Capabilities of

H. Paul Benton
Scripps Research

What does the current software do?

Philadelphia Police
@PhillyPolice

Please don't call 911 to ask if we're hearing "Laurel" or "Yanny". The only thing we hear is the creation of another bad hashtag. (And Laurel. We're definitely hearing Laurel).

5:31 AM - May 16, 2018

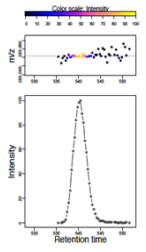
4,119 1,513 people are talking about this

Hear Both Yanny and Laurel

What is XCMS Online?

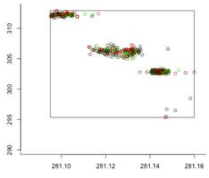
- The complete xcms system in a graphical web based system
- XCMS started in 2005
- First concept of XCMS Online was 2009 but production was started late 2011 (public mid 2012)
  - Approx. 25,000 users
  - Average 70 jobs a day
  - 150 Users logging in per day

Overview of XCMS

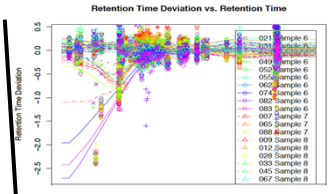


Peak Picking

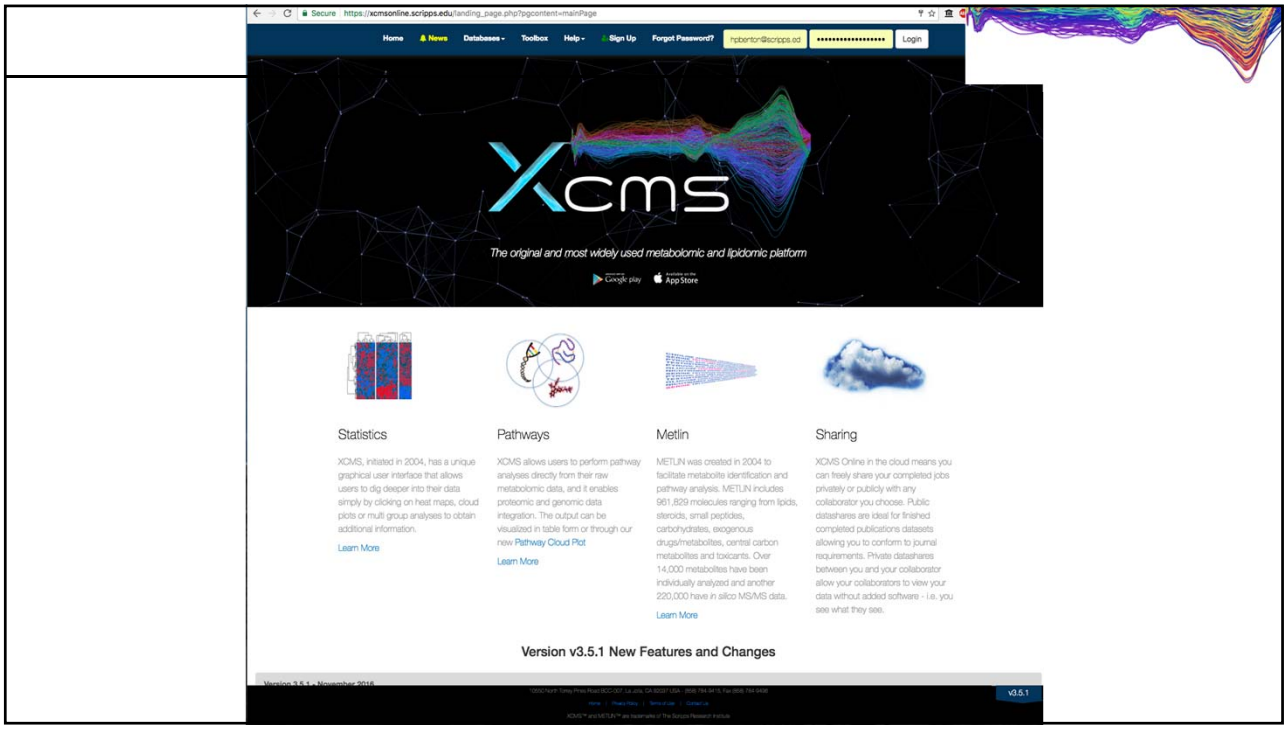
Grouping similar peaks across replicates



