Estrategias de expresión génica en la levadura *Saccharomyces cerevisiae*

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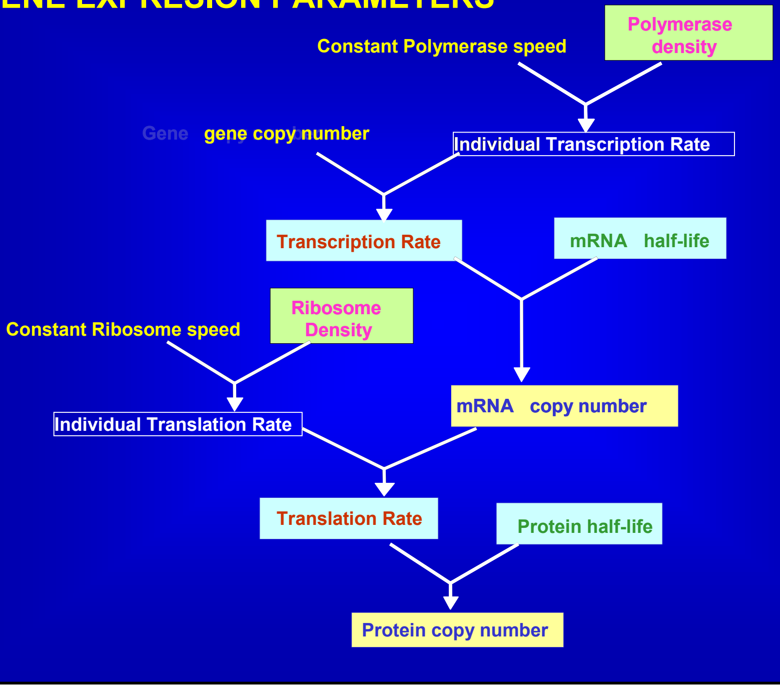
GENE EXPRESION PARAMETERS



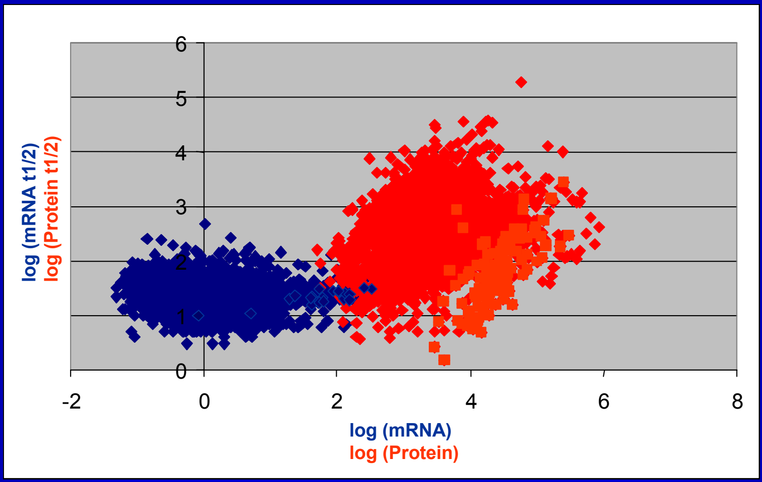
The 6 parameters characterizing gene expresion

(Condition: exponential growth in YPD)

