Regulatory sequence analysis

Position-specific scoring matrices (PSSM)

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Consensus representation

- The TRANSFAC database contains 8 binding sites for the yeast transcription factor Pho4p
  - 5/8 contain the core of high-affinity binding sites (CACGTG)
  - 3/8 contain the core of medium-affinity binding sites (CACGTT)
- The IUPAC ambigous nucleotide code allows to represent variable residues.
- 15 letters to represent any possible combination between the 4 nucleotides ($2^4 - 1 = 15$).
- This representation however gives a poor idea of the relative importance of residues.

```
R06098    \TCACACGTGGGA\
R06099    \GGCCACGTGCAG\
R06100    \TGACACGTGGGT\
R06102    \CAGCACGTGGGG\
R06103    \TTCCACGTGCGA\
R06104    \ACGCACGTTGGT\
R06097    \CAGCACGTTTTC\
R06101    \TACCACGTTTTC\

Cons         nnVCACGTKBDn
```

IUPAC ambiguous nucleotide code

A	A	Adenine
C	C	Cytosine
G	G	Guanine
T	T	Thymine
R	A or G	puRine
Y	C or T	pYrimidine
W	A or T	Weak hydrogen bonding
S	G or C	Strong hydrogen bonding
M	A or C	aMino group at common position
K	G or T	Keto group at common position
H	A, C or T	not G
B	G, C or T	not A
V	G, A, C	not T
D	G, A or T	not C
N	G, A, C or T	aNy

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From alignments to weights

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Sequence logo

Count matrix (TRANSFAC matrix F$PHO4_01)

Residue\position	1	2	3	4	5	6	7	8	9	10	11	12
A	1	3	2	0	8	0	0	0	0	0	1	2
C	2	2	3	8	0	8	0	0	0	2	0	2
G	1	2	3	0	0	0	8	0	5	4	5	2
T	4	1	0	0	0	0	0	8	3	2	2	2
Sum	8	8	8	8	8	8	8	8	8	8	8	8

Tom Schneider's sequence logo
(generated with Web Logo http://weblogo.berkeley.edu/logo.cgi)

