BGGN 213

Foundations of Bioinformatics

Lecture 3

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http://thegrantlab.org/bggn213

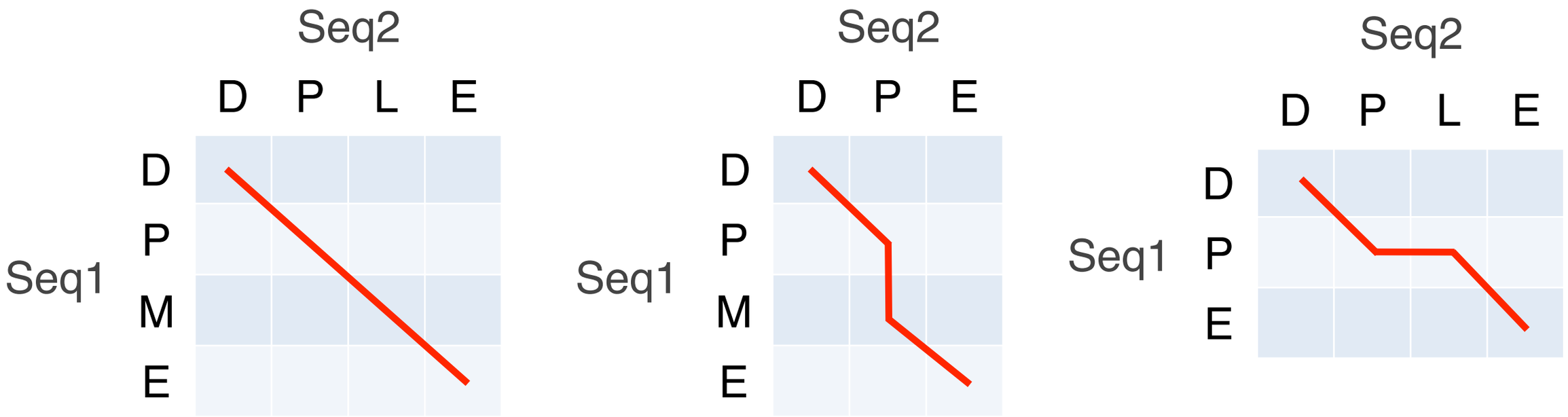
Recap From Last Time:

- Sequence alignment is a fundamental operation underlying much of bioinformatics.
- Introduced dot matrices, dynamic programing and the BLAST heuristic approaches.
  - ➡ *Key point*: Even when optimal solutions can be obtained they are not necessarily unique or reflective of the biologically correct alignment.
- Introduced classic global and local alignment algorithms (Needleman–Wunsch and Smith–Waterman) and their major application areas.
- Heuristic approaches are necessary for large database searches and many genomic applications.

Email: HW1

Feedback | **NW App**

Muddy Point: Different paths represent different alignments




```
Seq1: D P L E
      | |  :  |
Seq2: D P M E
```

```
Seq1: D P M E
      | |   |
Seq2: D P - E
```

```
Seq1: D P - E
      | |   |
Seq2: D P L E
```

(Mis)matches are represented by diagonal paths &

Indels with horizontal or vertical path segments

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BGGN 213

A hands-on introduction to the computer-based analysis of genomic and biomolecular data from the Division of Biological Sciences, UCSD.

Overview

Lectures

Computer Setup

Learning Goals

Assignments & Grading

Ethics Code

3: Advanced sequence alignment and database searching

Topics: Detecting remote sequence similarity, Database searching beyond BLAST, Substitution matrices, Using PSI-BLAST, Profiles and HMMs, Protein structure comparisons. Beginning with command line based database searches.

Goal:

- Be able to calculate the alignment score between two nucleotide or protein sequences using a provided scoring matrix
- Understand the limits of homology detection with tools such as BLAST
- Be able to perform PSI-BLAST, HMMER and protein structure based database searches and interpret the results in terms of the biological significance of an e-value.
- Run our first bioinformatics tool from the command line.

Material:

- Lecture Slides: Large PDF, Small PDF,
- Lab: Hands-on Worksheet,
- Bonus: Alignment App,
- Feedback: Muddy-Point-Assesment

Homework:

▶ **Details:**

Sequence 1 GATTAC

Sequence 2 GTCGACGC

Match Score	Mismatch Score	Gap Score
1	-1	-2

Compute Optimal Alignment | Clear Path | Custom Path

```
G  T  C  G  A  C  G  C
G  A  T  T  A  C  -  -
Score = -4
```

		G	T	C	G	A	C	G	C
	0	-2	-4	-6	-8	-10	-12	-14	-16
G	-2	1	← -1	← -3	↖ -5				
A	-4	↑ -1	↖ 0	← -2	← -4				
T	-6	↑ -3	0	↖ -1	← -3	← -5	← -5	← -7	← -9
T	-8	↑ -5	↖ -2	-1	↖ -2	← -4	← -6	-6	← -8
A	-10	↑ -7	↑ -4	↑ -3	-2	↖ -1	← -3	← -5	← -7
C	-12	↑ -9	↑ -6	↑ -3	↑ -4	↑ -3	↖ 0	← -2	← -4

Score from Diagonal cell
-6 + 1 (Due to a match between G & G) = -5

Score from Upper cell
-8 + -2 (The Gap score) = -10

Score from Side cell
-3 + -2 (The Gap score) = -5

Winning (max) score is -5

▼ **Reference**:
See the lecture and hands-on session for class 2 for a full discussion of Global, Local, and various Heuristic approaches to biomolecular sequence alignment.
Barry J Grant.

NW App Link

Today's Menu

- Sequence motifs and patterns: Simple approaches for finding functional cues from conservation patterns
- Sequence profiles and position specific scoring matrices (PSSMs): Building and searching with profiles, Their advantages and limitations
- PSI-BLAST algorithm: Application of iterative PSSM searching to improve BLAST sensitivity
- Hidden Markov models (HMMs): More versatile probabilistic model for detection of remote similarities

Side Note:

Q. Where do our alignment match and mis-match scores typically come from?

Protein BLAST (BLASTp)

▼ Algorithm parameters

General Parameters

Max target sequences: 100
Select the maximum number of aligned sequences to display

Short queries: ☑ Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 3

Max matches in a query range: 0

Scoring Parameters

Matrix: BLOSUM62

Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Conditional compositional score matrix adjus

Scoring matrix
For match & mis-match scores

Filters and Masking

Filter: ☐ Low complexity regions

Mask: ☐ Mask for lookup table only
☐ Mask lower case letters

BLAST

Search database Non-redundant protein sequences (nr) using Blastp
☐ Show results in a new window

By default BLASTp match scores come from the BLOSUM62 matrix

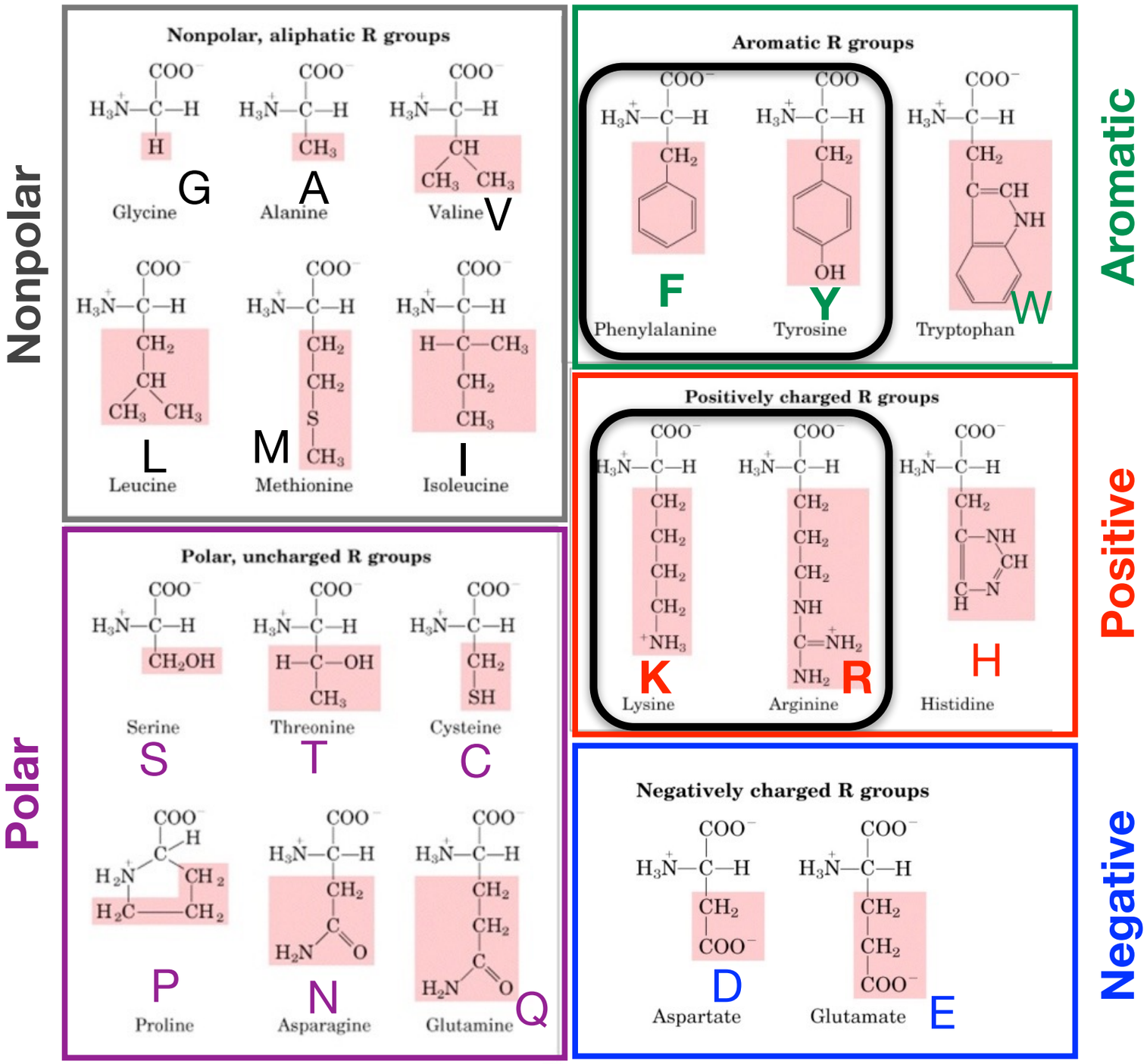
	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W
C	9																			
S	-1	4																		
T	-1	1	5																	
P	-3	-1	-1	7																
A	0	1	0	-1	4															
G	-3	0	-2	-2	0	6														
N	-3	1	0	-2	-2	0	6													
D	-3	0	-1	-1	-2	-1	1	6												
E	-4	0	-1	-1	-1	-2	0	2	5											
Q	-3	0	-1	-1	-1	-2	0	0	2	5										
H	-3	-1	-2	-2	-2	-2	1	-1	0	0	8									
R	-3	-1	-1	-2	-1	-2	0	-2	0	1	0	5								
K	-3	0	-1	-1	-1	-2	0	-1	1	1	-1	2	5							
M	-1	-1	-1	-2	-1	-3	-2	-3	-2	0	-2	-1	-1	5						
I	-1	-2	-1	-3	-1	-4	-3	-3	-3	-3	-3	-3	-3	1	4					
L	-1	-2	-1	-3	-1	-4	-3	-4	-3	-2	-3	-2	-2	2	2	4				
V	-1	-2	0	-2	0	-3	-3	-3	-2	-2	-3	-3	-2	1	3	1	4			
F	-2	-2	-2	-4	-2	-3	-3	-3	-3	-3	-1	-3	-3	0	0	0	-1	6		
Y	-2	-2	-2	-3	-2	-3	-2	-3	-2	-1	2	-2	-2	-1	-1	-1	-1	3	7	
W	-2	-3	-2	-4	-3	-2	-4	-4	-3	-2	-2	-3	-3	-1	-3	-2	-3	1	2	11

Blocks **Su**bstitution **M**atrix. Scores obtained from observed frequencies of substitutions in blocks of aligned sequences with no more than 62% identity.

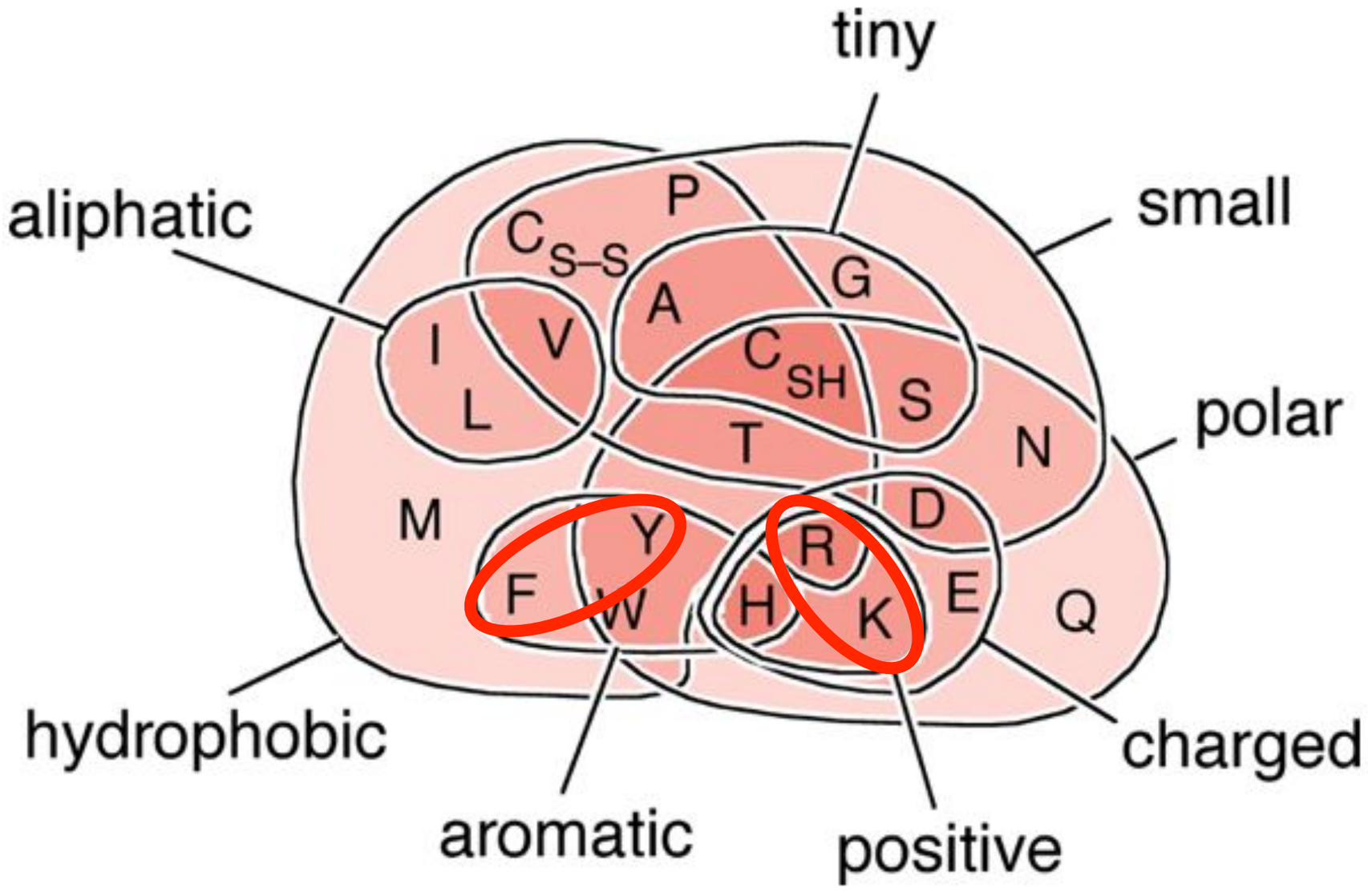
Note. Some amino acid mismatches have positive scores (highlighted in red) reflecting the shared physicochemical properties of these amino acids

Not all matches score equally (blue highlighted values)

Protein scoring matrices reflect the properties of amino acids



Protein scoring matrices reflect the properties of amino acids



Key Trend: High scores for amino acids in the same “biochemical group” and low scores for amino acids from different groups.

N.B. BLOUSM62 does <u>not</u> take the local context of a particular position into account

(*i.e.* all like substitutions are scored the same regardless of their location in the molecules).

