

Regulatory Sequence Analysis

Pattern discovery String-based approaches

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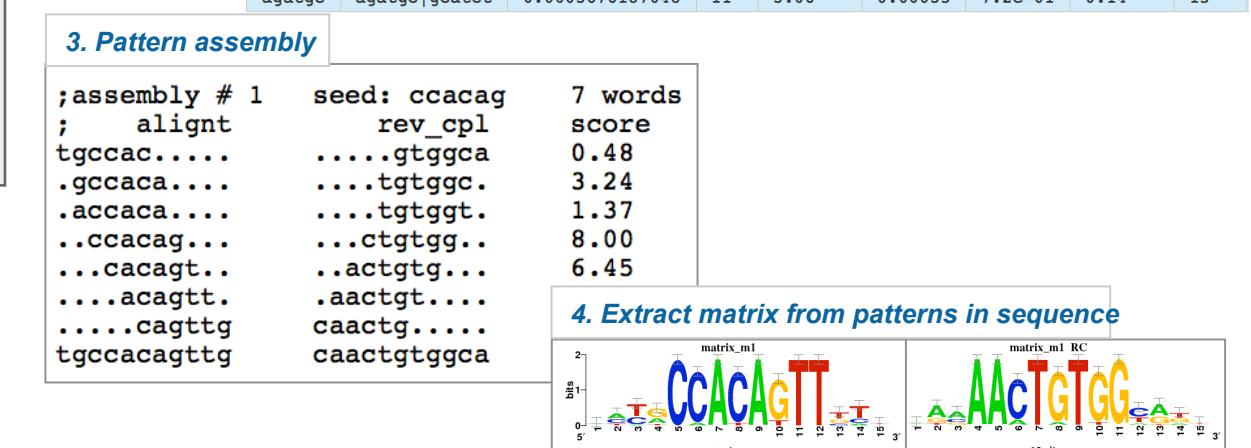
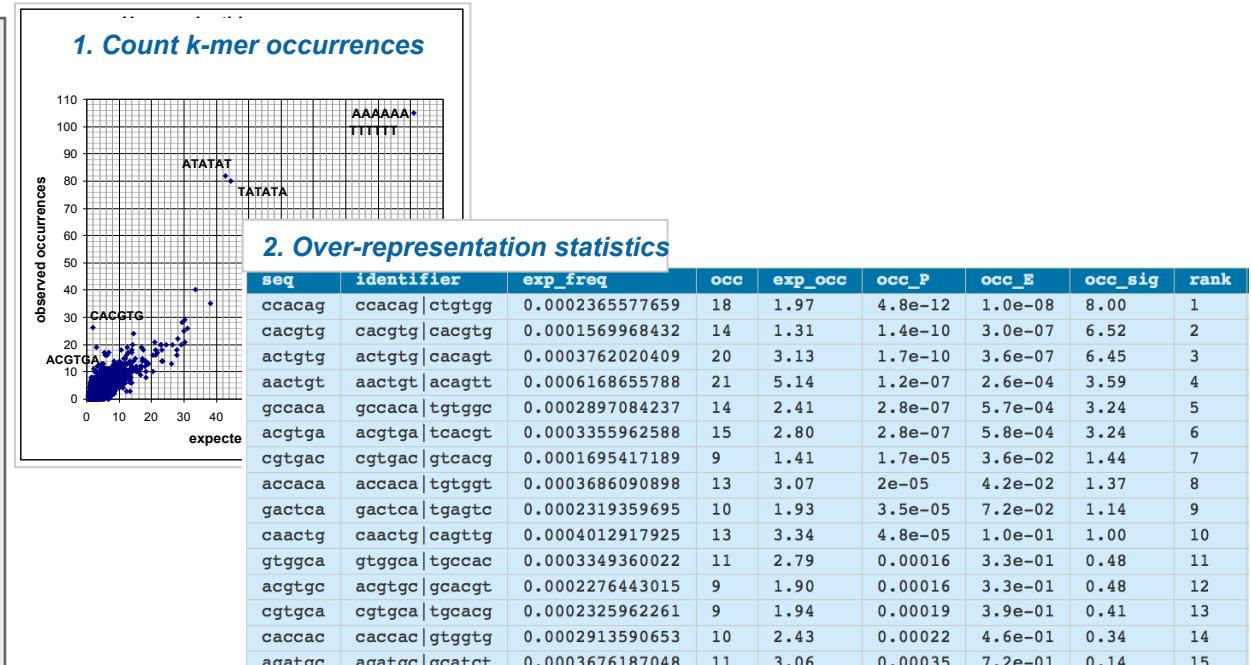
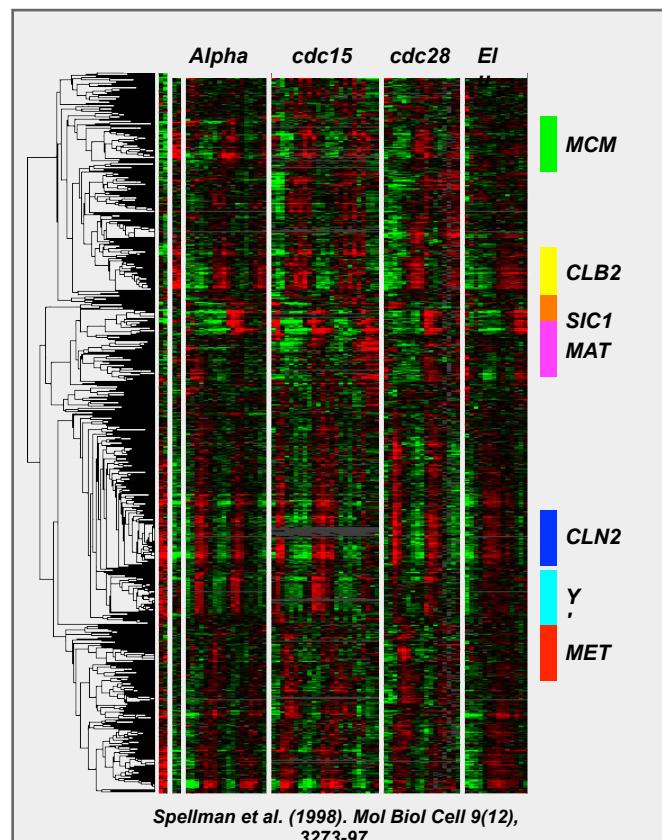
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Université Libre de Bruxelles, Belgique

Bioinformatique des Génomes et des Réseaux (BiGRe lab)

<http://www.bigré.ulb.ac.be/>

Motif discovery in promoters of co-expressed genes



Bruno André
(ULB, Bruxelles, Belgium)

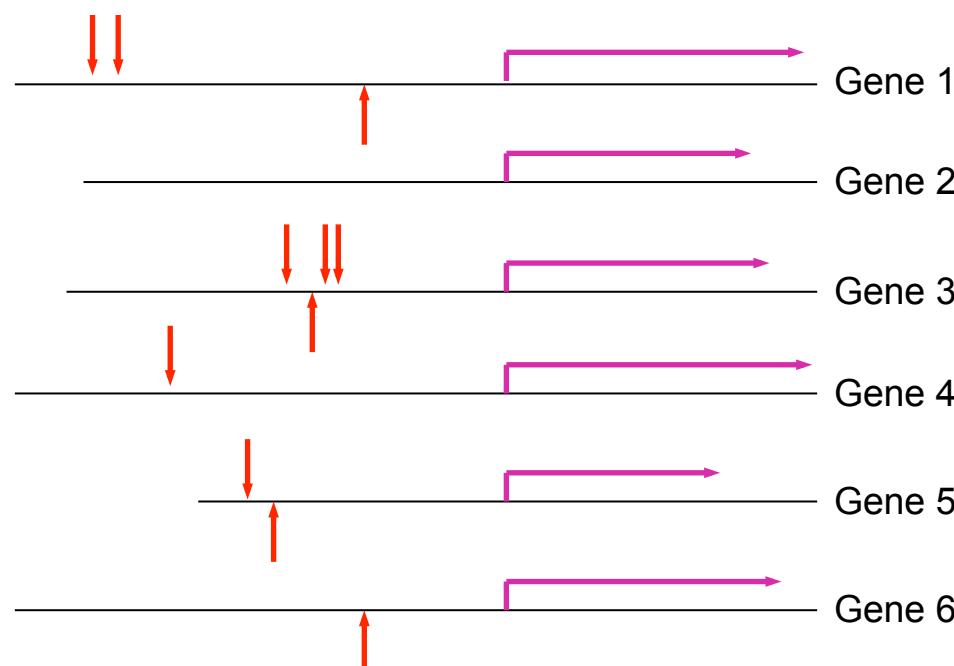


Julio Collado-Vides
(CCG, Cuernavaca – Mexico)

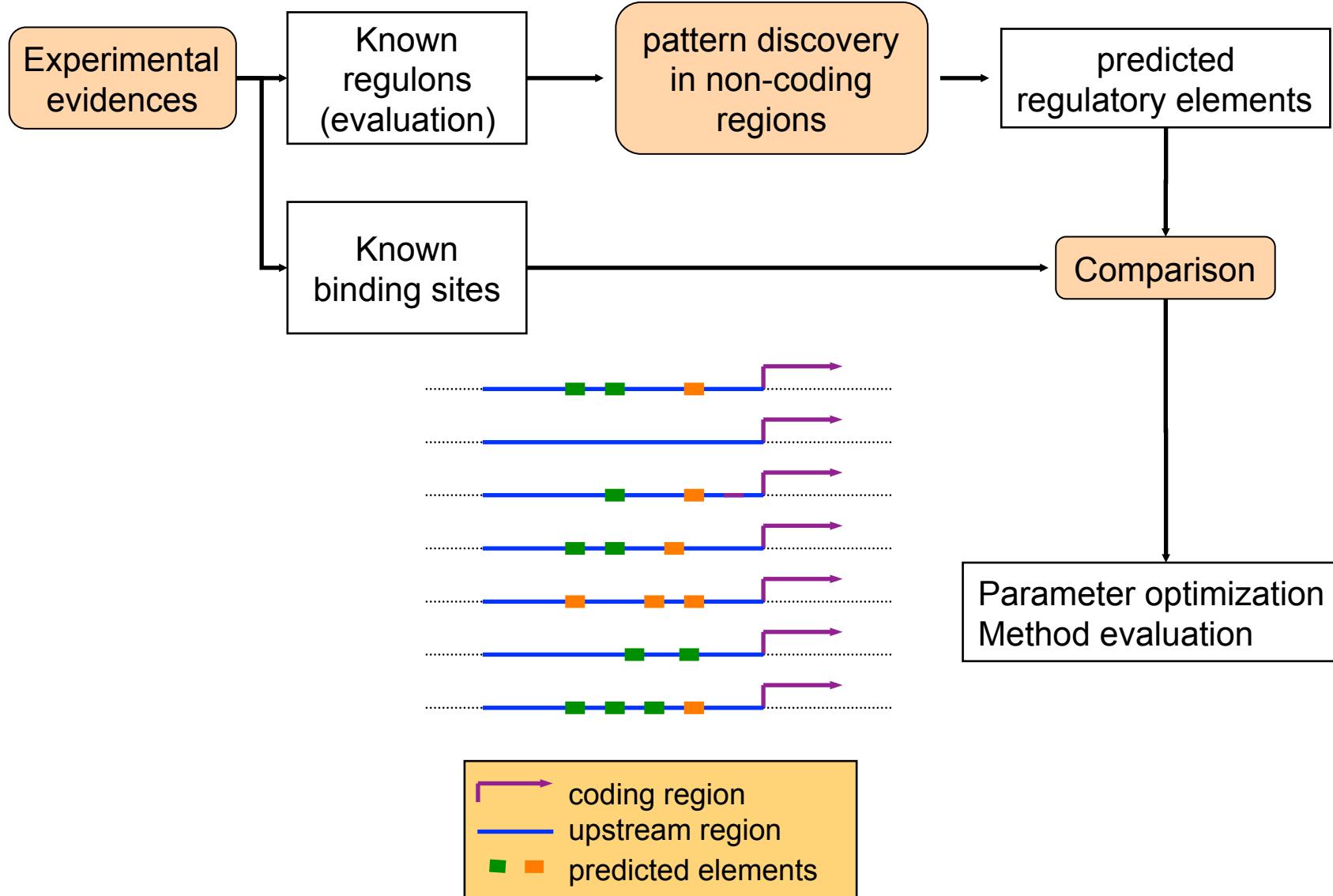


Detection of over-represented patterns

- Knowing that a set of genes are co-regulated, one can expect that their upstream regions contains some regulatory signal.
- This signal is likely to be more frequent in the upstream regions of the co-regulated genes than in a random selection of genes.
- In order to discover signals responsible for the co-regulation of a group of genes, we will thus detect over-represented patterns in their upstream sequences.



Evaluation with known regulons



Testing the performances with known regulons

- NIT
 - 7 genes expressed under low nitrogen conditions
- MET
 - 10 genes expressed in absence of methionine
- PHO
 - 5 genes expressed under phosphate stress
- GAL
 - 6 genes expressed in presence of galactose
- ...

Interface between the yeast Pho4p protein and one of its binding sites



Background model

- In order to detect over-represented patterns, the observed occurrences are compared to the random expectation.
- The random expectation can be estimated according to different models
 - Bernouilli model, with a specific probability for each nucleotide.
 - Markov model, estimated on the basis of the input sequence itself.
 - External background : occurrences for the same pattern in a reference data set
 - whole genome
 - intergenic sequences
 - set of all upstream sequences for the organism considered

The most frequent oligonucleotides are not informative

- A (too) simple approach would consist in detecting the most frequent oligonucleotides (for example hexanucleotides) for each group of upstream sequences.
- This would however lead to deceiving results.
 - In all the sequence sets, the same kind of patterns are selected: AT-rich hexanucleotides.

PHO		
aaaaaaa tttttt	51	
aaaaaag cttttt	15	
aagaaaa tttctt	14	
gaaaaaa tttttc	13	
tgccaa ttggca	12	
aaaaaat attttt	12	
aaatta taattt	12	
agaaaaa ttttct	11	
caagaaa ttcttg	11	
aaacgt acgttt	11	
aaagaaa ttcttt	11	
acgtgc gcacgt	10	
aataat attatt	10	
aagaag cttctt	10	
atataaa ttatat	10	

MET		
aaaaaaa tttttt	105	
atatat atatat	41	
gaaaaaa tttttc	40	
tatata tatata	40	
aaaaaat attttt	35	
aagaaa tttctt	29	
agaaaa ttttct	28	
aaaata tatttt	26	
aaaaag cttttt	25	
agaaat atttct	24	
aaataa ttattt	22	
taaaaa ttttta	21	
tgaaaa ttttca	21	
ataata tattat	20	
atataaa ttatat	20	

NIT		
aaaaaaa tttttt	80	
cttatc gataag	26	
tatata tatata	22	
ataaga tcttat	20	
aagaaa tttctt	20	
gaaaaaa tttttc	19	
atatat atatat	19	
agataa ttatct	17	
agaaaa ttttct	17	
aaagaa ttcttt	16	
aaaaca tggttt	16	
aaaaag cttttt	15	
agaaga tcttct	14	
tgataa ttatca	14	
atataa ttatat	14	

GAL		
aaaaaaa tttttt	47	
aaaaaat attttt	17	
aatata tatatt	17	
aaaattt aatttt	16	
aaaata tatttt	15	
attttc gaaaat	13	
aaataa ttattt	13	
aaatat atattt	13	
ataaaa ttttat	12	
atatta taatat	12	
atatat atatat	11	
tgaaaa ttttca	11	
caaaaa tttttg	11	
taaaaa ttttta	11	
agatat atatct	11	

A more relevant criterion for over-representation

- The most frequent patterns do not reveal the motifs specifically bound by specific transcription factors.
- They merely reflect the compositional biases of upstream sequences.
- A more relevant criterion for over-representation is to detect patterns which are more frequent in the upstream sequences of the selected genes (co-regulated) than the random expectation.
- The random expectation is calculated by counting the frequency of each pattern in the complete set of upstream sequences (all genes of the genome).

