

Homology and pairwise alignment

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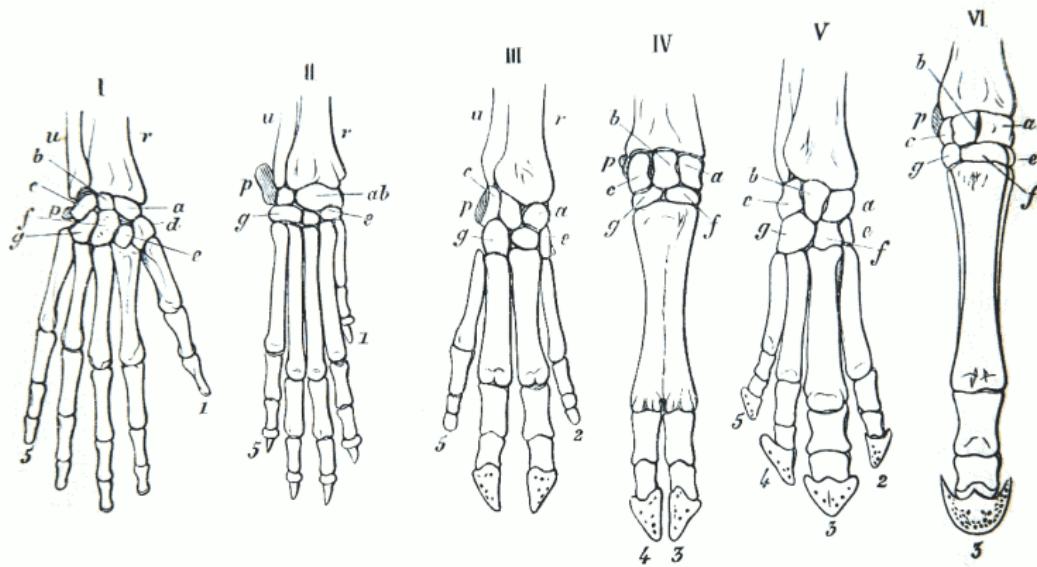
Ο βίος βραχύς,
ἡ δὲ τέχνη μακρή,
ό δὲ καιρὸς ὄξυς,
ἡ δὲ πεῖρα σφαλερή,
ἡ δὲ κρίσις χαλεπή.

— Ἰπποκράτης, Αφ. 1.1

Life is short,
and art long,
opportunity fleeting,
experience perilous,
and decision difficult.

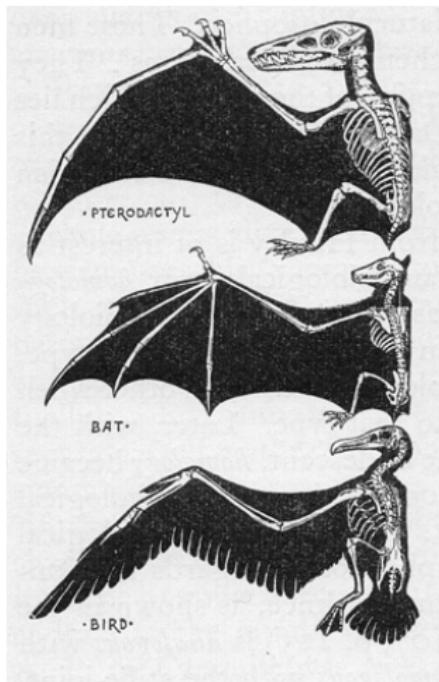
— Hippocrates, Aph. 1.1

Homologous traits descend from a common ancestor



Gegenbaur 1870

Homologous traits descend from a common ancestor



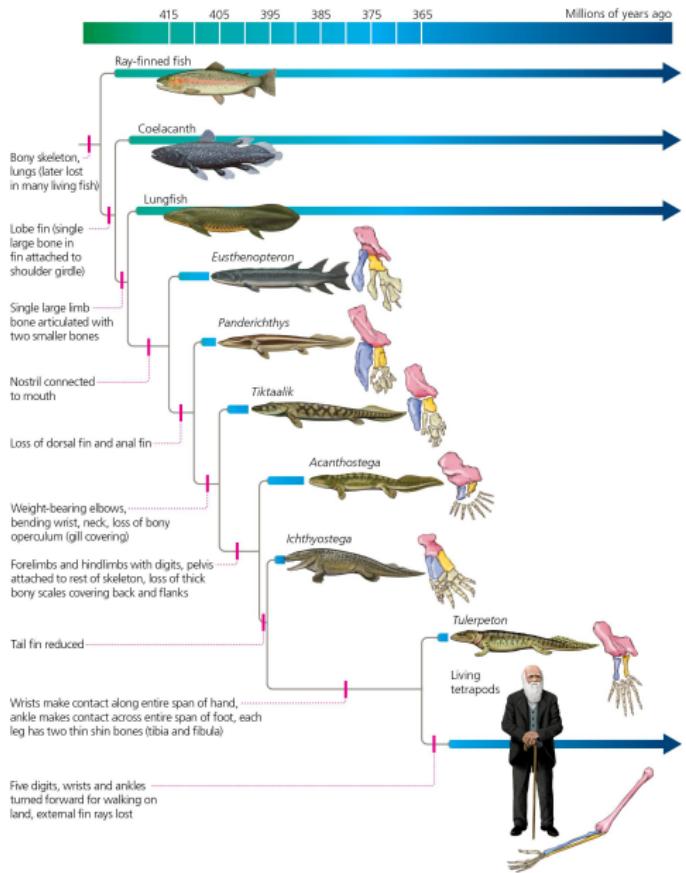
Forelimbs are homologous
(common descent)

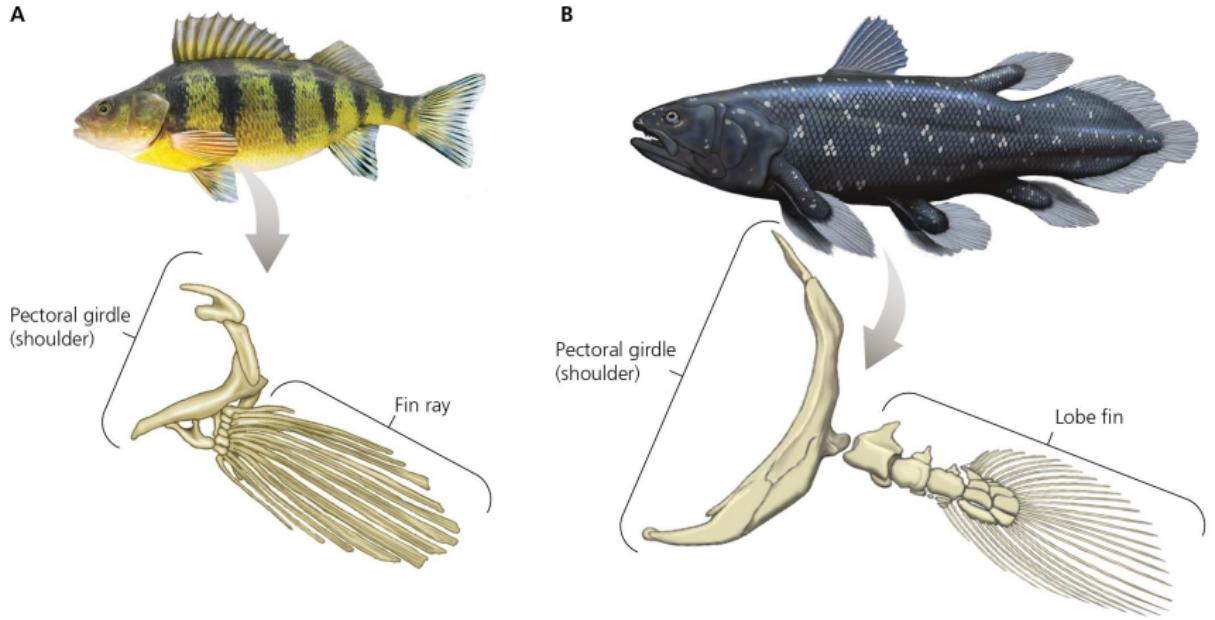
Wings are analogous
(common function)

Romanes 1892

How can we determine homology?

- Test hypotheses based on observations of:
 - morphological similarity (*briefly* discuss)
 - molecular sequence similarity (**mostly** discuss)
- Verify experimentally

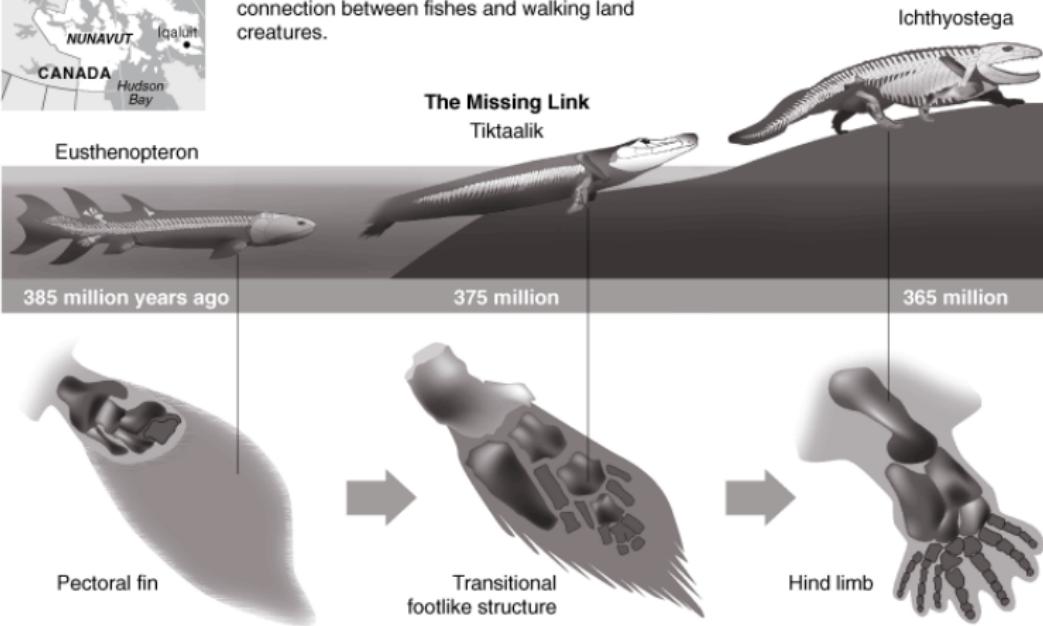






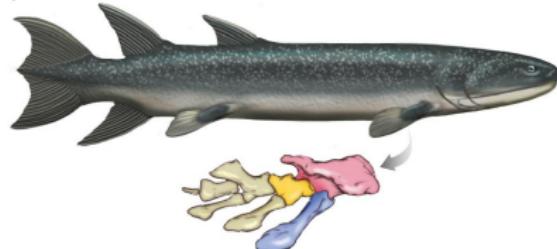
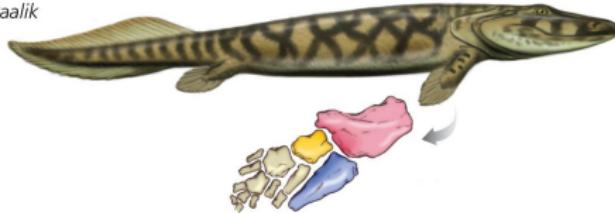
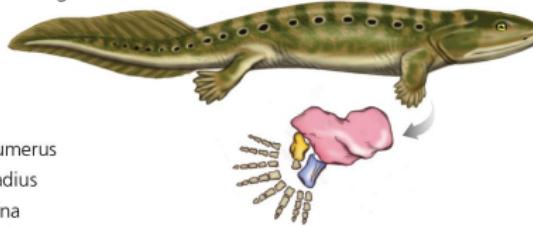
A 'Missing Link' Is Found

With the discovery of fossils of the Tiktaalik, or "large shallow water fish," scientists have found a missing connection between fishes and walking land creatures.



