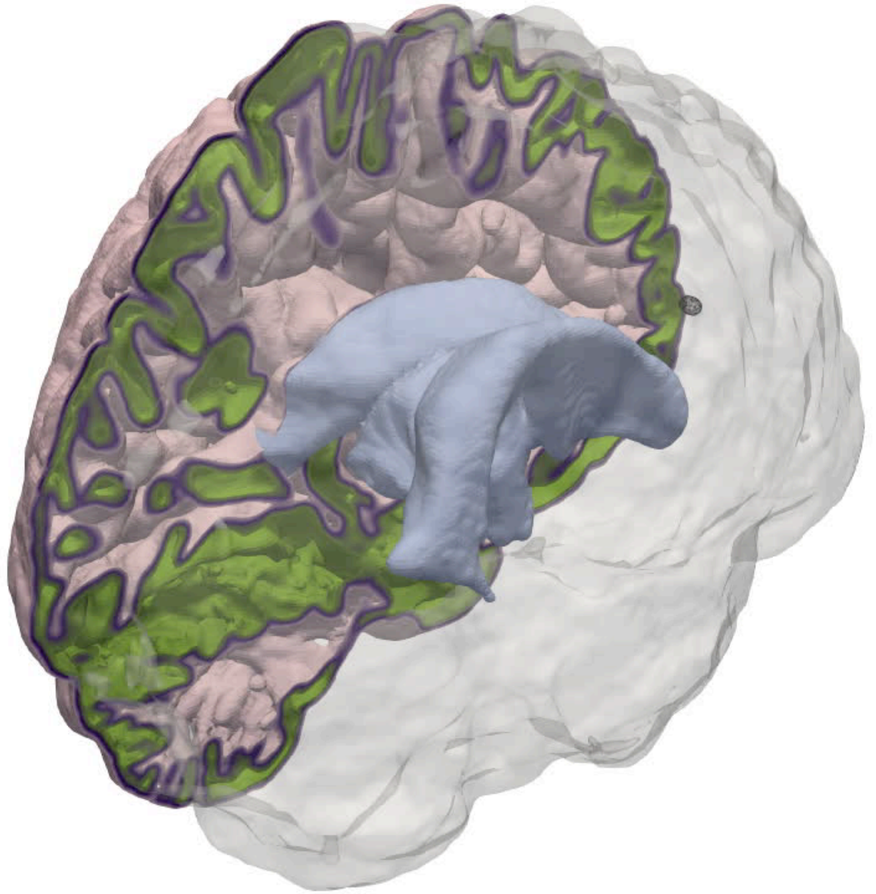
The University of Texas at Austin
Oden Institute for Computational Engineering and Sciences

A High-Performance Inversion Framework for Brain Tumor Growth Models in Personalized Medicine



