

A Case Study -- Chu et al.

- An interesting early microarray paper
- My goals
 - Show arrays used in a “real” experiment
 - Show where computation is important
 - Start looking at analysis techniques

The Transcriptional Program of Sporulation in Budding Yeast

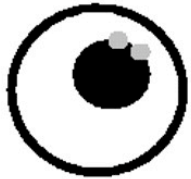
S. Chu, * J. DeRisi, * M. Eisen, J. Mulholland, D. Botstein, P. O. Brown, I. Herskowitz

Science, 282 (Oct 1998) 699-705

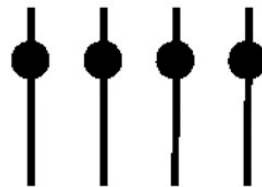
What is Sporulation?

- Under adverse conditions, one yeast cell transforms itself into “spores” -- tetrad of cells with tough cell wall, goes “dormant”
- Yeast is ordinarily diploid; spores are haploid. I.e., genetically, sporulation is analogous to formation of egg/sperm in most sexual organisms -- 2 rounds of meiotic (not mitotic) cell division.
 - And many of the genes/proteins involved in this are recognizably similar to human genes/proteins

Spore Formation



Meiotic Division



*replication
recombination*



meiosis I



meiosis II



spore maturation

Temporal Class

IME1
Early

NDT80
Middle

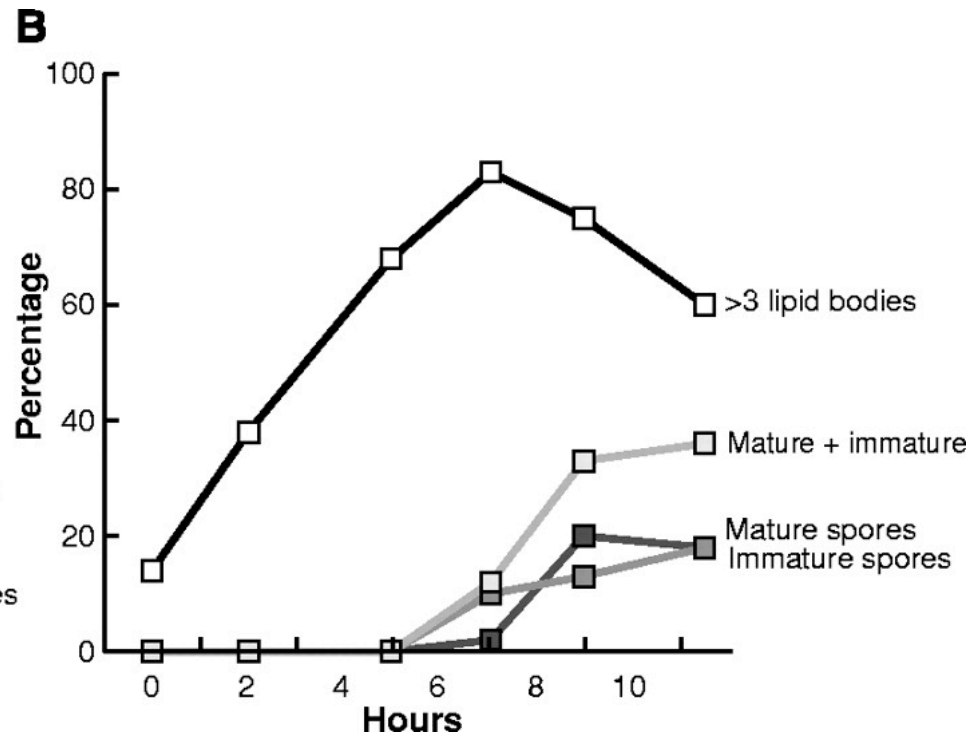
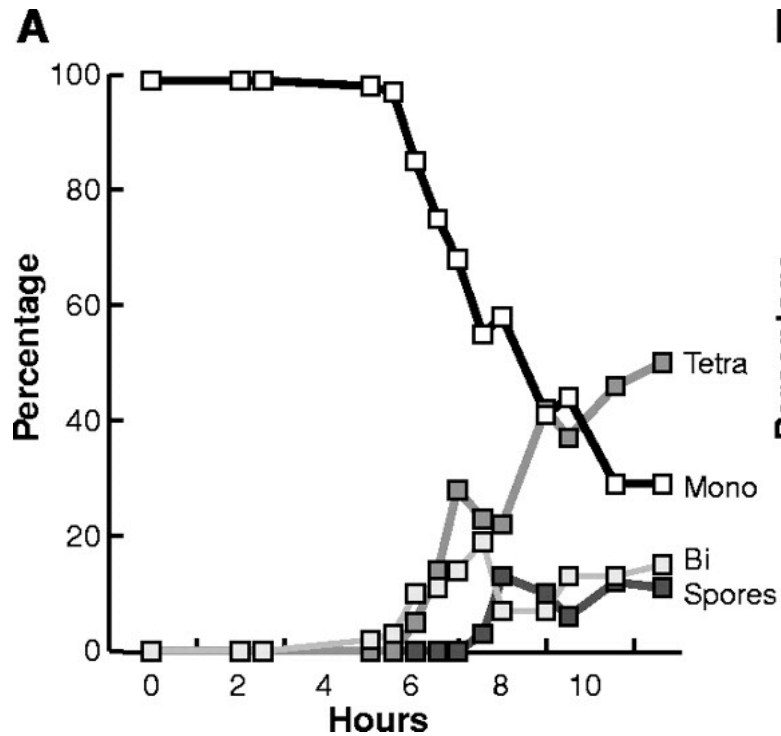
Mid-Late