weblogo.berkeley.edu
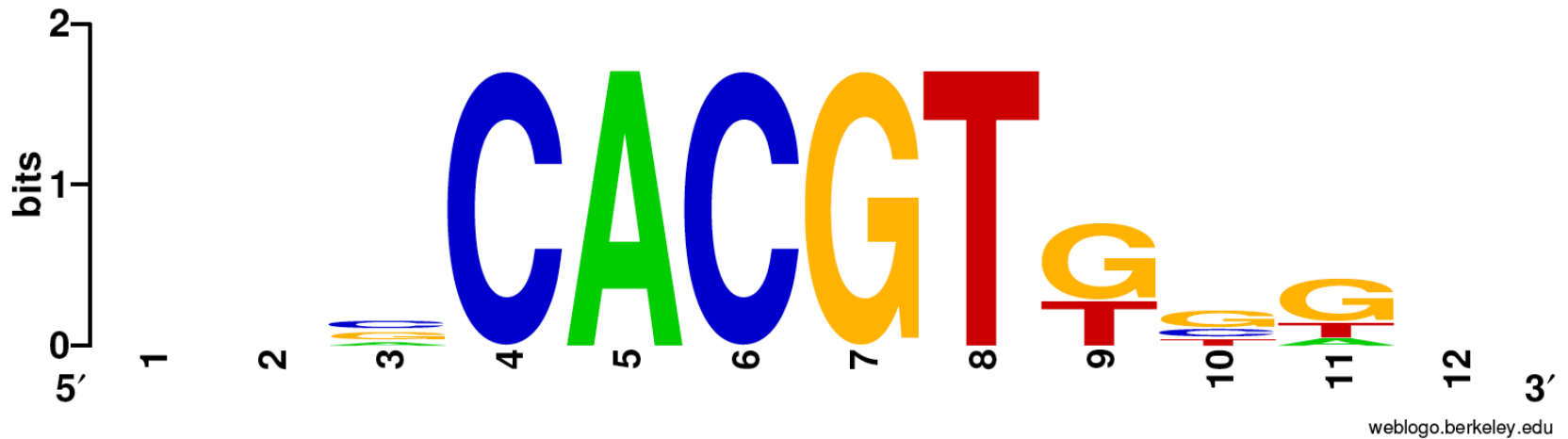
Frequency matrix

Pos	1	2	3	4	5	6	7	8	9	10	11	12
A	0.13	0.38	0.25	0.00	**1.00**	0.00	0.00	0.00	0.00	0.00	0.13	0.25
C	0.25	0.25	**0.38**	**1.00**	0.00	**1.00**	0.00	0.00	0.00	0.25	0.00	0.25
G	0.13	0.25	**0.38**	0.00	0.00	0.00	**1.00**	0.00	**0.63**	**0.50**	**0.63**	0.25
T	0.50	0.13	0.00	0.00	0.00	0.00	0.00	**1.00**	0.38	0.25	0.25	0.25
Sum	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

$$f_{i,j} = \frac{n_{i,j}}{\sum\limits_{i=1}^{A} n_{i,j}}$$

A *alphabet size (=4)*

$n_{i,j,}$ *occurrences of residue i at position j*

p_i *prior residue probability for residue i*

$f_{i,j}$ *relative frequency of residue i at position j*

Reference: Hertz (1999). Bioinformatics 15:563-577.

Corrected frequency matrix

P Pos	1	2	3	4	5	6	7	8	9	10	11	12
A	0.15	0.37	0.26	0.04	**0.93**	0.04	0.04	0.04	0.04	0.04	0.15	0.26
C	0.24	0.24	**0.35**	**0.91**	0.02	**0.91**	0.02	0.02	0.02	0.24	0.02	0.24
G	0.13	0.24	**0.35**	0.02	0.02	0.02	**0.91**	0.02	**0.58**	**0.46**	**0.58**	0.24
T	0.48	0.15	0.04	0.04	0.04	0.04	0.04	**0.93**	0.37	0.26	0.26	0.26
Sum	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

1st option: identically distributed pseudo-weight

$$f'_{i,j} = \frac{n_{i,j} + k/A}{\sum_{i=1}^{A} n_{i,j} + k}$$

2nd option: pseudo-weight distributed according to residue priors

$$f'_{i,j} = \frac{n_{i,j} + p_i k}{\sum_{i=1}^{A} n_{i,j} + k}$$

A alphabet size (=4)

$n_{i,j}$ occurrences of residue i at position j

p_i prior residue probability for residue i

$f_{i,j}$ relative frequency of residue i at position j

k pseudo weight (arbitrary, 1 in this case)

$f'_{i,j}$ corrected frequency of residue i at position j

Reference: Hertz (1999). Bioinformatics 15:563-577.

Weight matrix (Bernoulli model)

Prior	Pos	1	2	3	4	5	6	7	8	9	10	11	12
0.325	A	-0.79	0.13	-0.23	-2.20	1.05	-2.20	-2.20	-2.20	-2.20	-2.20	-0.79	-0.23
0.175	C	0.32	0.32	0.70	1.65	-2.20	1.65	-2.20	-2.20	-2.20	0.32	-2.20	0.32
0.175	G	-0.29	0.32	0.70	-2.20	-2.20	-2.20	1.65	-2.20	1.19	0.97	1.19	0.32
0.325	T	0.39	-0.79	-2.20	-2.20	-2.20	-2.20	-2.20	1.05	0.13	-0.23	-0.23	-0.23
1.000	Sum	-0.37	-0.02	-1.02	-4.94	-5.55	-4.94	-4.94	-5.55	-3.08	-1.13	-2.03	0.19

$$f'_{i,j} = \frac{n_{i,j} + p_i k}{\sum\limits_{r=1}^{A} n_{r,j} + k}$$

$$W_{i,j} = \ln\left(\frac{f'_{i,j}}{p_i}\right)$$

A — alphabet size (=4)
$n_{i,j}$ — occurrences of residue i at position j
p_i — prior residue probability for residue i
$f_{i,j}$ — relative frequency of residue i at position j
k — pseudo weight (arbitrary, 1 in this case)
$f'_{i,j}$ — corrected frequency of residue i at position j
$W_{i,j}$ — weight of residue i at position j

The use of a weight matrix relies on Bernoulli assumption

If we assume, for the background model, an independent succession of nucleotides (Bernoulli model), the weight W_S of a sequence segment S is simply the sum of weights of the nucleotides at successive positions of the matrix ($W_{i,j}$).