We will revisit this later…

Today's Menu

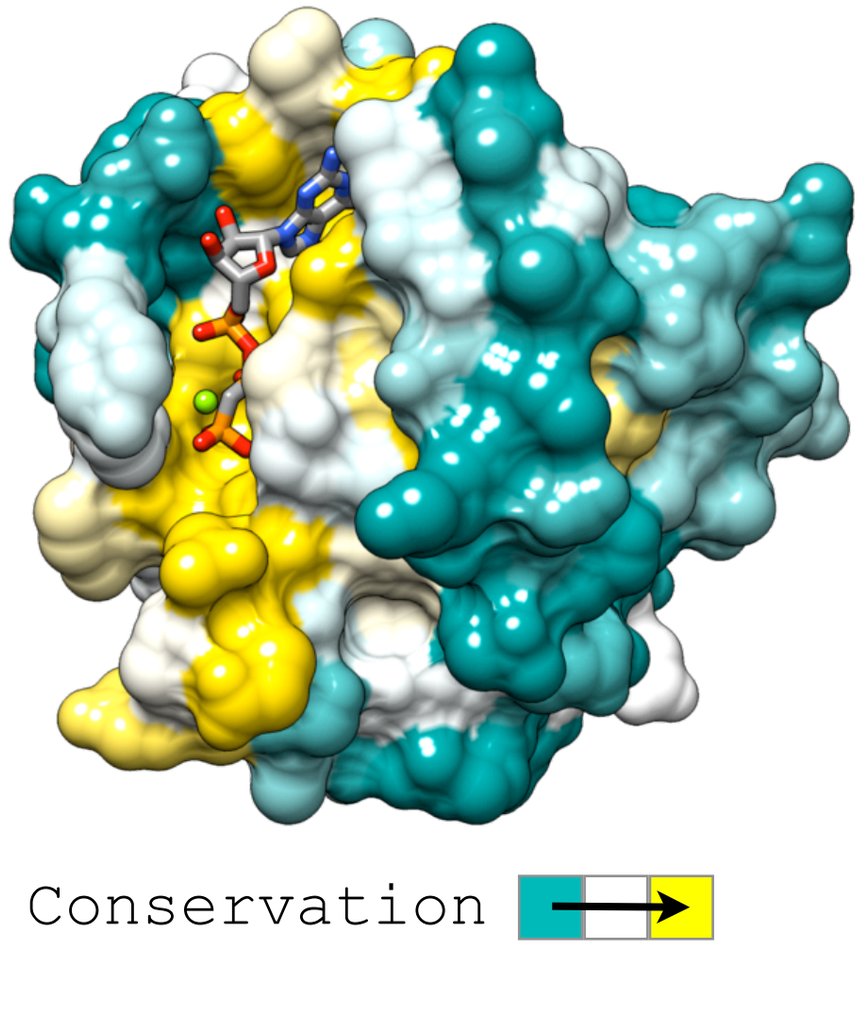
- **Sequence motifs and patterns:** Simple approaches for finding functional cues from conservation patterns
- Sequence profiles and position specific scoring matrices (PSSMs): Building and searching with profiles, Their advantages and limitations
- PSI-BLAST algorithm: Application of iterative PSSM searching to improve BLAST sensitivity
- Hidden Markov models (HMMs): More versatile probabilistic model for detection of remote similarities

Functional cues from conservation patterns

Within a protein or nucleic acid sequence there may be a small number of characteristic residues that occur consistently. These conserved "**motifs**" usually contain functionally important elements

- E.g., the amino acids that are consistently found at enzyme active sites (or the nucleotides that are associated with transcription factor binding sites).

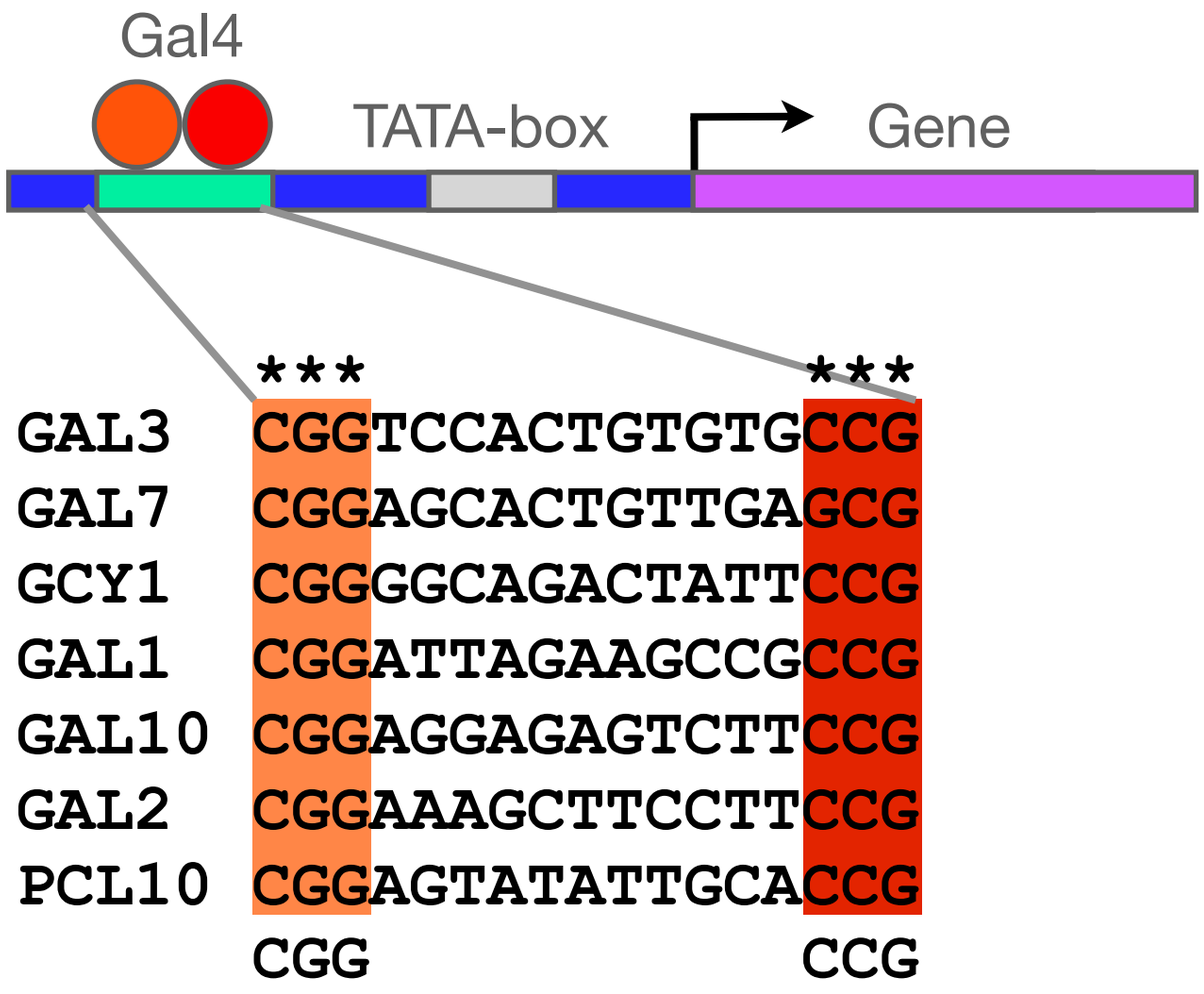
ATP/GTP-binding proteins: G-x(4)-G-K-T



Functional cues from conservation patterns...

Many DNA motif patterns are binding sites for Transcription Factors.

- E.g., The Gal4 yeast binding sequence
  C-G-G-N(11)-C-C-G



PROSITE is a popular protein pattern and profile database

Currently contains > 1790 patterns and profiles: http://prosite.expasy.org/
Example PROSITE patterns:

PS00087; SOD_CU_ZN_1
[GA]-[IMFAT]-**H**-[LIVF]-**H**-{S}-x-[GP]-[SDG]-x(2)-[STAGDE]
The two **H**istidines coordinate important copper ligands

- Each position in the pattern is separated with a hyphen
- x can match any residue
- [ ] are used to indicate ambiguous positions in the pattern
  e.g., [SDG] means the pattern can match S, D, or G at this position
- { } are used to indicate residues that are not allowed at this position
  e.g., {S} means NOT S (not Serine)
- ( ) surround repeated residues, e.g., A(3) means AAA

Information from http://ca.expasy.org/prosite/prosuser.html

Representing recurrent sequence patterns

Beyond knowledge of invariant residues we can define **position-based** representations that highlight the range of permissible residues per position.

- **Pattern**: Describes a motif using a qualitative consensus sequence (e.g., IUPAC or regular expression). N.B. Mismatches are not tolerated!

  [LFI]-x-G-[PT]-P-G-x-G-K-[TS]-[AGSI]

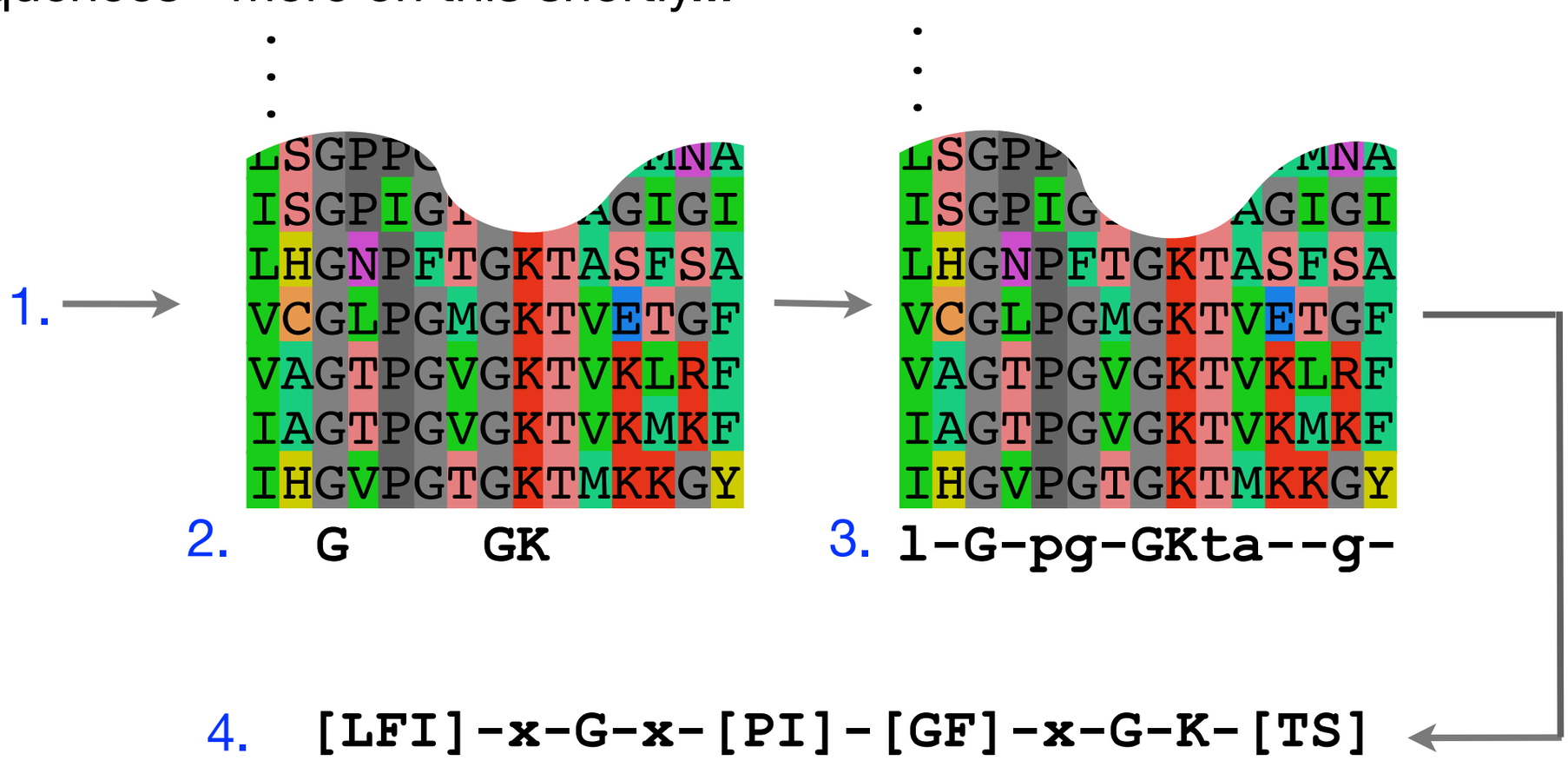
- **Logos**: A useful visual representation of sequence motifs.

Image generated by:
weblogo.berkeley.edu

Defining sequence patterns

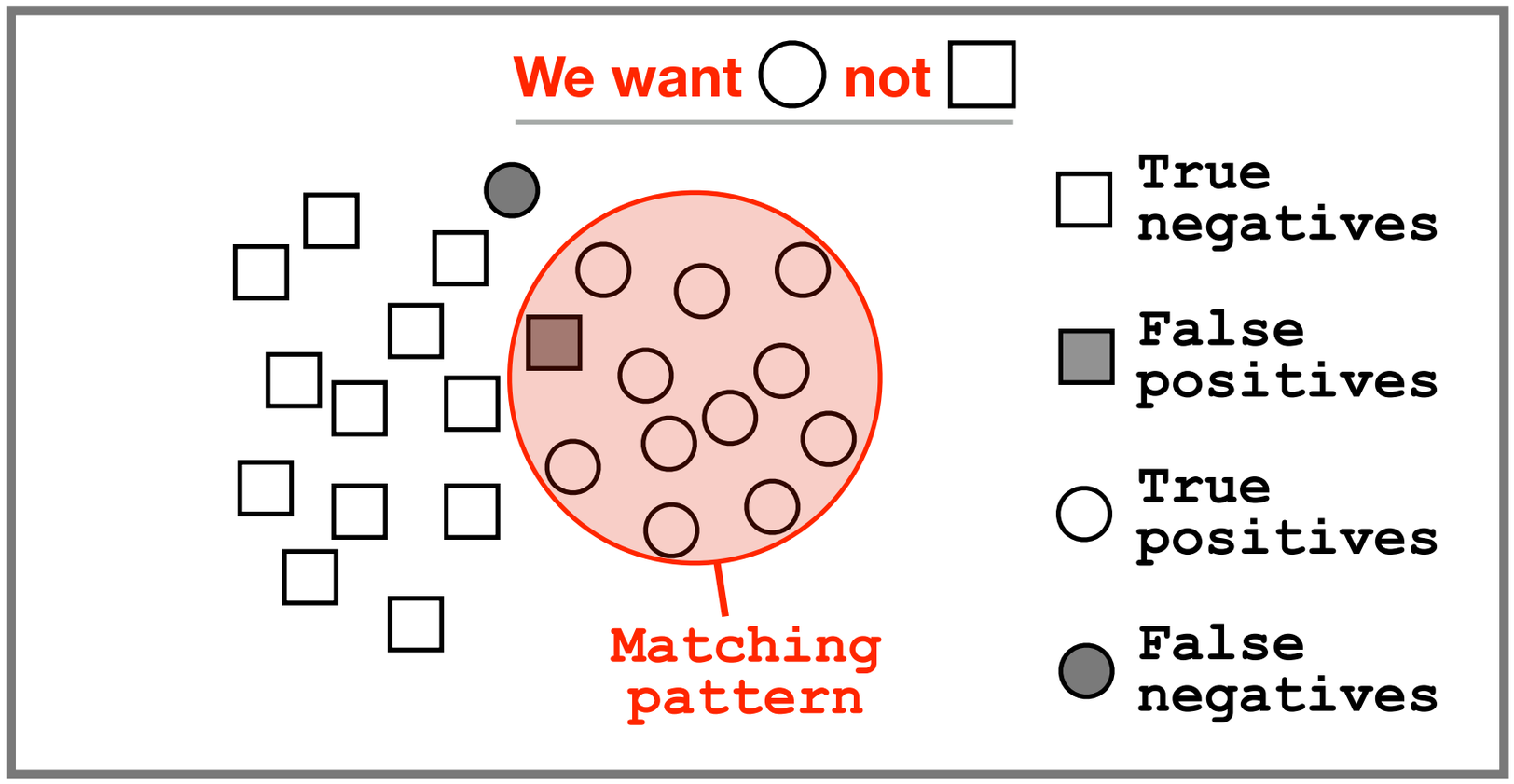
There are four basic steps involved in defining a new PROSITE style pattern:

1. Construct a multiple sequence alignment (MSA)
2. Identify conserved residues
3. Create a core sequence pattern (i.e. *consensus sequence*)
4. Expand the pattern to improve **sensitivity** and **specificity** for detecting desired sequences - more on this shortly...



Side note: pattern sensitivity and specificity

In practice it is not always possible to define one single regular expression type pattern which matches all family sequences (*true positives* ◯) while avoiding matches in unrelated sequences (*true negatives* □).

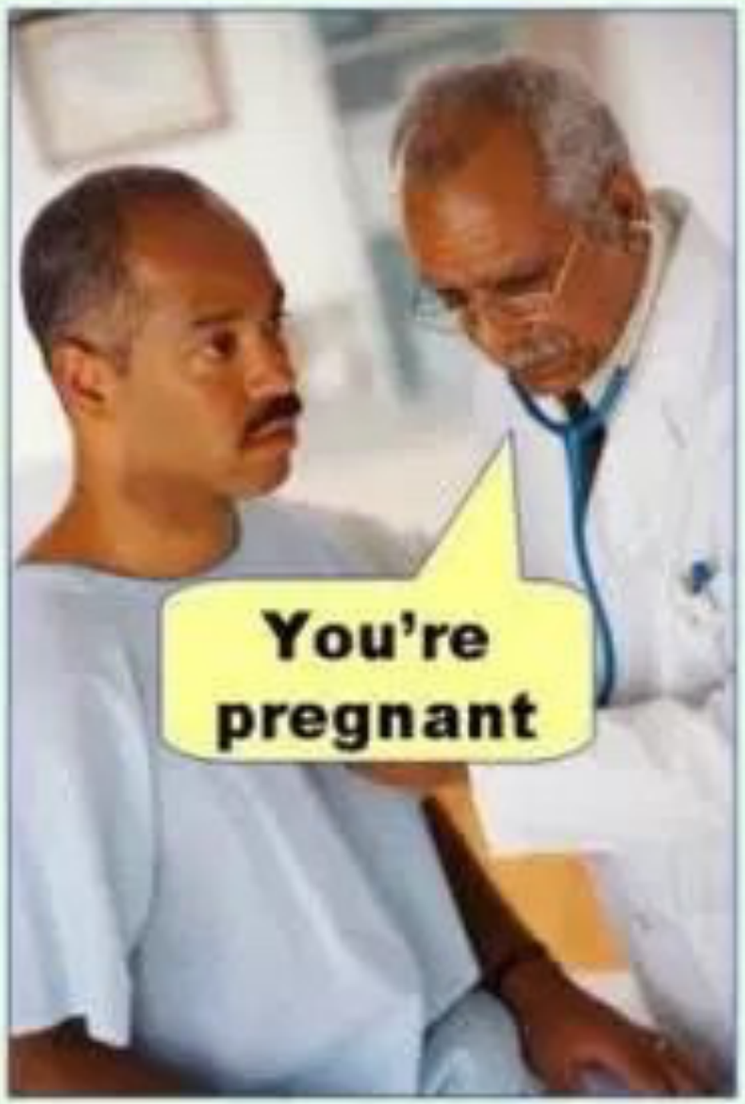


Sensitivity = TP/(TP+FN) ◯/(◯+●)

Specificity = TN/(TN+FP) □/(□+■)

