

clinical data

observational &
scientific data

computation &
visualization

decision support

cceHUB

Sharing , Exploring and Analyzing Data
An Environment for Collaborative Cancer Research

Ann Christine Catlin
HUBbub
04-06-2011

Master plan for the Cancer Care Engineering Colorectal Cancer Study

1. Blood Sample Acquisition

Sample Processing, Annotation, Distribution
Clinical Patient Data Collection

IU Simon Cancer Center

2. OMIC Laboratory Analysis

Data & Knowledge Acquisition

*Xu Lab **Lipidomics** IU School of Medicine*

*Raftery Lab **Metabolomics** Purdue*

*Regnier Lab **Glycoproteomics** Purdue*

*Bindley Lab **Global Proteomics** Purdue*

*Teegarden Lab **Vitamin D** Purdue*

*Klaunig Lab **Oxidative Stress** IU School of Medicine*

3. Predictive Modeling

Data Synthesis & Analysis

Knowledge Acquisition

*Zhang Group **Integrative Models** Purdue*

*Sherer **Population-based Models** VA Hospital*

*Chen **Biological Network Models** IUPUI*

4. Visual Analytics

Data Exploration & Analysis

Knowledge Acquisition

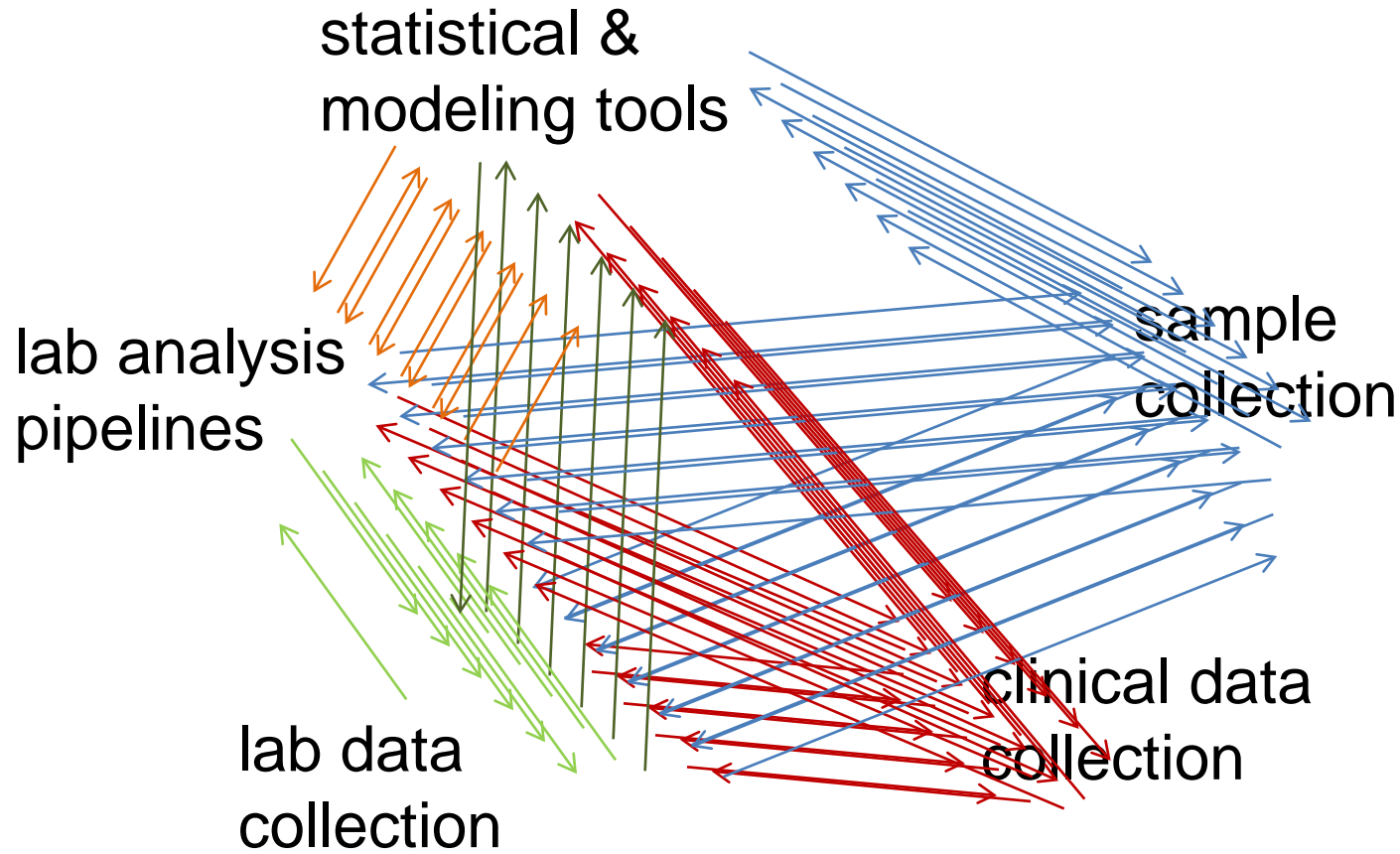
*Ebert Group **PURVAC** Purdue*

5. Iterative Feedback & Validation

CCE Research Community



molecular signatures for colorectal cancer that predict
susceptibility, treatment response and ultimate treatment outcome

