PortEco overview PortEco search Search for information about a particular gene Gene expression What genes are induced/repressed in some set of experiments? What genes are upregulated? What genes have expression patterns similar to my favorite gene? ChIP data Chemical Genomics Phenotypic Landscape Strain vs Condition Strain vs Strain Condition vs Condition Annotation with Students (CACAO) What is GO? Browsing GO

PortEco overview

PortEco is a portal for *E. coli* research (K-12 strains and their phage and mobile elements) that aims to:

- 1. facilitate access to E. coli information that is distributed over the web
- 2. make *E. coli* genomics data (currently gene expression data and chemical genomics data) easy to access, search and analyze.
- 3. enable the community to add information to the knowledgebase via EcoliWiki
- 4. provide <u>community features</u> such as a calendar, colleague search, blog entries mentioning *E. coli*; and educational materials

Access to E. coli information

PortEco search: aggregated search results for 14 different web resources EcoliHouse: a data warehouse with information from multiple data resources, including EcoCyc and EcoGene

Genomics data

Gene expression data and analysis tools at http://<u>expression.porteco.org</u> Chemical genomics data at <u>http://ecoliwiki.net/tools/chemgen/</u>

PortEco search

PortEco Search (search box at <u>http://porteco.org/</u>, or page at <u>http://porteco.org/AjaxSearch.jsp</u>) launches searches of 14 different web resources for *E. coli* information, and organizes the results onto a single results page. The page loads each result as it comes back from the

respective web resource: the progress bar on the page keeps track of how many resources have returned results.

If an *E. coli* gene name is entered in the search box, the results are formatted into the "Gene Results view." The full results display can be shown by clicking on the "Show full search results" button:

	PORTECO	1Ĉ	12						
portal fo	or <i>E. coli</i> research	00							
Home	About PortEco	About E. coli	Help/Tutorials	Contact Us					
	PortEco Search: muts Co Searches 13 different web resources (more) Gene Results view (your query is associated with a gene name). Show full search results								
Finished Loading									
Gene mutS Encodes DNA mismatch repair protein mutS									
The resou	The resources searched are listed at http://porteco.org/help/general.jsp.								

Search for information about a particular gene

Try entering a gene name in the search box, and press the **Search** or **Go** button. An example is shown below for the search string "muts" (note that the search is not case-sensitive):

portal for E. c	oli research	S BORAV							
Home	About PortEco About E.	coli Help/Tutorials	Contact Us						
Por Ger	tEco Search: muts ne Results view (your query is ass	Go Searches 13 diffe	rent web resources (more) w full search results						
	Fills								
Ge En Su stru dim	ene mutS codes DNA mismatch repair protein r mmary (from EcoCyc):MutS is cture of MutS bound to a 30 base pair D er that clasps the DNA. Only the DNA-bi	nutS one of the components of the MutHLS (NA oligomer containing a G:T mismatch nding domain of one of the monomers is	complex. MutHLS functions in the methyl-direc has been resolved at 2.2Å [CITS:[11048711] in direct contact with the mismatch.	cted mismatch repair pathway in <i>Escherichia coli</i> . The crystal I. In this structure two MutS monomers form an asymmetric					
De	tailed gene/protein information at:								
Ec	оСус	EcoliWiki	EcoGene	Uniprot					
Ger	nomics data								
Ge P C	Gene expression data at SMD Profiles in 68 experiments (and other genes with correlated profiles) Conditions with significant expression patterns across 615 samples								
Ch	emical genomics of knockout	(Nichols et al., Cell 144:143, 2011)						
G	Frowth rates under 318 different ch	emical exposures							
C	Aner gene knockouts with correlation	ed patterns							
Ger	netics, phenotypes and cellular loc	alization							
Kn	ockout phenotype, gene essentiali	ty, GFP localization at Genobase							
Alle	eles and phenotypes at EcoliWiki								
Str	Strain availability at EcoliWiki								
Oth	er information								
Int	eractions								
P	Predicted gene-gene and protein-protein interactions at STRING								
P	Protein-protein interactions at PathwayCommons								
Ge	ne family and evolution at PAN	ITHER							
L	ocation in phylogenetic tree								
C	orthologs in other organisms								
Pro	tein 3D structures and models at I	Protein Model Portal							
339	published journal articles mention	ning mutS in TextPresso							

Search for general information

You can enter other search terms as well. For example, you can search for

- a person in the EcoliWiki colleague pages (e.g. "paul thomas", see results page),
- a meeting in our PortEco Calendar (e.g. "phage meeting", see results page),
- a general biological search term (e.g. "kinase", see results page).

