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PDXportal as an Integration Tool for Image Features Indicative of Treatment Response in PDX Models and Patients as a Predictor of Patient Outcomes

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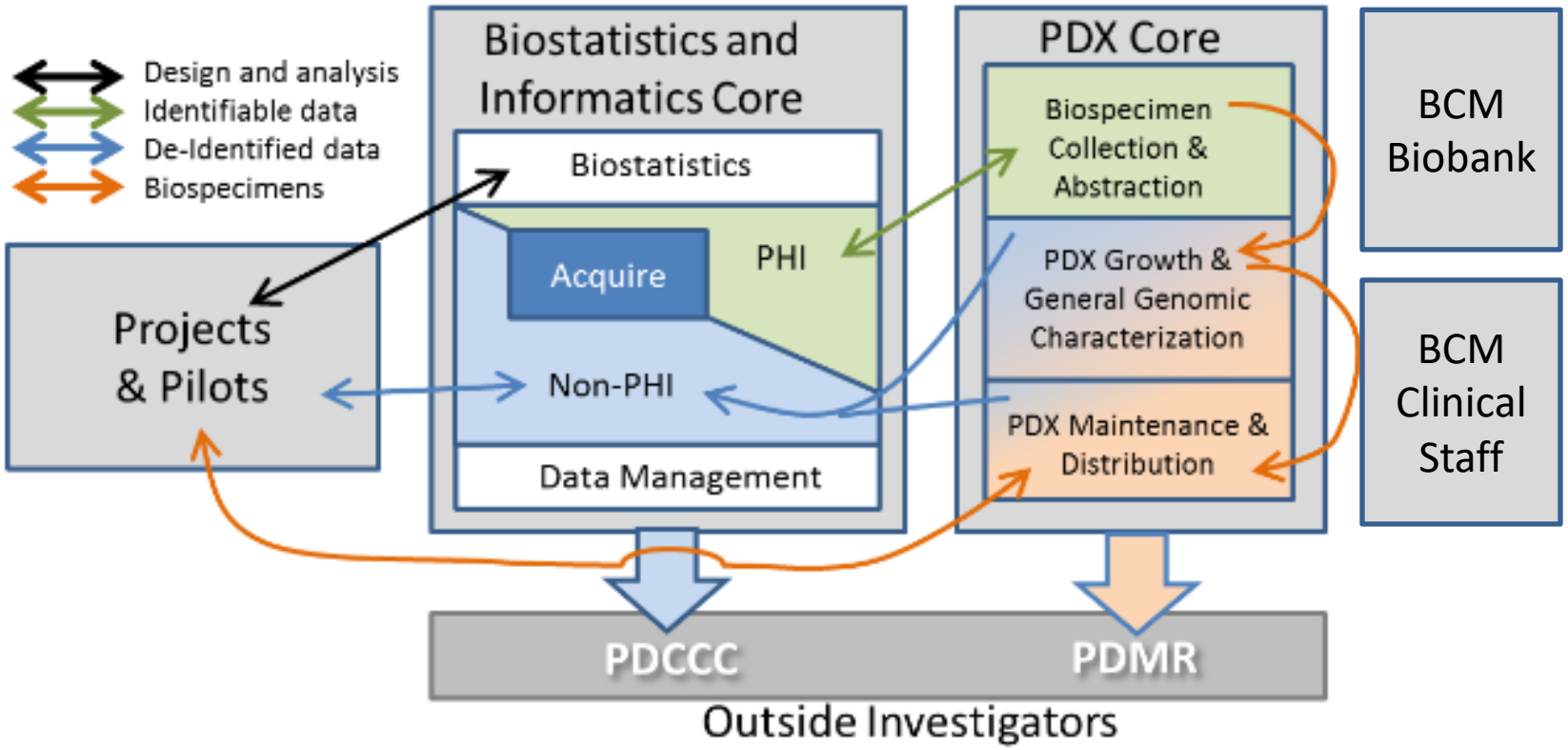
PDXportal: Solution for a Complex Problem

