Prediction of Pathological Complete Response to Neoadjuvant Chemotherapy in Breast Cancer Using Deep Learning with Integrative Imaging, Molecular and Demographic Data

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Motivations & Challenges

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- Early prediction on PCR to Neoadjuvant chemotherapy can help in treatment planning.

- Main problem we attempt to solve is:
  - CNN system can predict PCR before the chemotherapy
  - CNN system can process MR images, Molecular and Demographic Data
  - What is the best way in CNN to combine different resources of information

Methods – Image-only model

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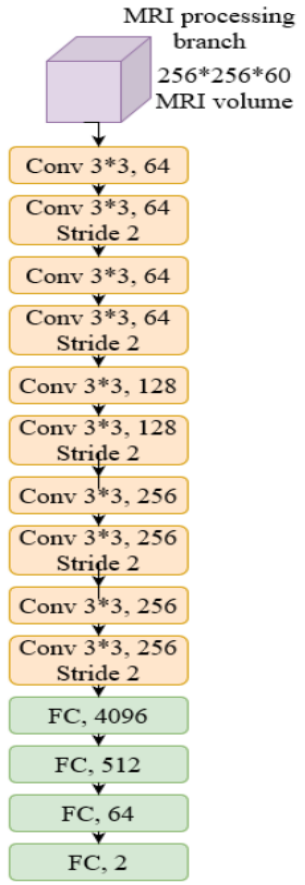
- The basic CNN model for processing the MR images.
- VGG-like model consisting of 10 convolutional layers.
- Replace maxpooling layer with convolutional layer with stride set as 2.
- Four fully connected layers at the end are in charge of the final prediction.



Methods – Parallel model

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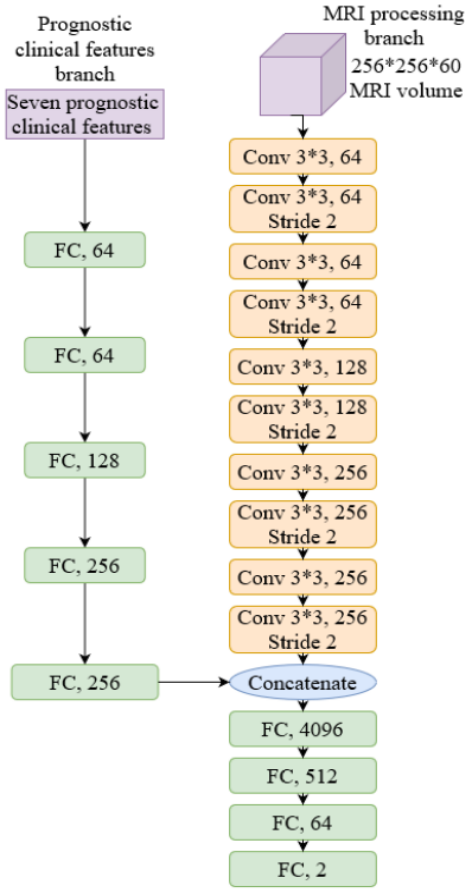
- Based on the basic image-only model, we proposed one more system to integrate non-imaging information into the CNN.
- One more branch consisting of five fully connected layers to process non-imaging data.
- Features extracted from imaging module and non-imaging module are concatenated before the last four fully connected layers.



Methods – Problems of parallel model

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1. P: Only one connection is established between imaging and non-imaging branches.
   - A: Multiple connections should be built in different intermediate levels.
2. P: Two branches are independent with each other.
   - A: Simulating radiologists reference imaging and non-imaging data at the same time, more interaction between two branches are needed.
3. P: Concatenation cannot solve the problem that features are in different scales.
   - A: Rather than simply putting two features together, other operations like multiplication can be deployed into the system.

