Integrated Biology

A Pathway-centric Approach to Multiomics Research Powered by GeneSpring Analytics

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Presentation Outline

- 1. Multi-omics Integration: Why?
- 2. Multi-omics Research: How? (Case Studies)
 - Metabolomics + Transcriptomics → Targeted Proteomics : In search of new anti-TB drugs
 - Proteomics + Transcriptomics:
 - PD Biomarkers for Cancer Chemoprevention
- 3. Summary





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What is the "common coordinate" that enables integrative analysis?





Common Reference: Pathway Representation









- Identifies why the pathway is active
- Suggests follow-on experiments





Agilent Integrated Biology Workflows: Practically any –omics technology type imaginable



"Omics" ↔ Biology

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The Challenge







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Pathway-informed Drug Discovery for Tuberculosis (Dr. Kyu Rhee, Weill Cornell Medical College)



"TB can usually be cured with a combination of firstline drugs taken for several months. Shown here are the four drugs in the standard regimen of first-line drugs and their modes of action. Also shown are the dates these four drugs were discovered—all more than 40 years ago."

NIAID

http://www.niaid.nih.gov/topics/tuberculosis/Understanding/ WhatIsTB/ScientificIllustrations/Pages/firstLineIllustration.aspx



Multi-omics Workflow: Transcriptomics + Metabolomics

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Example Analysis– Drug X



All Genes

(Note increased change with dose)

Example Analysis– Drug X



Genes among top 5% up-regulated in all dosages

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Genes among bottom 5% downregulated in all High dosages



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Pathway & GO Enrichment: Drug X

DOWNREGULATED p-value <u>Pat</u>hway GO Term Mx Oxidative phosphorylation WP1680 41452 1.38E-04 phospholipase C activity 3.34E-04 Mx Peptidoglycan biosynthesis WP1685 41461 0.002111 lipase activity 2.01E-04 Mx D-Glutamine and Dglutamate metabolism WP1643 41425 0.002212 phospholipase activity 0.001113 Mx Ether lipid metabolism WP1645 41436 0.00711 Mx Inositol phosphate metabolism WP1664 414 80 0.014402 Mx Riboflavin metabolism WP1696 41424 0.023819

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		p-value		
Path	way	(Genes)	GO Term	P-value
Mx	Glyoxylate_and_dicarboxylate_metabolism	ı_W		
P166	51 41479	0.030887	biological regulation	9.75E-06
		0.074453	regulation of biological process	7.11E-06
			response to chemical stimulus	3.50E-06
RNA	Mode		response to stimulus	1.42E-05
rolymerube	Gyrase Of			
	action		negative regulation of biological process	2.97E-05
mPNIA	DNA		regulation of growth	8.20E-05
			negative regulation of growth	1.85E-04
some	/		propionate catabolic process, 2-methylcitrate	
200			cycle	5.96E-04
Protein	Macrolides		propionate metabolic process, methylcitrate	
A	Inhibit protein		cycle	5.96E-04
	synthesis		regulation of metabolic process	4 66F-04

• MOA

- Suggestion of secondary mechanisms
- Direction for further exploration

Ribos



Multi-omics Analysis: Learning more about significant genes, metabolites, paths, etc.

DOWNREGULATED			
	p-value		
athway	(Genes)	GOTerm	P-value
1x_Oxidative_phosphorylation_WP1680_41452	1.38E-04	phospholipase C activity	3.34E-0
1x_Peptidoglycan_biosynthesis_WP1685_41461	0.002111	lipase activity	2.01E-0
<pre>//x_D-Glutamine_and_D-</pre>			
lutamate_metabolism_WP1643_41425	0.002212	phospholipase activity	0.0011
1x_Ether_lipid_metabolism_WP1645_41436	0.00711		
Ix_Inositol_phosphate_metabolism_WP1664_414			
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Ix_Riboflavin_metabolism_WP1696_41424	0.023819		
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661 41479	0.030887	biological regulation	9 75F-
	0.074453	regulation of biological process	7 11E-
	0.074400	response to chemical stimulus	3 50E-
Mode		response to stimulus	1.42E
Gyrase Of		negative regulation of biological process	2 97F-
		regulation of growth	8.20F-
DNA PCtio		negative regulation of growth	1.85E
h		propionate catabolic process, 2-methylcitrate	
1		cycle	5.96E-
		propionate metabolic process, methylcitrate	
Macmus		cycle	5.96E-
Inhibit protein		regulation of metabolic process	4.66E-
A Contract BLOMPT		- 0	
Inhan 1065		regulation of metabolic process	4.66E-
Marrier		cvcle	5.96E-
		propionate metabolic process, methylcitrate	
		cvcle	5.96E-
19		propionate catabolic process, 2-methylcitrate	
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Peptidoglycan biosynthesis Question: How can I understand what is biologically relevant about this pathway?

