The Cancer imaging Phenomics Toolkit (CaPTk)

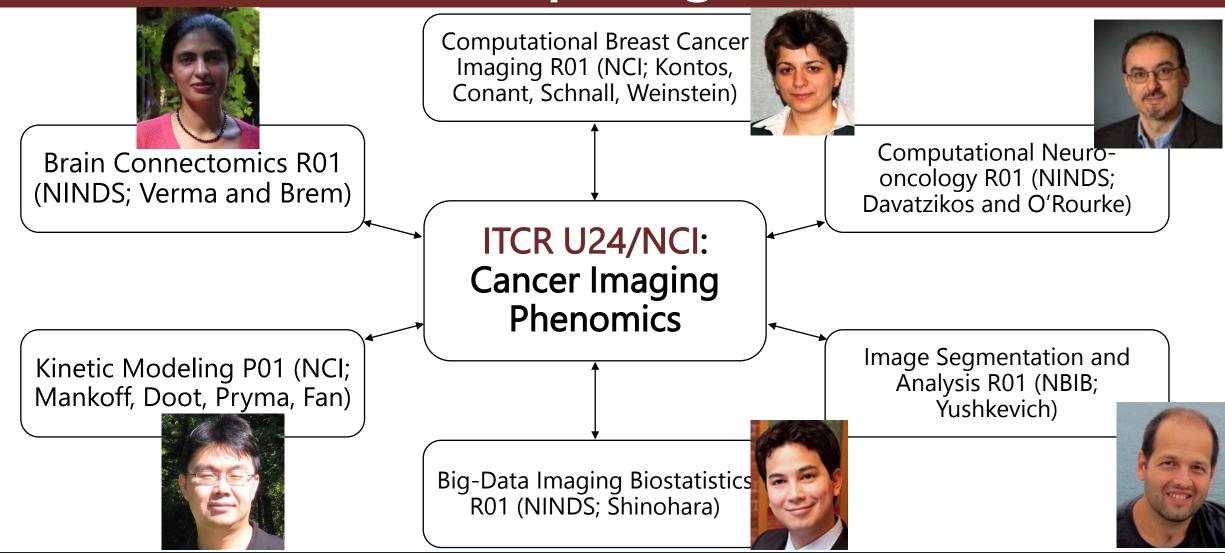
Christos Davatzikos, on behalf of the team



Center for Biomedical Image Computing and Analytics

Computational Breast Imaging Group Penn Image Computing and Science Lab Penn Statistical Imaging and Visualization Endeavor Section for Biomedical Image Analysis

