

# FOCUS: HOW DOES GENE EXPRESSION CHANGE AT DIFFERENT RpoS LEVELS?

The protein RpoS regulates the general stress response of the bacteria.



Chris Bickel, Science (2016)

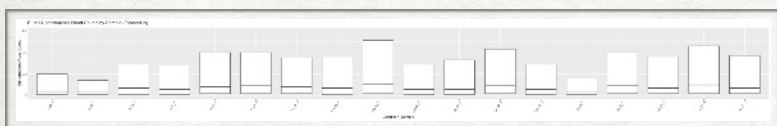
## GOAL: FIND PATTERNS

What are the patterns of gene expression across all RpoS-regulated genes as RpoS level changes?

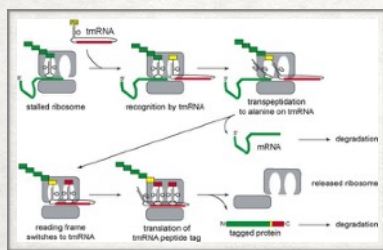
## GOAL: COMPARE TO OLD DATA

Dr. Stoebel, Dr Hardin and their lab conducted a similar investigation with three levels of RpoS. Now, with six RpoS levels, we wish to compare.

## CAVEATS AND OPEN QUESTIONS



The vast majority of genes have very low counts with a few genes in each sample dominating.



ssrA (tmRNA) has very high counts, and further investigation would be interesting.

Keiler KC (2007) Curr Opin Microbiol 10:169-75

hhmi | Howard Hughes Medical Institute

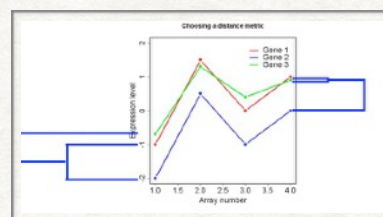
SCRIPPS  
THE WOMEN'S COLLEGE • CLAREMONT

Pomona College

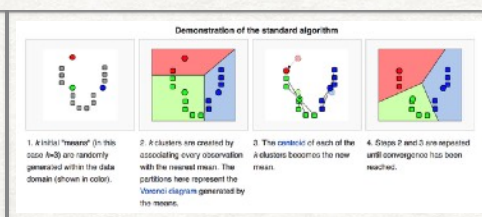
HARVEY MUDD  
COLLEGE

## PROCESS

- 1) Perform quality control.
- 2) Normalize all counts.
- 3) Find the regulon using differential expression analysis.
- 4) Design profiles and sort genes using Pearson correlation.
- 5) K-means clustering; Spearman correlation as dissimilarity metric.
- 6) K-medoids (PAM) clustering; Spearman correlation as dissimilarity metric.



Dr. Elena Marchiori, Institute for Computing and Information Science, Radboud University

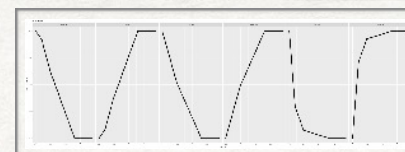


K-means Algorithm, Wikipedia

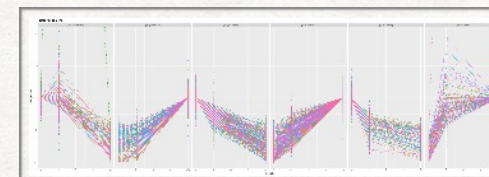
## RpoS-Regulated Gene Expression Patterns in *E. coli*

DR. DAN STOEDEL, HARVEY MUDD COLLEGE  
DR. JO HARDIN, POMONA COLLEGE  
MADISON HOBBS, SCRIPPS COLLEGE

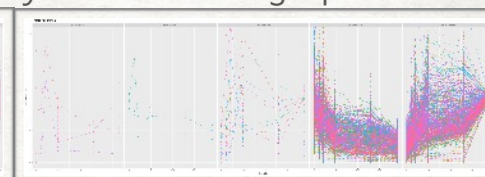
## METHOD 1: DESIGN PROFILES



Design 6 profiles, modeled after the profiles presented by Dr. Hardin and Dr. Stoebel's lab, to group genes by sensitivity to increasing RpoS.