In this case, it is convenient to convert the PSSM into a weight matrix, which can then be used to assign a score to each position of a given sequence.

Reference: Hertz (1999). Bioinformatics 15:563-577.

Properties of the weight function

$$W_{i,j} = \ln\left(\frac{f'_{i,j}}{p_i}\right)$$

$$f'_{i,j} = \frac{n_{i,j} + p_i k}{\sum\limits_{i=1}^{A} n_{i,j} + k}$$

$$\sum\limits_{i=1}^{A} f'_{i,j} = 1$$
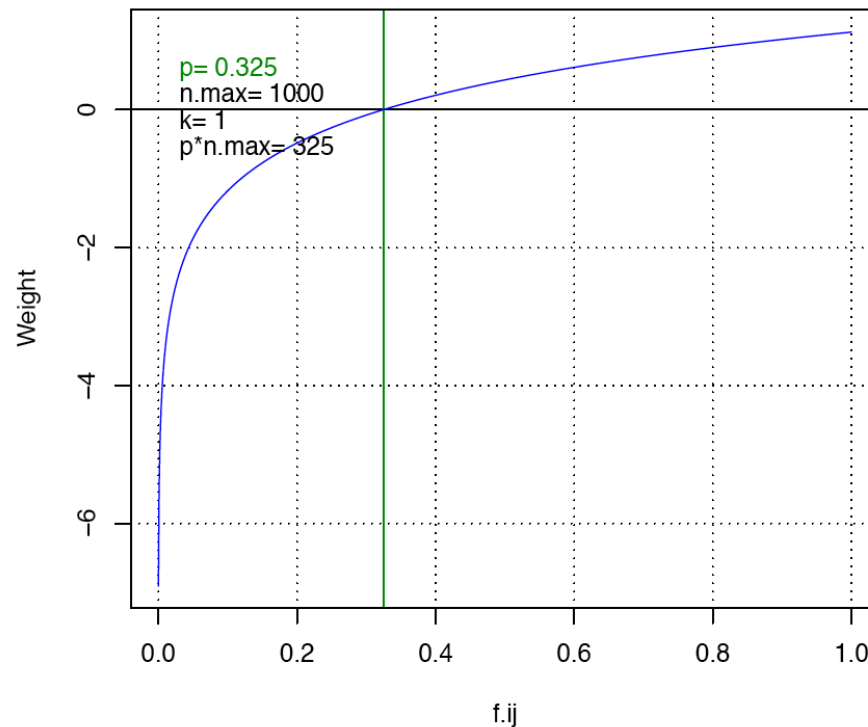
- The weight is
  - *positive* when $f'_{i,j} > p_i$
    (*favourable* positions for the binding of the transcription factor)
  - *negative* when $f'_{i,j} < p_i$
    (*unfavourable* positions)

p= 0.325
n.max= 1000
k= 1
p*n.max= 325

Regulatory sequence analysis

Information content

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Shannon uncertainty

- Shannon uncertainty
  - $H_s(j)$: uncertainty of a column of a PSSM
  - Hg: uncertainty of the background (e.g. a genome)
- Special cases of uncertainty (for a 4 letter alphabet)
  - $min(H)=0$
    - No uncertainty at all: the nucleotide is completely specified (e.g. p={1,0,0,0})
  - $H=1$
    - Uncertainty between two letters (e.g. p= {0.5,0,0,0.5})
  - $max(H) = 2$ *(Complete uncertainty)*
    - One bit of information is required to specify the choice between each alternative (e.g. p= {0.25,0.25,0.25,0.25}).
    - Two bits are required to specify a letter in a 4-letter alphabet.

