The Cancer imaging Phenomics Toolkit (CaPTk)

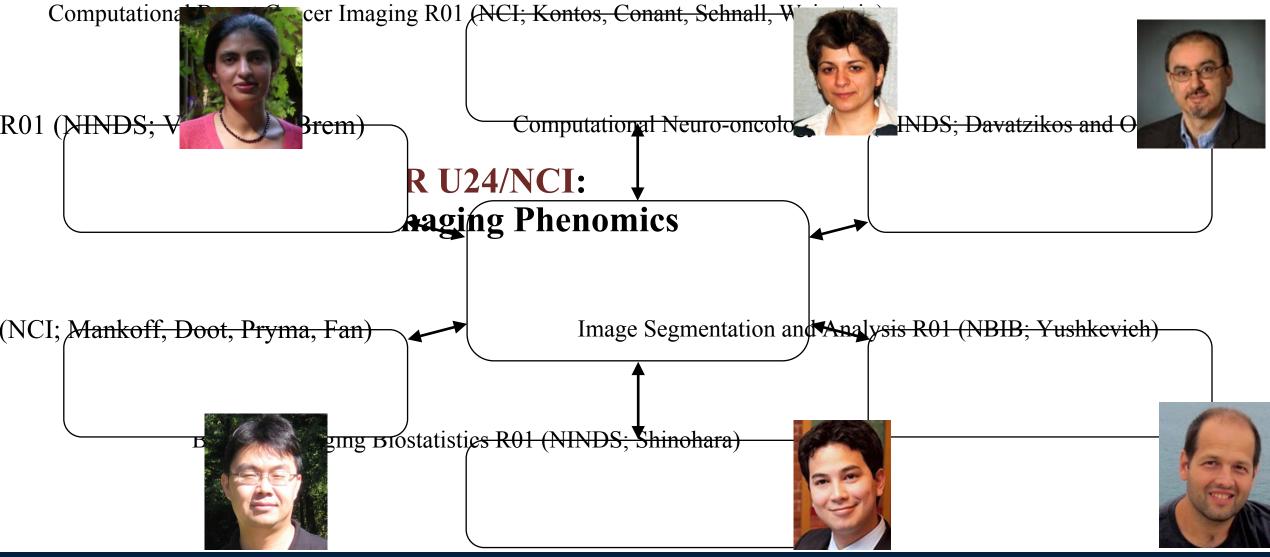
Christos Davatzikos, on behalf of the team