Retention time alignment

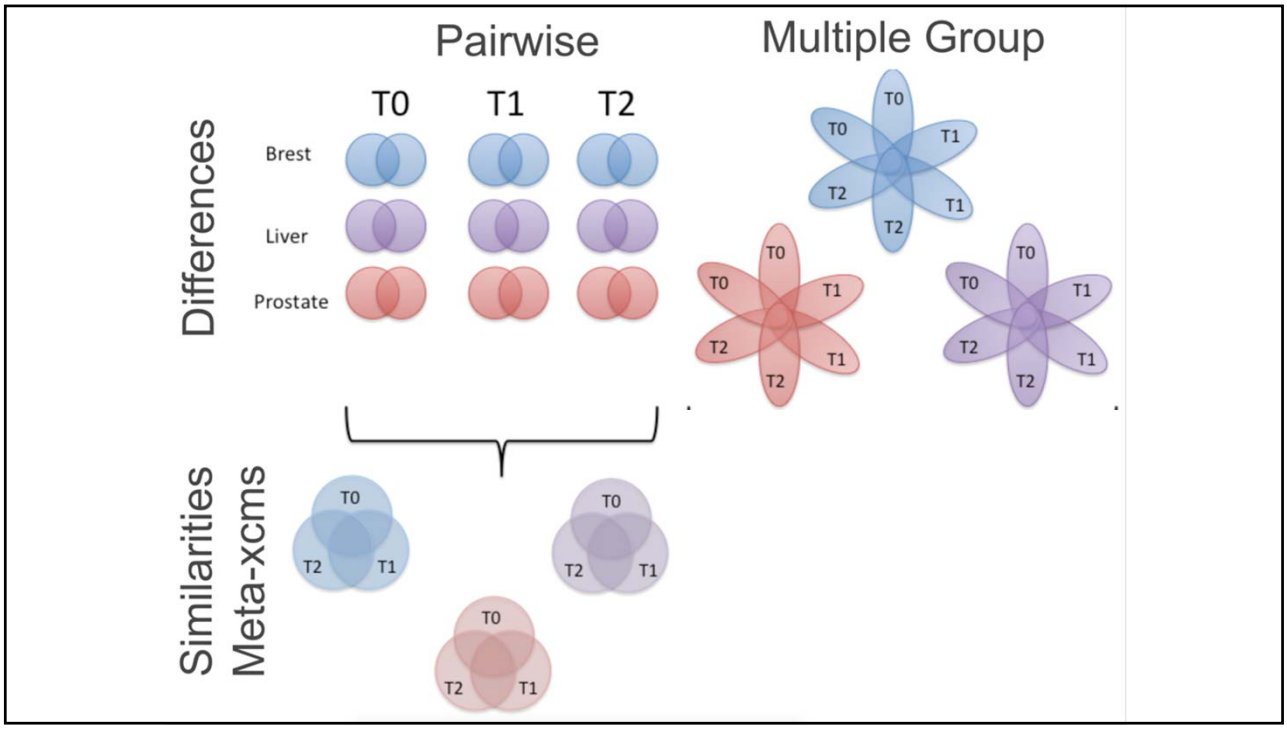


Statistical analysis of Peaks Between classes

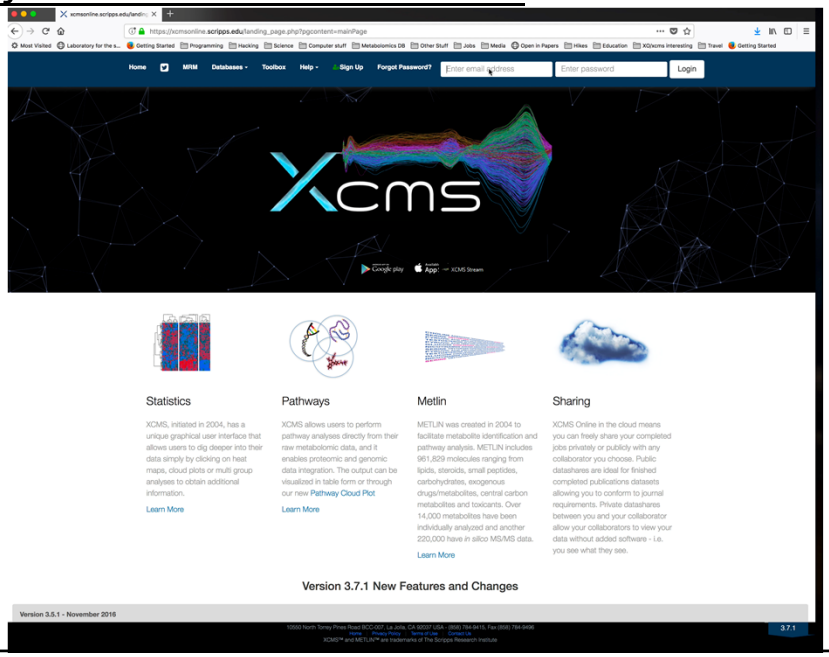


Job types in XCMS Online

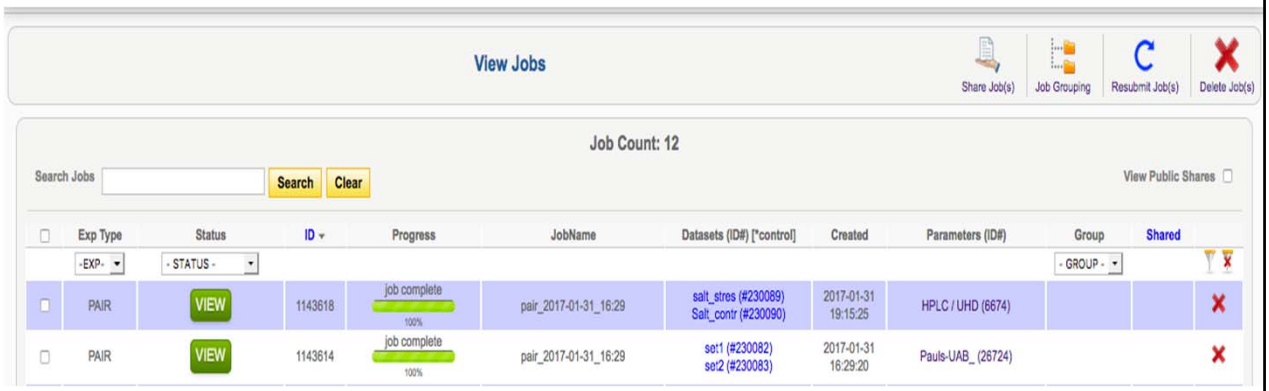
- Single Class Jobs – Either single file or single dataset (class or unknown classes)
- Pairwise analysis Jobs – Two class comparison, works best with KO –vs- WT type experiments
- Multigroup/class Jobs – Multiple classes including Quality control samples. Great for Time series jobs or multiple knockouts.
- meta-XCMS- Finds the overlap between many pairwise jobs. (Must have same control samples)
- MultiModal – Combining multiple polarities for better identification.