Sources: "Book of Life," edited by Stephen Jay Gould; *Nature*

The New York Times; illustrations by Graham Roberts

Eusthenopteron*Tiktaalik**Acanthostega*

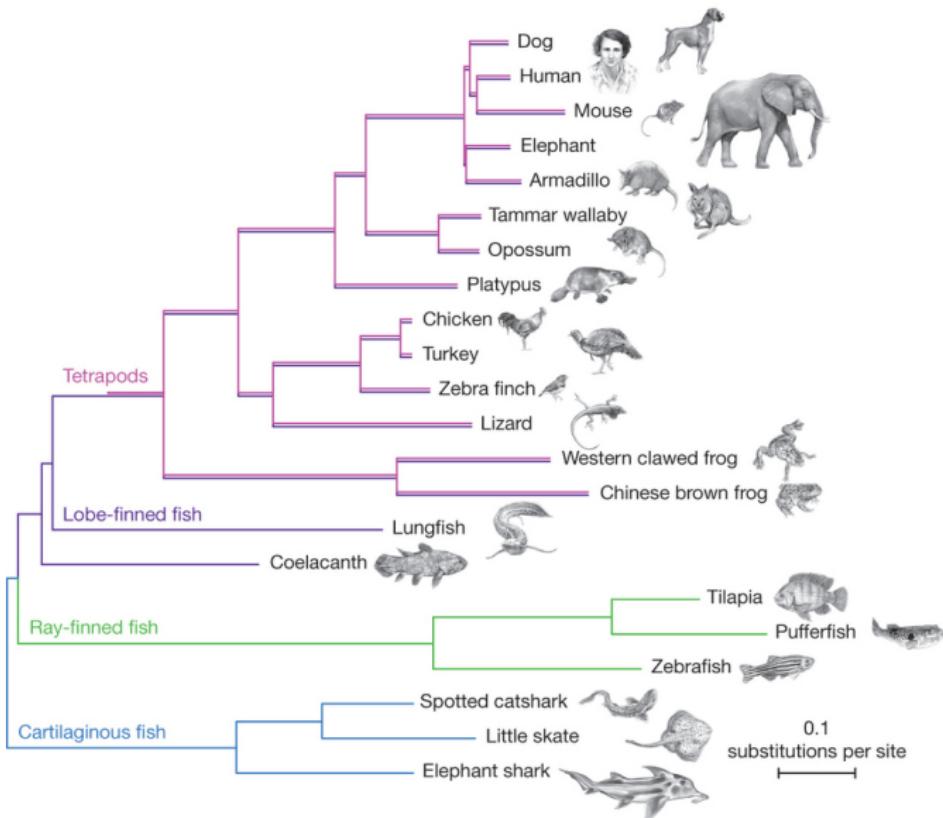
■ Humerus

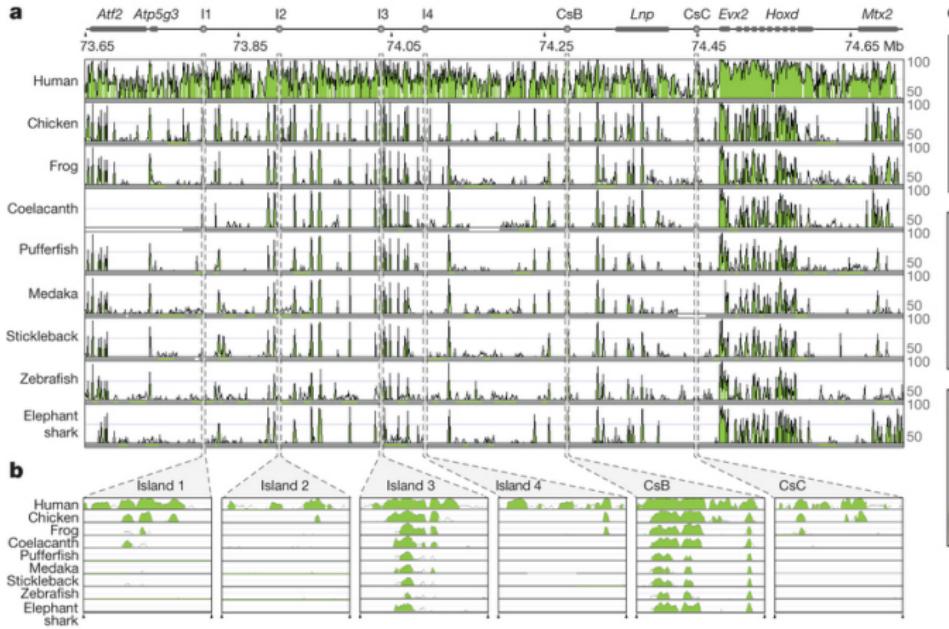
■ Radius

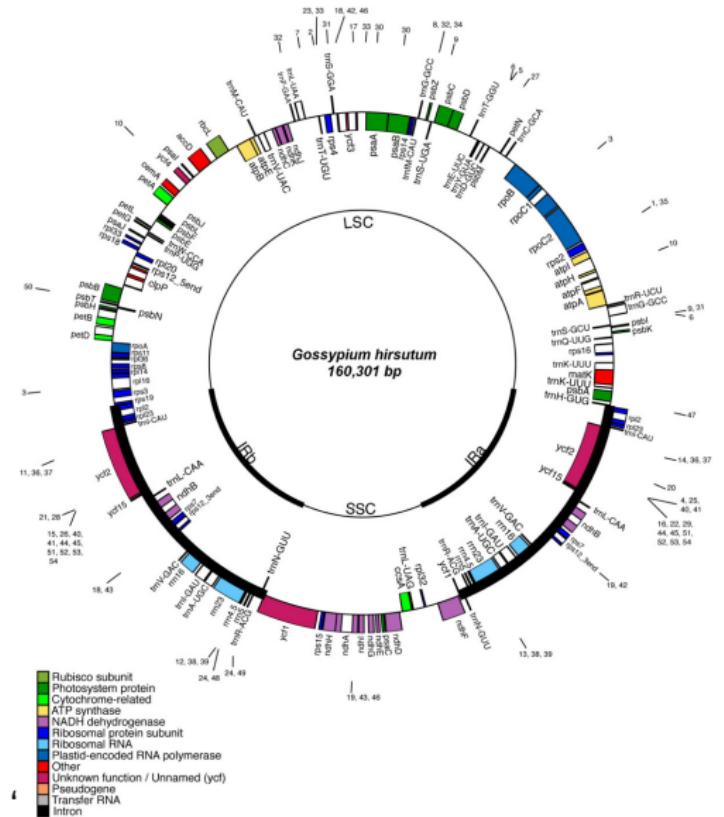
■ Ulna

Coelacanth

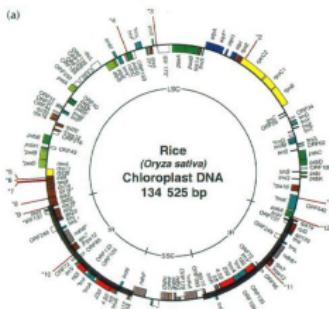
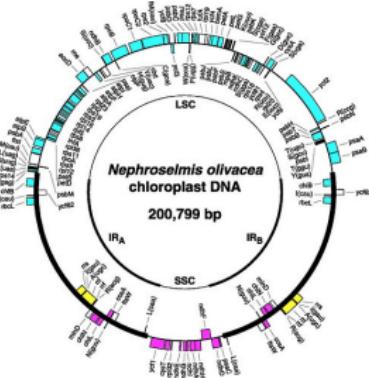
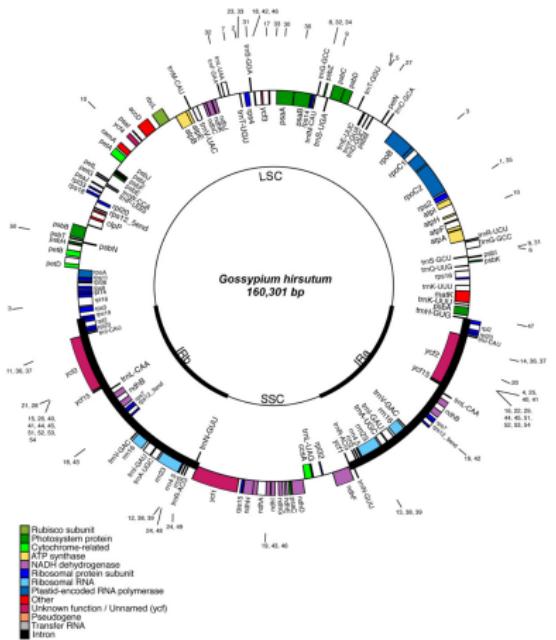


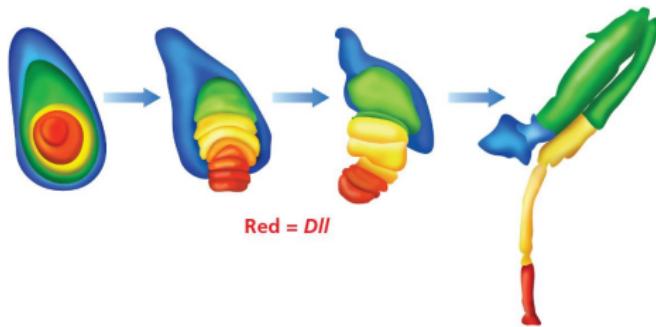
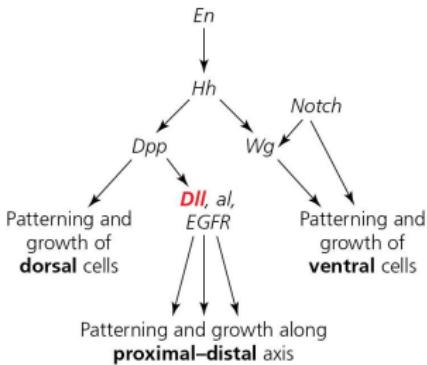
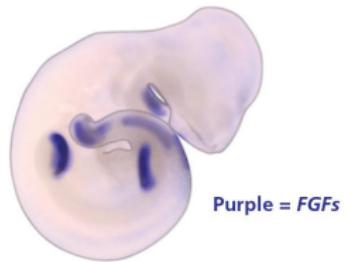
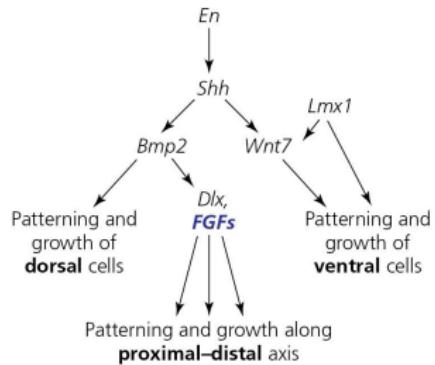




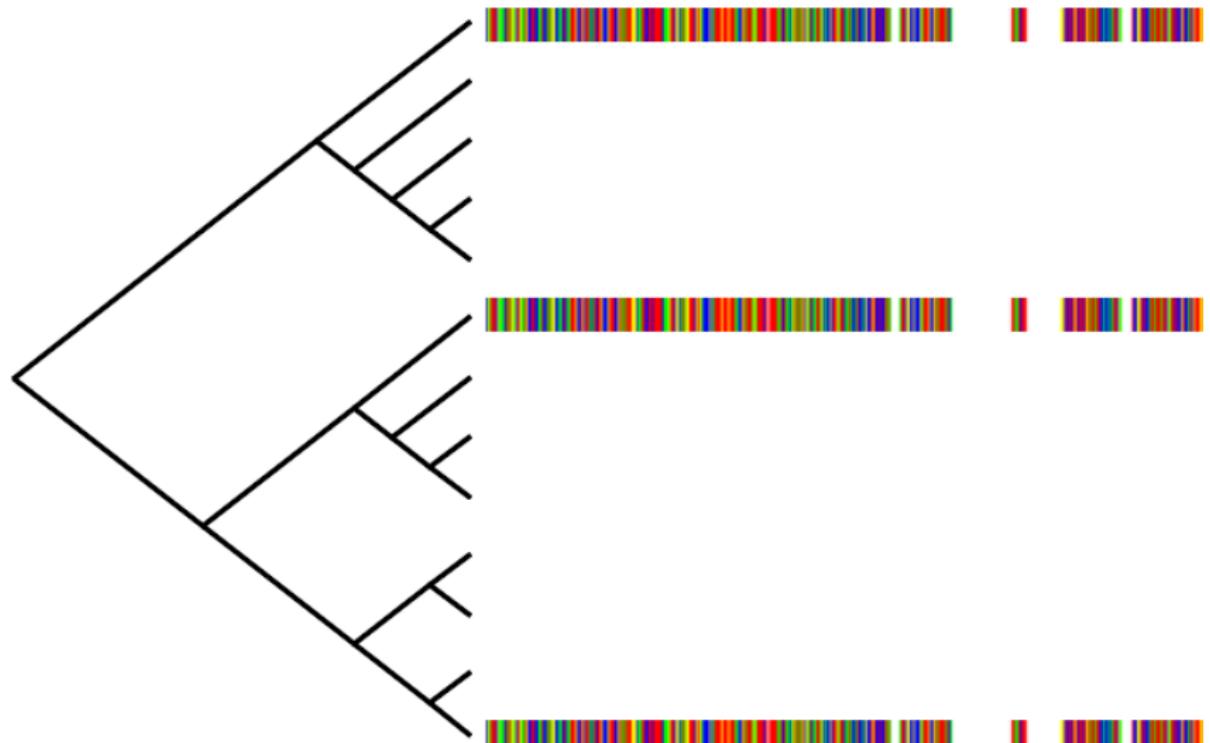


Sequence similarity

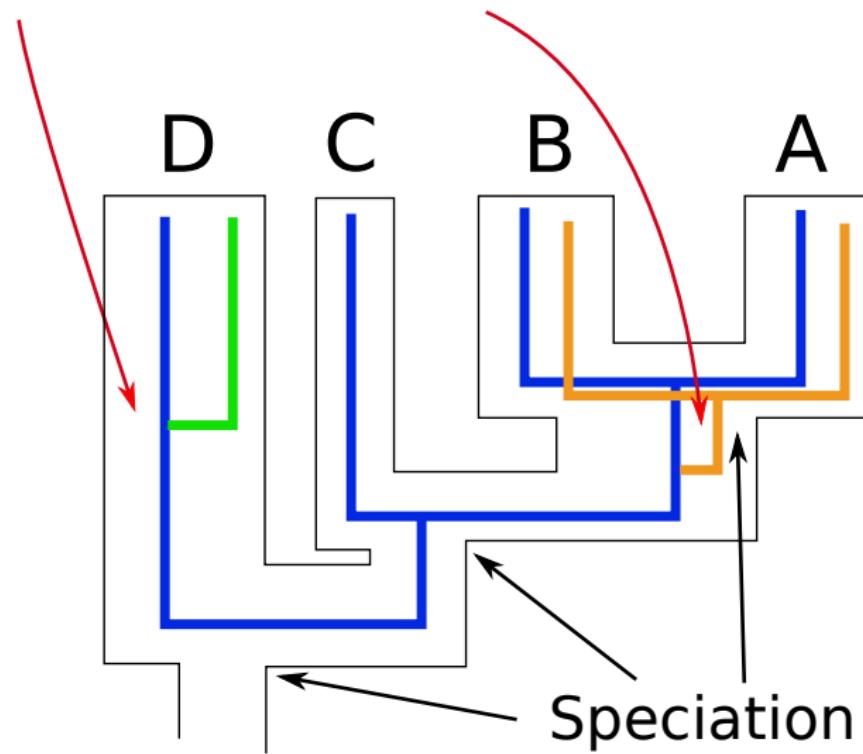


FLY LEG**MOUSE LEG**

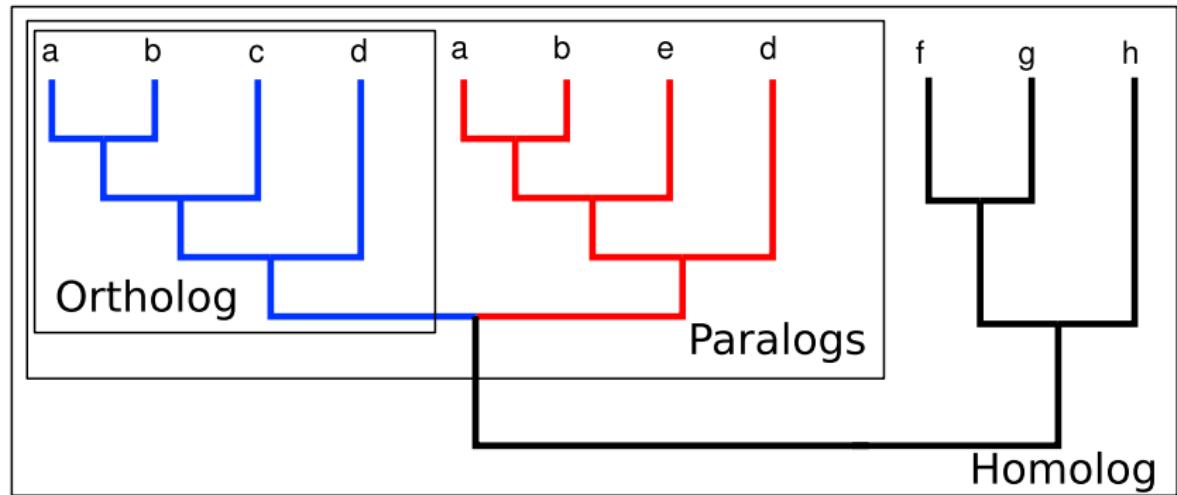
- **rbcL**
 - Ribulose-1,5-bisphosphate carboxylase/oxygenase (large subunit)
 - RuBisCO (large subunit)
- **ITS**
 - internal transcribed spacer
 - ITS1 ITS2



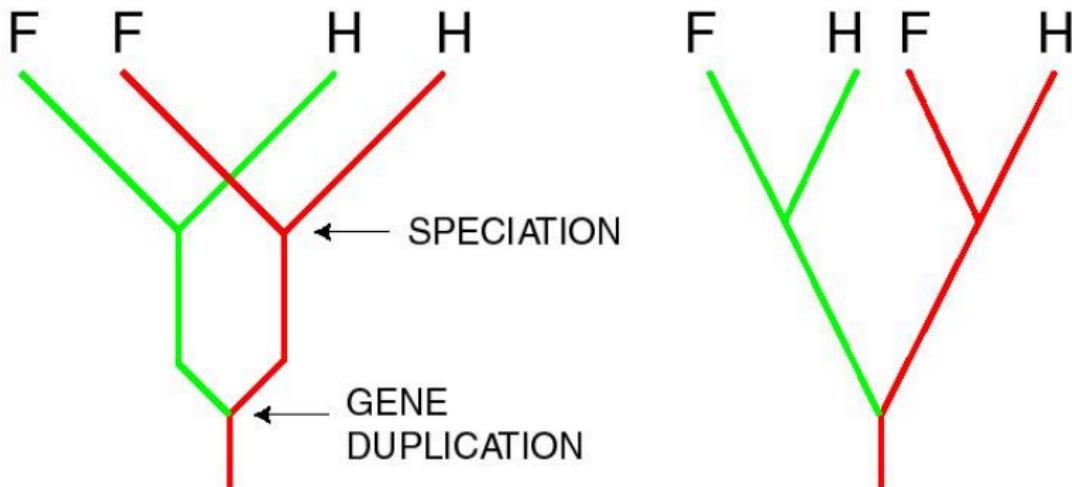
Gene Duplication



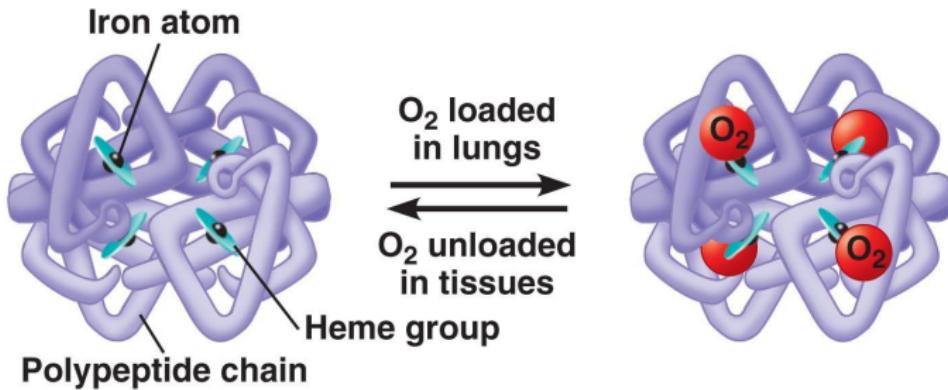
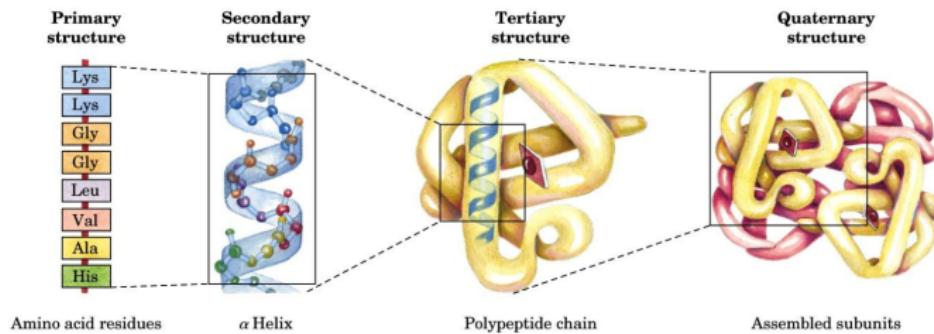
Homology, Orthology, and Paralogy



