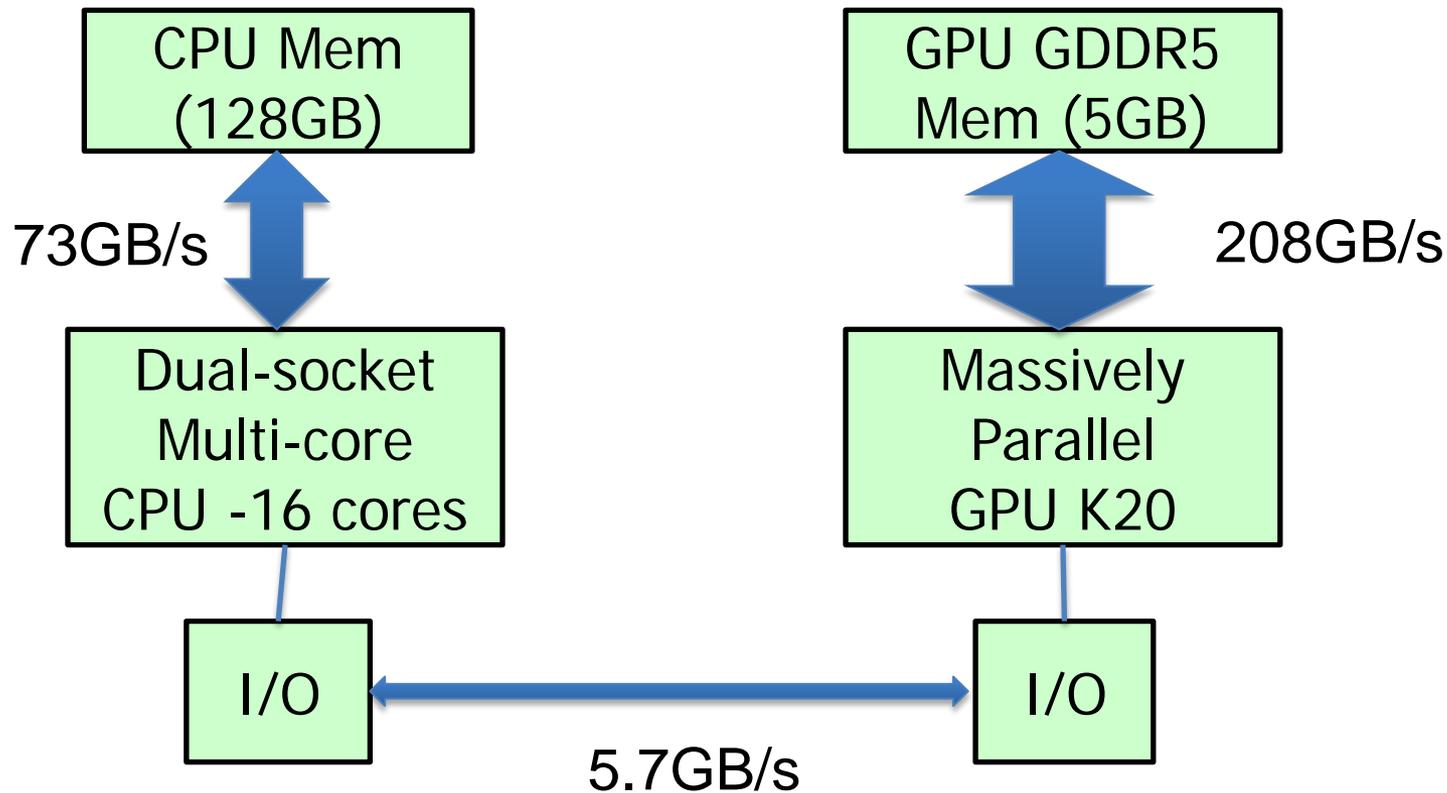
* Number of cells increase throughout the simulation due to proliferation. Current model shows a doubling of number of cells after the end of “5-day” simulation.

Characteristic Features of Applications



- Computationally demanding applications with irregular memory access patterns and involving large data sizes that cannot fit on the GPU memory
- Need to use heterogeneous platforms involving multicore CPU with one or more many-core GPUs.
- Performance Goal: try to achieve the same performance rate or throughput as in the case when the data fits on the GPU.

