

Lawrence Berkeley National Laboratory
Lawrence Berkeley National Laboratory

Title

Information Dashboards

Permalink

<https://escholarship.org/uc/item/1x41h374>

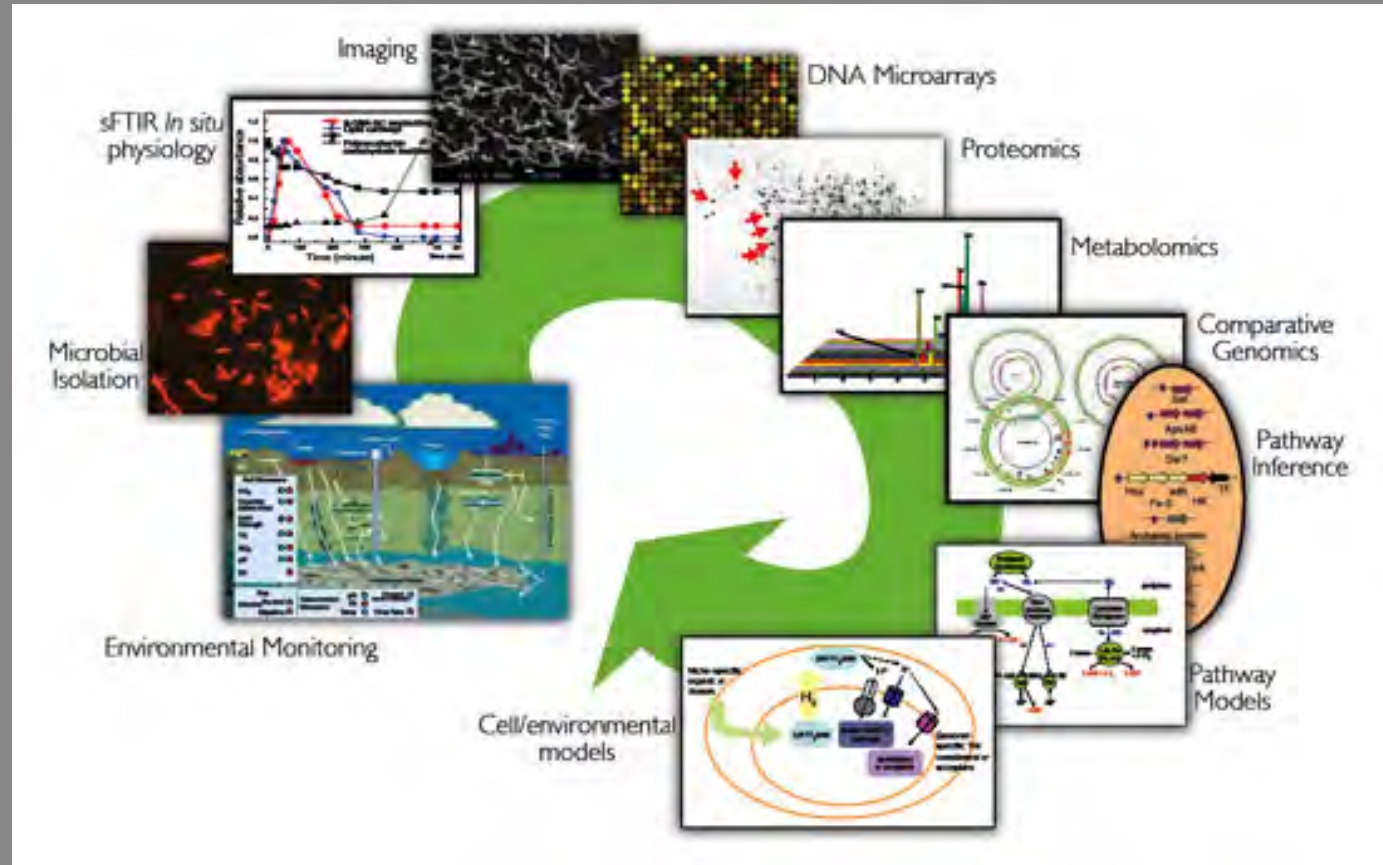
Author

Shutkin, Amy

Publication Date

2008-06-10

- Dashboard Design
- Team Science Approach
- Project Milestones & WBS & Budgets
- Working Dashboards



Amy Shutkin, CPM
ashutkin@lbl.gov
Ernest Orlando Lawrence Berkeley National
Laboratory
Physical Biosciences Division

ACKNOWLEDGEMENT

ESPP2 is part of the Virtual Institute for Microbial Stress and Survival supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics Program:GTL through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.

Information Dashboard Design: The Effective Visual Communication of Data

INFORMATION DASHBOARD DESIGN

The Effective Visual Communication of Data



Stephen Few

O'REILLY®

About the Author

Stephen Few has worked for over 20 years as an IT innovator, consultant, and teacher. Today, as Principal of the consultancy Perceptual Edge, Stephen focuses on data visualization for analyzing and communicating quantitative business information. He teaches in the MBA program at the University of California, Berkeley. You can learn more about Stephen's work and access an entire library of articles at www.perceptualedge.com.

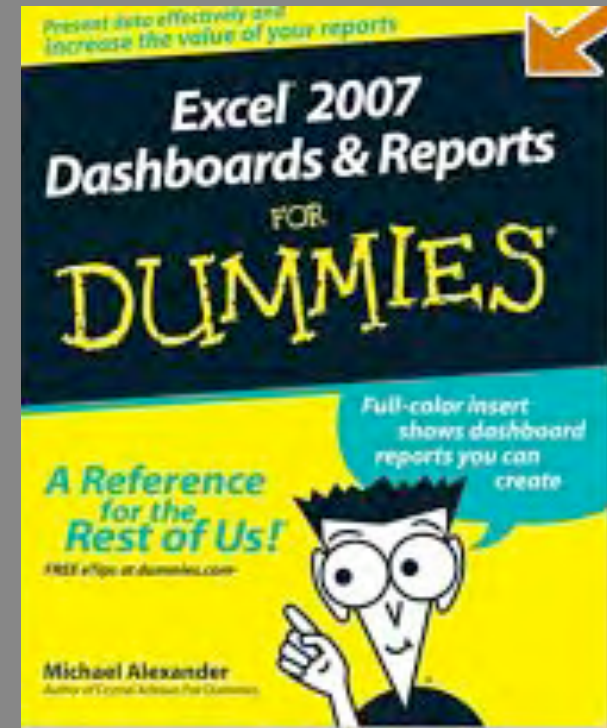
Dashboards - defined

“A dashboard is a visual interface that provides at-a-glance views into key measures relevant to a particular objective or business process.”

Key Attributes:

- ✓ Graphical to focus attention on key trends, comparisons and exceptions
- ✓ Display only relevant data
- ✓ Inherently contain predefined conclusions

Note: Collecting user requirements is KEY



*from 'Excel 2007 Dashboards & Reports for Dummies'
by Michael Alexander*

Dashboards - bad examples

The screenshot shows a website titled "perceptual edge" with a navigation menu including Home, About, Consulting, Workshops, Courses, Examples, Library, Blog, Discussion, and Contact. A search bar is located in the top right. The main content area is titled "Examples" and contains the following text:

Each of the examples that appear below illustrates quantitative information that is **poorly designed** for communication. Click on any of these examples to see an analysis of its problems and my proposed solutions.