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 PIs



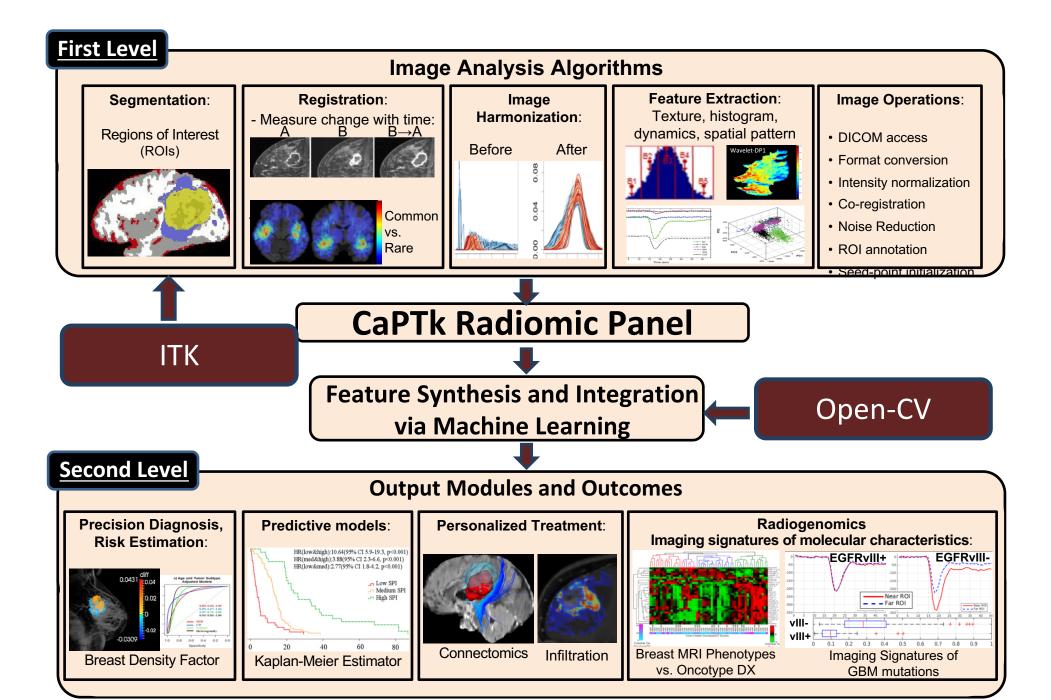


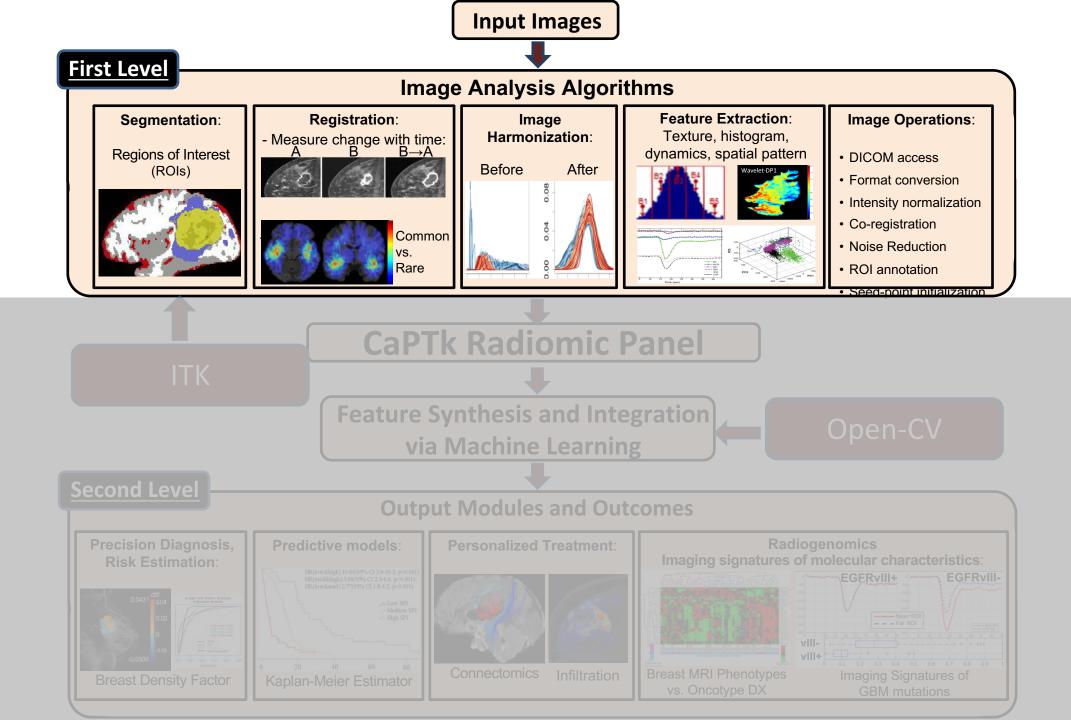
Two Major Goals

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

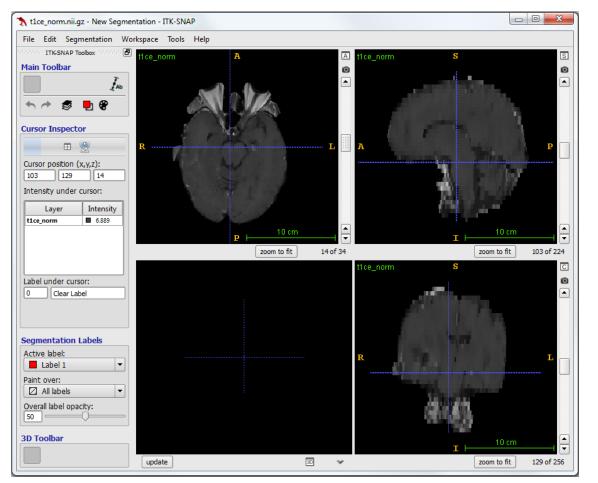
• To leverage extensive and long-standing <u>collaborations with clinical</u> <u>teams</u> who have provided input in the development of the algorithms, as well as data for training and validation of models







