CLINICAL PROTEOMIC TECHNOLOGIES FOR CANCER

Integrating Biospecimen Collection, Clinical Information and Proteomics for Cancer Biomarker Research

The Analytical Proteomics Team

NATIONAL CANCER INSTITUTE

Agenda

CLINICAL PROTEOMIC TECHNOLOGIES FOR CANCER

1. Introductions
2. Opening statements
3. Methods
4. Sample collection
5. Clinical data management
6. Follow-up samples
7. Recent studies
8. Concluding remarks

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Analytical Proteomics Team (APT)

- **Member of Clinical Proteomic Technology Assessment for Cancer (CPTAC) Consortium**
- **APT includes:**
  - Purdue University
  - Indiana University
  - Indiana University School of Medicine
  - University of Louisville
  - Hoosier Oncology Group

Opening Statement

CLINICAL PROTEOMIC TECHNOLOGIES FOR CANCER

High quality biospecimens along with corresponding anonymized patient clinical information are fundamental to successful cancer biomarker research.

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Methods

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1. Professional sample collection and management
2. Flexible and intuitive web-based clinical data management system
3. Follow-up samples from all enrolled patients at 3 month intervals

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Sample collection

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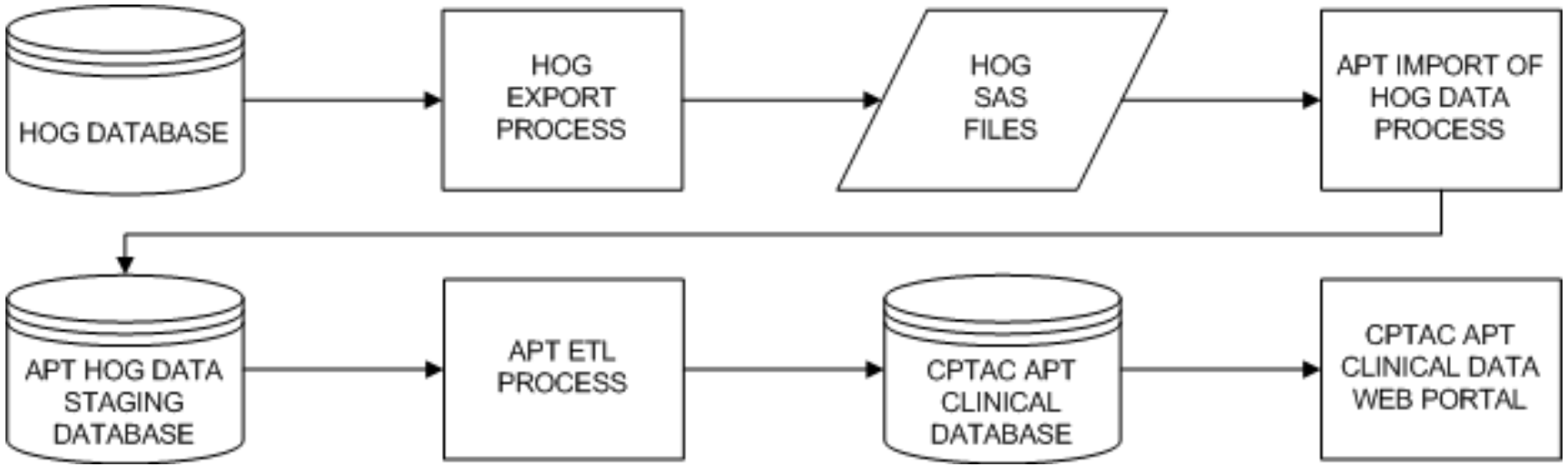
Hoosier Oncology Group (HOG)

- A not-for-profit providing management of oncology patient recruitment for clinical trials and biospecimen procurement
- Provide high quality and standardized biospecimens
- Activates an extensive network of oncologists to implement the sample collection protocol
- De-identified patient clinical information is supplied with the biospecimens to the research team
- Our sample collection = a professional clinical trial
- Utilizes sample collection kit to standardize collection

Clinical data management

- Flexible and intuitive web-based system
- Clinical information provided by HOG
- Aim to help researchers and clinicians procure the clinical data required for their experiments
- Main qualitative objective was to ease the process of finding relevant clinical information to match experimental data
- Researchers and clinicians can invest time in data analysis instead of attempting to track and coordinate clinical metadata.