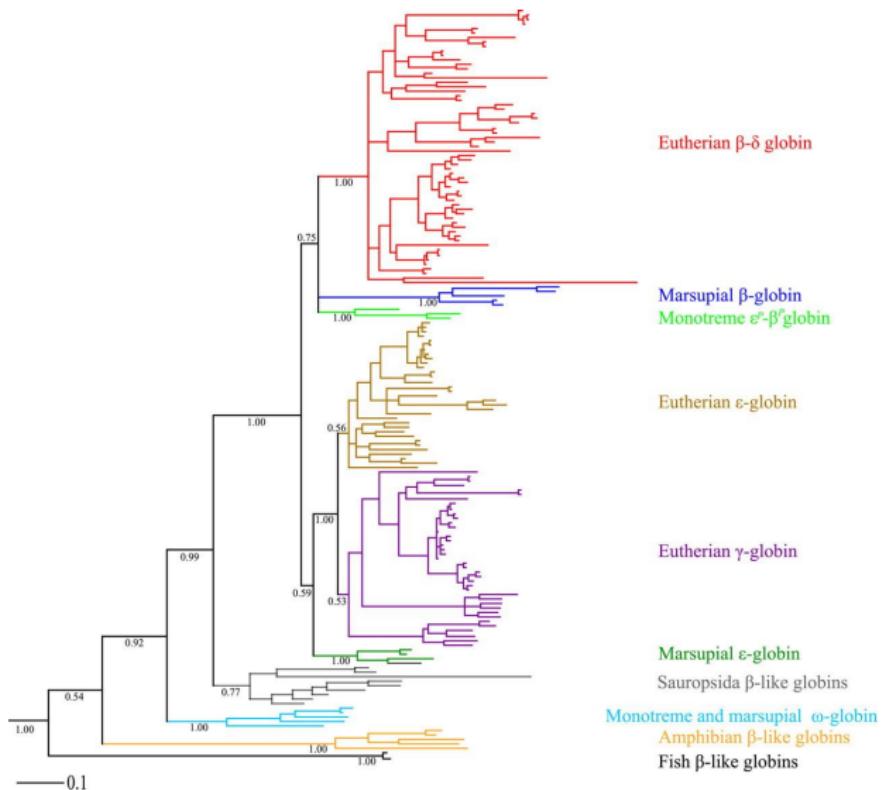
- **Homologs:** descended from a common ancestor
- **Paralogs:** descended from a common ancestor and split by a gene duplication event
- **Orthologs:** descended from a common ancestor and split by a speciation event



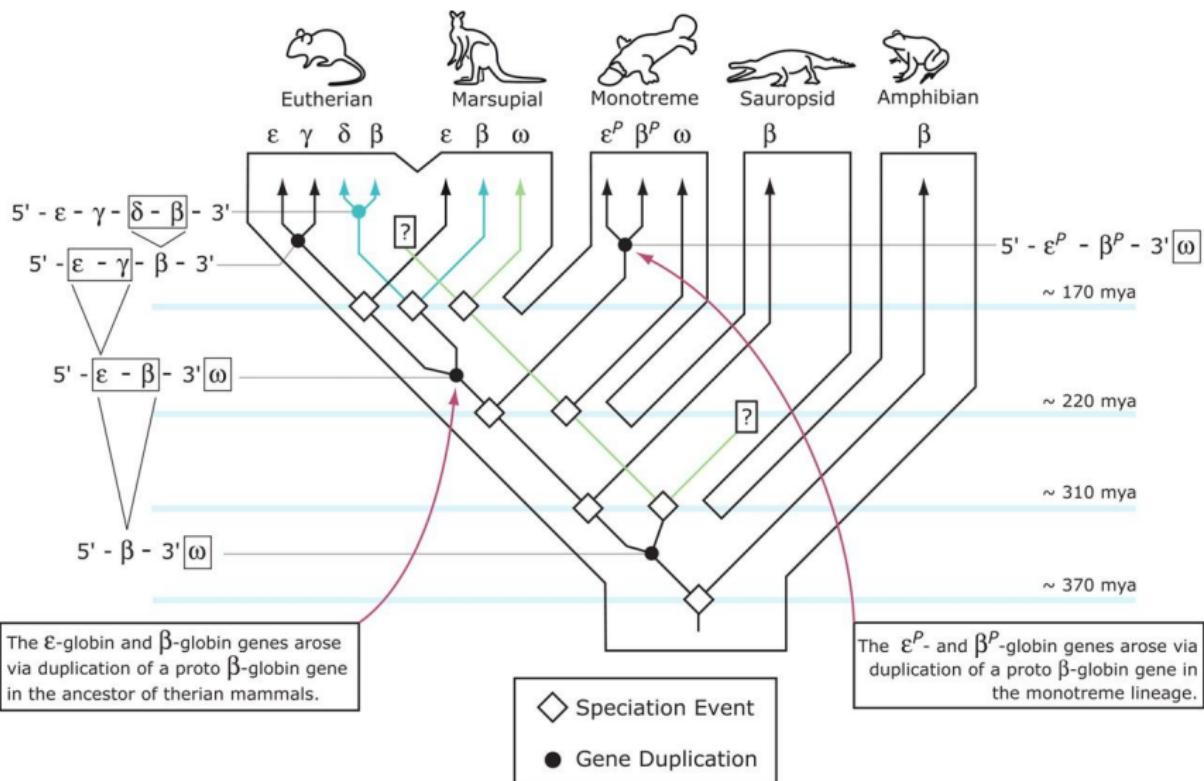
Hemoglobin



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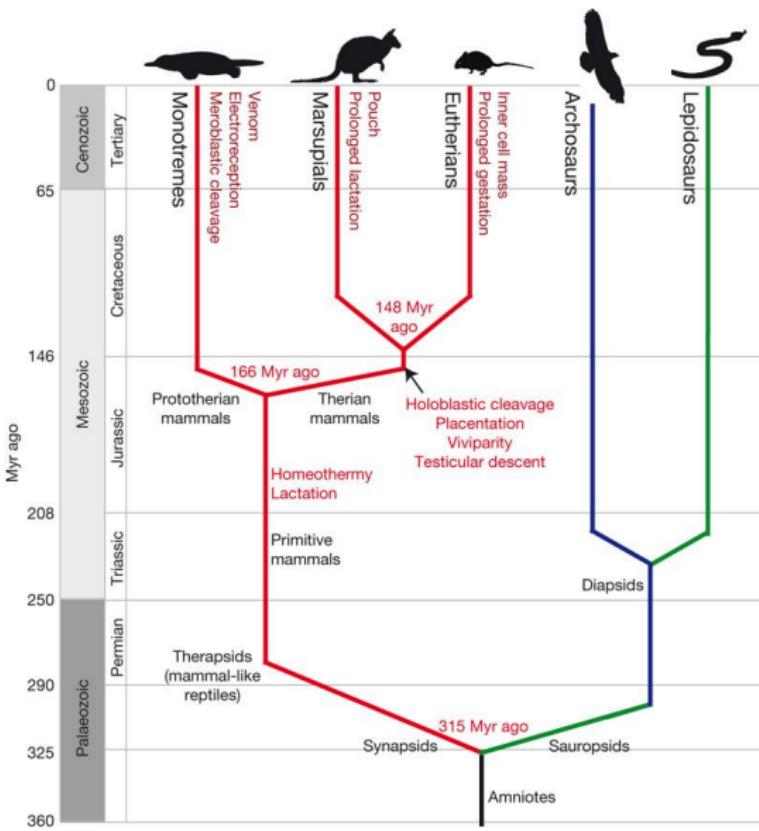


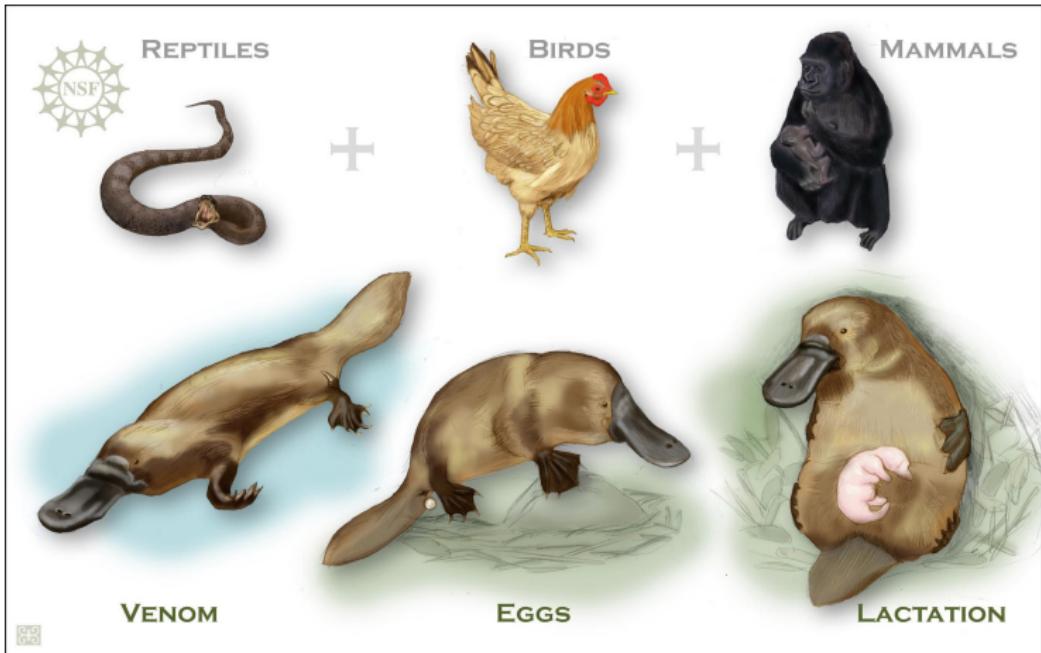
Opazo, Hoffman, and Storz 2008



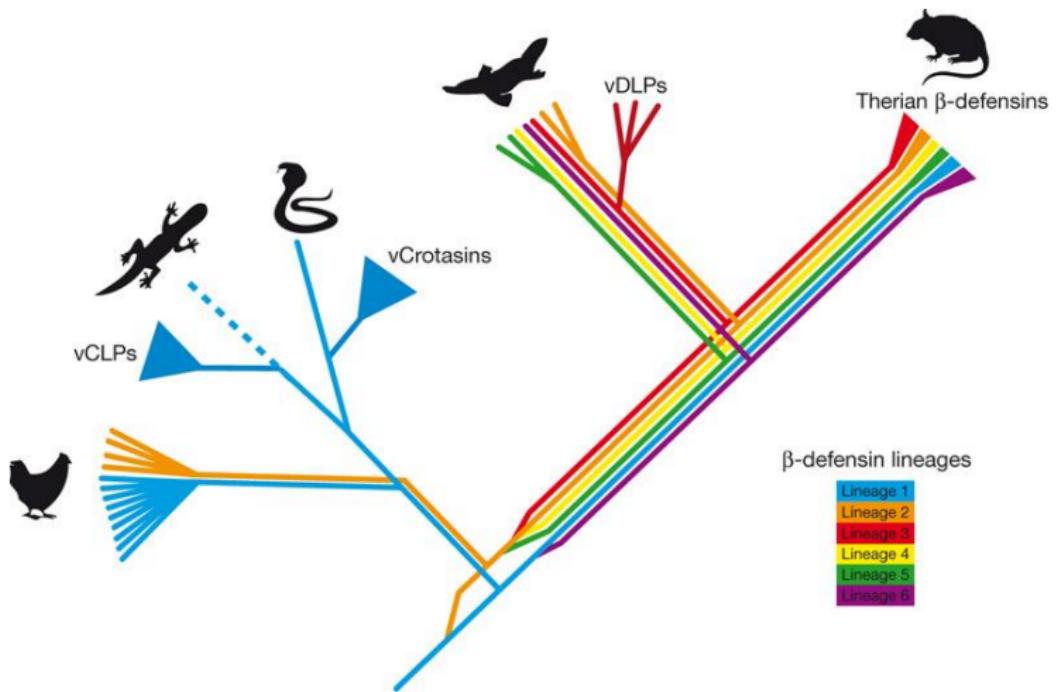
Opazo, Hoffman, and Storz 2008





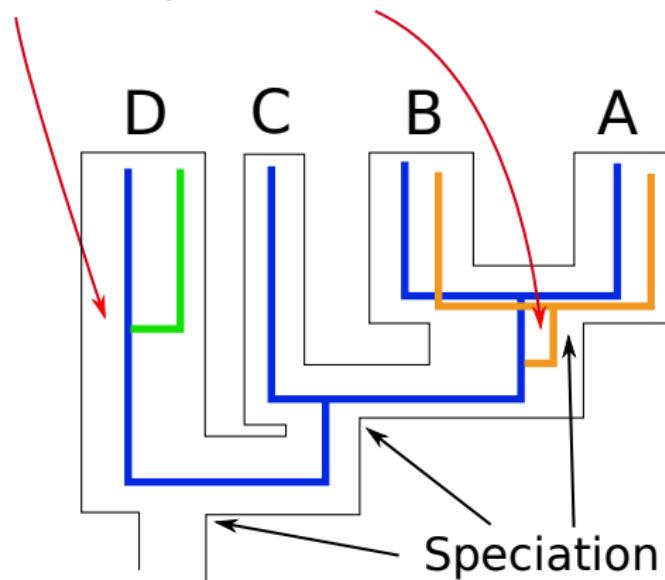


Platypus venom proteins are transcribed in part from duplicated beta defensin genes (vDLPs, venom defensin like proteins)



Why do we need homologs?

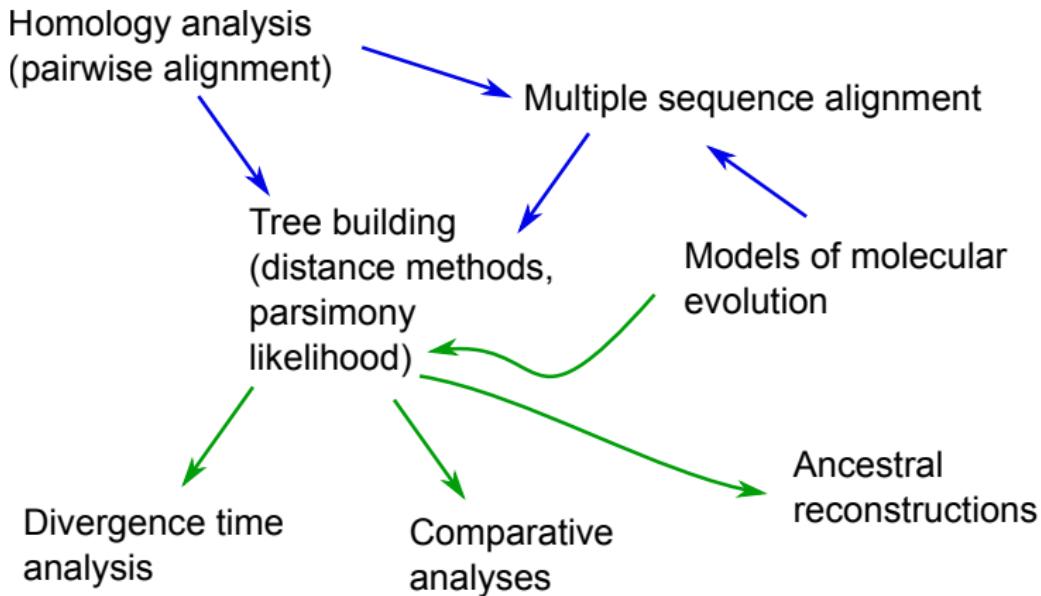
Gene Duplication



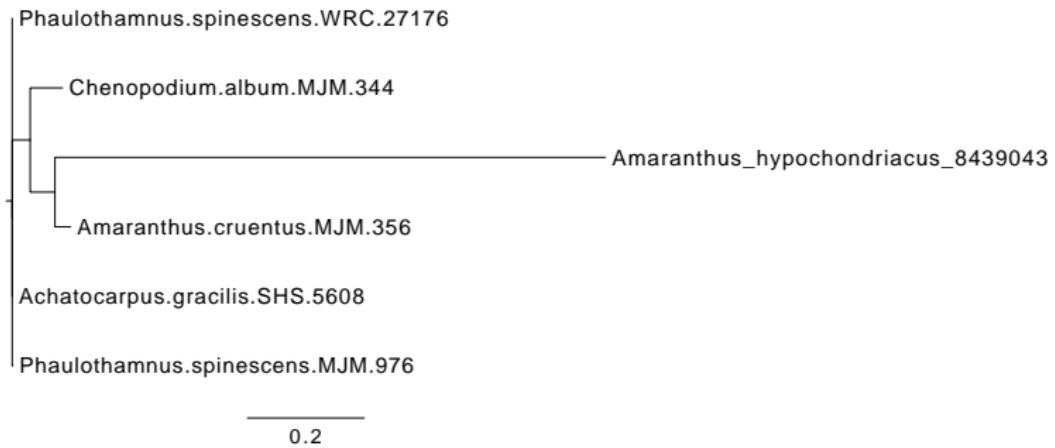
Why do we need homologs?