ITK-SNAP

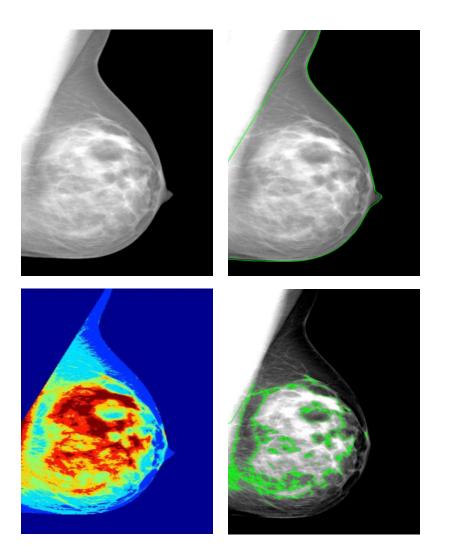


Screenshot of ITK-SNAP's interface

- 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

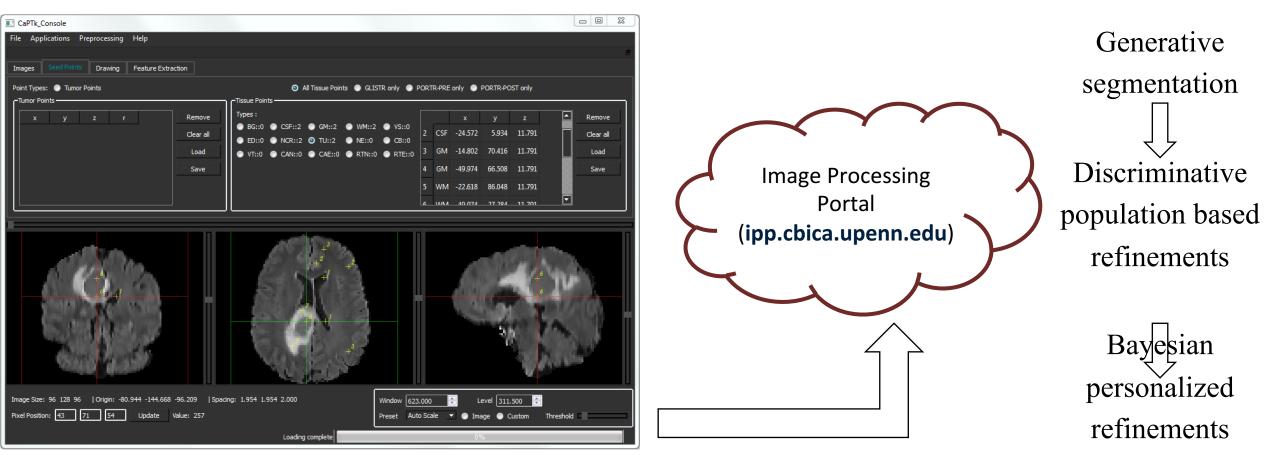


- Fully-automated segmentation of the breast area and the dense breast tissue, estimation of Percent Density (PD%)
- Adaptive fuzzy-c-mean (FCM) clustering based on intensity histogram and acquisition parameters
- Well calibrated versus radiologists estimates ^[9] demonstrated associations to breast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

