Cancer Imaging Phenomics Toolkit (CaPTk):

A Radio(geno)mics Software Platform for Leveraging Quantitative Imaging Analytics for Computational Oncology

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Primary Aim: To enable swift and efficient translation of cutting-edge academic research into clinically useful tools[1].

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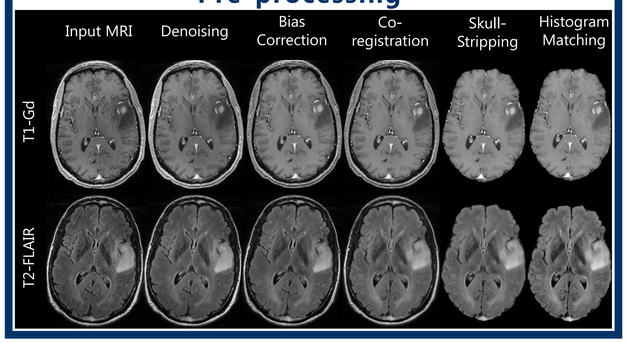
Target Audience:

1. ***Non-computational experts (radiologists, oncologists, clinicians, neuroscientists)*:** facilitating use of complex algorithms for clinically relevant studies through a user-friendly, light-weight interface.
2. ***Computational Imaging Scientists*:** allowing for batch-processing, as well as integration of new algorithms into a GUI based on ITK, VTK, and OpenCV.

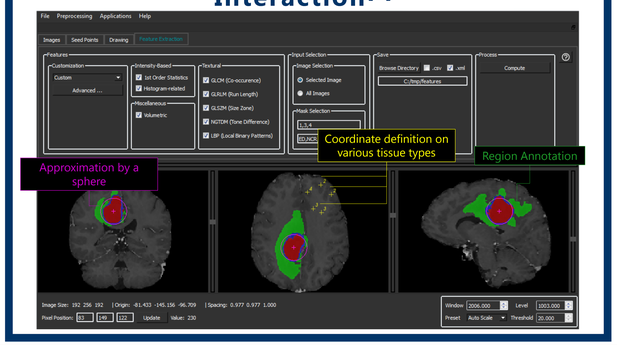
· Functionality ·

· 1st level ·

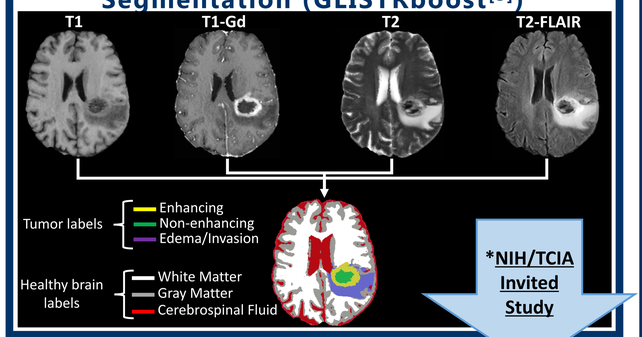
Pre-processing[2]



Interaction[1]

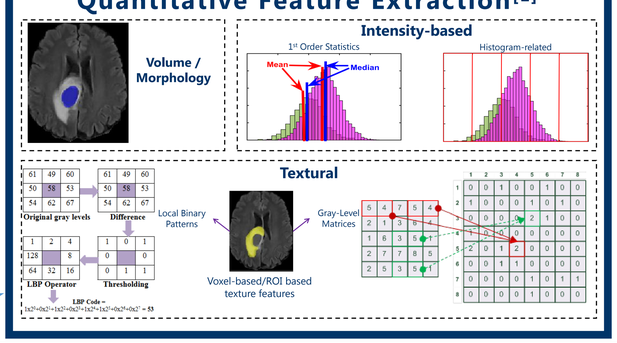


Segmentation (GLISTRboost[3])



***NIH/TCIA Invited Study**

Quantitative Feature Extraction[1]