- In order to **analyze changes in molecular sequences** among species/populations/individuals, we need to find **comparable sequences**.
- Homology is central to:
 - multiple sequence alignment
 - each column is assumed to be a homologous site
 - phylogenetic trees
 - A tree models ancestry relationships, so sequences need to be homologous
 - short read alignment
 - clustering genes

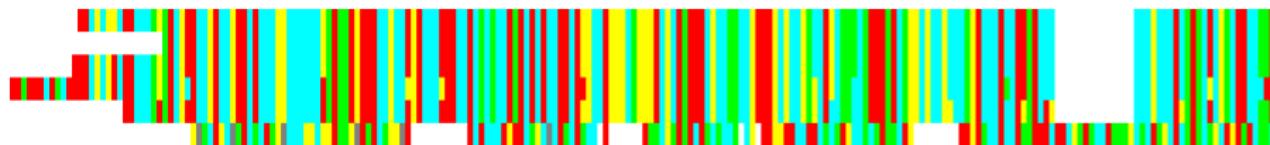
Overview

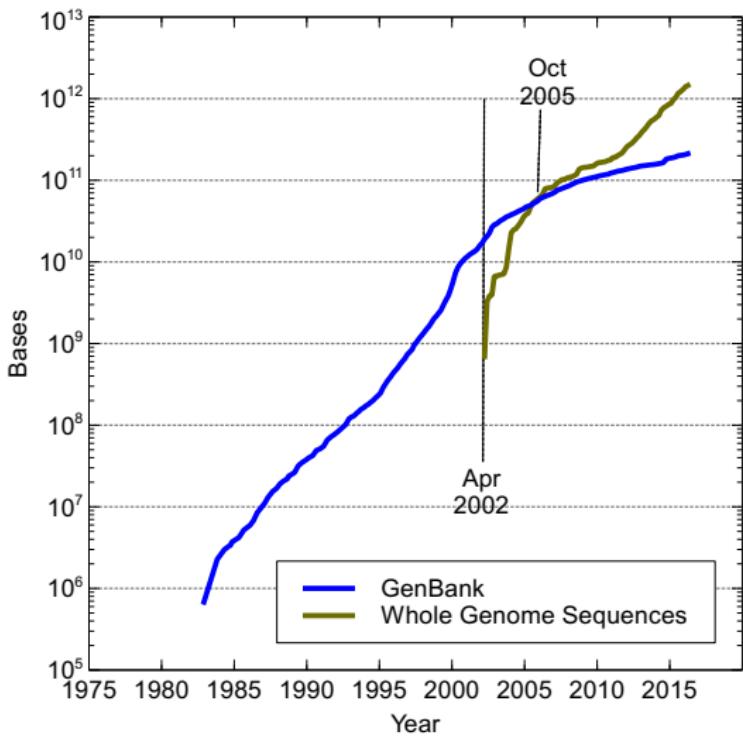


Tree



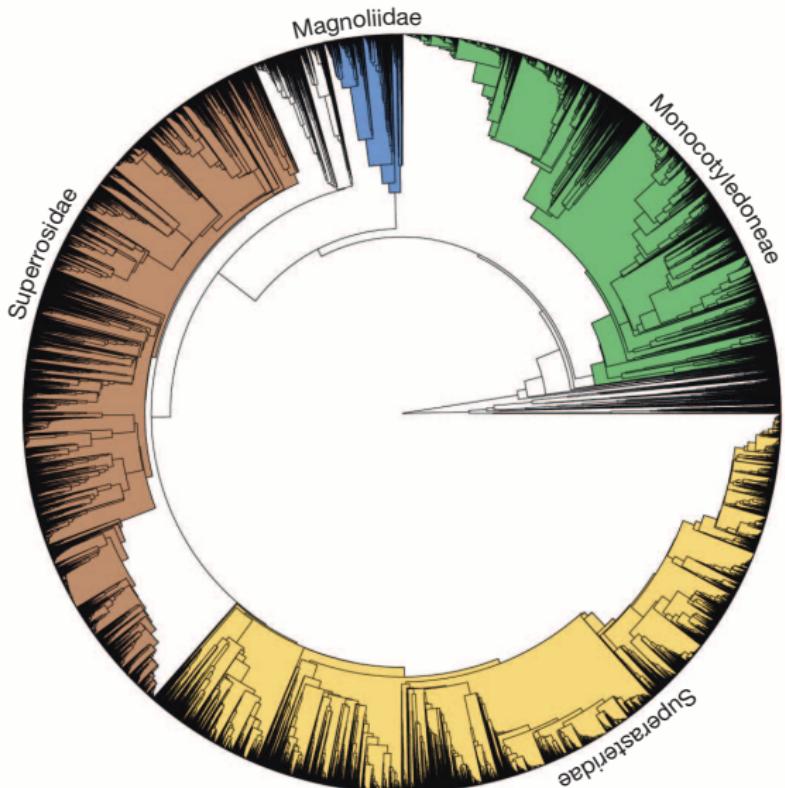
Alignment





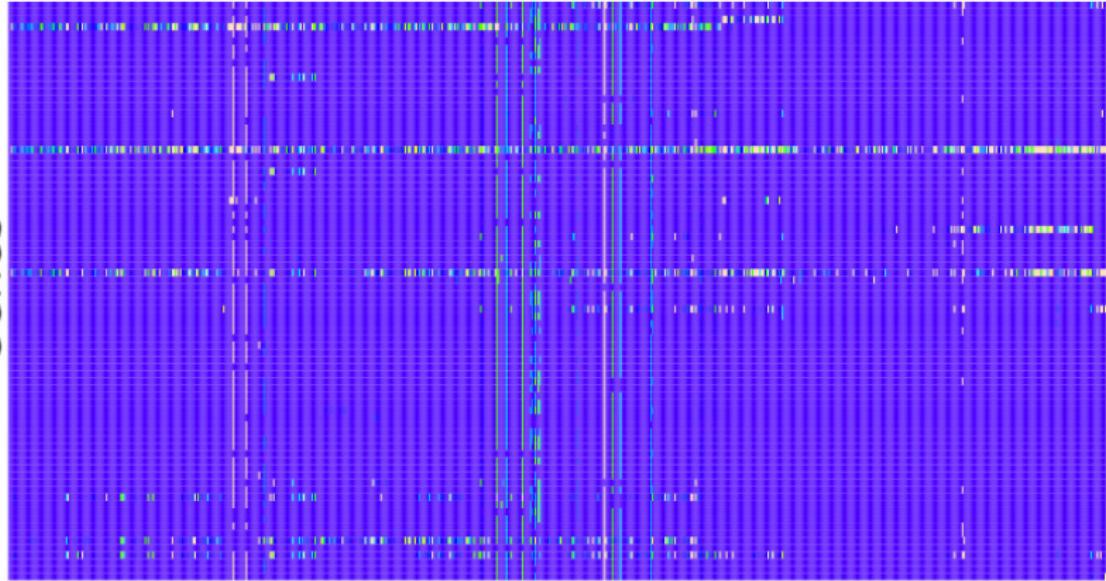
Can we get homology from a database?

- GenBank stores species taxonomy, but not gene taxonomy
- hard to get gene identifications/categories for all of GenBank (e.g., clustering)
- all genes for species *x*, but NOT all species for gene *y*



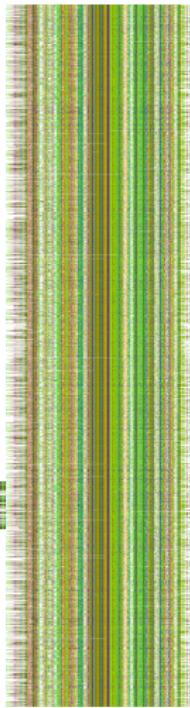
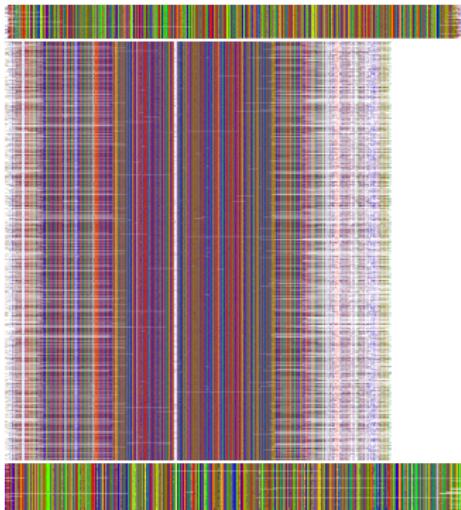
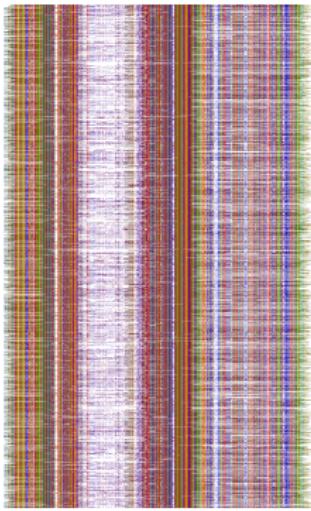
Zanne et al., Nature, 2013

Genes



Families





$\text{trnL-trnF} = 2485$

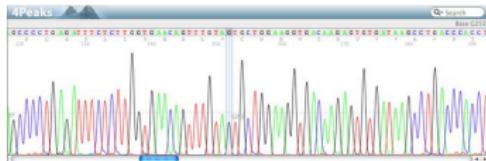
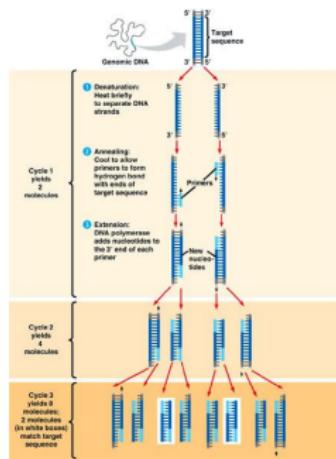
$\text{atpB} = 107$

$\text{matK} = 2182$

$\text{rbcL} = 924$

$\text{ITS} = 3725$

Massive parallel sequencing



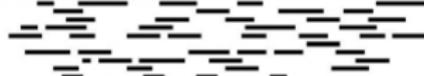
a) Multiple copies of genome



b) Sheared random fragments



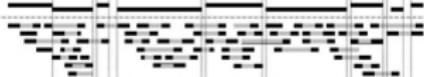
c) Size fractionated fragments



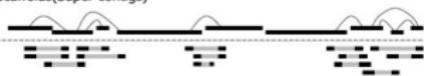
d) Reads



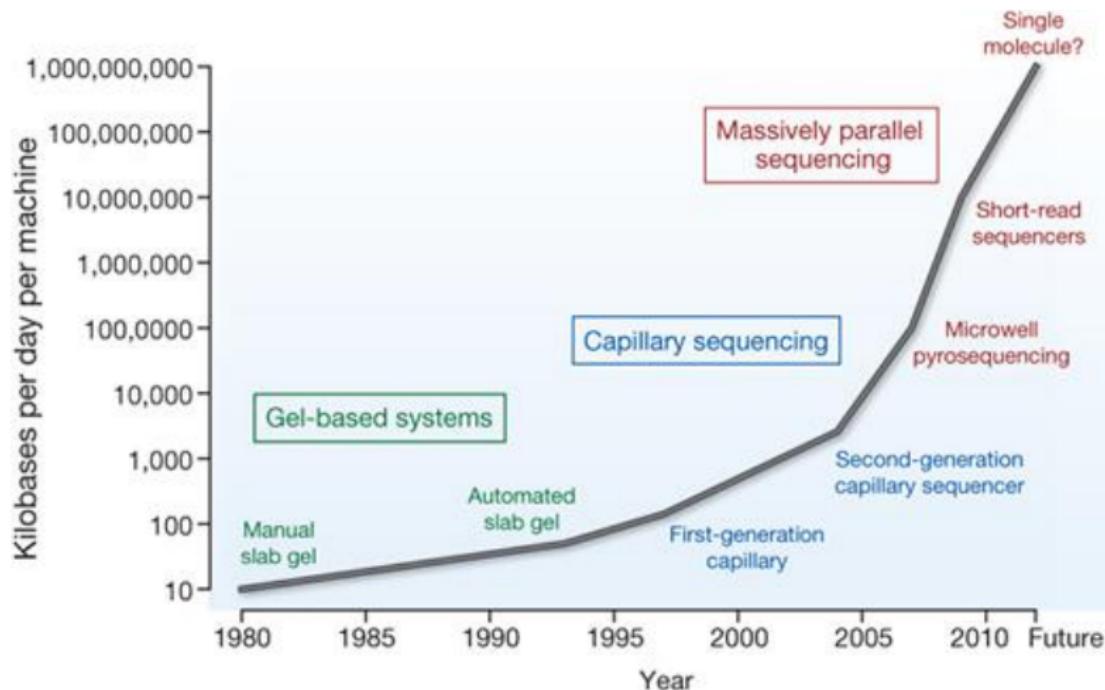
e) Contigs



f) Scaffolds(Super contigs)



Sequencing technology has improved exponentially



How many genes are used for a phylogenetic analysis?