Estimation of word-specific expected frequencies with a Markov model

- In a Markov model, the probability to find a letter at position i depends on the residues found at the m preceding residues.
- The tables represent the transition matrices for Markov chain models of order 1 (top) and 2 (bottom).
- Expected frequencies can be estimated
 - On the basis of a set of **background sequences** (e.g. the whole set of upstream sequences of the considered organism).
 - On the basis of the **input sequence set** itself: the probability of larger words is estimated from the observed frequencies of the sub-words that compose them.

$$P(S,m) = P(S_{1,m}) \prod_{i=m+1}^L P(r_i | S_{i-m,i-1})$$

Transition matrix, order 1

	g	a	c	t
a	0.178	0.369	0.165	0.288
c	0.166	0.327	0.191	0.316
g	0.190	0.313	0.211	0.286
t	0.175	0.273	0.180	0.372

Transition matrix, order 2

	g	a	c	t
aa	0.185	0.411	0.152	0.252
ac	0.171	0.348	0.186	0.296
ag	0.193	0.337	0.201	0.269
at	0.163	0.343	0.167	0.326
ca	0.181	0.344	0.184	0.291
cc	0.168	0.313	0.198	0.321
cg	0.194	0.283	0.227	0.295
ct	0.187	0.240	0.189	0.384
ga	0.186	0.407	0.145	0.262
gc	0.180	0.331	0.194	0.295
gg	0.192	0.318	0.216	0.274
gt	0.199	0.305	0.159	0.338
ta	0.160	0.304	0.182	0.354
tc	0.151	0.313	0.192	0.344
tg	0.184	0.302	0.210	0.304
tt	0.168	0.220	0.195	0.417

Estimation of word-specific expected frequencies from a set of background sequences

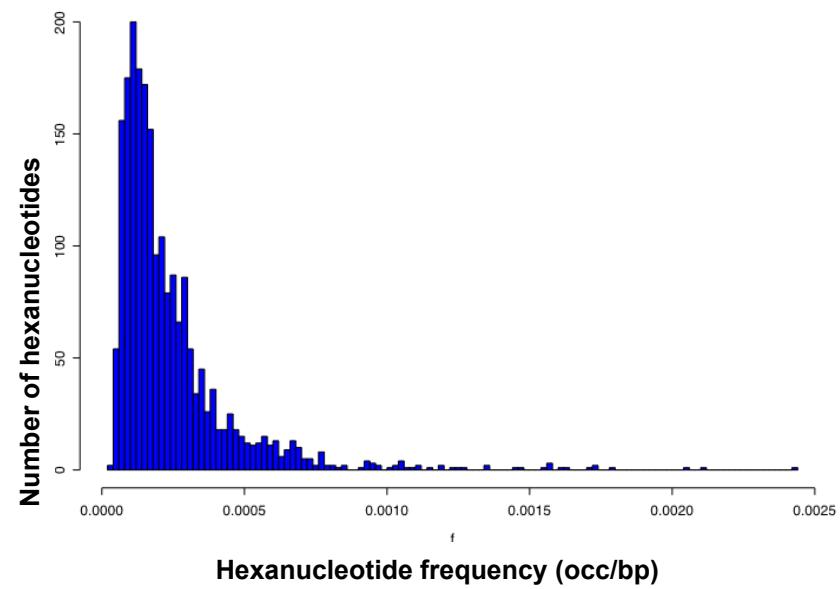
Example:

6nt frequencies in the whole set of yeast upstream sequences
Words are grouped by pairs of reverse complements.

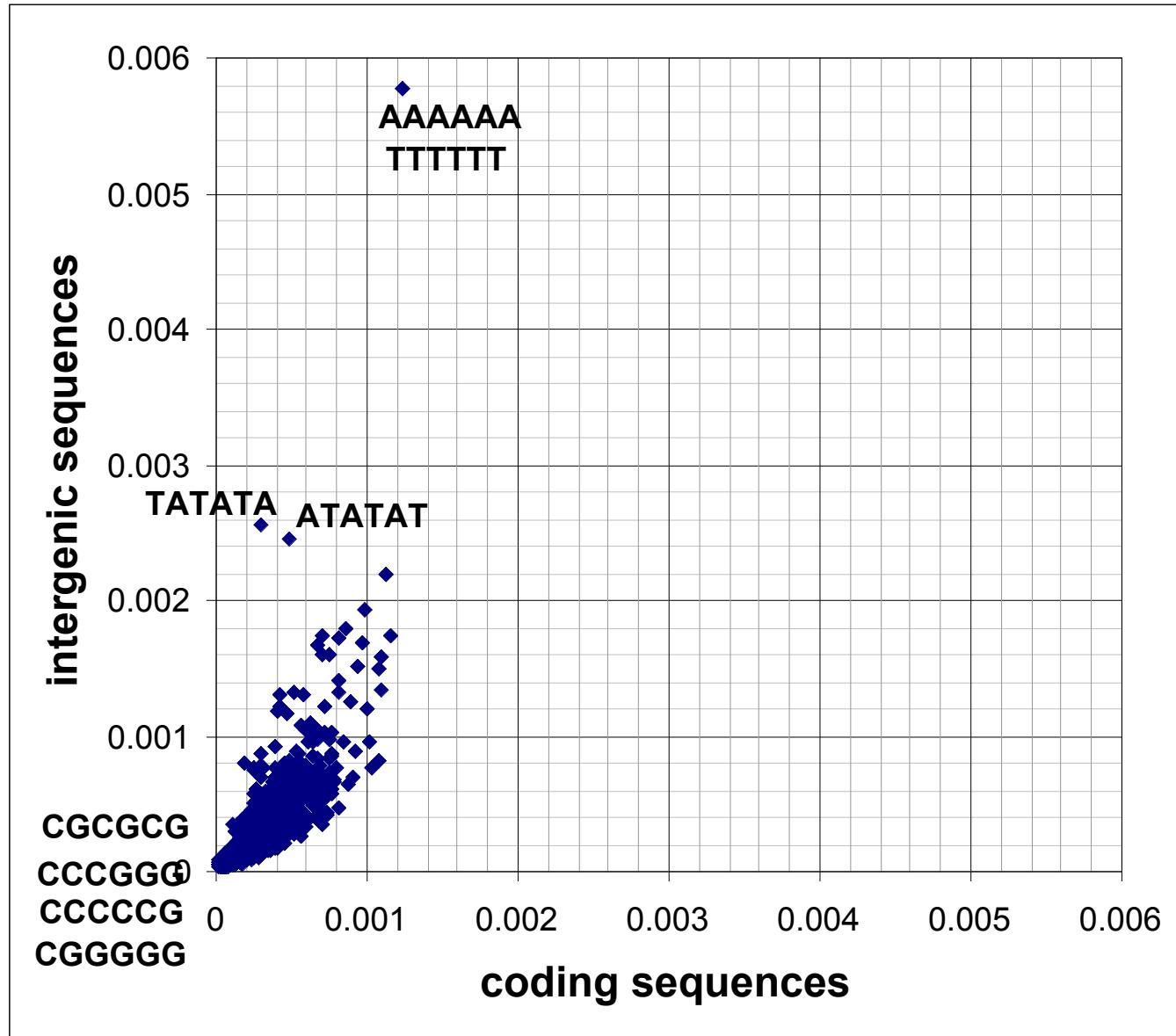
;seq	identifier	observed_freq	occ
aaaaaaa	aaaaaaa ttttt	0.00510699	14555
aaaaaac	aaaaaac gtttt	0.00207402	5911
aaaaaag	aaaaaag ctttt	0.00375191	10693
aaaaaat	aaaaaat atttt	0.00423577	12072
aaaaca	aaaaca tgttt	0.0019828	5651
aaaacc	aaaacc ggttt	0.00088526	2523
aaaacg	aaaacg cggtt	0.00090105	2568
aaaact	aaaact agttt	0.0014621	4167
aaaaga	aaaaga tcctt	0.00323016	9206
aaaagc	aaaagc gcttt	0.00135824	3871
aaaagg	aaaagg ccctt	0.0017849	5087
aaaagt	aaaagt acttt	0.0019035	5425
aaaata	aaaata tattt	0.00336805	9599
aaaatc	aaaatc gattt	0.00131368	3744
aaaatg	aaaatg cattt	0.00185648	5291
aaaatt	aaaatt aattt	0.00269156	7671
aaacaa	aaacaa ttgtt	0.00209999	5985
aaacac	aaacac gtgtt	0.00071684	2043
aaacag	aaacag ctgtt	0.00096491	2750
aaacat	aaacat atgtt	0.00108982	3106
aaacca	aaacca tggtt	0.00074421	2121

- Hexanucleotide frequencies have been measured in the whole set of 6000 yeast upstream sequences.
- Some words are very frequent, others are rare.
 - range 4.5e^{-5} to 1.2e^{-2}
 - Ratio between the most frequent and less frequent hexanucleotide:
 - $\max(f)/\min(f)=268$

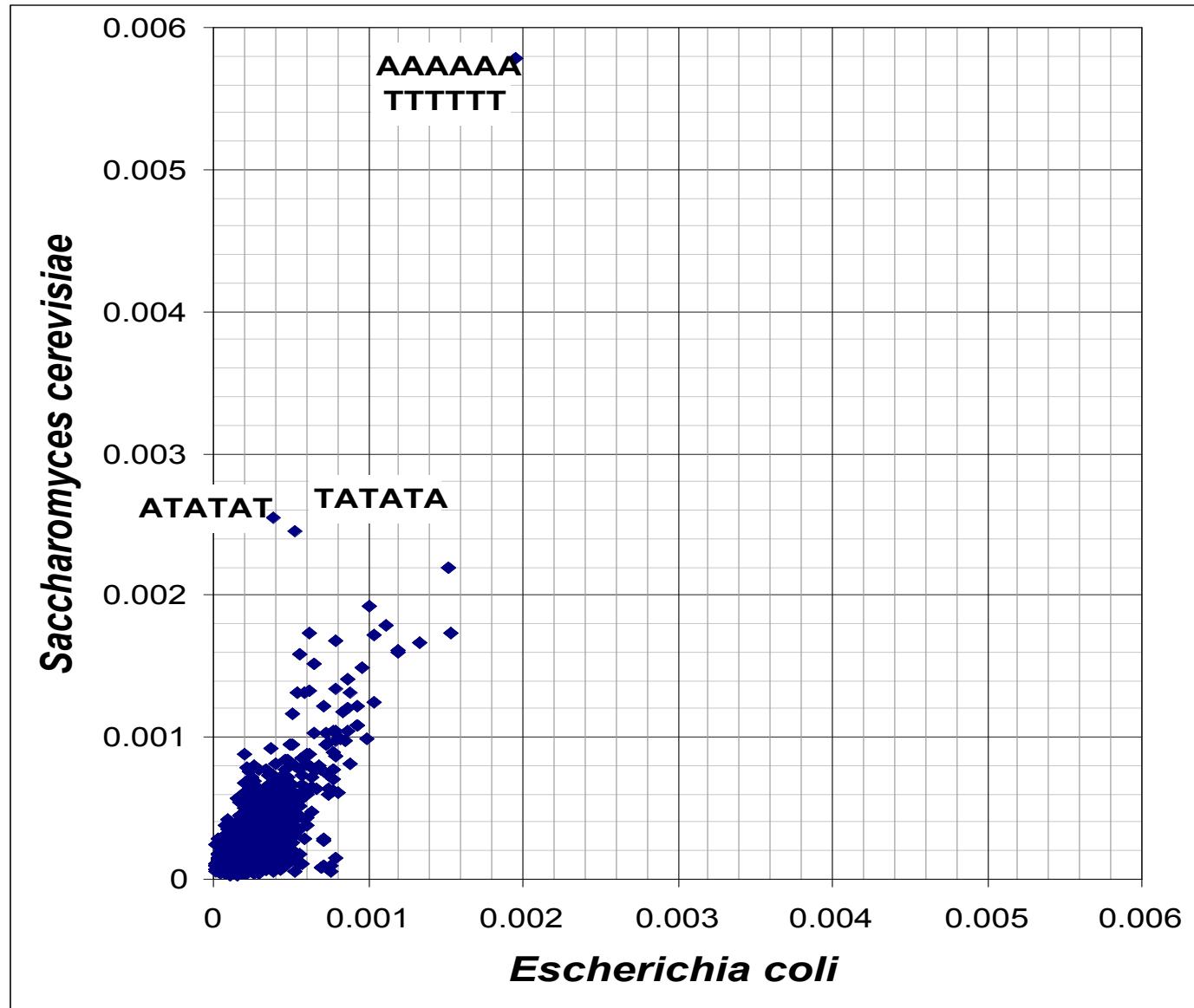
Hexanucleotide frequencies in yeast upstream sequences



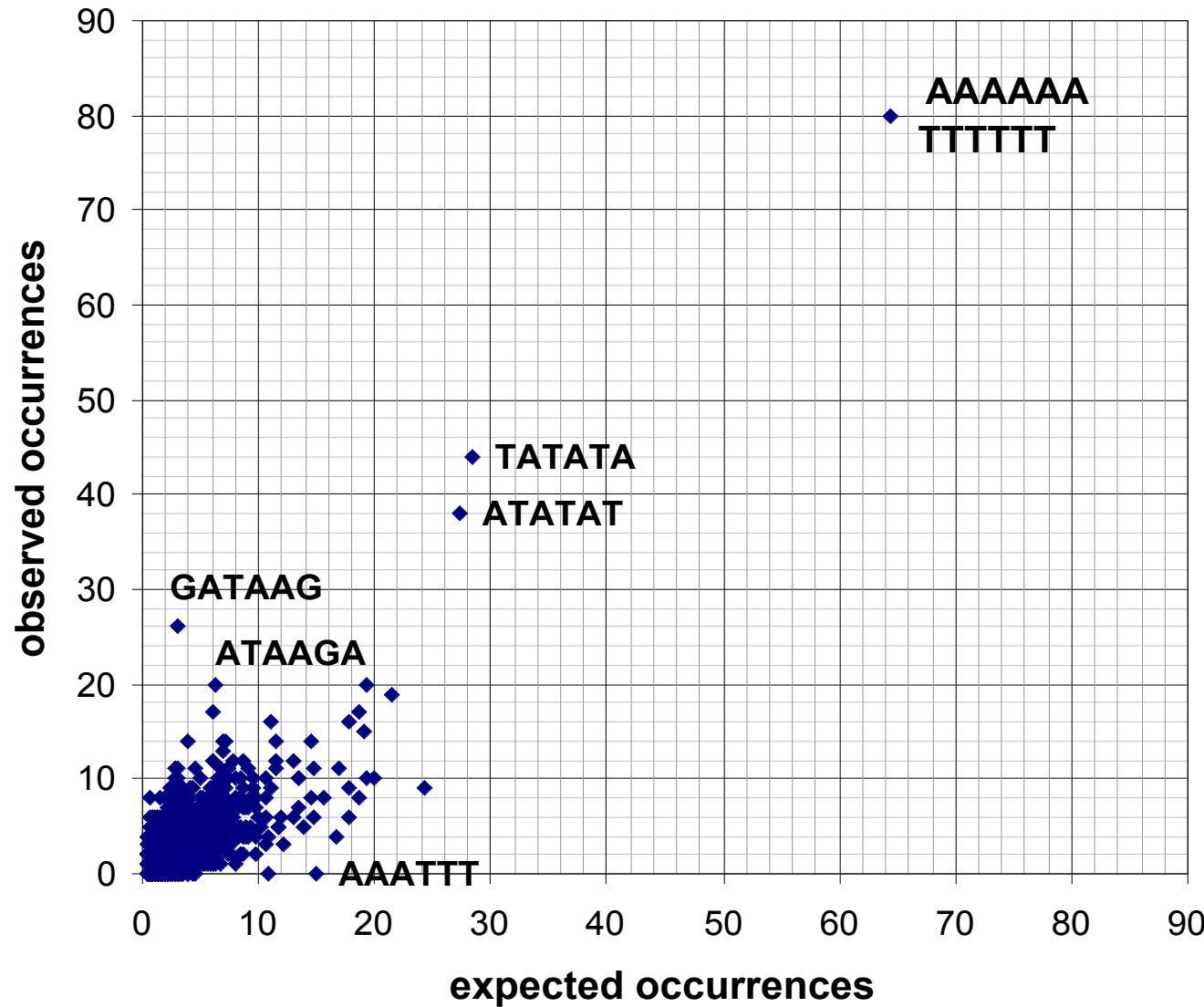
6nt frequencies differ between coding and non-coding sequences



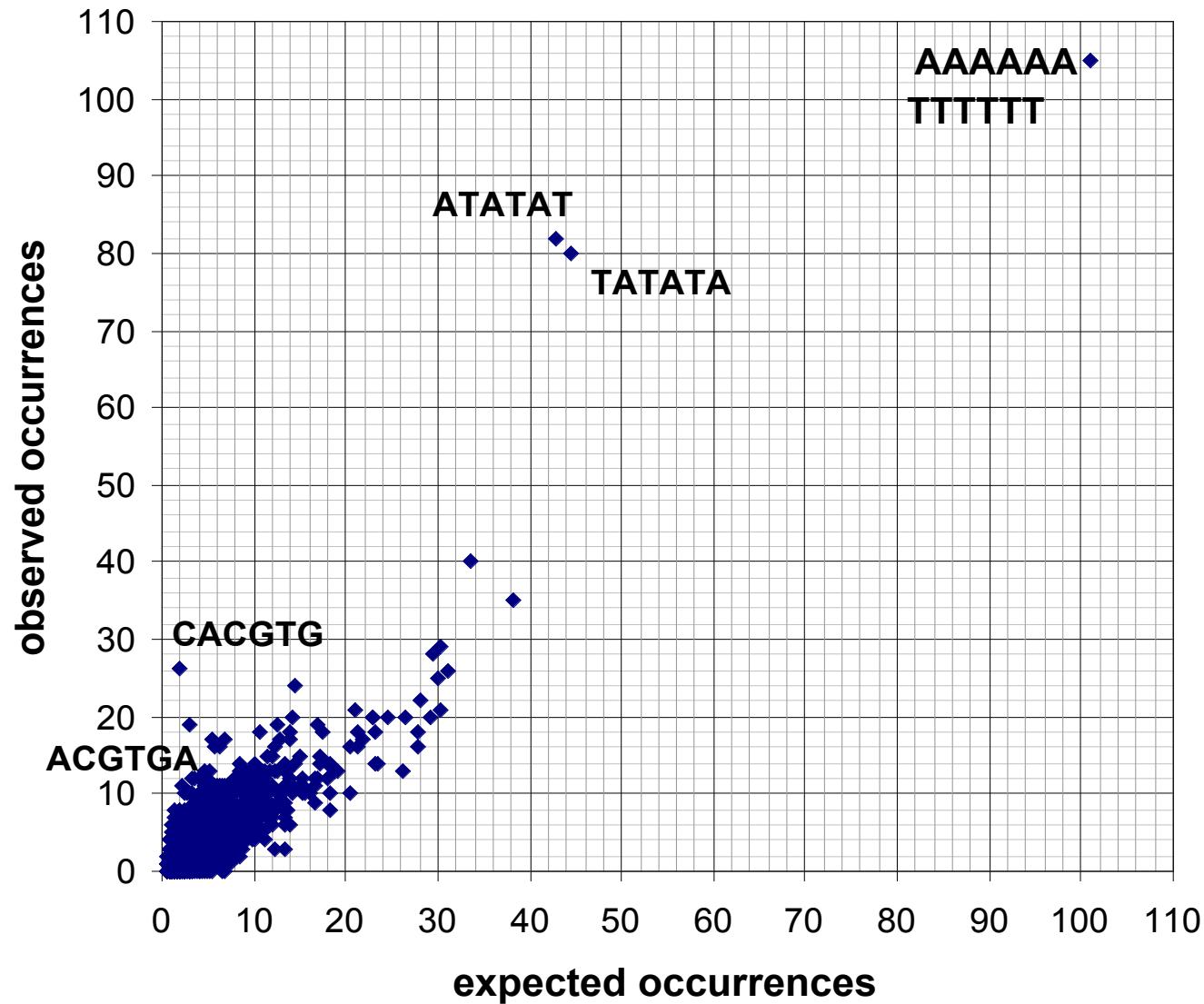
Inter-species variations in intergenic 6nt frequencies