In this view, you can jump to different sections of the page by clicking on the name of the section in blue, in the yellow summary box:



For example, clicking on "Pathways and Interactions" will scroll down to the section of the page with results of searches at websites that have information about pathways and molecular interactions in *E. coli*, that contain the search term.

Gene expression

<u>expression.porteco.org</u> offers a variety of tools to let you explore expression data for *E. coli*. We have been curating expression data available from GEO and ArrayExpress to allow comparisons across different studies. Although we have loaded over 1,000 arrays from 75 publications, this is only about 35% of the available studies for *E. coli*.

The results of analyses we will demo in this workshop are likely to change as additional datasets are added, and as we incorporate data from RNA-seq studies.

What genes are induced/repressed in some set of experiments?

We will find what genes have significant expression changes when subjected to one of the chemical treatments studied in the set of transcriptome experiments in the database.

- Choose Cluster My Genes.
- Click Chemical Treatments.
- Select Indole Acrylic Acid.
- o Click the Most Significant Genes button

Cluster My Genes	Help
Cluster My Genes Cluster My Genes Cluster My Genes tool allows you to retrieve and cluster gene like experimental Conditions or Mutant or Strain or from a Pul Condition Mutant Strain Publication Antibiotics - Inhibitors of LPS biosynthesis (6) Antibiotics - Inhibitors of Rho (16) Charliel treatment (20) Acidified Na Nitrite - control (2) Autoinducer-2 + Mutant (7) Autoinducer-2 + Mutant (1) Butanol (8) Carbon monoxide (20) Carbon monoxide (20) Copper (6)	Help expression data for a given set of genes in samples based on your selection criteria blication. Samples selected: 8 Genes: Enter gene names or symbols. Leave blank to use all genes Cluster My Genes
Copper (6) Copper - control (3) Epiper-brine + Mutant (1) Ethanol (17) Ethanol - control (11) Formate (2) Hydrogen perxide (6) Isobutanol (10) Isobutanol + arcA- (8) Isobutanol + fur- (8) Isobutanol + infA- (8)	Show Most Significant Genes Show Most Significant Up-regulated Genes Show Most Significant Down-regulated Genes Reset form

You should get a list like this:

Gene	Median Z Score (Absolute Value)	Number of Samples
trpE	7.067	8
yjiC	6.679	1
trpD	6.288	8
trpC	5.311	8
mtr	5.115	8
puuB	5.024	8
aceK	4.855	6
eamB	4.670	8
gatB	4.623	6
trpB	4.610	8
puuE	4.585	8
oppC	4.411	8
pstS	4.377	8
trpA	4.289	8
fliK	4.288	7
yfjZ	4.280	1
ycjV	4.267	1
cysC	4.251	2
gatC	4.209	5
fliI	4.205	6
frdB	4.136	8
sucB	4.040	7
nuoH	4.032	5
argF	3.943	8

Individual conditions: Indole acrylic acid

Indole Acrylic Acid is an inhibitor of tryptophan synthetase, and is known to induce expression of the trp operon. It makes sense that the trpE, trpD, trpC, trpB, and trpA all have significant changes in gene expression. To see a "heat map" of the data, click on **Go To Gene Profiles** at the bottom of the page to get this:

Zoom				
5° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 70 00 10° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 70 00 10° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 70 00 10° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 70 10° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 70 10° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 70 10° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 70 10° us 0° indole acrylic acid (10 ug/ml) (Indole acrylic acid) 80° us 0° indole acrylic acid (15 ug/ml) (Indole acrylic acid) 80° us 0° indole acrylic acid (15 ug/ml) (Indole acrylic acid) 80° us 0° indole acrylic acid (15 ug/ml) (Indole acrylic acid)	< 1/20.8 < 5' vs 0' ind 15' vs 0' in 30' vs 0' in 5' vs 0' in 30' vs 0' in 30' vs 0' in 60' vs 0' in 60' vs 0' in	ole acrylic dole acryli dole acryli dole acryli ole acryli dole acryli dole acryli dole acryli dole acryli	1/4.6 < acid (10 c acid (10 c acid (10 c acid (15 c aci	ug/ml) (indole acrylic acid) 0 ug/ml) (indole acrylic acid) 0 ug/ml) (indole acrylic acid) 0 ug/ml) (indole acrylic acid) ug/ml) (indole acrylic acid) 5 ug/ml) (indole acrylic acid)
	EG10814	rbsA	948264	fused D-ribose transporter subunits of ABC superfamily: ATP-binding components
	EG10503	☑ IIVY	948284	DNA-binding transcriptional dual regulator
	EG14066	🗹 yegW	946639	predicted DNA-binding transcriptional regulator
	EG11088	g pdhR	944827	DNA-binding transcriptional dual regulator
	EG11929	🗹 zur	948552	DNA-binding transcriptional repressor, Zn(II)-binding
	EG10281	🗹 fadR	948652	DNA-binding transcriptional dual regulator of fatty acid metabolism
	EG10260	🗹 entB	946178	isochorismatase
	EG13810	IsrF	946071	putative autoinducer-2 (AI-2) aldolase
	EG10544	🗹 lpp	946175	murein lipoprotein
	EG11105	entH	945215	thioesterase required for efficient enterobactin production
	EG11849	🗹 yihW	948381	predicted DNA-binding transcriptional regulator
	EG12427	M modA	945364	molybdate transporter subunit
	EG12460	✓ yjcZ	948633	mutational suppressor of yhjH motility mutation, function unknown
	EG13907	Dunb	946287	putrescine importer
	EG12094	SgrR	944788	transcriptional DNA-binding transcriptional activator of sgrS sRNA
	EG10036	Dunc 🖸	947003	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent
	EG11544	adE	948023	DNA-binding transcriptional activator

The small, almost unreadable graph shows a thumbnail of the clustering of the *E. coli* genes with significant expressions changes in the 8 selected samples. The red dotted lines show the area that is expanded below. You can move the selection by clicking.

What pathways are upregulated?

Click on the patch of bright red in the heat map to select the genes that are strongly upregulated. The select a subset of the samples.

	0 2 2 2 0 2 2 2										
	10000000000000000000000000000000000000	< 1/20.8 <	< 1/9.7 <	1/4.6 <	1/2.1 1:1 > 2.1 > 4.6 > 9.7 > 20.8						
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	,	15' vs 0' in	dole acrvli	c acid (15	ug/mi) (indole acrylic acid)						
	30' vs 0' indole acrylic acid (15 ug/ml) (indole acrylic acid)										
	5 5 5 5 5 5 60' vs 0' indole acrylic acid (15 ug/m) (indole acrylic acid) Show Pathways										
	GO Term Find	ler) - Dow	nload all (data (.pcl							
	View Data										
		EG10603	🗹 mprA	945282	DNA-binding transcriptional repressor of microcin B17 synthesis and multidrug efflux						
		EG10080	🗹 aroH	946229	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tryptophan repressible						
		EG11028	🗹 trpE	945846	component I of anthranilate synthase						
		EG11027	🗹 trpD	945109	fused glutamine amidotransferase (component II) of anthranilate synthase/anthranilate phosphoribosyl transferase						
		EG11026	🗹 trpC	945519	fused indole-3-glycerolphosphate synthetase/N-(5-phosphoribosyl)anthranilate isomerase						
		EG11025	🗹 trpB	945768	tryptophan synthase, beta subunit						
U .IV		EG11024	🗹 trpA	946204	tryptophan synthase, alpha subunit						
		EG11354	🗹 emrA	947166	multidrug efflux system						
🏭		EG12822	🗹 aaeB	947747	p-hydroxybenzoic acid efflux system component						
		EG11435	🗹 marR	945825	DNA-binding transcriptional repressor of multiple antibiotic resistance						
401		EG12600	🗹 yjjX	948919	inosine/xanthosine triphosphatase						
		EG11369	🗹 ubiC	948545	chorismatepyruvate lyase						
ليتعاد		EG10491	🗹 iclR	948524	DNA-binding transcriptional repressor						
		EG14033	🗹 cmoA	946380	tRNA cmo(5)U34 methyltransferase, SAM-dependent						
		EG13397	🗹 iscR	945279	DNA-binding transcriptional repressor						
		EG10443	🗹 hipA	946064	serine protein kinase required for perister formation; toxin of HipAB toxin-antitoxin system						
		EG10442	🗹 hipB	946065	antitoxin of HipAB toxin-antitoxin system						
		EG11755	hchA	946481	Hsp31 molecular chaperone						
		EG20255	🗹 sapB	946191	antimicrobial peptide transport ABC transporter permease						
		EG13547	🗹 ivy	946530	inhibitor of c-type lysozyme, periplasmic						
		EG13218	🗹 ybaO	945091	predicted DNA-binding transcriptional regulator						
		EG10325	🗹 fnr	945908	DNA-binding transcriptional dual regulator, global regulator of anaerobic growth						
		EG13326	🗹 ybiU	945439	predicted protein						
		EG12571	🗹 yjij	948859	predicted inner membrane protein						
		EG12570	🗹 kptA	948858	RNA 2'-phosphotransferase						
		EG11684	V yicH	948171	conserved protein						
		EG12824	🗹 aaeX	947751	membrane protein of efflux system						
		EG12174	🗹 vdaG	945907	Rac prophage: predicted protein						