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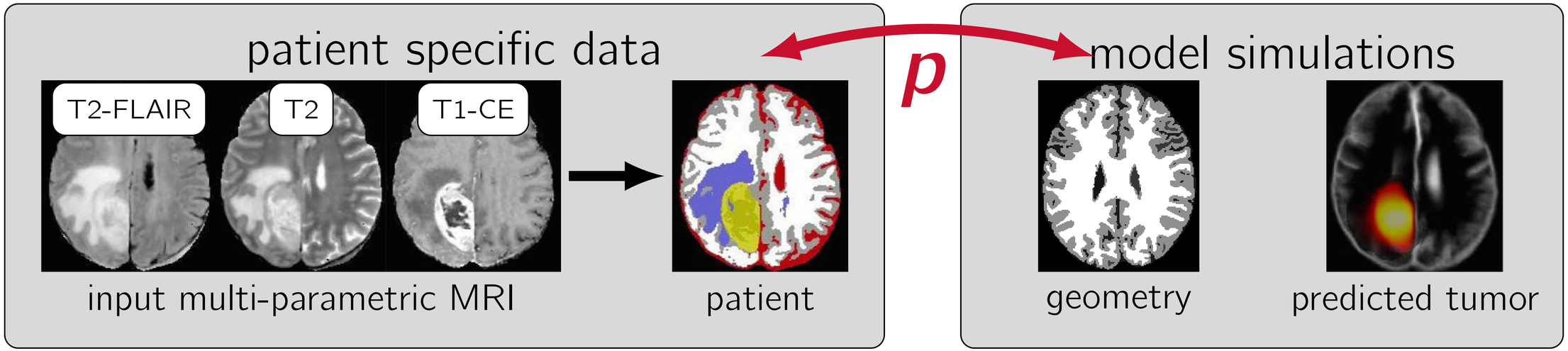
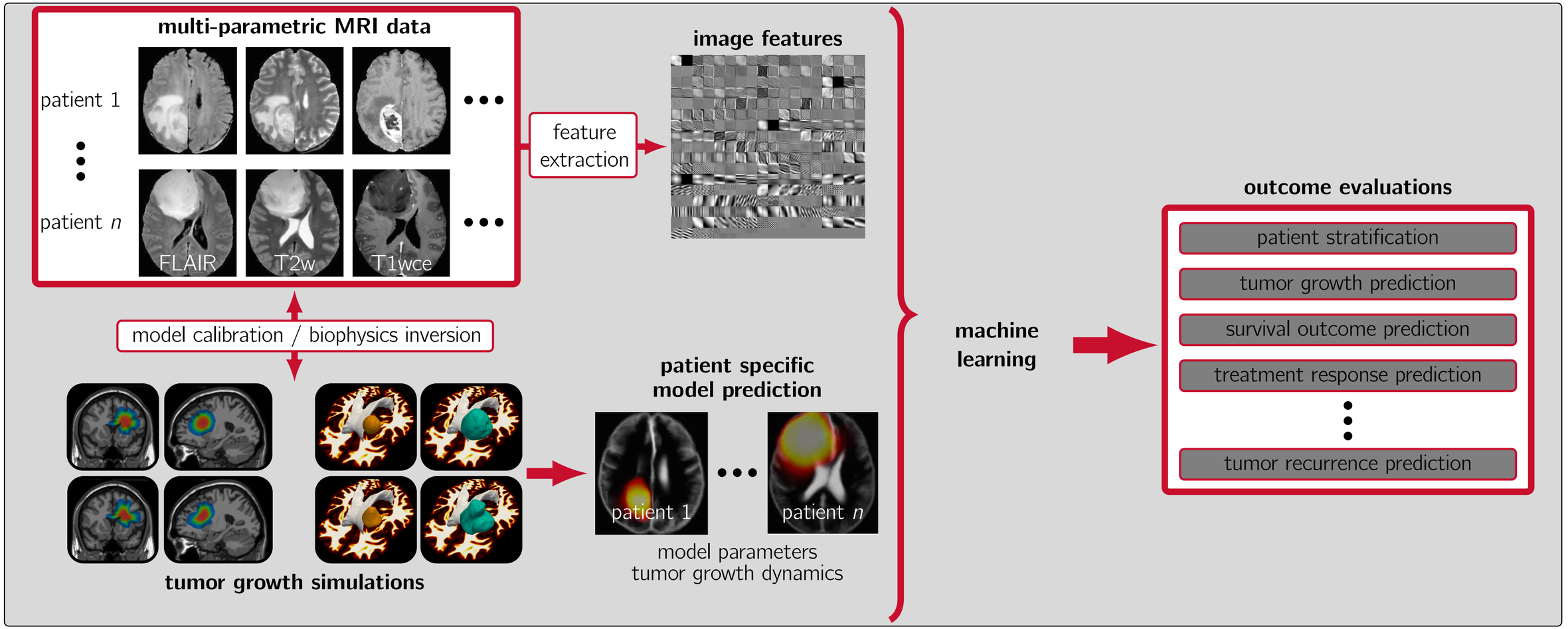
BIG PICTURE



- Brain cancer — aggressive tumors, poor prognosis, challenging to characterize
- *Data-informed* mathematical models of cancer growth hold an enormous promise
  - Explainable models that connect biophysics to clinical observables
  - Can assist in diagnosis and treatment planning
  - Provide a complete understanding of this complex dynamical system
- Our goal: an *end-to-end computational framework* to integrate cancer models with medical imaging data

AN END-TO-END FRAMEWORK



A Mang, S Bakas, S Subramanian, C Davatzikos, G Biros. Integrated biophysical modeling and image analysis: Application to neuro-oncology. Annual Review 22 2020
S Subramanian, K Scheufele, M Mehl, G Biros. Where did the tumor start? An inverse solver with sparse localization for tumor growth models. Inverse Problems 36 2020.

ALGORITHMS

- Multistage convolutional neural nets for semantic segmentation of MRIs
- Medical imaging data is sparse = a formidable large-scale non-convex inverse problem
  - Biophysically-inspired regularization strategies with sophisticated non-linear optimization algorithms
- Tumor growth models are complex PDEs = 3D non-linear forward problems
  - Fast spectral algorithms with efficient preconditioners

SOFTWARE

- Very expensive calculations — optimized software which exploits distributed memory parallelism and GPU-acceleration
  - Strong scaling efficiency > 95% up to 4000 CPU cores on the Frontera system
  - GPU-optimized computational kernels
- Inversion on clinical medical image data sizes can be done within 2 hours using the V100 GPUs on the Longhorn system; 5x faster than single node (48 cores) CPU performance.