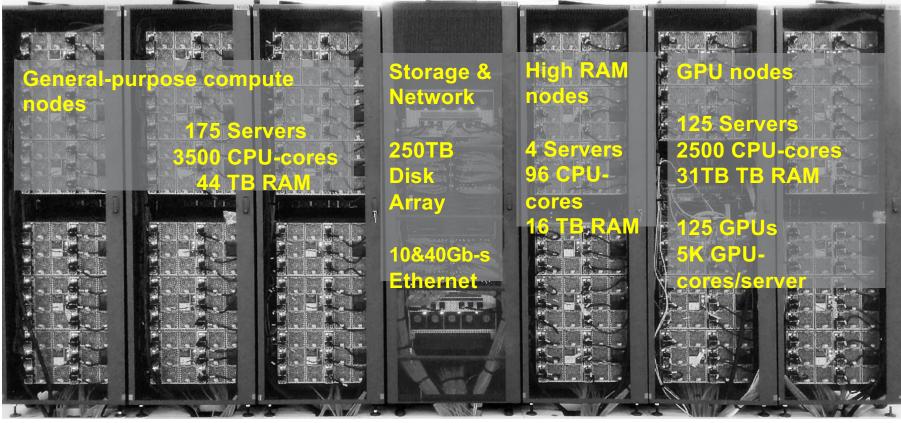


Initialize seed points for the MICCAI BRATS 2015 awardwinning GLISTRboost method using CaPTk Console

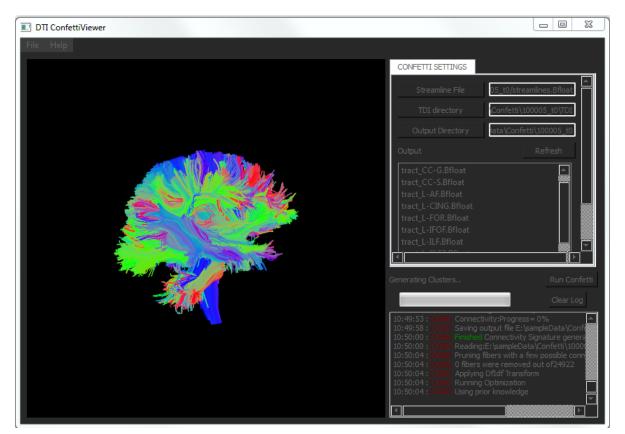


GLISTRboost: Combining Multimodal MRI Segmentation, Registration, and Biophysical Tumor Growth Modeling with Gradient Boosting Machines for Glioma Segmentation - Bakas et. al

