Brain Cancer Modeling and Forecasting in Patients



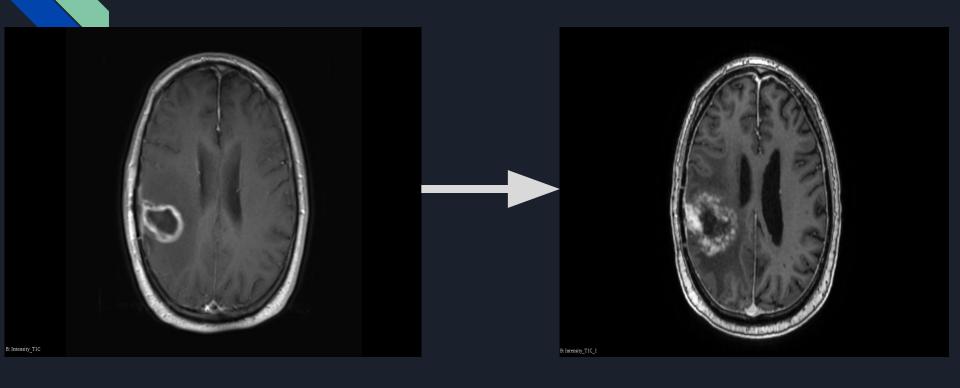


Agustin Garcia Flores, Patrick Hoover, Ashley Nichols

Mentor: Dr. Kostelich; Duane Harris

Background

- GBM (Glioblastoma Multiforme) is an aggressive brain cancer with a low survival rate.
- Different treatments include radiation, chemotherapy, and surgical resection
- Patients usually die within 15 months of diagnosis
- Our goal is to create a way for doctors to better counsel GBM patients through accurate simulations of brain tumor proliferation.
- Several parameters to consider (proliferation rate, diffusion rate, model type, etc.)
- GBM has both diffusive and growth behaviors (Neumann boundaries)
- There is still a degree of uncertainty when it comes to these simulations



Scan 1 Scan 6

Harris-Kuang Model

$$\frac{\partial p}{\partial t} = \nabla * (D\nabla p) + \rho g(p+q)p - k\delta(p+q)p$$

$$\frac{\partial q}{\partial t} = k\delta(p+q)p$$

- Representative of a 2 Cell Population Model
 - Proliferating cells
 - Quiescent cells
 - Necrotic dead
 - Hypoxic lack of oxygen
- G is a decreasing function of population
- Delta is an increasing function of population

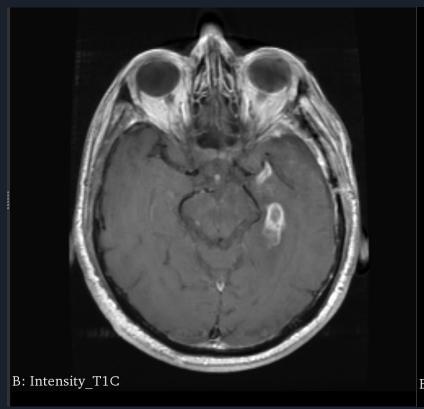
Image Processing

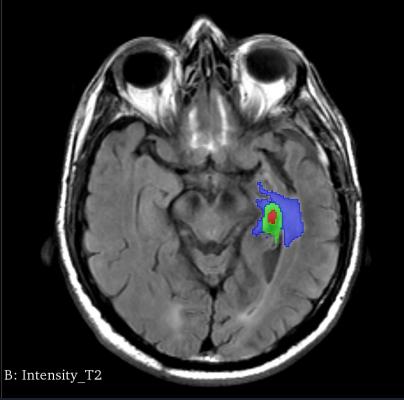
- Preprocessing
 - MATLAB code SPM12
 - Bias Correction 3D Slicer
 - MATLAB code SPM12
 - Reduce dimensions, align the scans, tissue classification
- Segmentation

Segmentations

- 3D Slicer
- We look for high intensity regions in every scan and label them:
 - Rim, core, and edema
- Each scan is a resection of the patient's tumor
- Variability of scans in each person
- We were helped by Dr. Preul and Dr. Mignucci

Segmentation Example - Pt 17









- High-Performance Computing (HPC) cluster
- Cluster has computer servers to help user optimize research
 - High memory computation and storage (>34TB RAM)
 - Separate server rather than local computer.
 - Parallel programming



Source: researchcomputi ng.asu.edu "Core Facilites"