Methods – Interactive model

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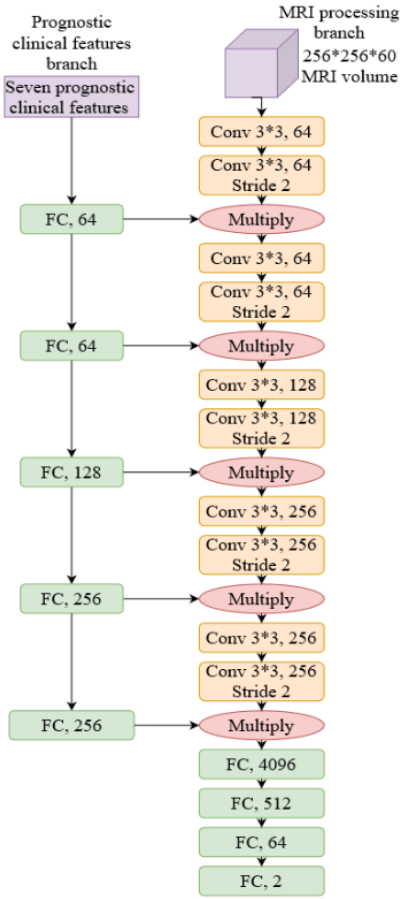
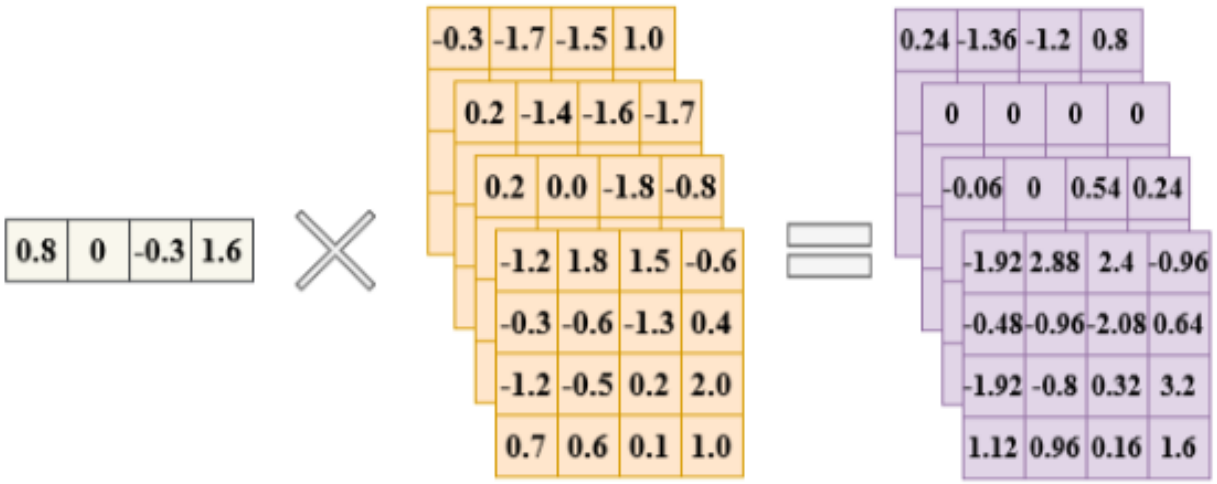
- To solve the problem discussed, we have the final version of the system.
- In the intermediate levels of the system, we deployed 5 connections between two branches.
- The connection is operated by channel-wise multiplication.
- By channel-wise multiplication, non-imaging features will guide the imaging branch in feature maps extraction and selection.



Methods – Channel-wise Multiply



Features from non-imaging branch will emphasis or restrain the corresponding feature maps from imaging branch

Dataset

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- 112 patients from I-SPY-1 TRIAL (2002-2006)
- stage 2 or 3 breast cancer
- breast tumors at least 3 cm in size
- T1 post-contrast breast MR images obtained at pre-neoadjuvant chemotherapy
- Seven non-imaging features

Parameter	Description	Data Type
Age	Patient Age (Years)	Demographic
Race	1=Caucasian 2=African American 3=Asian 4=Native Hawaiian/Pacific Islander 5=American Indian/Alaskan Native 6=Multiple race	Demographic
Estrogen Receptor (ER)	0=Negative 1=Positive 2=Indeterminate	Molecular
Progesterone Receptor (PR)	0=Negative 1=Positive 2=Indeterminate	Molecular
HER2 Status	0=Negative 1=Positive -1=indeterminate or not done	Molecular
3-level HR/HER2 category	1=HR Positive, HER2 Negative 2=HER2 Positive 3=Triple Negative	Molecular
Ki-67	1=<10% 2=10-20% 3=>20%	Molecular

Results

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Table 2. Prediction performance comparison.