Participating Pls



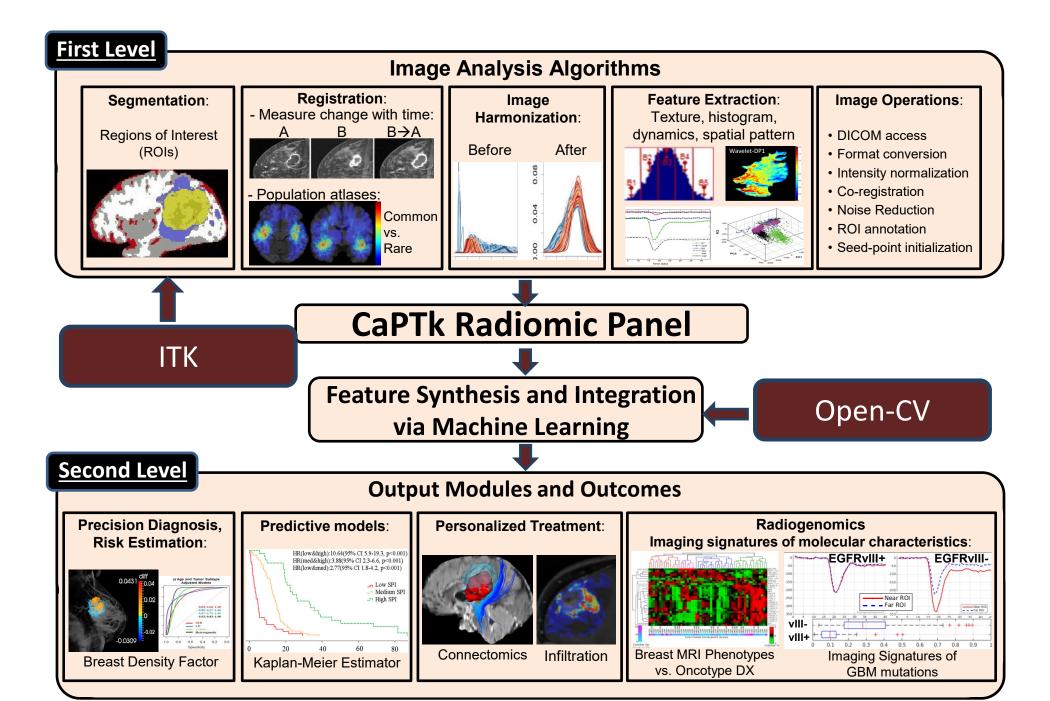


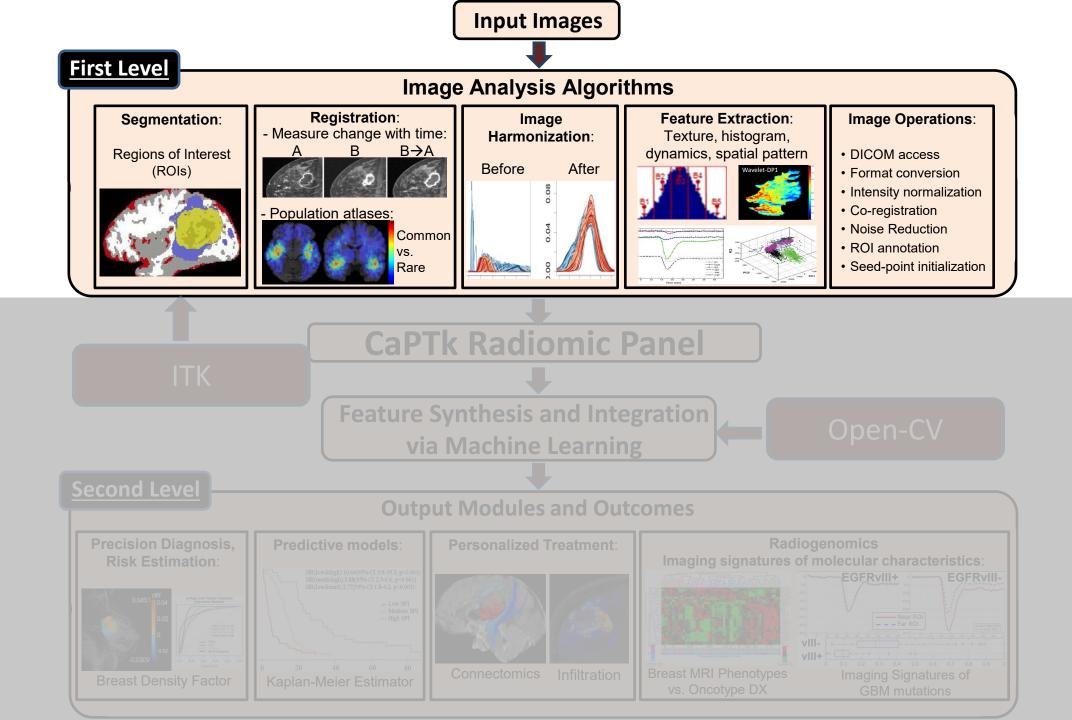
Two Major Goals

• To leverage a rich family of <u>advanced image computing algorithms</u>

 To leverage extensive and long-standing <u>collaborations with clinical</u> <u>teams</u> who have provided input in the development of the algorithms, as well as data for training and validation of models











General purpose semi-automated segmentation: ITK-SNAP; Weighted geodesic segmentation

• Organ/Cancer-specific tools (GLISTR for brain gliomas; Breast cancer tools, fiber tract extraction for neurosurgical planning)