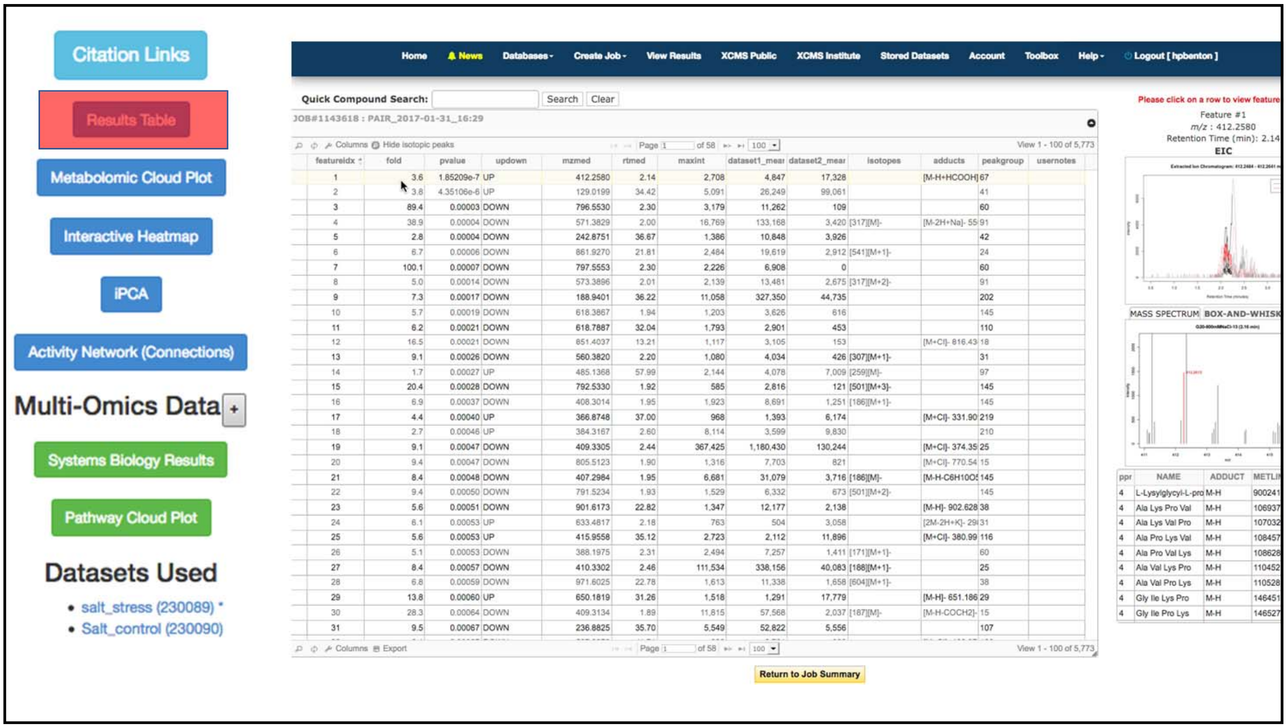


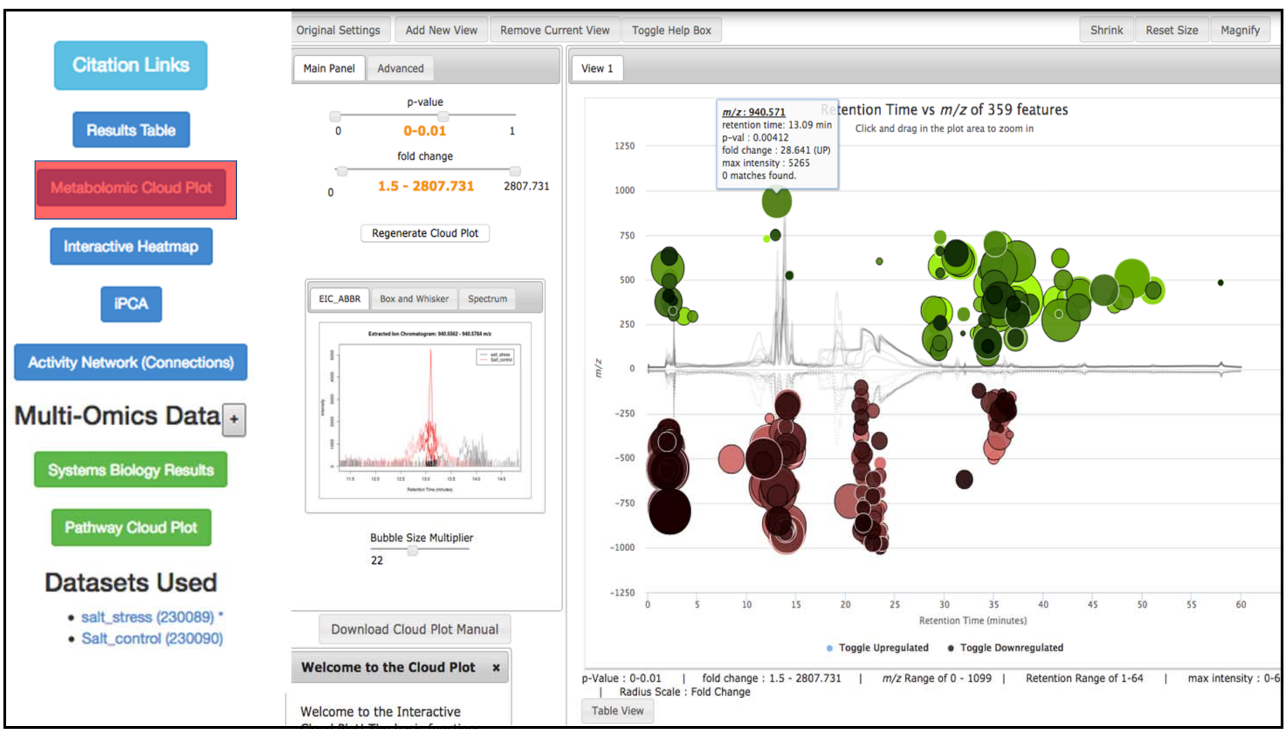
Running a job



View Results section




Citation Links
Results Table
Metabolomic Cloud Plot
Interactive Heatmap
iPCA
Activity Network (Connections)
Multi-Omics Data
Systems Biology Results
Pathway Cloud Plot
Datasets Used
salt_stress (230089) *
Salt_control (230090)
Home
News
Databases
Create Job
View Results
XCMS Public
XCMS Institute
Stored Datasets
Account
Toolbox
Help
Quick Compound Search:
Search
Clear
Return to Job Summary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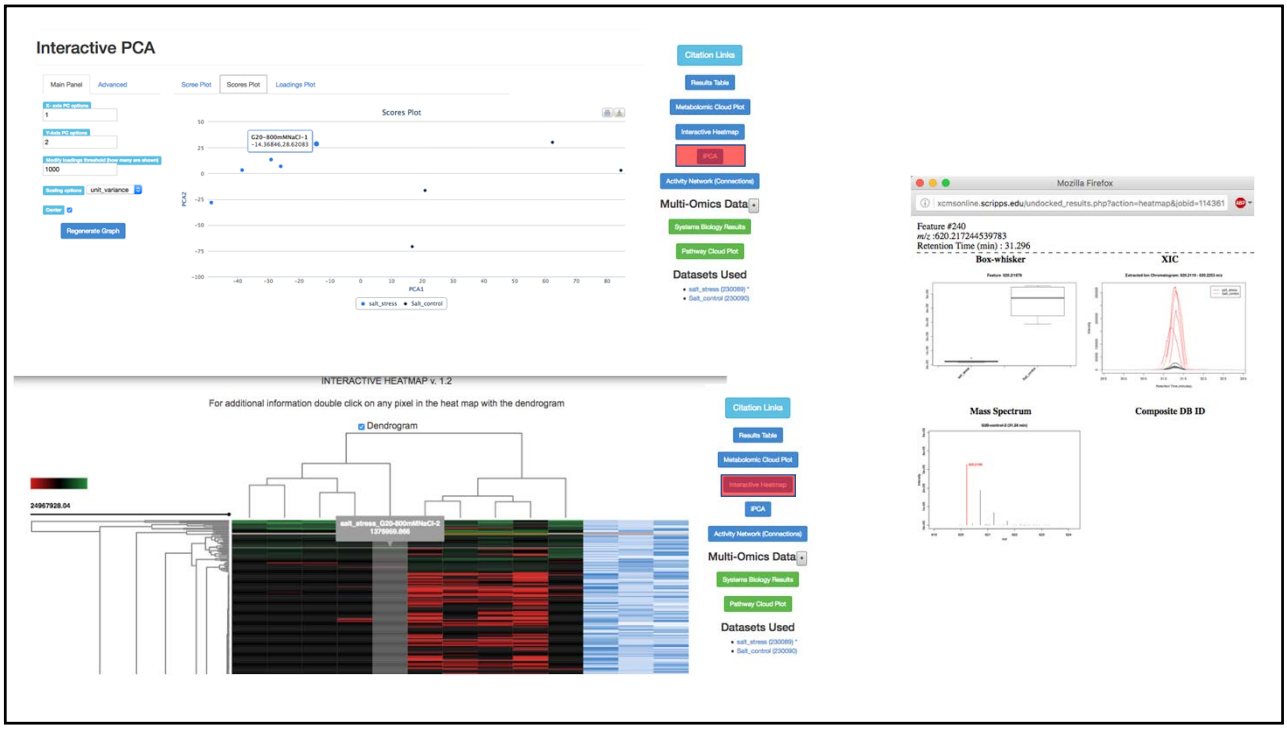
Datasets Used
salt_stress (230089) *
Salt_control (230090)
Original Settings
Add New View
Remove Current View
Toggle Help Box
Shrink
Reset Size
Magnify
Main Panel
Advanced
View 1
p-value
0-0.01
fold change
1.5 - 2807.731
Regenerate Cloud Plot
EIC_ABBR
Box and Whisker
Spectrum
Bubble Size Multiplier
22
Download Cloud Plot Manual
Welcome to the Cloud Plot
Welcome to the Interactive
Retention Time vs m/z of 359 features
Click and drag in the plot area to zoom in
m/z : 940.571
retention time: 13.09 min
p-val : 0.00412
fold change : 28.641 (UP)
max intensity : 5265
0 matches found.
Retention Time (minutes)
Toggle Upregulated
Toggle Downregulated
p-Value : 0-0.01 | fold change : 1.5 - 2807.731 | m/z Range of 0 - 1099 | Retention Range of 1-64
Radius Scale : Fold Change
Table View