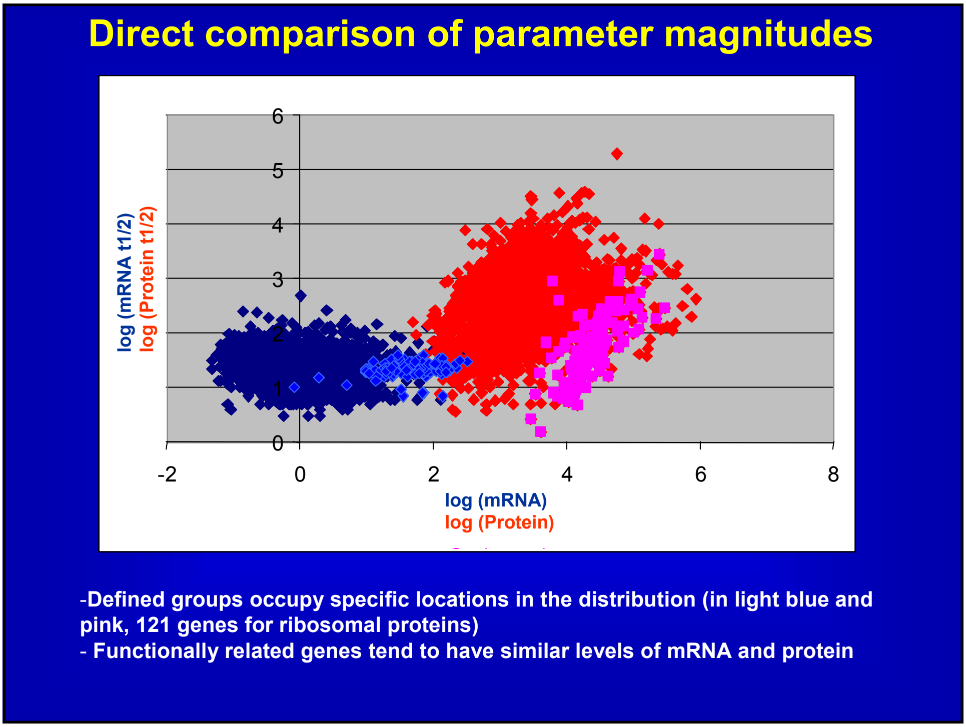
Parameter (units)	Used in this study	Alternative(s) tested
RA (molec./cell)	Reference set from Beyer et al. (2004) by combining 36 microarray experiments	Set from García-Martínez et al. (2004)
TR (molec./min)	Direct measurements by using GRO methodology from García-Martínez et al. (2004)	
RS (min)	Direct measurements of overall mRNA from Wang et al. (2002) by using the *rpb1-1* ^{ts} mutant	Indirect estimation by using RA and TR from García-Martínez et al. (2004)
PA (molec./cell)	Reference set from different sources constructed by Beyer et al. (2004)	
TLR (molec./min)	Calculated by using the ribosome density data from Arava et al. (2003) and the RA reference set	Calculated by using the ribosome density data from Arava et al. (2003) and RA estimations from García-Martínez et al. (2004)
PS (min)	Calculated by using the reference sets for PA and TLR	Calculated by using the reference set for PA and the alternative TLR set

Yeast: complete dataset (6 parameters) for 3138 genes)

Direct comparison of parameter magnitudes

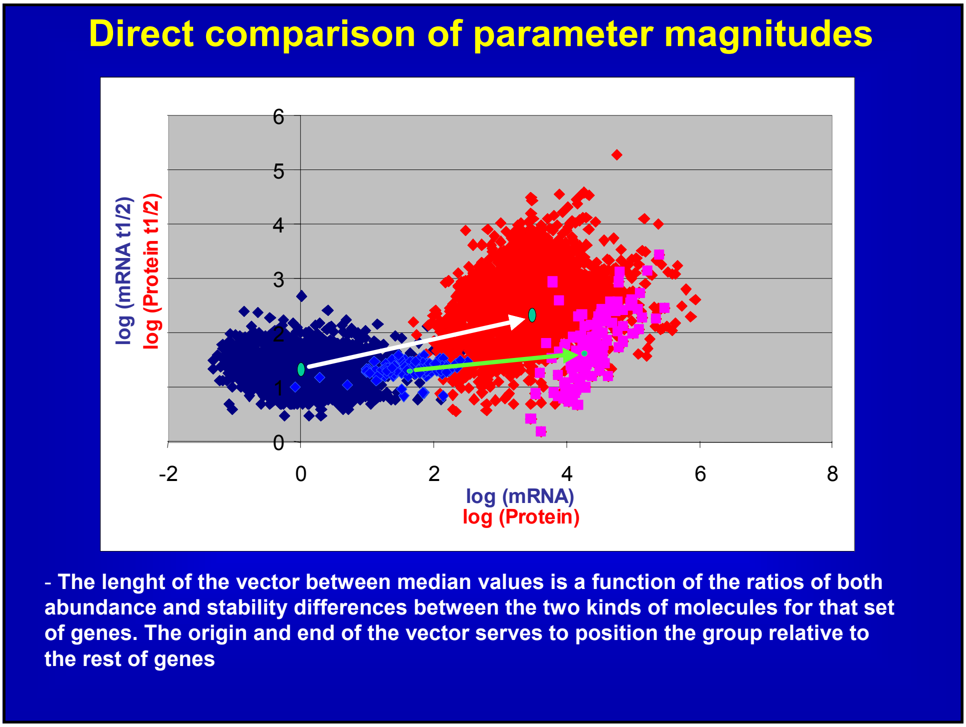


- Proteins are 3 magnitude orders more abundant than mRNA
- Both mRNA and protein display a range of about 3.5 orders when comparing the less and the most abundant molecules
- While mRNA half-lives span 1.5 orders, protein stabilities display a range of, again, about 3.5 orders, producing a round-shaped cloud