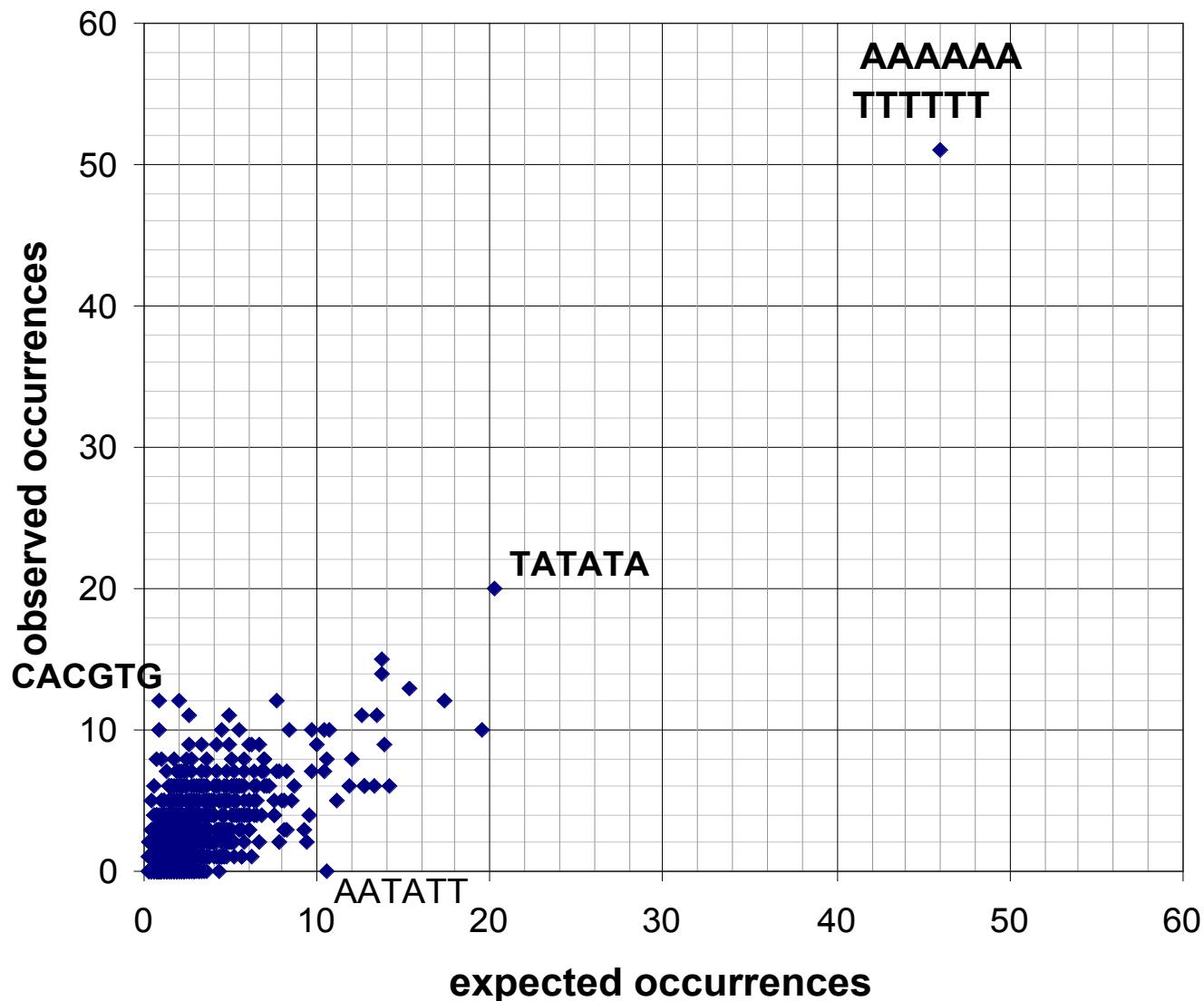
Hexanucleotide occurrences in upstream sequences of the NIT family



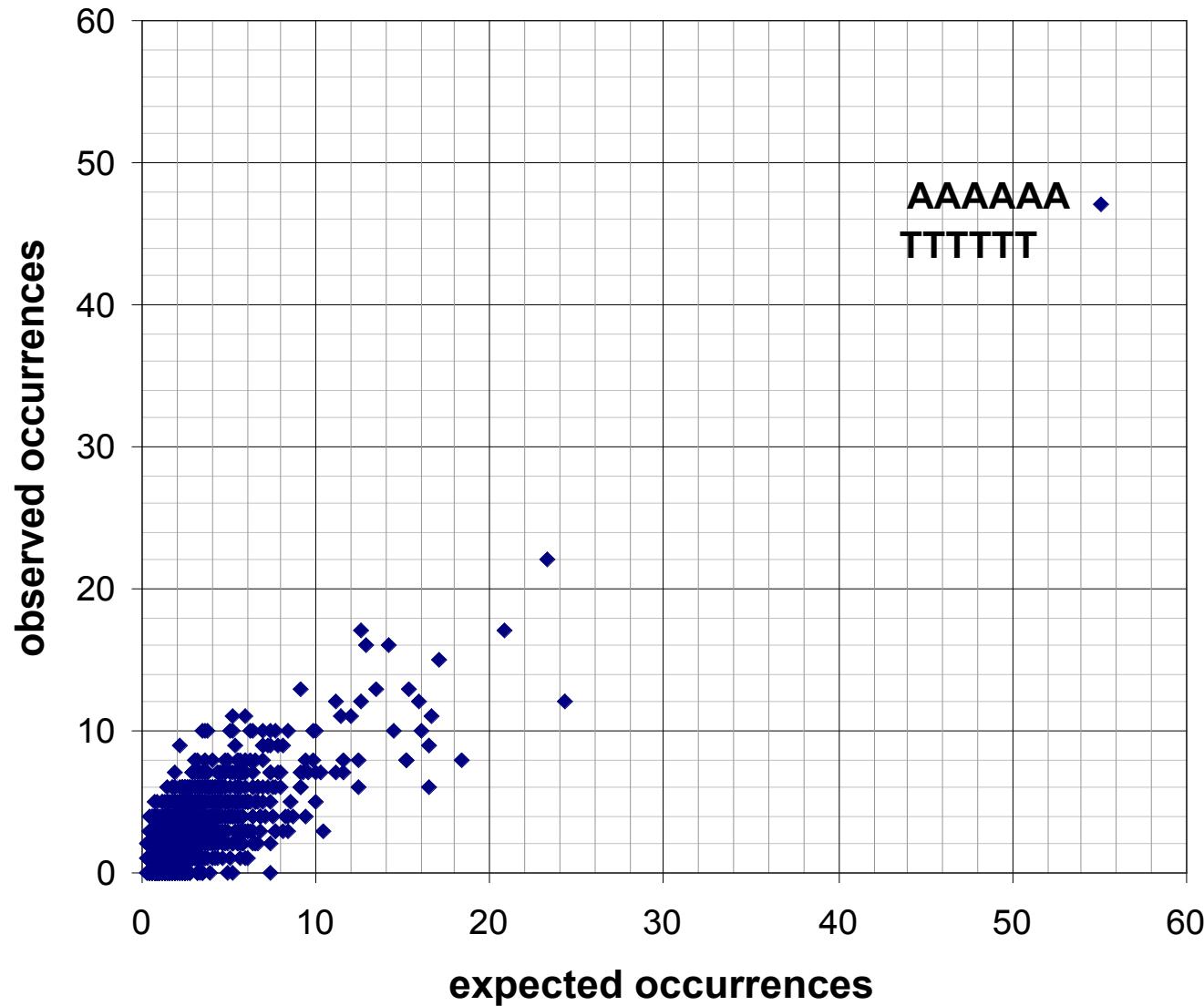
Hexanucleotide occurrences in upstream sequences of the MET family



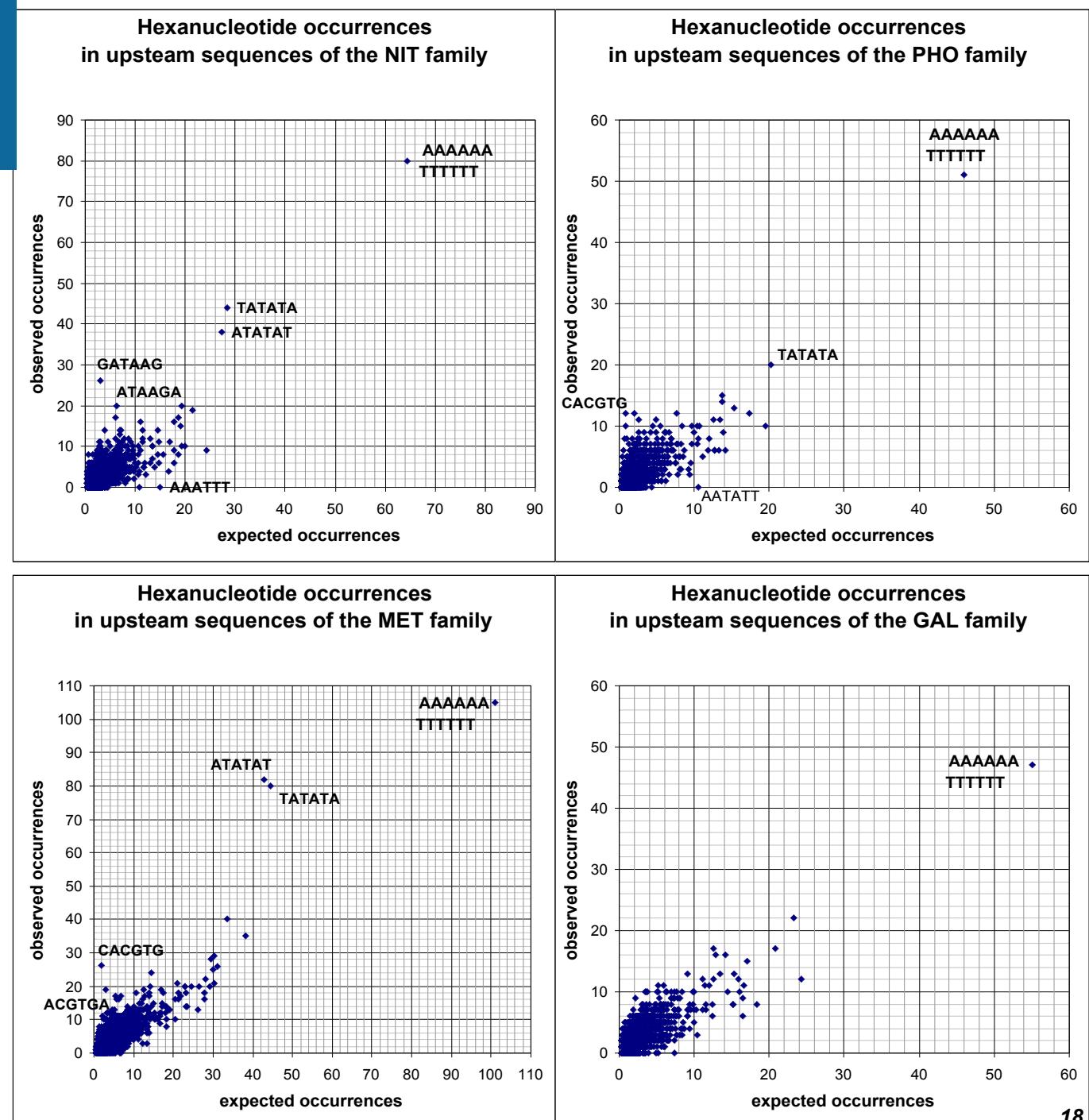
Hexanucleotide occurrences in upstream sequences of the PHO family



Hexanucleotide occurrences in upstream sequences of the GAL family

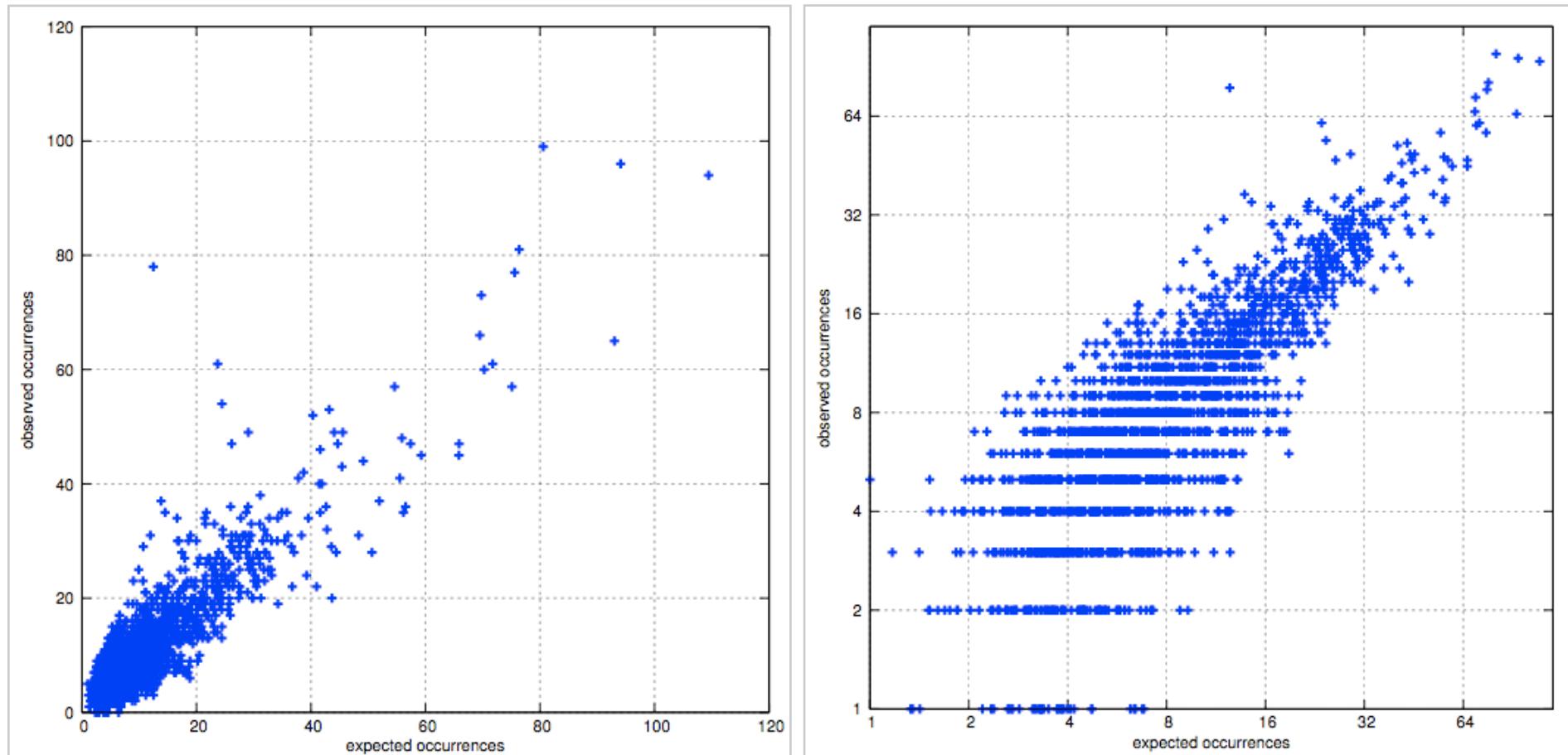


Hexanucleotide occurrences in yeast NIT, PHO, MET and GAL upstream sequences



Hexanucleotide occurrences in an extended NIT family

- We analyzed here an extended set of 41 NIT genes (taken from Godard et al., 2006).
- The number of genes affects the dispersion around the diagonal on the plot of observed versus expected occurrences.
- The signal-to-noise separation increases when more genes are analyzed.
- The logarithmic axes better emphasize the words with low expected and observed occurrences but does not allow to display words with 0 occurrences.
- Words with very low expected frequencies are sensitive to low-number fluctuations. For such cases, the observed/expected ratio is misleading (e.g. exp=1, obs=4).