ITK-SNAP

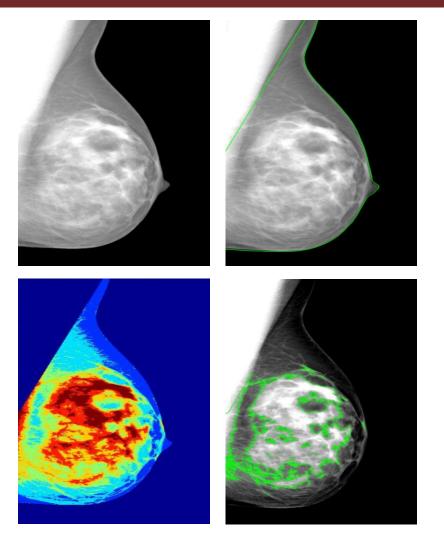


Screenshot of ITK-SNAP's interface

- Support for color, multi-channel, and timevariant images
- Segmentation done using Random Forest and Level Sets algorithms
- Transfer of data between ITK-SNAP and CaPTk is seamless – giving users the option to use the former's segmentation and user interaction functionality with latter's computation capabilities



Breast Segmentation

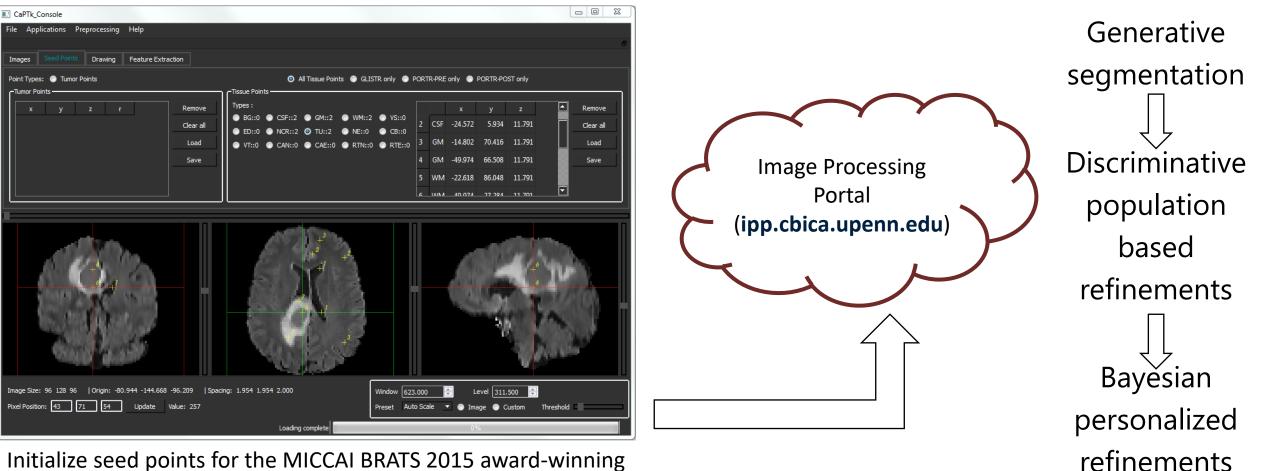


- Fully-automated segmentation of the breast area and the dense breast tissue, estimation of Percent Density (PD%)
- Adaptive fuzzy-c-mean (FCM) clustering based on intensity histogram and acquisition parameters
- Well calibrated versus radiologists estimates ^[9] demonstrated associations to breast cancer risk ^[10] for raw and processed FFDM.