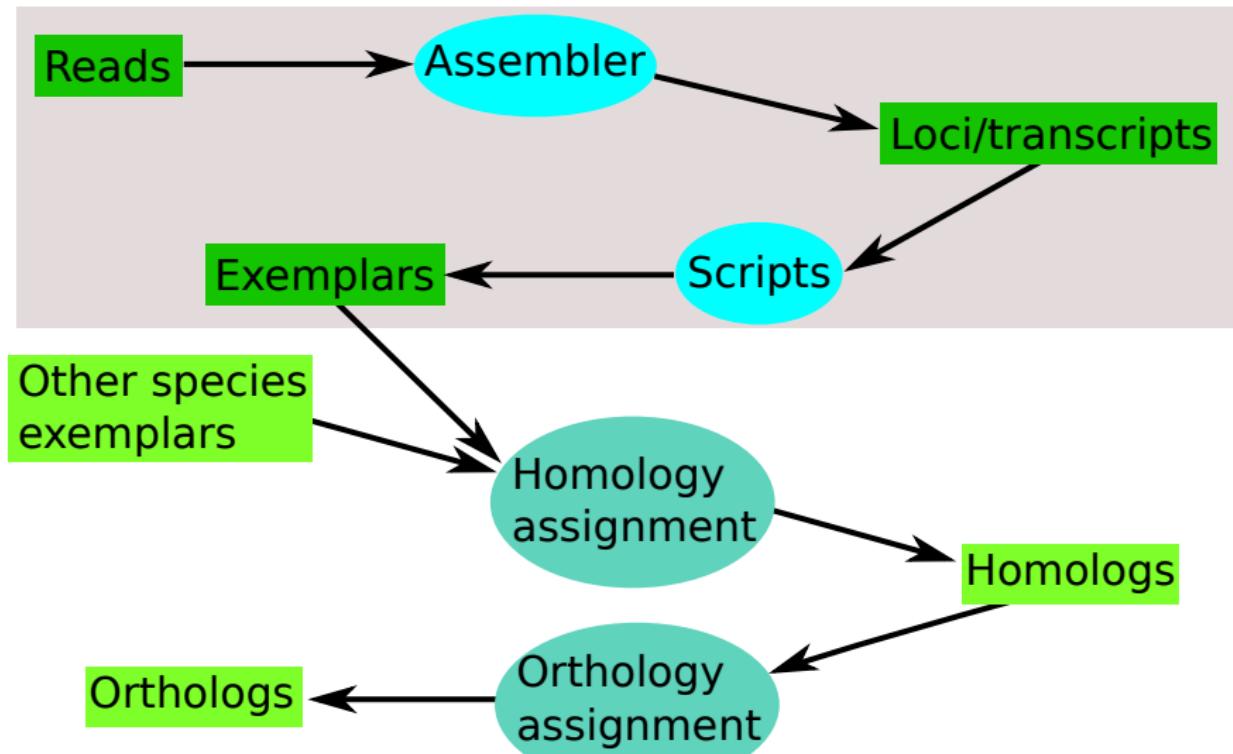
Typical phylogenetic analyses

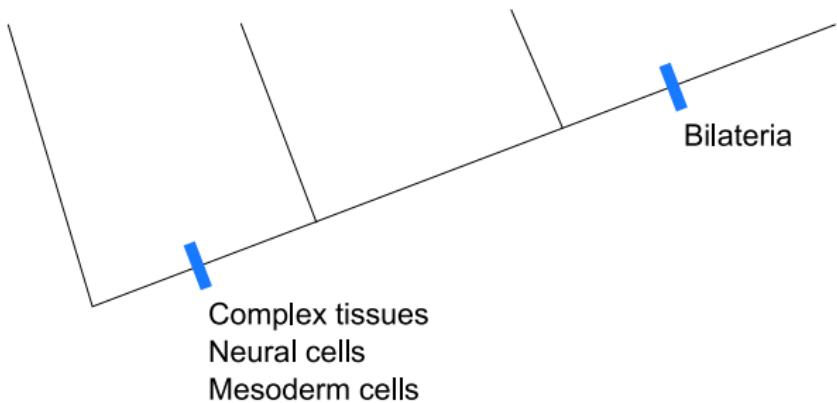
- 1-10 genes
- 17 genes. Plants
(Soltis et al. 2011)
- 19 genes. Birds
(Hackett et al. 2007)

Transcriptomic and genomic phylogenetic analyses

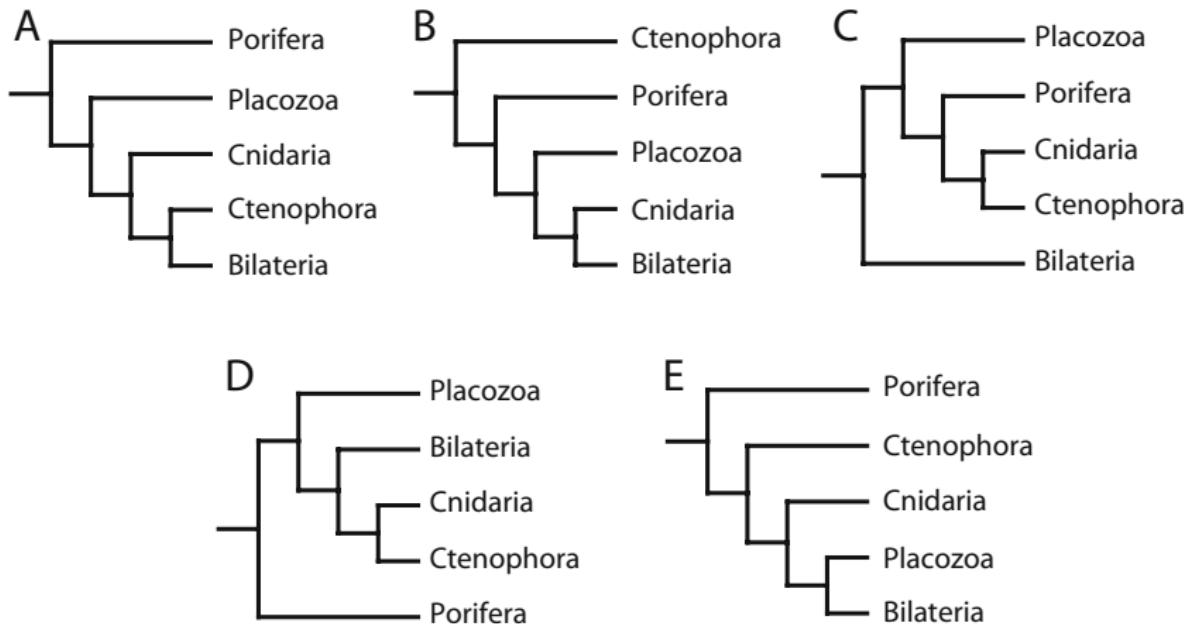
- 140 genes. Metazoa
(Dunn et al. 2008)
- 1185 genes. Molluscs
(Smith et al. 2011)
- 2970 genes. Seed plants
(Lee et al. 2011)
- 8251 genes. Birds
(Jarvis et al. 2014)
- 20,374 genes. Equids.
(Jónsson et al. 2014)

Pipeline



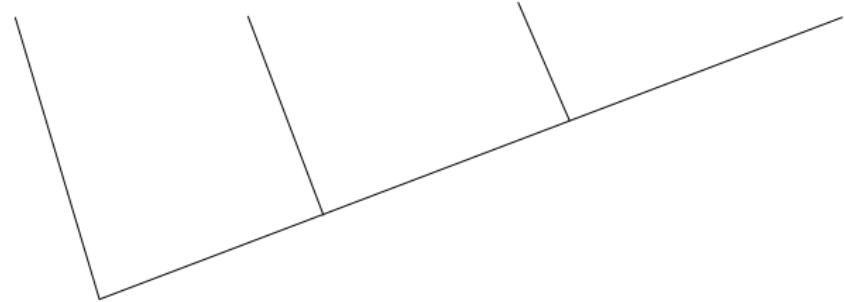
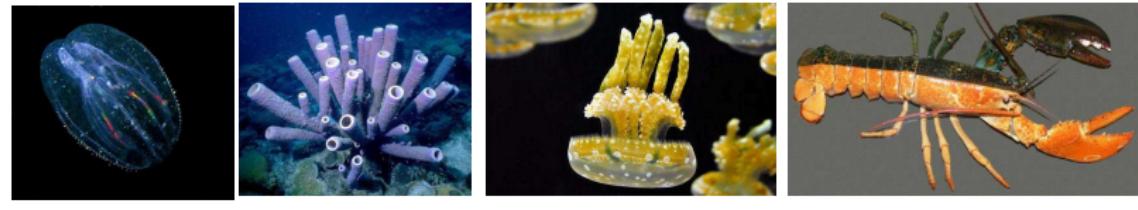


Phylogenetic discordance in animals

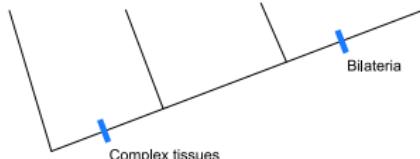
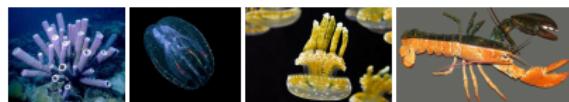


Edgecombe et al. 2011

Alternative phylogeny also has support

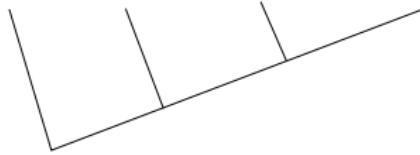
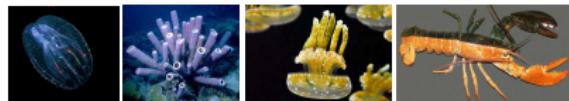


Which is the actual order of divergence?

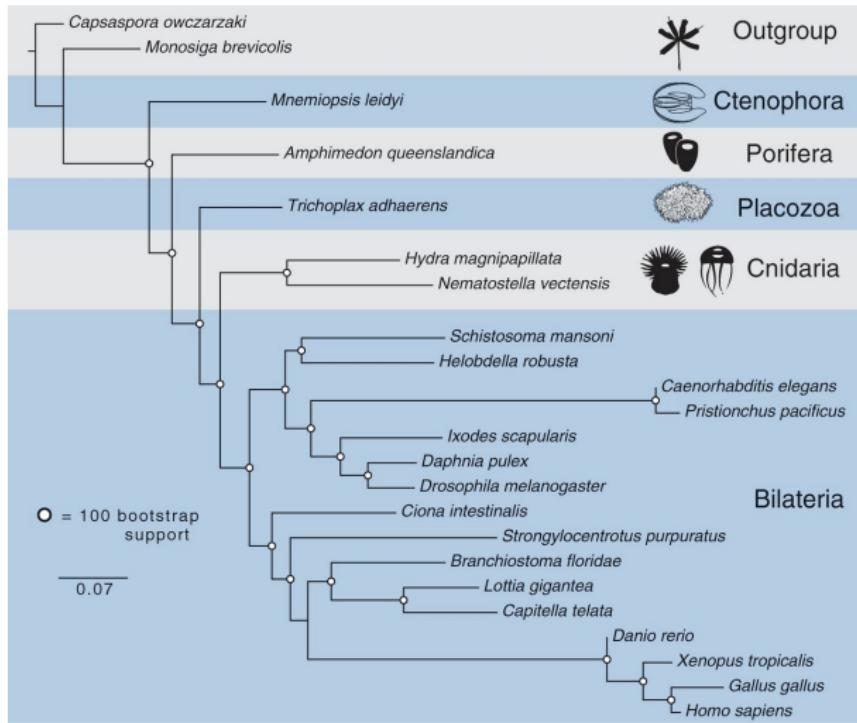


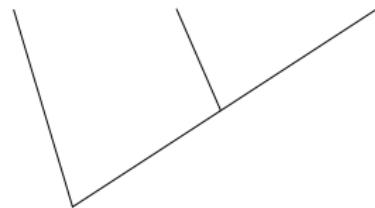
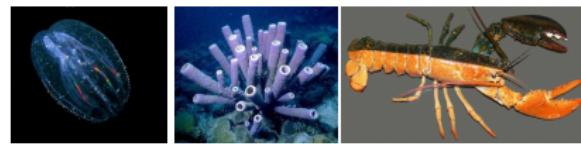
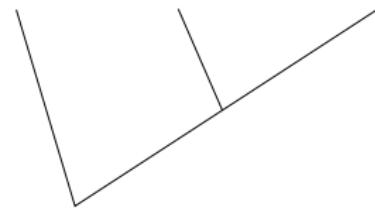
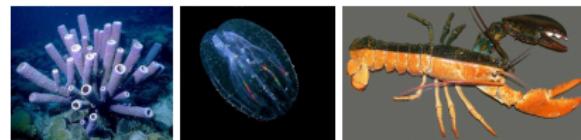
Traits

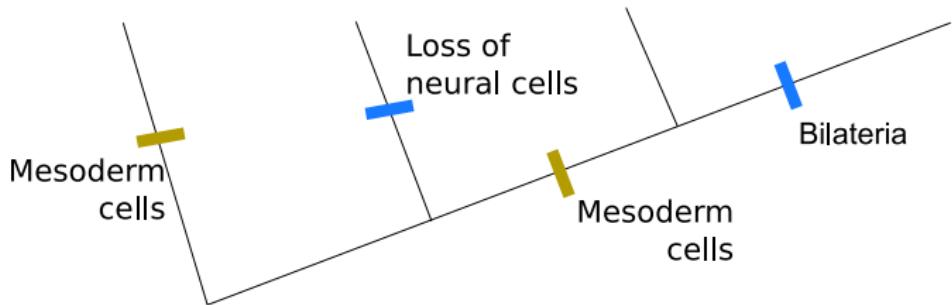
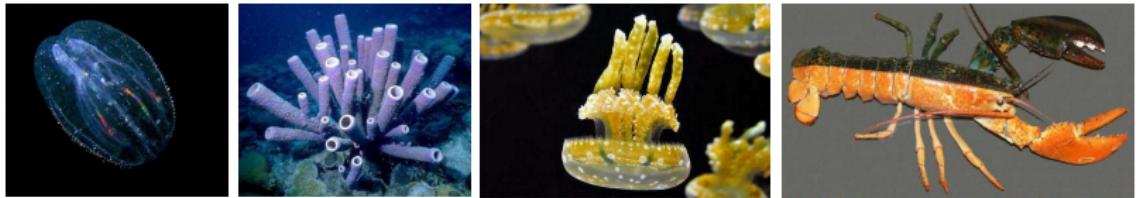
- tissue present
- cell types
- motility
- symmetry
- ...



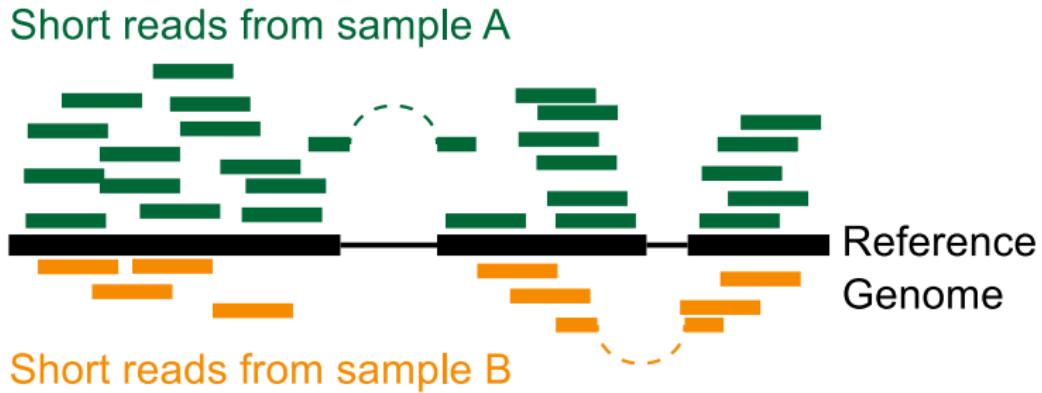
242 genes; Ryan et al., 2013



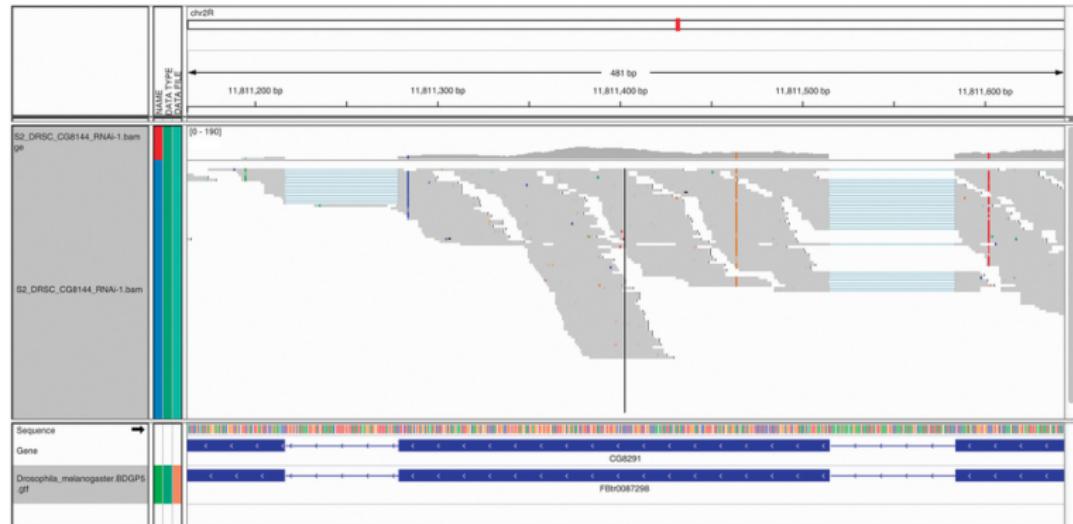




Short read “mapping” (i.e., aligning to a reference)