Scoring statistics

- Several scoring statistics have been used to assess the statistical significance of word over-representation
- Observed/expected ratio
 - Never use this statistic !
 - The ratio can be misleading, because it over-emphasizes the patterns with a very low number of expected number of occurrences
 - Example:
 - $x_{obs}/x_{exp} = 10/1$ is quite significant, but $x_{obs}/x_{exp} = 1/0.1$ is not.
- Log-likelihood ratio
 - $LLR = F_{obs} * \log(F_{obs}/F_{exp})$
- Z-score (Matthieu Blanchette)
 - $Z\text{-score} = (x_{obs} - x_{exp})/s_x$
 - Only valid for very large sequences ($exp \gg 10$ for each word)
- Poisson (Andreas Wagner)
- Compound Poisson (Sophie Schbath)
- Binomial (Jacques van Helden)

Scoring scheme - Binomial

- Advantages
 - Allows to estimate a P-value.
 - Appropriate for small sequence sets, where some words have a very low expected number of occurrences (<1).
 - Allows to detect over- and under-representation.
- Weaknesses
 - Bias for self-overlapping words (but this can be circumvented by preventing the counting of overlapping occurrences).
 - Assumes that sequence length is much larger than word length
- Probability to observe exactly x occurrences

$$P(X = x) = \frac{T!}{x!(T-x)!} p^x (1-p)^{T-x}$$

- Probability to observe at least s occurrences

$$P(X \geq x) = \sum_{i=x}^T \frac{T!}{i!(T-i)!} p^i (1-p)^{T-i}$$

Where

x = observed occurrences

$T = \text{Sum}_{i=1 \rightarrow n}(L_i - k + 1)$ = number of possible positions for a word of length k in a sequence of n sequences of length L_i

p = word probability

Hexanucleotide analysis of the NIT regulon



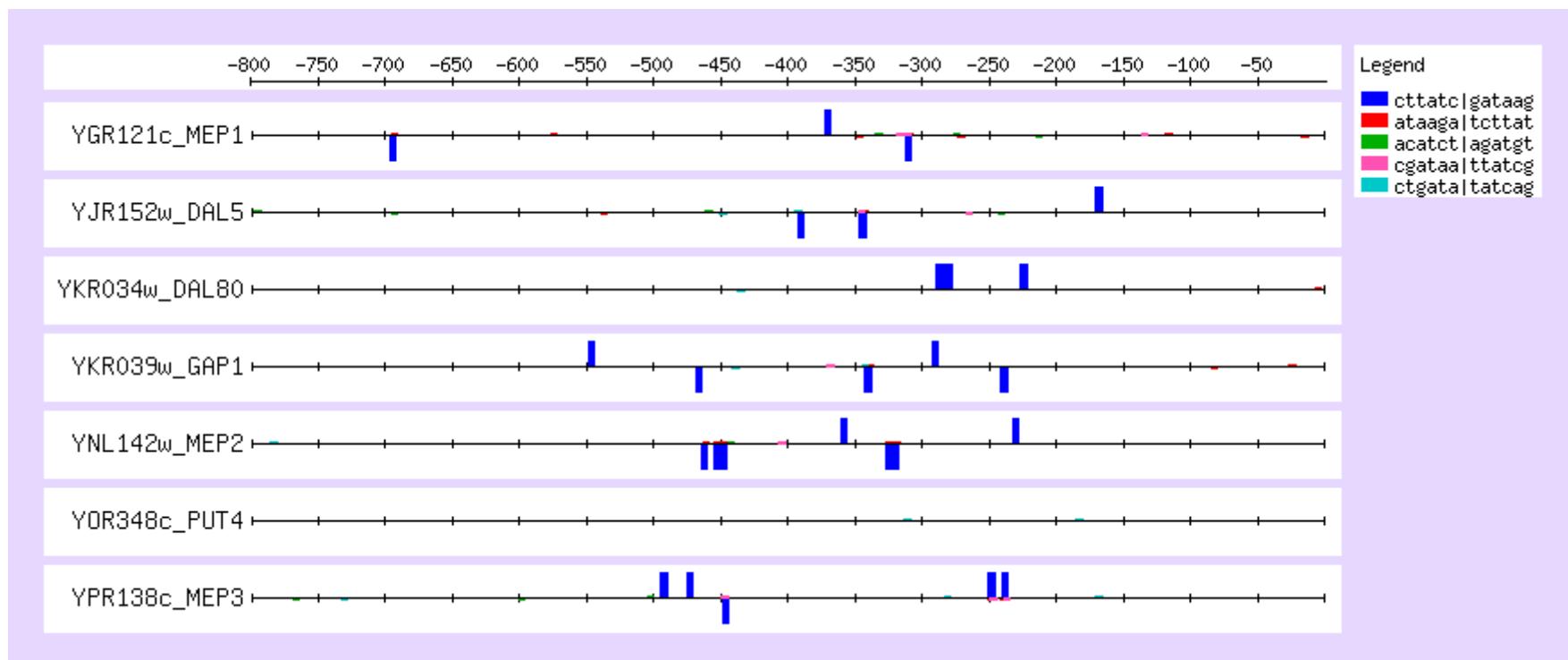
Impossible d'afficher l'image. Votre ordinateur manque peut-être de mémoire pour ouvrir l'image ou l'image est endommagée. Redémarrez l'ordinateur, puis ouvrez à nouveau le fichier. Si le x rouge est toujours affiché, vous devrez peut-être supprimer l'image avant de la réinsérer.

Genes
Known motifs
GATAAg

DAL5, DAL80, GAP1, MEP1, MEP2, MEP3, PUT4
Factors
Gln3p; Nil1p; Gzf3p; Uga43p

Feature-map of discovered patterns - NIT regulon

- Typical features of yeast GATA-boxes
 - Multiple occurrences per sequences.
 - Occurrences generally appear clustered (at least two with a spacing of 0-60bp).
 - This probably stimulates synergic effects.
- Remark: PUT4 does not contain a single optimal motif



Hexanucleotide analysis of the PHO regulon

Sequence	exp freq	occ	exp occ	P-value	E-value	sig	matching sequences
.....CGTGGG	0.00013	5	0.5	0.00021	4.30E-01	0.36	3
....ACGTGc.	0.00021	9	0.8	2.50E-07	5.20E-04	3.29	5
....ACGTGG.	0.00018	7	0.7	9.00E-06	1.90E-02	1.73	5
...CACGTG..	0.00012	6	0.5	8.90E-06	1.90E-02	1.73	5
.cgCACG....	0.00013	6	0.5	1.40E-05	2.90E-02	1.54	5
ctgCAC....	0.00024	8	1.0	7.80E-06	1.60E-02	1.79	4
....ACGT <u>TT</u> .	0.00061	10	2.4	0.00019	3.90E-01	0.41	5
...CACGT <u>T</u> ..	0.00030	7	1.2	0.00024	5.00E-01	0.3	5
tgc ₄ aa	0.00048	12	1.9	7.40E-07	1.50E-03	2.81	4

Genes

PHO5, PHO8, PHO11, PHO84, PHO81

Known motifs

Factors

CACGTGGG

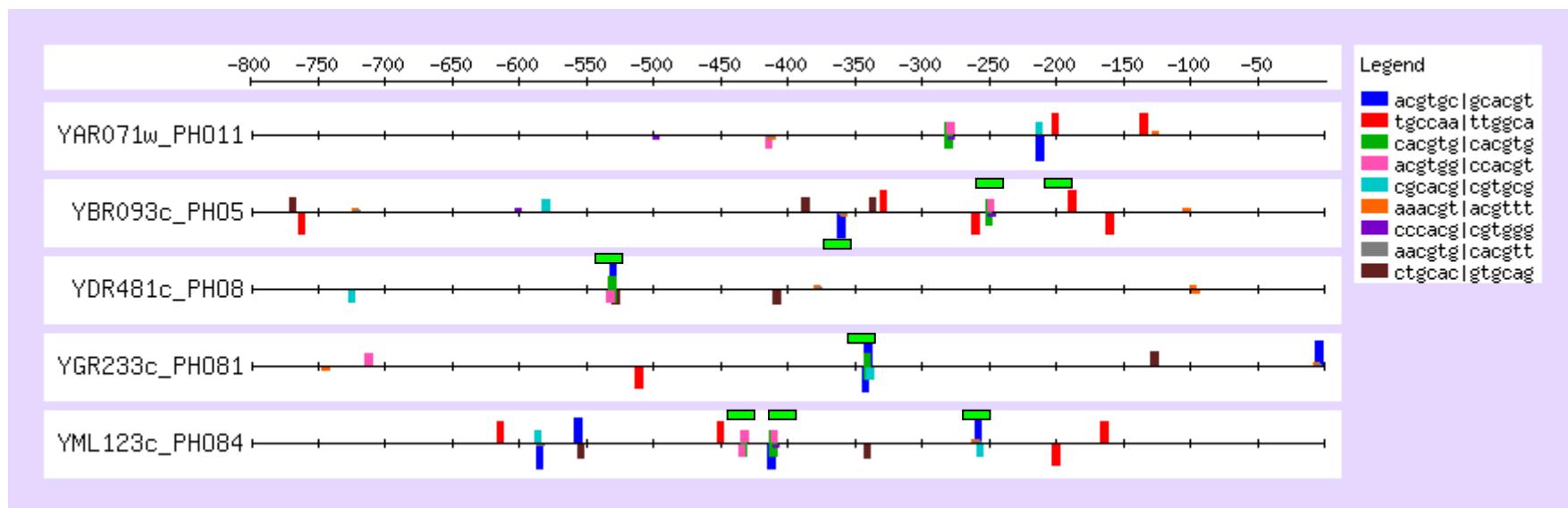
Pho4p (high affinity)

CACGTTTT

Pho4p (medium affinity)

Feature-map of discovered patterns - PHO regulon

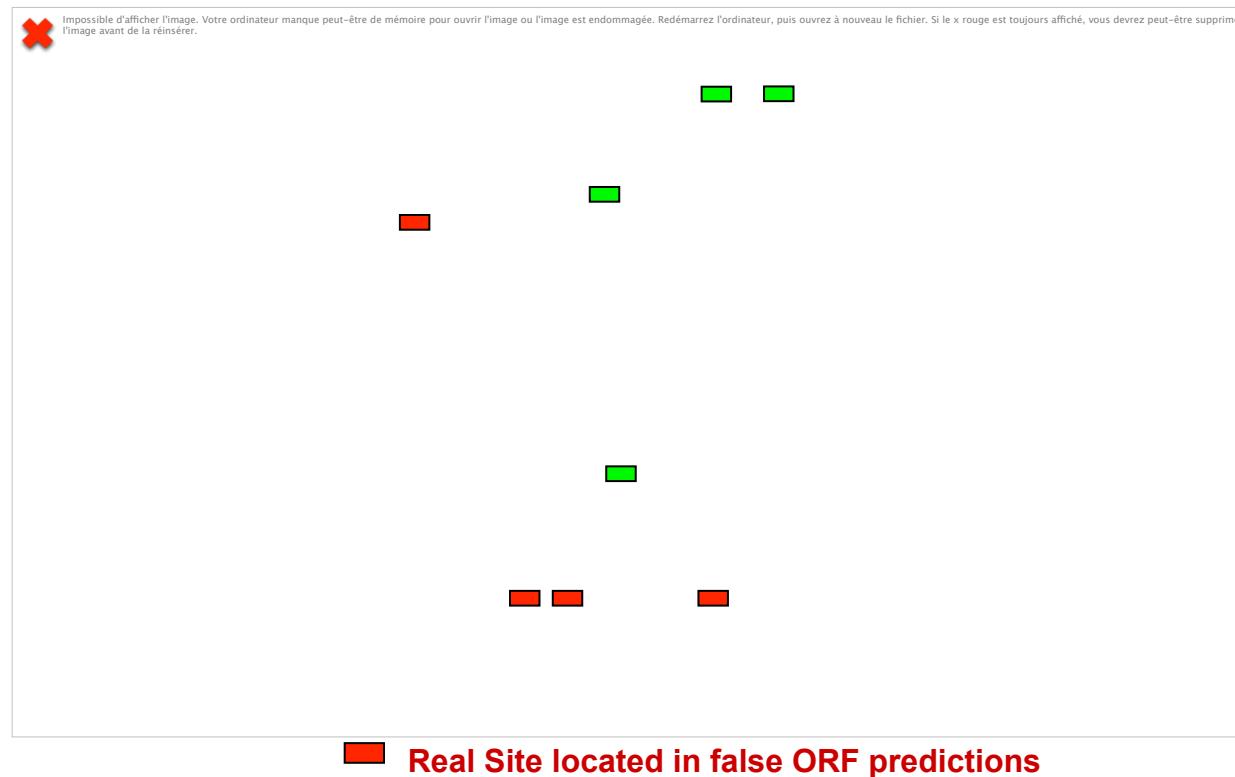
- The feature-map provides a convenient representation of the discovered patterns
 - Each colour represents one pattern.
 - Box height reflects pattern significance.
 - Clusters of mutually overlapping words represent sites larger than 6 bp.
- Green bars were superimposed, to indicate the positions of experimentally proven sites, and compare predictions with experimental knowledge.
 - For PHO11, no site is documented, we can thus not check the predictions.
 - For the other genes, the proven sites are detected as clusters of overlapping words



■ Site with experimental evidence █

Clipping of upstream coding sequences

- In the particular case of the yeast *Saccharomyces cerevisiae*, the initial annotations were over-predictive, and contained many false ORFs.
- Clipping upstream ORFs sometimes results in a loss of information.
- In the case of the PHO family, half of the known sites would be clipped, and the pattern discovery program would not identify any significant motif anymore.
- This problem has recently been solved, with the new annotations based on comparative genomics.



Hexanucleotide analysis of the MET regulon

Sequence	exp freq	occ	exp occ	P-value	E-value	sig	matching sequences
..ACGTGa	0.00033	13	2.9	1.00E-05	2.20E-02	1.67	9
.CACGTG.	0.00012	13	1.0	6.90E-11	1.40E-07	6.84	9
tCACGTG.	0.00033	13	2.9	1.00E-05	2.20E-02	1.67	9
tCACGTGa	consensus						
....TGTGGc	0.00027	10	2.3	1.50E-04	3.20E-01	0.49	7
...CTGTGG.	0.00022	11	1.9	4.30E-06	8.90E-03	2.05	8
..aCTGTG..	0.00036	12	3.1	9.90E-05	2.10E-01	0.69	9
.aaACTGT...	0.00063	17	5.4	4.90E-05	1.00E-01	0.99	11
aaaACTG....	0.00074	17	6.4	0.00037	7.60E-01	0.12	11
aaaACTGTGGc	consensus						
gcttcc	0.00039	12	3.4	0.00021	4.50E-01	0.35	7

Genes

SAM2, MET6, MUP3, MET30, MET3, MET14, MET1, SAM1, MET17, ZWF1, MET2

Known motifs

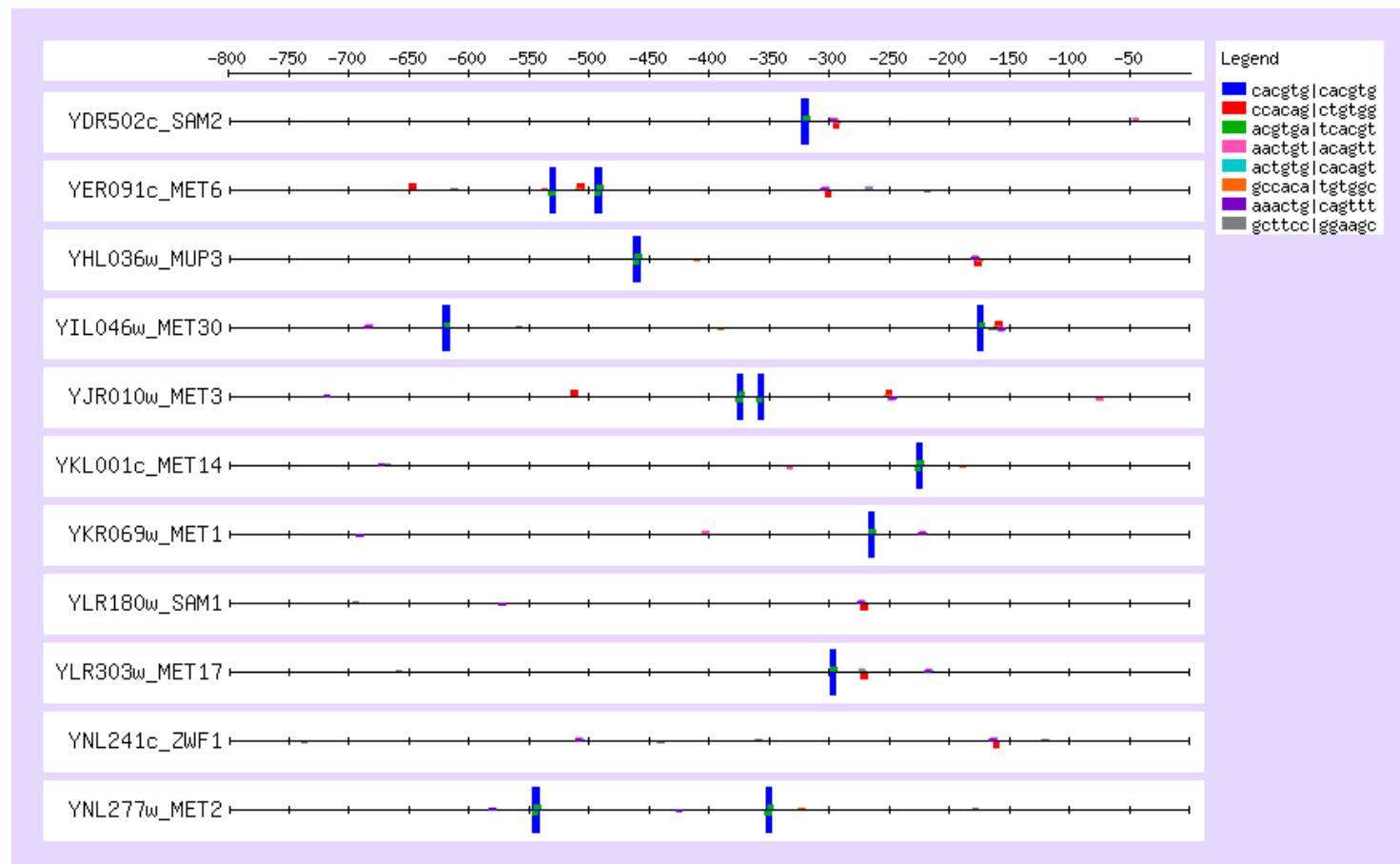
Factors

TCACGTG
AAAACTGTGG

Cbf1p/Met4p/Met28p *Met31p; Met32p*

Feature-map of discovered patterns - MET family

- Two distinct motifs (combinations of words) are apparent.
 - blue-green TCACGTGA Met4p/Met28p/Cbf1p
 - red-violet AAACTGTG Met31p; Met32p
- Multiple clustered motifs are sometimes found, but not always.