Estimation of breast PD via adaptive FCM clustering and SVM segmentation – Keller et al.; Medical Physics, 2012 Evaluation of Laboratory for Breast Radiodensity Assessment (LIBRA) software – Keller et al.; Breast Cancer Research, 2015

GLISTRboost Segmentation

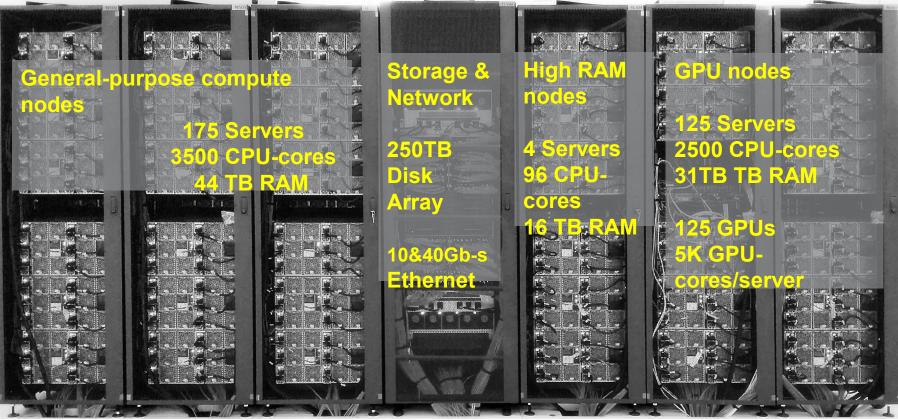


Initialize seed points for the MICCAI BRATS 2015 award-winning GLISTRboost method using CaPTk Console

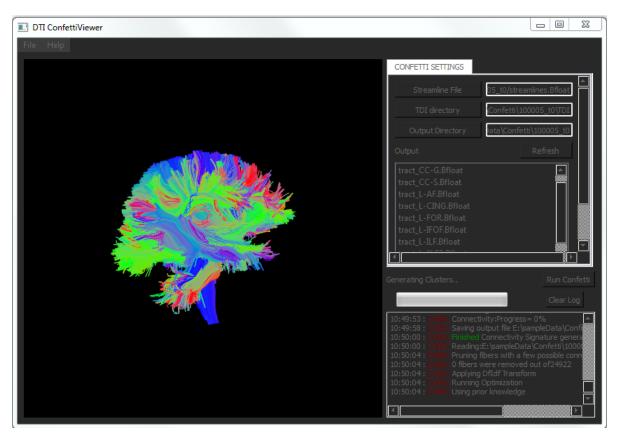


Modeling with Gradient Boosting Machines for Glioma Segmentation - Bakas et. al

Web Portal for Compute-heavy CaPTk Functions: CBICA cluster via high-end NIH instrumentation grant:



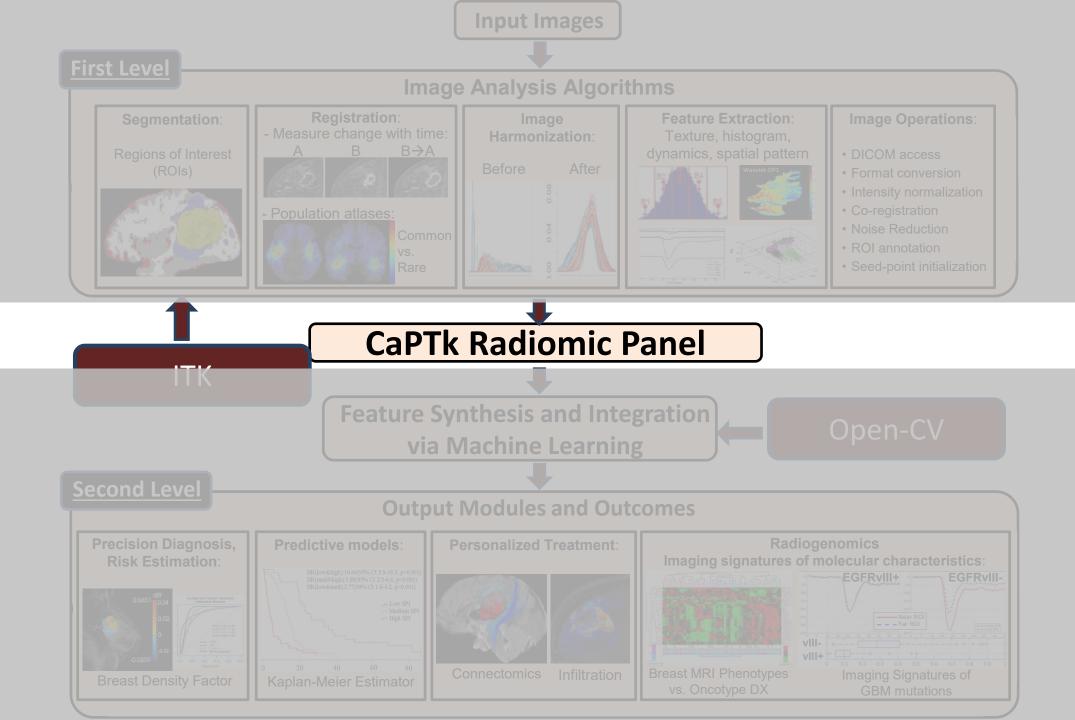
Confetti – Visualizing Fiber Tracts



Confetti interface is dedicated for fiber tract visualization and it is integrated with CaPTk Console Advances in tractography enhance neurosurgical planning, but are limited by edema, mass effect, and tract infiltration

- Confetti facilitates automated identification of all tracts (including eloquent tracts) without manual drawing of ROIs, making the tracts robust and replicable
- Confetti enhances the primary objective of neurosurgery: maximal safe resection in the presence of tumor edema and infiltration





CapTk Radiomic Panel

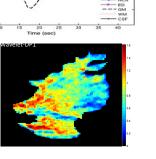
• Segmentations: volumes and signals within ROIs

- Histogram based x10⁻³ features B2 B4 B1 B2 B4 B5 0 50 100 150 200 256
- Normalized histograms of different protocols; optimized binning