Direct comparison of parameter magnitudes

-Defined groups occupy specific locations in the distribution (in light blue and pink, 121 genes for ribosomal proteins)
- Functionally related genes tend to have similar levels of mRNA and protein



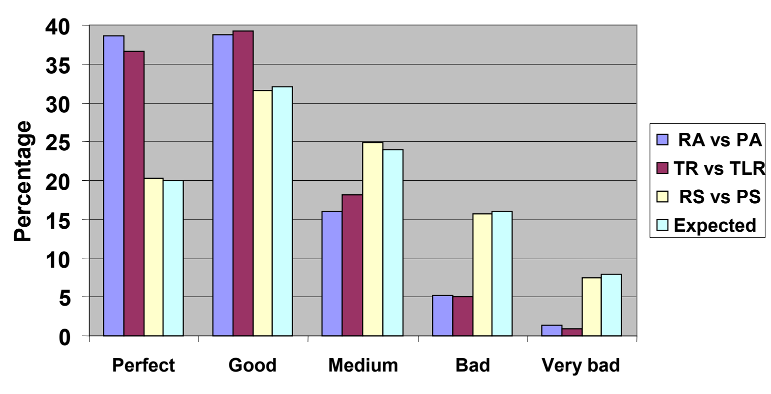
Direct comparison of parameter magnitudes

- The lenght of the vector between median values is a function of the ratios of both abundance and stability differences between the two kinds of molecules for that set of genes. The origin and end of the vector serves to position the group relative to the rest of genes

Correlations between parameters

A. Same type of parameters

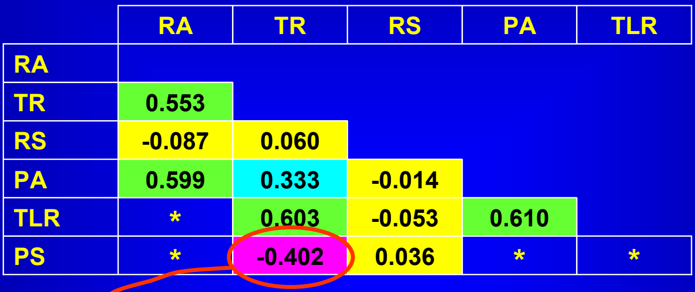
→ Ordered quintiles



- **Perfect for RA/PA & TR/TLR:** ***cytosolic ribosome, cytosol, metabolism, alcohol metabolism***
- **Perfect only for RA/PA:** ***amino acid metabolism, translation, tRNA ligase***
- **Very bad correlation for: RA/PA** ***(endoplasmic reticulum, transporter, membrane)*** **and TR/TLR** ***(glucanosyltranferase*** **activity)**

Correlations between parameters

A. Cross-correlation between all parameters (Spearman rank correlation)



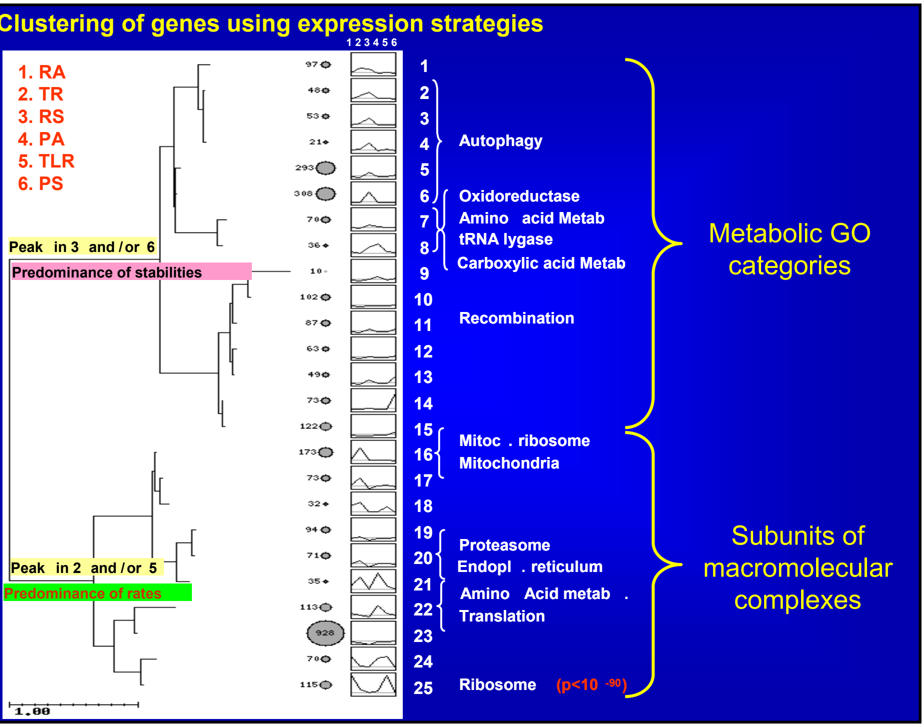
	RA	TR	RS	PA	TLR
RA					
TR	0.553				
RS	-0.087	0.060			
PA	0.599	0.333	-0.014		
TLR	*	0.603	-0.053	0.610	
PS	*	-0.402	0.036	*	*