Expected frequency calibration

- The results of string-based pattern discovery depend drastically on the choice of a background model.
- Taking the MET family as example
 - With 6nt calibration in intergenic sequences, the Met4p binding site appears at rank 1, and Met31p at rank 3
 - With equiprobable nucleotides, Met4p only appears at rank 20, and Met31p at rank 32. In other terms, they will never be considered as the most interesting motifs
 - With a single-nucleotide calibration, the Met4p appears at rank 4 and Met31p at rank 13. The first motif would thus have been easily detected, but not the second one.

pattern	rev compl	Background model		
		intergenic	Bernoulli	equiprobable
atcacg....cgtgat	9	44	139
gtcacg....cgtgac	5	34	266
.tcacgt...	...acgtga.	2	4	20
..cacgtg..	..cacgtg..	1	3	23
...acgtga.	.tcacgt...	2	4	20
....cgtgac	gtcacg....	5	34	266
....cgtgat	atcacg....	9	44	139
gccaca....tgtggc	7	17	164
.ccacag...	...ctgtgg.	3	13	99
..cacagt..	..actgtg..	6	21	75
...acagtt.	.aactgt...	4	19	32
....cagttt	aaactg....	10	18	33
gcttcc	ggaagc	8	10	77

Effect of oligonucleotide size on the significance

Family	Pattern	oligonucleotide length					
		4	5	6	7	8	9
NIT	aGATAAGa	1.8	4.1	9.1	4.6	0.9	-
MET	gTCACGTG	4.4	4.1	7	8.2	3.2	-
	AAACTGTGg	1.5	2.3	1.6	4.8	5.2	4.9
PHO	CACGTggg	4.7	8.4	4.4	4.3	4.3	-
	aTGCCAA	2.6	1.5	2.6	0.6	-	-
	CTGCAC	-	-	1.7	-	-	-
INO	CAACAAg	2.9	2.1	3.7	1.3	-	-
	cCATGTGAA	-	-	2.7	3.2	6.4	0.4
PDR	tCCGTGGa	1.5	3.3	7.4	6.9	4.2	1.4
	tCCGCGGa	6.9	7.1	4.5	5.6	1.8	1
GCN4	GCNgGTGACTCa	5.4	8.8	8.2	7.7	4.7	-
	CAGCGGta	3.3	3.5	4	0.6	-	-
YAP	CATTACTAA	-	-	1	2.3	2.1	3.2
	cCGTTCC	0.1	0.5	3.3	0.3	-	-
YAP (400bp)	cATTACTAA	-	-	0.7	4.5	2.5	3.5
	cCGTTCC	0.8	0.5	2.4	0.7	0.2	-
TUP	gtGGGGta	10.1	9	8.6	5.6	3	-
	catAGGCAC	3.3	3.3	4.3	2.6	3.3	1.7

oligo-analysis results with known regulons ($\text{sig} > 1$)

Family	Factor	DNA-binding Domain	Known motifs	oligont	reverse oligont	score
NIT	GATA factors	Zn finger	GATAAG	TCTTATCT	AGATAAGA	20.0
MET	Cbf1p/Met4p/Met28p	bHLH/bLZ/bLZ	TCACGTG	CACGTGAT	ATCACGTG	9.0
	Met31p, Met32p	Zn finger	AAACTGTGG	CACGTGAC AACTGTGGCG	GTCACGTG CGCCACAGTT	9.0 3.6
PHO	Pho4p (high affinity)	bHLH	GCACGTGGG	CCCACGTGCG	CGCACGTGGG	4.4
	Pho4p (medium affin.)	bHLH	GCACGTTTT	AAACGTGCG TGCCAA CTGCAC	CGCACGTGTT TTGGCA GTGCAG	4.4 2.6 1.8
PDR	Pdr1p, Pdr3p	Zn ₂ Cys ₆ binuclear cluster	t _y tCCGYGG _y	TCCGTGGAA TCCGCGG	TTCCACGGA CCGCGGA	7.4 4.5
GCN4	Gcn4p	bZip	RRTGACTCTT	ATGACTCA	TGAGTCAT	8.5
				AGTGACTCA	TGAGTCACT	8.5
				ATGACTCT	AGAGTCAT	8.5
				ATGACTCC	GGAGTCAT	8.5
				ATGACTA	TAGTCAT	3.8
				CCGCTG	CAGCGG	3.7
				GCCGGT	ACCGGC	1.3
INO	Ino2p/Opi1p	bHLH/leucine zipper	CATGTGAAWT	CAACAACG CAACAAG TTCACATG	CGTTGTTG CTTGTG CATGTGAA	3.8 3.8 2.8
HAP 2/3/4	Hap2/3/4/5p		CCAAY	AGAGAGA	TCTCTCT	2.8
GAL4	Gal4p	Zn ₂ Cys ₆ binucl. cluster	CGGn ₁₁ CCG	no significant pattern		

Hexanucleotide analysis of the GAL family

Sequence	exp freq	occ	exp occ	P-value	E-value	sig	matching sequences
agacat	0.00044	9	2.1	0.00033	0.69	0.16	4

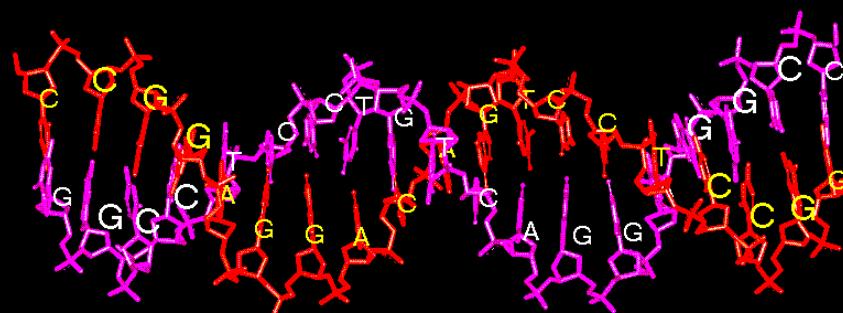
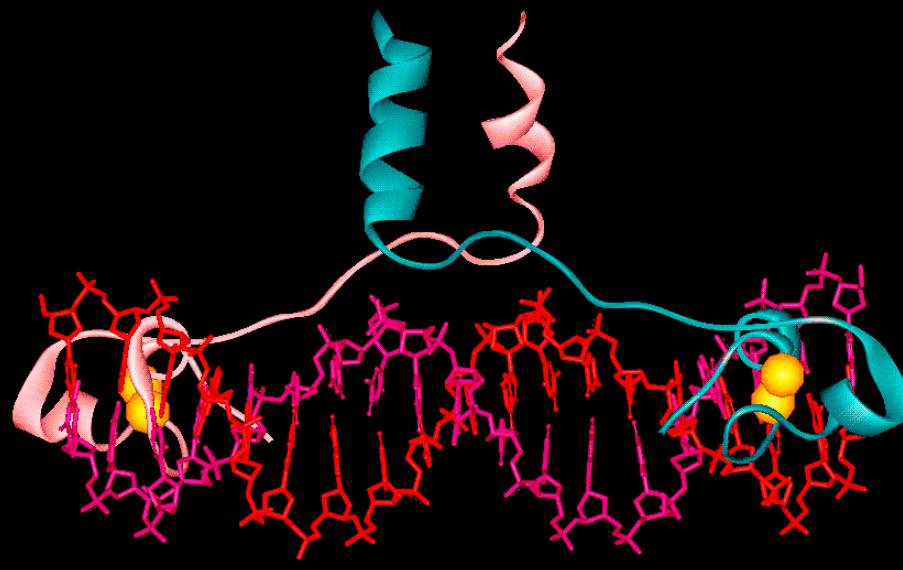
Genes *GAL1, GAL2, GAL7, GAL80, MEL1, GCY1*

Known motifs *Factors*

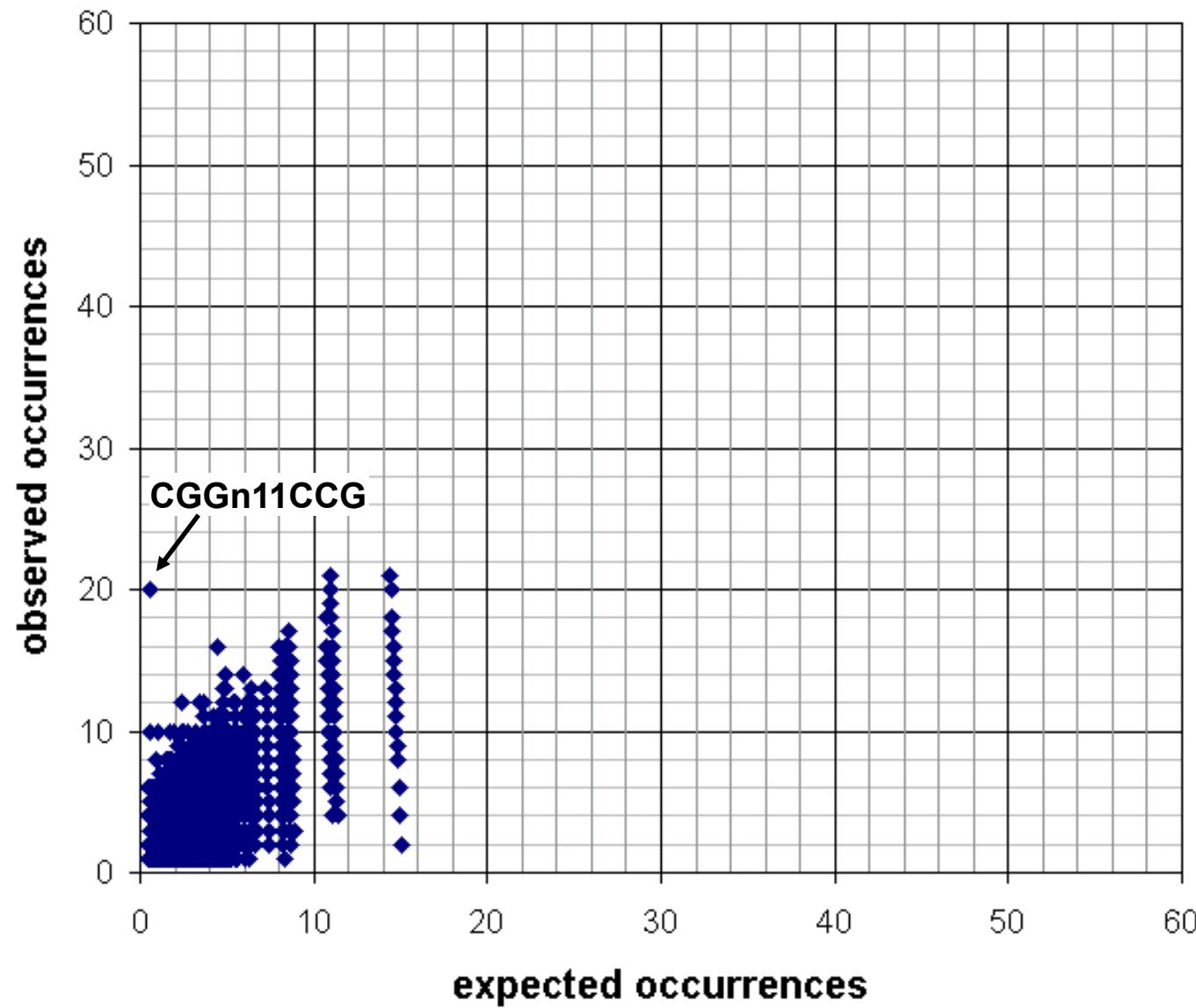
CGGn₅wn₅CCG *Gal4p*

- With the GAL family, the program returns a single pattern.
 - The significance of this pattern is very low.
 - This level of significance is expected at random ~ once per sequence set.
 - This can be considered as a negative result: the program did not detect any really significant pattern.
- Why did the program fail to discover the GAL4 motif ?

DNA/protein interface of the yeast transcription factor Gal4p



**spaced pairs of trinucleotides
in upstream sequences of the GAL family**



Dyad analysis of the *GAL* family

Sequence	exp freq	obs occ	exp occ	P-value	E-value	sig
..GGa.....CCG.	0.00006	10	0.5	2.70E-10	1.20E-05	4.92
.CGG.....Cga	0.00006	10	0.5	4.80E-10	2.10E-05	4.68
.CGG.....CCG.	0.00007	20	0.6	2.10E-12	9.20E-08	7.03
.CGG.....tCC..	0.00006	10	0.5	2.70E-10	1.20E-05	4.92
.CGG.....cgC...	0.00004	6	0.4	5.30E-06	2.30E-01	0.64
tCG.....CCG.	0.00006	10	0.5	4.80E-10	2.10E-05	4.68
cCG.....CCG.	0.00005	6	0.4	6.40E-06	2.80E-01	0.55
yCGGa.....ckCCGa						
AGA.....CCG	0.00010	8	0.9	7.00E-06	3.10E-01	0.51
CCG.GCG	0.00005	6	0.5	9.30E-06	4.00E-01	0.39

Genes

GAL1, GAL2, GAL7, GAL80, MEL1, GCY1

Known motifs

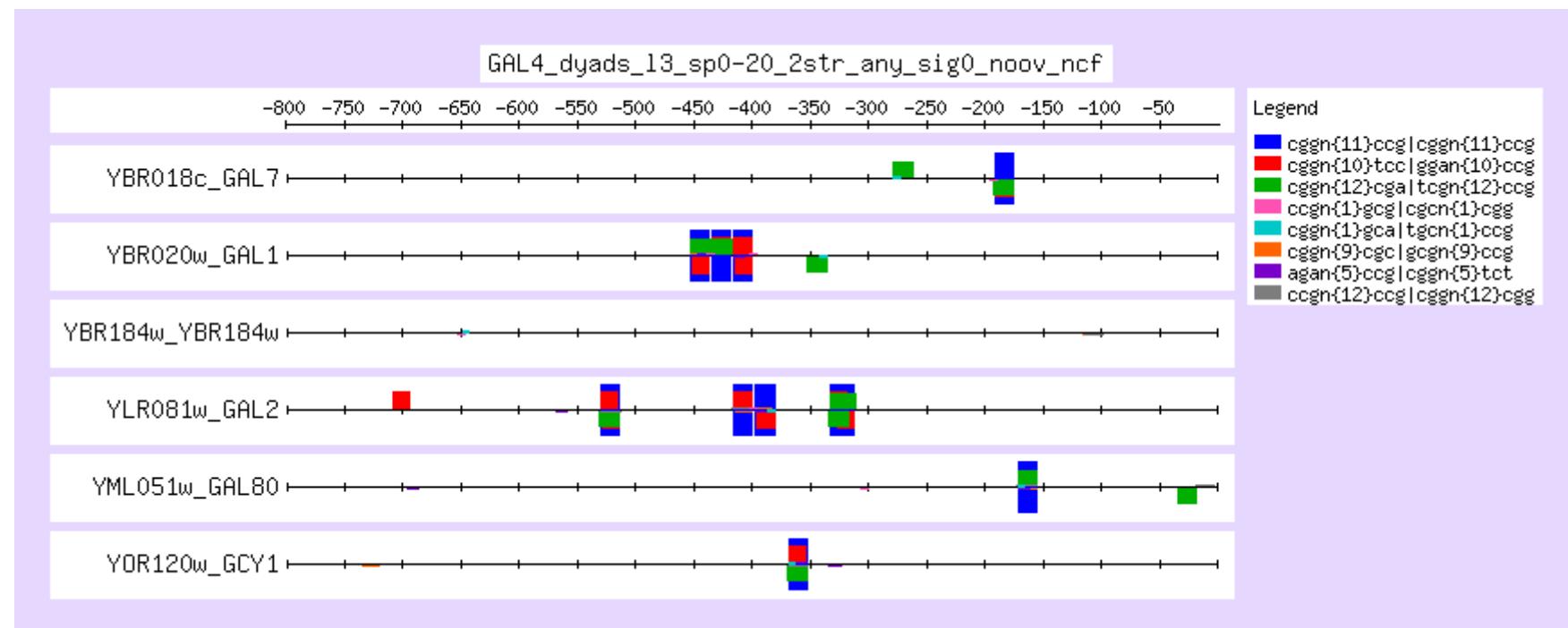
Factors

CGGn₅wn₅CCG

Gal4p

Feature-map of discovered patterns - GAL family

- Clusters of overlapping dyads indicates that conservation extends over 3 bp on each side of the dyad.
- Some genes, but not all, contain multiple motifs (synergic effect).