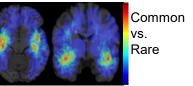
• Textures

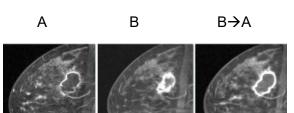
Kinetics

•

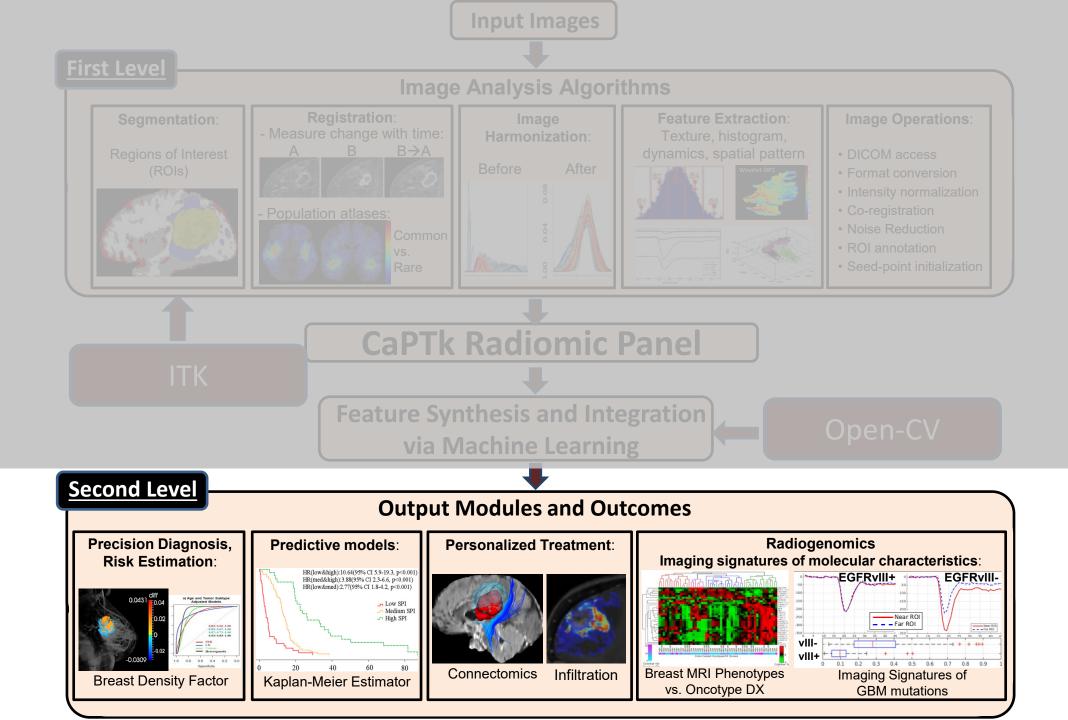


- Spatial patterns/distributions
- Parametric maps from longitudinal scans



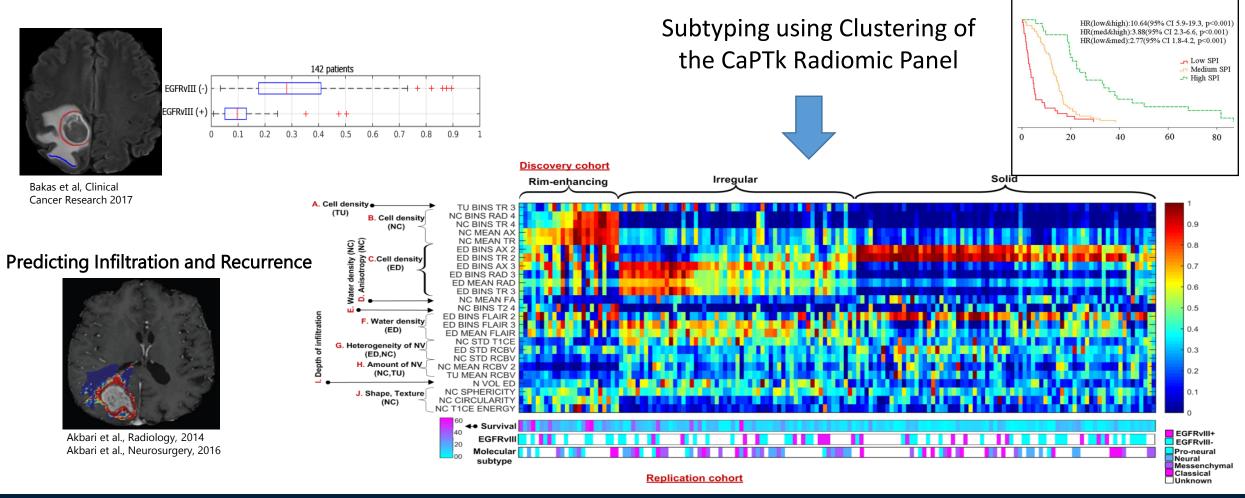






Computational Neuro-Oncology

Imaging Signatures of Molecular Characteristics

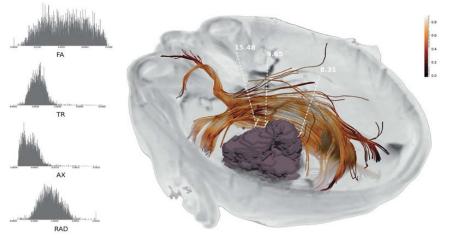




Predicting Survival:

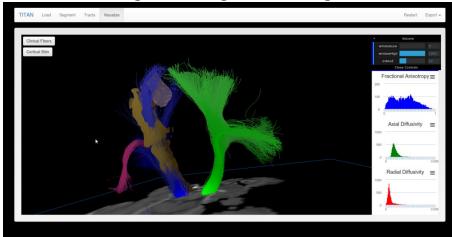
Computational study of Brain Connectivity

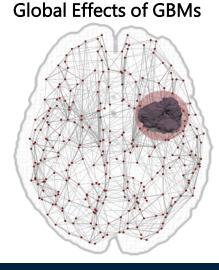
Peri-lesional Effects of GBMs



- Automated atlas-based tract extraction (using connectivity signatures instead of shape help address mass effect)
- Edema invariant tractography (using multicompartment models fitted to multishell imaging)
- Tumor connectome (effect of tumor on distant regions, regional vulnerability and functional rerouting)