Type I error

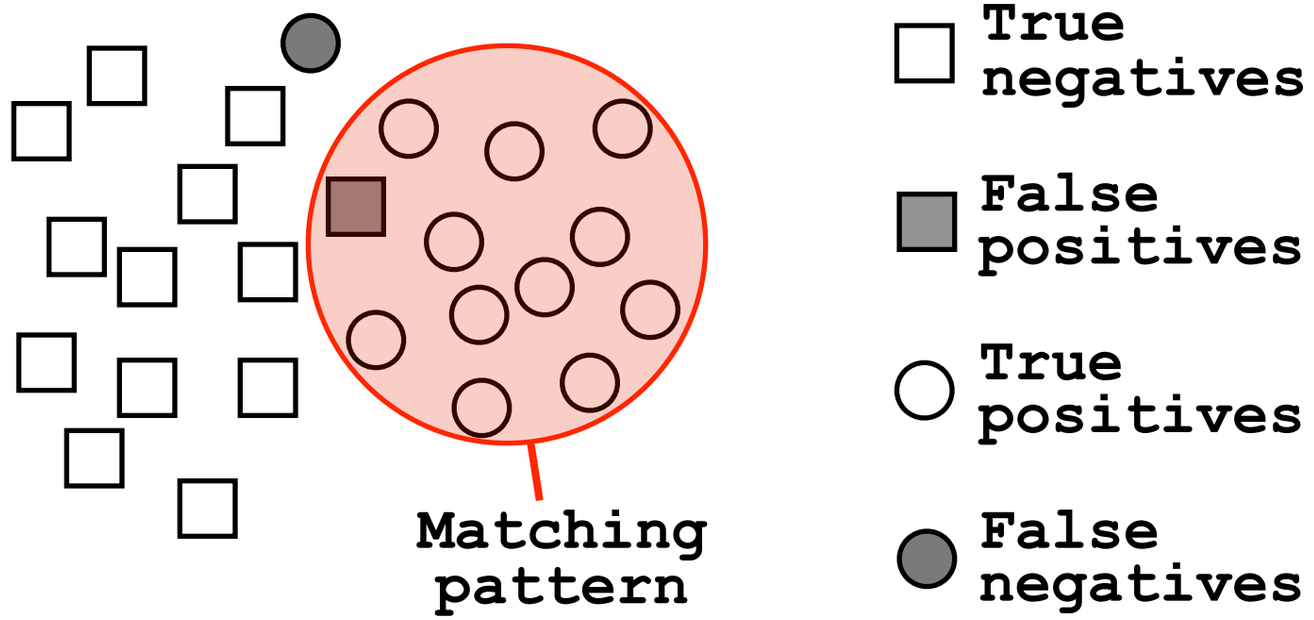
(false positive)



Type II error

(false negative)

Side note: pattern sensitivity, specificity, and PPV



Sensitivity = TP/(TP+FN) = Fraction of total circles we found
(i.e. things we want!) ○/(○+●)

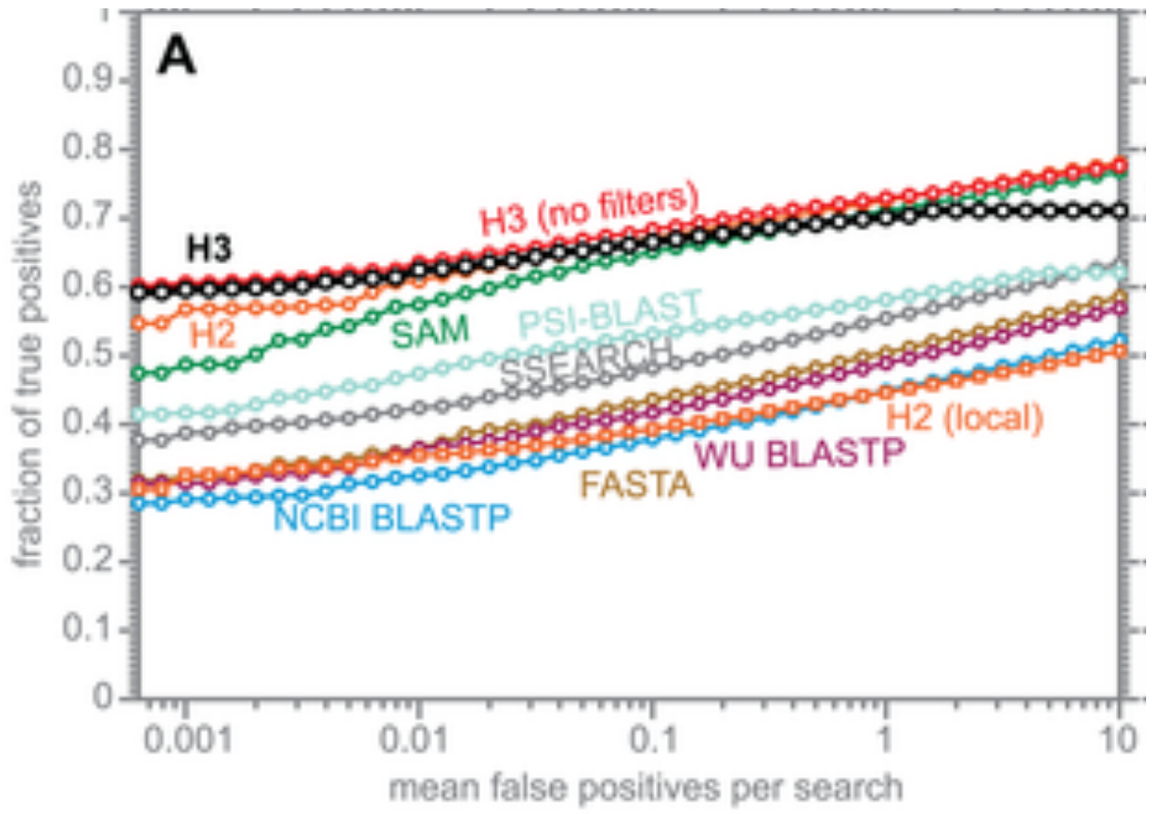
Specificity = TN/(TN+FP) = Fraction of total squares we missed
(i.e. things we **don't** want!) □/(□+■)

PPV = TP/(TP+FP) = Fraction of our highlighted matches that are actually circles
(i.e. proportion of the things we found that are what we want!)

○/(○+■)

ROC plot example

ROC plot of sequence searching performance...



H3 (HMMER3) has a much higher search sensitivity and specificity than BLASTp

In each benchmark, true positive subsequences have been selected to be no more than 25% identical to any sequence in the query alignment ... (see paper for details).

See: Eddy (2011) PLoS Comp Biol 7(10): e1002195

Pattern advantages and disadvantages

Advantages:

- Relatively straightforward to identify (exact pattern matching is fast)
- Patterns are intuitive to read and understand
- Databases with large numbers of protein (e.g., PROSITE) and DNA sequence (e.g., JASPER and TRANSFAC) patterns are available.

Disadvantages:

- Patterns are qualitative and *deterministic*
  (i.e., either matching or not!)
- We lose information about relative frequency of each residue at a position
  E.g., [GAC] *vs* 0.6 G, 0.28 A, and 0.12 C
- Can be difficult to write complex motifs using regular expression notation
- Cannot represent subtle sequence motifs

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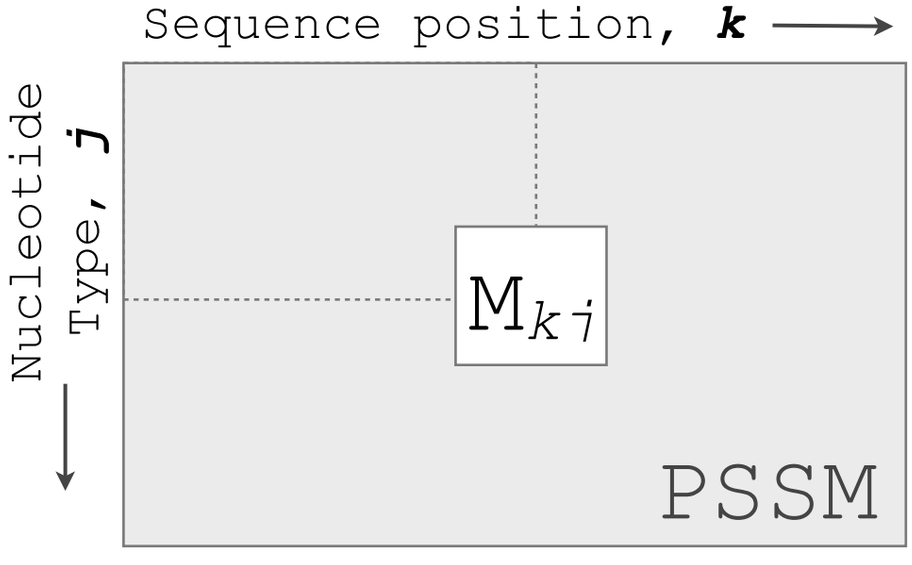
Sequence profiles

A sequence profile is a **position-specific scoring matrix** (or **PSSM**, often pronounced 'possum') that gives a *quantitative* description of a sequence motif.

Unlike deterministic patterns, profiles assign a score to a query sequence and are widely used for database searching.

A simple PSSM has as many columns as there are positions in the alignment, and either 4 rows (one for each DNA nucleotide) or 20 rows (one for each amino acid).



$$M_{kj} = \log\left(\frac{p_{kj}}{p_j}\right)$$

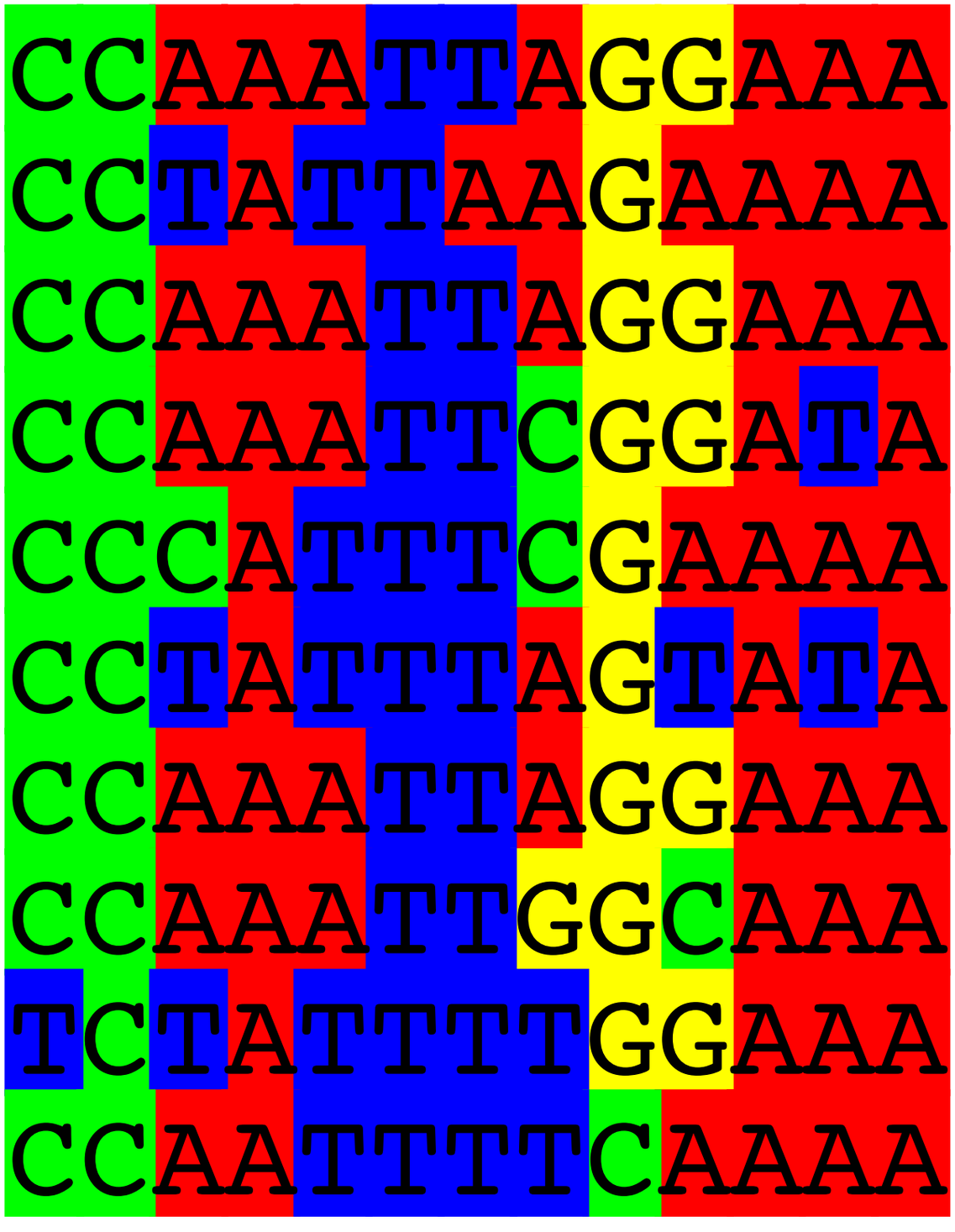
$\mathbf{M_{kj}}$ score for the *j*th nucleotide at position *k*

$\mathbf{p_{kj}}$ probability of nucleotide *j* at position *k*

$\mathbf{p_j}$ "background" probability of nucleotide *j*

See Gibskov *et al.* (1987) PNAS 84, 4355

Computing a transcription factor bind site PSSM

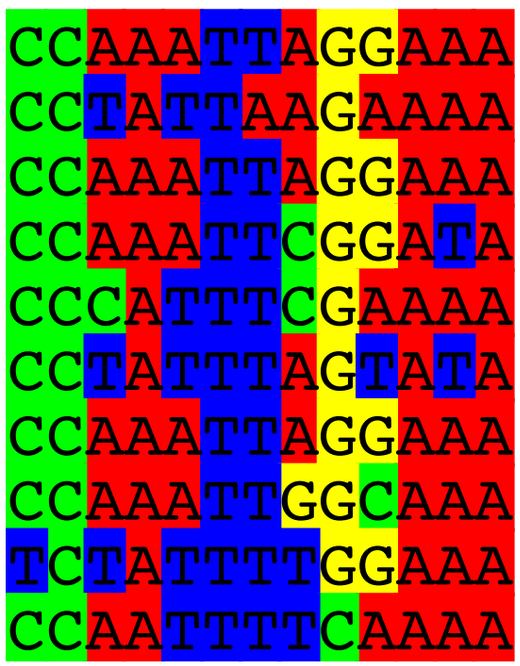


Here we have **10 aligned** transcription factor binding site nucleotide sequences

That span **13 positions** (i.e. columns of nucleotides).

We will build a 13 x 4 **PSSM** (*k*=13, *j*=4).

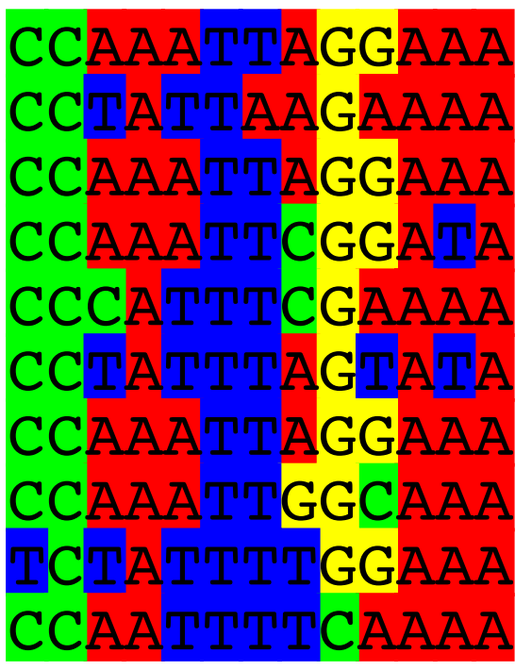
Computing a transcription factor bind site PSSM



First we will build an alignment **Counts matrix**

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:													
C:													
G:													
T:													

Computing a transcription factor bind site PSSM

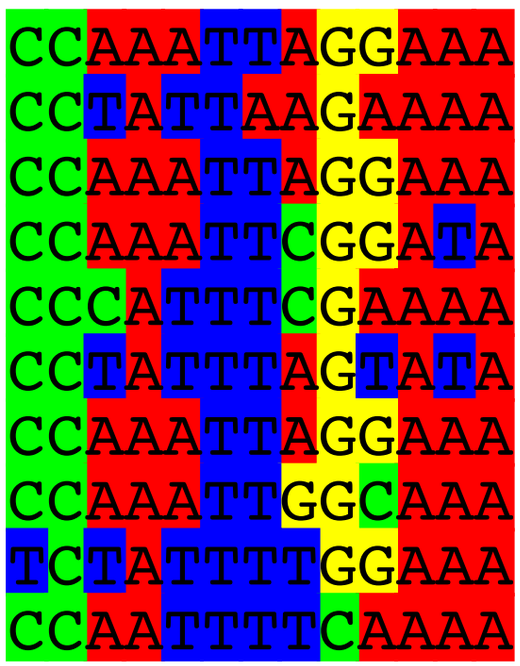


Alignment Counts matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:													
C:													
G:													
T:													

Position k = 1

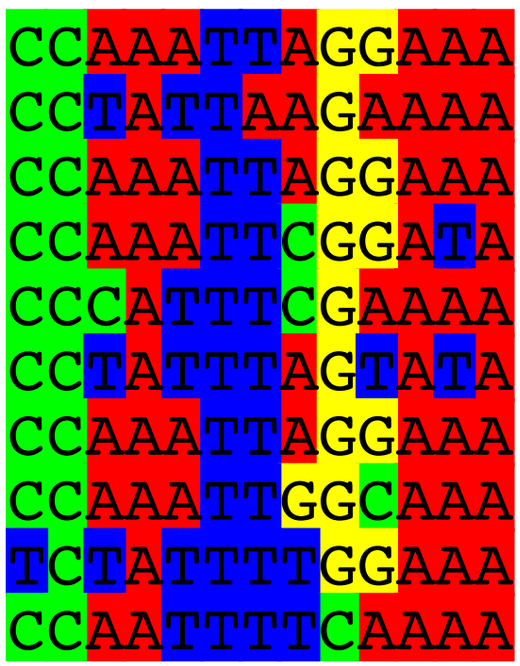
Computing a transcription factor bind site PSSM