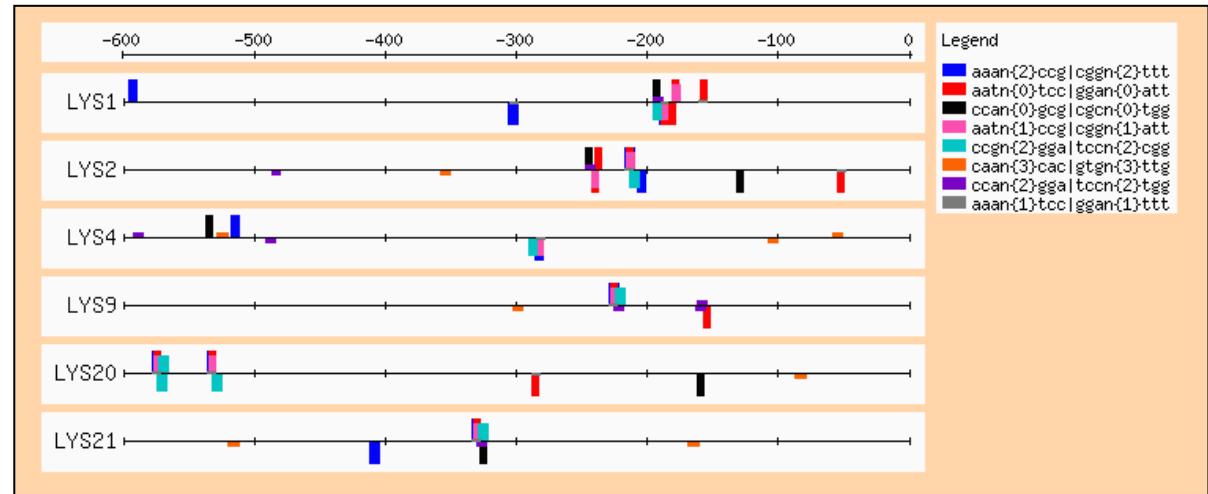


Dyad analysis: regulons of Zn cluster proteins

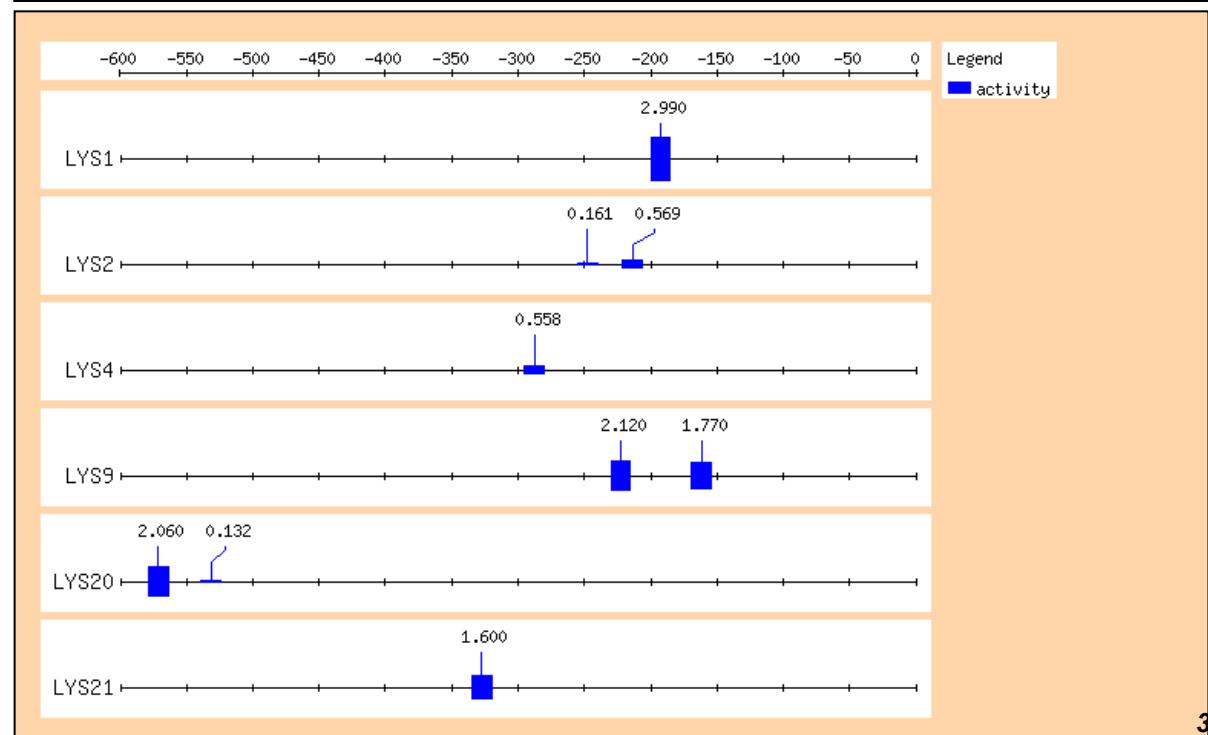
FACTOR	# genes	KNOWN MOTIFS	DYADS	REVERSE DYADS	SCORE
GAL4	6	CGGn ₁₁ CCG	TCGGAn ₉ TCCGG TCGGCGCAGAn ₄ TCCGG	CCGGAn ₉ TCCGA CCGGAn ₄ TCTGCGCCGA	7.8 7.8
HAP1	9	CGGnnntanCGG	GGAn ₅ CGGC GGGGGn ₁₂ GGC CCTn ₁₀ GGC	GCCGn ₅ TCC GCCn ₁₂ CCCCC GCCn ₁₀ AGG	1.8 1.4 1.1
LEU3	5	RCCggnncGGY	CCGn ₃ CCG	CGGn ₃ CGG	1.0
LYS	6	wwwTCCrnyGGAwWW	AAATTCCG TCCGCTGGA	CGGAATTT TCCAGCGGA	1.9 1.0
PDR	6	tytCCGYGGary	CTCCGTGGA _A CTCCGCGGA _A	TTCCACGGAG TTCCGCGGAG	6.7 6.7
PPR1	3	wyCGGnnwwykCCGaw		CGGn ₆ CCG	0.5
PUT3	2	yCGGnangcgnannnCCGa	CGGn ₁₀ CCG	CGGn ₁₀ CCG	1.2
UGA3	3	aaarccgcsggcggssawt	CGGn ₁₄ AGG GCCn ₁₁ TCC	CCTn ₁₄ CCG GGAn ₁₁ GGC	1.7 1.0
UME6	25	tagccgccga	TCGGCGGCTA	TAGCCGCCGA	4.9
CAT8	5	CGGnnnnnnGGA	CGGn ₄ ATGGAA	TTCCATn ₄ CCG	6.0

Comparison of discovered patterns with known sites (LYS family)

Patterns discovered
by dyad analysis

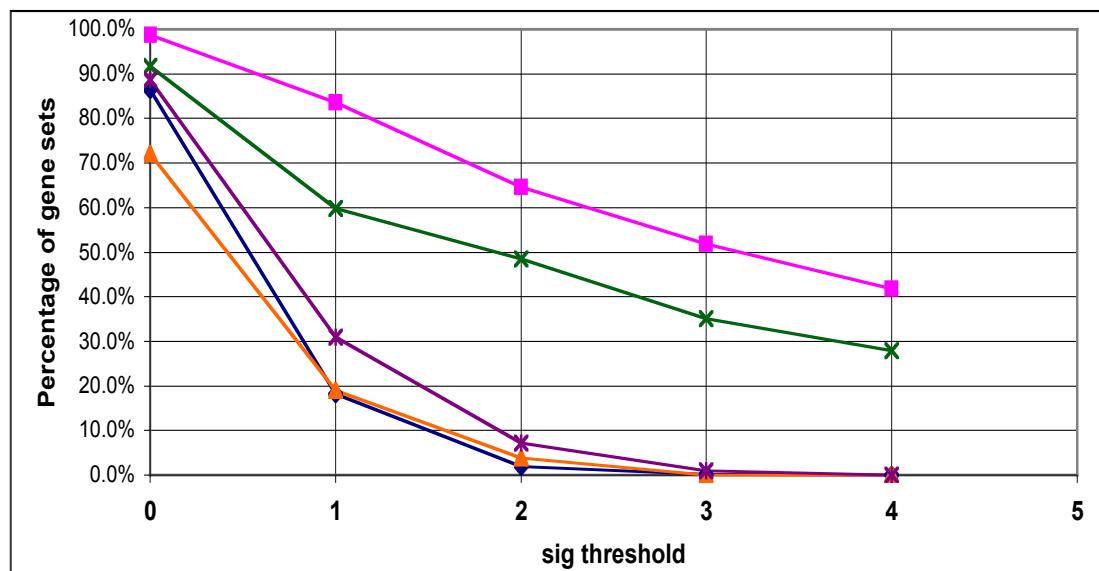
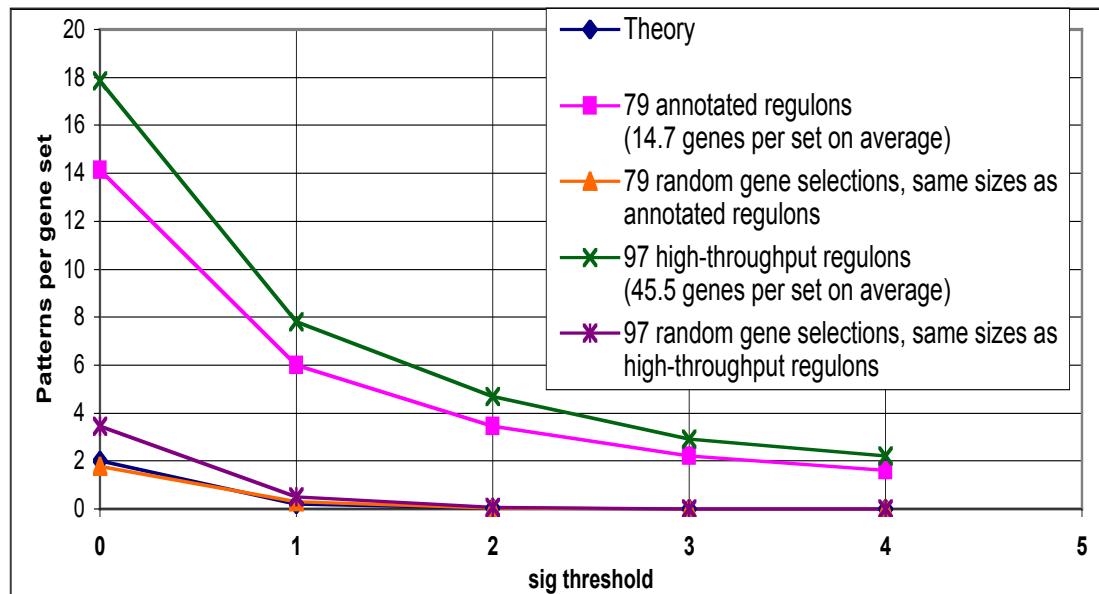


Experimental
measurement of
activity



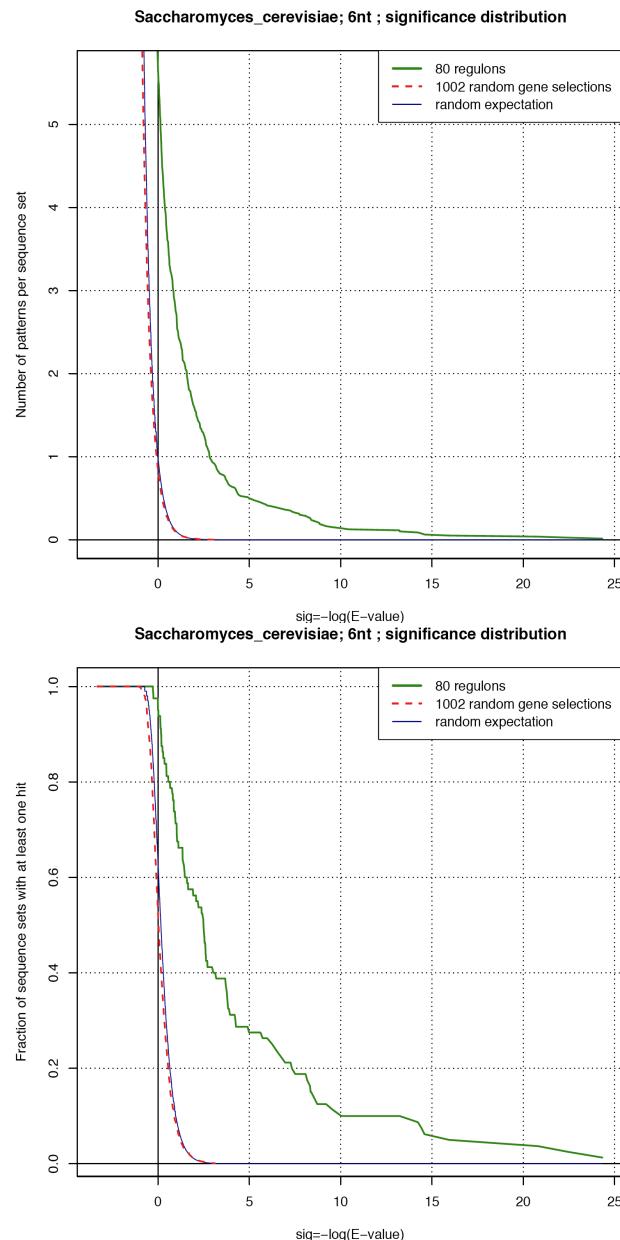
Quantitative evaluation of pattern discovery results

Validation of pattern discovery with yeast regulons

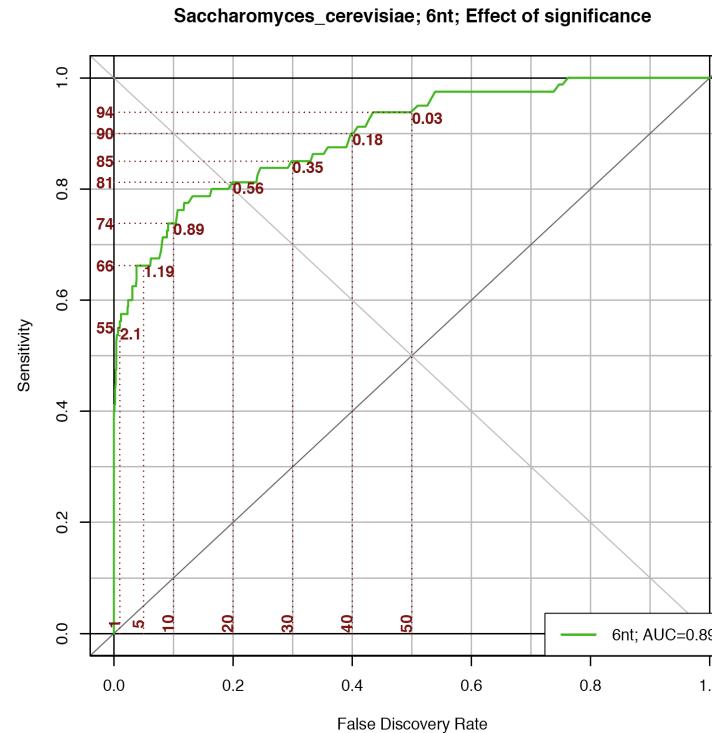


- These figures regroup patterns detected with
 - oligo-analysis*
 - dyad-analysis*
- Regulons were collected from TRANSFAC and aMAZE.
- All the regulons with ≥ 5 genes were analyzed.
 - Significant patterns ($\text{sig} \geq 2$) are detected in 65% of the regulons.
- As a negative control, sets of random genes were analyzed.
 - The rate of false positive follows pretty well the statistical expectation.