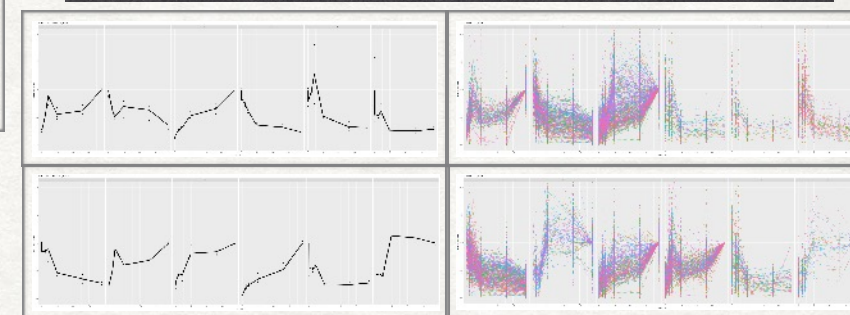


old data set: profile assignment with 3 RpoS levels



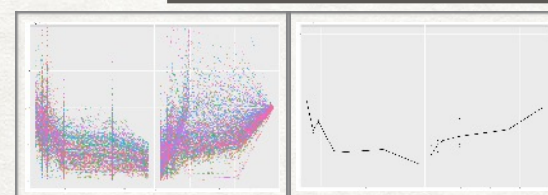
new data set: profile assignment with 6 RpoS levels

## METHOD 2: K-MEANS CLUSTERING

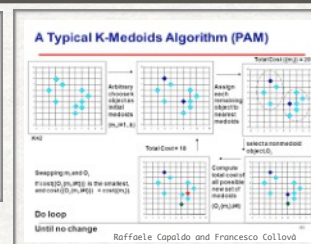


Adjusted Rand Index for K-means #1 vs. K-means #2: 0.515  
The cluster centers change each time through the algorithm, even with the same value for k.

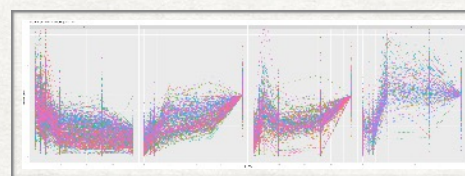
## METHOD 3: PARTITIONING AROUND MEDOIDS CLUSTERING (K-MEDOIDS)



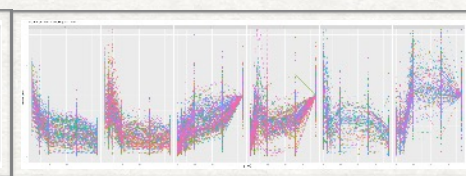
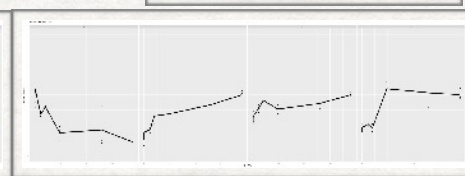
average silhouette width: 0.834



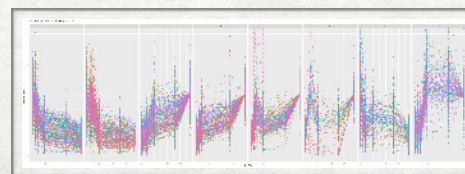
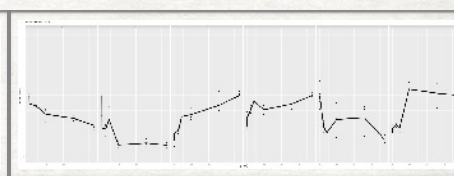
average silhouette width: 0.568



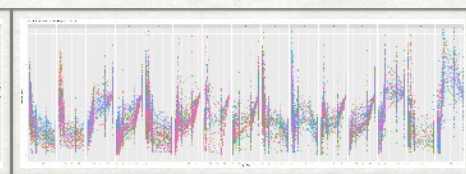
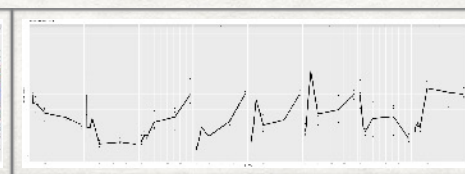
average silhouette width: 0.561



average silhouette width: 0.322, ARI with profiles: 0.369



average silhouette width: 0.256



average silhouette width: 0.203