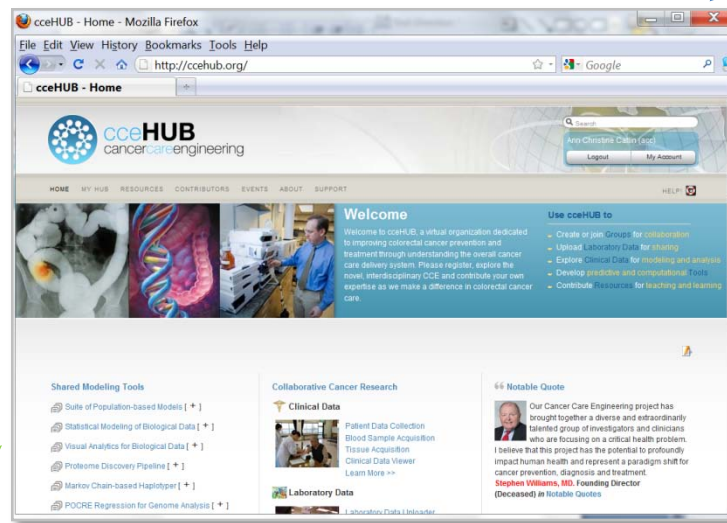


A single portal : sharing data, tools, analysis & knowledge

statistical &
modeling tools

sample
collection

lab analysis
pipelines

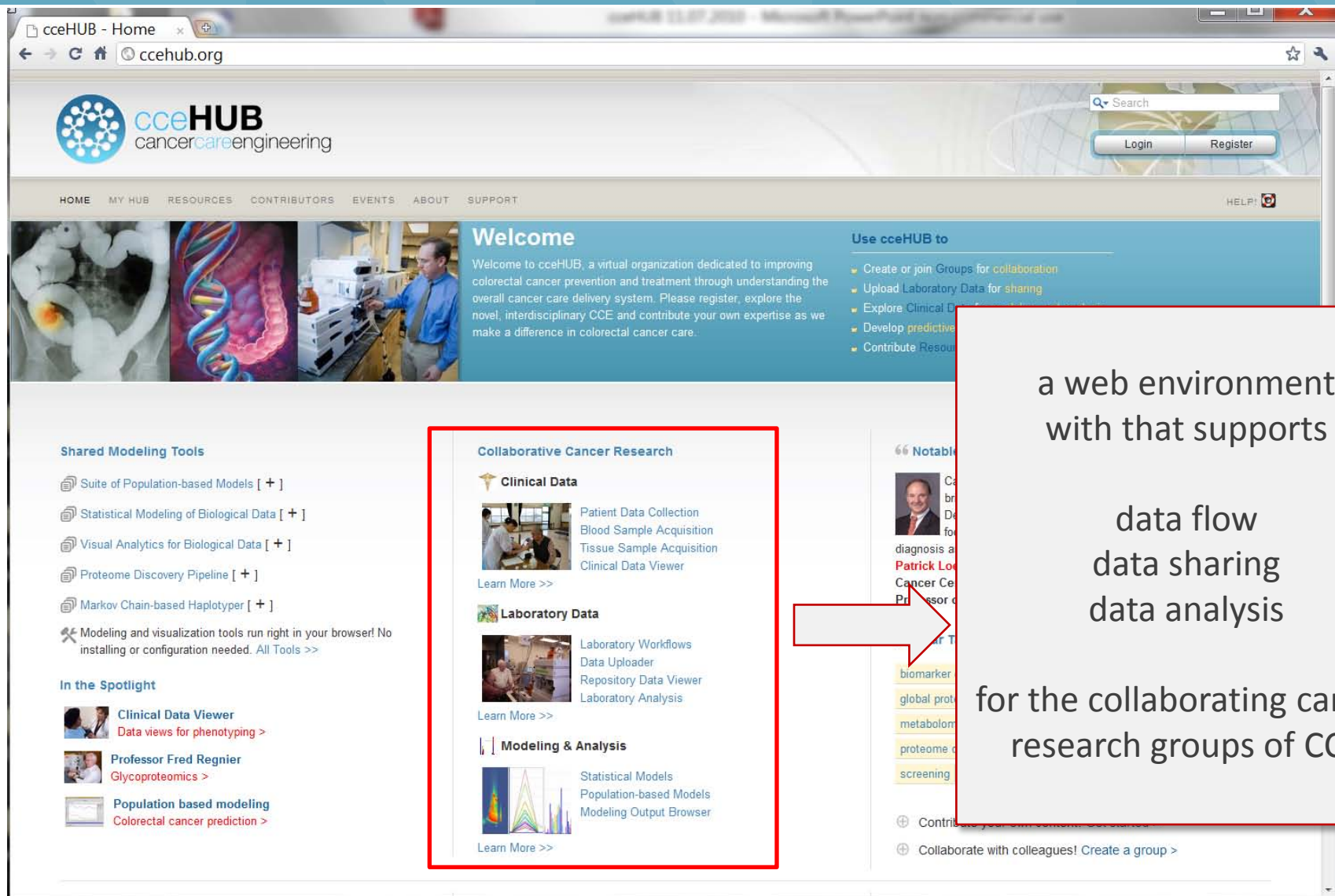


clinical data
collection

lab data
collection

cancer research
groups worldwide

A single portal: sharing data, tools, analysis & knowledge



The screenshot shows the cceHUB website interface. At the top, there is a search bar and buttons for 'Login' and 'Register'. Below the navigation menu, a 'Welcome' message is displayed, followed by a list of features under 'Use cceHUB to'. The main content area is divided into several sections: 'Shared Modeling Tools', 'Collaborative Cancer Research', and 'In the Spotlight'. The 'Collaborative Cancer Research' section is highlighted with a red box and contains sub-sections for 'Clinical Data', 'Laboratory Data', and 'Modeling & Analysis'. A red arrow points from this section towards a text box on the right.

a web environment with that supports

- data flow
- data sharing
- data analysis

for the collaborating cancer research groups of CCE

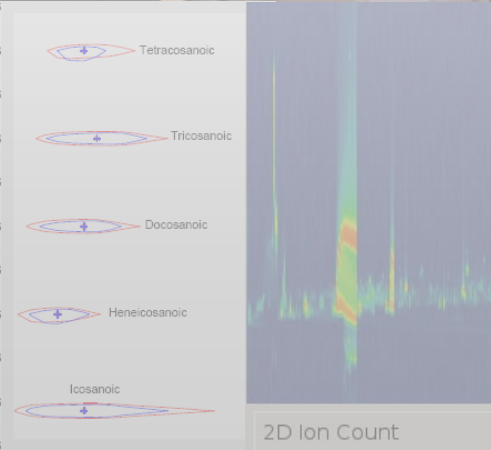


clinical data

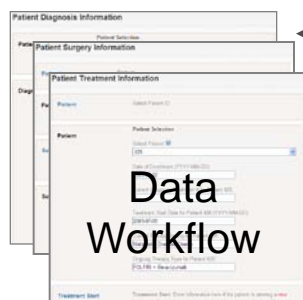
Clinical Research Team and Physicians



laboratory analysis



predictive modeling tools

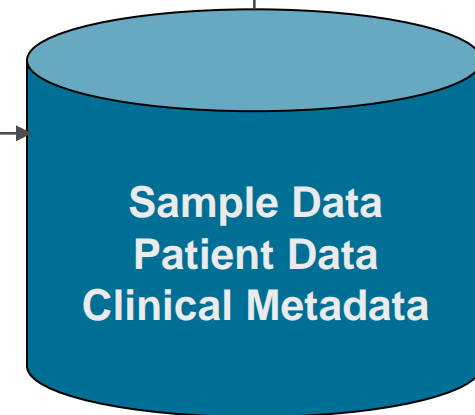


Data contribution from clinical team

Patients Diagnosis, Treatments, Surgeries, Lifestyle, Diet, Demographics, ...

Samples Collection, Processing, Protocols, Distribution, Tracking, ...

Automatic Metadata Processing



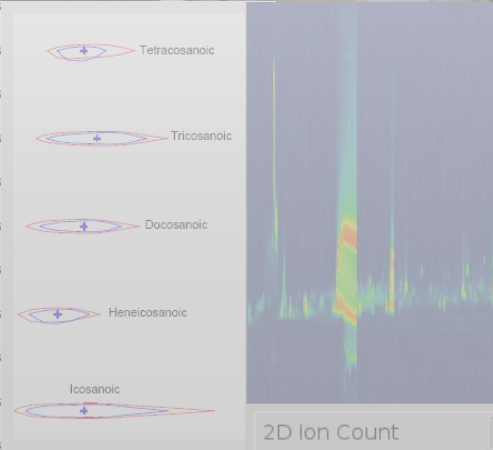
cceHUB Database



clinical data




laboratory analysis




predictive modeling tools

CL



Clinical Data



- [Patient Data Collection](#)
- [Blood Sample Acquisition](#)
- [Tissue Acquisition](#)
- [Clinical Data Viewer](#)
- [Learn More >>](#)