- R_{seq}
  - Schneider (1986) defines an **information content** based on Shannon's uncertainty.

- R^*_{seq}
  - For skewed genomes (i.e. unequal residue probabilities), Schneider recommends an alternative formula for the information content . This is the formula that is nowadays used.

$$H_s(j) = -\sum_{i=1}^{A} f_{i,j} \log_2(f_{i,j})$$

$$H_g = -\sum_{i=1}^{A} p_i \log_2(p_i)$$

$$R_{seq}(j) = H_g - H_s(j) \qquad R_{seq} = \sum_{j=1}^{w} R_{seq}(j)$$

$$R^*_{seq}(j) = \sum_{i=1}^{A} f_{i,j} \log_2\left(\frac{f_{i,j}}{p_i}\right) \qquad R^*_{seq} = \sum_{j=1}^{w} R^*_{seq}(j)$$

Adapted from Schneider (1986)
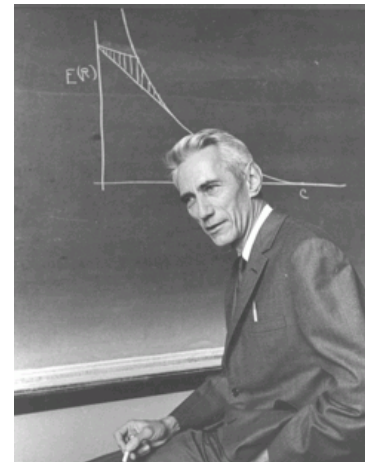
Information content

Prior	Pos	1	2	3	4	5	6	7	8	9	10	11	12
0.325	A	-0.12	0.05	-0.06	-0.08	0.97	-0.08	-0.08	-0.08	-0.08	-0.08	-0.12	-0.06
0.175	C	0.08	0.08	0.25	1.50	-0.04	1.50	-0.04	-0.04	-0.04	0.08	-0.04	0.08
0.175	G	-0.04	0.08	0.25	-0.04	-0.04	-0.04	1.50	-0.04	0.68	0.45	0.68	0.08
0.325	T	0.19	-0.12	-0.08	-0.08	-0.08	-0.08	-0.08	0.97	0.05	-0.06	-0.06	-0.06
1.000	Sum	0.11	0.09	0.36	1.29	0.80	1.29	1.29	0.80	0.61	0.39	0.47	0.04