Click Show Pathways to send data for the selected genes to the EcoCyc Omics viewer



The trp biosynthetic pathway, along with a few other reactions, is highlighted. You can pan and zoom on the map to see more detail.

What genes have expression patterns similar to my favorite gene?

Genes that act in the same biological process often have similar patterns of gene expression. However, the converse is often not true: similar patterns of gene expression do not mean common biological functions. A major reason for this is that in most transcriptome studies, the majority of genes do not change their expression. Thus, many genes of unrelated function will cluster together by virtue of not doing anything.

To avoid this, we would like to see what genes have common expression with our favorite genes under conditions where the expression of our favorite gene is doing something interesting.

Type dinB in search box for Samples and Conditions.



The histogram shows the distribution of significance scores for *dinB* across the studies available at expression.porteco.org. The adjustable light blue area selects studies from a range of values. These are listed on the right. To view a cluster across these studies, click on the cluster icon next to the Download Table link.

Wait for the clustering heatmap to come up, and enter *dinB* in the search box that will appear in the top banner.

4

ortEcol Exproscion		gene	lorer	SAV7 3	100
orteco. Expression	Put your mouse over elements	to see more information here			
n-throughput biological data powered by the Stanford Microarray Database		Search for dinB	90	2R37/3	1 2 - 2 - 2
Most similar (orange) and dissimilar (gray) expression patterns for: sulA /	EG10984				
Mbro1)					
8 22.4					
4 5 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					
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출출 출출 경험 등 10min after UVtreatment 1', 40J, MG1655 in Davis+0.4%gl	u (Ultraviolet light)				
40min after UVtreatment 1, 40J, MG1655 in Davis+0.4%gi	u (Ultraviolet light – control)				
នុន្ននួន * * មុ bomin after Uvtreatment 1, 40J, MG1655 in Davis+0.4%gli និតិទីទី៤ មិនិចិ	(Ultraviolet light)	Show Pathways			
GO Term Finder - Download all data (.pcl)					
EG10984 e sulA 947335 SOS cell division	n inhibitor				
EG10923 I ruvA 946369 component of R	uvABC resolvasome, regulatory su	ubunit			

Clicking GO or pressing return will give you a view like this, showing only dinB:

atment 1', 40J atment 1', 40J atment 1, 40J, atment 1, 40J, al medium +0.2 mal medium +0. mal medium +0.	< 1/4.8	< 1/3.2	< 1/2.2	< 1/1.5	1:1	> 1.5	> 2.2	> 3.2	> 4.8			
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Sometimes there is no heat map to the left of the gene information - this is a bug. Mouse over that area and you will see that there is a link. You may see a tooltip popup that says "View this gene's profile". Click there.