Alignment Counts matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0												
C:	9												
G:	0												
T:	1												

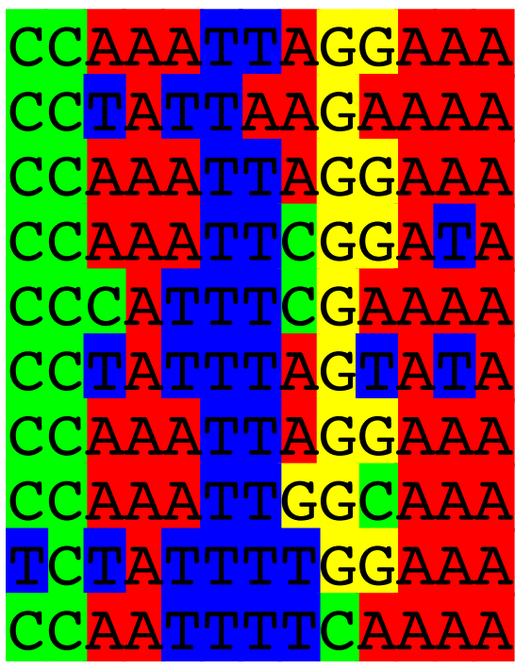
Computing a transcription factor bind site PSSM



Alignment Counts matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0												
C:	9												
G:	0												
T:	1												
Consensus	C												

Computing a transcription factor bind site PSSM

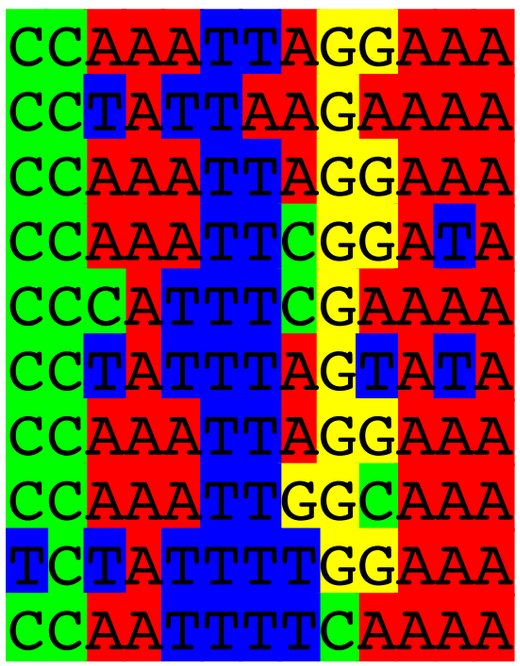


Alignment Counts matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0	0											
C:	9	10											
G:	0	0											
T:	1	0											
Consensus	C	C											

Position k = 2

Computing a transcription factor bind site PSSM

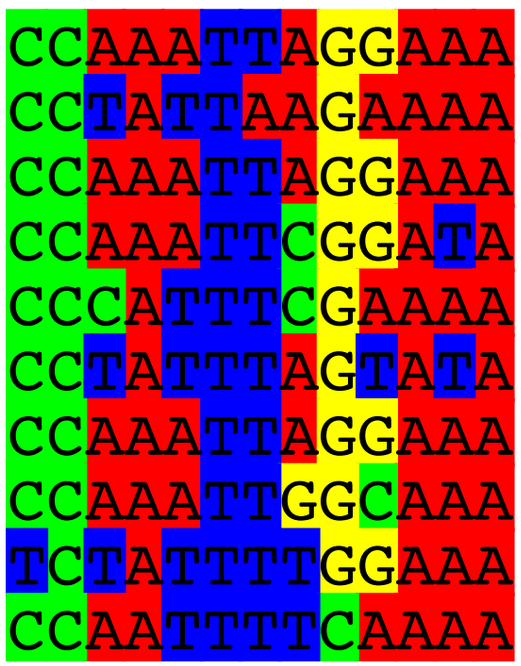


Alignment Counts matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0	0	6										
C:	9	10	1										
G:	0	0	0										
T:	1	0	3										
Consensus	C	C	[AT]										

Position k = 3

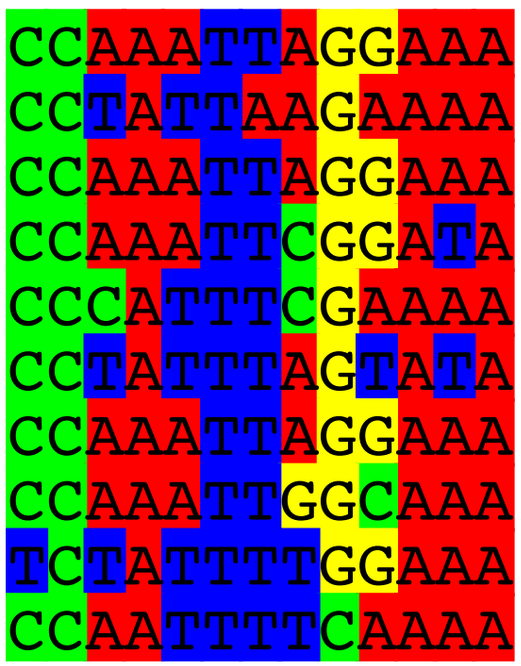
Computing a transcription factor bind site PSSM



Alignment Counts matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0	0	6	10	5	0	1	5	0	3	10	8	10
C:	9	10	1	0	0	0	0	2	1	1	0	0	0
G:	0	0	0	0	0	0	0	1	9	5	0	0	0
T:	1	0	3	0	5	10	9	2	0	1	0	2	0
Consensus	C	C	[AT]	A	[AT]	T	T	[ACT]	G	[GA]	A	[AT]	A

Computing a transcription factor bind site PSSM



Alignment Counts matrix:

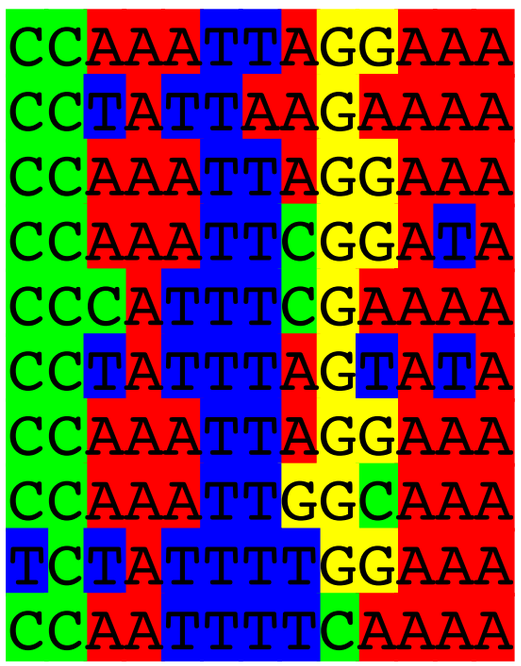
Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0	0	6	10	5	0	1	5	0	3	10	8	10
C:	9	10	1	0	0	0	0	2	1	1	0	0	0
G:	0	0	0	0	0	0	0	1	9	5	0	0	0
T:	1	0	3	0	5	10	9	2	0	1	0	2	0
Consensus	C	C	[AT]	A	[AT]	T	T	[ACT]	G	[GA]	A	[AT]	A

Often we will not communicate with the count matrix but rather the derived **average profile** (a.k.a. frequency matrix).

Average Profile (Frequency) matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0	0	0.6	1	0.5	0	0.1	0.5	0	0.3	1	0.8	1
C:	0.9	1	0.1	0	0	0	0	0.2	0.1	0.1	0	0	0
G:	0	0	0	0	0	0	0	0.1	0.9	0.5	0	0	0
T:	0.1	0	0.3	0	0.5	1	0.9	0.2	0	0.1	0	0.2	0
Consensus	C	C	[AT]	A	[AT]	T	T	[ACT]	G	[GA]	A	[AT]	A

Computing a transcription factor bind site PSSM



Alignment Counts matrix:

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0	0	6	10	5	0	1	5	0	3	10	8	10
C:	9	10	1	0	0	0	0	2	1	1	0	0	0
G:	0	0	0	0	0	0	0	1	9	5	0	0	0
T:	1	0	3	0	5	10	9	2	0	1	0	2	0
Consensus	C	C	[AT]	A	[AT]	T	T	[ACT]	G	[GA]	A	[AT]	A

Or the "score (M_{kj}) matrix" = PS**S**M

C_{kj} Number of *j*th type nucleotide at position *k*

Z Total number of aligned sequences

p_j "background" probability of nucleotide *j*

p_{kj} probability of nucleotide *j* at position *k*

$$M_{kj} = \log\left(\frac{p_{kj}}{p_j}\right) \qquad p_{kj} = \frac{C_{kj} + p_j}{Z + 1}$$

$$M_{kj} = \log\left(\frac{C_{kj} + p_j / Z + 1}{p_j}\right)$$

Adapted from Hertz and Stormo, Bioinformatics 15:563-577

Computing a transcription factor bind site PSSM...

Alignment Matrix: C_{kj}

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	0	0	6	10	5	0	1	5	0	3	10	8	10
C:	9	10	1	0	0	0	0	2	1	1	0	0	0
G:	0	0	0	0	0	0	0	1	9	5	0	0	0
T:	1	0	3	0	5	10	9	2	0	1	0	2	0

k=1, j=A: $M_{kj} = \log\left(\frac{C_{kj} + p_j / Z + 1}{p_j}\right) = \log\left(\frac{0 + 0.25/10 + 1}{0.25}\right) = -2.4$

k=1, j=C: $M_{kj} = \log\left(\frac{C_{kj} + p_j / Z + 1}{p_j}\right) = \log\left(\frac{9 + 0.25/10 + 1}{0.25}\right) = 1.2$

k=1, j=T: $M_{kj} = \log\left(\frac{C_{kj} + p_j / Z + 1}{p_j}\right) = \log\left(\frac{1 + 0.25/10 + 1}{0.25}\right) = -0.8$

PSSM: M_{kj}

Position k =	1	2	3	4	5	6	7	8	9	10	11	12	13
A:	-2.4	-2.4	0.8	1.3	0.6	-2.4	-0.8	0.6	-2.4	0.2	1.3	1.1	1.3
C:	1.2	1.3	-0.8	-2.4	-2.4	-2.4	-2.4	-0.2	-0.8	-0.8	-2.4	-2.4	-2.4
G:	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-0.8	1.2	0.6	-2.4	-2.4	-2.4
T:	-0.8	-2.4	0.2	-2.4	0.6	1.3	1.2	-0.2	-2.4	-0.8	-2.4	-0.2	-2.4

Scoring a test sequence

Query Sequence

CCTATTTAGGATA

PSSM:

Position k =	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
A:	-2.4	-2.4	0.8	**1.3**	0.6	-2.4	-0.8	**0.6**	-2.4	0.2	**1.3**	1.1	**1.3**
C:	**1.2**	**1.3**	-0.8	-2.4	-2.4	-2.4	-2.4	-0.2	-0.8	-0.8	-2.4	-2.4	-2.4
G:	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-0.8	**1.2**	**0.6**	-2.4	-2.4	-2.4
T:	-0.8	-2.4	**0.2**	-2.4	**0.6**	**1.3**	**1.2**	-0.2	-2.4	-0.8	-2.4	**-0.2**	-2.4

Test seq: **C C T A T T T A G G A T A**

Query Score = 1.2 + 1.3 + 0.2 + 1.3 + 0.6 + 1.3 + 1.2
+ 0.6 + 1.2 + 0.6 + 1.3 + -0.2 + 1.3
= 11.9

Scoring a test sequence

Query Sequence

CCTATTTAGGATA

PSSM:

Position k =	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
A:	-2.4	-2.4	0.8	**1.3**	0.6	-2.4	-0.8	**0.6**	-2.4	0.2	**1.3**	1.1	**1.3**
C:	**1.2**	**1.3**	-0.8	-2.4	-2.4	-2.4	-2.4	-0.2	-0.8	-0.8	-2.4	-2.4	-2.4
G:	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-0.8	**1.2**	**0.6**	-2.4	-2.4	-2.4
T:	-0.8	-2.4	**0.2**	-2.4	**0.6**	**1.3**	**1.2**	-0.2	-2.4	-0.8	-2.4	**-0.2**	-2.4

Test seq:	**C**	**C**	**T**	**A**	**T**	**T**	**T**	**A**	**G**	**G**	**A**	**T**	**A**

Query Score = 1.2 + 1.3 + 0.2 + 1.3 + 0.6 + 1.3 + 1.2
+ 0.6 + 1.2 + 0.6 + 1.3 + -0.2 + 1.3
= 11.9

Q. Does the query sequence match the DNA sequence profile?

Scoring a test sequence...

Query Sequence

CCTATTTAGGATA

Best Possible Sequence

CCAATTTAGGAAA

PSSM:

Position k =	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
A:	-2.4	-2.4	**0.8**	**1.3**	0.6	-2.4	-0.8	**0.6**	-2.4	0.2	**1.3**	**1.1**	**1.3**
C:	**1.2**	**1.3**	-0.8	-2.4	-2.4	-2.4	-2.4	-0.2	-0.8	-0.8	-2.4	-2.4	-2.4
G:	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-2.4	-0.8	**1.2**	**0.6**	-2.4	-2.4	-2.4
T:	-0.8	-2.4	0.2	-2.4	**0.6**	**1.3**	**1.2**	-0.2	-2.4	-0.8	-2.4	-0.2	-2.4

Max Score: **C C A A T T T A G G A A A**

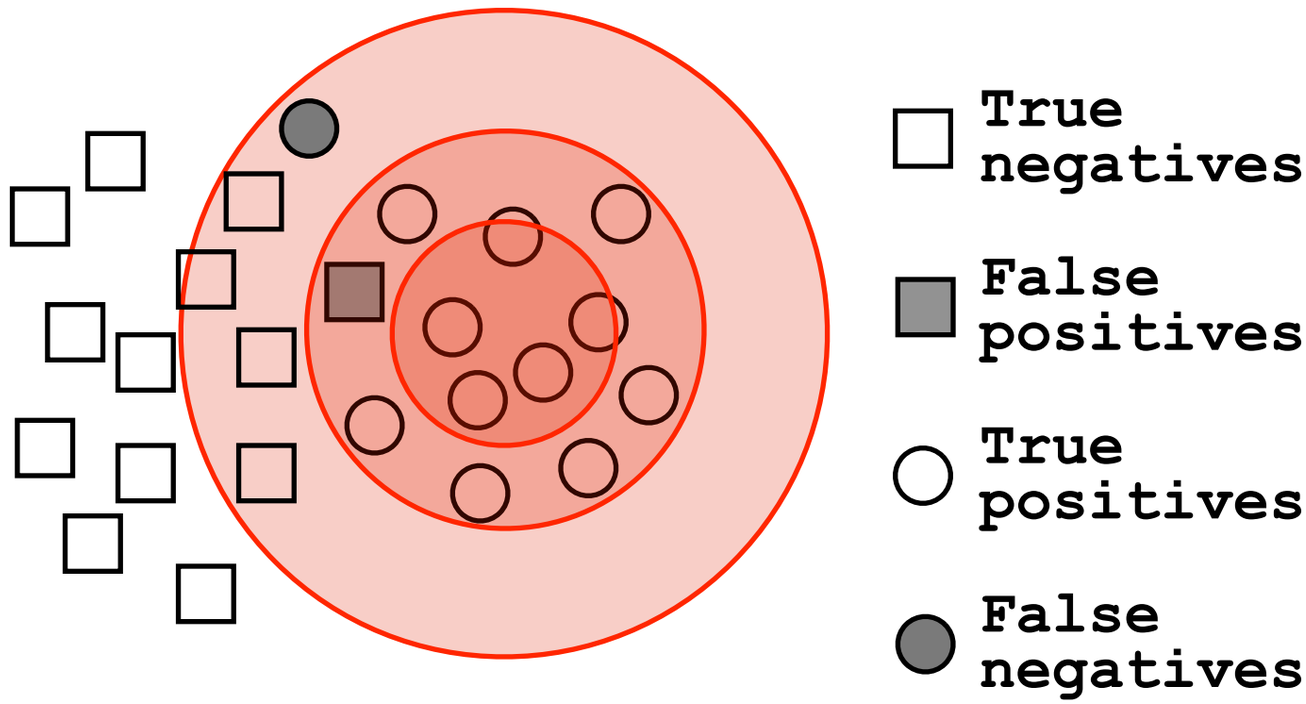
Max Score = 1.2 + 1.3 + 0.8 + 1.3 + 0.6 + 1.3 + 1.2
+ 0.6 + 1.2 + 0.6 + 1.3 + 1.1 + 1.3
= 13.8

A. Following method in Harbison *et al.* (2004) Nature 431:99-104

Heuristic threshold for match = 60% x Max Score = (0.6 x 13.8 = 8.28);
11.9 > 8.28; Therefore our query is a potential TFBS!

Picking a threshold for PSSM matching

Again, you want to select a threshold that **minimizes FPs** (e.g., how many shuffled or random sequences does the PSSM match with that score) and **minimizes FNs** (e.g., how many of the 'real' sequences are missed with that score).