Data import


HOG DATABASE
HOG EXPORT PROCESS
HOG SAS FILES
APT IMPORT OF HOG DATA PROCESS
APT HOG DATA STAGING DATABASE
APT ETL PROCESS
CPTAC APT CLINICAL DATABASE
CPTAC APT CLINICAL DATA WEB PORTAL

Web portal

Select	Patient ID	Age	Race	Ethnicity	Medical History	Details	Invasive Comment	Both Breast	Surgery	Tumor Size	Grade
☐	120-0001	79	White	Non-Hispanic	Cardiovascular, Musculoskeletal/Soft Tissue	Show	UNKNOWN	No	Yes	.5	G1
☐	120-0002	44	White	Non-Hispanic	UNKNOWN	Show	10% DCIS	No	Yes	1.1	G3
☐	120-0004	39	White	Non-Hispanic	UNKNOWN	Show	UNKNOWN	No	Yes	.2	G2
☐	120-0006	72	White	Non-Hispanic	UNKNOWN	Show	UNKNOWN	No	Yes	.35	G1

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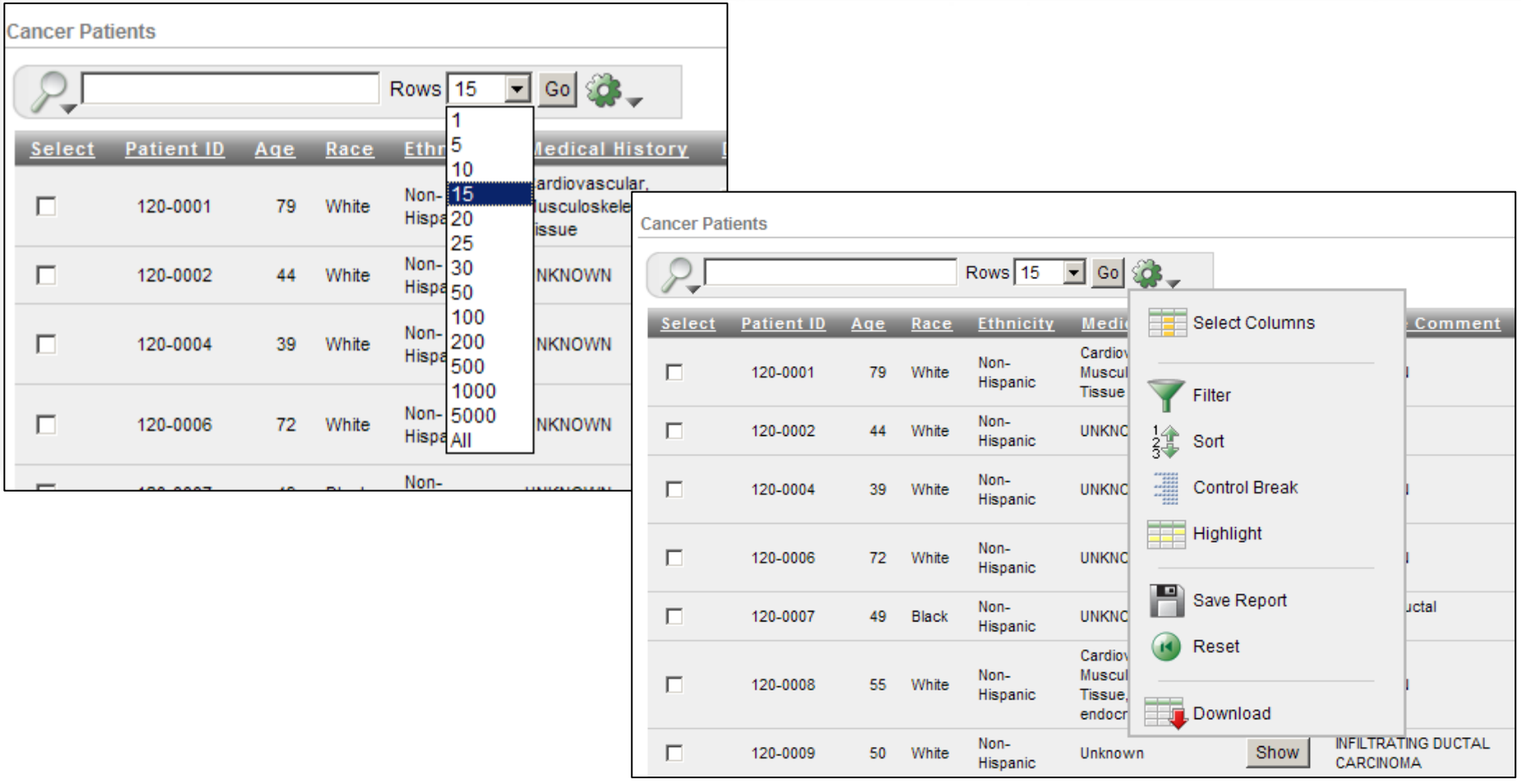
Functionality