Late

The Chu et al. Experiment

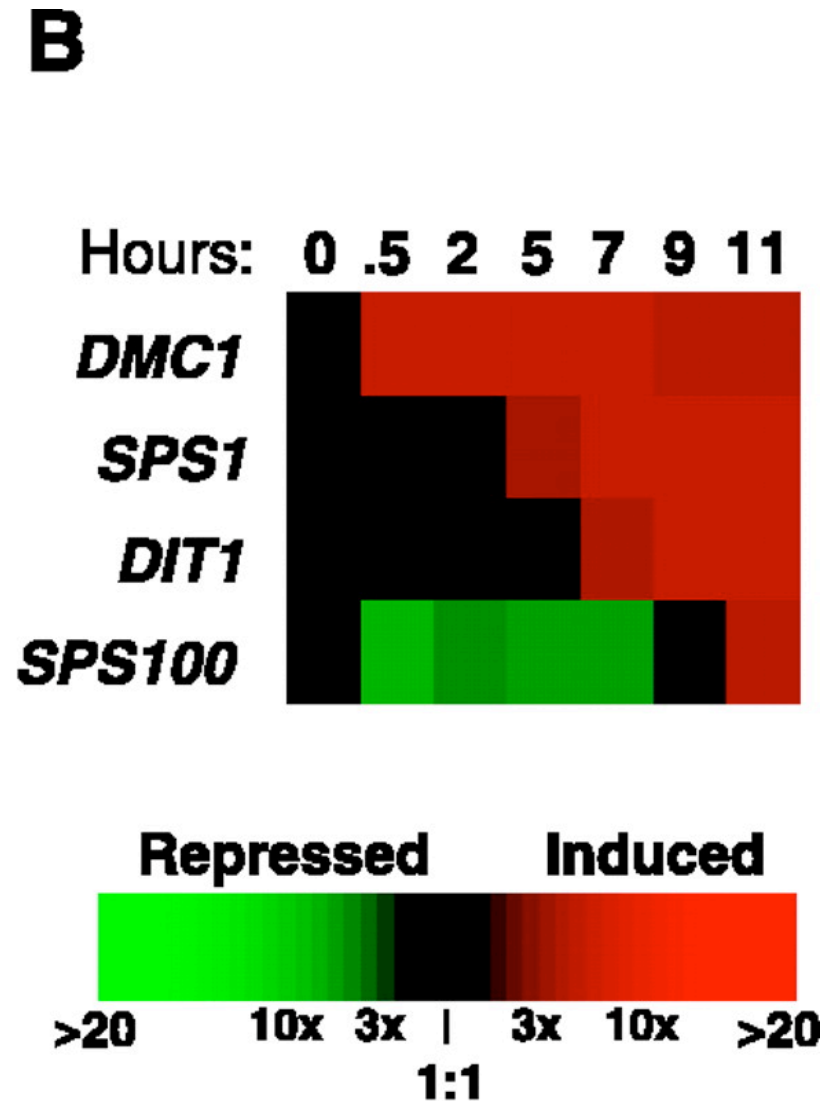
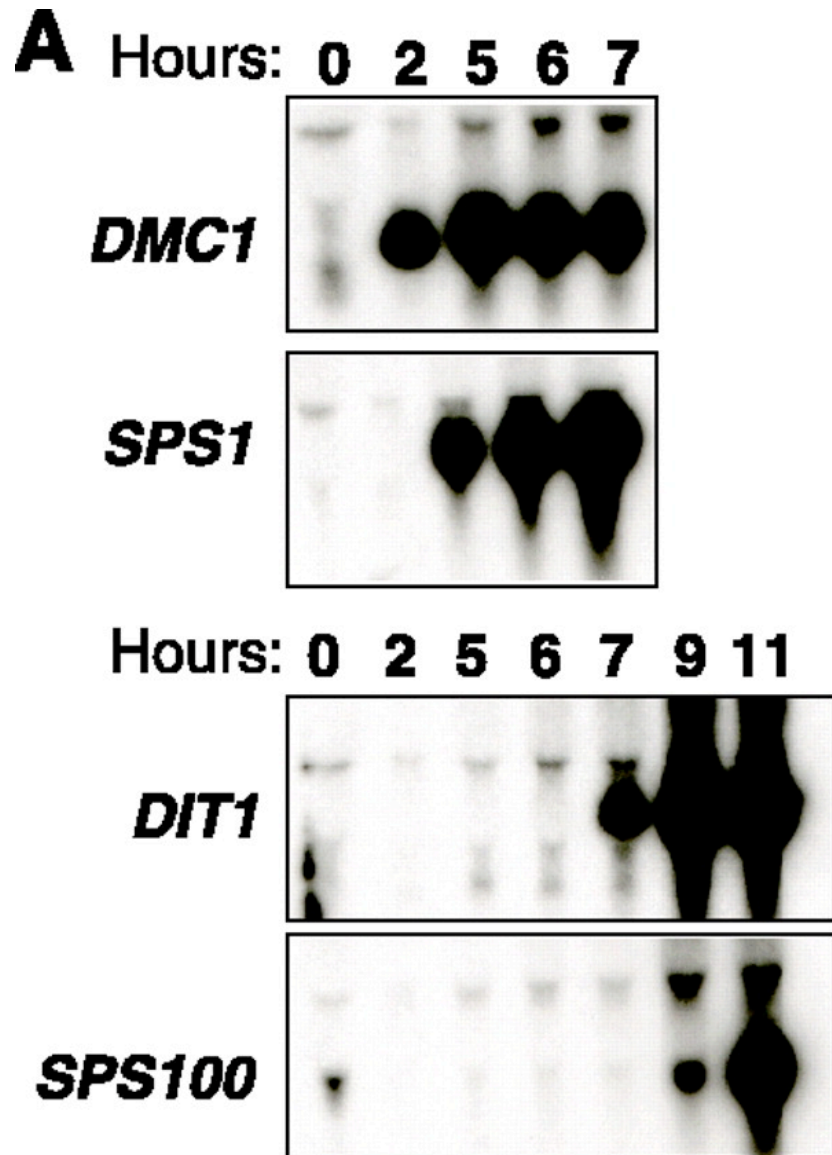
- Measure mRNA expression levels of all 6200 yeast genes in 7 time points (0-11 hours) in a (loosely synchronized) sporulating yeast culture
- Compare level at time t to level at time 0 on 2-color cDNA array
- Plus some more standard tests as controls