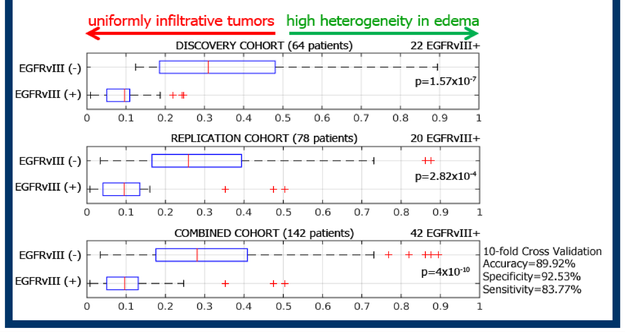
Feature Integration via Machine Learning

Published in Nature Scientific Data[4], enriching the TCGA-GBM & TCGA-LGG datasets with publicly available manual tumor segmentations and radiomic features[5,6].
A contribution towards repeatable, reproducible and comparative quantitative studies:

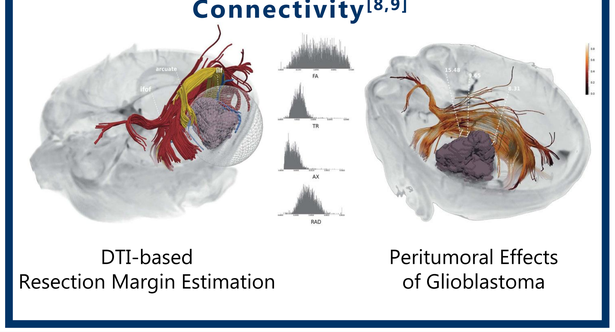
- Enabling direct utilization of the TCGA/TCIA glioma collections
- Allowing full utilization of their potential in clinical and computational studies

· 2nd level ·

Imaging Signature of EGFRvIII in GBM[7]



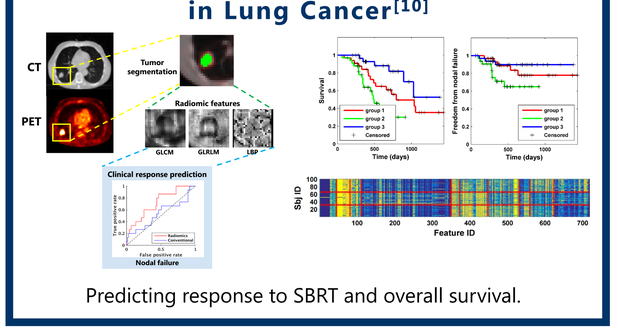
Computational Study of Brain Connectivity[8,9]



DTI-based Resection Margin Estimation

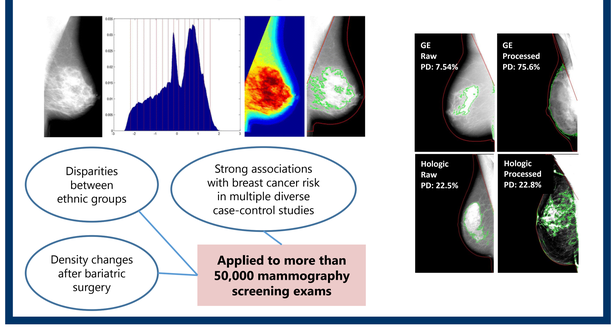
Peritumoral Effects of Glioblastoma

Radiomics Predicting Patient Outcomes in Lung Cancer[10]



Predicting response to SBRT and overall survival.

Breast Density Assessment[11-14]



· Extendibility ·

External algorithm integration in CaPTk, is possible in:

Source level

Tightest integration, providing memory-level access to all interactive functionalities, hence allowing for maximum optimization. The external application should be written in C++ and compiled alongside CaPTk.

Executable level

CaPTk offers a graphical interface to an existing application (not necessarily written in C++), allowing users to leverage CaPTk's functionality (e.g., interaction, feature extraction, modeling). Executable-level integration requires minor additions to CaPTk's source to create a menu option for the new application.

· Future Work ·

- **Application to other neurological diseases:** Meningioma; Multiple sclerosis
- **Additional predictive tools for GBM:** Survival[15]; Recurrence[16]; Distinct radiographic subtypes[17]
- **Integration of brain cognitive deficit measurement:** Vulnerability maps depicting brain connectivity, lead to future cognitive deficits
- Incorporation of a lattice-based strategy for **Breast Parenchymal Tissue Characterization**
- **Deep Learning** pipelines for segmentation[18] and prediction tasks.

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