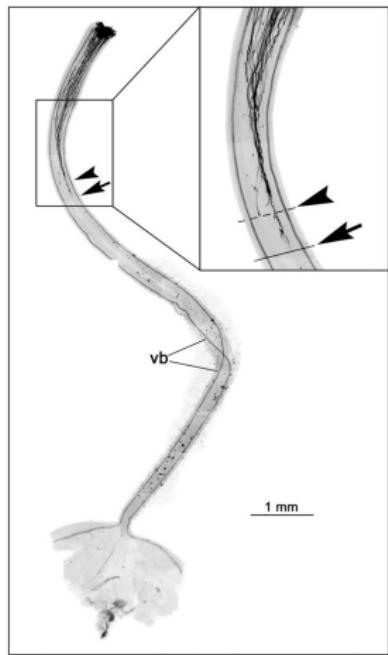


Short read mapping also used for populations to map variation

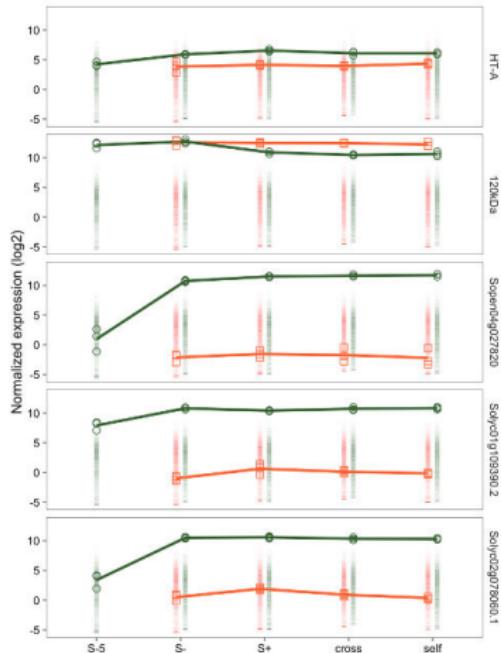


Anders et al., 2013, Nature Protocols

Using aligned read counts to determine pollen tube rejection genes



Baek et al 2015 Am J Bot



Pease et al. 2016 Molecular Ecology

All these techniques require some sort of pairwise alignment (and homology assessment)

Major topics covered

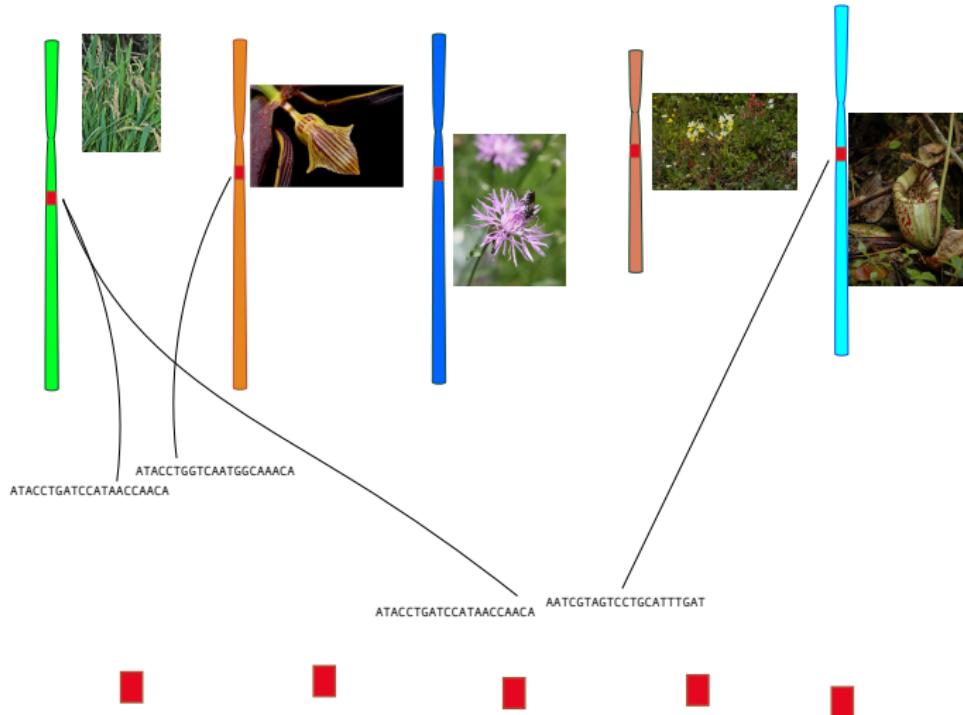
- Detecting homologous sequences (one-to-one) with pairwise sequence alignment
 - global → Needleman-Wunsch-Gotoh algorithm
 - local → Smith-Waterman algorithm
 - BLAST → heuristic search
- Grouping homologs (many-to-many)
 - Markov clustering
 - other clustering methods

Schedule

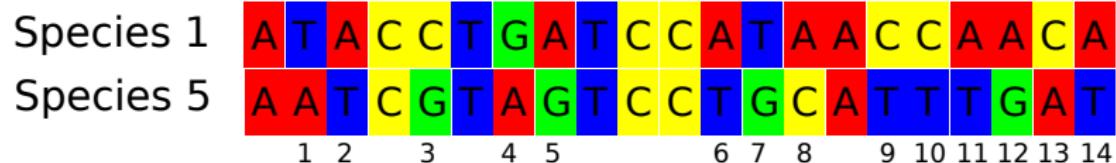
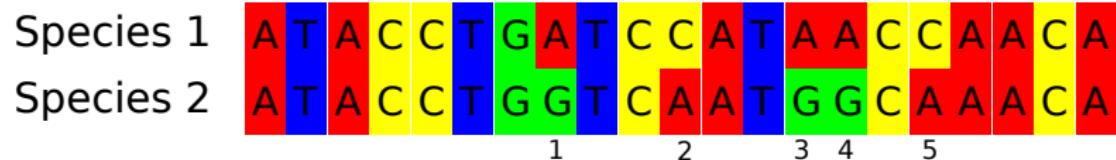
- First
 - Detecting homologous sequences
 - Lab for detecting homologous sequences
- Second
 - Clustering sequences
 - Short lab for clustering sequences

What are we going to address with pairwise alignment?

- Questions from a biological perspective:
 - Are these sequences homologous?
 - Do they share common ancestry?
- Questions from an informatics perspective:
 - Should a sequence be removed? Too short or too noisy (information poor)?
 - Are these sequences “similar enough” to include in analysis? (cut-offs)



Comparisons



Aligning words can be trivial...

- Species 1: SOMEONE
- Species 2: AWESOME

Aligning words can be trivial...

- Species 1: SOMEONE
- Species 2: AWESOME

- Species 1: ---SOMEONE
- Species 2: AWESOME---

... or less trivial

- Species 1: ACGTTAGA
- Species 2: CGTTGAA

... or less trivial

- Species 1: ACGTTAGA
- Species 2: CGTTGAA

- Species 1: -----ACGTTAGA
- Species 2: CGTTGAA-----

... or less trivial

- Species 1: ACGTTAGA
- Species 2: CGTTGAA

- Species 1: -----ACGTTAGA
- Species 2: CGTTGAA-----

- Species 1: ACGTTAGA-
- Species 2: -CGTT-GAA

Alignments are evaluated by a quantitative score

- Species 1: -----ACGTTAGA
- Species 2: CGTTGAA-----
 - score: -15 (gaps = -1, match = 1)
- Species 1: ACGTTAGA-
- Species 2: -CGTT-GAA
 - score: 3

Example for you to try:

- Species 1: TTGGCACGTTAGA
- Species 2: TGCACCTTAGTTA

How do we get the “best” alignment?

- We cannot enumerate all of the possible alignments
- We **can** find the best alignments algorithmically
 - using Dynamic Programming (no be covered here, but there are great resources if you are interested)
 - solve a large problem by breaking it down and solve sub-problems
- Needleman-Wunsch is the standard global alignment algorithm
 - published in 1970
 - cited over 7000 times

Example to try:

- Species 1: TTGGCACGTTAGA
- Species 2: TGCACCTTAGTTA
- +1 match, -1 mismatch

Needleman-Wunsch result

- Species 1: TTGGCACGTTAGA
 - Species 2: TGCACCTTAGTTA
-

- Species 1: TTGGCA-CGTTAG--A
- Species 2: -T-GCACC-TTAGTTA

Amino acids often use more complex score matrices

- Don't just have to have match and mismatch
- NUC.4.4 from NCBI also known as "EDNAFULL"
 - <ftp://ftp.ncbi.nih.gov/blast/matrices/>

	A	T	G	C	S	W	R	Y	K	M	B	V	H	D	N	U
A	5	-4	-4	-4	-4	1	1	-4	-4	1	-4	-1	-1	-1	-2	-4
T	-4	5	-4	-4	-4	1	-4	1	1	-4	-1	-4	-1	-1	-2	5
G	-4	-4	5	-4	1	-4	1	-4	1	-4	-1	-1	-4	-1	-2	-4
C	-4	-4	-4	5	1	-4	-4	1	-4	1	-1	-1	-1	-4	-2	-4
S	-4	-4	1	1	-1	-4	-2	-2	-2	-2	-1	-1	-3	-3	-1	-4
W	1	1	-4	-4	-4	-1	-2	-2	-2	-2	-3	-3	-1	-1	-1	1
R	1	-4	1	-4	-2	-2	-1	-4	-2	-2	-3	-1	-3	-1	-1	-4
Y	-4	1	-4	1	-2	-2	-4	-1	-2	-2	-1	-3	-1	-3	-1	1
K	-4	1	1	-4	-2	-2	-2	-2	-1	-4	-1	-3	-3	-1	-1	1
M	1	-4	-4	1	-2	-2	-2	-2	-4	-1	-3	-1	-1	-3	-1	-4
B	-4	-1	-1	-1	-1	-3	-3	-1	-1	-3	-1	-2	-2	-2	-1	-1
V	-1	-4	-1	-1	-1	-3	-1	-3	-3	-1	-2	-1	-2	-2	-1	-4
H	-1	-1	-4	-1	-3	-1	-3	-1	-3	-1	-2	-2	-1	-2	-1	-1
D	-1	-1	-1	-4	-3	-1	-1	-3	-1	-3	-2	-2	-2	-1	-1	-1
N	-2	-2	-2	-2	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-2
U	-4	5	-4	-4	-4	1	-4	1	1	-4	-1	-4	-1	-1	-2	5

How we score gaps can vary considerably among models

- constant gap model
 - one gap = one penalty
 - Species 1: GTTAGTTAC
 - Species 2: GTTA----C
 - match = 1, gap = -1, score = 4 (+5,-1)
- linear gap model (what we have done)
 - gap still has the one parameter, but take into account length
 - match = 1, gap = -1, score = 1 (+5,-4)
- affine gap model
 - parameter for **opening** a gap
 - AND a separate parameter for **extending** a gap
 - match = 1, open = -2, ext = -1, score = -1 (+5,-2+(-1*4))

More complicated gap models can also exist
(or be specified)

- Species 1: TTGGCACGTTAGA
 - Species 2: TGCACCTTAGTTA
-

- Species 1: TTGGCA-CGTTAG--A
 - Species 2: -T-GCACC-TTAGTTA
-

- Gap open: -100, Gap extend: -0.0005
- Species 1: TTGGCACGTTAGA--
- Species 2: --TGCACCTTAGTTA
- play around on
https://www.ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html

Protein

- Algorithmically, protein (amino acid) alignments are not different
- The major differences involve the scoring matrices
- Major choices are PAM and BLOSUM
 - PAM: Point Accepted Mutation (Dayhoff et al.)
 - this was typically used before the 1990s
 - BLOSUM
 - has generally replaced PAM as the common matrix

PAM matrices indicate divergence

- refers to evolutionary difference
(higher the number → more divergent)
- based on evolutionary models and empirical data
- ranges from closely related to completely random
- includes {PAM250, PAM120, PAM1}

A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	B	Z	X	*	
A	3	-3	-1	0	-3	-1	0	1	-3	-1	-3	-2	-2	-4	1	1	1	-7	-4	0	0	-1	-1	-8
R	-3	6	-1	-3	-4	1	-3	-4	1	-2	-4	2	-1	-5	-1	-1	-2	1	-5	-3	-2	-1	-2	-8
N	-1	-1	4	2	-5	0	1	0	2	-2	-4	1	-3	-4	-2	1	0	-4	-2	-3	3	0	-1	-8
D	0	-3	2	5	-7	1	3	0	0	-3	-5	-1	-4	-7	-3	0	-1	-8	-5	-3	4	3	-2	-8
C	-3	-4	-5	-7	9	-7	-7	-4	-4	-3	-7	-7	-6	-6	-4	0	-3	-8	-1	-3	-6	-7	-4	-8
Q	-1	1	0	1	-7	6	2	-3	3	-3	-2	0	-1	-6	0	-2	-2	-6	-5	-3	0	4	-1	-8
E	0	-3	1	3	-7	2	5	-1	-1	-3	-4	-1	-3	-7	-2	-1	-2	-8	-5	-3	3	4	-1	-8
G	1	-4	0	0	-4	-3	-1	5	-4	-4	-5	-3	-4	-5	-2	1	-1	-8	-6	-2	0	-2	-2	-8
H	-3	1	2	0	-4	3	-1	-4	7	-4	-3	-2	-4	-3	-1	-2	-3	-3	-1	-3	1	1	-2	-8
I	-1	-2	-2	-3	-3	-3	-3	-4	-4	6	1	-3	1	0	-3	-2	0	-6	-2	3	-3	-3	-1	-8
L	-3	-4	-4	-5	-7	-2	-4	-5	-3	1	5	-4	3	0	-3	-4	-3	-3	-2	1	-4	-3	-2	-8
K	-2	2	1	-7	0	-1	-3	-2	-3	-4	5	0	-7	-2	-1	-1	-5	-5	-4	0	-1	-2	-8	
M	-2	-1	-3	-4	-6	-1	-3	-4	-4	1	3	0	8	-1	-3	-2	-1	-6	-4	1	-4	-2	-2	-8
F	-4	-5	-4	-7	-6	-6	-7	-5	-3	0	0	-7	1	8	-5	-3	-4	-1	4	-3	-5	-6	-3	-8
P	1	-1	-2	-3	-4	0	-2	-2	-1	-3	-3	-2	-3	5	6	1	-1	-7	-6	-2	-2	-1	-2	-8
S	1	-1	1	0	0	-2	-2	1	-2	-2	-4	-1	-2	-3	1	3	2	-2	-3	-2	0	-1	-1	-8
T	1	-2	0	-1	-3	-2	-2	-1	-3	0	-3	-1	-1	-4	-1	2	4	-6	-3	0	0	-2	-1	-8
W	-7	1	-4	-8	-8	-6	-8	-8	-3	-6	-3	-5	-6	-1	-7	-2	-6	12	-2	-8	-6	-7	-5	-8
Y	-4	-5	-2	-5	-1	-5	-5	-6	-1	-2	-2	-5	-4	-4	-6	-3	-3	-2	8	-3	-3	-5	-3	-8
V	0	-3	-3	-3	-3	-3	-3	-2	-3	3	1	-4	1	-3	-2	-2	0	-8	-3	5	-3	-3	-1	-8
B	0	-2	3	4	-6	0	3	0	1	-3	-4	0	-4	-5	-2	0	0	-6	-3	4	2	-1	-8	
Z	-1	-1	0	3	-7	4	4	-2	1	-3	-3	-1	-2	-6	-1	-1	-2	-7	-5	-3	2	4	-1	-8
X	-1	-2	-1	-2	-4	-1	-1	-2	-2	-1	-2	-2	-2	-3	-2	-1	-1	-5	-3	-1	-1	-1	-2	-8
*	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	1

BLOSUM matrices indicate percent identity

- refers to percent identity
(higher the number → *less* divergent)
- based on empirical data
- BLOSUM has a narrower range than PAM
- includes {BLOSUM45, BLOSUM62, BLOSUM80}