Measures of Sporulation

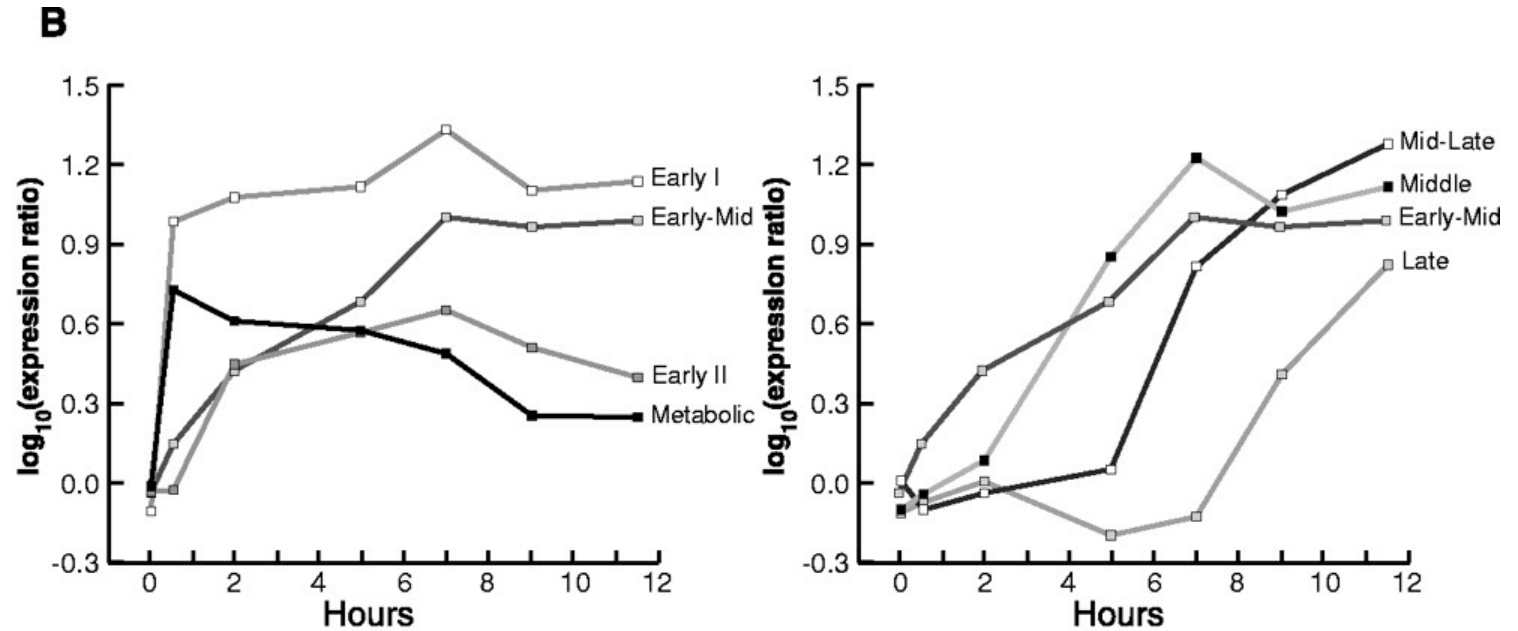
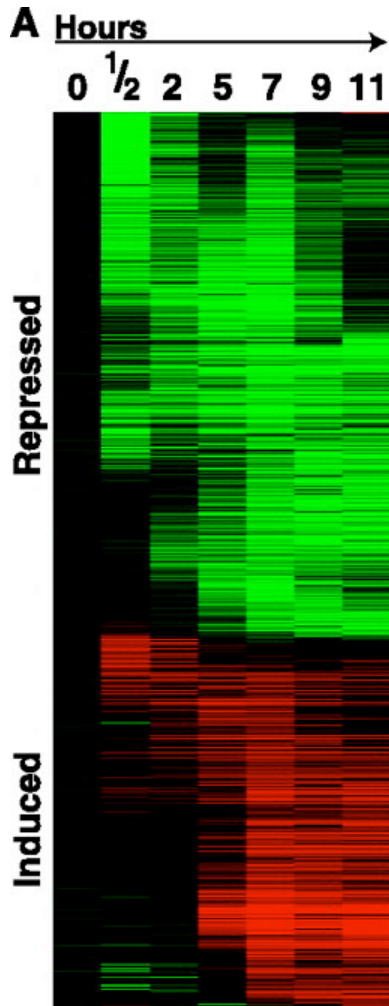


NB: < 20% spores, so data are *mixtures* of cell stages

Standard Test (Western) vs Array



Prototype Expression Profiles



Genes used to create average temporal profiles

<u>Metabolic</u>	<u>Early I</u>	<u>Early II</u>	<u>Early-Mid</u>	<u>Middle</u>	<u>Mid-Late</u>	<u>Late</u>
ACS1	ZIP1	KGD2	YBL078C	YSW1	CDC27	SPS100
PYC1	YDR374C	AGA2	QRI1	SPR28	DIT2	YKL050C
SIP4	DMC1	YPT32	PDS1	SPS2	DIT1	YMR322C
CAT2	HOP1	MRD1	APC4	YLR227C		YOR391C
YOR100C	IME2	SPO16	KNR4	ORC3		
CAR1		NAB4	STU2	YLL005C		
		YPR192W	YNL013C	YLL012W		
			EXO1			

"Sporulation" Summary, I

- What they did:
 - measured mRNA expression levels of all 6200 yeast genes in 7 time points in a (loosely synchronized) sporulating yeast culture
 - plus some more standard tests as controls
- What they learned:
 - 3-10x increase in number of genes implicated in various subprocesses
 - several subsequently verified by direct knockouts
 - further evidence for significance of some known transcription factors and/or binding motifs
 - several potential new ones
 - evidence for existence of others