Assessment of motif discovery in yeast regulons - *Saccharomyces cerevisiae*



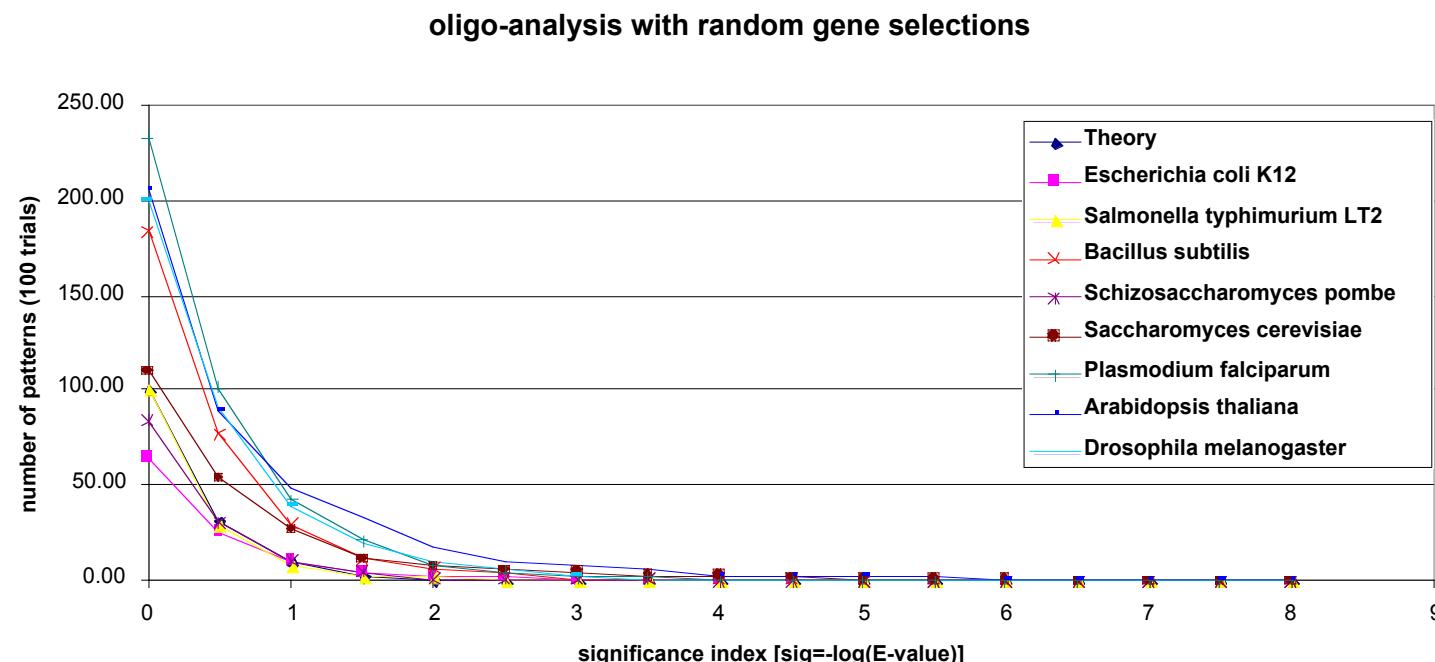
- As a control, we compare the significance of patterns discovered
 - **in regulons** (*positive control*)
 - **in random gene selections** (*negative control*)
- In the yeast *Saccharomyces cerevisiae*
 - The rate of false positive corresponds remarkably well with the theoretical expectation.
 - When the score increases,
 - the sensitivity (patterns discovered in regulons) decreases,
 - the specificity increases (less patterns in random selections)



Sand, O., Turatsinze, J. V. and van Helden, J (2008). Evaluating the prediction of cis-acting regulatory elements in genome sequences In *Modern genome annotation: the BioSapiens network* (Springer).

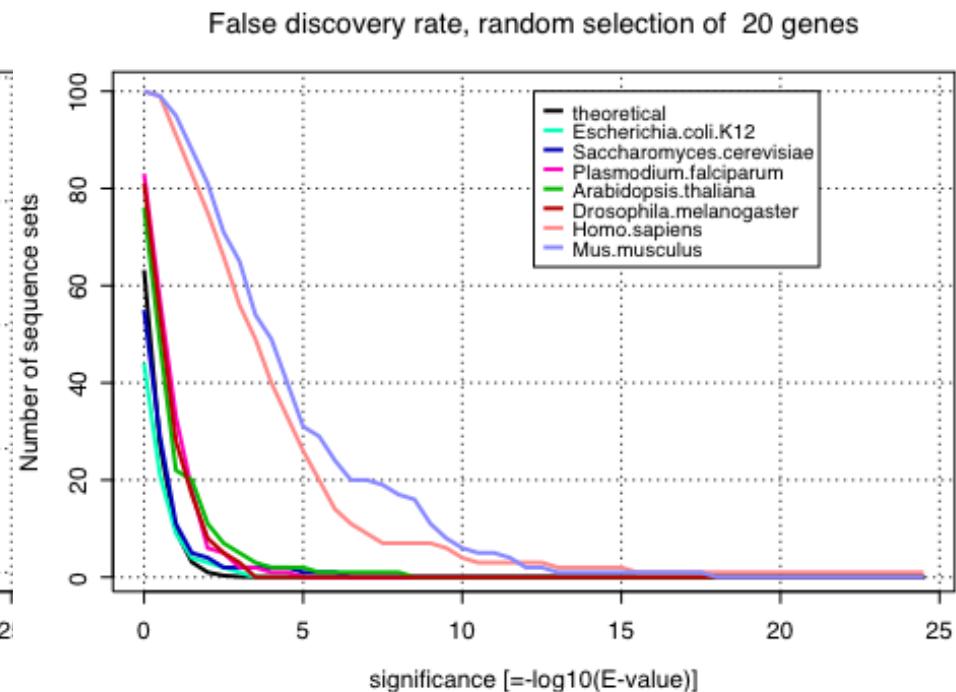
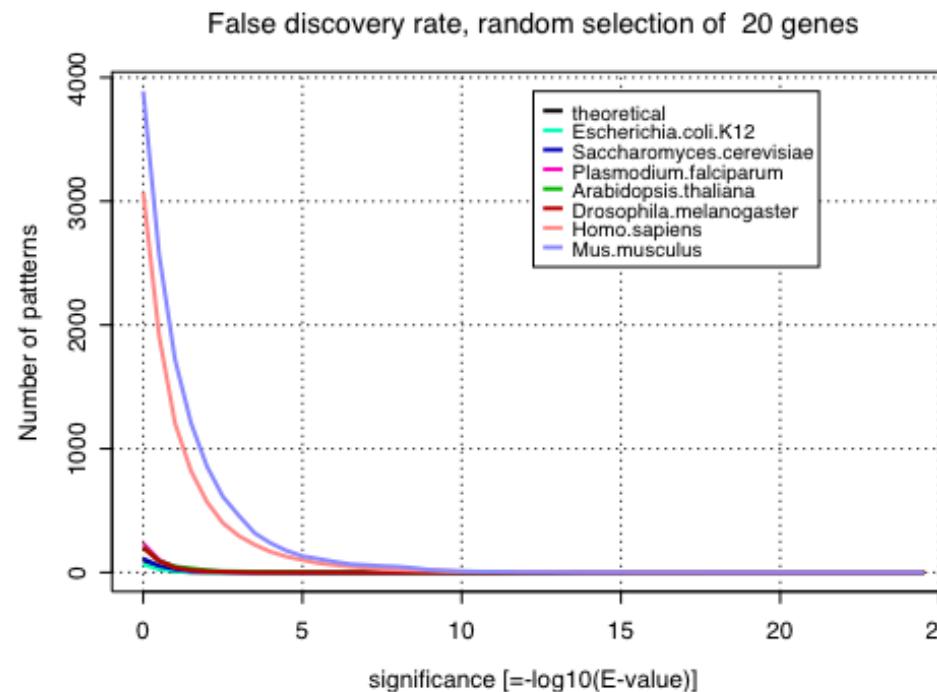
Rate of false positive in different organisms

- The analysis of random gene selections allows to evaluate the rate of false positive returned by a pattern discovery program.
- The rate of false positive is good for microbes (bacteria, yeasts, ...), but increases for multicellular organisms (e.g. the fly *Drosophila*, the plant *Arabidopsis thaliana*, ...).
- The rate of false positive is also higher in the protozoan *Plasmodium falciparum* (the agent of the malaria) than in bacteria and yeast.

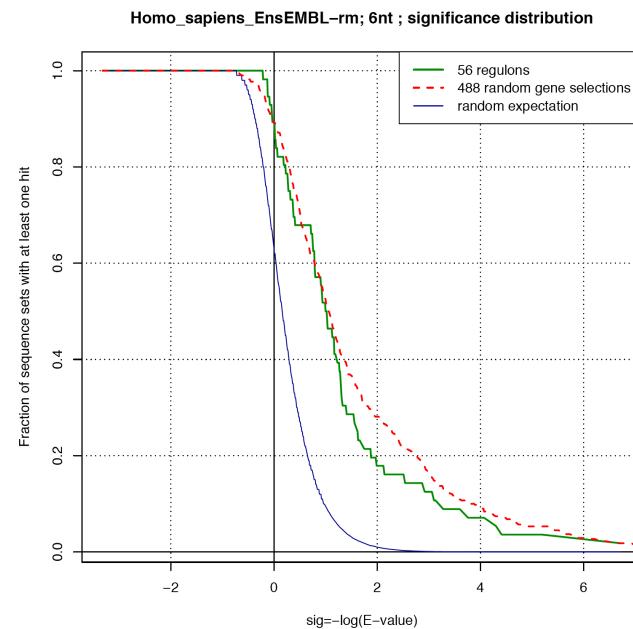
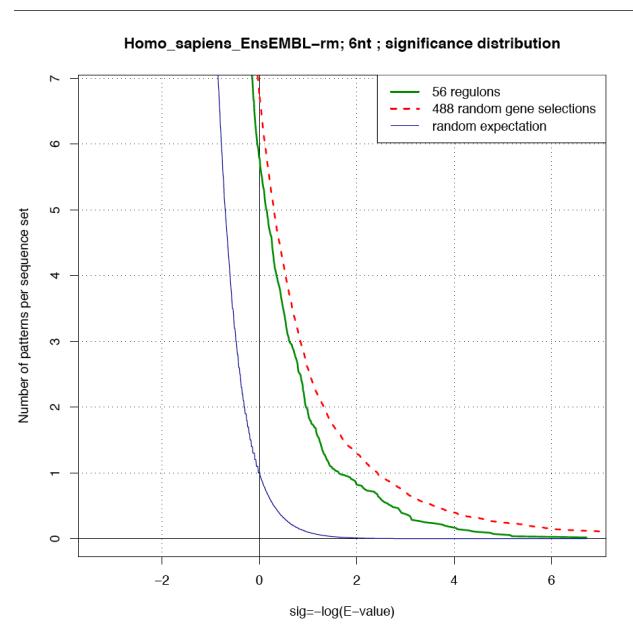


Rate of false positive in higher organisms

- The rate of false positive increases dramatically with higher organisms.
- This is likely to come from
 - a bad treatment of repetitive elements : genome-scale calibration does not account for local frequencies
 - positional heterogeneities : oligonucleotide frequencies depend on the distance from the gene
 - the higher heterogeneity of genomic sequences in these organisms (GC-rich vs AT-rich promoters)
- We are currently developing more elaborate background models to treat this problem.

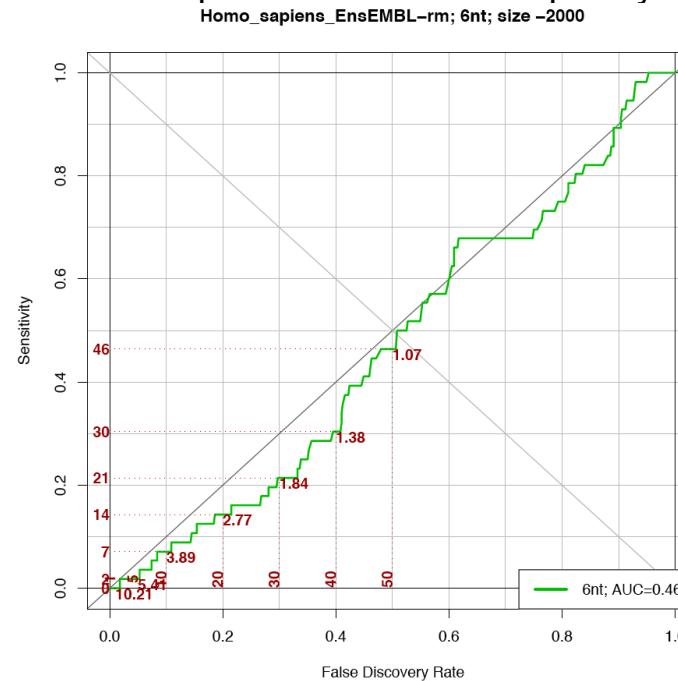


Pattern significance in regulons - *Homo sapiens*



In *Homo sapiens*

- The rate of false positive is much higher than the theoretical expectation
- The number of patterns detected in regulons is still higher, but the significance score is quite inefficient to distinguish between reliable motifs and false positives.
- This indicates that the background model is inadequate to treat the complexity of human



Sand, O., Turatsinze, J. V. and van Helden, J (2008). Evaluating the prediction of cis-acting regulatory elements in genome sequences In *Modern genome annotation: the BioSapiens network* (Springer).

String-based pattern discovery: strengths

- Deterministic (not heuristic) and exhaustive
 - all possible words/dyads are tested
 - ability to return several patterns in a single run
- Speed
 - co-expression clusters are treated within seconds
- Time increases linearly with sequence set
 - Can be applied to very large sequence sets (full genomes)
 - Realistic application: ChIP-seq peaks generally cover several Mb or even tens of Mb.
Such files are treated in a few minutes on a personal laptop.
- Ability to return a negative answer
 - "not a single over-represented pattern in this sequence set"
 - Corollary: very low false positive rate
- Ability to detect over-represented, but also under-represented motifs
 - (e.g. restriction sites in bacterial genomes)
- Pattern assembly refines the result
 - ability to detect some level of degeneracy
(result contains words differing by single substitutions)
 - ability to detect motifs larger than the oligonucleotide size
(result contains strongly overlapping words)

String-based pattern discovery: weaknesses

- No direct treatment of pattern degeneracy
 - NB: degenerated words can be analyzed with similar statistics, but it is not tractable due to the increase of the number of patterns: 15k possible words of length k.
- String patterns are poor descriptions for genome-scale pattern matching.
 - Matrices are more appropriate to describe the weight of each substitution at a given position.
- Solution
 - string-based approach for pattern discovery (RSAT programs *oligo-analysis*, *dyad-analysis*, *position-analysis*, *local-words*).
 - use discovered strings as seeds for building a matrix, which can be used for pattern search (RSAT program *matrix-from-patterns*)

Position-analysis

Regulatory Sequence Analysis

Examples of applications

Analysis of cell cycle data : results

family	oligo-analysis				dyad-analysis (non-coding dyad frequency calibration)					
	word	reverse	clpt	sig	remark	dyad	reverse	clpt	sig	remark
CLN2	TACGCGAA	.	TTCGCGTA	30.5	MBF; SBF variant	TTTACGCGAAAA	TTTCGCGTAAA		29.0	MBF; SBF variant
	TACGCGTA	.	TACGCGTA	30.5	MBF; SBF	GAAAACGCGTAAA	TTTACGCGTTTC		29.0	MBF; SBF
	TTCGCGTCG	CGACGCGAA		30.5	MBF; SBF variant	TTTCGCGTCA	.	TGACGCGAAAA	29.0	MBF; SBF variant
	AAACGCGAA	.	TTCGCGTTT	30.5	MBF; SBF variant	TTTACGCGTCA	.	TGACGCGTAAA	29.0	MBF; SBF
	TTCGCGTCA	TGACGCGAA		30.5	MBF; SBF variant	CGACGCGAAAA	TTTCGCGTCG		29.0	MBF; SBF variant
	TGCCAA	TTGGCA		1.8		GAAAACGCGTCA	.	TGACGCGTTTC	8.1	MBF; SBF
	ATCAAG	CTTGAT		1.3		AAAn8CGC	GCGn8TTT		1.9	
Y' (purged)	CTCGTC	GACGAG		1.8		CAAn5CGC	GCGn5TTG		1.1	
	AGTATC	GATACT		1.2		AGTnGAG	CTCnACT		3.0	
						CAGn{10}ATC	GATn{10}CTG		2.0	
histone (purged)	CGCCCG	CGGGCG		2.6		ATCn{12}GAG	CTCn{12}GAT		1.2	
	CCAGAA	TTCTGG		1.7	Mcm1	GCGn8AGAAC	GTTCTn8CGC		3.0	
						CGCCCG	CGGGCG		1.3	
Cell cycle MET	TGCCACAGTT	AACTGTGGCA		10.1	Met31; Met32	ATTn2GCG	CGCn2AAT		1.3	
	TCACGTGA	TCACGTGA		10.1	Met4/Met28/Cbf1	GCCACAGTT	AACTGTGGC		8.6	Met31; Met32
	ACAGAG	CTCTGT		1.9		GTCACGTGAC	GTCACGTGAC		6.9	Met4/Met28/Cbf1
	GACTCA	TGAGTC		0.9						
CLB2	CCAAAG	CTTTGG		1.3		CCCn6GAA	TTCn6GGG		2.5	ECB
	CCTTCA	TGAAGG		0.9	NEG	CAAn13GCC	GGCn13TTG		0.9	
						ACCn14AAT	ATTn14GGT		0.9	
MCM	AGAGCA	TGCTCT		1.4		TCCCn4GGGA	TCCCN4GGGA		3.9	ECB variant
	TCCTAA	TTAGGA		1.0	Mcm1	AAAnAGG	CCTnTTT		2.8	ECB ?
						AGGn10ACT	AGTn10CCT		1.2	
SIC1	AACCAGCAA	TTGCTGGTT		20.0	Swi5; Ace2	AACCAGCATGCTGGTT		20.0	Swi5; Ace2
	AGCCAGCAA	TTGCTGGCT		20.0	Swi5; Ace2	AACCAGC	CAGCA TGCTGGCTGGTT		20.0	Swi5; Ace2
	AACCAGCC	GGCTGGTT		8.0	Swi5; Ace2					

Gene clusters from Spellman et al. (1998). Mol Biol Cell 9(12), 3273-97

Pattern discovery : van Helden et al. (2000). Nucleic Acids Res 28: 1808-1818.