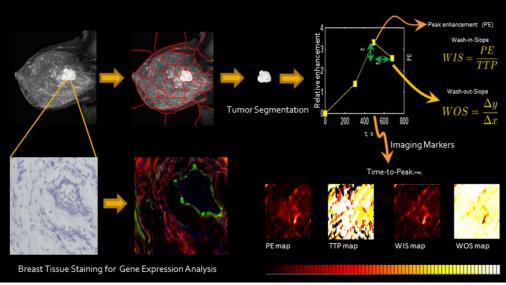
Web-based Integrated Surgical Planning Environment





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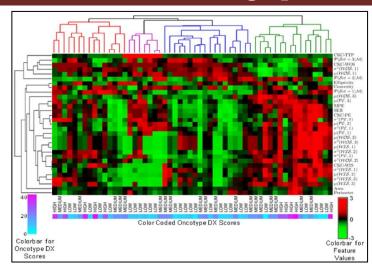
Radiomic Breast Cancer Phenotypes



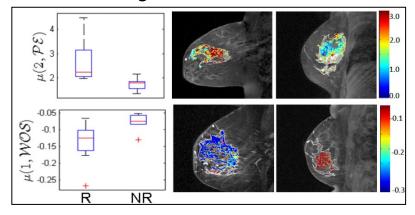
Ashraf et al., IEEE TMI 2013; Mahrooghy et al. IEEE TBME 2015

Breast Cancer Phenotyping via Imaging:

- Segmentation and multi-parametric feature extraction
- Identification of <u>intrinsic</u> phenotype patterns
- Prognostication and treatment response prediction

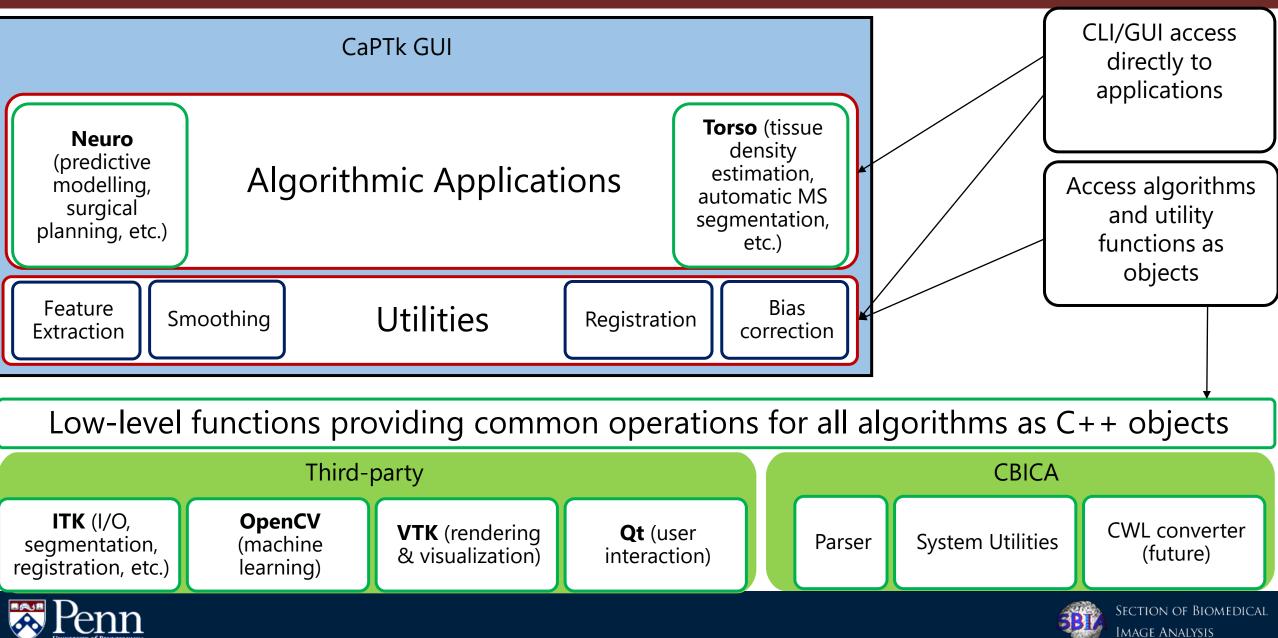


Intrinsic Imaging Phenotypes for Breast Cancer <u>Prognostic</u> and <u>Predictive Value</u>