The examples shown are:

- Example 1:** A page titled "Getting to Know the Revenue" with a dense, repetitive pattern of small text and lines, making it unreadable.
- Example 2:** A "CONSERVATIVE ASSET ALLOCATION MODEL" section featuring two pie charts. The first chart lists: 8% International, 2% Small Cap, 2% Mid Cap, 8% Large Cap, 2% Real Estate Securities, 5% High Yield Bonds, 60% Bonds, and 15% Cash/Cash Equivalents. The second chart lists: 12% International, 3% Small Cap, 5% Mid Cap, 17% Large Cap, 3% Real Estate Securities, and 4% High Yield Bonds. The text is small and the layout is cluttered.
- Example 3:** A stacked bar chart showing revenue for Nike, Reebok, Adidas, Fila, and Converse. Nike's revenue is \$6,437 and Reebok's is \$2,635. The bars are cluttered with labels and values.
- Example 4:** A grouped bar chart showing the "Number of Staff" from 1983 to 2005, comparing "Time" (grey bars) and "Newsweek" (red bars). The Y-axis ranges from 160 to 360.
- Example 5:** A grouped bar chart titled "Chart Title" showing data for North America, South America, Europe, Africa, Asia, Australia, and Antarctica for the years 2006, 2007, and 2008. The Y-axis ranges from 0 to 90.
- Example 6:** A 3D pie chart with many slices of different colors, making it difficult to distinguish between categories.

Common Problems:

Positioning content in places that don't fit its importance

Positioning content in places that fail to support its use

Including items that serve no useful purpose

Sizing content larger than it deserves

Separating content excessively

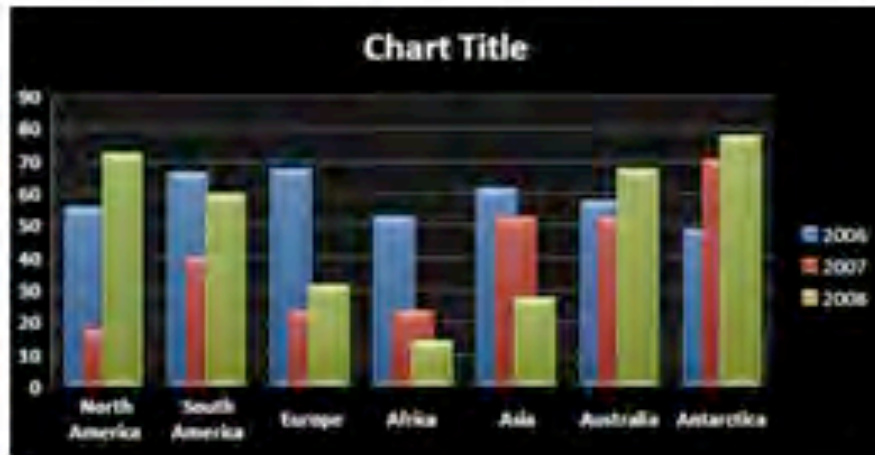
Visually featuring content & other items more than they deserve

Failing to link contents & other items that are related

Visually suggesting links between unrelated content

Enforcing a rigid symmetrical grid

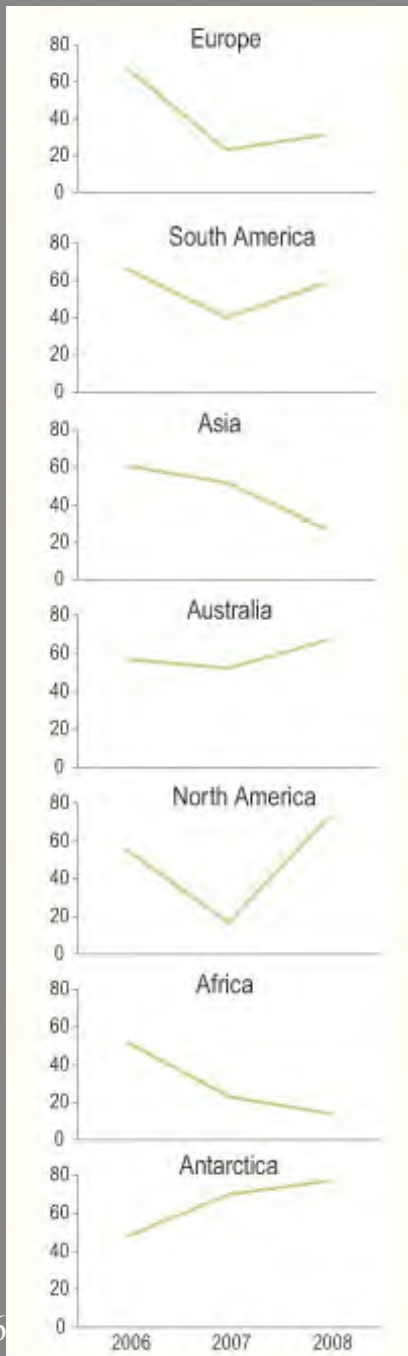
Dashboards - bad examples



Here are a few of this graph's problems:

- There are several distracting (and detracting) visual effects: the reflection of light, transparency, and 3-D effects on the bars (and squares in the legend) add no value.
- The bars have been overlaid on one another, which partially obscures the first two sets and gives them different visual salience. Because the bars for the year 2008 appear in the forefront of each cluster, their greater importance is implied, which was probably not intended. While I can't be sure, the graph's original post date of 2005, suggests that these values are projections, albeit unbelievably volatile ones. Without knowing more about the data, I can't say for sure, but the 2006 projections are probably the surest and most relevant, yet they are partly obscured by the other two years.
- Although the gridlines in this graph are thin and light, because these values are projections, we probably don't need to know precise values. As such, the gridlines are not necessary.
- The bar colors are more intense than they should be. The use of high-intensity colors should be reserved for making important data salient. Regular data should be shown using less intense colors. After all, when you display all of your data to stand out, nothing does.
- The continents have not been ordered in a logical way. At the very least they could have been alphabetized, but, as we'll see below, there's almost always a better way to order your data.
- Although bar graphs are great for showing and comparing the magnitudes of different variables, they are inferior to lines for showing how the values change through time. Because the pattern of change through time is likely more important than the actual magnitudes of the individual values, a line graph would have worked better.

Dashboards - solutions



Line graphs make it especially easy to see the patterns of change and to focus on trends. To avoid the clutter of seven lines on a single graph, I used "small multiples," a series of seven small graphs, which vary by region, but otherwise look and work the same. Small multiples may be arranged vertically (shown above), horizontally, or in a matrix. Because this information is a projection (and so the exact magnitudes are probably not as important), I have made the assumption that the graphs should be arranged to make it easiest to compare the patterns of change for the various regions, which is why I aligned the years by arranging the graphs vertically. If the magnitudes of the lines were more important, then a horizontal layout would have been preferable, for easier magnitude comparisons. Notice that the horizontal label (showing the years) is only shown on the very bottom of the graph. This is all that's necessary to show which part of each line belongs to which year. Duplicating these labels for each graph would have resulted in redundancy and clutter.

I have reordered the continents based on the 2006 values, with the highest at the top and the lowest at the bottom. I based the sequence on the 2006 value because, as these values are projections, the first year is likely to be most reliable and of greatest interest to decision-makers.