Clinical Data Flow

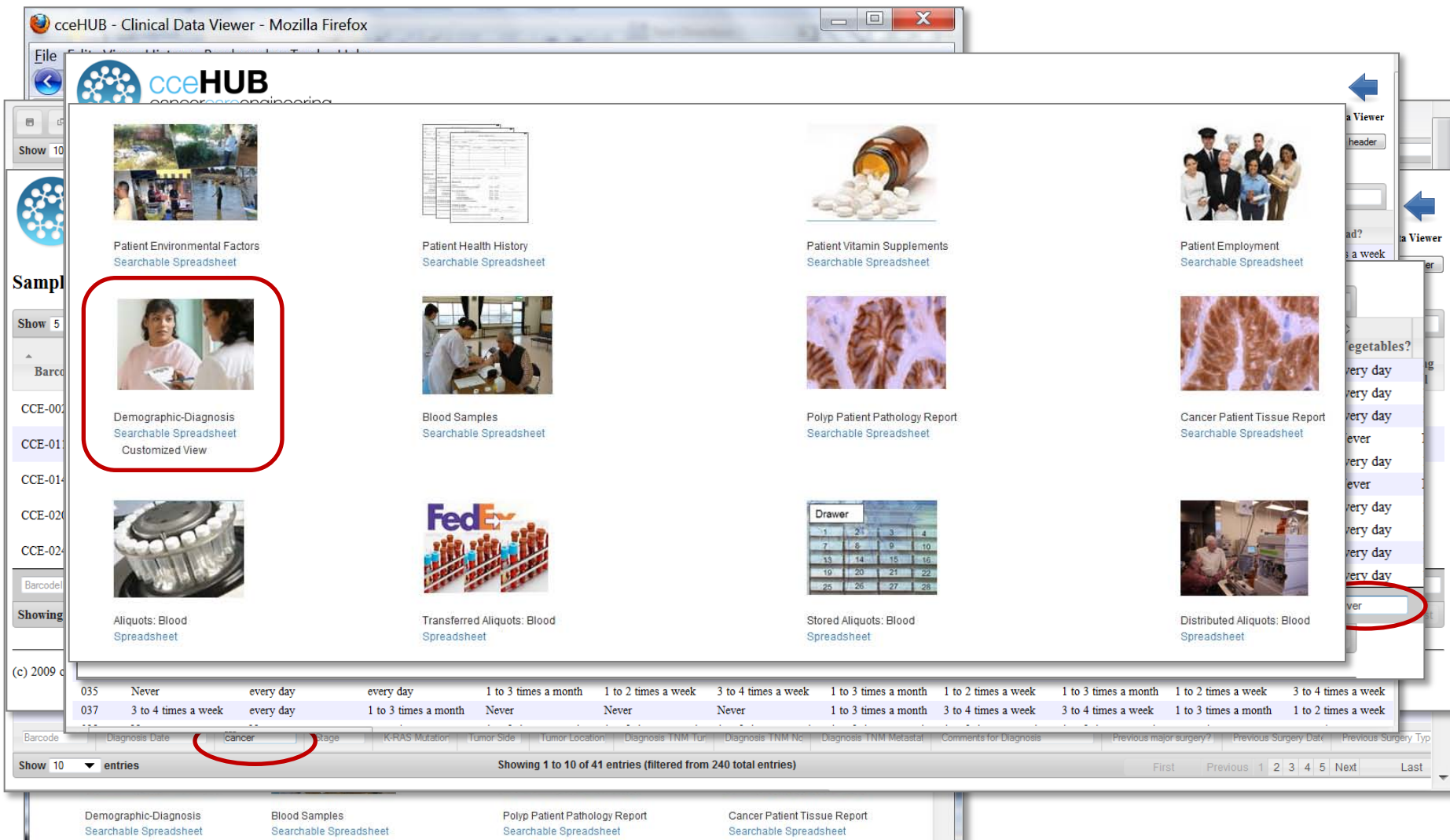
- nightly pull from hospital e-records
- patient data collection
- sample tracking
- data annotation

- clinical data archive
- blood sample bio-repository
- patient and sample linkage

- data viewing
- data search, filter & explore



cceHUB - Clinical Data Viewer - Mozilla Firefox



The interface displays a grid of data view options, each with a representative image and a title:

- Patient Environmental Factors Searchable Spreadsheet
- Patient Health History Searchable Spreadsheet
- Patient Vitamin Supplements Searchable Spreadsheet
- Patient Employment Searchable Spreadsheet
- Demographic-Diagnosis Searchable Spreadsheet Customized View** (highlighted with a red circle)
- Blood Samples Searchable Spreadsheet
- Polyp Patient Pathology Report Searchable Spreadsheet
- Cancer Patient Tissue Report Searchable Spreadsheet
- Aliquots: Blood Spreadsheet
- Transferred Aliquots: Blood Spreadsheet
- Stored Aliquots: Blood Spreadsheet
- Distributed Aliquots: Blood Spreadsheet

Below the grid is a table of filtered results. The 'Diagnosis' column is highlighted with a red circle, and the value 'cancer' is selected. The table shows 10 entries, with the first two rows highlighted in blue.

Barcode	Diagnosis Date	Diagnosis	Stage	K-RAS Mutation	Tumor Side	Tumor Location	Diagnosis TNM Tumor	Diagnosis TNM N	Diagnosis TNM Metastasis	Comments for Diagnosis	Previous major surgery?	Previous Surgery Date	Previous Surgery Type
035	Never	every day	every day	1 to 3 times a month	1 to 2 times a week	3 to 4 times a week	1 to 3 times a month	1 to 2 times a week	1 to 3 times a month	1 to 2 times a week	3 to 4 times a week		
037	3 to 4 times a week	every day	1 to 3 times a month	Never	Never	Never	1 to 3 times a month	3 to 4 times a week	3 to 4 times a week	1 to 3 times a month	1 to 2 times a week		

Showing 1 to 10 of 41 entries (filtered from 240 total entries)

Demographic-Diagnosis Searchable Spreadsheet | Blood Samples Searchable Spreadsheet | Polyp Patient Pathology Report Searchable Spreadsheet | Cancer Patient Tissue Report Searchable Spreadsheet

Clinical data : some stats

Database	Total Patients	Diagnosis % Data	Lifestyle % Data	Cancer/Polyp Patients	Treatment % Data
patients	240	100%	70%	41 / 92	100%

First patient CCE001 enrolled on 04/02/2009 (the day cceHUB went live)

Most recent patient CC285 enrolled on 02/15/2011

Most recent data : neoadjuvant chemoradiation treatment for patient CCE156 on 04/02/2011

Maximum patients enrolled on a single day 09/23/2009 = 9

web-forms to track patient and sample data flow : 12

accesses to clinical data viewer 04/02/2009 – 05/25/2010 : > 15,000

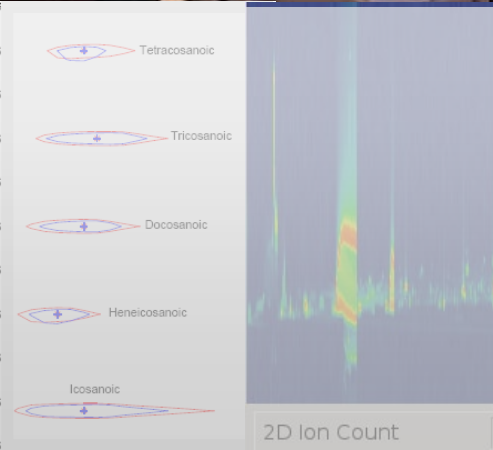
Database	Total Samples	Total Aliquots	Sample Tracking Web-forms	# instances cceHUB used to find missing aliquot
samples	267	5073	sample processing sample transfer sample storage sample distribution	52 (we track sample barcodes, location, entry person, entry date)



clinical data



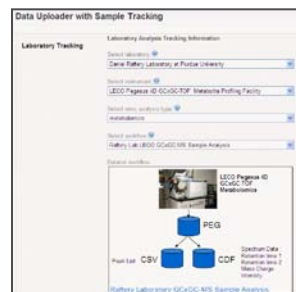
laboratory analysis



predictive modeling tools

Research Labs

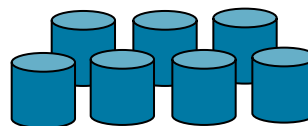
Metabolomics, Lipidomics,
Global Proteomics,
Glycoproteomics, Vitamin D,
Oxidative Stress, Genomics