Green: Positive correlations
Light blue: low positive correlations
Yellow: absence of correlation
Pink: Negative correlations
Asterisks indicate cases for which no correlation analysis can be done because of the mathematical relationship between both variables

Besides the global tendency, some GO categories appear over-represented in the corners of the distribution:

↑TR / ↓PS → Ribosome, cytosol
↓TR / ↑PS → Mitosis

Clustering of genes using expression strategies



Autophagy

Oxidoreductase

Amino acid Metab

tRNA lygase

Carboxylic acid Metab

Recombination

Mitoc. ribosome

Mitochondria

Proteasome

Endopl. reticulum

Amino Acid metab.

Translation

Ribosome ($p<10^{-90}$)

Metabolic GO categories

Subunits of macromolecular complexes

Analysis of functionally related gene groups

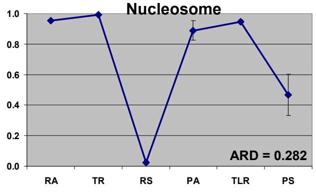
- **Analysis of macomolecular complexes** (Nucleosome, Cytosolic ribosome, Mitochondrial ribosome, Proteasome, Spliceosome, SAGA, TOM-TIM, Mediator, Respiatory chain, ATP synthase, Nuclear pore, RNA polymerase) **and functionally related groups of genes no-forming complexes** (Mitosis, Carboxylic Acid Metabolism, TCA, Glycolysis + Gluconeogenesis, Fermentation, Ionic homeostasis, Cell wall organization, Phosphate metabolism, Translation, Vacuole, Lipid metabolism)

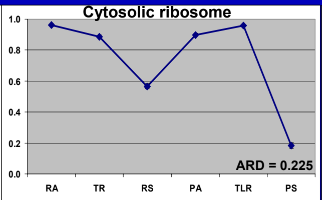
- Represented the average of percentil value for each parameter (with its Standard Error)

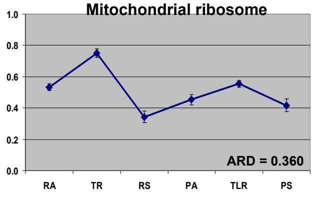
- Calculated an Average of Relative Deviation (ARD) in relation to the average

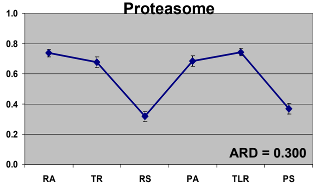
$$ARD = \sum_{i=1}^{n} [(x_i - \bar{x}) / \bar{x}] / n$$