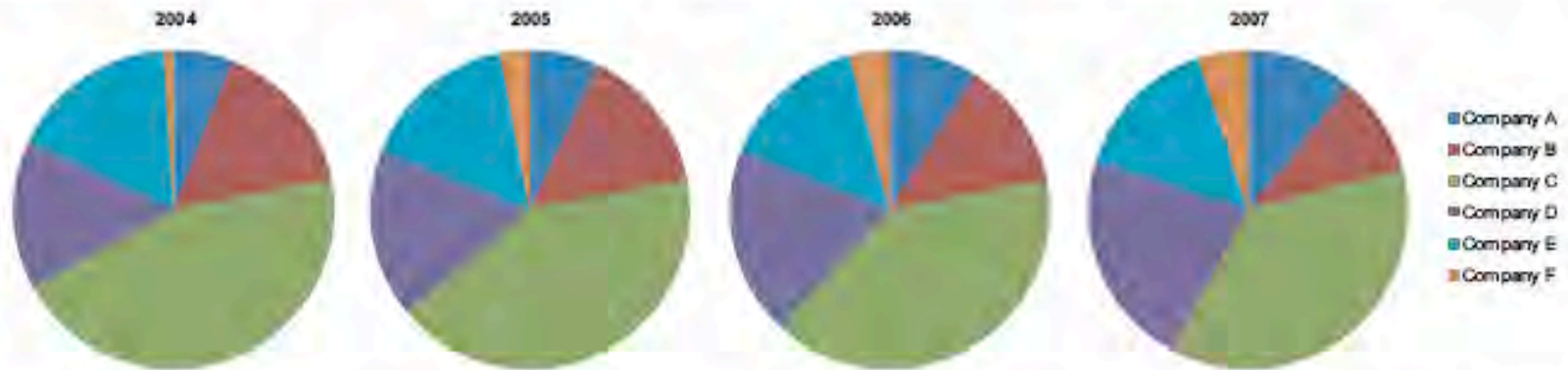
This new design is clean and clear—free of the visual distractions in the first two examples. Anyone viewing the graph would be able to examine the data, focusing perhaps on the large declines that are projected to occur in Europe and Africa, instead of the pretty, shiny bars.

Reduce the non-data ink

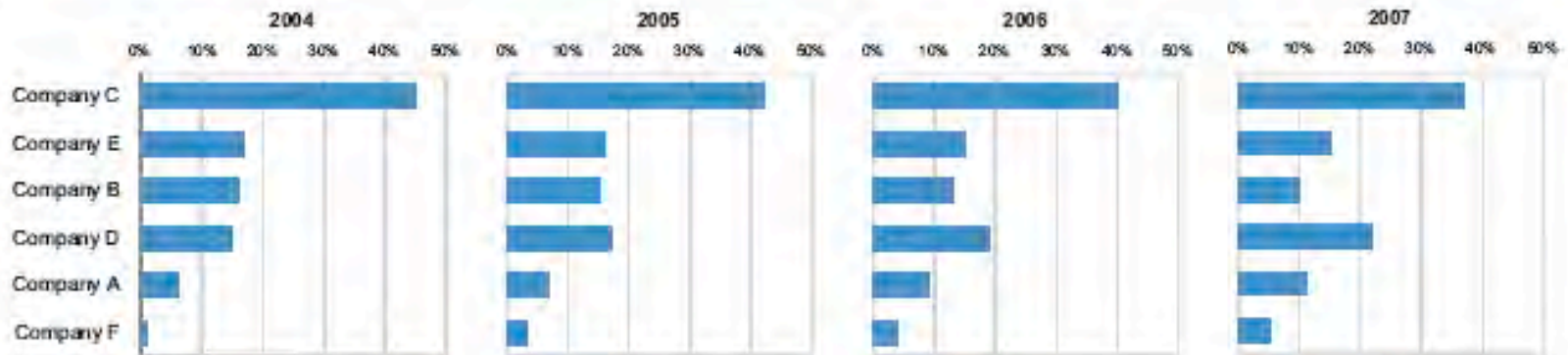
Enhance the data ink

Dashboards - evil pies

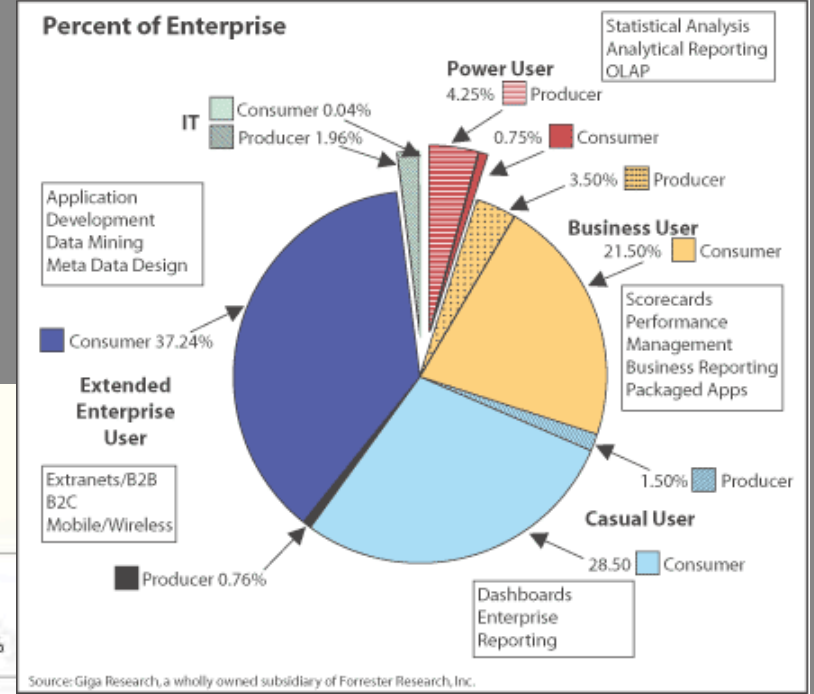
Let's examine another ineffective use of pie charts. Edward Tufte once said that "the only worse design than a pie chart is several of them, for then the viewer is asked to compare quantities located in spatial disarray both within and between pies" (Edward Tufte, *The Visual Display of Quantitative Information*, Graphics Press, 1983, p. 178.) I share Tufte's opinion that this is an ineffective way to compare multiple part-to-whole relationships.



Try to follow the changes of these various companies and how they compare to one another through time. It is nearly impossible. Notice how easily you can do it, however, using the following display:



Dashboards - evil pies



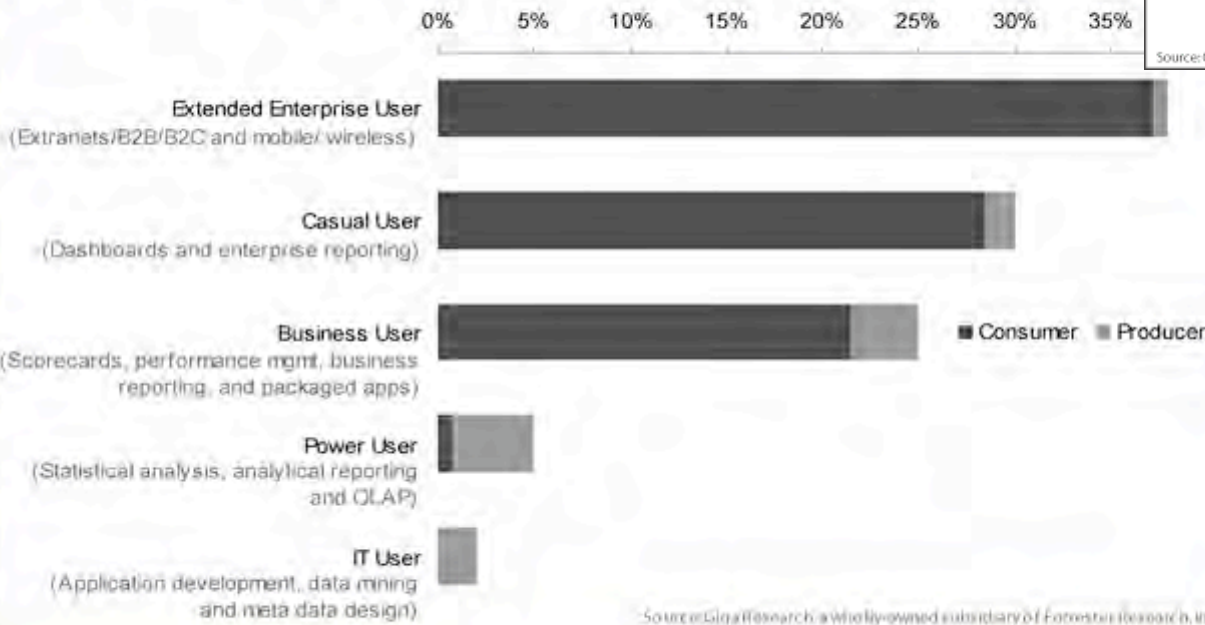
My Analysis

The data is great but the display is a jumbled mess.