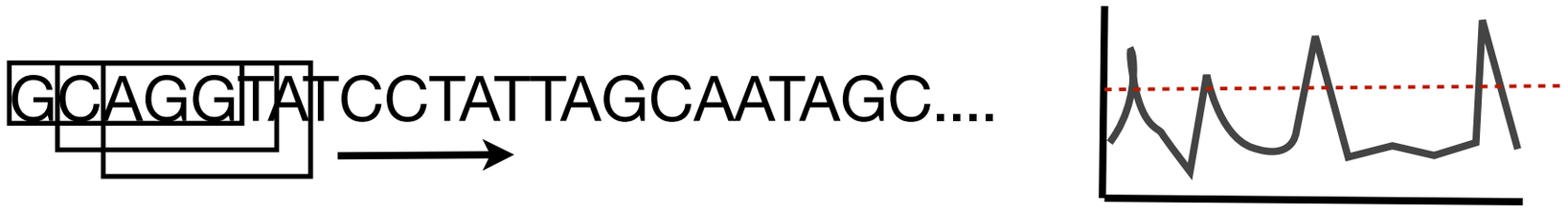
FP=0, FN=7, TP=5	5/(5+0) = 1
FP=1, FN=1, TP=11	11/(11+1) = 0.92
FP=5, FN=0, TP=12	12/(12+5) = 0.71

Q. Which threshold has the best PPV (TP/(TP+FP)) ?

Searching for PSSM matches

If we do not allow gaps (i.e., no insertions or deletions):

- Perform a linear scan, scoring the match to the PSSM at each position in the sequence - the “sliding window” method



If we allow gaps:

- Can use dynamic programming to align the profile to the protein sequence(s) (with gap penalties)
  We will discuss PSI-BLAST shortly...
  see Mount, Bioinformatics: sequence and genome analysis (2004)

- Can use hidden Markov Model-based methods
  We will cover HMMs at the end of today's lecture...
  see Durbin et al., Biological Sequence Analysis (1998)

Side note: Profiles software and databases...

InterPro is an attempt to group a number of protein domain databases.
http://www.ebi.ac.uk/interpro

It currently includes:

- PFAM
- PROSITE
- PRINTS
- ProDom
- SMART
- TIGRFAMs

- InterPro tries to have and maintain a high quality of annotation
- The database and a stand-alone package (**iprscan**) are available for UNIX platforms, see:
  ftp://ftp.ebi.ac.uk/pub/databases/interpro

Today's Menu

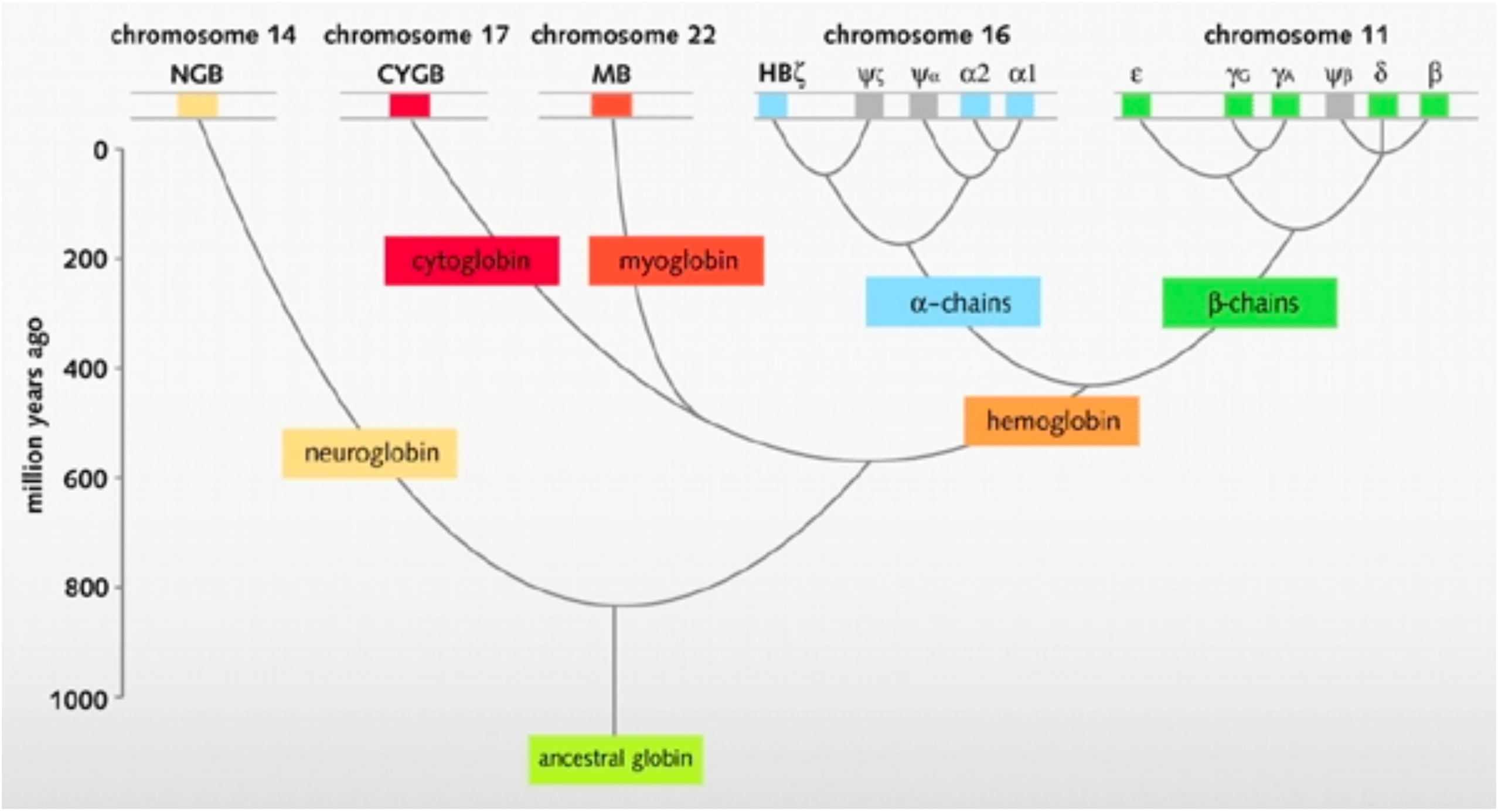
- Sequence motifs and patterns: Simple approaches for finding functional cues from conservation patterns
- Sequence profiles and position specific scoring matrices (PSSMs): Building and searching with profiles, Their advantages and limitations
- PSI-BLAST algorithm: Application of iterative PSSM searching to improve BLAST sensitivity
- Hidden Markov models (HMMs): More versatile probabilistic model for detection of remote similarities

Your Turn!

Hands-on sections 1 & 2:
Comparing methods and the trade-off between sensitivity, selectivity and performance

~50 mins

Side Note: Human Globins



An evolutionary model of human globins.
The different locations of globin genes in human chromosomes are reported at the top of the figure, distinguishing between the functional genes (in color) and the pseudogenes (in grey).

Recall: BLOUSM62 does not take the local context of a particular position into account

(*i.e.* all like substitutions are scored the same regardless of their location in the molecules).

By default BLASTp match scores come from the BLOSUM62 matrix

	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W
C	9																			
S	-1	4																		
T	-1	1	5																	
P	-3	-1	-1	7																
A	0	1	0	-1	4															
G	-3	0	-2	-2	0	6														
N	-3	1	0	-2	-2	0	6													
D	-3	0	-1	-1	-2	-1	1	6												
E	-4	0	-1	-1	-1	-2	0	2	5											
Q	-3	0	-1	-1	-1	-2	0	0	2	5										
H	-3	-1	-2	-2	-2	-2	1	-1	0	0	8									
R	-3	-1	-1	-2	-1	-2	0	-2	0	1	0	5								
K	-3	0	-1	-1	-1	-2	0	-1	1	1	-1	2	5							
M	-1	-1	-1	-2	-1	-3	-2	-3	-2	0	-2	-1	-1	5						
I	-1	-2	-1	-3	-1	-4	-3	-3	-3	-3	-3	-3	-3	1	4					
L	-1	-2	-1	-3	-1	-4	-3	-4	-3	-2	-3	-2	-2	2	2	4				
V	-1	-2	0	-2	0	-3	-3	-3	-2	-2	-3	-3	-2	1	3	1	4			
F	-2	-2	-2	-4	-2	-3	-3	-3	-3	-3	-1	-3	-3	0	0	0	-1	6		
Y	-2	-2	-2	-3	-2	-3	-2	-3	-2	-1	2	-2	-2	-1	-1	-1	-1	3	7	
W	-2	-3	-2	-4	-3	-2	-4	-4	-3	-2	-2	-3	-3	-1	-3	-2	-3	1	2	11

Note. All matches of Alanine for Alanine score +4 regardless of their position or context in the molecule.

PSI-BLAST: Position specific iterated BLAST

- The purpose of PSI-BLAST is to look deeper into the database for matches to your query protein sequence by employing a scoring matrix that is customized to your query
  - PSI-BLAST constructs a multiple sequence alignment from the results of a first round BLAST search and then creates a “profile” or specialized position-specific scoring matrix (PSSM) for subsequent search rounds

Inspect the blastp output to identify empirical “rules” regarding amino acids tolerated at each position

```
730496     66   FTVDENGQMSATAKGRVRLFNNWDVCADMIGSFTDTEDPAKFKMKYWGVASFLQKGNDDH 125
200679     63   FSVDEKGHMSATAKGRVRLLSNWEVCADMVGTFTDTEDPAKFKMKYWGVASFLQRGNDDH 122
206589     34   FSVDEKGHMSATAKGRVRLLSNWEVCADMVGTFTDTEDPAKFKMKYWGVASFLQRGNDDH 93
2136812    2          MSATAKGRVRLLNNWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDH 53
132408     65   FKIEDNGKTTATAKGRVRILDKLELCANMVGTFIETNDPAKYRMKYHGALAILERGLDDH 124
267584     44   FSVDESGKVTATAHGRVIILNNWEMCANMFGTFEDTPDPAKFKMRYWGAASYLQTGNDDH 103
267585     44   FSVDGSGKVTATAQGRVIILNNWEMCANMFGTFEDTPDPAKFKMRYWGAAAYLQSGNDDH 103
8777608    63   FTIHEDGAMTATAKGRVIILNNWEMCADMMATFETTPDPAKFRMRYWGAASYLQTGNDDH 122
6687453    60   FKVEEDGTMTATAIGRVIILNNWEMCANMFGTFEDTEDPAKFKMKYWGAAAYLQTGYDDH 119
10697027   81   FKVQEDGTMTATATGRVIILNNWEMCANMFGTFEDTEEPARFKMKYWGAAAYLQTGYDDH 140
13645517   1                                  MVGTFTDTEDPAKFKMKYWGVASFLQKGNDDH 32
13925316   38   FSVDGSGKMTATAQGRVIILNNWEMCANMFGTFEDTPDPAKFKMRYWGAAAYLQSGNDDH 97
131649     65   YTVEEDGTMTASSKGRVKLFGFWVICADMAAQYTDPTTPAKMYMTYQGLASYLSSGGDNY 126
```

R,I,K C D,E,T K,R,T N,L,Y,G

		A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	M	-1	-2																		
2	K	-1	1																		
3	W	-3	-3	-4	-5	-3	-2	-3	-3								-3	-3	12	2	-3
4	V	0	-3	-3	-4	-1	-3	-3	-4								-2	0	-3	-1	4
5	W	-3	-3	-4	-5	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-3	12	2	-3
6	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
7	L	-2	-2	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	1
8	L	-1	-3	-3	-4	-1	-3	-3	-4	-3	2	2	-3	1	3	-3	-2	-1	-2	0	3
9	L	-1	-3	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	2
10	L	-2	-2	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	1
11	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
12	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
13	W	-2											-3	2	1	-3	-3	-2	7	0	0
14	A	3											-1	-2	-3	-1	1	-1	-3	-3	-1
15	A	2											0	-2	-3	-1	3	0	-3	-2	-2
16	A	4											-1	-1	-3	-1	1	0	-3	-2	-1
...																					
37	S	2	-1	0	-1	-1	0	0	0	-1	-2	-3	0	-2	-3	-1	4	1	-3	-2	-2
38	G	0	-3	-1	-2	-3	-2	-2	6	-2	-4	-4	-2	-3	-4	-2	0	-2	-3	-3	-4
39	T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5	-3	-2	0
40	W	-3	-3	-4	-5	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-3	9	2	-3
41	Y	-2	-2	-2	-3	-3	-2	-2	-3	2	-2	-1	-2	-1	3	-3	-2	-2	2	7	-1
42	A	4	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0

20 amino acids

All the amino acids from position 1 to N (the end of your query protein)

		A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	M	-1	-2	-2	-3	-2	-1	-2	-3	-2	1	2	-2	6	0	-3	-2	-1	-2	-1	1
2	K	-1	1	0	1	-4	2	4	-2	0	-3	-3	3	-2	-4	-1	0	-1	-3	-2	-3
3	W	-3	-3	-4	-5	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-3	12	2	-3
4	V	0	-3	-3	-4	-1	-3	-3	-4	-4	3	1	-3	1	-1	-3	-2	0	-3	-1	4
5	W	-3	-3	-4	-5	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-3	12	2	-3
6	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
7	L	-2	-2	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	1
8	L	-1	-3	-3	-4	-1	-3	-3	-4	-3	2	2	-3	1	3	-3	-2	-1	-2	0	3
9	L	-1	-3	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	2
10	L	-2	-2	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	1
11	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
12	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
13	W	-2	-3	-4	-4	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-2	7	0	0
14	A	3	-2	-1	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	-1	-3	-3	-1
15	A	2	-1	0	-1	-3	-1	-1	-2	-2	-3	-1	0	-1	-3	-1	3	0	-3	-2	-2
16	A	4	-2	-1	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	-1
...																					
37	S	2	-1	0	-1	-3	-1	-1	-2	-2	-3	-2	0	-1	-3	-1	4	1	-3	-2	-2
38	G	0	-3	-1	-2	-3	-2	-2	6	-2	-4	-3	-2	-3	-3	-2	0	-2	-3	-3	-4
39	T	0	-1	0	-1	-3	-1	-1	-2	-2	-3	-2	0	-1	-3	-1	1	5	-3	-2	0
40	W	-3	-3	-4	-5	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-3	9	2	-3
41	Y	-2	-2	-2	-3	-3	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	-1
42	A	4	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0

Note: A given amino acid (such as alanine) in your query protein can receive different scores for matching alanine depending on the position in the protein (BLOSUM S_{AA} = +4)

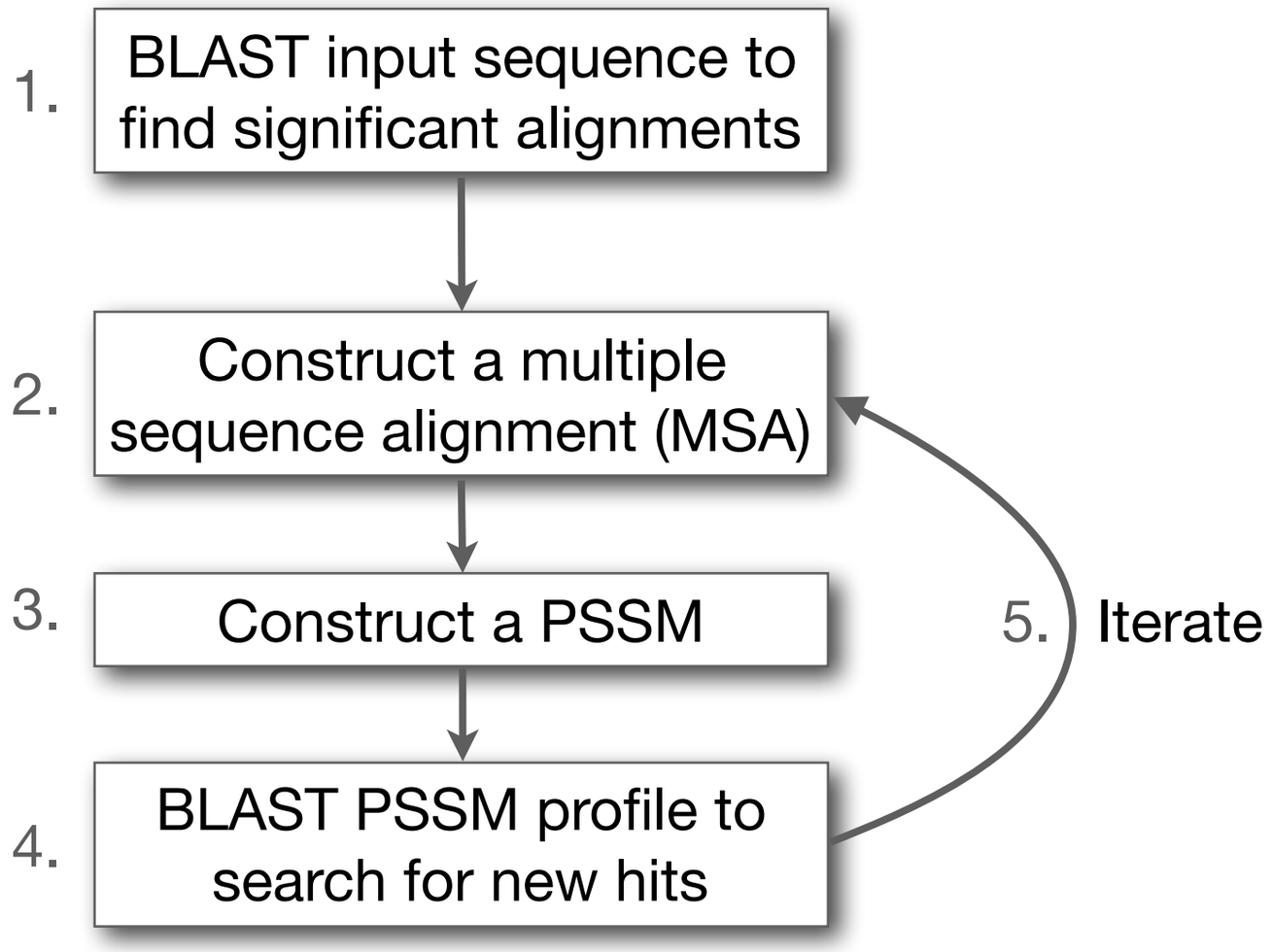
		A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
1	M																				
2	K																				
3	W																				
4	V																				
5	W	-3	-3	-4	-5	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-3	12	2	-3
6	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
7	L	-2	-2	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	1
8	L	-1	-3	-3	-4	-1	-3	-3	-4	-3	2	2	-3	1	3	-3	-2	-1	-2	0	3
9	L	-1	-3	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	2
10	L	-2	-2	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-1	-2	-1	1
11	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
12	A	5	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0
13	W	-2	-3	-4	-4	-1	-2	-3	-4	-3	2	4	-3	2	0	-3	-3	-2	7	0	0
14	A	3	-2	-1	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	-1	-3	-3	-1
15	A	2	-1	0	-1	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	3	0	-3	-2	-2
16	A	4	-2	-1	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	-1
...																					
37	S	2	-1	0	-1	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	4	1	-3	-2	-2
38	G	0	-3	-1	-2	-1	-2	-2	6	-2	-3	-3	-2	-2	-3	-2	0	-2	-3	-3	-4
39	T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5	-3	-2	0
40	W	-3	-3	-4	-5	-3	-2	-3	-3	-3	-3	-2	-3	-2	1	-4	-3	-3	9	2	-3
41	Y	-2	-2	-2	-3	-3	-2	-2	-3	-2	-2	-1	-2	-1	3	-3	-2	-2	2	7	-1
42	A	4	-2	-2	-2	-1	-1	-1	0	-2	-2	-2	-1	-1	-3	-1	1	0	-3	-2	0

The PSI-BLAST PSSM is essentially a query customized scoring matrix that is more sensitive than BLOSUM.