Software Architecture Overview



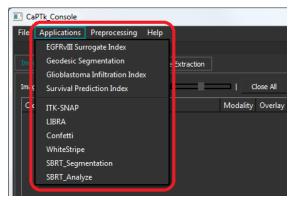
Application Integration Levels

GUI with no integration API	GUI with integration API	Stand-alone CLI app	Application functions	Library functions	
LIBRA	ITK-SNAP	SBRT Lung	Brain <i>Radiomic</i> Signatures	ITK Filters	
Language independent (including Python)			Native C++		
/				N	
Low	Low Integration with Console and Optimization			High 🔶	

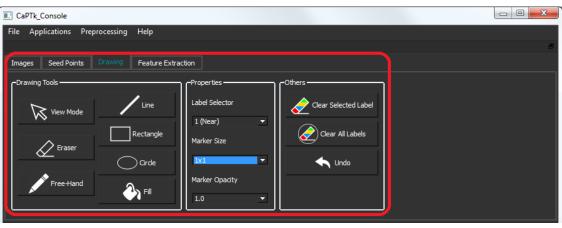




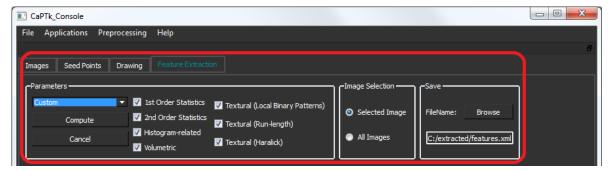
User Interface Screenshots



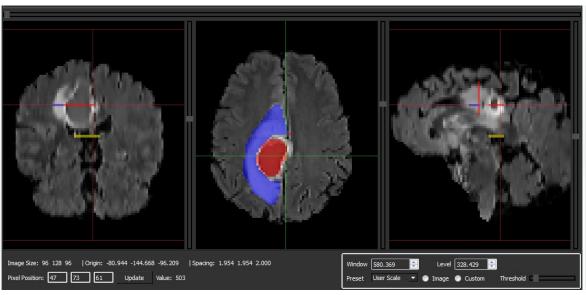
All available Applications



Drawing annotations



Feature Panel



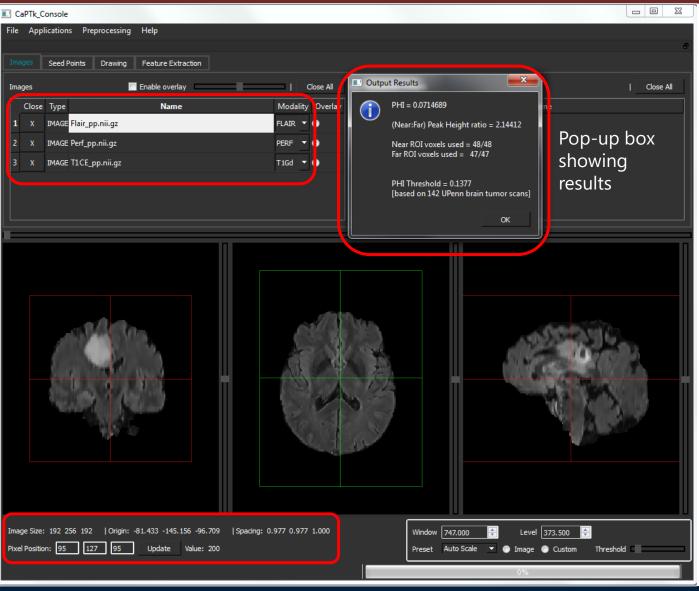
Visualization Pane





EGFR Radiogenomic Signature Example Screenshot

Loaded Images and modalities



Various image properties









Section of Biomedical Image Analysis

User Workflow