A Solution

Here's the same data displayed simply and clearly:

Percentage of Analytic Computer Usage by Type



Reduce the non-data ink
Enhance the data ink

I could have used colors but, frankly, this graph doesn't need them. Limiting it to black and white allows you to photocopy this useful information and pass it on without any loss of quality. Can you imagine what the original pie chart would look like if you photocopied it in black and white?

Dashboards - real estate

“The relative prominence of screen space on a dashboard can be divided into quadrants... Whenever possible, place information that is considered most important in the upper left hand region and that which is least important in the lower right hand corner.”

Emphasized

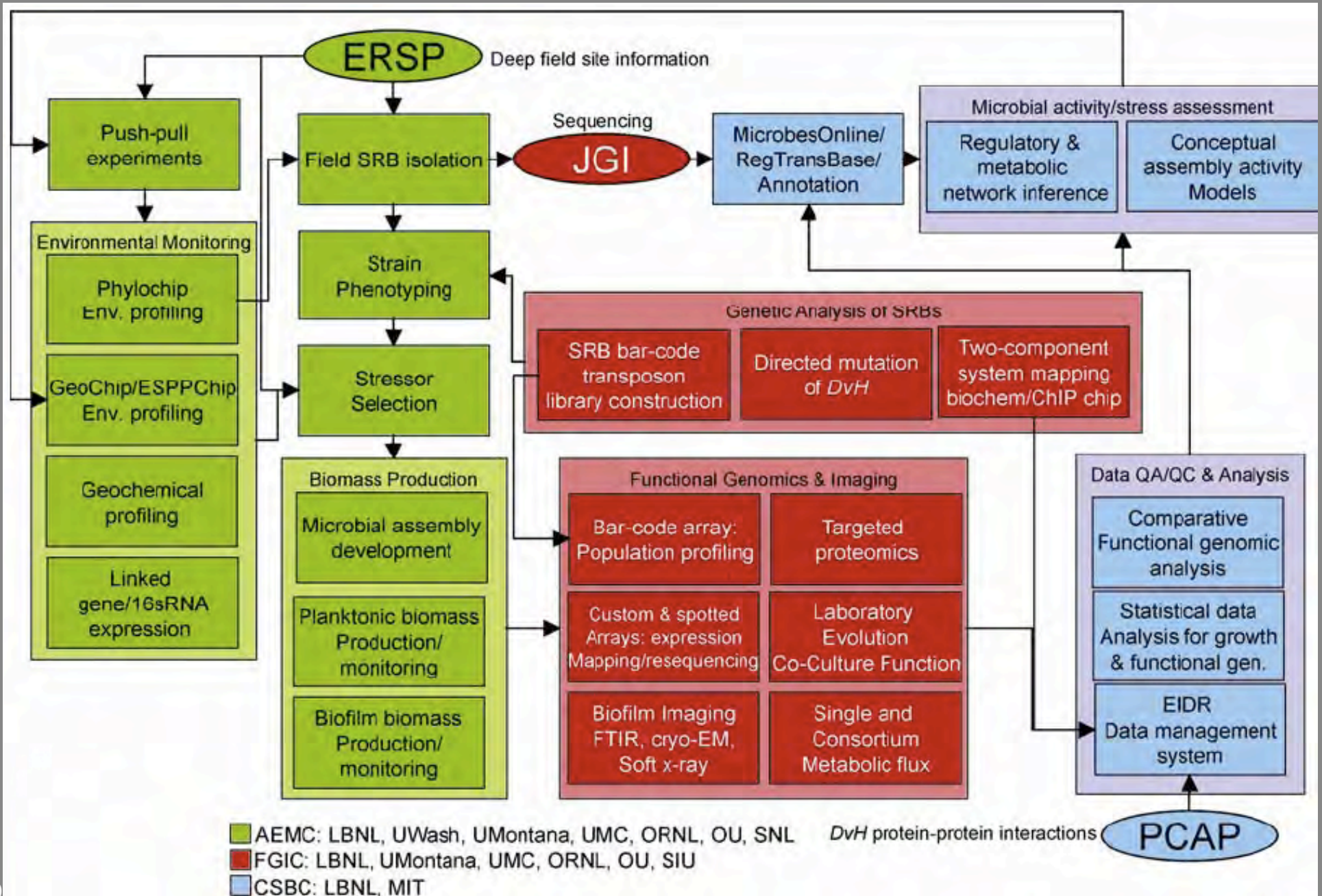
Neither emphasized
nor de-emphasized

Emphasized

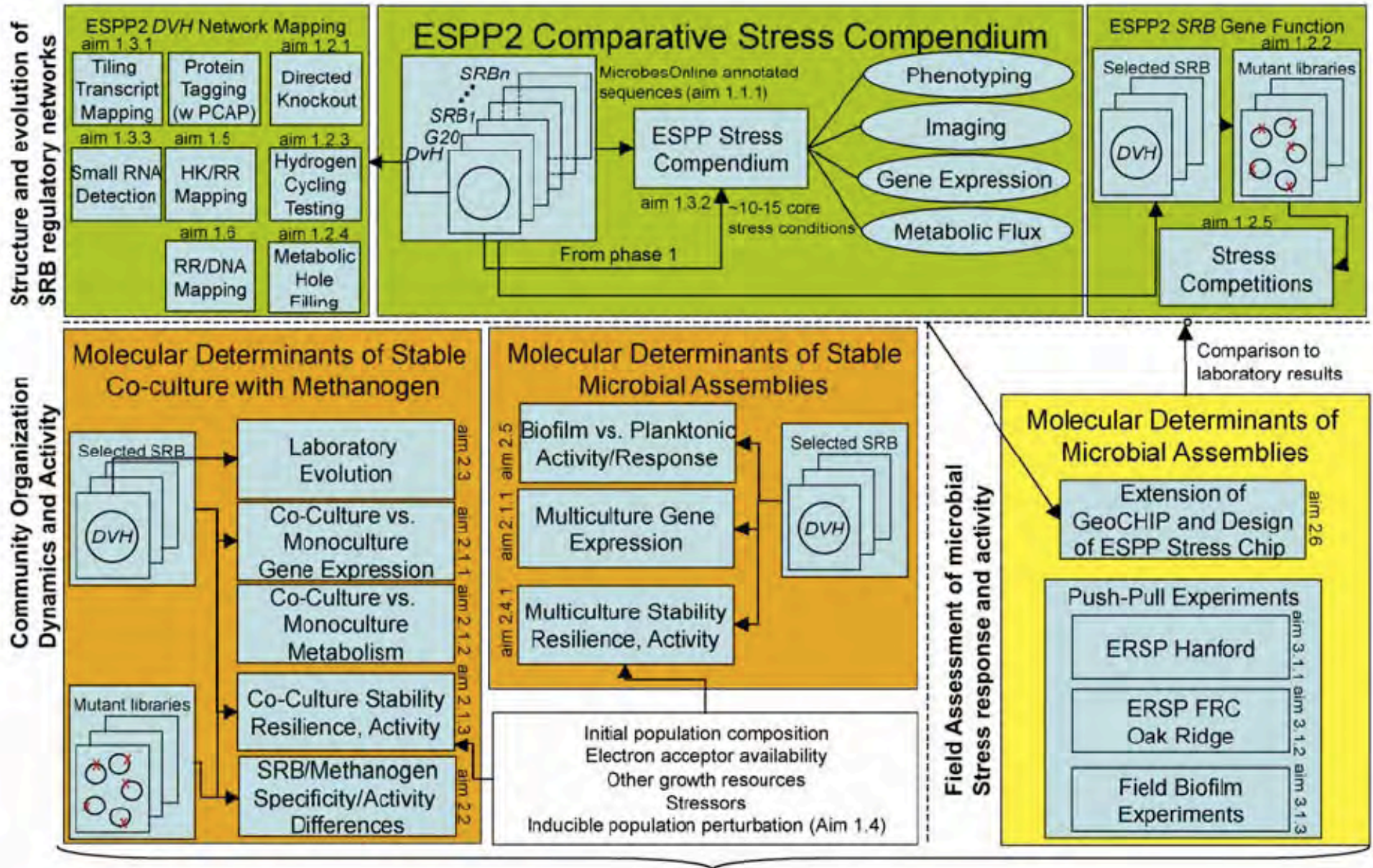
Neither emphasized
nor de-emphasized

De-emphasized

Team Science Approach



Team Science Approach



Milestones: Year One 09/30/2008

AEMC

- Obtain previously isolated SRB (especially for DOE contaminated sites), prepare DNA for sequencing submit to JGI.
- Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species.
- Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation & steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.
- Initial tests of multiculture conditions.
- Initiation of co-culture evolution experiments.
- Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co-culture.
- Complete membrane profiling of *D. vulgaris* and *M. maripaludis* in mono culture and together in syntrophic culture.
- Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry and Hanford and Oak Ridge, including initial testing of in well sediment/attachment simulation systems.
- Design larger scale attached stress experiments for comparison with planktonic experiments (transcriptomics).
- Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.

FGIC

- Create and sequence-verify saturating tagged transposon library of *D. vulgaris* and *D. alaskensis* G20.
- Prioritize HK/RR pair characterization with Computational Core.
- Tag and purify HK/RR pairs.
- Initial HK/RR mapping by biochemical assay.
- Initial proof of concept RR/DNA mapping using CHIP-chip.
- Optimize barcode array design.
- Optimize tiling array for transcription start-stop mapping, small RNA detection and CHIP-chip in SRB for G20 and DvH.
- Optimize multiplex gene expression design for G20.
- Complete stress response transcriptomics for G20.
- Initial survey of possible small RNA regulators.
- Complete design and testing of ESPPChip microarray.

CSBC









- Extension of MicrobesOnline for 16SRNA, GeoCHIP/ESPPChip, Phenotype, metagenomic data.
- Complete computational analysis of DvH and G20 and methanogen metabolism.
- Establish flux model analysis methods for mono- and multicultures.
- Developing tiling array and bar-code array design and analysis techniques.
- Complete annotation of Dv Miyazaki, Ds 27774, and one Dv Hanford isolate.
- Complete initial reannotation of DvH.
- Begin design of conceptual model of stress, ED, TEA responses for Hanford Cr and Oak Ridge U contaminated sites.

Work Breakdown Structure by Milestones

Schedule Development & Execution

VIMSS/ESPP2 Annual Milestones by Core Groups						
ID	WBS	Task Name	Predecessors	Resource Names	2007	2008
1	1	AEMC Year One		Terry Hazen		
2	1.1	Obtain previously isolated SRB, prepare DNA for sequencing submit to JGI		Terry Hazen		10/1
3	1.2	Begin isolation of SRB from ORNL/FRC and Hanford Sites		Matthew Fields, Martin Keller		10/1
4	1.3	Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species		David Stahl		10/1