"Sporulation" Summary, II

- Where computation fits in
 - automated sample handling
 - image analysis
 - data storage, retrieval, integration
 - visualization
 - clustering
 - sequence analysis
 - similarity search
 - motif discovery
 - structure prediction
- More on these topics later in the course

More on Computation

- Similarity Search -- given a loosely defined sequence “motif”, e.g. a transcription factor binding site, scan genome for “matches”
 - “Which genes have an MSE element?”
 - E.g., weight matrix models, Markov models
- Motif discovery -- given a collection of sequences presumed to contain a common pattern, e.g. a transcription factor binding site, find it & characterize it
 - “What motifs are common to Early Middle genes?”
 - E.g., MEME, Gibbs Sampler, Footprinter, ...

More on Computation

- Finding groups of sequences that plausibly contain common sequence motifs
 - E.g., clustering (co-varying because co-regulated?)

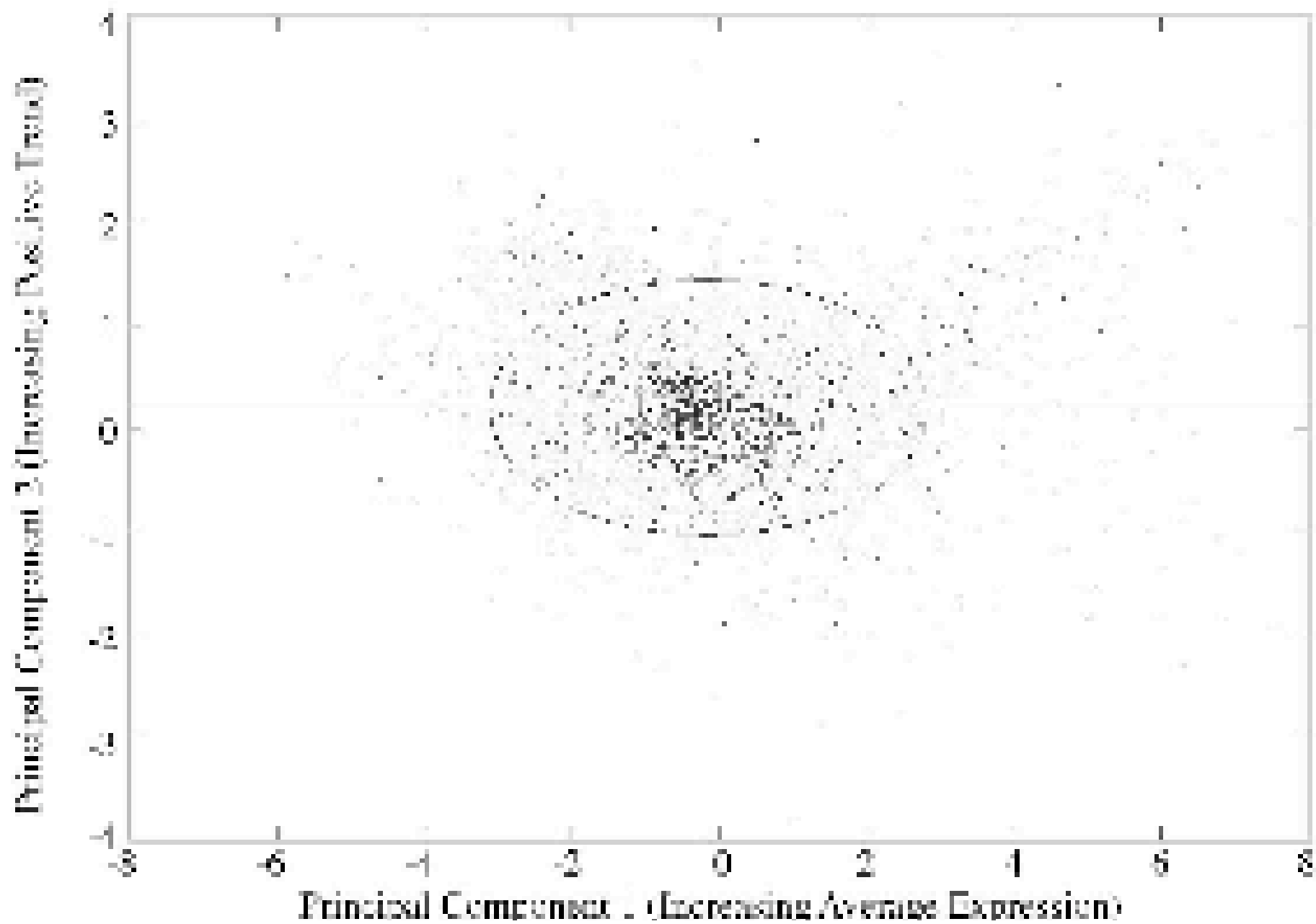
Chu's "Supervised" Clustering

- Hand picked ~ 40 prototype genes
 - With significant variation in data set
 - With known function
- Hand-segregated into 7 groups ("Early", ...)
- Assign all others to "nearest" group
 - Based on Pearson correlation to per-group averages of prototypes
- For visualization, order within groups by correlation to neighboring groups