Agave Simulation Predictions

Name/Model

Population

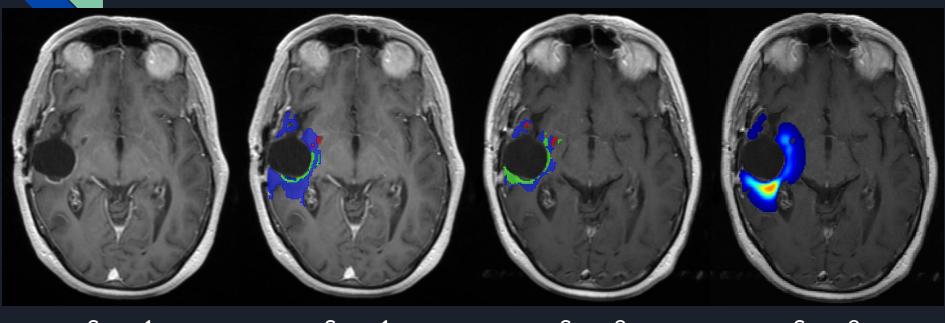
Parameters

```
RNAME
  model name='harris'
  Unspecified values are zero
RPOPULATION
                       ! proliferating cells
  pmin edema = 0.01
  pmax edema = 0.05
  pmin t1c = 0.05
  pmax t1c = 0.75
  qratio edema = 0
  qratio t1c = 0.0625
                       ! quiescent cells
  qmin core = 0.75
  amax core = 0.99
  pratio core = 0.125
RBASEPARAM
 d0(1,1)=0.4
              ! white matter diffusion rate, proliferating cells
 d0(2,1)=0.2 ! gray matter diffusion rate, proliferating cells
 d0(3.1)=0.2 ! edema diffusion rate, proliferating cells
 d0(4,1)=0.2 ! enhancing rim diffusion rate, proliferating cells
 d0(5,1)=0.2 ! tumor core diffusion rate, proliferating cells
 d0(1,2)=0.04 ! white matter diffusion rate, quiescent cells
 d0(2,2)=0.02 ! gray matter diffusion rate, quiescent cells
 d0(3,2)=0.02 ! edema diffusion rate, quiescent cells
 d0(4.2)=0.02 ! enhancing rim diffusion rate, quiescent cells
 d0(5,1)=0.02 ! tumor core diffusion rate, quiescent cells
 r0(1,1)=0.028 ! white matter growth rate, proliferating cells (rho1 in paper)
 r0(2,1)=0.032 ! gray matter growth rate, proliferating cells (rho2 in paper)
 r0(3,1)=0.04 ! edema growth rate, proliferating cells (rho1 in paper)
 r0(4:5,1)=0.02 ! enhancing rim growth rate, proliferating cells
 r0(5,1)=0.02 ! tumor core growth rate, proliferating cells
 q0(1,1)=0.01
              ! quiescence rate, white matter (k1 in paper)
              ! quiescence rate, gray matter (k1)
 q0(2,1)=0.01
              ! quiescence rate, edema (k1)
 q0(3,1)=0.01
              ! quiescence rate, enhancing rim (k2)
 q0(4,1)=0.02
 q0(5,1)=0.04 ! quiescence rate, core (k3)
 beta g = 1, 3 ! Taken from Lifeng's paper
 beta d = 2, 2 ! see Fig. 4 in Lifeng's paper
 hmax = 1 ! initial maximum time step
 verblev = 2 ! verbose
 days = 56 ! update
```

Comparing Our Results

- Agave gives a prediction based on the parameters
- Compare Agave prediction to our own segmented scans
- Segmentations are up to interpretation,
 segmentations may not be 100% accurate