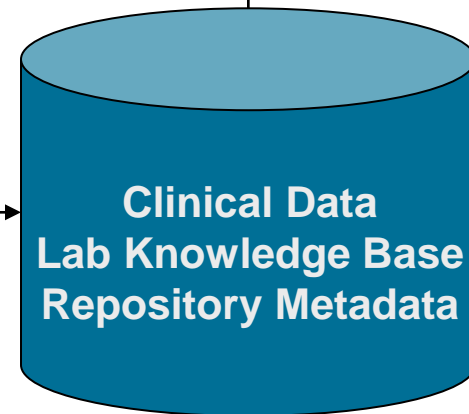
Lab Workflow Knowledge

Sample-Dataset tracking
Massive instrument-generated datasets

Data Upload

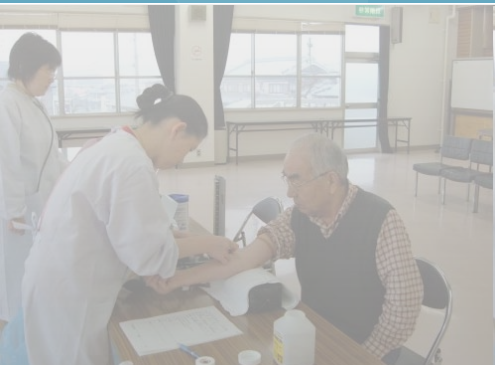


cceHUB
Lab Instrument Data Repository

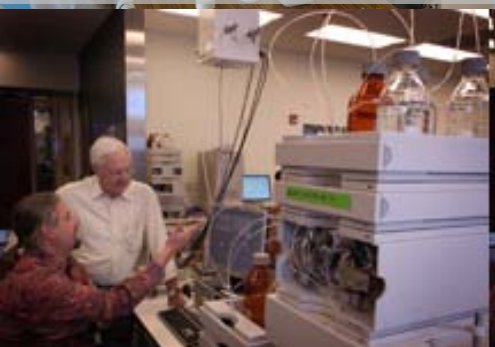


cceHUB
Database

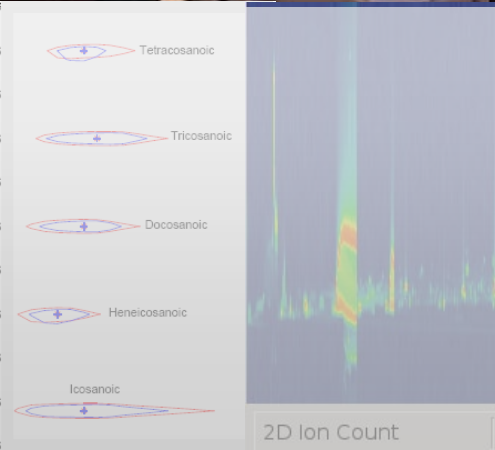
Clinical Data
Lab Knowledge Base
Repository Metadata



clinical data



laboratory analysis



predictive modeling tools

Laboratory Data



- Laboratory Data Uploader
- User Collections Uploader
- Repository Data Viewer
- Track Laboratory Analysis 2011, 2010
- [Learn More >>](#)

Laboratory Data Flow

- "knowledge base" resources (protocols, sample preparation, instruments, standards, file formats, analysis)
- annotation for lab data files
- lab data files tracked to samples/patients
- data files upload with provenance
- metadata processing
- lab data collections
- data view & explore
- data access for analysis tools



Laboratory Knowledge Base for Instruments, Standards, Data Flow and Data Formats

Use the [Data Uploader Form](#) to upload laboratory analysis datasets generated for the Colorectal Cancer OMIC Pilot Study. This form is restricted to authorized members of the CCE OMIC Laboratory Analysis Group.

[Learn more](#) about the CCE biological data analysis Laboratories ...

▶ [Global Proteomics analysis laboratory](#) in the Purdue University Bindley Bioscience Center.

The instrument-generated datasets and their formats are shown in this [LC-MS global proteomics workflow diagram](#).

▶ [Xu Lipidomics analysis laboratory](#) in the Indiana University Simon Cancer Center.

The instrument-generated datasets and their formats are shown in this [LC-MS lipidomics workflow diagram](#).

▶ [Klaunig Oxidative Stress analysis laboratory](#) in the Indiana University Department of Pharmacology and Toxicology

The instrument-generated datasets and their formats are shown in the [comet assay workflow diagram](#) and the [teac assay workflow diagram](#).

▶ [Rafferty Metabolomics analysis laboratory](#) in the Department of Chemistry's Rafferty Group at Purdue University.

The instrument-generated datasets and their formats are shown in the [GCxGC-MS metabolomics workflow diagram](#) and the [NMR metabolomics workflow diagram](#).

▶ [Regnier Glycoproteomics analysis laboratory](#) in the Purdue University Bindley Bioscience Center

The instrument-generated datasets and their formats are shown in this [LC-MS glyco-proteomics workflow diagram](#).

▶ [Teegarden Vitamin D analysis laboratory](#) in the Foods and Nutrition Department at Purdue University.

Follow the links to the laboratories for more detailed information about the workflow, instruments, sample preparation protocols, instrument setup methods, generated datasets, formats, conversions, and laboratory analysis.

In the Spotlight



Regnier Glycoproteomics Analysis Laboratory

Posted 07 Feb, 2009 in [Series](#)

About

Reviews

Citations

Contributor

Step9 Process the mass spectral data

1st

MS

Data Processing and Generated Datasets

Data processing will be achieved in two ways. The first will be to transfer the raw MS/MS data containing m/z values and signal intensity to the [statistical models and pattern recognition group](#). The relative amount of peptides will be judged directly from their signal intensity in spectra. The second mode of data processing will be to identify the individual peptides obtained from RPC fractions and their protein parent. This will be done using the MASCOT, Sorcerer or Spectrum Mill search engines.

The XCT PLUS ESI ion trap in LC-MS mode generates ".D" files during instrument sample analysis. For peptide quantification, Bruker's CompassXport software is used to convert the XCT PLUS ".D" files to [Level 1 LC-MS mzXML](#) files. The mzXML file generated by the XCT PLUS in LC-MS mode has more detailed m/z information than the XCT PLUS run in LC-MS-MS mode. The LC-MS mzXML file can be used as input to the [Proteomics Discovery Pipeline](#) for data mining. [You must be logged in to access the Proteomics Discovery Pipeline link.]