Data associated with PDX modeled is multilayered and involves many moving parts and stakeholders: patient data, biospecimens, HIPPA & privacy considerations, PDX transplantation conditions, model testing, model selection & study design, model & data distribution



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PDXportal

- Patient-Derived Xenografts (PDX) are developed by transplanting human tumor specimen into mice.
- The PDX models enable translational research on living patient tissues and are frequently used for drug testing and pre-clinical trials.
- To fully utilize PDX models several types of data must be collected and managed including de-identified clinical patient, patient genomic, PDX model laboratory and PDX study data generated from multiple sources.
- To facilitate usability of these data, the BCM biomedical informatics core created a PDX visualization portal, **BCM PDXportal** (https://pdxportal.research.bcm.edu/), by combing the patient clinical data, sequencing data, and model data and applying web-based data visualization tools.

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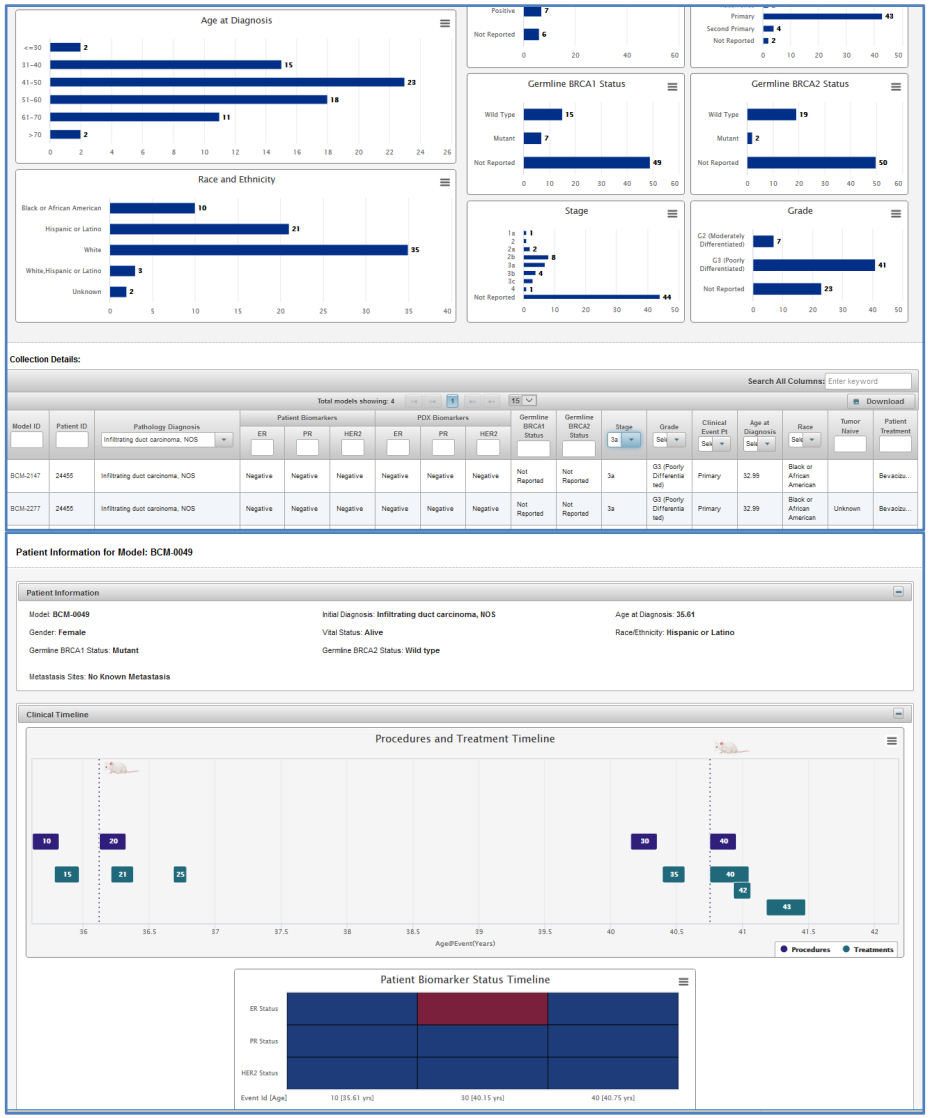
Public Model Selection & Private Model Management