Critique

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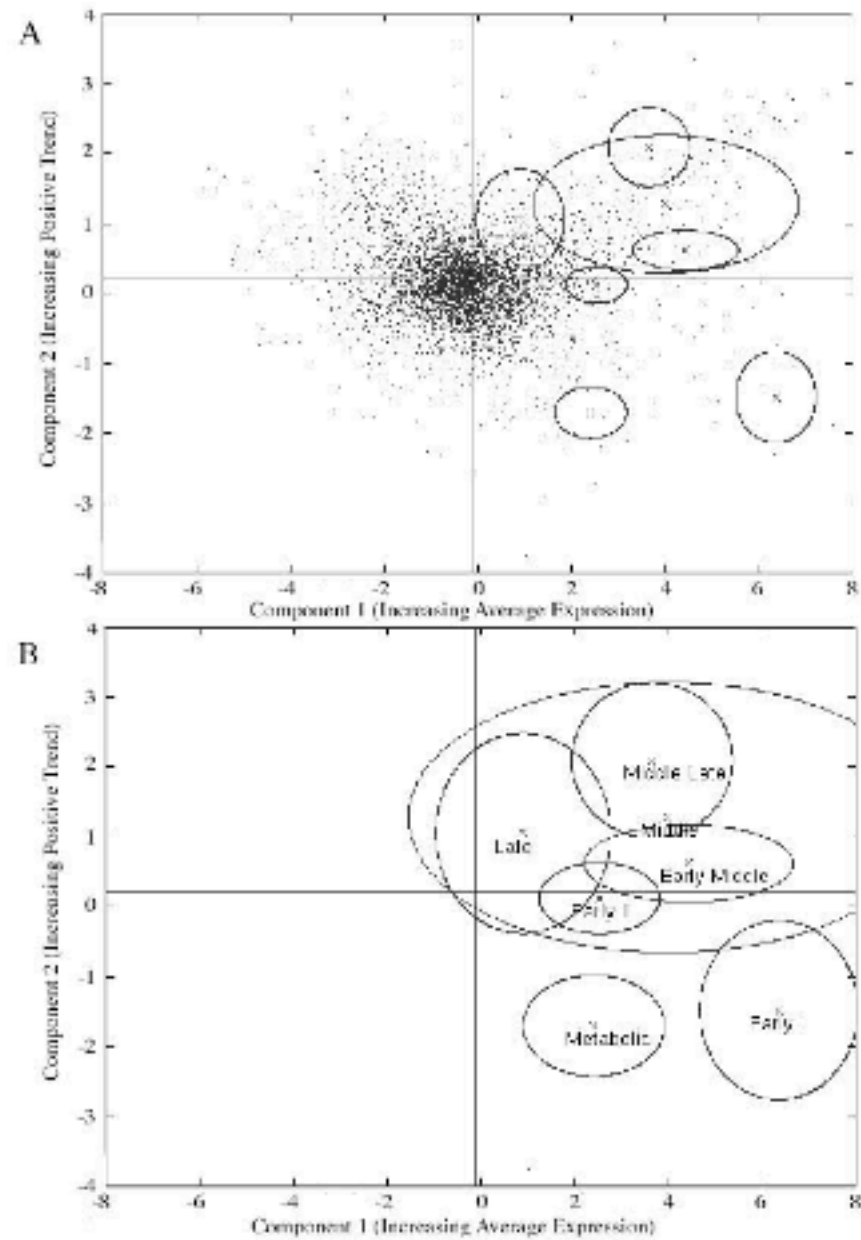


Figure 4. A. All genes plotted with respect to first and second principal components. Ellipses represent clusters identified in the original publication of the sporulation data. Ellipses are drawn to include 68% of the genes in the cluster. B. Ellipses are labelled using labels reported by the original investigators (Chiu et al. 1998) and drawn to include 95% of genes in the cluster.