Answer: Pathway visualization to find enriched paths



Peptidoglycan Biosynthesis





Mapping Metabolites across Databases: UDP-N-acetylmuramate

METABOLITE DBs

Human Metabolome Database Version 3.5					
Search	Search type: Metabolites • Search [Advanced]				
HMDB has recent	tly undergone some major changes, if you are experiencing problems please click here to provide us with feedback.				
	Showing metabocard for UDP-N-acetyImuraminate (HMDB11720)				
Metabolite Identif	cation				
Common Name	UDP-N-acetylmuraminate				
Description	UDP-N-acety/muraminate is a nucleoside diphosphate sugar which is formed from UDP-N-acety/glucosamine and phosphoenolpyruvate. It serves as the building block upon which peptidoglycan is formed.				
Structure	Download: MOL SDF SMILES InChi Display: 2D Structure 3D Structure				
Synonyms	N-Acetylmuramoyl-UDP UDP-Murt/Ac UDP-M-Acetyl-D-muramate UDP-N-Acetyl-muramate UDP-N-Acetylmuramate UDP-N-Acetylmuramic acid Uridine diphosphate N-acetylmuramic acid				
Chemical Formula	C ₂₀ H ₃₁ N ₃ O ₁₉ P ₂				
Average Molecular Weight	679.4164				
Monoisotopic Molecular Weight	679.102698849				

PATHWAYS DBs



K	COMPOUND: C01050		
Entry	C01050 Compound		
Name	UDP-N-acetylmuramate; UDP-N-acetyl-alpha-D-muramate; UDP-N-acetylmuramic acid; UDP-MurNAc		
Formula	C20H31N3019P2		
Exact mass	679.1027		
Mol weight	679.4164		
structure	$HO^{+} O^{+} O^{-} P^{-} O^{-} P^{-} O^{-} O^{+} O^{$		
Reaction	R03191 R03192 R03193		
Pathway	ko00471 D-Glutamine and D-glutamate metabolism ko00520 Amino sugar and nucleotide sugar metabolism ko00550 Peptidoglycan biosynthesis		



Same?

BridgeDb: Mapping Entities Onto Pathways Resolves Mapping Problem Between Databases



Metabolite Identifiers •KFGG •HMDB ChEBI •CAS **Protein Identifiers:** Swiss-Prot UniProt UniProt/TrEMBL Gene Identifiers : Entrez Gene, GenBank, Ensembl •EC Number, RefSeq, UniGene, HUGO •HGNC, EMBL



Multi-omics Workflow: Transcriptomics + Metabolomics

+ 4





Multi-omics Workflow: Transcriptomics + Metabolomics → Targeted Proteomics







Enhancing Targeted Proteomics Experiments: Integrating Prior knowledge and Community-based Tools into the IB Ecosystem







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Case Study:

Looking for Evidence of Pathway Intervention to Advance the Search for New Breast Cancer Chemopreventives

Breast Cancer Res Treat DOI 10.1007/s10549-011-1536-9

PRECLINICAL STUDY

Transcriptomic and proteomic profiling of KEAP1 disrupted and sulforaphane-treated human breast epithelial cells reveals common expression profiles

Abena S. Agyeman · Raghothama Chaerkady · Patrick G. Shaw · Nancy E. Davidson · Kala Visvanathan · Akhilesh Pandey · Thomas W. Kensler

Received: 15 April 2011 / Accepted: 17 April 2011 © Springer Science+Business Media, LLC. 2011



Suhr Y-J. Nat. Rev. Cancer, 2003, 768-80.



The Workflow: Manual





10011010



Keap1- Nrf2 Pathway: 3100101010 **Transcriptome in GeneSpring Integrated Biology**







Keap1- Nrf2 Pathway: Proteome in GeneSpring Integrated Biology





Western blot validation of SILAC data





Insights from Integrated Analysis

• "Big Picture" view

Key Pathways from SFN Exploration

- Xenobiotic metabolism and antioxidants
- Glutathione metabolism
- Carbohydrate metabolism and NAD(P)H generation
- Identify activated pathways
 ...including known cytoprotective pathways
- Identify off-target behaviors, and theorize as to mechanism (or even toxicity) (e.g. SFN does more than inhibit KEAP1)



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Pathway-directed re-mining of data or designing the next experiment

Propose new experiments based on pathway analysis

- 1. Re-mine originally acquired (or legacy) untargeted metabolomics data based on pathway analysis—create db
- 2. Design new experiments (metabolite, protein or genes) based on pathway results interpretation



Multi-Omic Analysis in GeneSpring





Thank you!

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- Allan Kuchinsky, Agilent Labs

Learn more!

New Agilent IB Website: http://biology.chem.agilent.com/