$$f'_{i,j} = \frac{n_{i,j} + p_i k}{\sum_{i=1}^{A} n_{i,j} + k}$$

$$I_{i,j} = f'_{i,j} \ln\left(\frac{f'_{i,j}}{p_i}\right)$$

$$I_j = \sum_{i=1}^{A} I_{i,j}$$
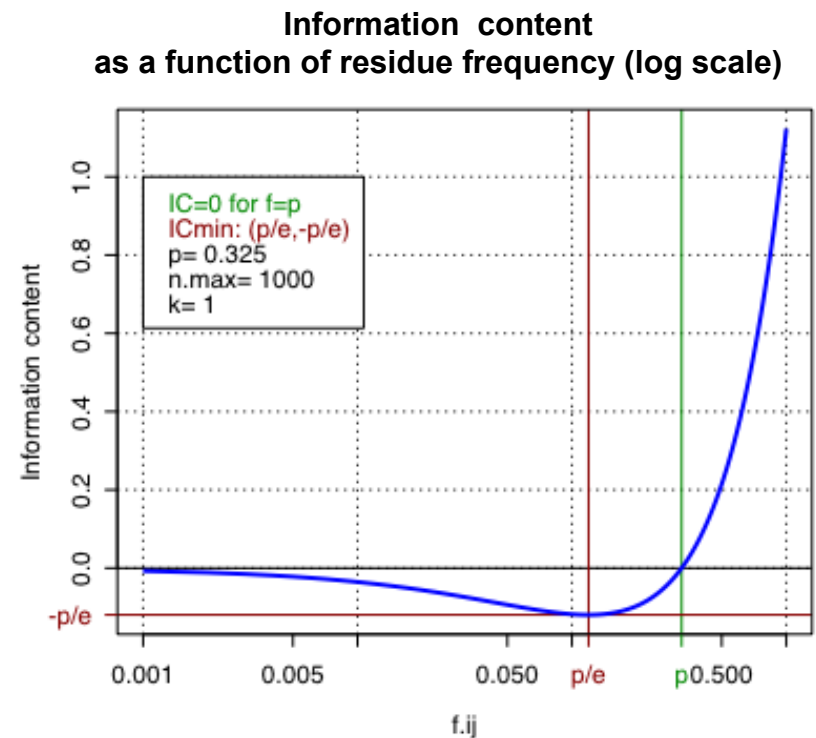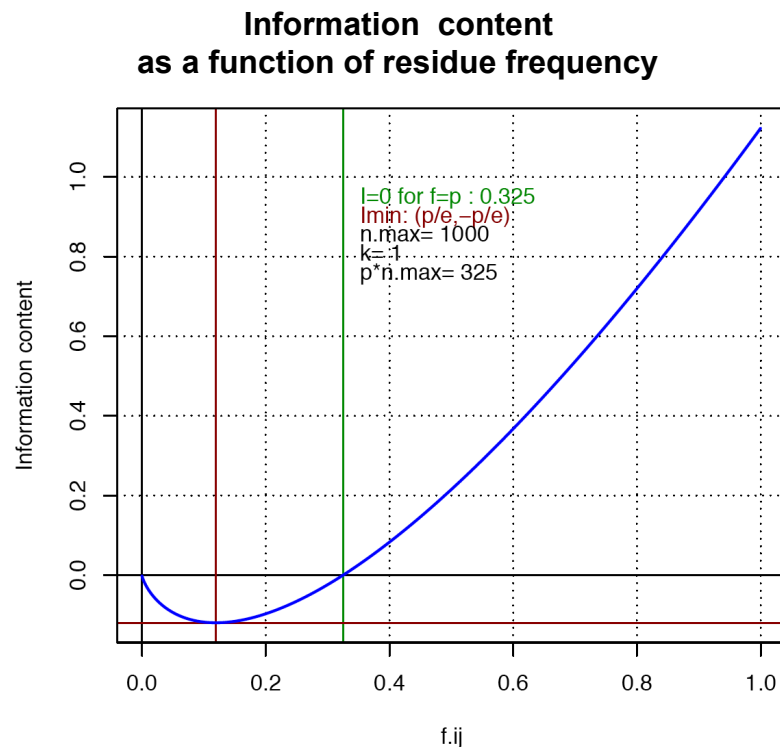
$$I_{matrix} = \sum_{j=1}^{w} \sum_{i=1}^{A} I_{i,j}$$

A *alphabet size (=4)*

$n_{i,j,}$ *occurrences of residue i at position j*

w *matrix width (=12)*

p_i *prior residue probability for residue i*

$f_{i,j}$ *relative frequency of residue i at position j*

k *pseudo weight (arbitrary, 1 in this case)*

$f'_{i,j}$ *corrected frequency of residue i at position j*

$W_{i,j}$ *weight of residue i at position j*

$I_{i,j}$ *information of residue i at position j*

Reference: Hertz (1999).

Bioinformatics 15:563-577[11]

- For a given cell of the matrix
  - I_{ij} is positive when $f'_{ij} > p_i$
    (i.e. when residue *i* is more frequent at position *j* than expected by chance)
  - I_{ij} is negative when $f'_{ij} < p_i$
  - I_{ij} tends towards 0 when $f'_{ij} \rightarrow 0$ (because $limit_{x \rightarrow 0}\ x*ln(x) = 0$)