5	1.4	Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation and steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.	4SS	Terry Hazen, David Stahl		10/1
6	1.5	Initial tests of multi-culture conditions.		David Stahl, Martin Keller, Joe Zhou		10/1
7	1.6	Initiation of co-culture evolution experiments.		Kristina Hillesland		10/1
8	1.7	Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co-culture.		Judy Wall, Adam Deutschbauer		10/1

Project: Year 5 Milestones
Date: Tue 4/17/07

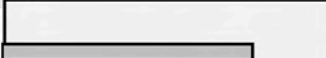
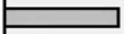

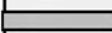



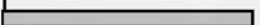


Task		Rolled Up Task	
Progress		Rolled Up Milestone	
Milestone		Rolled Up Progress	
Summary		Split	

VIMSS/ESPP2 Annual Milestones by Core Groups						
ID	WBS	Task Name	Predecessors	Resource Names	2007	2008
9	1.8	Complete membrane profiling of <i>D. vulgaris</i> in mono culture.		Terry Hazen		10/1
10	1.9	Complete membrane profiling <i>M. maripaludis</i> in mono culture.		Terry Hazen		10/1
11	1.10	Complete membrane profiling of <i>D. vulgaris</i> / <i>M. maripaludis</i> in syntrophic culture.	9,10	David Stahl		10/2
12	1.11	Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry.	3	Terry Hazen, Martin Keller, Matthew Fields, Joe Zhou		10/2
13	2	FGIC Year One		Jay Keasling, Aindri		
14	2.1	Create and sequence-verify saturating tagged transposon library of <i>D. vulgaris</i> and <i>D. alaskensis</i> G20.		Judy Wall		10/1
15	2.2	Prioritize HK/RR pair characterization with Computational Core		Aindria Mukhopadhyay, Adam Deutschbauer		10/1
16	2.3	Initial HK/RR mapping by biochemical assay.	15	Aindria Mukhopadhyay		10/2
17	2.4	Tag and purify HK/RR base pairs.	16	Aindria Mukhopadhyay		10/3
18	2.5	Initial proof of concept RR DNA mapping using CHIP chip.	15	Adam Deutschbauer		10/2
19	2.6	Optimize barcode array design.		Adam Deutschbauer		10/1
20	2.7	Optimize tiling array for transcription start-stop mapping, small RNA detection and CHIP-chip in SRB for G20 and DvH.		Adam Deutschbauer, Kelly Bender		10/1

Project: Year 5 Milestones
Date: Tue 4/17/07

Task		Rolled Up Task	
Progress		Rolled Up Milestone	
Milestone		Rolled Up Progress	
Summary		Split	

Dashboard Milestone Reports

FY08 Milestones: AEMC	% Complete	as of 04/01/08		Notes
Obtain previously isolated SRB, prepare DNA for JGI sequencing.	70%			<i>D. vulgaris</i> Hanford HBL5, <i>D. hanfordii</i> HMW + others
Syntrophic co-culture assemblies: Growth optimization & stability studies: Alternative Dv strains/species.	30%			<i>need update</i>
BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%			<i>need update</i>
Initial tests of multiculture conditions.	30%			
Initiation of co-culture evolution experiments.	70%			U WA & OK
Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.	50%			<i>ongoing</i>
Complete membrane profiling of <i>D. vulgaris</i> and <i>M. maripaludis</i> in mono culture and in syntrophic culture.	<i>need update</i>			<i>Aindrila</i>
Design push-pull experiments & initial characterization of site bacterial populations and geochemistry @ Hanford & ORNL, including initial testing of in well sediment/attachment simulation systems.	70%			<i>under way</i>
Design larger scale attached stress experiments for comparison w/ planktonic *experiments (transcriptomics).	<i>need update</i>			<i>Matt Fields</i>
Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.	50%			<i>CSBC: Metagenome FRC grdwater - DNA sequencing complete, annotation completed, draft circulating.</i>
		Oct 07- Mar 08	Apr - Sep 08	

Key Performance Indicators (KPI) ~ essential tasks draw attention to problem areas