Interactive PCA
Main Panel
Advanced
Scree Plot
Scores Plot
Loadings Plot
Scores Plot
Regenerate Graph
Citation Links
Results Table
Metabolomic Cloud Plot
Interactive Heatmap
PCA
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Multi-Omics Data
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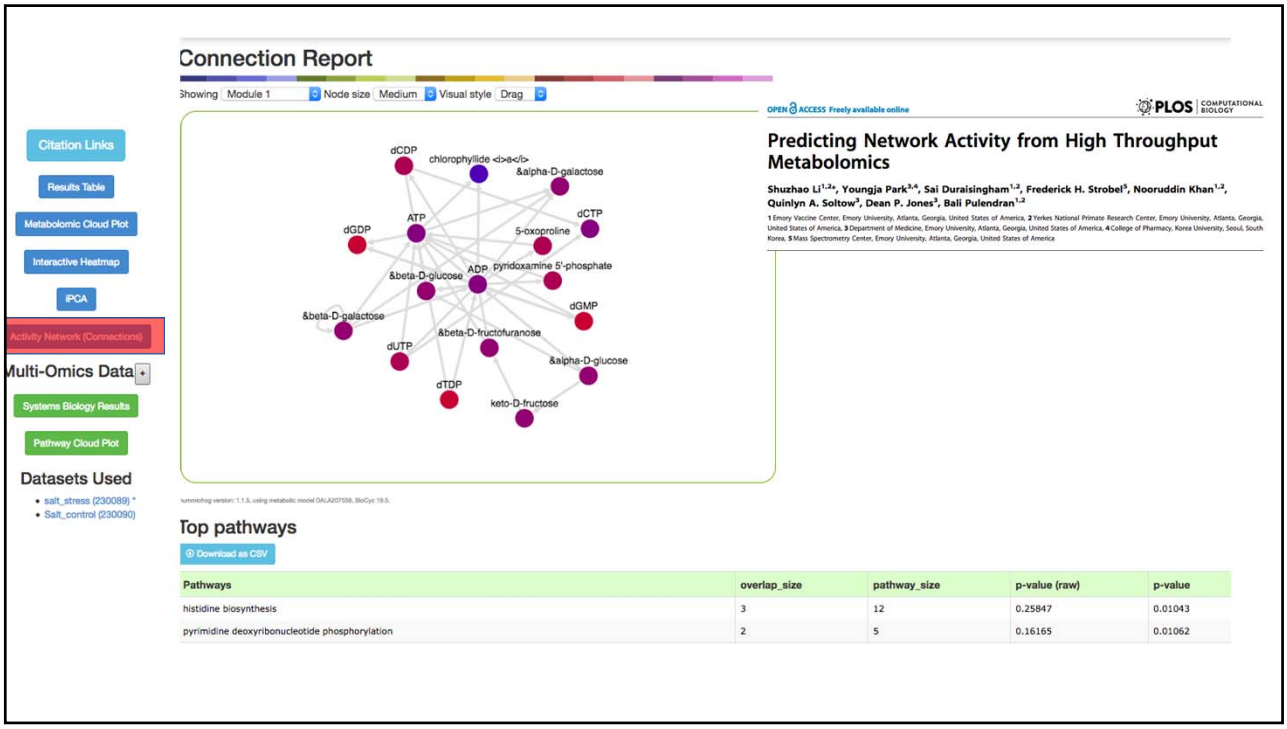
Datasets Used
INTERACTIVE HEATMAP v. 1.2
For additional information double click on any pixel in the heat map with the dendrogram
Dendrogram
Mozilla Firefox
Feature #240
m/z :620.21724539783
Retention Time (min) : 31.296
Box-whisker
XIC
Mass Spectrum
Composite DB ID