**Information content
as a function of residue frequency**

**Information content
as a function of residue frequency (log scale)**

I=0 for f=p : 0.325
Imin: (p/e,–p/e)
n.max= 1000
k= 1
p*n.max= 325

IC=0 for f=p
ICmin: (p/e,-p/e)
p= 0.325
n.max= 1000
k= 1

- For a given column i of the matrix
  - The information of the column (I_j) is the sum of information of its cells.
  - I_j is always positive
  - I_j is 0 when the frequency of all residues equal their prior probability ($f_{ij}=p_i$)
  - I_j is maximal when
    - the residue i_m with the lowest prior probability has a frequency of 1
      (all other residues have a frequency of 0)
    - and the pseudo-weight is null ($k=0$).

$$I_j = \sum_{i=1}^{A} I_{i,j} = \sum_{i=1}^{A} f'_{i,j} \ln\left(\frac{f'_{i,j}}{p_i}\right)$$

$$i_m = \arg\min_i(p_i) \qquad k = 0$$

$$\max(I_j) = 1 \cdot \ln\left(\frac{1}{p_i}\right) = -\ln(p_i)$$

Schneider logos

$$H_s(j) = -\sum_{i=1}^{A} f_{ij} \log_2(f_{ij})$$

$$R_{seq}(j) = 2 - H_s(j) + e(n)$$

$$h_{ij} = f_{ij} R_{seq}(j)$$

Pho4p binding motif

weblogo.berkeley.edu

- Schneider (1990) proposes a graphical representation based on his previous entropy (H) for representing the importance of each residue at each position of an alignment. He provides a new formula for R_{seq}
    - $H_s(j)$ uncertainty of column j
    - $R_{seq}(j)$ "information content" of column j (beware, this definition differs from Hertz' information content)
    - $e(n)$ correction for small samples (pseudo-weight)
- Remarks
    - This information content does not include any correction for the prior residue probabilities (p_i)
    - This information content is expressed in bits.
- Boundaries
    - $min(Rseq)=0$ equiprobable residues
    - $max(Rseq)=2$ perfect conservation of 1 residue with a pseudo-weight of 0,
- Sequence logos can be generated from aligned sequences on the *Weblogo* server
    - http://weblogo.berkeley.edu/
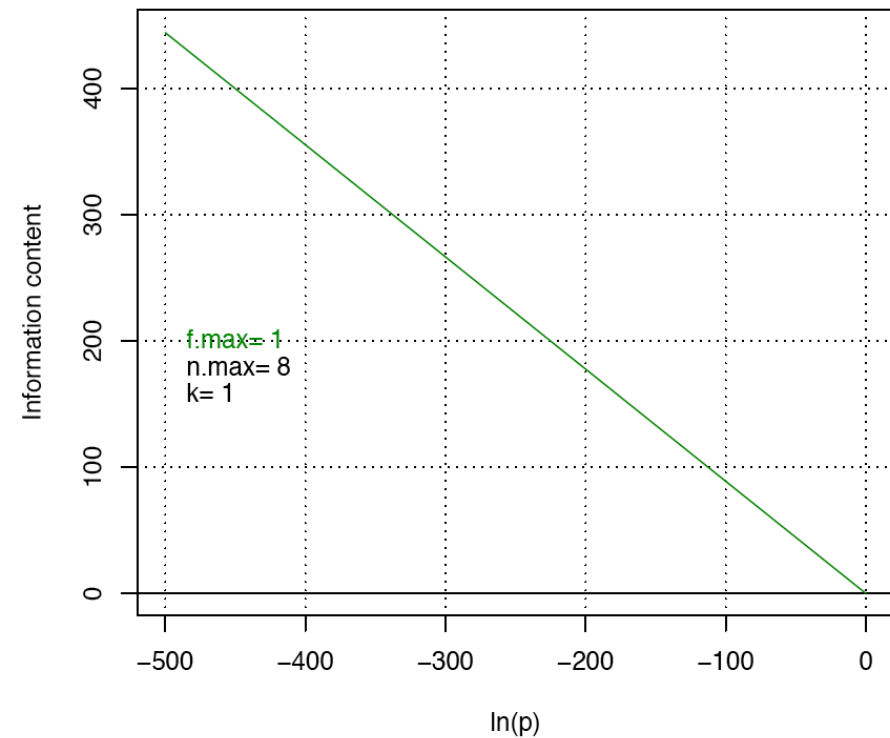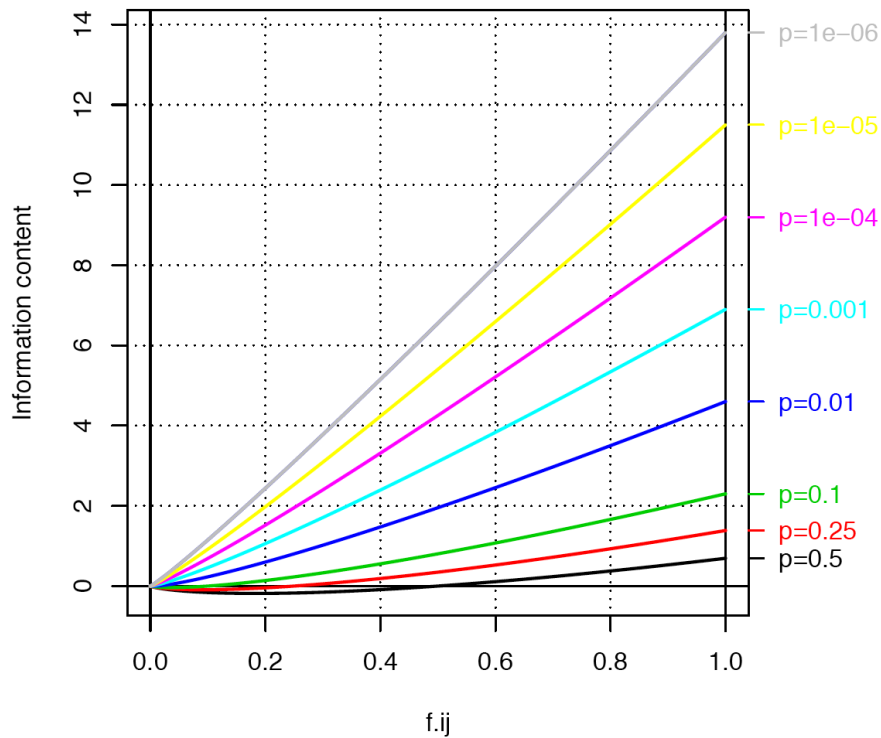
Information content of the matrix