ESPP2 Milestones – Espwiki

https://vimss.lbl.gov/espwiki/index.php/ESPP2_Milestones


AShutkin my talk my preferences my watchlist my contributions close browser to log out

article discussion edit history move watch

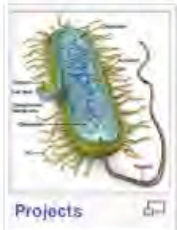
ESPP2 Milestones

Main Page > ESPP2 Milestones

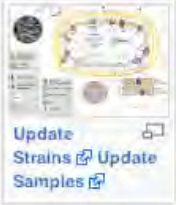
ESPP Wiki Toolbar



Progress Reports



Projects



Update Strains Update Samples

navigation

- Main Page
- Community portal
- Current events
- Recent changes
- Random page
- Help
- Donations

search

Go Search


toolbox

- What links here
- Related changes
- Upload file
- Special pages
- Printable version
- Permanent link

VIMSS/ESPP2 Milestones Summary [edit]

Projected Milestone Date: 09/30/2008 [edit]

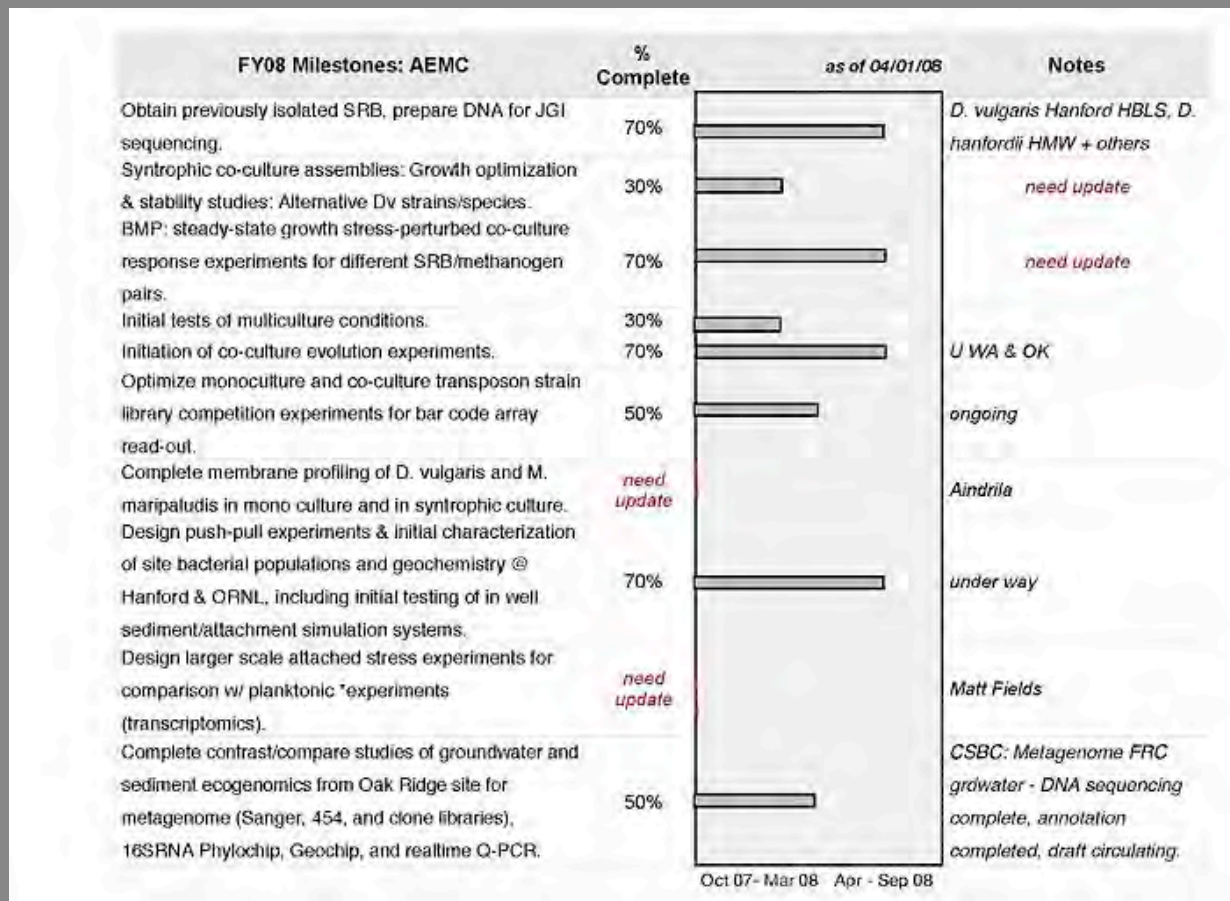
AEMC [edit]



FY08 1st 6 months

- Obtain previously isolated SRB (especially for DOE contaminated sites), prepare DNA for sequencing submit to JGI.
- Growth optimization and stability studies of different syntrophic co-culture assemblies: Alternative Dv strains/species.
- Full scale biomass production for steady-state growth stress-perturbed co-culture response experiments (perturbation & steady state analyses using optimized co-culture conditions) for different SRB/methanogen pairs.
- Initial tests of multiculture conditions.
- Initiation of co-culture evolution experiments.
- Optimize transposon strain library competition experiments for read-out by bar code arrays both in monoculture and co-culture.
- Complete membrane profiling of *D. vulgaris* and *M. maripaludis* in mono culture and together in syntrophic culture.
- Design of push-pull experiments and initial characterization of site bacterial populations and geochemistry and Hanford and Oak Ridge, including initial testing of in well sediment/attachment simulation systems.
- Design larger scale attached stress experiments for comparison with planktonic *experiments (transcriptomics).
- Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.

Dashboard Milestone Reports



Size of this preview: 776 x 600 pixels

Full resolution (2200 x 1700 pixel, file size: 276 KB, MIME type: image/jpeg)
 ESPP2 Milestones > Images:AEMC.jpg > Main Page > ESPP2 Milestones > Images:AEMC.jpg

File history

Legend: (cur) = this is the current file, (del) = delete this old version, (rev) = revert to this old version.
 Click on date to see the file uploaded on that date.

■ (del) (cur) 20:29, 7 April 2008 ... Ashutkin (Talk | contribs) ... 2200x1700 (282,122 bytes)

- Upload a new version of this file.
- Edit this file using an external application.



Cost Estimation & Budget Oversight

Rate Type FY07 FY08 FY09 FY10 FY11 FY12 (est) 5 Year Totals

Escalation Rates

LBNL Labor	3.5%	3.0%	3.0%	3.0%		
LBNL Supplies & Other Expenses (OMB)						

Total Labor \$3,77

Total Supplies & Other Expenses (OMB) \$4,26

Totals \$8,04

Original Project Budget Assumptions

LBNL Labor
Equipment, Supplies & Other Expenses, LBNL (OMB)