Detailed Patient Information

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☐	120-0008	55	White	Non-Hispanic	Cardiovascular, Musculoskeletal/Soft Tissue, Neurological, endocrine	Hide	UNKNOWN		No		

Significant Medical History

☐	120-0004	39	White	Non-Hispanic	UNKNOWN	Show	UNKNOWN	No	Yes	2	G2
☐	120-0006	72	White	Non-Hispanic	UNKNOWN	Show	UNKNOWN	No	Yes	35	G1

120-0008	endocrine	thyroid disorder

1 - 4

Prior Chemotherapy Treatment

Patient Id	Chemotherapy Type	Chemotherapy Description	Setting	Start Date	Stop Date
120-0008	Chemotherapy Multiple Agent Systemic	"Adriamycin, Cytoxan"	UNKNOWN	UNKNOWN	UNKNOWN

1 - 1

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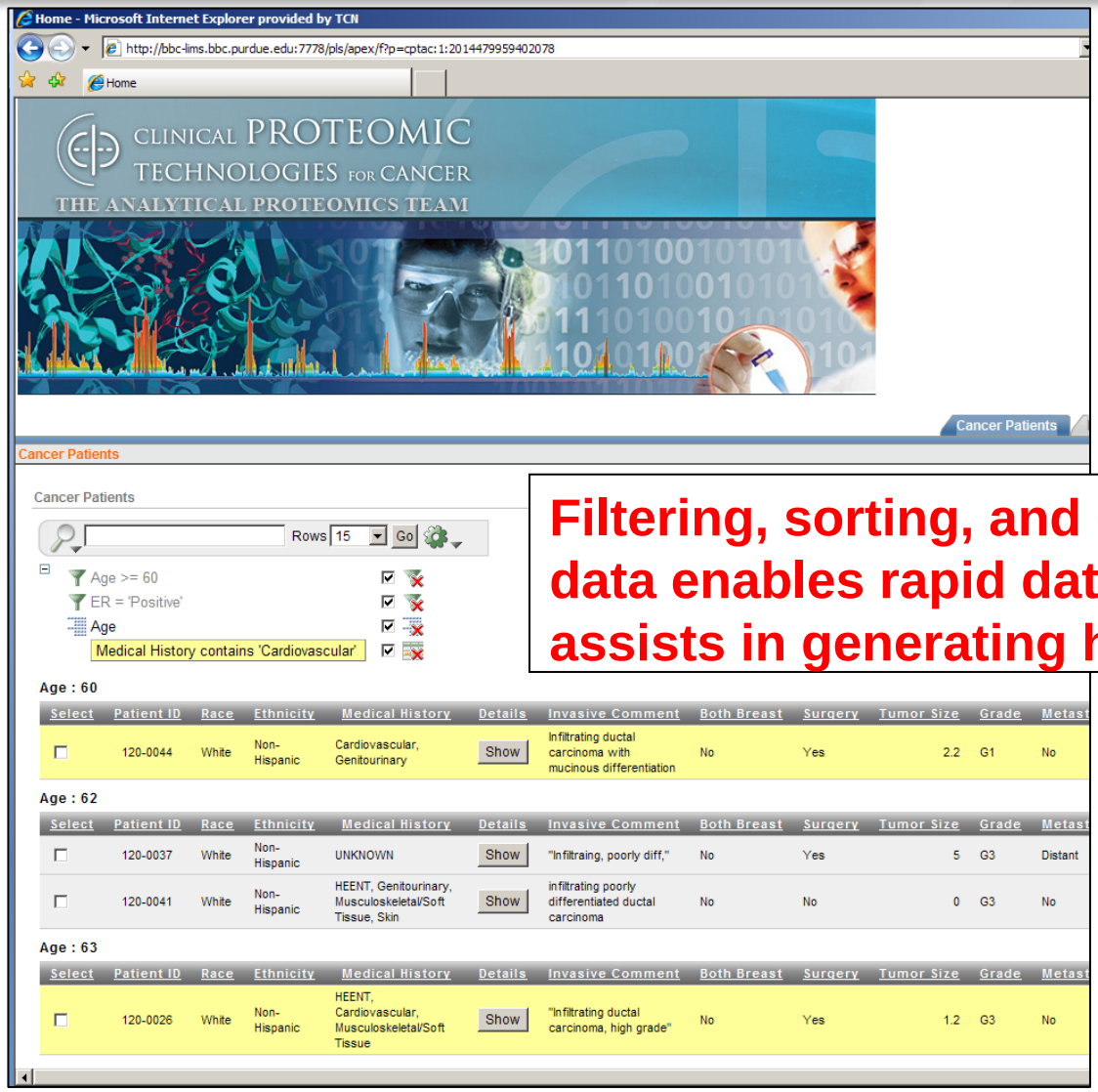
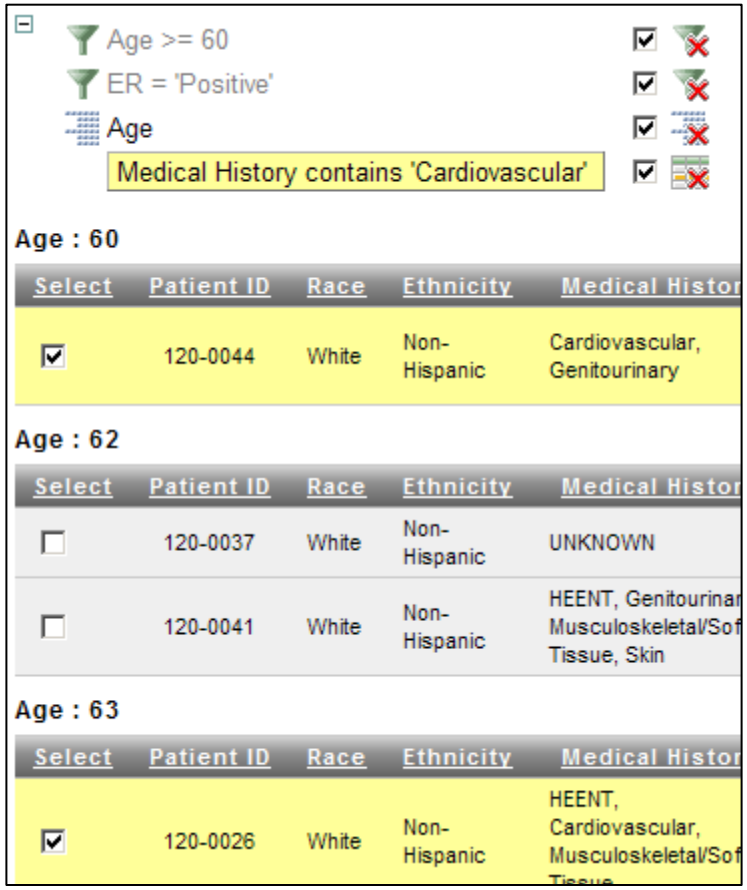
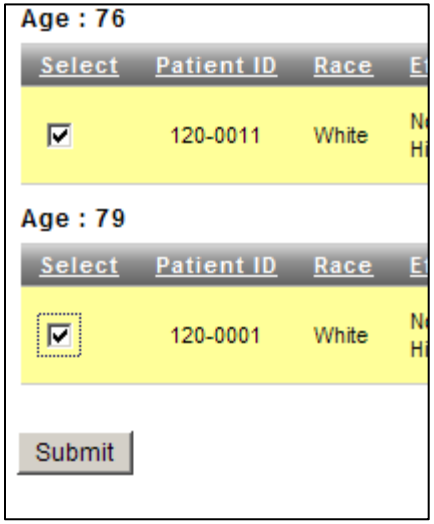
Data reduction and hypothesis generation