- Collections are arranged by disease groups
- Collections are summarized in graphs representing standardized and disease specific clinical treatment determinants
- Data is represented in a table with multi-factor filtering to enable model selection
- Detailed patient chronological clinical history is provided.
- Private models are blocked from public viewing and selection
- Private models can be shared with specific collaborators
- Clinical timeline identifies when the model specimen was collected and when multiple models are created on a patient
- Patient treatment regimes and responses are captured.



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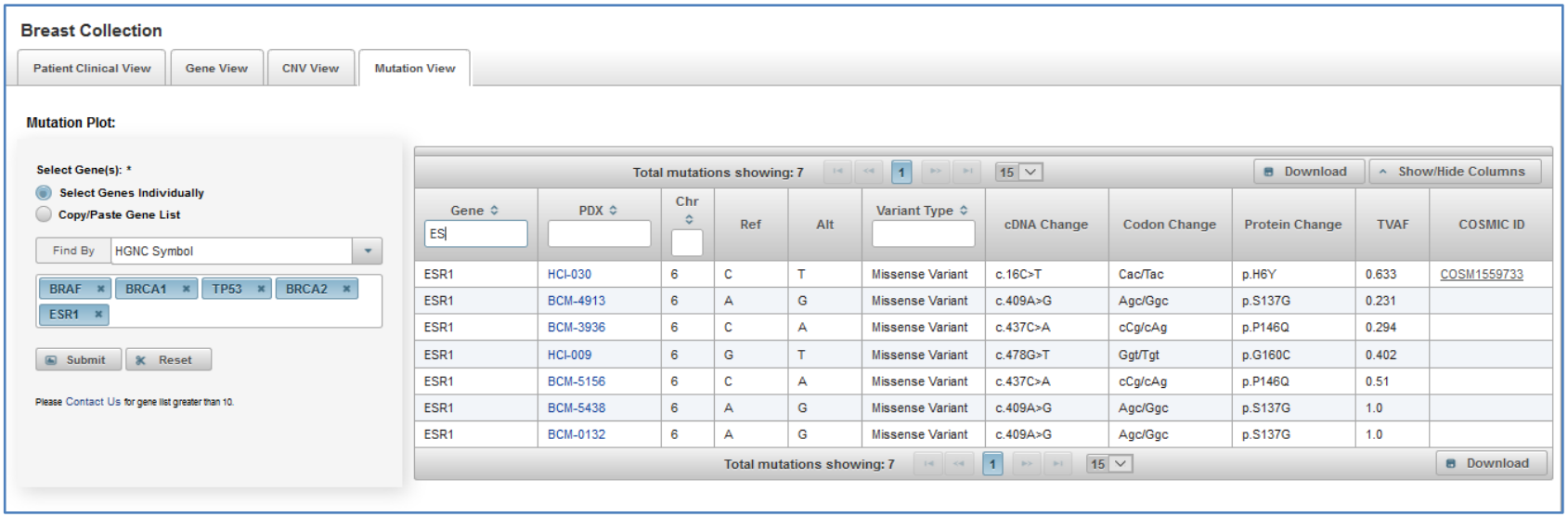
Omics & Imaging Integration

- Gene data is captured within the Gene Expression View, Copy Number Variations, and Gene Mutation Views. The PDXportal integrates with the multi-omics analysis tool, LinkedOmics (Zhang) to provide gene mutation frequency plots and CNV heat maps.
- PDX model and patient hematoxylin and eosin (H& E) slides and immunohistochemistry (IHC) slides are stored in a noSQL data base, for side by side comparisons. Future directions include integration with Stanford's ePAD (Rubin) MRI image viewer as predictive evidence of treatment response.



Acknowledgements

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