- The total information content represents the capability of the matrix to make the distinction between a binding site (represented by the matrix) and the background model.

$$I_{matrix} = \sum_{j=1}^{w} \sum_{i=1}^{A} I_{i,j}$$

- The information content also allows to estimate an upper limit for the expected frequency of the binding sites in random sequences.

$$P(site) \leq e^{-I_{matrix}}$$

- The pattern discovery program *consensus* (developed by Jerry Hertz) optimises the information content in order to detect over-represented motifs.

- Note that this is not the case of all pattern discovery programs: the gibbs sampler algorithm optimizes a log-likelihood.

Reference: Hertz (1999). Bioinformatics 15:563-577.

- The upper bound of I_j increases when p_i decreases
  - $I_j \to Inf$ when $p_i \to 0$
- The information content, as defined by Gerald Hertz, has thus no upper bound.

References - PSSM information content

- **Papers by Tom Schneider**
  - Schneider, T.D., G.D. Stormo, L. Gold, and A. Ehrenfeucht. 1986. Information content of binding sites on nucleotide sequences. J Mol Biol 188: 415-431.
  - Schneider, T.D. and R.M. Stephens. 1990. Sequence logos: a new way to display consensus sequences. Nucleic Acids Res 18: 6097-6100.
  - Tom Schneider's publications online
    - http://www.lecb.ncifcrf.gov/~toms/paper/index.html

- **Papers by Gerald Hertz**
  - Hertz, G.Z. and G.D. Stormo. 1999. Identifying DNA and protein patterns with statistically significant alignments of multiple sequences. Bioinformatics 15: 563-577.