GO Term Finder	Download all	data (.ncl)		
View Data	boundad and	autu (.per)		
	EG13141	e dinB	944922	DNA polymerase IV
	EG11808	✓ yebG	946364	conserved protein regulated by LexA
		✓ yeeL_2	946497	
	EG11472	Image: Image: wide manual state of the s	948966	predicted recombination limiting protein
	EG10823	I recA	947170	DNA strand exchange and recombination protein with protease and nuclease activity
	EG11193	🕑 dinD	948153	DNA-damage-inducible protein
	EG12080	✓ recX	947172	regulatory protein for RecA
	EG13153	✓ yafP	944912	predicted acyltransferase with acyl-CoA N-acyltransferase domain
	EG11056	🕑 umuC	946359	DNA polymerase V, subunit C
	EG10831	recN	947105	recombination and repair protein
	EG11062	le uvr₿	945385	excinulease of nucleotide excision repair, DNA damage recognition component
	EG11393	✓ dsbB	946344	oxidoreductase that catalyzes reoxidation of DsbA protein disulfide isomerase I
	EG13993	🕑 cho	948996	endonuclease of nucleotide excision repair
	EG11807	yebF	946363	secreted protein
	EG14333	⊌ ykfI	946726	CP4-6 prophage; toxin of the YkfI-YafW toxin-antitoxin system
	EG12894	🕑 gspK	947831	general secretory pathway component, cryptic
	EG13338		945373	CP4-6 prophage; conserved protein
	EG13667	ybhK	945390	predicted transferase with NAD(P)-binding Rossmann-fold domain
	EG11434	🕑 marA	947613	DNA-binding transcriptional dual activator of multiple antibiotic resistance
	EG13367	⊌ ydaY	946208	
	EG13013	🕑 yqhC	947491	transcriptional activator of yqhD
	EG10035		945672	aldehyde dehydrogenase A, NAD-linked
	EG11391	✓ osmY	948895	periplasmic protein
	EG13690	✓ ItaE	944955	L-allo-threonine aldolase, PLP-dependent
	EG13625	🕑 mhpF	945008	acetaldehyde-CoA dehydrogenase II, NAD-binding
	EG11233	✓ rstB	948870	sensory histidine kinase in two-component regulatory system with RstA
	EG10207	🕑 dapD	944862	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
	EG11441	g priC	948016	oligopeptidase A
	5010310	of whole	047621	and shed DNA bladles becaused able as includes.

The orange bars indicate genes that cluster with *dinB*, while the grey bars indicate anticorrelation. The many of the genes we see are known members of the SOS response regulon, so this is an expected result. However some are genes of unknown function.

Interestingly, some other genes known to be in the SOS response are not clustering with *dinB* in these studies. Let's compare some expression patterns over several studies.

Cluster My Genes

Cluster My Genes tool allows you to retrieve and cluster gene expression data for a given set of genes in samples based on your selection criteria like experii from a Publication.



Here, I've selected other studies that are annotated as involving DNA damage, and I've focused the clustering on the genes that clustered with dinB in the previous analysis, plus some other genes I think should have been in this cluster. For example, *sulA* is often used as a reporter for the SOS response. UmuD is in a complex with UmuC. The *umuC* gene clustered with *dinB*, so let's see what's going on with *umuD*. Click **Cluster My Genes**, and find *dinB* again.



Note a few things. First, Cluster My Genes picked up some genes that were not on our list; this is because it's looking for matches not just in the gene name but also in the rest of the gene information. Second, in the larger comparisons, the other known SOS genes look similar to

dinB. This second point illustrates how transcriptome analysis, and, more generally, cluster analysis does not have a unique "right answer".

ChIP data

http://ecoliwiki.net/gbrowse will redirect you to the EcoliWiki genome browser.

File - Help -
E coli K 12 MC1655, 100 kbp from NC, 000012;2 100 000, 2 200 000
E. coli k-12 Mc1055: 100 kbp iroli NC_000913:3,100,0003,200,000
Browser Select Tracks Custom Tracks Preterences
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Examples: argl, argR, parC, phoA, sucB, ssrA.
E. coli K-12 MG1655
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lac PM-b Rac PK-X EUC/DZ-00 Pm-1 mmE lac PM-67 Pm-6
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Select Tracks to see available ChIP and other data types

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Sanches-Romero 2010 All on All off								
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Cho et al. 2011 All on All off								
SImA density	SImA xy							
Cho et. at. 2009 All on All off								
RNAp heat-shocked, negative	RNAp rifampicin treated, negative	RNAp stationary phase, negative						
RNAp heat-shocked, positive	RNAp rifampicin treated, positive	RNAp stationary phase, positive						
RNAp log phase, negative	RNAp glutamine as nitrogen source, negative							
RNAp log phase, positive	RNAp glutamine as nitrogen source, positive							
Grainger 2006 All on All off								
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Mooney 2009 All on All off								
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NusA	✓ RNAp							
Vora 2009 All on All off								
Protein Occupancy. Vora 2009.								
General All on All off								
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Select one or more tracks and return to the browser



Generic Genome Browser version 2.26. For questions about the data at this site, please contact its webmaster. For support of the browser software *only*, send email to gmod-gbrowse@lists.sourceforge.net or visit the GMOD Project web pages.