Heterogeneous Platforms





Dense Matrix Multiplication

- DGEMM: $C = \alpha AB + \beta C$
where the matrices are of dimensions:

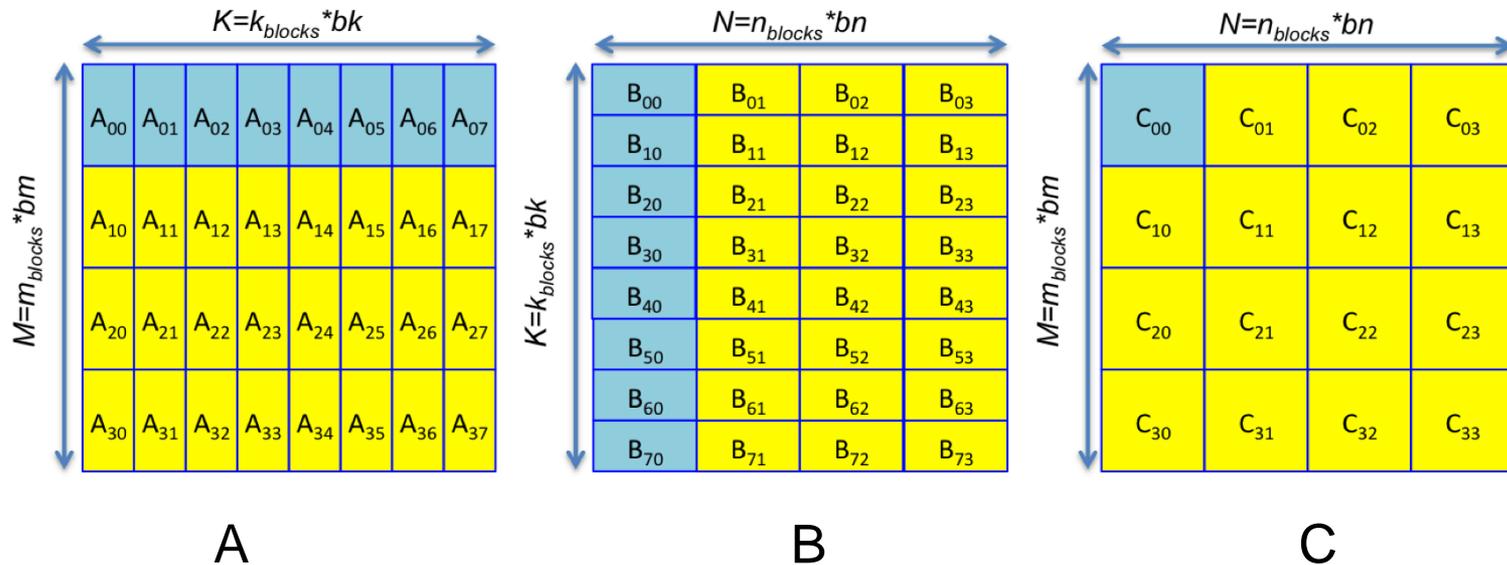
$$A : m \times k, B : k \times n, C : m \times n$$

- Why?
 - An important kernel for many problems
 - Optimization ideas can be used in other problems
 - Perhaps the most-studied algorithm in high performance computing
 - Can we solve very large DGEMM with the same performance throughput as small DGEMM?
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Block Matrix Multiplication

- Decompose into blocks

$$C_{ij} = \alpha \sum_{k=0}^{K/bk} A_{ik}^{(0)} B_{kj}^{(0)} + \beta C_{ij}^{(0)}$$