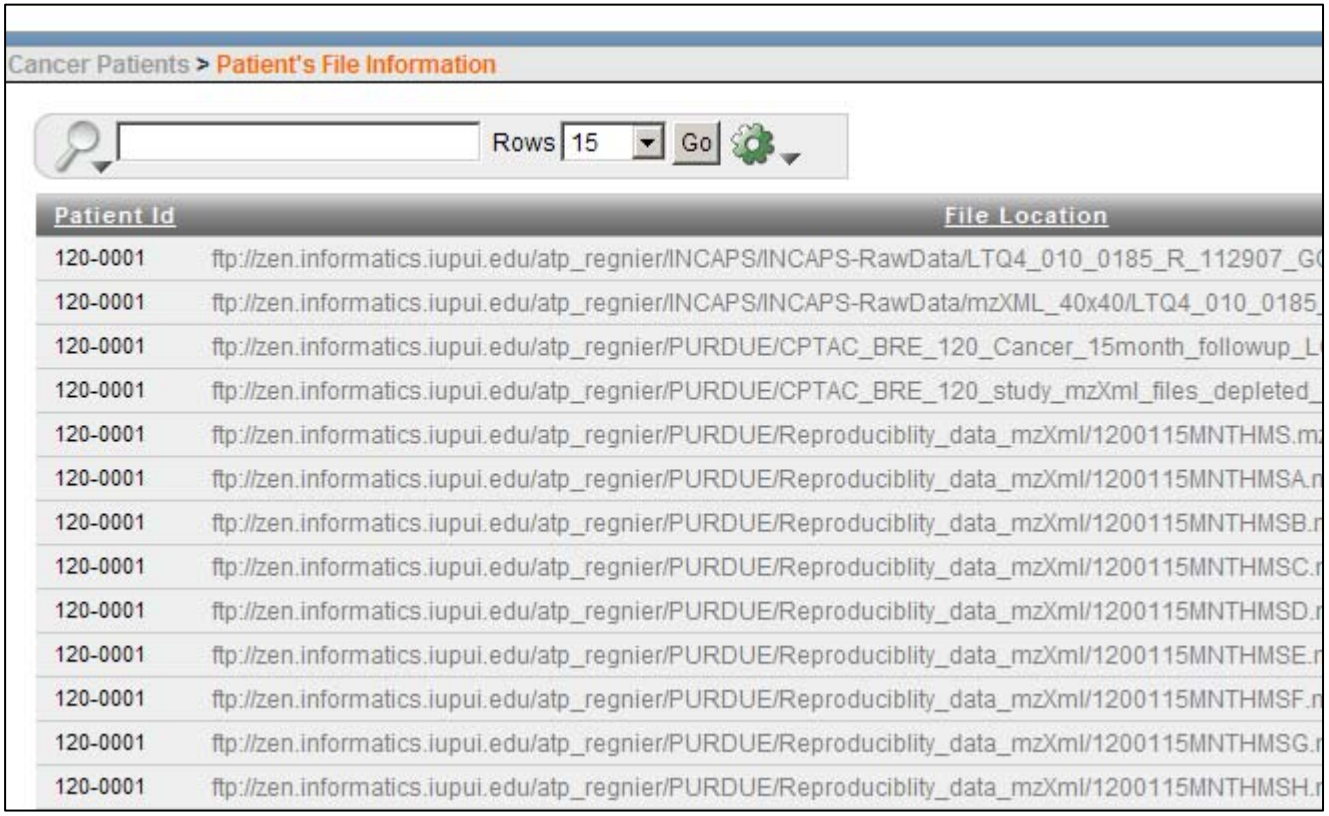
Filtering, sorting, and grouping of data enables rapid data reduction and assists in generating hypotheses.