Gbrowse allows you to upload your own private tracks to compare with our tracks. For example, try this file:

http://ecoliwiki.net/files/phage2011/pec_nonessential.gff

Chemical Genomics Phenotypic Landscape

Carol Gross' keynote will describe some of the work her lab based on high-throughput phenotyping (<u>Nichols et al. (2010) Phenotypic Landscape of a Bacterial Cell. Cell 143, 1097–1109</u>). We have a tool to allow you to browse the data at: <u>http://ecoliwiki.net/tools/chemgen/</u>

There are three kinds of searches you can do.

Strain vs Condition

This allows you to search for the behavior of a knockout mutant on one of the 324 conditions. Enter *recA* and sort the score to show the most negative first. This data browser is for data from Nichols et al. (2010) Phenotypic Landscape of a Bacterial Cell. Cell 143, 1097–1109 Search data

Go to help

Select a search type: List strains List conditions		
Growth data (Strain/Condition) strain Correlations among strains Correlations among conditions conditi	n recA on	Please enter at least one query. If you leave a field empty, the search will look for all.
Submit		

item 1:recA => strain(s):'recA', 'ECK2694-RECA'
item 2: => cond(s):all

ving 1 to 50 of 318 entries Fi	iter:	Fir	irst Previous 1 2 3 4 5 Next
strain	\$	cond	🔶 score 🔺
ECK2694-RECA	NITROFURANTO	IN-1.5	-14.6681570
ECK2694-RECA	NORFLOXACIN-0	0.01	-14.1697920
ECK2694-RECA	NITROFURANTO	IN-2.0	-12.6568720
ECK2694-RECA	MITOMYCINC-0.	1	-11.7342480
ECK2694-RECA	CIPROFLOXACIN	I-0.006	-10.4311280
ECK2694-RECA	MMS-0.05%		-10.0342640
ECK2694-RECA	LEVOFLOXACIN-	0.002	-9.1689430
ECK2694-RECA	NORFLOXACIN-0	0.02	-9.0748700
ECK2694-RECA	NITROFURANTO	IN-1.0	-8.9442600
ECK2694-RECA	ETHIDIUMBROM	IDE-50	-8.4857310
ECK2694-RECA	STREPTONIGRIM	1-0.5	-7.9777590
ECK2694-RECA	CIPROFLOXACIN	I-0.008	-7.8658110
ECK2694-RECA	STREPTONIGRIM	-0.1	-7.8588390
ECK2694-RECA	ACRIFLAVINE-10	D	-7.4681000
ECK2694-RECA	DOXORUBICIN-	10.0	-5.9352350
ECK2694-RECA	ETHIDIUMBROM	IDE-10	-4.2397480
ECK2694-RECA	NITROFURANTO	IN-0.5	-4.1312820
ECK2694-RECA	ETHIDIUMBROM	IDE-2	-4.0370300
ECK2694-RECA	NORFLOXACIN-0	0.04	-3.8086930
ECK2694-RECA	TRITONX-0.2%		-3.2498870
ECK2694-RECA	PHLEOMYCIN-1.	0	-3.1218900
ECK2694-RECA	BILE-1.0%		-2.6684770

Fitness is based on colony size doubly normalized for the sizes of all colonies on the plate and the size of the specific strain under other conditions. Scores are not directly correlated to doubling times or growth rates: they're a statistical measure of how far this sample is from the average behavior of all strains on this condition and this strain on all conditions. Positive scores mean better than average fitness, while negative scores mean greater than average sensitivity.

In the example, we can see that *recA* is more sensitive to nitrofurantoin, norfloxacin, cipro, mitomycin etc. These all make physiological sense, as they lead to DNA damage.

Strain vs Strain

We can look at what other genes have similar patterns of increased or decreased fitness by changing to a strain vs strain comparison. Leave *recA* in strain 1 and leave the other blank.