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



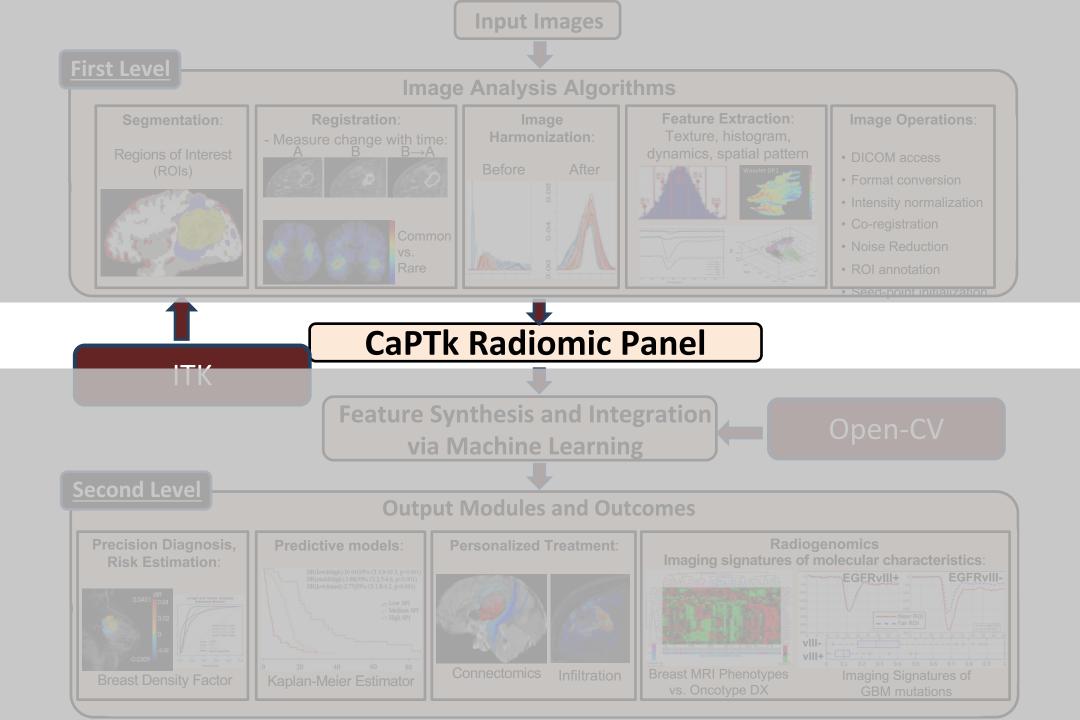
Confetti – Visualizing Fiber Tracts



Confetti interface is dedicated for fiber tract visualization and it is integrated with CaPTk Console

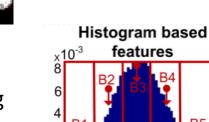
- Advances in tractography enhance neurosurgical planning, but are limited by edema, mass effect, and tract infiltration
- Confetti facilitates automated identification of all tracts (including eloquent tracts) without manual drawing of ROIs, making the tracts robust and replicable
- Confetti enhances the primary objective of neurosurgery: maximal safe resection in the presence of tumor edema and infiltration





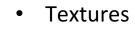
CaPTk Radiomic Panel

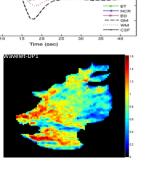
Segmentations: volumes and signals within ROIs •



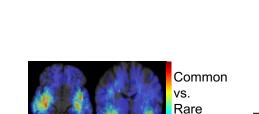
Normalized histograms of different protocols; optimized binning ٠