	Imaging-Only-Model	Parallel-Model	Interactive-Model
Accuracy	0.7407	0.7846	0.8300
AUC	0.5758	0.5871	0.8035
Sensitivity	0.2229	0.4000	0.6822
Specificity	0.9222	0.8929	0.8822
F1 score	0.3590	0.5525	0.7694

Results

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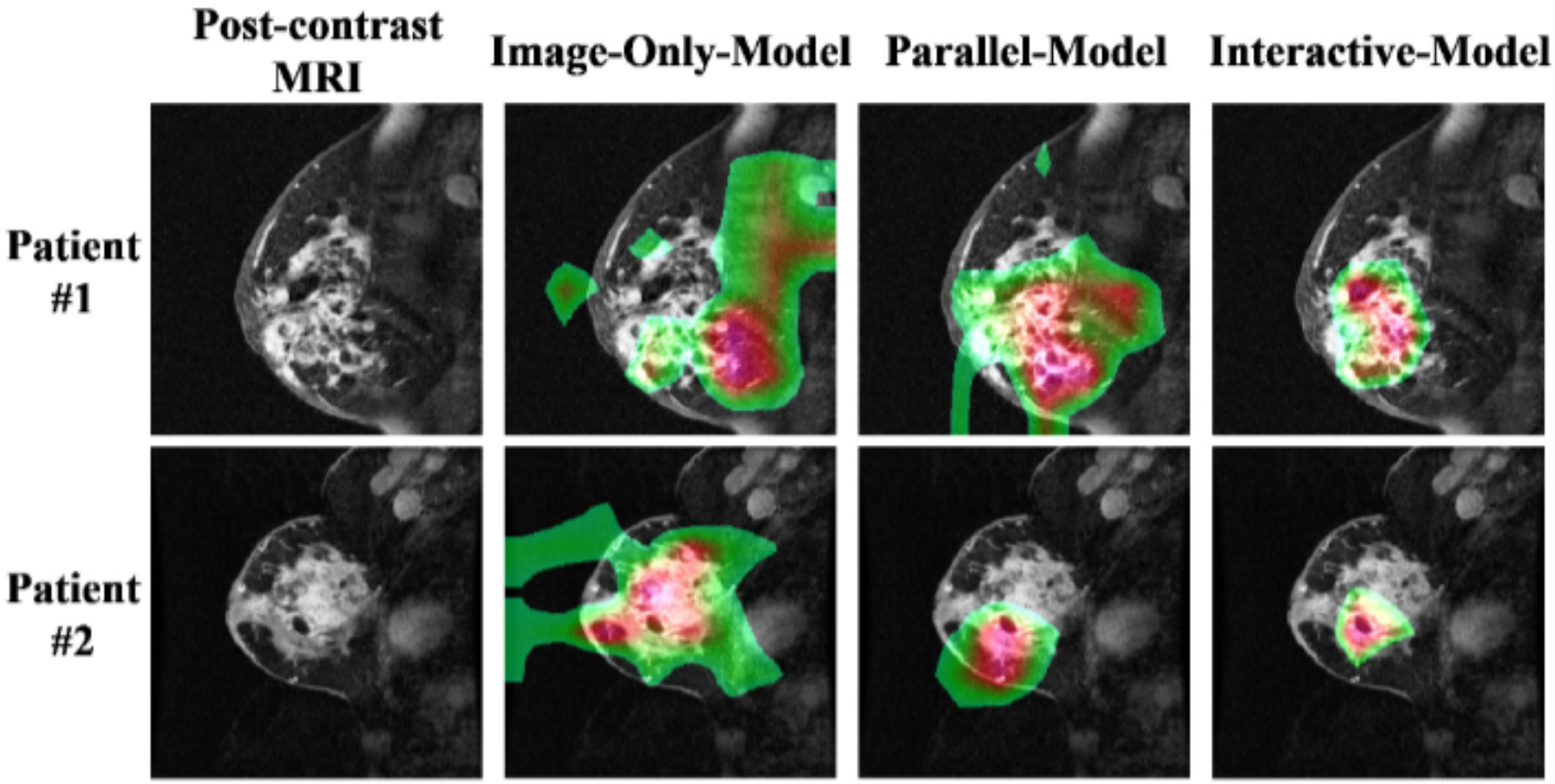

Limits &Future Work

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- A larger dataset should be used to train the model to improve generalizability of the model.
- We also plan to incorporate multiple time points during NAC instead of only pre-treatment time point.
- More modality of MRI (i.e., T2-weighted MRI and diffusion-weighted MRI) should be incorporated into the system.