Search data

Go to help		
Select a search type:		
Growth data (Strain/Condition) strain 1	recA	Please enter at least one query.
Correlations among strains strain 2		If you leave a field empty, the search will look for all.
Submit		

item 1:recA => strain(s):'recA', 'ECK2694-RECA'
item 2: => strain2(s):all

	Filter:		First Previous 1 2 3 4 5 Next 1
strain	▲ ²	strain2	correlation_coefficient
ECK2694-RECA	ECK2694-RECA		1.00000000
ECK2694-RECA	ECK1862-RUVA		0.588771000
ECK2694-RECA	ECK2818-RECC		0.544787000
ECK2694-RECA	ECK1864-RUVC		0.541649000
ECK2694-RECA	ECK3642-RECG		0.538428000
ECK2694-RECA	ECK2816-RECB		0.489492000
ECK2694-RECA	ECK4050-UVRA		0.483626000
ECK2694-RECA	ECK2612-RECN		0.438514000
ECK2694-RECA	ECK0768-UVRB		0.412939000
ECK2694-RECA	ECK0621-LIPA		0.407332000
ECK2694-RECA	ECK3808-UVRD		0.401450000
ECK2694-RECA	ECK3806-XERC		0.393383000
ECK2694-RECA	ECK1310-YCJS		0.360886000
ECK2694-RECA	ECK1912-UVRC		0.323210000
ECK2694-RECA	ECK2270-NUON		0.323139000
ECK2694-RECA	ECK4017-PGI		0.322410000
ECK2694-RECA	ECK0654-UBIF		0.319181000
ECK2694-RECA	ECK2889-XERD		0.311637000
ECK2694-RECA	ECK0388-RDGC		0.301641000
ECK2694-RECA	ECK3085-EXUR		0.296974000
ECK2694-RECA	ECK2281-NUOB		0.296758000
ECK2694-RECA	ECK2282-NUOA		0.294667000
ECK2694-RECA	ECK0398-ACPH		0.292268000

The score here is a correlation coefficient for all the phenotypes of each pair of strains. Based on Fig 3 of Nichols et al, the P-values for these correlation coefficients are

correlation coefficient	P-value
0.4	10 ⁻¹⁴
0.5	10 ⁻²²
0.6	10 ⁻³⁴
0.7	10 ⁻⁵⁰

0.8	10 ⁻⁷⁵
0.9	10 ⁻¹²⁰

The fitness effects of mutations in a particular condition are often due to complex indirect effects. This means looking at the strain-condition scores is often not informative in terms of the biological function of a gene. However, strain-strain correlation will pick up cases where both the direct and indirect effects are similar, making the strain-strain comparisons more informative.

Condition vs Condition

Similarly, we can compare conditions Search data

Go to help	
Select a search type: List strains List conditions	
Growth data (Strain/Condition) condition 1 nitrofurantoin-1.0 Correlations among strains Correlations among conditions condition 2 Submit	Please enter at least one query. If you leave a field empty, the search will look for all.
item 1:nitrofurantoin-1.0 => cond(s):'nitrofurantoin-1.0', 'NITROFURA item 2: => cond2(s):all	NTOIN-1.0'

Showing 1 to 50 of 317 entries		
Filter:		First Previous 1 2 3 4 5 Next Last
cond	cond 2	correlation_coefficient
NITROFURANTOIN-1.0	NITROFURANTOIN-1.0	1.00000000
NITROFURANTOIN-1.0	NITROFURANTOIN-0.5	0.632582000
NITROFURANTOIN-1.0	NITROFURANTOIN-1.5	0.534356000
NITROFURANTOIN-1.0	ACTINOMYCIND-2.5	0.395206000
NITROFURANTOIN-1.0	ACTINOMYCIND-5.0	0.377339000
NITROFURANTOIN-1.0	PROCAINE-1	0.359892000
NITROFURANTOIN-1.0	NITROFURANTOIN-2.0	0.309719000
NITROFURANTOIN-1.0	ACTINOMYCIND-10.0	0.295500000
NITROFURANTOIN-1.0	EGTA-0.5	0.287543000
NITROFURANTOIN-1.0	EGTA-0.1	0.283845000
NITROFURANTOIN-1.0	TOBRAMYCIN-0.05	0.271015000
NITROFURANTOIN-1.0	PROCAINE-5	0.270544000
NITROFURANTOIN-1.0	UV-24SEC	0.265810000
NITROFURANTOIN-1.0	UV-12SEC	0.265127000
NITROFURANTOIN-1.0	TOBRAMYCIN-0.1	0.263121000
NITROFURANTOIN-1.0	TUNICAMYCIN-1.0	0.250606000
NITROFURANTOIN-1.0	TUNICAMYCIN-3.0	0.246792000
NITROFURANTOIN-1.0	UV-18SEC	0.244157000
NITROFURANTOIN-1.0	SPIRAMYCIN-1	0.243117000
NITROFURANTOIN-1.0	GENTAMICIN-0.1	0.236867000
NITROFURANTOIN-1.0	CCCP-0.1	0.231874000
NITROFURANTOIN-1.0	NITROFURANTOIN-0.1	0.220140000
NITROFURANTOIN-1.0	CCCP-0.5	0.215787000