Connection Report
Showing Module 1 Node size Medium Visual style Drag
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Activity Network (Connections)
Multi-Omics Data
Systems Biology Results
Pathway Cloud Plot
Datasets Used
salt_stress (230089) *
Salt_control (230090)
dCDP
chlorophyllide
&alpha-D-galactose
dCTP
ATP
dGDP
5-oxoproline
&beta-D-glucose
ADP
pyridoxamine 5'-phosphate
dGMP
&beta-D-galactose
&beta-D-fructofuranose
dUTP
&alpha-D-glucose
dTDP
keto-D-fructose
OPEN ACCESS Freely available online
PLOS COMPUTATIONAL BIOLOGY
Predicting Network Activity from High Throughput Metabolomics
Top pathways
Download as CSV
Pathways
overlap_size
pathway_size
p-value (raw)
p-value
histidine biosynthesis
3
12
0.25847
0.01043
pyrimidine deoxyribonucleotide phosphorylation
2
5
0.16165
0.01062

Top metabolite predictions

Download as CSV

Compound_ID	name(input_mz)	evidence_score(match_form)	MW(mz_diff)
DCDP	dCDP	5	387.0233
	386.017400	M-H[-]	0.001400
2-D-THREO-HYDROXY-3-CARBOXY-ISOCAPROATE	(2*R*,3*S*)-3-isopropylmalate	9	176.0685
	196.036600	M+Na-2H[-]	0.000700
	175.061400	M-H[-]	0.000200
	235.082800	M+CH3COO[-]	0.001000
	157.051200	M-H2O-H[-]	0.000600
5-OXOPROLINE	5-oxoproline	8	129.0426
	149.009700	M+Na-2H[-]	-0.000300
	128.035900	M-H[-]	0.000600
	164.011900	M+Cl[-]	0.000400
	128.035800	M-H[-]	0.000500
CHLOROPHYLLIDE-A	chlorophyllide *a*	6	614.238
	613.230100	M-H[-]	-0.000600
	659.238500	M+HCOO[-]	0.002900
CPD-1130	3-ethylmalate	6	162.0528
	161.046300	M-H[-]	0.000800
	197.021200	M+Cl[-]	-0.000500
UDP-MANNACA	UDP-*N*-acetyl-α-D-mannosaminouronate	8	621.0608

- Adding MS/MS checks to confirm the predicted metabolites.
  - This will result in an increased/decreased score for the pathway

Citation Links

Results Table

Metabolomic Cloud Plot

Interactive Heatmap

iPCA

Activity Network (Connections)