LBNL Total

Total Direct Costs, LBNL

Total Indirect Costs, LBNL

Total Direct Costs less Other Inst. Indirect Costs, LBNL

SNL

ORNL

ESPP2 Total

% original projection

DOE F 4820.1 (04-03) All Other Editions Are Obsolete		U.S. Department of Energy Budget Page (See reverse for Instructions)		
ORGANIZATION Ernest O. Lawrence Berkeley National Laboratory				
PRINCIPAL INVESTIGATOR/PROJECT DIRECTOR Arkin, Adam Overall Project Budget				
A. SENIOR PERSONNEL: PFD, Co-Pfs, Faculty and Other Senior Associates (List each separately with title; A.S. show number in brackets)		DOE Funded Personnel		
		CAL	ACAD	SUMR
1.	Arkin, Adam	15.00		
2.	Kearns, Jay	6.00		
3.	Hazen, Leity	6.00		
4.	Duchas, Irma	18.00		
5.				
A. (0)	OTHERS (LIST INDIVIDUALLY ON BUDGET EXPLANATION PAGE)	231.00		
7.	(11) TOTAL SENIOR PERSONNEL (1-6)	336.00		
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)				
1.	(0) POST DOCTORAL ASSOCIATES	108.00		
2.	(25) OTHER PROFESSIONAL (TECHNICIAN, PROGRAMMER, ETC.)	699.00		
3.	(2) GRADUATE STUDENTS	54.60		
4.	(0) UNDERGRADUATE STUDENTS	0.00		
5.	(2) SECRETARIAL - CLERICAL	30.00		
6.	(0) OTHER	0.00		
TOTAL SALARIES AND WAGES (A+B)				
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)				
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A+B+C)				
D. PERMANENT EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM)				
TOTAL PERMANENT EQUIPMENT				
E. TRAVEL		1. DOMESTIC (INCL CANADA AND U.S. POSSESSIONS)		
		2. FOREIGN		
TOTAL TRAVEL				
F. TRAINEE/PARTICIPANT COSTS				
1. STIPENDS (Specify levels, types + totals on budget justification page)				
2. TUITION & FEES				
3. TRAINEE TRAVEL				
4. OTHER (Fully explain on justification page)				
TOTAL PARTICIPANTS (0)		TOTAL COST		
G. OTHER DIRECT COSTS				
1. MATERIALS AND SUPPLIES				
2. PUBLICATION COSTS/DOCUMENTATION/COMMUNICATION				
3. CONSULTANT SERVICES				
4. COMPUTER (ADPE) SERVICES				
5. SUBCONTRACTS				
6. OTHER				
TOTAL OTHER DIRECT COSTS				
H. TOTAL DIRECT COSTS (A THROUGH G)				
I. INDIRECT COSTS (SPECIFY RATE AND BASE) Please see the indirect calculation sheets				
TOTAL INDIRECT COSTS				
J. TOTAL DIRECT AND INDIRECT COSTS (H+I)				
K. AMOUNT OF ANY REQUIRED COST SHARING FROM NON-FEDERAL SOURCES				
L. TOTAL COST OF PROJECT (J+K)				

LBNL Forward Pricing Rates Effective October 1, 2006 Revision 5

Rate Type

Escalation Rates

- Labor
- Supplies & Other Expenses (OMB)
- Construction Projects (OECM)

Institutional Rates

- General and Administrative
- G&A (Off Site) Rate - OFF
- Site Support (Fabrication) Rate - FAB
- Gretina
- Animal Care
- General Rate - GR1

LDRD Rate

- LDRD Operating and Equipment
- (LDRD rate is based on proposed structure, which is currently being reviewed by DOE)

IGPP Rate

IGPP

Procurement Burdens (Base: Cost of procured materials & services)

- PO's \$1-\$500,000
- PO's Over \$500,000 (per PO)
- R&D subcontract's \$1-\$300,000
- R&D subcontract's over \$300,000
- Intra-University Transfers (IUTs) \$1-\$200,000
- Intra-University Transfers (IUTs) over \$200,000
- Genomics Procurements (PO's \$1-\$500,000)
- Molecular Foundry (PO's \$1-\$500,000)
- Project Management (PO's \$1-\$500,000)

Travel (Base: Travel Costs)

Travel Rate

Payroll Burden (Base: Delivered effort cost only)

- Career & Term Employees
- Post Docs, Visiting Post Docs, Limited Employees, and Visiting Researchers
- GSRAs
- Students/Rehired Retirees/Employees working variable time
- Summer Faculty

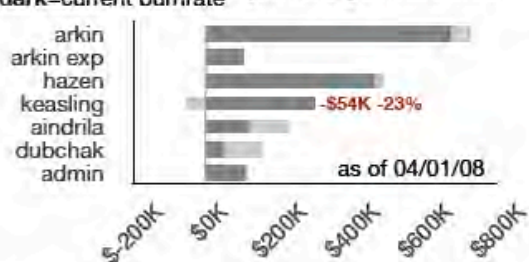
Fringe Benefits Only (Base: FTE gross pay only)

- Career & Term Employees
- Post Docs, Visiting Post Docs, Limited Employees, and Visiting Researchers
- GSRAs
- Students/Rehired Retirees/Employees working variable time
- Summer Faculty

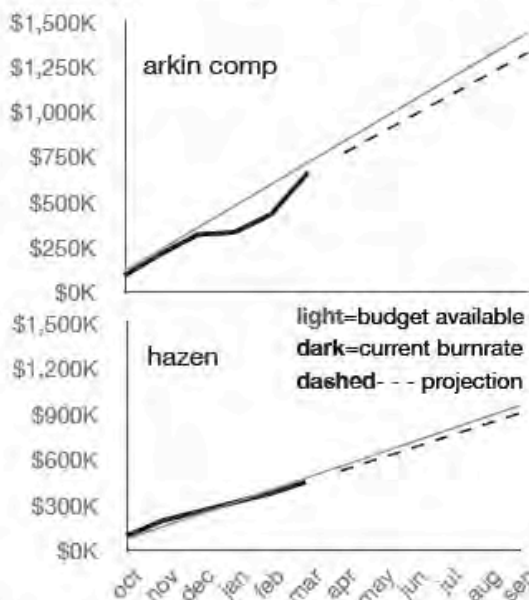
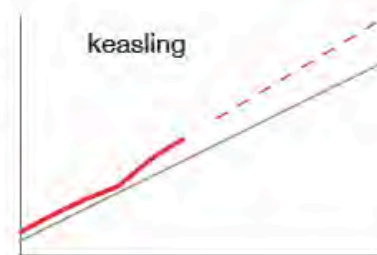
Dashboard Integrated Milestone & Budget Reports

“How then do we make it easy for people to compare related sets of values when they are associated with different units of measure? Two answers come to mind. The first and most obvious is to place them in separate graphs, positioned close to one another so that the patterns in each can be compared to one another, but magnitude comparisons will be discouraged.” *Stephen Few*

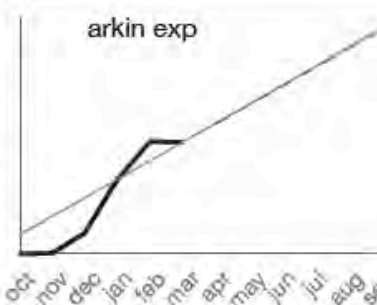
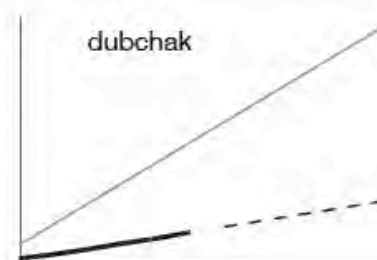
light=budget available
dark=current burnrate



\$580.20K
\$464.16K
\$348.12K
\$232.08K
\$116.04K
\$0K



\$550K
\$440K
\$330K
\$220K
\$110K
\$0K
\$300K
\$225K
\$150K
\$75K
\$0K
\$300K

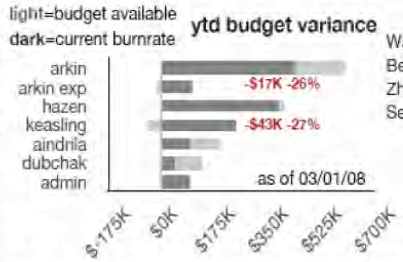


PI	wiki update	Critical Events, Milestones & Top Projects
Arkin - internal for others	3/25/08	Metabolic profile analysis
Hazen	3/31/08	Co-culture Biomass, IMS
Keasling	3/12/08	Flux work
Mukhopadhyay	3/24/08	HK knock-outs, HK/RR
Alm	2/14/08	Compendium analysis, FRC
Dubchak	3/25/08	Integrate, annot. metab. pathway
Fields	2/18/08	DvH Cr transcriptomics: biofilm vs planktonic
Keller	3/10/08	Env mRNA profiling, consortia
Singh	3/7/08	Tri-culture & Mesocosm
Stahl	2/29/08	Methanococcus transcriptional/proteomic/mutant analysis in coculture
Wall	1/31/08	Deletions via marker xchange
Bender	2/7/08	Small RNA's - ongoing
Zhou	3/6/08	Evolution, Hanford, FRC
Sequencing	9/7/07	Need update