Annotation with Students (CACAO)

Our ability to mine data about *E. coli,* or any other organism, is limited by how well we capture what is in the literature. To speed up curation of the literature, we have created a way for people to get teaching credit for having students do curation using the Gene Ontology (GO).

Brenley McIntosh will present a poster with more detail about this activity, which we call Community Assessment of Community Annotation with Ontologies. Today we're just going to show you:

- What GO is
- How to browse in GONUTS
- How to create an editable page

What is GO?

Ontologies can be thought of as vocabularies for types or classifications combined with defined relationships between those types.

Example:

phosphofructokinase activity is_a carbohydrate kinase activity

Relationships between types in ontologies can be complex directed acyclic graphs (DAG). Ontologies can be thought of as concept maps for different areas of knowledge. Below is a DAG for the GO term integral to plasma membrane.



Although it is counterintuitive, the DAG is usually drawn with the **root node** at the top. The terms at the ends of the branches are often referred to as **leaf nodes**. As you move from the root toward the leaves, the terms become more specific. The more specific terms below a term are also called **child terms**, while the less specific relatives are **parent terms**.

GO consists of three DAGs for three different aspects of gene function

- Molecular function what a gene product does on its own
- Biological process pathways or processes the product participates in
- Cellular component where it acts; compartments and complexes

Browsing GO in GONUTS

There are many tools to browse GO. The Gene Ontology Normal Usage Tracking System (GONUTS) at <u>http://gowiki.tamu.edu</u> has a couple of important features that make it different from other GO browsers.

- Users can add notes about terms
- Users can add annotations for anything in UniProt

Go to GONUTS and log in. You should have received an email to set up your account. If not, we can create one for you.

	main page discussion view source history purge	
1978	CACAO competition Sign up for CACAO Fall 2011 today. Email Branky or Jim.	
navigation	Main Page	
Main Page Enter GO at the top Help Report Bug Update log Annotation Jamborees Recent changes	GONUTS is a Gene Ontology Normal Usage Tracking System. The GONUTS wiki has been set up to provide third-party documentation for users of the Gene Onto rationale for this wiki is described in About GONUTS. To enter the ontology pages, go to the GO page, or search for a term ⁴ . For more information about h = See Current events for what new with the GONUTS wiki. = Leave comments and suggestions on our Known Issues page.	ogy Project g. The GO wiki is not an official product of the GO consortium. It was built by users at TAMU for newcorners to GO who want to explore GO usage. The ow this wiki is automatically updated, see GO wiki scripts. For Help using the system, see Help:Contents, which is available in the navigation links from all pages.
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toolbox	 Or go to the Special:Search page, where you can set which namespaces are searched. 	
 What links here Related changes 	Joining GONUTS	
 Special pages Printable version Permanent link 	GONUTS is currently set up so anyone can view or search, but only registered users can edit or adc registered users at EcoliHub, EcoCyc, GOA, BeeBase, SGD, dictyBase, FlyBase, WormBase, TAIR	pages. Currently registered users can create new users, and we are working to add at least one registered user for each participating database (So far we have Rat Genome Database, ZFIN, MGI, UCL and AgBase please edit this #1 forgot yout)

In the search box, enter some words that sound like a function. If you match a GO term name, you'll go straight to a term page; otherwise you will get a list of possible matches. If you go to one of those, you can often find what you want by navigating up or down the DAG.

Creating gene pages



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