The mzXML files will also be used by the Cancer Care Engineering statistical modeling group for [integrative mathematical modeling](#).

For protein identification, the XCT PLUS LC-MS-MS generated ".D" files are converted to either

- **mzXML Level 2 LC-MS-MS** format file used for analysis by **Sorcerer** software
- **PKL** format file generated by DataExtractor, a component of Agilent's **Spectrum Mill** software
- **MGF**, the MASCOT generated format file used for **MASCOT** database searching.

These [formats](#) produce peak lists and fragmentation patterns which are matched against databases to identify proteins. Users can access the mzXML and MGF files converted from the D format, as use them as input to other identification software or databases. The PLK file is not accessible after conversion from the D format.

In general, the LC-MS and LC-MS-MS phases are separate runs of the XCT PLUS. The LC-MS phase includes hundreds of samples, and the LC-MS-MS phase includes only a handful of the original sample group.

Laboratory data flow, standards, data annotations & upload

Sample Tracking - Cancer Care Engineering

cceHUB - cceHUB - Mozilla Firefox

File Edit View History Bookmarks Tools Help

https://ccehub.org/uploader

cceHUB - cceHUB

Data Uploader with

Laboratory Tracking

Sample Tracking Information

Sample Preparation Information

Give your prepared sample a name:

Identify sample preparation start time (enter YYYY-MM-DD, e.g., 2009-09-28):

Sample preparation protocol:
<http://ccehub.org/site/documents/DOC0000AB4000SamplePreparation.pdf>

Sample preparation protocol accurate?:

Quality of sample preparation:

Annotation for sample preparation:
 All extractions were performed either in siliconized tubes or in glass tubes. We have developed a simple phospholipid extraction method and call it the MeOH method. In brief, when it is used for extraction of choline-containing lipids, 10 μ L of plasma or serum were added into 1 mL of MeOH with 100 μ mol of 12:0 LPC as the internal standard (IS). After vortex and incubation on ice for 10 min, the mixture was centrifuged (10,000g, 5min, room temperature), and 120 μ L of supernatant were directly used for MS analysis of lyso-PAF, LPCs, SMs and PCs. For natively-charged lipids, 10 μ L of plasma or serum were also added into 1 mL of MeOH with 100 μ mol of 14:0 IPA and 100 μ mol of 17:0 CoA as internal standards. After Instrument Setup and Run Information

Workflow Tracking

Workflow

Yan X

This shows selected workflow should be a

Sample Tracking


All barcodes in the table use patient - case number 0014

cceHUB - Repository Data Viewer - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://ccehub.org/?option=com_dataview&task=view&obj=datasets

cceHUB - Repository D...



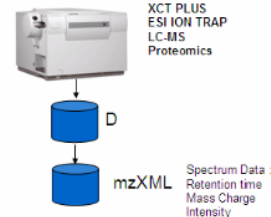
Search

- Daniel Raftery Laboratory at Purdue University
 - LECO Pegasus 4D GCxGC-TOF: Metabolite Profiling Facility
 - BRUKER AVANCE 500MHz SPECTROMETER: Purdue Interde
- James Klaunig Laboratory at Indiana University
 - Nikon Fluorescence Microscope: IU Simon Cancer Center
 - TECAN Infinite M200 Microplate Reader: IU Simon Cancer Center
 - TEAC 3-18-2011 : wsp : 02.14.2011
 - TEAC 3-18-2011 : xls : 02.14.2011
 - TEAC 3-18-2011 : csv : 02.14.2011
- Bindley Biosciences Center at Purdue University
 - XCT PLUS ESI Ion Trap: Bindley Biosciences Center
 - CCE-003-1: D : 09.10.2010
 - CCE-009-2: D : 09.29.2010
 - CCE-009-2A : D : 09.23.2010
 - CCE-009-2A : mzXML : 09.23.2010
 - CCE-012-1: D : 09.10.2010
 - CCE-013-2: D : 09.13.2010
 - CCE-013-2: MZXML : 09.13.2010
 - CCE-013-3: D : 09.13.2010
 - CCE-013-3: MZXML : 09.13.2010
 - CCE-014-2: D : 09.13.2010
 - CCE-014-3: D : 09.13.2010
 - CCE-014-3: MZXML : 09.13.2010
 - CCE-020-1: D : 09.14.2010
 - CCE-020-1: MZXML : 09.14.2010
 - CCE-022-1: D : 09.14.2010
 - CCE-022-1A : D : 09.23.2010
 - CCE-026-2: D : 09.15.2010
 - CCE-026-2: MZXML : 09.15.2010
 - CCE-028-1: D : 09.14.2010

[CCE-013-3.mzXML](#)

Lab: Bindley Biosciences Center at Purdue University

Workflow: Bindley Biosciences Center XCT LC-MS Sample Analysis
 Uploaded on Mon Sep 13 2010 13:10:30 GMT-0400 (Eastern Daylight Time)
 Jianming Lei [lei6@purdue.edu]



Adamec Laboratory LC-MS Sample Analysis

Instrument: XCT PLUS ESI Ion Trap: Bindley Biosciences Center

Name of the CCE Study: Cancer Care Engineering of Colorectal Cancer - OMICs Pilot Study

File generated for this analysis type:

File: CCE-013-3.mzXML
 Analysis Type Format: XCTPLUS-IONTRAP LC-MS mzXML
 File size: 75888049 bytes
 File Format: mzXML
 Repository Location:
 /data/XCTPLUS-IONTRAP/adamec/LC-MS/CCEColorectalCancer/mzXML

[\[CCE-013-3.mzXML \]](#)