Patient Selection





Experimental data



Cancer Patients > Patient's File Information

Rows 15 Go

Patient Id	File Location
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/INCAPS/INCAPS-RawData/LTQ4_010_0185_R_112907_G
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/INCAPS/INCAPS-RawData/mzXML_40x40/LTQ4_010_0185
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/CPTAC_BRE_120_Cancer_15month_followup_L
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/CPTAC_BRE_120_study_mzXml_files_depleted_
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/Reproduciblity_data_mzXml/1200115MNTHMS.m
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/Reproduciblity_data_mzXml/1200115MNTHMSA.r
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/Reproduciblity_data_mzXml/1200115MNTHMSB.r
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/Reproduciblity_data_mzXml/1200115MNTHMSC.r
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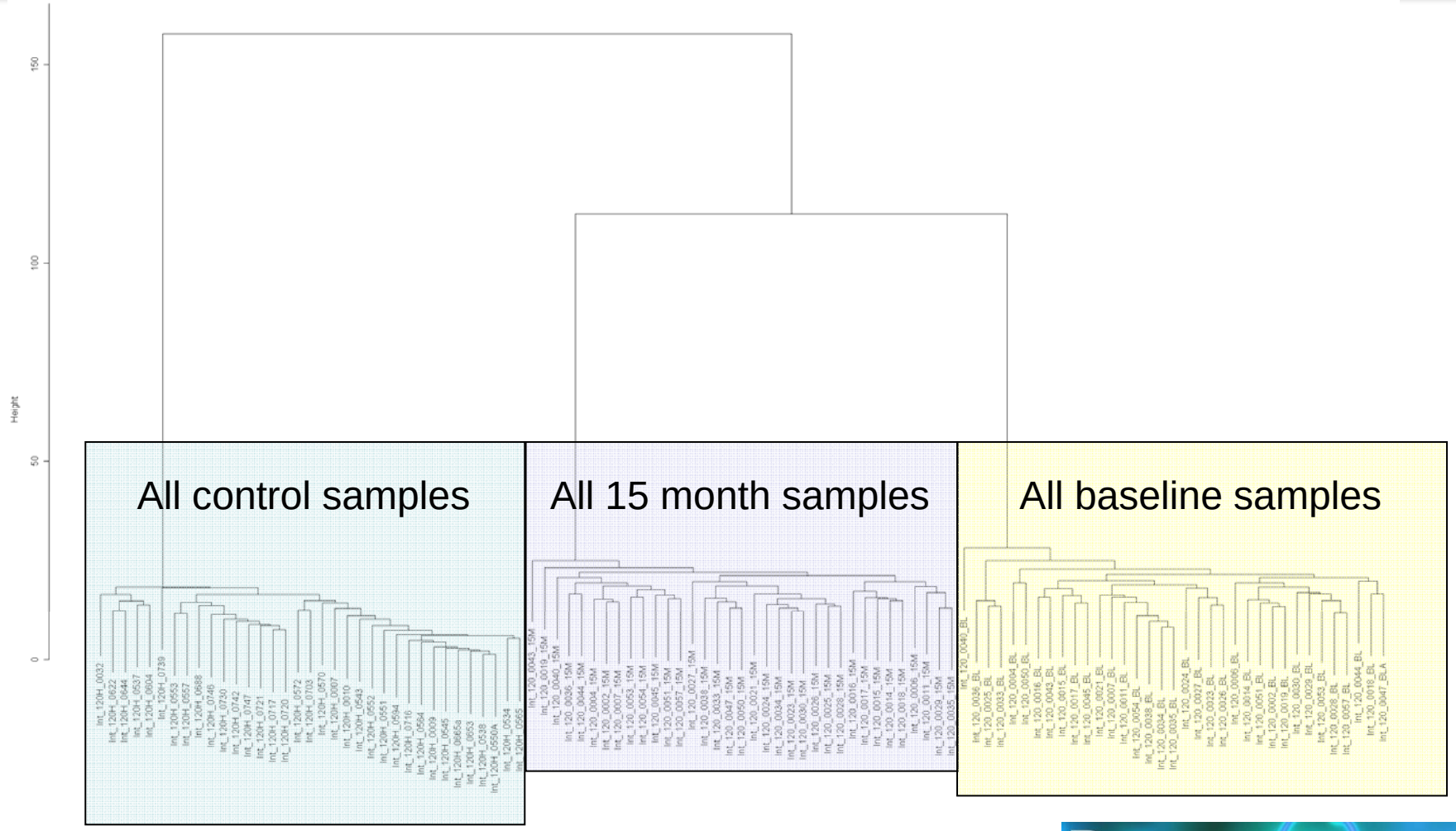
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/Reproduciblity_data_mzXml/1200115MNTHMSG.r
120-0001	ftp://zen.informatics.iupui.edu/atp_regnier/PURDUE/Reproduciblity_data_mzXml/1200115MNTHMSH.r

Follow-up samples

- **Follow-up samples from all enrolled patients at 3 month intervals**
- **Employed clinical data system to compare age-matched proteomic profiles (35 x 35 x 35)**
  - Control volunteer samples
  - Baseline breast cancer patients (with cancer diagnosis and about to begin a new treatment regime)
  - Same breast cancer patients at 15 months
- **Proteomic profiles of the 15-month samples group together and away from baseline samples suggesting that treatment affects the proteomic profile**

Hierarchical Clustering for 35 x 35 x 35 study



Concluding remarks

- High quality biospecimens along with corresponding anonymized patient clinical information provides a foundation for successful cancer biomarker research.
- Data-driven nature of cancer biomarker research requires software tools that enable researchers to generate hypotheses and perform data reduction
- Follow up samples provide another dimension for studies.
- Support from the NCI Clinical Proteomics Technology Assessment for Cancer (CPTAC) program is gratefully acknowledged