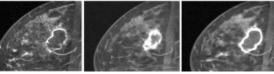


- Spatial patterns/distributions ٠
- Parametric maps from longitudinal scans ٠

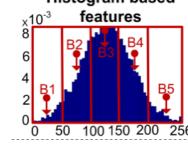


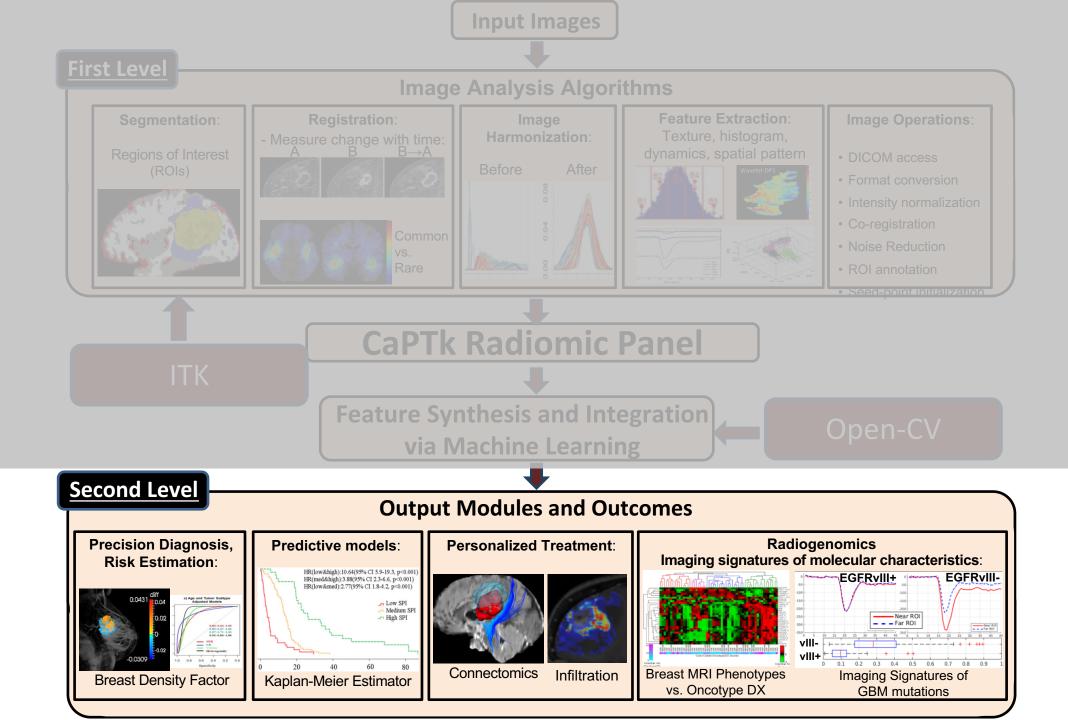






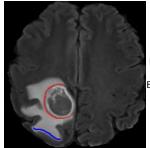






Computational Neuro-Oncology

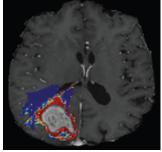
Imaging Signatures of Molecular Characteristics



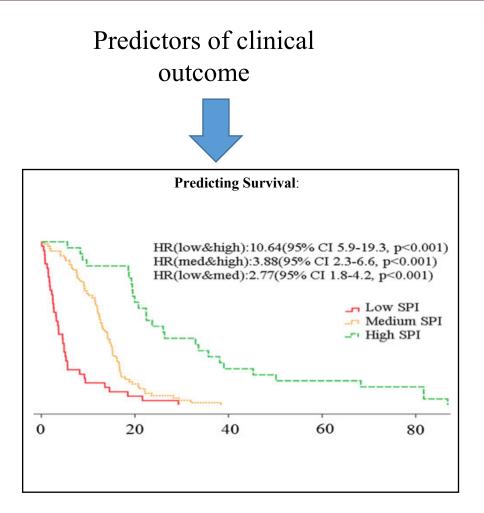
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Bakas et al, Clinical Cancer Research 2017

Predicting Infiltration and Recurrence



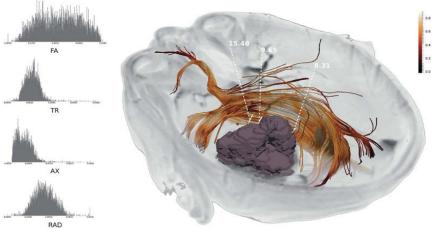
Akbari et al., Radiology, 2014 Akbari et al., Neurosurgery, 2016





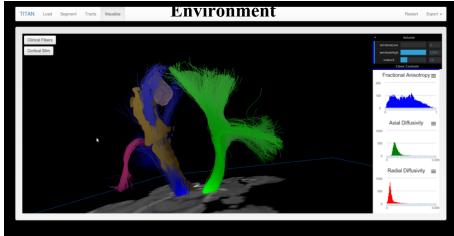
Brain Connectomics

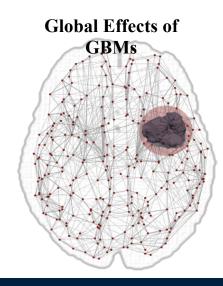
Peri-lesional Effects of GBMs



- 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)

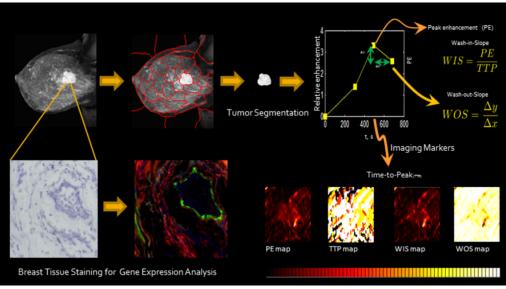
Web-based Integrated Surgical Planning





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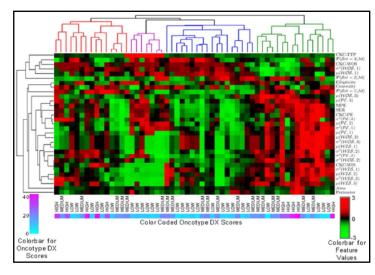
Radiomic Breast Cancer Phenotypes



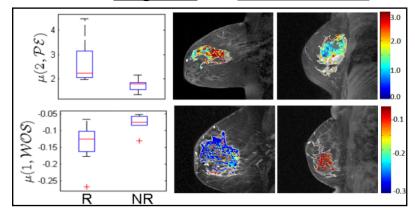
Ashraf et al., IEEE TMI 2013; Mahrooghy et al. IEEE TBME 2015