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

Differences between PAM and BLOSUM

- PAM120, BLOSUM30
- A-A: PAM=3, BLOSUM=4
- A-R: PAM=-3, BLOSUM=-1
- R-N: PAM=-1, BLOSUM=0

A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V	B	Z	X	*
A	3	-3	1	0	-3	-1	0	-3	-2	-4	1	1	-7	-4	0	-1	-1	-1	-8				
R	-3	6	-1	-3	-4	1	-3	-4	1	-2	-4	2	-1	-5	-1	-1	-2	1	-5	-3	-2	-1	-8
N	-1	-1	4	2	-5	0	1	0	2	-2	-4	1	-3	-4	-2	1	0	-4	-2	-3	3	0	-1
D	0	-3	2	5	-7	1	3	0	0	-3	-5	-1	-4	-7	-3	0	-1	-8	-5	-3	4	3	-2
C	-3	-4	-5	-7	9	-7	-7	-4	-4	-3	-7	-7	-6	-6	-4	0	-3	-8	-1	-3	-6	-7	-4
Q	-1	1	0	1	-7	6	2	-3	3	-3	-2	0	-1	-6	-2	-6	-5	-3	0	4	-1	-8	
B	0	-3	1	3	-7	2	5	-1	-1	-3	-4	-1	-3	-7	-2	-1	-2	-8	-5	-3	3	4	-1
Z	1	-4	0	0	-4	-3	-1	5	-4	-5	-3	-4	-5	-2	1	-1	-8	-6	-2	0	-2	-2	-8
X																							
H	-3	1	2	0	-6	-3	-1	4	7	-4	-3	-2	-4	-3	-1	-2	-3	-1	-3	1	1	-2	-8
I	-1	-2	-2	-3	-3	-3	-3	-4	-4	6	1	-3	1	0	-3	-2	0	-6	-2	3	-3	-3	-1
L	-3	-4	-5	-7	-7	-2	-4	-5	-3	1	5	-4	3	0	-3	-4	-3	-3	-2	1	-4	-3	-2
K	-2	2	1	-1	-7	0	-1	-3	-3	-2	-3	-4	5	0	-7	-2	-1	-1	-5	-5	-4	0	-1
M	-2	-1	-3	-4	-6	-1	-1	-3	-4	-4	1	3	0	8	-1	-3	-2	-1	-4	-6	1	-4	-2
F	-4	-5	-6	-7	-6	-7	-5	-3	0	0	-7	-1	8	-5	-3	-4	1	4	-3	-5	-6	-3	-8
P	1	-1	-2	-3	-4	-3	-2	-2	-1	-3	-3	-2	-5	6	1	-1	-7	-6	-2	-2	-1	-2	-8
S	1	-1	1	0	0	-2	-2	-1	1	-2	-2	-4	-1	-2	-3	1	3	2	-2	-3	0	-1	-1
T	1	-1	2	0	-1	-3	-2	-2	-1	-3	-1	-4	-1	2	4	-6	-3	0	0	-2	-1	-1	-8
W	-7	1	-4	-8	-8	-6	-8	-8	-3	-6	-3	-5	-6	-1	-7	-2	-6	12	-2	-8	-6	-7	-5
Y	-4	-5	-2	-5	-1	-5	-5	-6	-1	-2	-2	-5	-4	-4	-6	-3	-1	2	-8	-3	-5	-3	-8
V	0	-3	-3	-3	-3	-3	-2	-3	-3	1	-4	1	-3	-2	-2	0	-8	-3	-5	-3	-1	-1	
B	0	-2	3	4	-6	0	3	0	1	-3	-4	-5	-4	-2	0	0	-6	-3	4	2	4	1	
Z	2	-1	1	0	3	-7	4	-2	1	-3	-3	-1	-2	-6	-1	-1	-2	-7	-5	-3	2	4	-1
X	-1	-2	-1	-2	-4	-1	-1	-2	-2	-2	-3	-2	-1	-5	-3	-1	-1	-2	-8	-1	-1	-1	-8
*	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8	-8

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

- Species 1: HEAGAWGHEE
- Species 2: PAWHEAE

- Species 1: HEAGAWGHEE
 - Species 2: PAWHEAE
-

- BLOSUM62 and -2 gap
- Species 1: HEAGAWGHE-E
- Species 2: --P-AW-HEAE

- Species 1: HEAGAWGHEE
 - Species 2: PAWHEAE
-

- BLOSUM62 and -2 gap
 - Species 1: HEAGAWGHE-E
 - Species 2: --P-AW-HEAE
-

- BLOSUM30 and -2 gap
- Species 1: HEAGAWGHE-E
- Species 2: -P--AW-HEAE

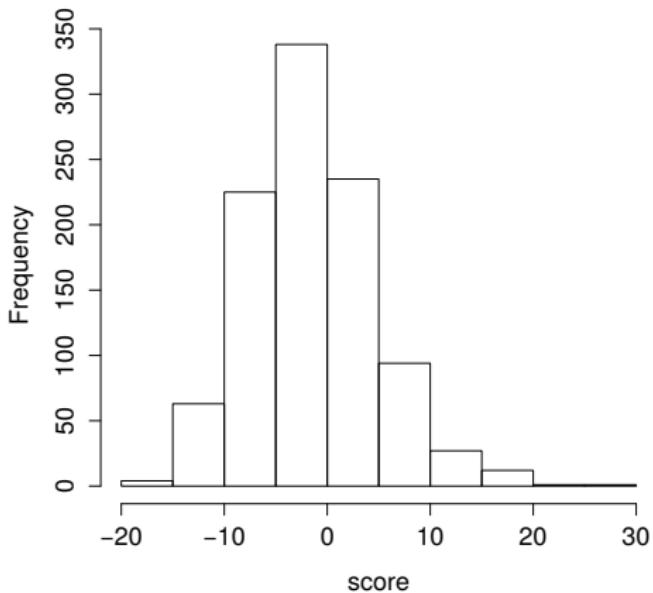
Significance

- How do we measure whether an alignment is significant?

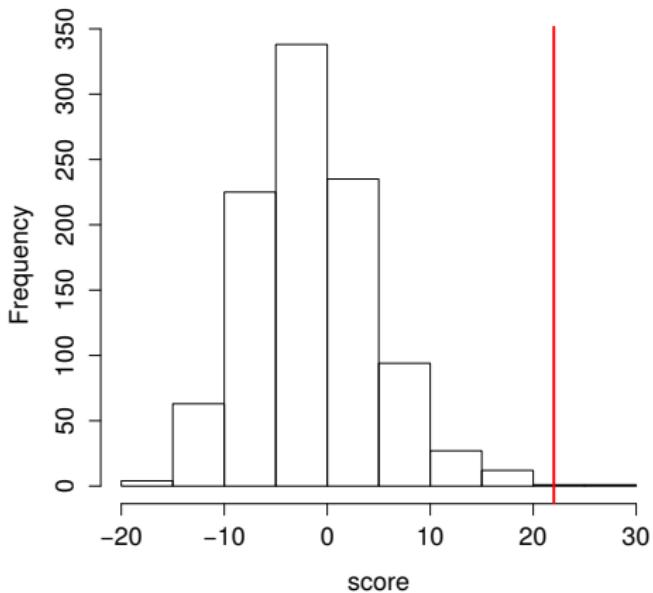
How do we assess alignment significance?

- Needleman-Wunsch will always give the best alignment (given the assumptions)
- **In theory:**
 - No method allows us to predict the distribution of alignment scores from random sequences
- **In practice:**
 - generate a distribution simulated alignments and get scores
 - compare our score to the distribution
 - if 100 random alignments give scores that are lower than the observed alignment score, then $P < 0.01$

- Species 1: HEAGAWGHE-E
- Species 2: --P-AW-HEAE
- score = 22 with BLOSUM62 and -2 gap
- $1/1000 > 22$



- Species 1: HEAGAWGHE-E
- Species 2: --P-AW-HEAE
- score = 22 with BLOSUM62 and -2 gap
- $1/1000 > 22$



Global alignment is not the same as local alignment

- Species 1: SOMEONE
- Species 2: AWESOME

Global alignment is not the same as local alignment

- Species 1: SOMEONE
- Species 2: AWESOME

- Species 1: ---SOMEONE
- Species 2: AWESOME---

Global alignment is not the same as local alignment

- Species 1: SOMEONE
- Species 2: AWESOME

- Species 1: ---SOMEONE
- Species 2: AWESOME---

- Species 1: SOME
- Species 2: SOME

Pairwise alignment

- **Needleman-Wunsch** is the standard **global alignment** algorithm
 - published 1970, cited over 9600 times
- **Smith-Waterman** is the standard **local alignment** algorithm
 - published 1981, cited over 8800 times
 - also a dynamic programming algorithm

Difference

- Species 1: ACGTTAGA
 - Species 2: CGTTGAA
-

- Species 1: ACGTTAGA
 - Species 2: -CGTTGAA
-

- Species 1: CGTTAGA
- Species 2: CGTTGAA

Another example

- (amino acids with BLOSUM 62)

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

- Species 1: HEAGAWGHEE
- Species 2: PAWHEAE

Global means full-sequence alignment, local focuses on best aligned subregion

- Species 1: HEAGAWGHEE
 - Species 2: PAWHEAE
-

- Species 1: AWGHE-E
 - Species 2: AW-HEAE
-

- Species 1: HEAGAWGHE-E
- Species 2: --P-AW-HEAE

When are sequences homologous? (decision is difficult)

- What properties are used to qualify/quantify homology?
 - sequences that are similar ***enough*** are homologous
 - find the best alignment defining similarity
 - calculate alignment scores
 - Other properties?
- What constitutes similar enough?
 - more similar than by chance?
 - how is the probability of this chance determined?

How do we calculate the significance of alignments?

- We have calculated the optimal alignment
 - the alignment with the best score
 - this doesn't depend on whether the sequences are related or not
 - call this the maximum segment pair (MSP)
- How many MSPs do we expect with at least the same score by chance?

How do we calculate the significance of alignments?

- We make use of the extreme value distribution (EVD) to calculate the number of alignments between random sequences that have at least (or better) our calculated alignment score
- This is known as the *E*-value or the number of distinct alignments with a score equal or better than our score
 - $E(S) = Kmne^{-\lambda S}$
 - K and λ = scaling parameters calculated based on the search space (K) and scoring scheme (λ)
 - $m * n$ = size of the search space
- The probability of finding at least one alignment with our score (the *p* value)
 - $1 - e^{-E(S)}$
- As both *E* and *p* values decrease, the biological significance increases

Calculating significance

- $m = 980, n = 10,030,834,086, K = 1.37, \lambda = 0.711$
- $m \times n \sim 10^{13}$

<i>score</i>	<i>e</i>	<i>p</i>
39	12	0.99
41	2.9	0.95
42	1.4	0.76
46	0.08	0.08
49	0.01	0.01
55	0.0001	0.0001







Software**Highly accessed****Open Access****CBESW: Sequence Alignment on the Playstation 3****Adrianto Wirawan*, Chee K Kwok, Nim T Hieu and Bertil Schmidt*** Corresponding author: Adrianto Wirawan adri0004@ntu.edu.sg

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For all author emails, please [log on](#).*BMC Bioinformatics* 2008, **9**:377 doi:10.1186/1471-2105-9-377The electronic version of this article is the complete one and can be found online at:
<http://www.biomedcentral.com/1471-2105/9/377>

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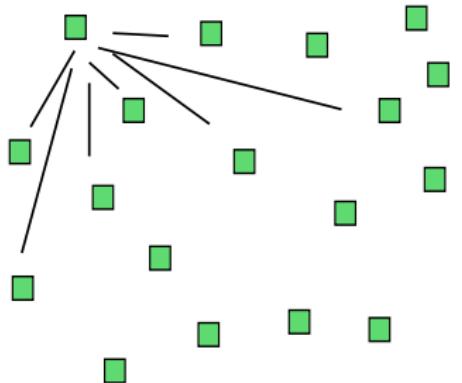
Published: 17 September 2008

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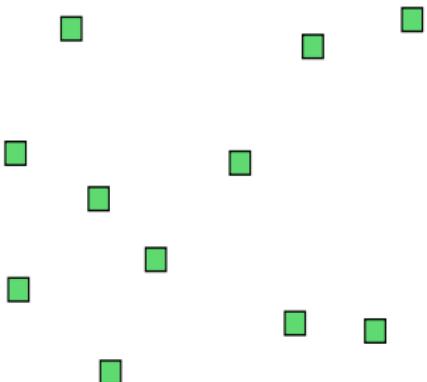
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.**Abstract**Formula display: **MathJax** 

Sets of sequences

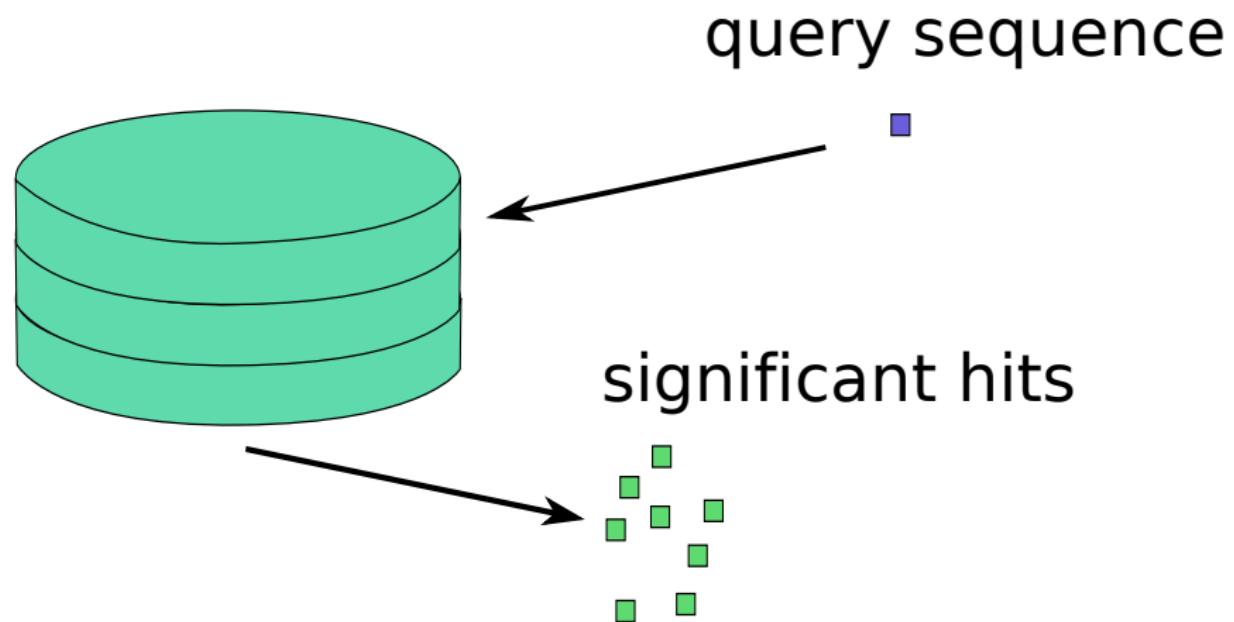
sequences



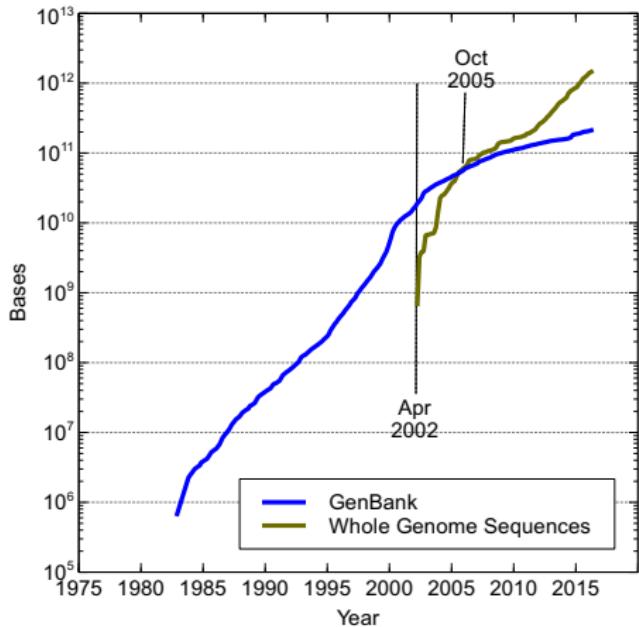
significant hits



From a database



Sequence databases growing exponentially (genomic data even faster)



- GSAFDACFDEADRKANTAYKNEQHPNDMFQTYEBLUEBERRYPANCAKESSHLEGQSC
- CTFQTYEBLUEBERRYPANCAKESQNPFEEQGPQMKVEVQAFNQDFWDLFRFFPQWHK

- GSAFDACFDEADRKANTAYKNEQHPNDMFQTYE**BLUEBERRY PANCAKES**SHLEGQSC
- CTFQTYE**BLUEBERRY PANCAKES**QNPFEEQGPQMKVEVQAFNQDFWDLFRFFPQWHK

- GSAFDACFDEADRKANTAYKNEQHPNDMFQTYEBLUEBERRY PANCAKESSHLEGQSC
- CTFFQTYEBLUEBERRY PANCAKESQNPFEEQGPQMKVEVQAFNQDFWDLFRFFPQWHK

Smith-Waterman does not always focus on biologically-relevant regions



BLAST: Basic Local Alignment Search Tool

- Smith-Waterman is often slow for local alignment
 - While getting to the human genome, needed something faster (50-100×)
- BLAST (Altschul et al., 1990, cited over 59,000 times)
 - Heuristic that produces an **approximate** best match (S-W is a guarantee)
 - calculate the high scoring matches instead of the maximum scoring matches (HSP instead of MSP)