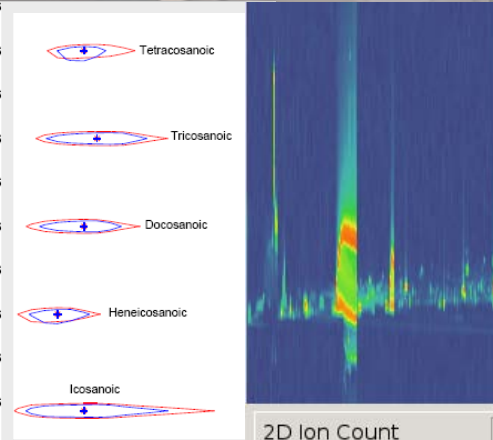
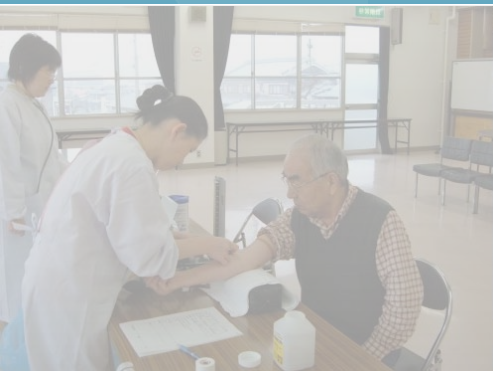
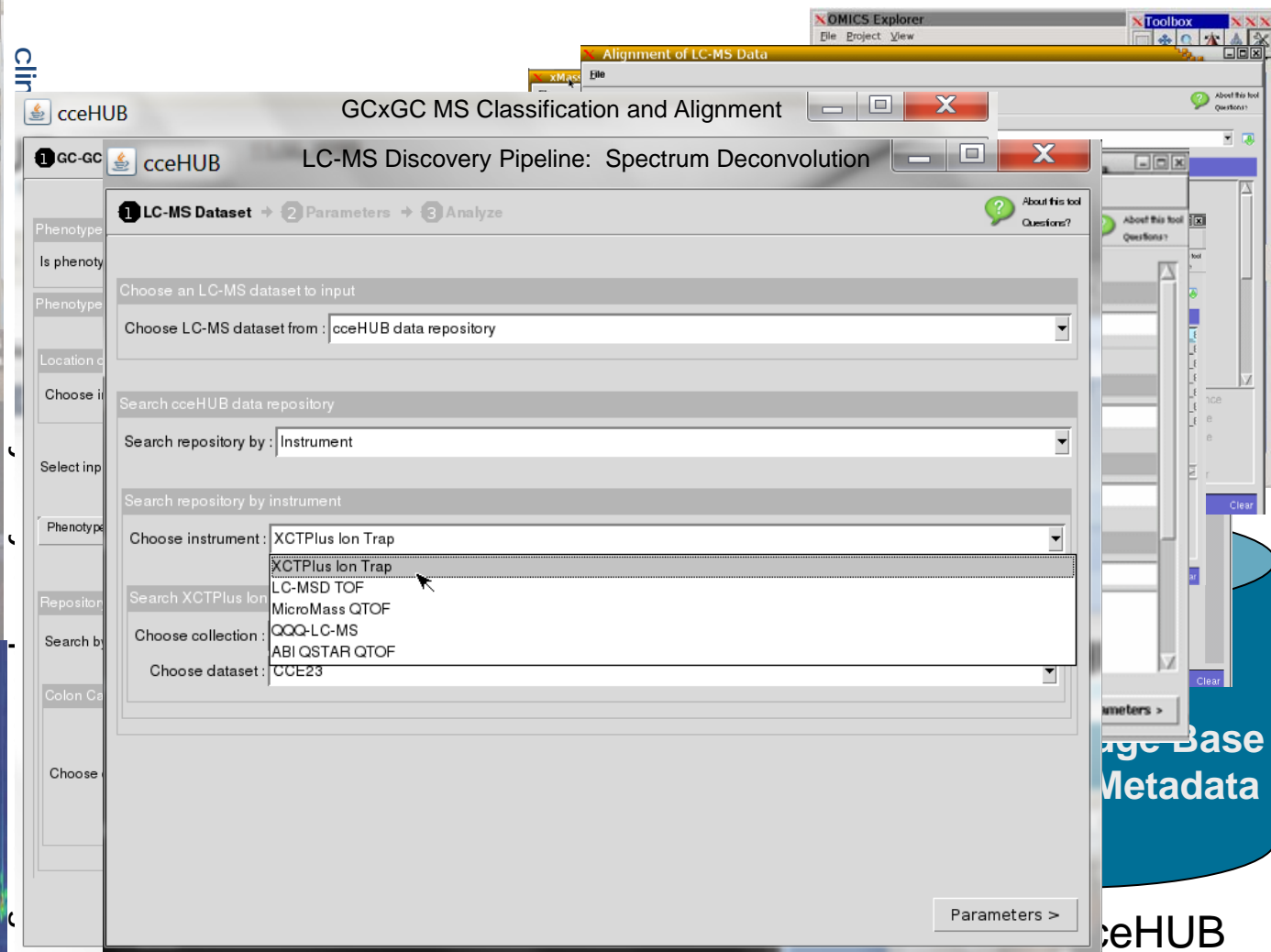
Comments: [+] [!]

Sample	Aliquot
CCE-013-3	0133PL07

Laboratory data : some stats

Lab	#Samples Analyzed % Total	Files/ Samples Uploaded	Average File Size	Analysis Tools at cceHUB	Using cceHUB tools ?
Bindley Biosciences Global Proteomics	193 73%	193 files 193 samples	80MB	Discovery Pipeline Results Visualize/Compare	500 runs through discovery pipeline
Teegarden Vitamin D	225 85%	4 files 225 samples	< 1MB	Vitamin D-Blood Draw - Clinical Data merge for SAS	Yes, DataView
Raftery Metabolomics GCGC-MS	230 87%	230 files 230 samples	1 GB	Peak classification and alignment GCGC-MS Visual Analytics	
Raftery Metabolomics NMR	110 41 %	1 file 110 samples	< 1MB		
Xu Lipidomics	143 54%	1 file 143 samples	< 1MB	Lipidomics-BloodDraw- Clinical Data merge for SAS	Yes, DataView
Klaunig TEAC analysis	259 98%	1 file 259 samples	< 1MB	TEAC-Blood Draw-Clinical Data merge for SAS	Yes, DataView
Klaunig Comet Assay	101 38%	1 file 101 samples	< 1MB	CometAssay-Blood Draw- Clinical Data merge for SAS	Yes DataView
Klaunig Genotyping Assay	--			POCRE, MaCH genotype imputation	(used by stat group on their own data)
Regnier Glycoproteomics	--				

Support for modeling and analysis

Lab Instrument Data Repository

Database

Large Base Metadata

cceHUB

Tools to support data exploration and synthesis

SHARED MODELING TOOLS

- Suite of Population-based Models
- Colorectal Cancer Incidence E
- GCxGC MS
- Monte Carlo S
- Patient Specif
- Statistical Modelin
- GCxGC-MS C
- Visual Analytics fo
- GCxGC-MS D
- Proteome Discove
- Spectrum Dec
- Peak Alignme
- Normalization
- Significance T
- Pattern Recognition