Breast Cancer Phenotyping via Imaging:

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

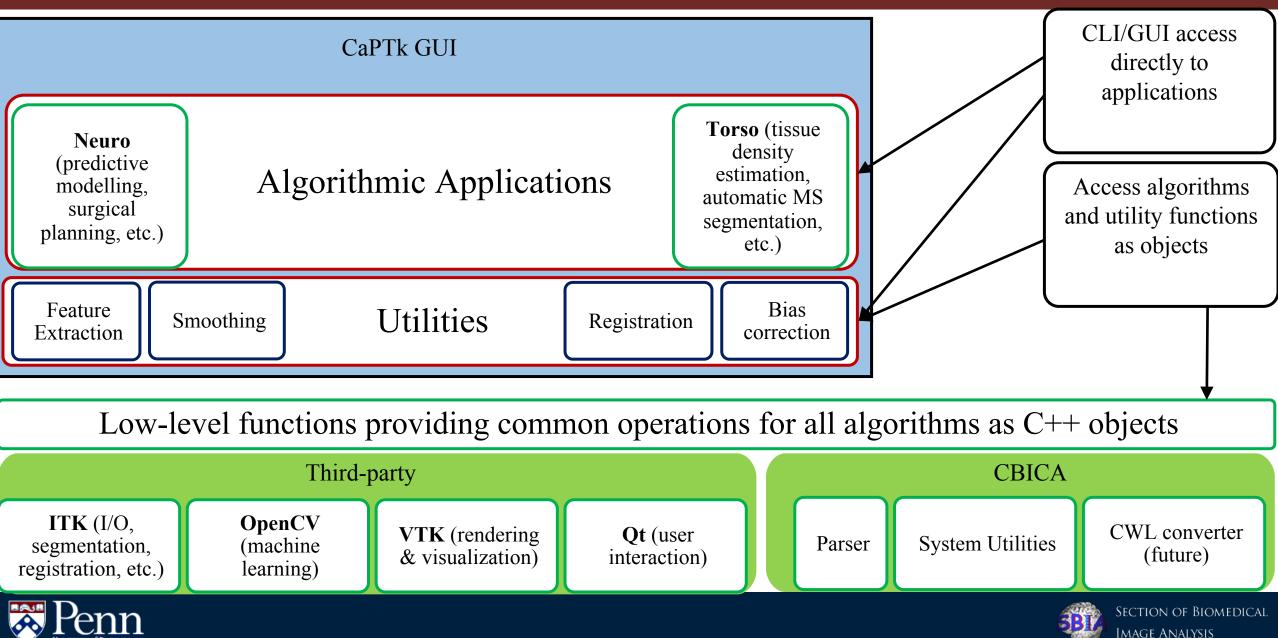


Intrinsic Imaging Phenotypes for Breast Cancer <u>Prognostic</u> and <u>Predictive Value</u>





Software Architecture Overview



Installation

- Only 64-bit machines supported due to processing requirement
- Installers are designed to work as double-click and install
- Windows and Linux installers are available and macOS to be ready soon
- The entire CaPTk (console and all applications) will also be available as docker images soon

Operating System	Version	Installer System
Windows	7+	MSI
macOS	Snow Leopard+	DMG
Ubuntu	14.04+	DEB
centOS	6+	RPM



Dependencies

• Core Application (written in C++ for efficiency):

Library	Utility	Reference
Qt	Graphical Framework of application	www.qt.io
Visualization Toolkit (VTK)	Visualization of images, charts, etc.	www.vtk.org
Insight Toolkit (ITK)	I/O, image processing, etc.	www.itk.org
OpenCV	Machine Learning	www.opencv.org

• Different Components (can be C++ or Python):

Library	Utility	Reference
numpy	Higher level math operations	numpy.org
pyqt	User interface of some applications	wiki.python.org/moin/ PyQt
dipy	Diffusion Imaging	nipy.org/dipy







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