Multiple CUDA Stream Scheduling

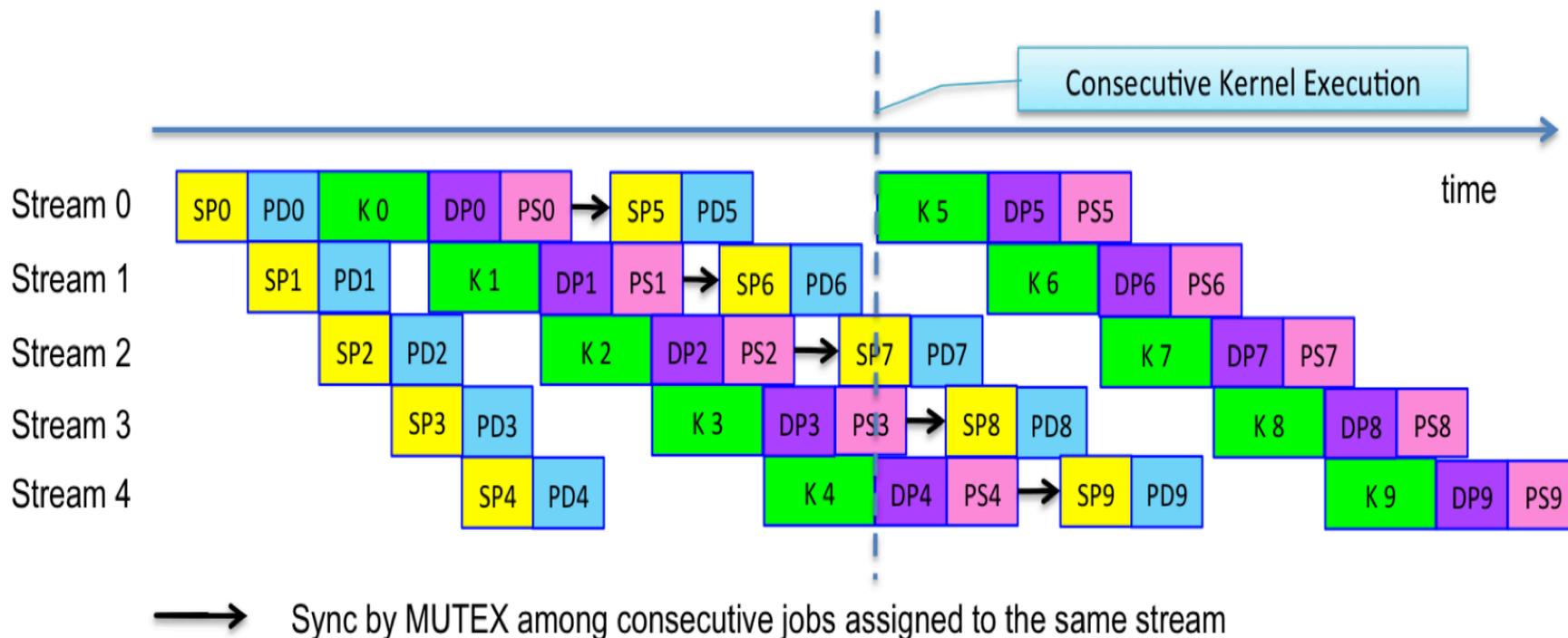


Figure 6: CPU-GPU Software Pipeline

Performance Evaluation

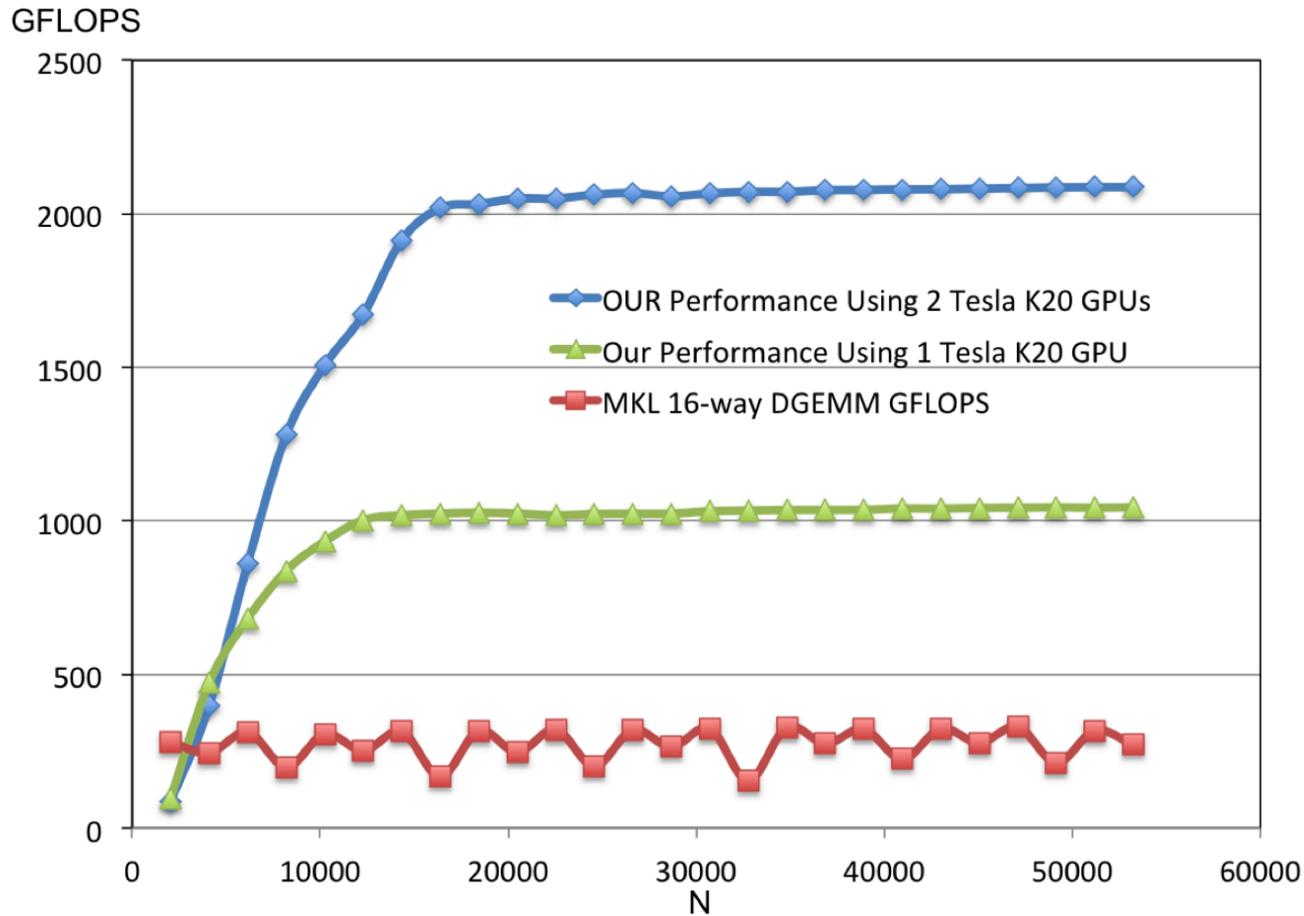
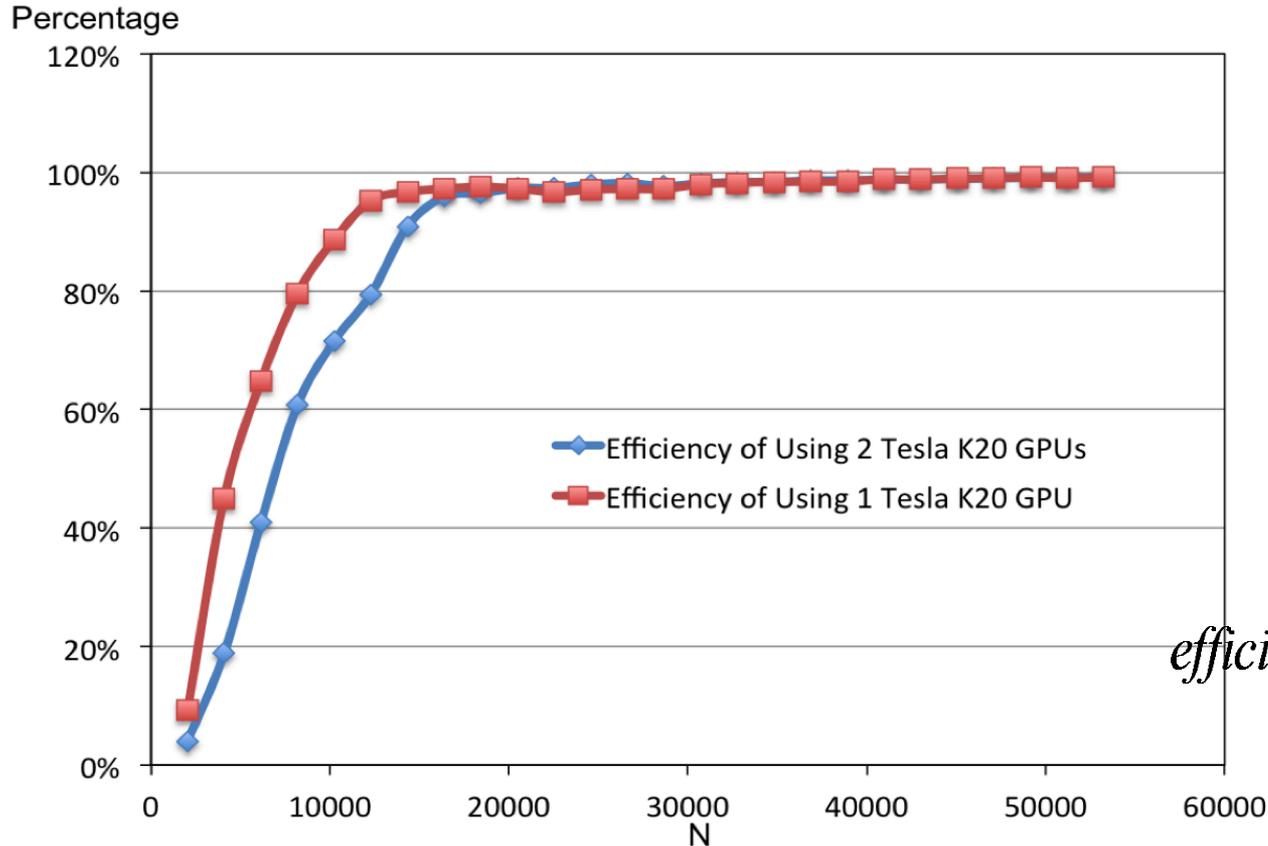


Figure 7: DGEMM Performance on *Sandy-Kepler* Node

Performance Evaluation



$$\text{efficiency} = \frac{GFLOPS_{\text{achieved}}}{GFLOPS_{\text{peak lib performance}}}$$

Figure 9: Efficiency on *Sandy-Kepler* Node

Conclusion

- Many biomedical applications can make effective use of heterogeneous platforms.
- But a significant amount of work is required to organize the computation into multi-stream of data transfers and kernel executions with no or very small stall time.
- Portability of high performance code remains a problem.