Patient 48: 68 Day Simulation



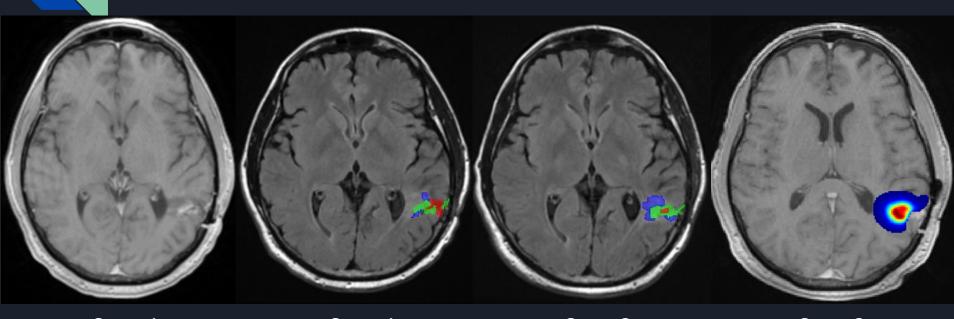
Scan 1
No Segmentation

Scan 1
Segmentation

Scan 2
Segmentation

Scan 2 Harris-Kuang Model

Patient 15: 56 Day Simulation



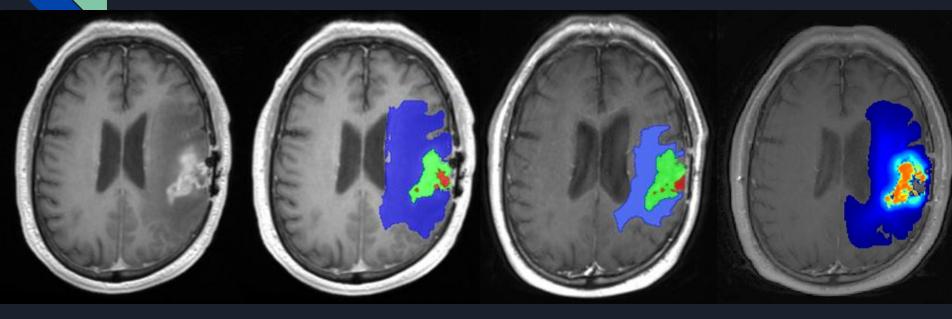
Scan 1
No Segmentation

Scan 1
Segmentation

Scan 2 Segmentation

Scan 2 Harris-Kuang Model

Patient 38: 56 Day Simulation



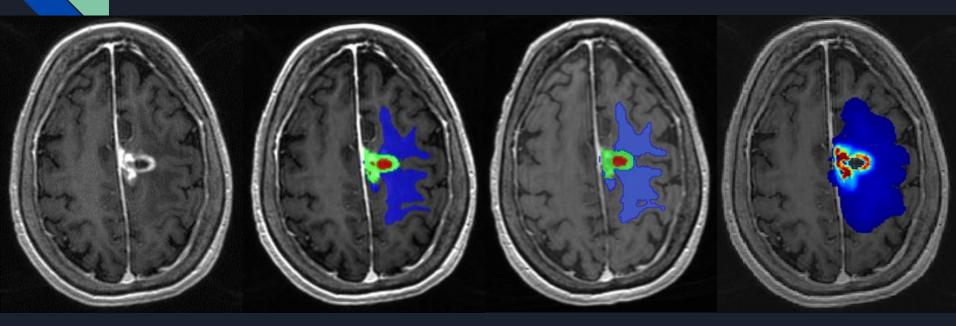
Scan 2 No Segmentation

Scan 2 Segmentation

Scan 3
Segmentation

Scan 3 Harris-Kuang Model Modified

Patient 40: 31 Day Simulation



Scan 1
No Segmentation

Scan 1
Segmentation

Scan 2 Segmentation

Scan 2 Harris-Kuang Model Modified

Image Subtraction

- Use image subtraction to find the difference between the Agave prediction and our own segmentation
 - Gives us an idea of how accurate the prediction was
- An accurate prediction = an accurate set of parameters (model, rate of diffusivity, etc.)

Image Subtraction Results

Patient	Rim Agreement	Core Agreement
Patient 48	9.75%	0%
Patient 15	14.39%	5.22%
Patient 38	26.47%	2.96%
Patient 40	35.60%	43.21%

^{*}Note: "Rim" = Proliferating cells, "Core" = Quiescent cells

Limitations of Image Subtraction

- -The subtraction method does not take into account the cell density at each location
- -Different parameter values will produce different results
- -Consider both proliferating and quiescent regions whereas a tumor/high intensity region radius may be more accurate for our purposes

Future Work and Improvements

- More trials of the Agave program in order to find a set of parameters that gives the best outcome
- If we find an accurate set of parameters that works from scan 1 to scan 2:
 - Will it work from scan 2 to scan 3 and so on?
 - Will it work for different patients?
- More biologically accurate segmentations and models



Thanks for listening!

Any questions?

Acknowledgments: Dr. Kostelich, Duane Harris, Dr. Preul, Dr. Mignucci

Thank you to the NSF (National Science Foundation) and Arizona Biomedical Research Center for sponsoring our program!