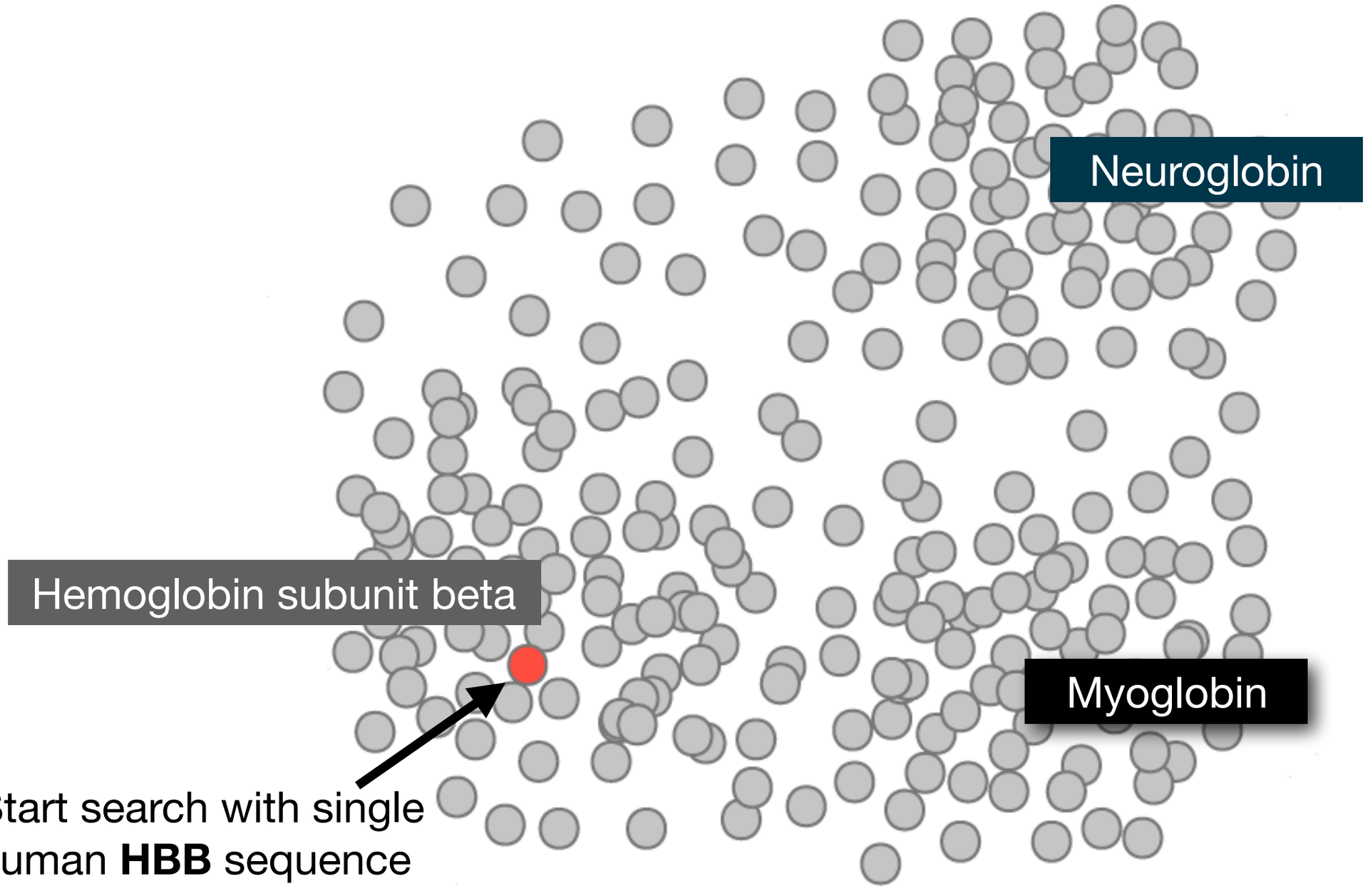
Note: A given amino acid (such as alanine) in your query protein can receive different scores for matching alanine depending on the position in the protein (BLOSUM S_{AA} = +4)

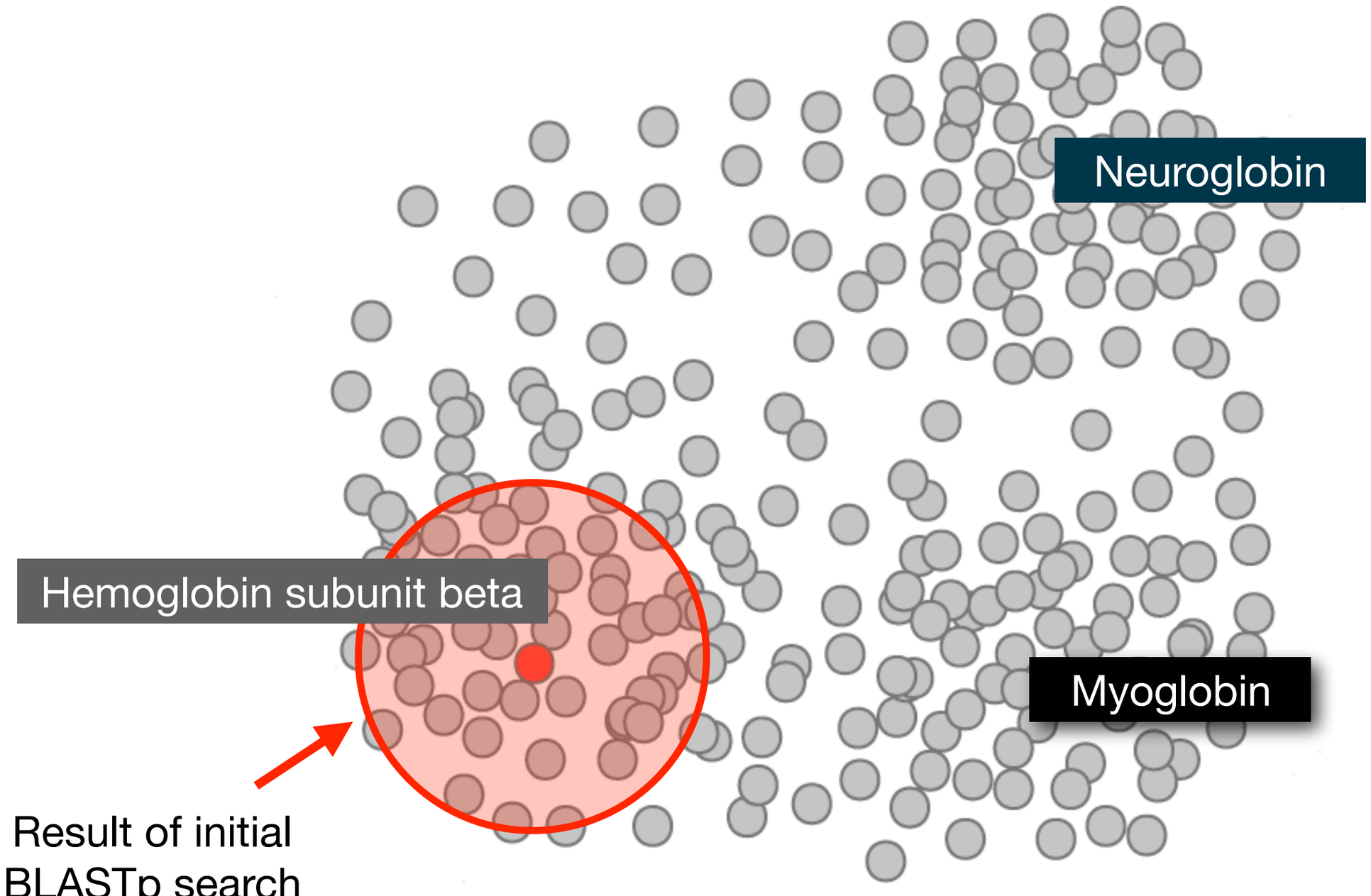
PSI-BLAST: Position-Specific Iterated BLAST

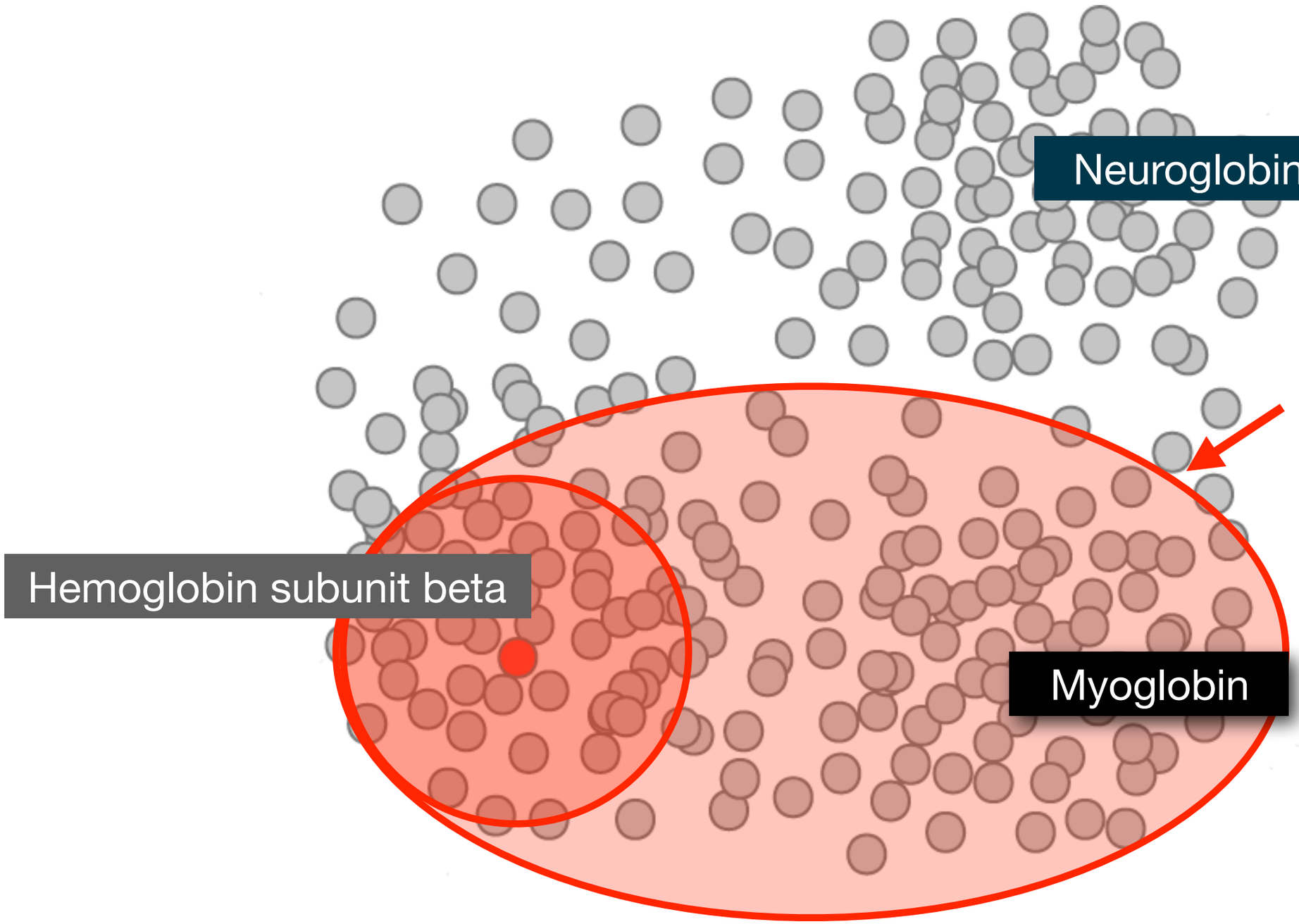
Many proteins in a database are too distantly related to a query to be detected using standard BLAST. In many other cases matches are detected but are so distant that the inference of homology is unclear. Enter the more sensitive PSI-BLAST



(see Altschul *et al.*, Nuc. Acids Res. (1997) 25:3389-3402)

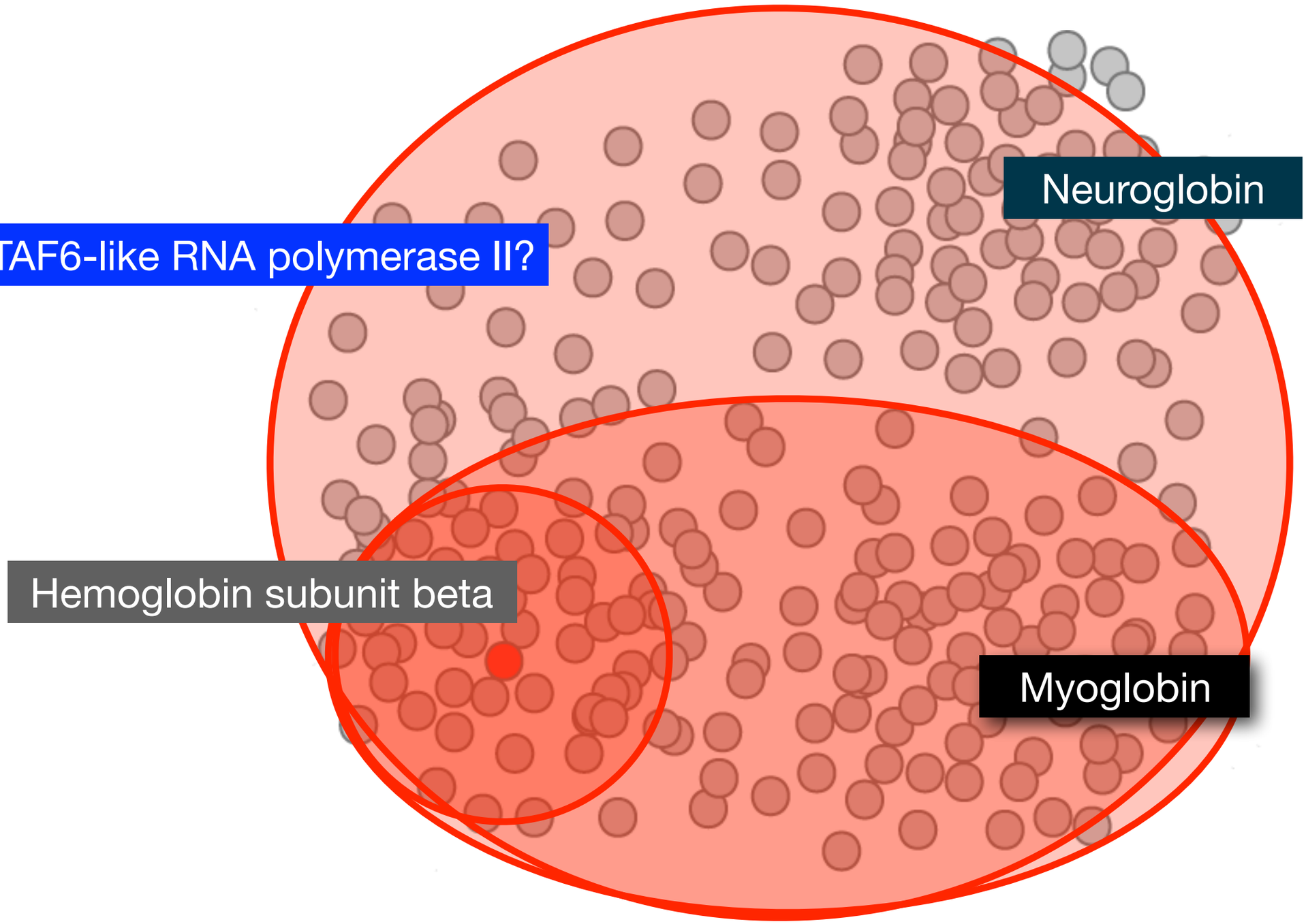

Neuroglobin
Hemoglobin subunit beta
Myoglobin
Start search with single human **HBB** sequence


Neuroglobin
Hemoglobin subunit beta
Myoglobin
Result of initial
BLASTp search



Result of subsequent **PSI-BLAST** iteration

(*note, more globin hits!*)



Result of later **PSI-BLAST** iteration

(*note, potential "corruption"!*)

Description	Max score	Total score	Query cover	E value	Ident	Accession
hemoglobin subunit beta [Homo sapiens]	301	301	100%	2e-106	100%	NP_000509.1
hemoglobin subunit delta [Homo sapiens]	284	284	100%	7e-100	93%	NP_000510.1
hemoglobin subunit epsilon [Homo sapiens]	240	240	100%	2e-82	76%	NP_005321.1
hemoglobin subunit gamma-2 [Homo sapiens]	235	235	100%	2e-80	73%	NP_000175.1
hemoglobin subunit gamma-1 [Homo sapiens]	232	232	100%	3e-79	73%	NP_000550.2
hemoglobin subunit alpha [Homo sapiens]	114	114	97%	7e-33	43%	NP_000508.1
hemoglobin subunit zeta [Homo sapiens]	100	100	97%	3e-27	36%	NP_005323.1

1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hemoglobin subunit beta [Homo sapiens]	301	301	100%	2e-106	100%	NP_000509.1
hemoglobin subunit delta [Homo sapiens]	284	284	100%	7e-100	93%	NP_000510.1
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hemoglobin subunit alpha [Homo sapiens]	114	114	97%	7e-33	43%	NP_000508.1
hemoglobin subunit zeta [Homo sapiens]	100	100	97%	3e-27	36%	NP_005323.1

1

myoglobin [Homo sapiens]	80.5	80.5	97%	2e-19	26%	NP_005359.1
neuroglobin [Homo sapiens]	54.7	54.7	92%	2e-09	23%	NP_067080.1

2

New relevant globins found only by PSI-BLAST

Description	Max score	Total score	Query cover	E value	Ident	Accession
hemoglobin subunit beta [Homo sapiens]	301	301	100%	2e-106	100%	NP_000509.1
hemoglobin subunit delta [Homo sapiens]	284	284	100%	7e-100	93%	NP_000510.1
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1

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neuroglobin [Homo sapiens]	54.7	54.7	92%	2e-09	23%	NP_067080.1

2

myoglobin [Homo sapiens]	159	159	97%	3e-50	26%	NP_005359.1
hemoglobin subunit alpha [Homo sapiens]	151	151	97%	3e-47	42%	NP_000508.1
hemoglobin subunit mu [Homo sapiens]	147	147	97%	6e-46	35%	NP_001003938.1
hemoglobin subunit theta-1 [Homo sapiens]	147	147	97%	2e-45	37%	NP_005322.1
neuroglobin [Homo sapiens]	134	134	92%	3e-40	23%	NP_067080.1
PREDICTED: cytoglobin isoform X2 [Homo sapiens]	115	115	66%	3e-33	25%	XP_016879605.1
PREDICTED: microtubule cross-linking factor 1 isoform X1 [Homo sapie	46.3	46.3	27%	7e-06	39%	XP_011523942.1
PREDICTED: microtubule cross-linking factor 1 isoform X4 [Homo sapie	46.3	46.3	27%	7e-06	39%	XP_005258156.1

3

?