Plasmodium erythrocytic cycle

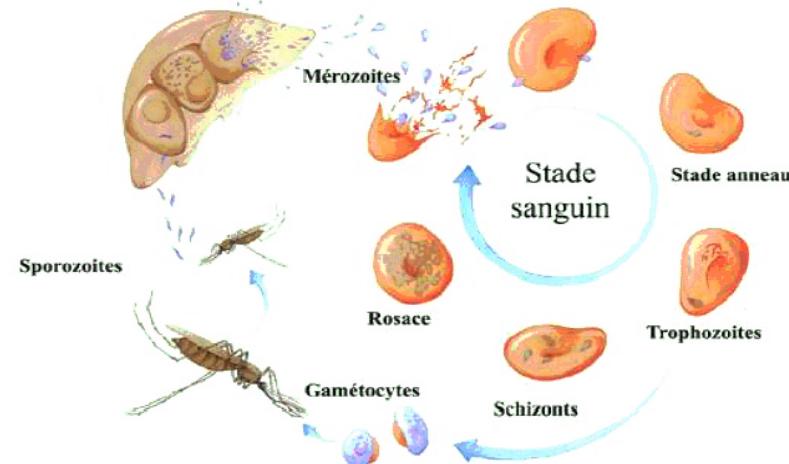
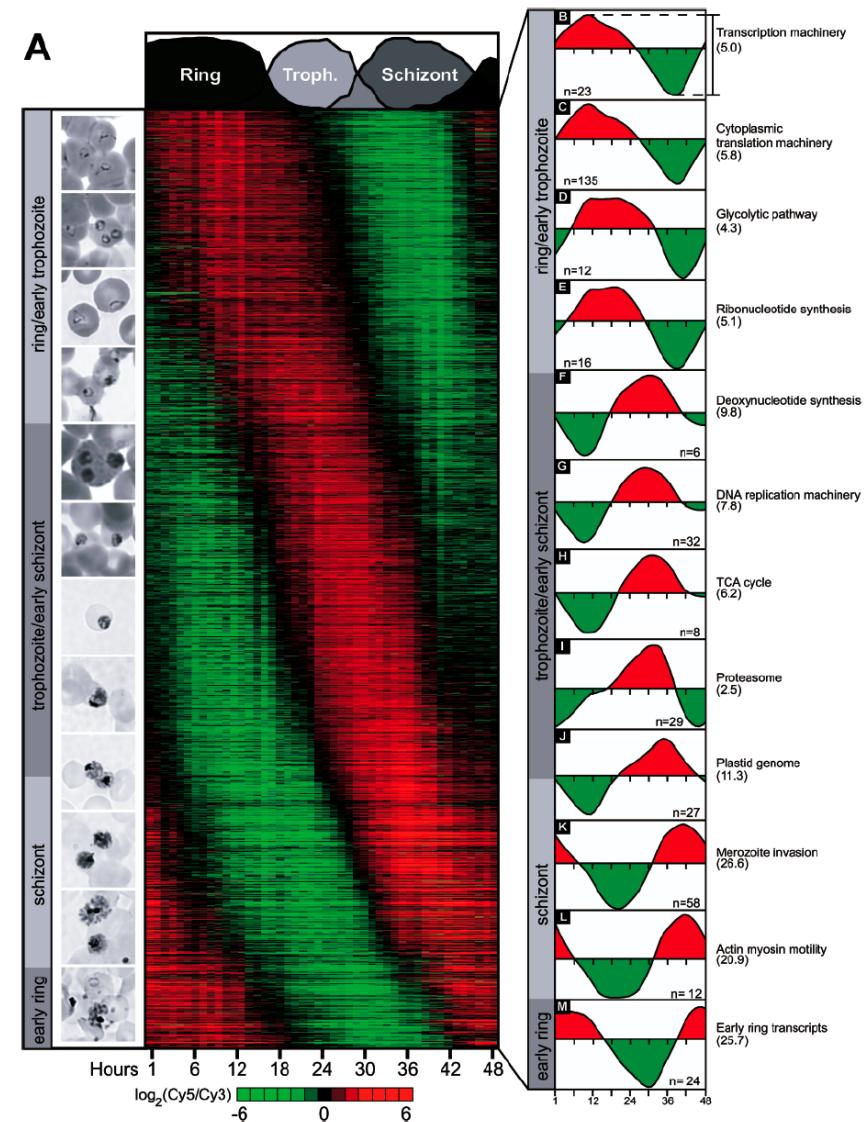
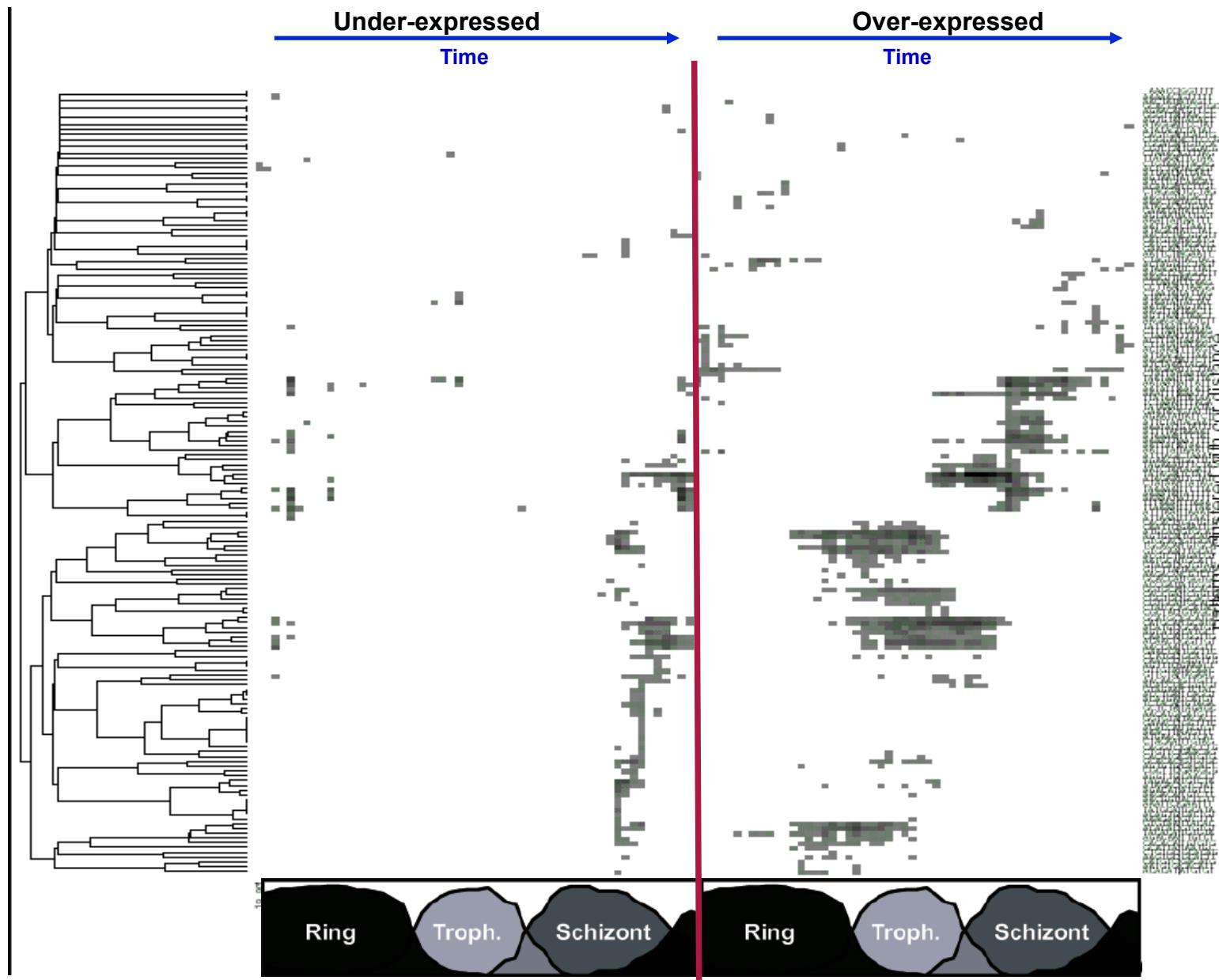


figure 2: Cycle de vie de *Plasmodium falciparum* (source :institut pasteur (France) page web)



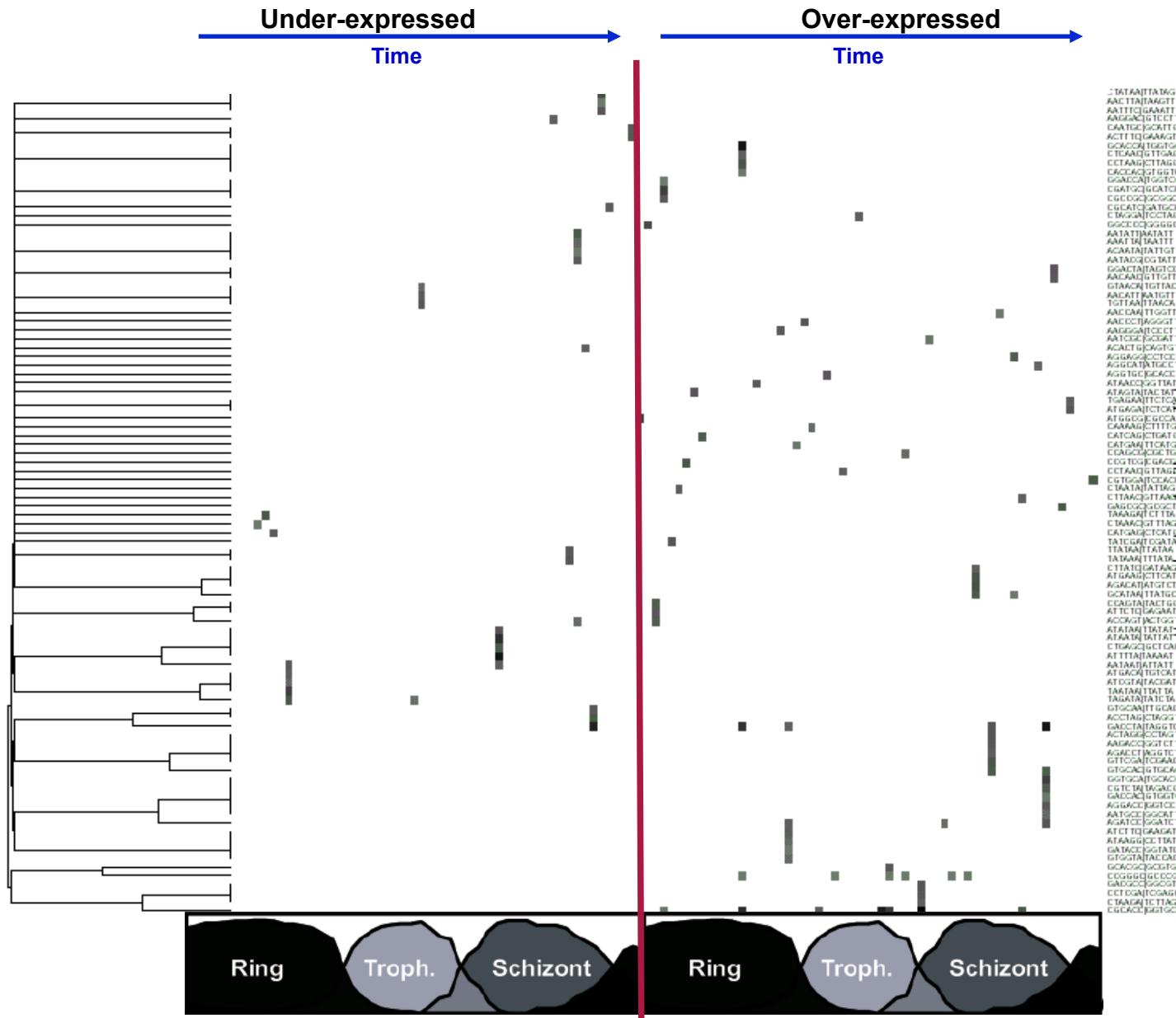
Bozdech et al. (2003). The Transcriptome of the Intraerythrocytic Developmental Cycle of *Plasmodium falciparum*. PLoS Biol 1: E5.

Over-represented oligos in promoters of under- and over-expressed genes at different time points of the erythrocytic cycle of *Plasmodium falciparum*



Erythrocytic cycle in Plasmodium falciparum

Under- and over-expressed oligonucleotides in random gene selections



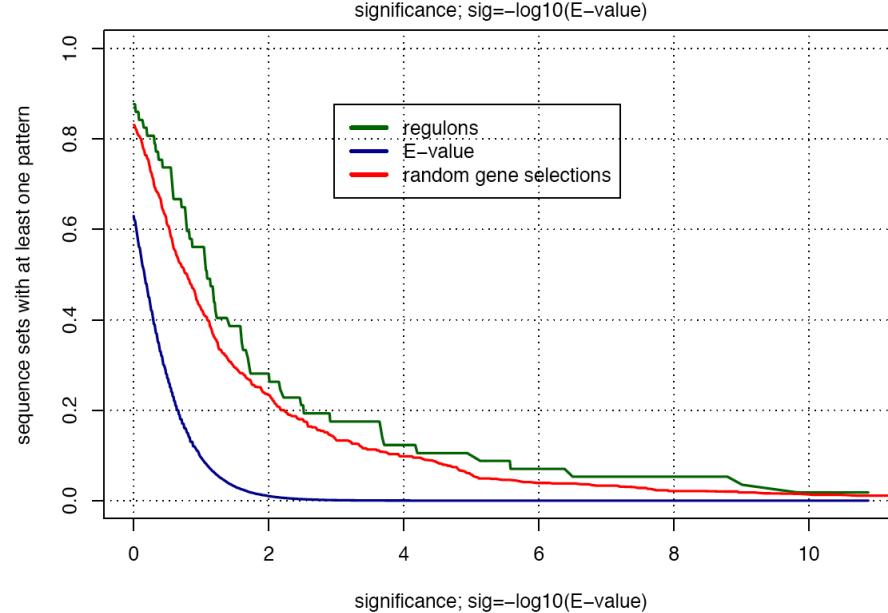
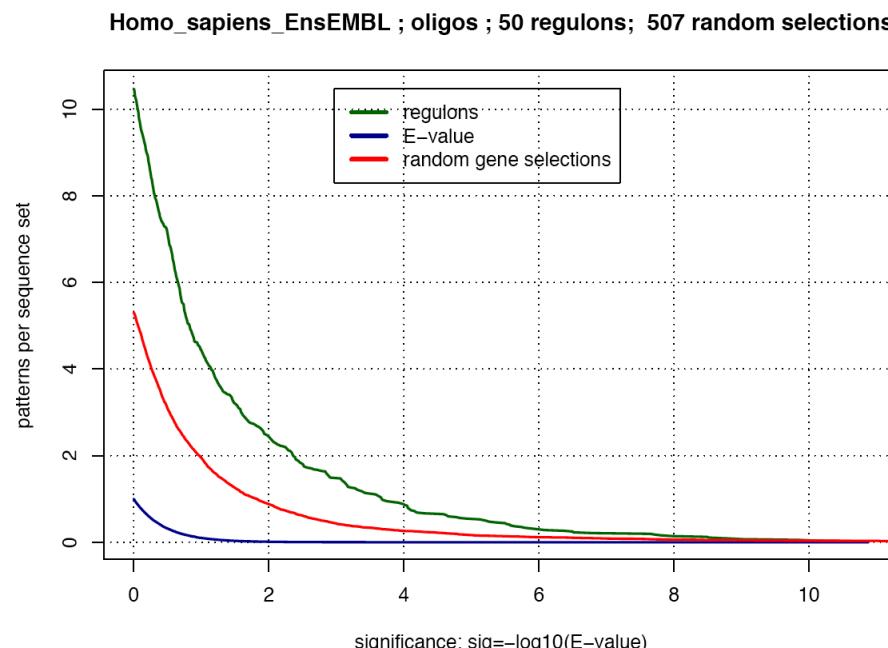
*Essaghir, Vaquero
& van Helden, in prep* 52

Supplementary material

Pattern discovery: string-based algorithms

- Count occurrences observed for each word
- Calculate expected word frequencies
 - Choice of a model :
 - independently distributed nucleotides
(equiprobable or biased alphabet utilization)
 - Markov chain : on basis of subword frequencies
 - External reference (e.g. word frequencies observed in the whole set of upstream sequences)
- Calculate a score for each word
 - obs/exp ratio (very bad)
 - log-likelihood
 - Z-value
 - binomial probability
- Select all words above a defined threshold
 - Statistical criterion for establishing the threshold

Pattern significance in regulons - *Homo sapiens*



In *Homo sapiens*

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- The number of patterns detected in regulons is still higher, but the significance score is quite inefficient to distinguish between reliable motifs and false positives.
- This indicates that the background model is inadequate to treat the complexity of human promoters.