\$225K
\$150K
\$75K
\$0K
\$200K
\$150K
\$100K
\$50K
\$0K

Dashboard Integrated Milestone & Budget Reports

FY08 Milestones: CSBC	% Complete	as of 04/01/08	Notes
Extension of MicrobesOnline for: 16SRNA	50%		
GeoCHIP/ESPPChip	0%		working w/ ORNL to incorporate Selexa data
Phenotype	50%		usefulness will depend on human (undergrads) annotation
Metagenomic data	25%		
Complete computational analysis of DvH & G20 + methanogen metabolism.	50%		Waiting on data.
Establish flux model analysis methods for mono- and multicultures.	50%		High potential value & high interest
Developing tiling array and bar-code array design and analysis techniques.	90%		Analysis techniques will continue to evolve & improve
Complete annotation of Dv Miyazaki, Ds 27774, and one Dv Hanford isolate.	50%		Waiting for these + other sequences before expression array & analysis
Complete initial reannotation of DvH.	50%		Additional data to include? Tiling array?
Begin design of conceptual model of stress, ED, TEA responses for Hanford Cr and Oak Ridge U contaminated sites.	0%		Participating in experimental design - conceptual model depends on data to be collected



PI	wiki update	Critical Events, Milestones & Top Projects
Arkin - internal	3/7/08	Microarray analysis
for others	3/11/08	Metabolomics condition set
Hazen	3/14/08	Co-culture Biomass, IMS
Keasling	3/12/08	Tryptophan biosynthesis
Mukhopadhyay	3/12/08	HK knock-outs, HK/RR
Alm	2/14/08	Compendium analysis, FRC
Dubchak	1/31/08	Hiring Pavel
Fields	2/18/08	DvH Cr transcriptomics: biofilm vs planktonic
Keller	2/7/08	Consortia culture
Singh	3/7/08	Tri-culture & Mesocosm
Stahl	2/29/08	Methanococcus transcriptional/proteomic/ mutant analysis in coculture
Wall	1/31/08	Deletions via marker xchange
Bender	2/6/08	Small RNA's
Zhou	3/6/08	Evolution, Hanford, FRC
Sequencing	9/7/07	Need update

FY08 Milestones: FGIC	% Complete	as of 04/01/08	Notes
Create and sequence-verify saturating tagged transposon libraries for: D. vulgaris	10%		Adam D. just started
D. alaskensis G20	50%		100% created, sequence verification ongoing
Prioritize HK/RR pair characterization w/ CSBC.	30%		
Tag and purify HK/RR pairs.	70%		RR - 90%, HK - 50%
Initial HK/RR mapping by biochemical assay.	50%		Post-doc to begin 08/01. All HK knock-outs: 12/64 genes completed, 2-3 checked. Paper in process.
Initial proof of concept RR/DNA mapping using ChIP-chip.	50%		Ready to go - waiting on Nimblegen chips (Adam D. & Paramvir)
Optimize barcode array design.	50%		(Adam D. & Paramvir)
Optimize tiling array for transcription start-stop mapping, small RNA detection and ChIP-chip in SRB for G20 and DvH.	0%		Will need to recast into year 2 milestones.
Optimize multiplex gene expression design for G20.	need update		Adam D.
Complete stress response transcriptomics for G20.	need update		Adam D.
Initial survey of possible small RNA regulators.	30%		Kelly Bender - 1 study complete
Complete ESPPChip microarray design & testing.	need update		Redundant? Combine w/ Chip-chip development?
Gene expression compendium	need update		
Metabolomics	need update		

FY08 Milestones: AEMC	% Complete	as of 04/01/08	Notes
Obtain previously isolated SRB, prepare DNA for JGI sequencing.	70%		D. vulgaris Hanford HBL5, D. hanfordii HMW + others
Syntrophic co-culture assemblies: Growth optimization & stability studies: Alternative Dv strains/species.	30%		need update
BMP: steady-state growth stress-perturbed co-culture response experiments for different SRB/methanogen pairs.	70%		need update
Initial tests of multiculture conditions.	30%		
Initiation of co-culture evolution experiments.	70%		U WA & OK
Optimize monoculture and co-culture transposon strain library competition experiments for bar code array read-out.	50%		ongoing
Complete membrane profiling of D. vulgaris and M. maripaludis in mono culture and in syntrophic culture.	need update		Aindria
Design push-pull experiments & initial characterization of site bacterial populations and geochemistry @ Hanford & ORNL, including initial testing of in well sediment/attachment simulation systems.	70%		under way
Design larger scale attached stress experiments for comparison w/ planktonic *experiments (transcriptomics).	need update		Matt Fields
Complete contrast/compare studies of groundwater and sediment ecogenomics from Oak Ridge site for metagenome (Sanger, 454, and clone libraries), 16SRNA Phylochip, Geochip, and realtime Q-PCR.	50%		CSBC: Metagenome FRC grdwater - DNA sequencing complete, annotation completed, draft circulating.

Adam P. Arkin and Terry C. Hazen, Directors

Applied Environmental Microbiology Core:

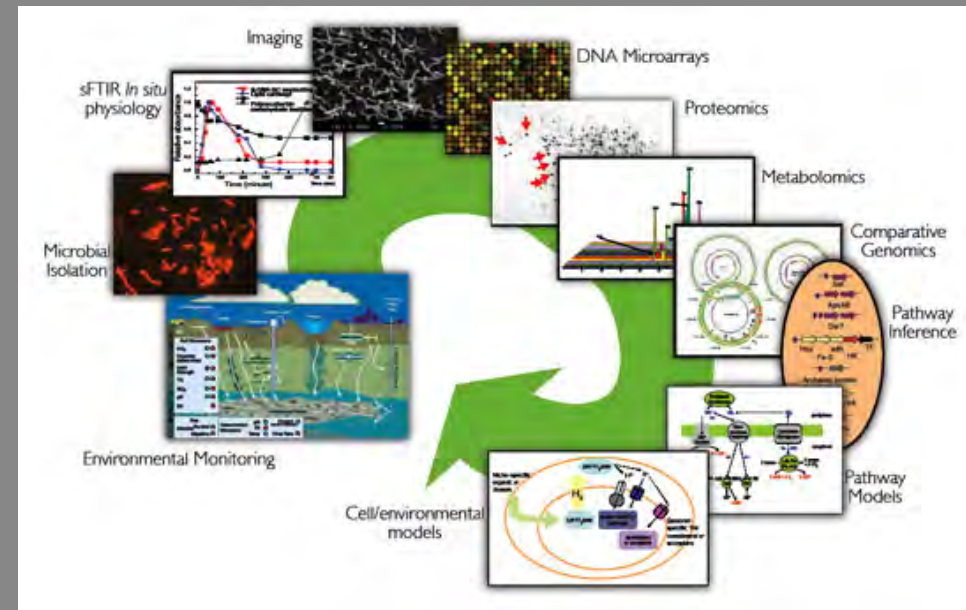
- LBNL, Terry C. Hazen
- University of Washington, David Stahl
- Montana State University, Matthew Fields

Functional Genomics and Imaging Core:

- LBNL, Jay Keasling and Aindrila Mukhopadhyay
- University of Missouri-Columbia, Judy Wall
- Southern Illinois University, Kelly Bender
- Sandia National Laboratory, Anup Singh
- Oak Ridge National Laboratory, Martin Keller
- University of Oklahoma, Jizhong (Joe) Zhou

Computational and Systems Biology Core:

- LBNL: Adam P. Arkin, Inna Dubchak, Paramvir Dehal
- MIT: Eric Alm



ACKNOWLEDGEMENT

ESPP2 is part of the Virtual Institute for Microbial Stress and Survival supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics Program:GTL through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.