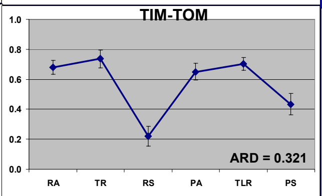
Macromolecular complexes

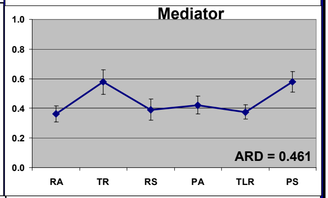

Nucleosome
ARD = 0.282

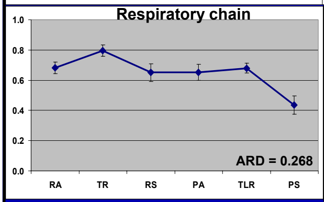

Cytosolic ribosome
ARD = 0.225

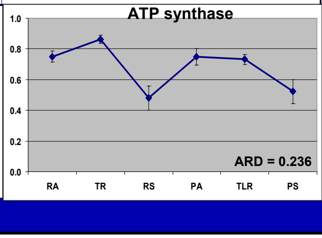

Mitochondrial ribosome
ARD = 0.360

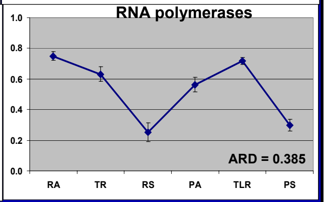

Proteasome
ARD = 0.300


TIM-TOM
ARD = 0.321

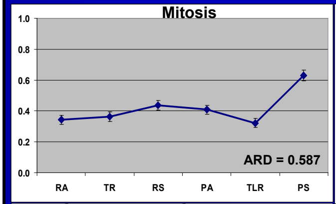

Mediator
ARD = 0.461

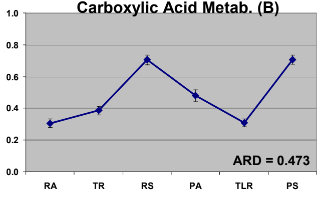

Respiratory chain
ARD = 0.268

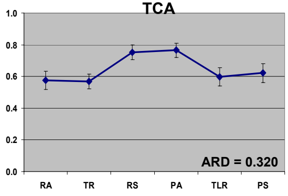

ATP synthase
ARD = 0.236

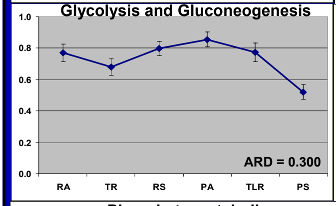

RNA polymerases
ARD = 0.385

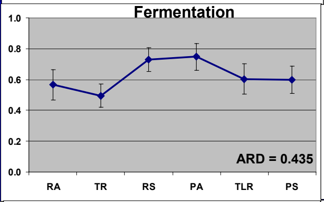
Functionally related gene groups (no-complexes)

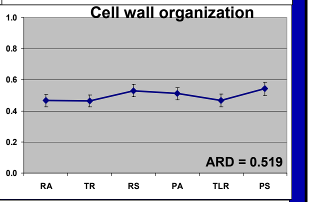

Mitosis
ARD = 0.587

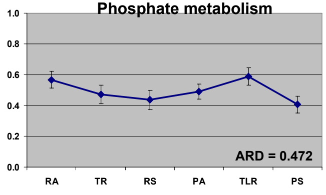

Carboxylic Acid Metab. (B)
ARD = 0.473

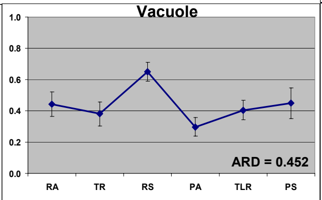

TCA
ARD = 0.320

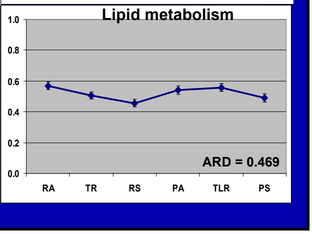

Glycolysis and Gluconeogenesis
ARD = 0.300


Fermentation
ARD = 0.435


Cell wall organization
ARD = 0.519

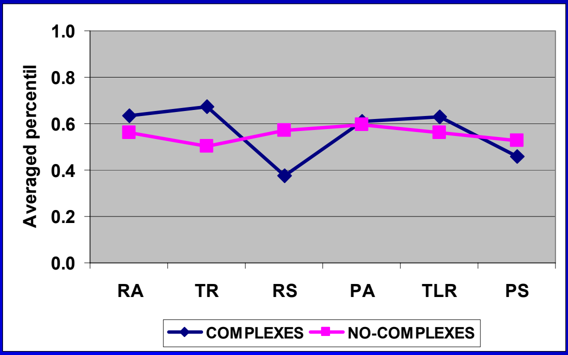

Phosphate metabolism
ARD = 0.472


Vacuole
ARD = 0.452


Lipid metabolism
ARD = 0.469

Summary

A. Parameter values



B. ARD

	RA	TR	RS	PA	TLR	PS	ARD
COMPLEXES	0.245	0.279	0.561	0.306	0.238	0.506	0.356
NO COMPLEXES	0.440	0.455	0.420	0.394	0.432	0.471	0.435