Multi-Omics Data

Systems Biology Results

Pathway Cloud Plot

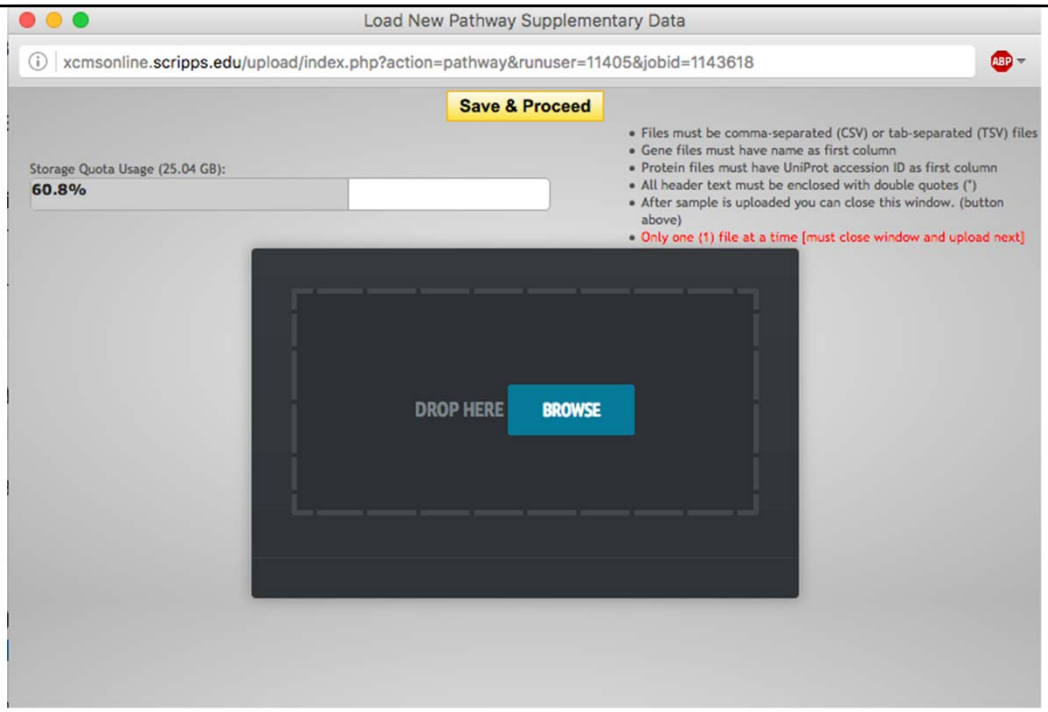
Datasets Used

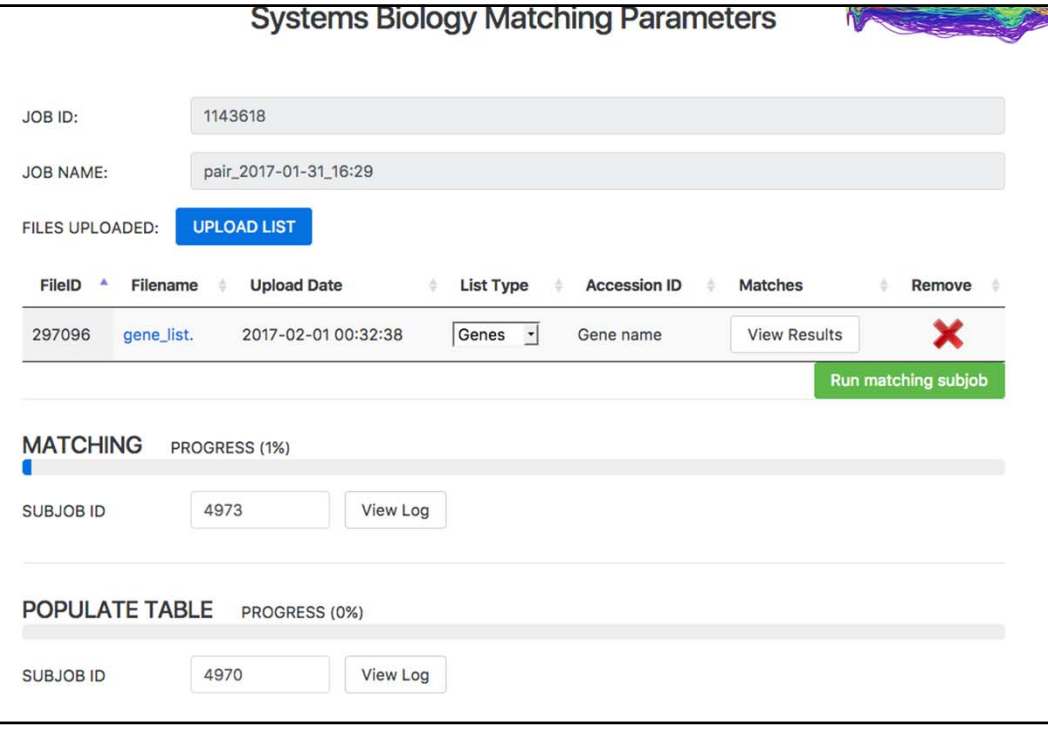
- salt_stress (230089) *
- Salt_control (230090)

Systems Biology Analysis Results

Show 25 rows | VALUES <> PERCENT | TSV | PDF | Print

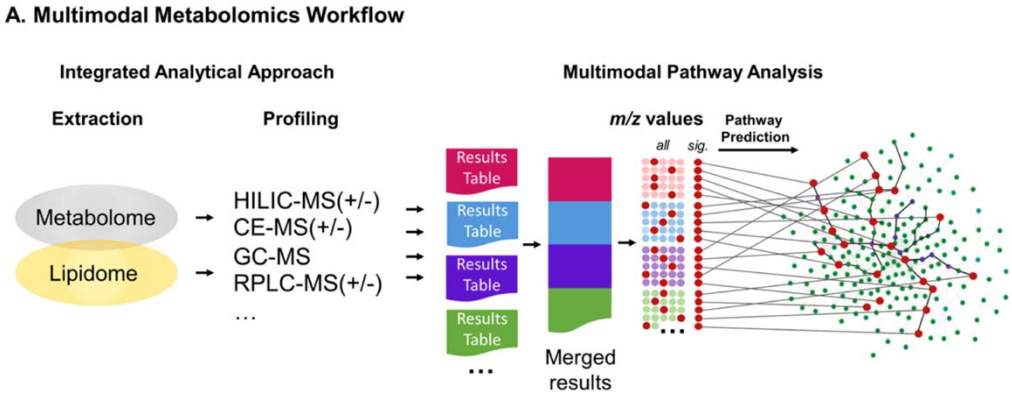
Pathway	Overlapping genes	All genes*	Overlapping proteins	All proteins*	Overlapping putative metabolites[1]	All metabolites[2]*	p-values
histidine biosynthesis	0	0	0	0	3	12	1.0e-2
pyrimidine deoxyribonucleotide phosphorylation	0	0	0	0	2	5	1.1e-2
UDP-*N*-acetyl-α-D-mannosaminouronate biosynthesis	0	0	0	0	2	5	1.1e-2
NAD salvage pathway I	0	0	0	0	2	5	1.1e-2
pyrimidine deoxyribonucleotides *de novo* biosynthesis III	0	0	0	0	3	13	1.3e-2
NAD biosynthesis from 2-amino-3-carboxymuconate semialdehyde	0	0	0	0	2	6	1.5e-2
ethanol degradation II	0	0	0	0	2	6	1.5e-2


Load New Pathway Supplementary Data
xcmsonline.scripps.edu/upload/index.php?action=pathway&runuser=11405&jobid=1143618
Save & Proceed
Storage Quota Usage (25.04 GB):
60.8%
• Files must be comma-separated (CSV) or tab-separated (TSV) files
• Gene files must have name as first column
• Protein files must have UniProt accession ID as first column
• All header text must be enclosed with double quotes (")
• After sample is uploaded you can close this window. (button above)
• Only one (1) file at a time [must close window and upload next]
DROP HERE
BROWSE