Inclusion of irrelevant hits can lead to PSSM corruption

Description	Max score	Total score	Query cover	E value	Ident	Accession
hemoglobin subunit beta [Homo sapiens]	301	301	100%	2e-106	100%	NP_000509.1
hemoglobin subunit delta [Homo sapiens]	284	284	100%	7e-100	93%	NP_000510.1
hemoglobin subunit epsilon [Homo sapiens]	240	240	100%	2e-82	76%	NP_005321.1
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1

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2

myoglobin [Homo sapiens]	159	159	97%	3e-50	26%	NP_005359.1
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PREDICTED: microtubule cross-linking factor 1 isoform X4 [Homo sapie	46.3	46.3	27%	7e-06	39%	XP_005258156.1

3

Score and E value depends on PSSM

PSI-BLAST is performed in five steps

- A normal blastp search uses a scoring matrix (e.g., BLOSUM62) to perform pairwise alignments of your query sequence (such as RBP) against the database. PSI-BLAST also begins with a protein query that is searched against a database of choice.

- PSI-BLAST constructs a multiple sequence alignment (MSA) from an initial blastp-like search. It then creates a **PSSM** based on that multiple alignment.

- This **PSSM** is then used as a query to search the database again.

- PSI-BLAST estimates the statistical significance of the database matches, essentially using the parameters we described for gapped alignments.

- The search process is continued iteratively, typically 3 to 5 times. At each step a new PSSM is built.

PSI-BLAST returns dramatically more hits

You must decide how many iterations to perform and which sequences to include!

> You can stop the search process at any point - typically whenever few new results are returned or when no new “sensible” results are found.

Iteration	Hits with E < 0.005	Hits with E > 0.005
1	34	61
2	314	79
3	416	57
4	432	50
5	432	50

Human retinol-binding protein 4 (RBP4; P02753) was used as a query in a PSI-BLAST search of the RefSeq database.

PSI-BLAST errors: the corruption problem

The main source of error in PSI-BLAST searches is the spurious amplification of sequences that are unrelated to the query.

There are three main approaches to stopping corruption of PSI-BLAST queries:

- Perform multi-domain splitting of your query sequence
  If a query protein has several different domains PSI-BLAST may find database matches related to both individually. One should not conclude that these hits with different domains are related.
  - Often best to search using just one domain of interest.

- Inspect each PSI-BLAST iteration removing suspicious hits.
  E.g., your query protein may have a generic coiled-coil domain, and this may cause other proteins sharing this motif (such as myosin) to score better than the inclusion threshold even though they are not related.
  - Use your biological knowledge!

- Lower the default expect level (e.g., E = 0.005 to E = 0.0001).
  This may suppress appearance of FPs (but also TPs)

Profile advantages and disadvantages

Advantages:

- Quantitate with a good scoring system
- Weights sequences according to observed diversity
  Profile is specific to input sequence set
- Very sensitive
  Can detect weak similarity
- Relatively easy to compute
  Automatic profile building tools available

Disadvantages:

- If a mistake enters the profile, you may end up with irrelevant data
  The corruption problem!
- Ignores higher order dependencies between positions
  i.e., correlations between the residue found at a given position and those found at other positions (e.g. salt-bridges, structural constraints on RNA etc...)
- Requires some expertise and oversight to use proficiently

Today's Menu

- Sequence motifs and patterns: Simple approaches for finding functional cues from conservation patterns
- Sequence profiles and position specific scoring matrices (PSSMs): Building and searching with profiles, Their advantages and limitations
- PSI-BLAST algorithm: Application of iterative PSSM searching to improve BLAST sensitivity
- Hidden Markov models (HMMs): More versatile probabilistic model for detection of remote similarities

Your Turn!

Hands-on sections 3 & 4:
Comparing methods and the trade-off between sensitivity, selectivity and performance

~30 mins

Problems with PSSMs: Positional dependencies

Do not capture positional dependencies

WEIRD
WEIRD
WEIQH
WEIRD
WEIQH

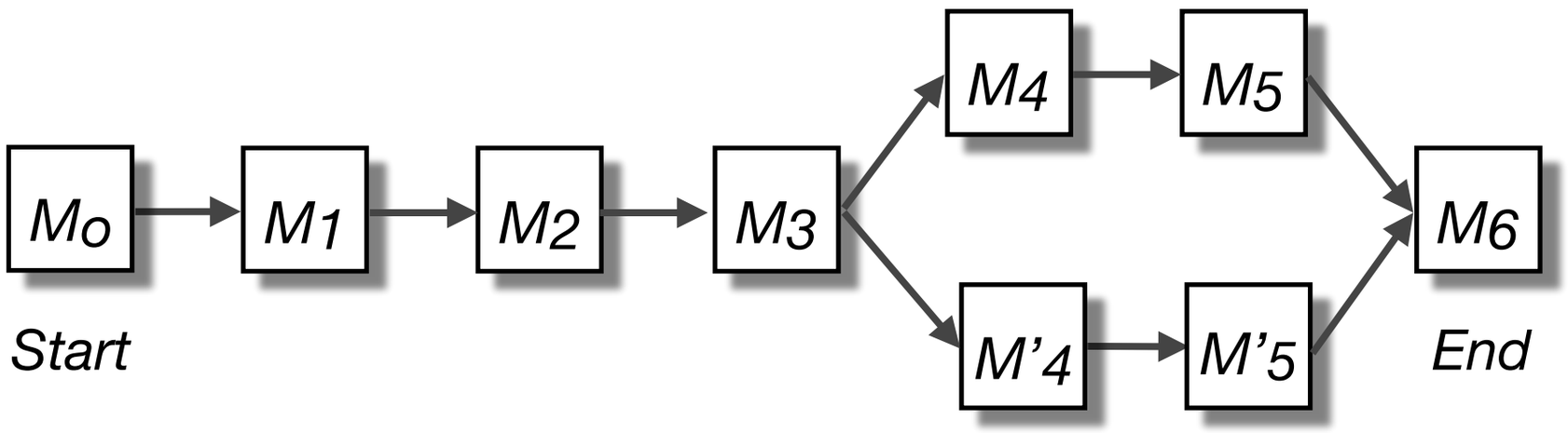
D					0.6
E		I			
H					0.4
I			I		
Q				0.4	
R				0.6	
W	I				

Note: We <u>never</u> see **QD** or **RH**, we only see **RD** and **QH**.
However, P(RH)=0.24, P(QD)=0.24, while P(QH)=0.16

Markov chains: Positional dependencies

The connectivity or **topology** of a Markov chain can easily be designed to capture dependencies and variable length motifs.

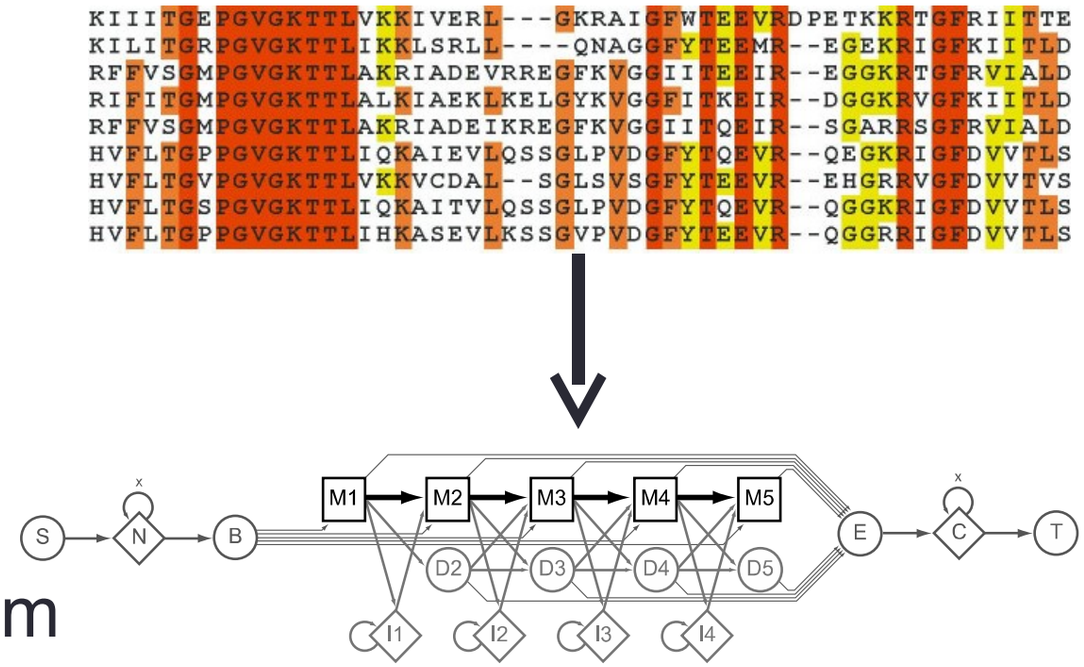
WEIRD
WEIRD
WEIQH
WEIRD
WEIQH



Recall that a PSSM for this motif would give the sequences **WEIRD** and **WEIRH** equally good scores even though the **RH** and **QR** combinations were not observed

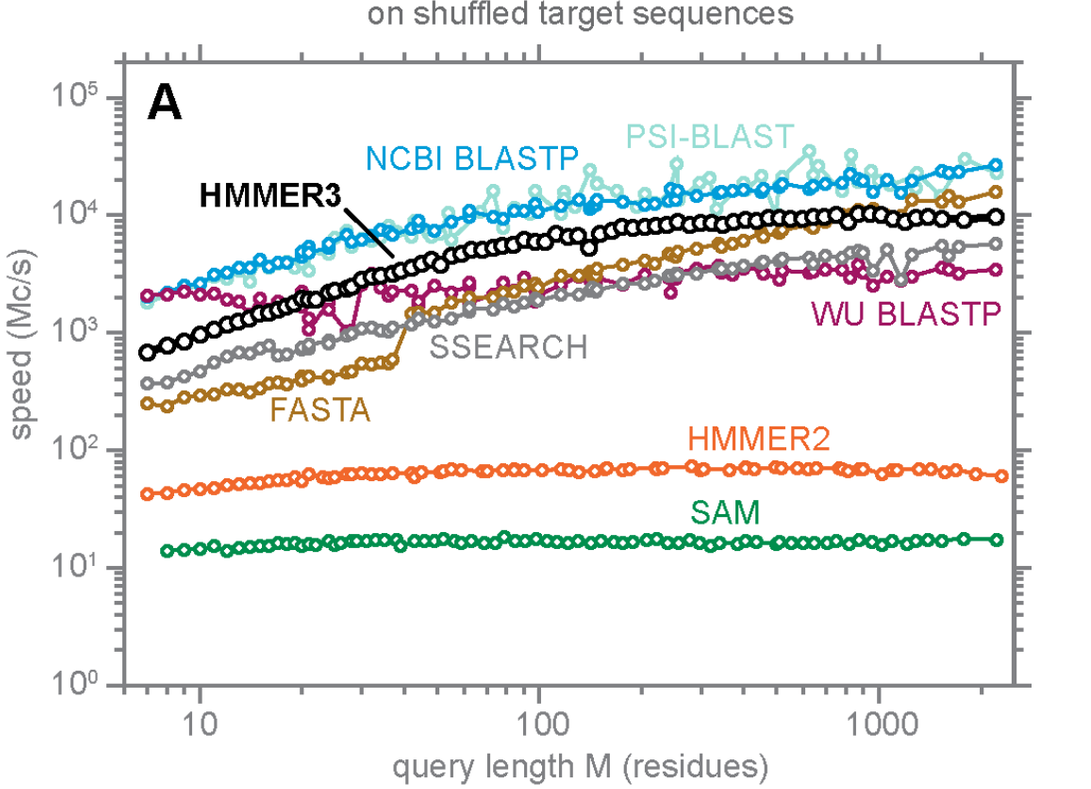
Use of HMMER

- Widely used by protein family databases
  - Use ‘seed’ alignments
- Until 2010
  - Computationally expensive
  - Restricted to HMMs constructed from multiple sequence alignments
- Command line application



HMMER vs BLAST

	HMMER	BLAST
Program	*PHMMER*	*BLASTP*
Query	Single sequence	
Target Database	Sequence database	
Program	*HMMSCAN*	*RPSBLAST*
Query	Single sequence	
Target Database	Profile HMM database, e.g. Pfam	PSSM database, e.g. CDD
Program	*HMMSEARCH*	*PSI-BLAST*
Query	Profile HMM	PSSM
Target Database	Sequence database	
Program	*JACKHMMER*	*PSI-BLAST*
Query	Single sequence	
Target Database	Sequence database	



Modified from: S. R. Eddy
PLoS Comp. Biol., 7:e1002195, 2011.

Fast Web Searches

- Parallelized searches across compute farm
  - Average query returns ~1 sec
- Range of sequence databases
  - Large Comprehensive
  - Curated / Structure
  - Metagenomics
  - Representative Proteomes
- Family Annotations
  - Pfam
- Batch and RESTful API
  - Automatic and Human interface

HMMER

Biosequence analysis using profile hidden Markov Models

phmmer | hmmscan | hmmsearch | jackhmmer

protein sequence vs protein sequence database

Paste a Sequence | Upload a File | Accession Search

Paste in your sequence or use the example

```
>NP_000509.1 hemoglobin subunit beta [Homo sapiens]
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLG
AFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVAN
ALAHKYH
```

Submit | Reset

▼ **Sequence Database**

Frequently used databases: Reference Proteomes | UniProtKB | SwissProt | PDB | Ensembl

Current database selection:

SwissProt

▼ **Restrict by Taxonomy**

Taxon search | Pre-defined representatives

Organism:

Significant Query Matches (12) in *swissprot* (v.2018_11)

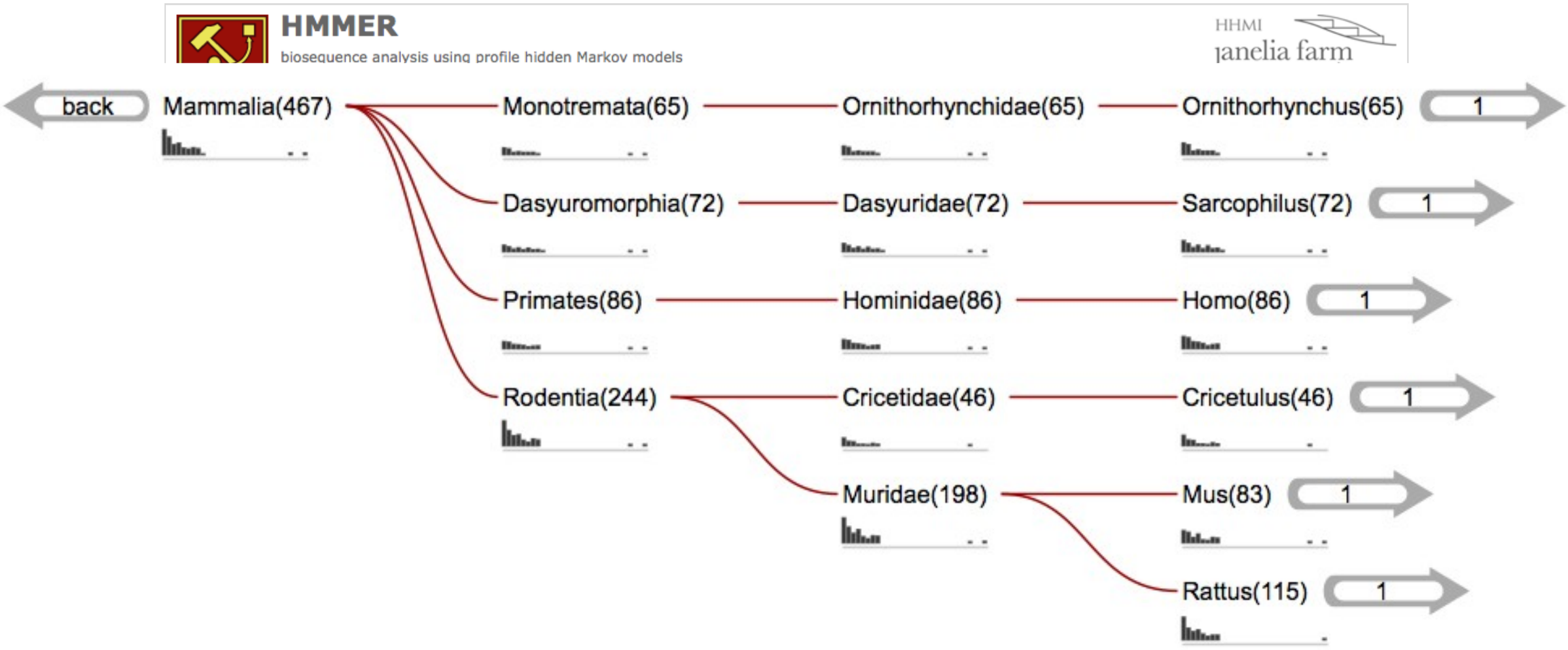
Customise Customise

	Target	Description	Species	Cross-references	E-value
>	HBB_HUMAN	Hemoglobin subunit beta	Homo sapiens		6.8e-99
>	HBD_HUMAN	Hemoglobin subunit delta	Homo sapiens		1.6e-91
>	HBE_HUMAN	Hemoglobin subunit epsilon	Homo sapiens		1.5e-74
>	HBG2_HUMAN	Hemoglobin subunit gamma-2	Homo sapiens		8.8e-73
>	HBG1_HUMAN	Hemoglobin subunit gamma-1	Homo sapiens		6.2e-72
>	HBA_HUMAN	Hemoglobin subunit alpha	Homo sapiens		3.8e-29
>	HBAZ_HUMAN	Hemoglobin subunit zeta	Homo sapiens		4.5e-23
>	HBAT_HUMAN	Hemoglobin subunit theta-1	Homo sapiens		5.2e-22
>	HBM_HUMAN	Hemoglobin subunit mu	Homo sapiens		3.4e-19
>	CYGB_HUMAN	Cytoglobin	Homo sapiens		3.1e-14
>	MYG_HUMAN	Myoglobin	Homo sapiens		2.3e-06
>	NGB_HUMAN	Neuroglobin	Homo sapiens		0.0017

(show all) alignments Your search took: 0.06 secs showing rows 1 - 12 of 12

Local Link

Visualization of Results – By Taxonomy



Species Distribution

Species	Count	View
Rattus norvegicus	115	Show
Homo sapiens	86	Show
Mus musculus	83	Show
Sarcophilus harrisii	72	Show
Ornithorhynchus anatinus	65	Show
Cricetulus griseus	46	Show

Show All Visible

Search Details
Jump to threshold page

PFAM: Protein Family Database of Profile HMMs

Comprehensive compilation of both multiple sequence alignments and profile HMMs of protein families.