OMICS

File Name

Colon_15

Colon_22

Spectrum Deconvolution of LC-MS Data

File

Result: 1 result

Peak Alignment of Deconvoluted Data

File

Result: 1 result

Normalization of Aligned LC-MS Data

File

Result: 1 result

Significance Testing of LC-MS Data

File

Result: 1 result

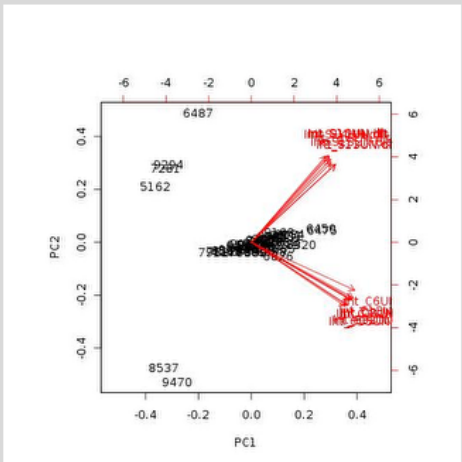
Pattern Recognition for LC-MS Data

File

Result: 1 result

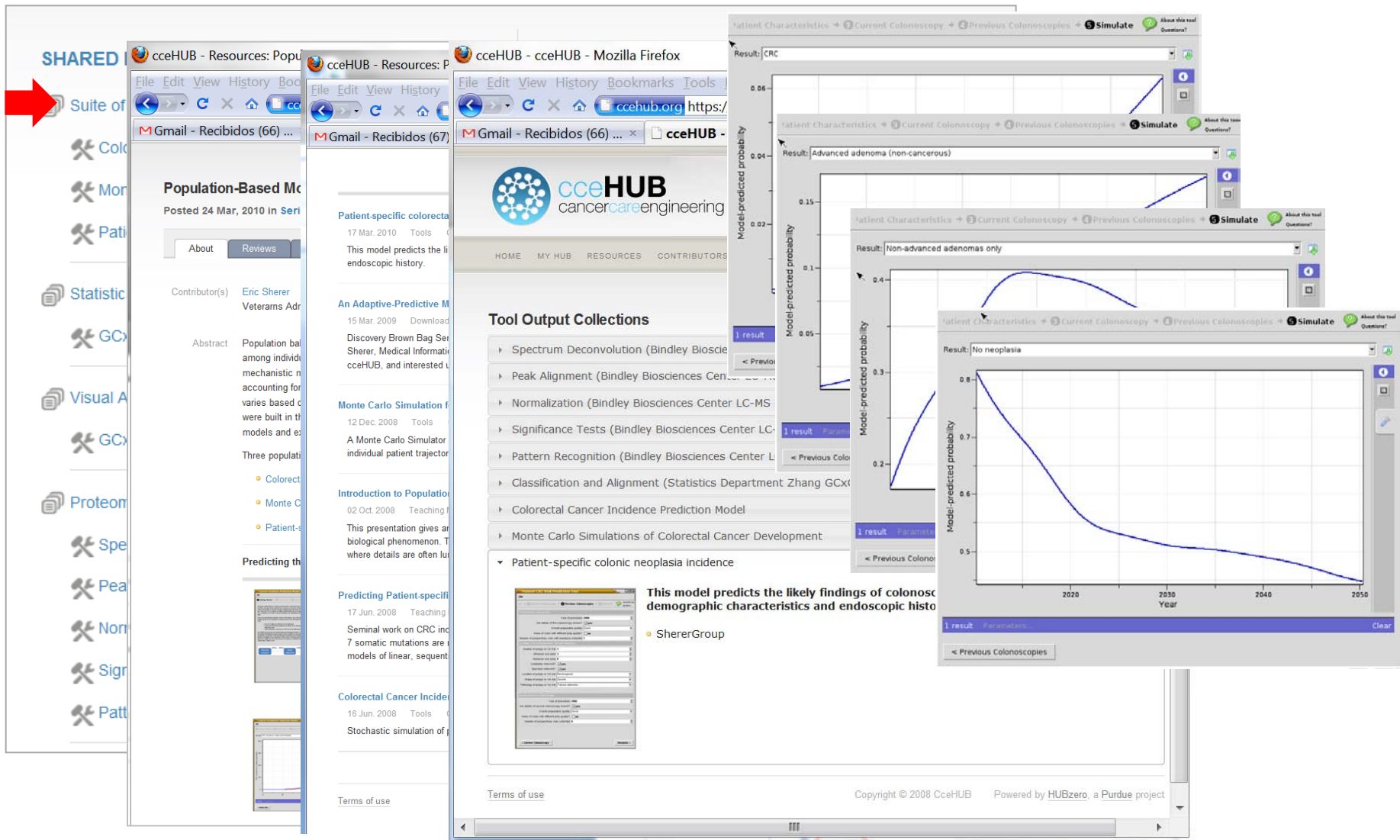
1 Normalized Dataset → 2 Parameters → 3 Analyze

Result: Principal Component Analysis



1 result Parameters... Clear

Tools for physician decision support



SHARED

- Suite of
- Colo
- Mon
- Pati
- Statistic
- GC
- Visual A
- GC
- Proteom
- Spe
- Pea
- Non
- Sign
- Patt

Population-Based Model
Posted 24 Mar, 2010 in Seri

Contributor(s) Eric Sherer, Veterans Adr

Abstract Population bal among indivi mechanistic n accounting for varies based c were built in th models and es

Three populati

- Colorect
- Monte C
- Patient-s

Predicting th

Tool Output Collections

- Spectrum Deconvolution (Bindley Biosci
- Peak Alignment (Bindley Biosciences Cen
- Normalization (Bindley Biosciences Center LC-MS
- Significance Tests (Bindley Biosciences Center LC-
- Pattern Recognition (Bindley Biosciences Center L
- Classification and Alignment (Statistics Department Zhang GCX
- Colorectal Cancer Incidence Prediction Model
- Monte Carlo Simulations of Colorectal Cancer Development
- Patient-specific colonic neoplasia incidence
 - ShererGroup

This model predicts the likely findings of colonosc demographic characteristics and endoscopic histo

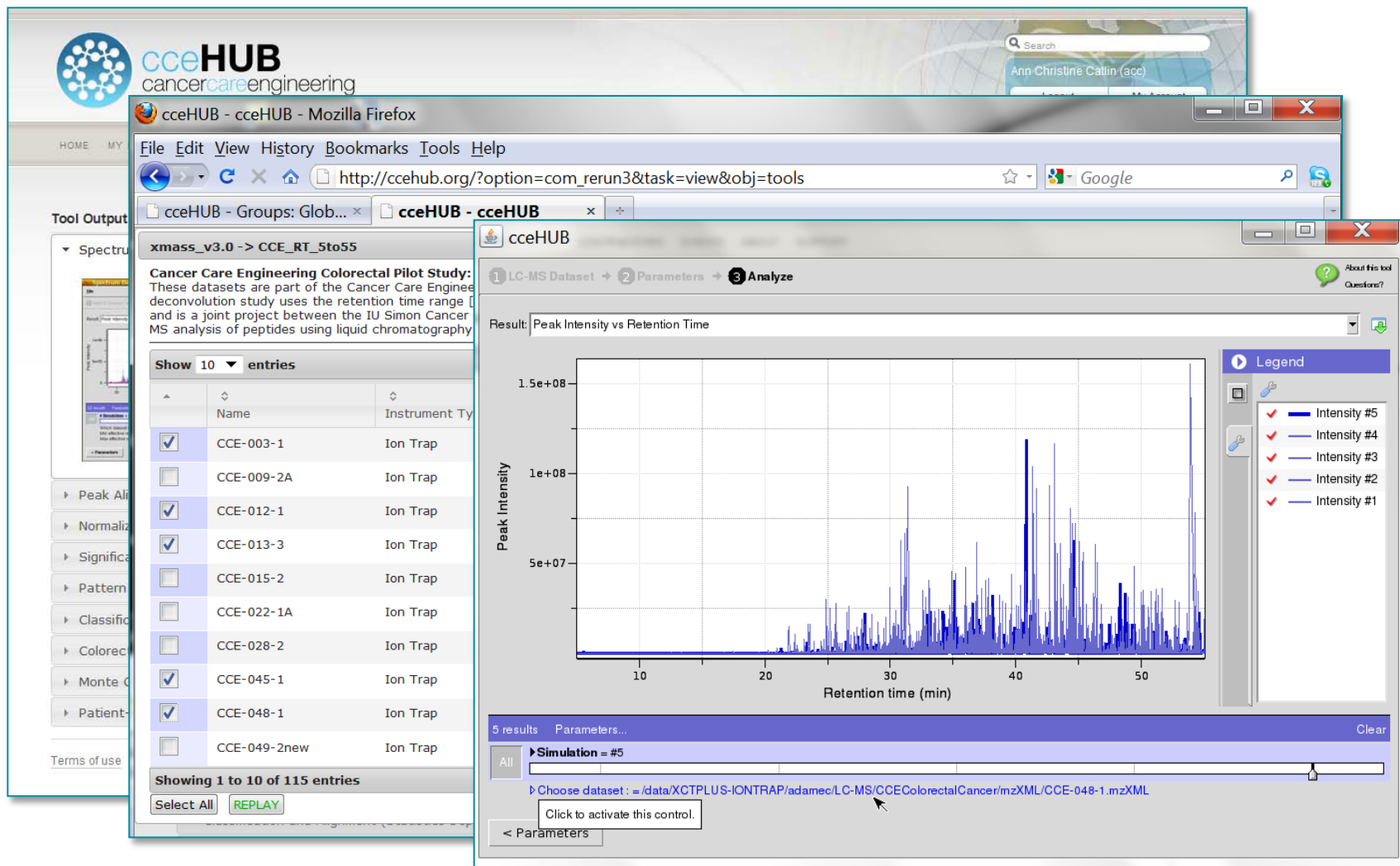
Simulation Results:

- Result: CRC
- Result: Advanced adenoma (non-cancerous)
- Result: Non-advanced adenomas only
- Result: No neoplasia

Model-predicted probability vs. Year (2020-2050)

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Tool Results Collections and Analysis Browser



The screenshot displays the cceHUB web interface. On the left, a sidebar shows a list of datasets under the heading "xmass_v3.0 -> CCE_RT_5to55". The main content area shows a table of datasets and a chromatogram plot.

Dataset List:

Name	Instrument Type
<input checked="" type="checkbox"/> CCE-003-1	Ion Trap
<input type="checkbox"/> CCE-009-2A	Ion Trap
<input checked="" type="checkbox"/> CCE-012-1	Ion Trap
<input checked="" type="checkbox"/> CCE-013-3	Ion Trap
<input type="checkbox"/> CCE-015-2	Ion Trap
<input type="checkbox"/> CCE-022-1A	Ion Trap
<input type="checkbox"/> CCE-028-2	Ion Trap
<input checked="" type="checkbox"/> CCE-045-1	Ion Trap
<input checked="" type="checkbox"/> CCE-048-1	Ion Trap
<input type="checkbox"/> CCE-049-2new	Ion Trap

Chromatogram Plot:

The plot shows Peak Intensity (Y-axis, ranging from 0 to 1.5e+08) versus Retention time (min) (X-axis, ranging from 0 to 60). The plot displays a complex signal with multiple peaks. A legend on the right indicates five intensity levels: Intensity #1 (red), Intensity #2 (blue), Intensity #3 (green), Intensity #4 (purple), and Intensity #5 (orange).

Simulation Parameters:

5 results Parameters... Clear

Simulation = #5

Choose dataset : = /data/XCTPLUS-IONTRAP/adamec/LC-MS/CCEColorectalCancer/mzXML/CCE-048-1.mzXML

Click to activate this control.

Collaboration for Cancer Care Engineering Research

cceHUB - Groups: Global Proteomics Analysis Group - Mozilla Firefox

File Edit View History Bookmarks Tools Help

Yanzhu Lin Proteomics Data Meeting 02/21/2011

ID	Diagnosis	ID	Diagnosis
0011	Healthy	0021	Healthy
0041	Polyp	0051	Colo
0061	Health		
0091	Colo		
0111	Colo		
0131	Colo		
0151	NA		
0181	Health		
0202	Recta		
0231	Polyp		
0251	Health		
0291	Polyp		
0311	Health		
0351	Polyp		
0381	Polyp		
0401	Health		

02/21/2011
yanzhulin_pdm_report

03/04/2011

CCE Analysis Monthly Meetings

Swank, Kristine A.

Outlook Web Access was not able to show all the images in this message. You can use Microsoft Outlook to access the missing content.

Sent: Thursday, March 17, 2011 10:33 AM

To: Catlin, Ann Christine; 'Chen, Jake' [jakechen@iupui.edu]; 'Ebert, David' [ebert@purdue.edu]; Gough, Erik S; Harrison, Marietta L.; 'Lin, Yanzhu' [lin43@purdue.edu]; 'Maciejewski, Ross' [rmacieje@purdue.edu]; Regnier, Fred E; 'Wu, Xiaogang' [wu33@iupui.edu]; Zhang, Dabao; Zhang, Min

Cc: Hewitt, Elizabeth E.; Swank, Kristine A.; Nagel, Julie S

Attachments:  [CampusMap_052510.pdf \(322 KB\)](#) [Open as Web Page];

The CCE Proteomics meetings have been renamed to **CCE Analysis** meetings and will meet once a month in the **Burton Morgan Center for Entrepreneurship (MRGN), room 206** on the following days/times:

Tuesday, April 12 from 2-3pm
 Tuesday, May 10 from 9-10am
 Tuesday, June 14 from 9-10am
 Tuesday, July 12 from 9-10am
 Tuesday, August 16 from 9-10am
 (so please mark your calendars)


ITMIG Global Prospective Database just underway ...

cceHUB - ITMIG Global Prospective Database - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://ccehub.org/itmig

cceHUB - ITMIG Global ...



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Ann-Christine Catlin (acc)

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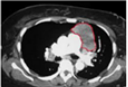



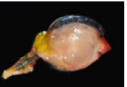
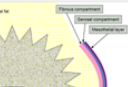


HELP!

ITMIG Global Prospective Database

Learn more about the ITMIG Global Prospective Database from the [ITMIG November 2010 Workshop publications](#) and [database development documents](#).

Web Forms for Submitting Patient Data for the Prospective Database

Web-forms are used by contributing institutions to submit patient data to the ITMIG Prospective Global Database. Send us feedback about the web-forms and data elements so we can ensure that the appropriate data is requested from the contributing institutions.

<p>Instructions for entering enrollment and presentation data</p>  <p>Patient Enrollment Jim Huang Send Comments</p>	<p>Initial Presentation</p>  <p>Initial Presentation Enrico Ruffini Jim Huang Send Comments</p>							
<p>Instructions for entering patient episode data</p>  <p>Imaging (Staging) Edith Marom Jim Huang Send Comments</p>	<p>Biopsy (Pathology)</p>  <p>Biopsy (Pathology) Alberto Marchevsky Jim Huang Philip Strobel Nicolas Girard Send Comments</p>	<p>Primary Treatment</p>  <p>Primary Treatment Nicolas Girard Daniel Gomez Jim Huang Send Comments</p>	<p>Imaging (Response)</p>  <p>Imaging (Response) Edith Marom Jim Huang Send Comments</p>	<p>Surgery</p>  <p>Surgery Alper Toker Frank Detterback Jim Huang Send Comments</p>	<p>Resection (Pathology)</p>  <p>Resection (Pathology) Alberto Marchevsky Jim Huang Philip Strobel Nicolas Girard Send Comments</p>	<p>Staging</p>  <p>Staging Frank Detterback Jim Huang Send Comments</p>	<p>Postoperative Treatment</p>  <p>Postoperative Treatment Nicolas Girard Daniel Gomez Jim Huang Send Comments</p>	<p>Followup Surveillance</p>  <p>Followup Surveillance Enrico Ruffini Jim Huang Send Comments</p>

Our technology extends to other cancer research workflows

Using the HUB cyber infrastructure
and cceHUB data technology
to further collaborative
Cancer Care Engineering Research