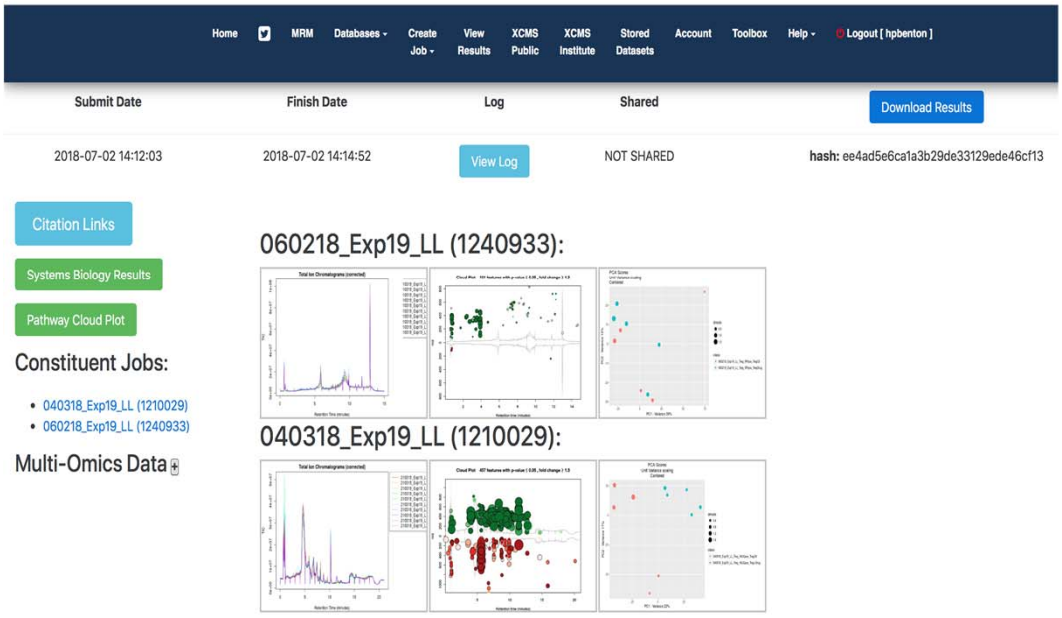

Systems Biology Matching Parameters
JOB ID:
1143618
JOB NAME:
pair_2017-01-31_16:29
FILES UPLOADED:
UPLOAD LIST
FileID
Filename
Upload Date
List Type
Accession ID
Matches
Remove
297096
gene_list.
2017-02-01 00:32:38
Genes
Gene name
View Results
Run matching subjob
MATCHING
PROGRESS (1%)
SUBJOB ID
4973
View Log
POPULATE TABLE
PROGRESS (0%)
SUBJOB ID
4970
View Log

System Biology

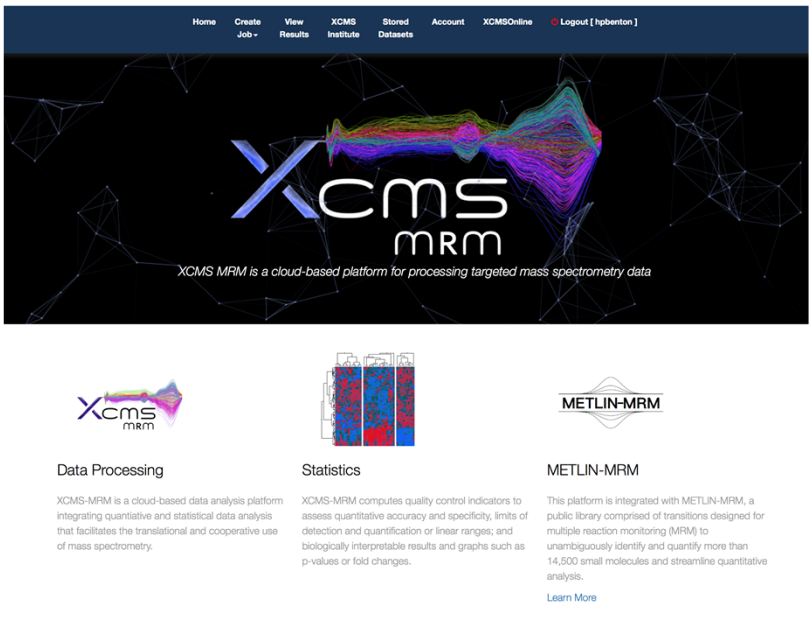
Multimodal metabolomics



Multimodal metabolomics

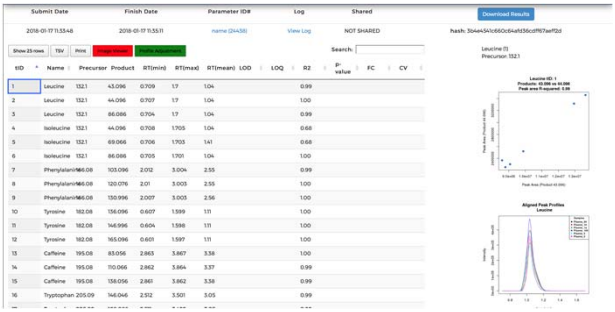


XCMS-MRM



XCMS-MRM

- XCMS – MRM – a central cloud based targeted analysis software
- With METLIN-mrm allows a standard for MRM analysis and optimization across multiple standards



Taking a step back

- We can automatically get to System level data quickly.
  - Where are the other dead time events?
- Sharing is caring : The future is sharing your data with others
- How can we make the data even better?

Thank you ! Questions ?

Prof. Gary Siuzdak

The Scripps Research Institute

Aries Aisporna

Duane Rinehart