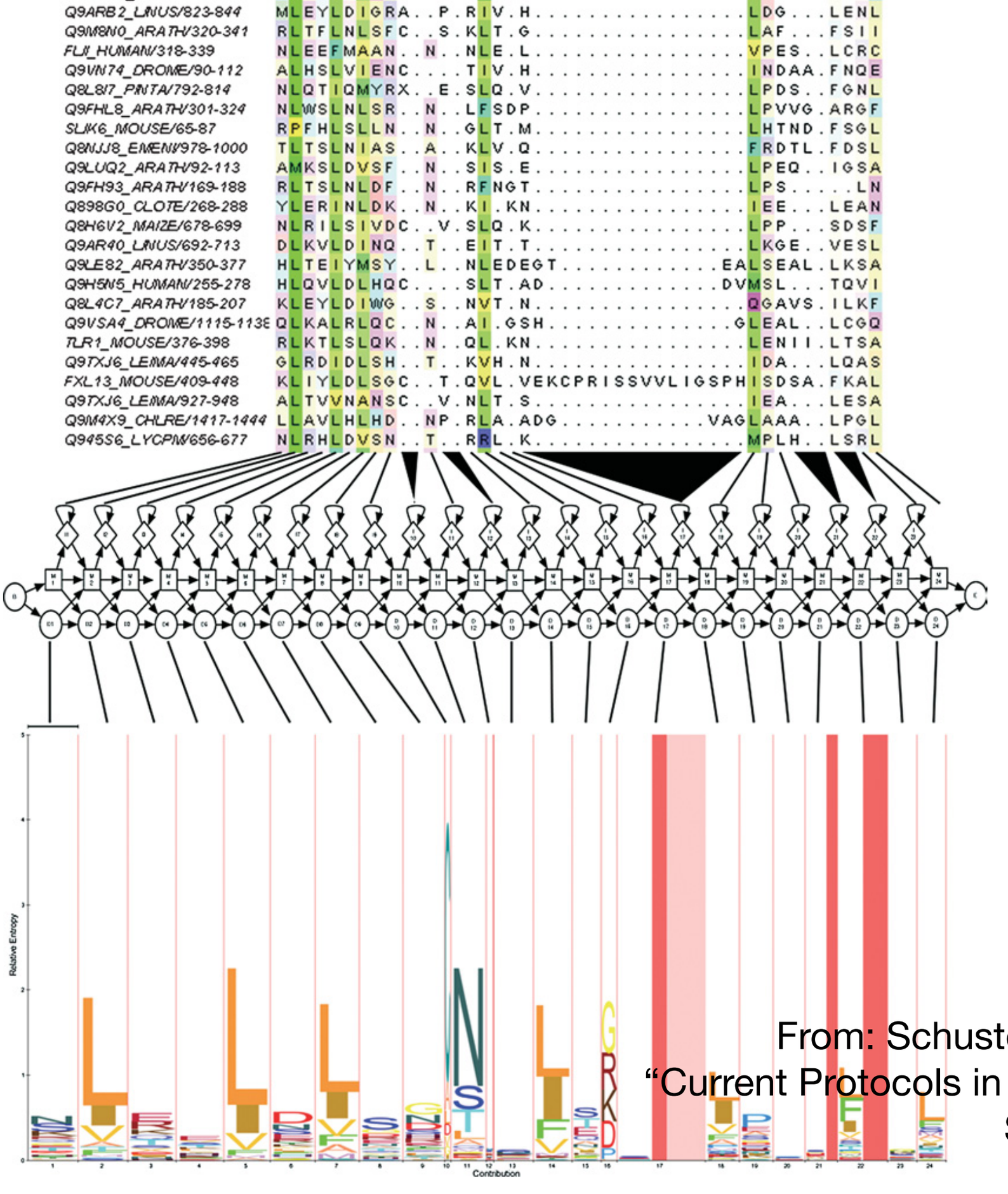
http://pfam.sanger.ac.uk/

PFAM consists of two databases:

- **Pfam-A** is a manually curated collection of protein families in the form of multiple sequence alignments and profile HMMs. HMMER software is used to perform searches.

- **Pfam-B** contains additional protein sequences that are automatically aligned. Pfam-B serves as a useful supplement that makes the database more comprehensive.

- Pfam-A also contains higher-level groupings of related families, known as **clans**



From: Schuster-Bockler *et al.*
"Current Protocols in Bioinformatics"
Supplement 18.

Summary

- Sequence motifs and patterns: Simple approaches for finding functional cues from conservation patterns
- Sequence profiles and position specific scoring matrices (PSSMs): Building and searching with profiles, Their advantages and limitations
- PSI-BLAST algorithm: Application of iterative PSSM searching to improve BLAST sensitivity
- Hidden Markov models (HMMs): More versatile probabilistic model for detection of remote similarities

Homework: DataCamp!

Install R and RStudio (see website)

Complete the Introduction to R course on DataCamp
(Check your email for your DataCamp invite and sign up with your UCSD email (i.e. first part of your email address) please.

Let me know NOW if you don't have access to DataCamp!

That’s it!

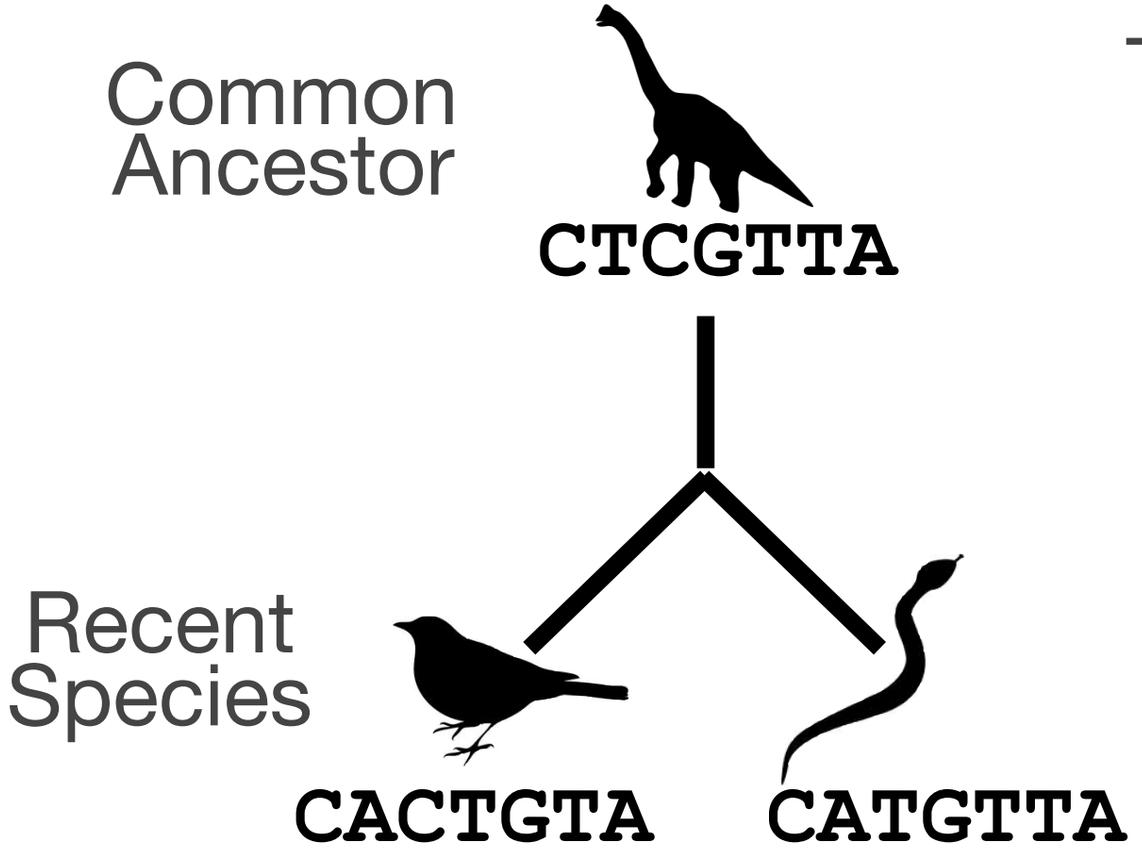
Reference Slides:

Side Note: Orthologs *vs* Paralogs

Sequence comparison is most informative when it detects homologs

Homologs are sequences that have common origins i.e. they share a common ancestor

- They may or may not have common activity



Can be used to establish evolutionary relationships

Key terms

When we talk about related sequences we use specific terminology.

Homologous sequences may be either:

– Orthologs or Paralogs

(Note. these are all or nothing relationships!)

Any pair of sequences may share a certain level of:

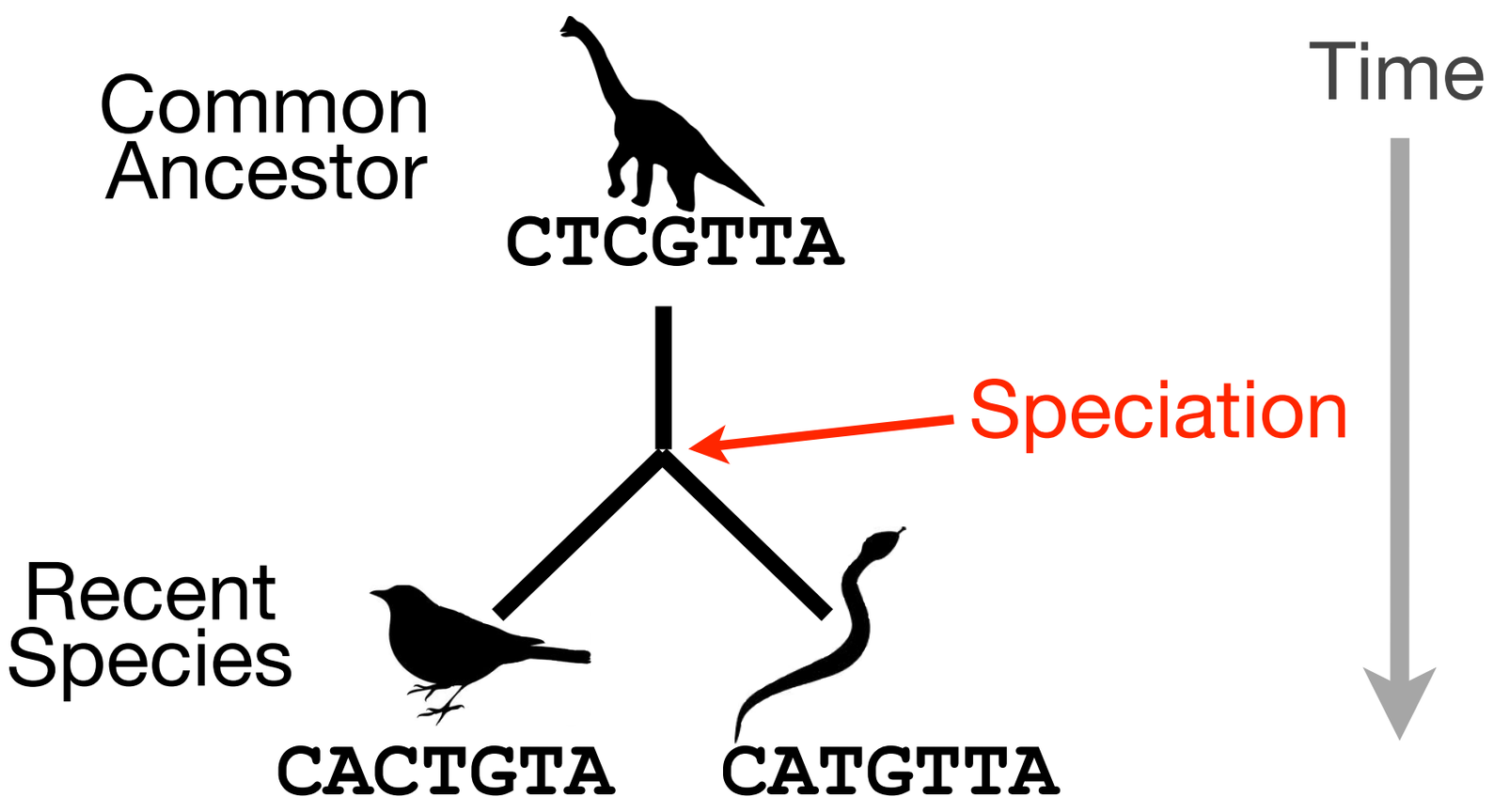
– Identity and/or Similarity

(Note. if these metrics are above a certain level we often infer homology)

Orthologs tend to have similar function

Orthologs: are homologs produced by speciation that have diverged due to divergence of the organisms they are associated with.

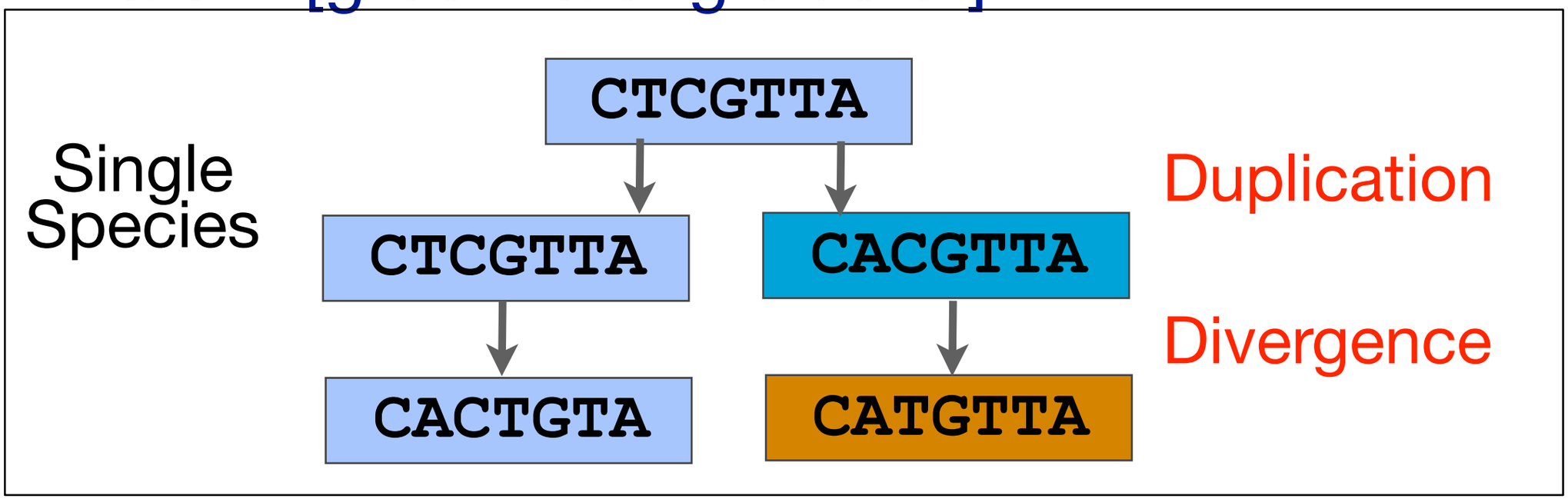
- Ortho = [greek: straight] ... implies direct descent



Paralogs tend to have slightly different functions

Paralogs: are homologs produced by gene duplication. They represent genes derived from a common ancestral gene that duplicated within an organism and then subsequently diverged by accumulated mutation.

– Para = [greek: along side of]



Orthologs vs Paralogs

- In practice, determining ortholog vs paralog can be a complex problem:
  - gene loss after duplication,
  - lack of knowledge of evolutionary history,
  - weak similarity because of evolutionary distance
- Homology does not necessarily imply exact same function
  - may have similar function at very crude level but play a different physiological role