BLAST

- filter out repeats and low complexity regions (this is different than FASTA)

```
>gi|195593191|gb|EU940837.1| Zea mays clone 1158441 mRNA sequence

GTTCACATCATCCTGCAGGACTGCCTGAGGAGGGATCACACTGCCTCTCAGGCTTCAGTTAGTGCTTA
TGGCGTTCTGTTAGAACCTGTATTGTATTCTGCTGGGAGCCTGAGTTCCATTCCGTGCAAAGATAAAAT
CATGTGTGACGACACGTTGCAACAGCATTATGCTAAACTGCATTAATGATGATGCGTTGAGCTCCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ATTTTTTTTTTTTTTTTTAAAAAAA
```

BLAST

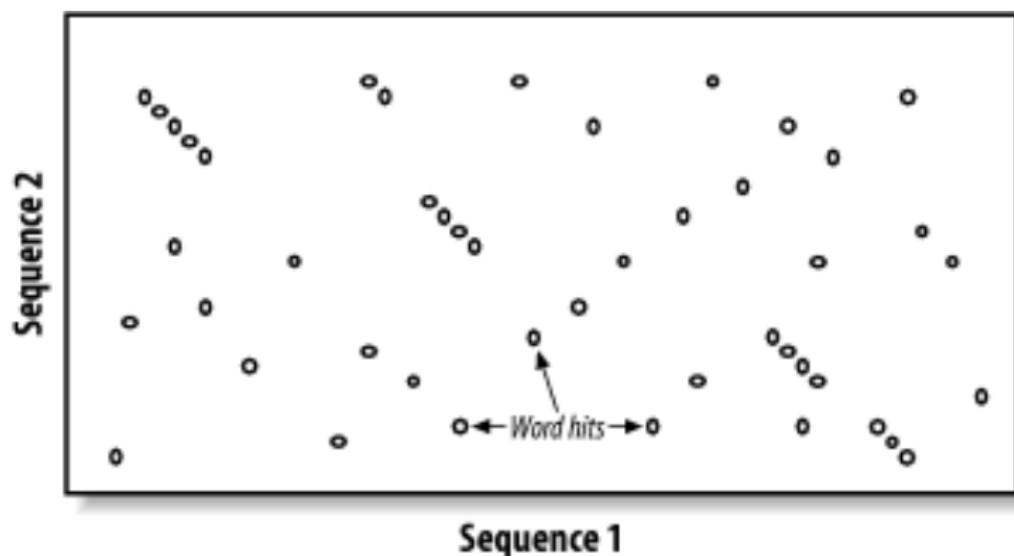
- filter out repeats and low complexity regions
- break the sequence into “words” of a length (default for nucleotides is 28, we will look at 4)
- GTTCACATCATCCTGC
 - GTTC
 - TTCA
 - TCAC
 - CACA
 - ACAT
 - CATC
 - ATCA
 - ...

BLAST

- for each word, look at “likely” mutants (based on scoring matrices)
- you could call this the word’s sequence “neighborhood”
- GTTCACATCATCCTGC
 - GTTC: CTTC, GTTC, GATC...
 - TTCA: TTCT, TTGA, TTGT...
 - TCAC: AGAC, CCAC, TCTG...
 - CACA: ...
 - ACAT: ...
 - CATC: ...
 - ATCA: ...
 - ...

BLAST

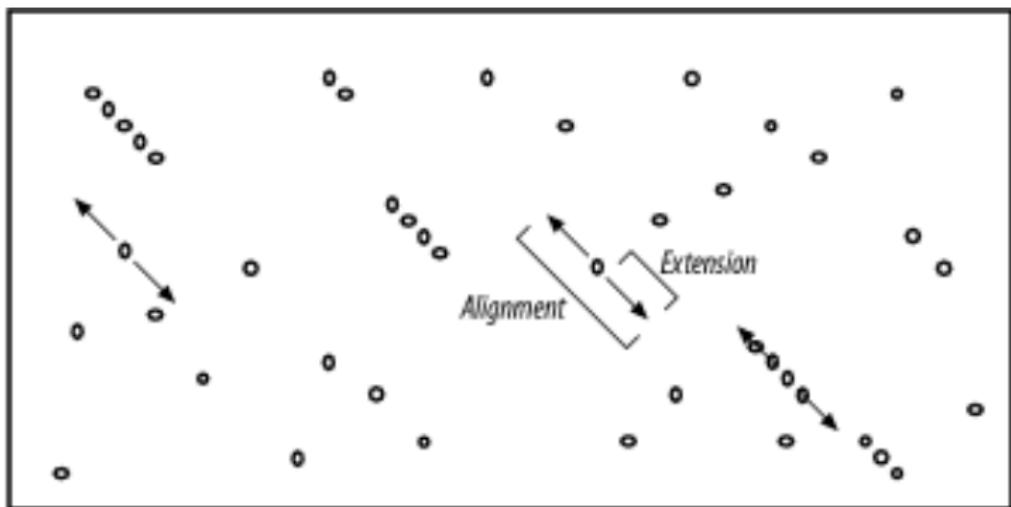
- organize the words into a form best for searching
- scan the other sequence for words that match



from Korf et al.

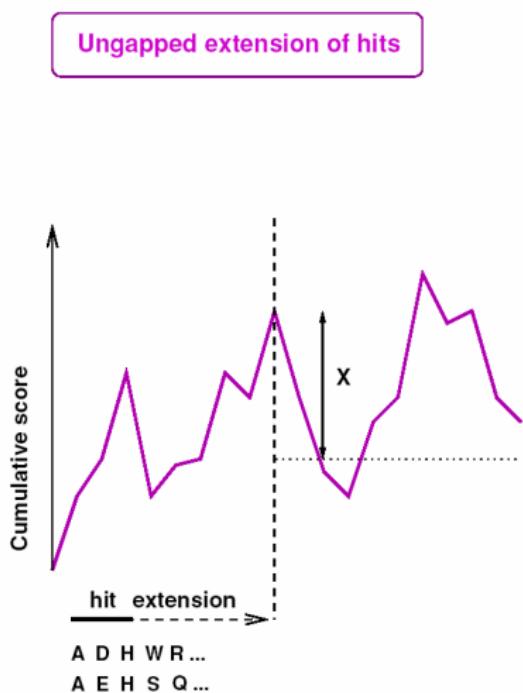
BLAST

- extend these matches in the local neighborhood (these are going to be HSP or high scoring segment pairs)



from Korf et al.

- Extension stops when the score decreases past a certain point (X) when compared to the highest score



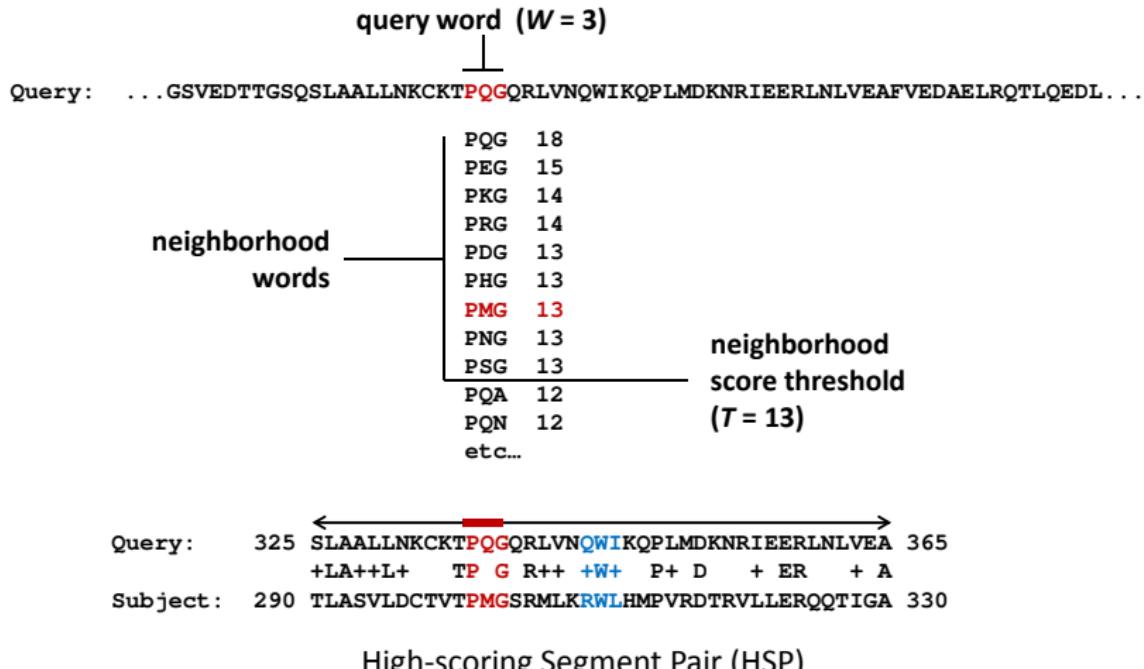


figure from Altschul

BLAST

- calculate E -values and return significant results
 - expectation that you would get that alignment by chance given the database of sequences
- we already talked about these E -values and p -values with Smith-Waterman significance

BLAST

- Because of the speed, BLAST has been used in many different ways
 - identification of homologs
 - organism identification
 - translation (at least the first steps)
 - putative function
- Here, we mainly search for sequences that will have significant matches
- Can search a custom set of sequences or a standard database of sequences
- First lets look at results from our own sequences

>18S_Abelia

NNNNNNNNNNNNNNNNNNTAGTCATGCTGTCAAAGATTAAGCCATGATGTGAAGTATGAACATAATTCAAGACTGTGAAAC
 TCGGAATGGCTCATTAATCAGTTAGTTGTTGATGGACTCTGCATAACCGTAGTAACTTAGAGCTAATACGTGCAA
 CAAACCCCCGACTTCGGAAGGGATGCACTTTAGATAAAAGGTCAGCGGGCTCTGCCTGCTGCAGTATTCACTG
 ACGGATCGCAGGGCCTCTGCGGCAGCGCATCTAACATTCTGCCTATCACATTCTGGATGAGTAGTGGCTACTATGGT
 GGTGACGGGTGACGGAGAATTAGGGTCGATTCCGGAGAGGGAGCGTGGAGAACCGCTACACATCCAAGAAGGACAGCGCG
 AATTACCCAATCTGACACGGGGAGGTAGTGACAATAACATACCCGGCTTTGAGTCTGTAATTGGAAATGAGTACAATCTA
 AATCCCTTAACAGGGATCGTGGAGGCAAGCTCTGGTGCCAGCACCCGGCTAACTTGAGCTCATGAGATATTAAAGTTG
 CGTTAAAAGGGCTGAGTGGACTTTGGGTTGGCGCTCAGGGCTTGAGTACCGGCTCGTCCCTCTGCGCG
 ATGCGCTCTGGCTTAACCTGTCGGGTGCTCGGCTGTTACTTTGAAAGAAATTAGGTGCTCAAAGCAAGCTACGCTCG
 GATACATTAGCATGGGATAACATCATAGGATTCTGGTCTTACGGTTGCCCTCGGATCGGAGATAATGATTAACAGGGACAGTC
 GGGCATTGTTAGTGGATAGCTGGAGGTAACATTGAGAGGATGGAGGACTGGGAGGATGGGAGGATCTGG
 TAATCAAGAACAGGGGGCTGAAGAAGCATAGATACTGGCCTAGTGGCTGCAACCTAACAGATGCCGACCCGGGATCTGG
 GTTGCTTTAGGAACTTCACTGGCCTATTGAGAAATCAAAGGTTGGGGGGAGTAGTGTGCAAGGCTGAAACTAAAG
 GAATTGACGGAGGGCACCCAGGAGTGGGGCTGCGCTTAATTGGACTAACACGGGAAACTTACGGCTCAGACATAGTAAG
 GATTGACAGACTGAGAGCTTCTGTGATTCTATGGGTGGGGTGATGCCGTTCTAGTTGGGGCGATTTGCTGGTTAATC
 CGTTAACGACAGACCTCGCCTGCTAAGCTAGTGGGAGGATCTCCCTCGCGGCAGCTTCAAGGGACTATGCCCTTCAG
 GCCCGGAAGGTTGGAGCAAAACAGGCTGAGCTTGGGTTGGGCTAGCTGGGGGGAGCAGCGCCTACACTGATGTATTCAACGAGCC
 TATAGCCCTGGGAGGCAAGGCCGGAAATCTTCACTGATGGGGATAGATCATTGCAATTGGTGTCTAAACGAAGAA
 TTCCCTAGTAAGCGCGAGTCATCAGCTCGCTGTTGACTACGTCCCTGCCCTTGACACACCAGCGCGTCGCTCCTACCGATTG
 CGGTGAAGTGTCCGATCGCGCAGCTGGCGGTTGCTGCCGAGCTCGCAGAGTCCACTGAACTTATCATTGAGAGGAAG
 GAGAGTC

>18S_Acorus

CAGANTGTGAAGANTCGAATGGCTCATTAATCAGTTAGTTGTTGATGGTATCTGACTCGGATAACCGTAGTAACTTAGA
 CTAATAGTCGACCAAAACCCGACTTCTGGGAAGGGATGCACTTTAGAAAAAAGGTCATGGGGCTCTGCCCTGCTCTGG
 TTCATGATAACTCGAGGGTGCACGCCCTTGTGCTCGAGGCATCTAACATTCTGCCCTATCAACTTCTGGTAGAGGAT
 TGGCCTACCATGTTGTGACGGAGATAGGGTGGCATTCCGGAGAGGGGAGCTGGAGAACCGGCTACACATCAGGAAG
 GCAGCAGCCGCAAATTACCAATCTGACACGGGGAGGTAGTAGCAAAATAAACACCGGCTTTGAGTCTGTAATTG
 ATGAGTACAATCTAAACCCCTAACGAGGANCAATAGTCAGAGGCTGAAATTCTGGATTATGAAAGACGAACACKGCAAAGCA
 TTGCAAGGGATTTCTTAATCAAGAACGAAAGTTGGGAGTCGAAGACGATCACAGATAACCGCTCTAGTCTCAACCTAACGATG
 CGGACCAAGGGATCGGGTGGATGGCTTACAGGACTCGCCGCCACCTTGGAGAACATCTGGGTTCCGGGGGGAGTAG
 NNNNNNNNNNNNNNNNNNNNNNNAATTGACGGGAAGGGCACCAGGGAGTCGGGACTTGGCTTAATTGACTCAACACGGGAAACT
 CCAGGTTCCAGACATAGCAAGGATTGACAGACTGAGAGCTTTCTGATCTGGGGGGGGGGGGAGTAG
 GCGATTGGTCTGGTTAATTCCGTTAACGAACGAGACTCAGCCGCTAATCAGTCAGTCAGGGGGAGTACTCTCCACGGCCAGCTCT
 GAGGGACTATGCCGCTTACGGCNNN
 NNN
 AATTGTTGGCTTCAAGGGAGAGTTCTCCTAAKYRNTGAAGTAATTNCAGSCCNGTTGACKACKCCTCTGCTSCWtgwnn
 NNNNNNNNNNNNTCTACCGATTGAATGGTCCGGTAGAGTGTGCGCTGCCGAGCAGGGCGGTSCGCCGGCAGCTGTGAGAAGT
 CCATT

Score = 785 bits (425), Expect = 0.0
 Identities = 457/474 (96%), Gaps = 1/474 (0%)
 Strand=Plus/Plus

Query	76	CAGACTGTGAAACTCGAATGGCTCATTAATCAGTTAGTTGTTGATGGTACCTGC	135
Sbjct	1	CAGANTGTGAAANTCGAATGGCTCATTAATCAGTTAGTTGTTGATGGTATCTGC	60
Query	136	TACTCGGATAACCGTAGTAATTCTAGAGCTAACAGTGCAACAAACCCGACTTCTGGAA	195
Sbjct	61	TACTCGGATAACCGTAGTAATTCTAGAGCTAACAGTGCAACAAACCCGACTTCTGGAA	120
Query	196	GGGATGCATTATTAGATAAAAGGTCGACGCCGGC-TCTGCCGTTGCTGCATGATTCA	254
Sbjct	121	GGGATGCATTATTAGAAAAAGGTCATGCCGGCTCTGCCGTCCTGGTATTCA	180
Query	255	TGATAACTCGACGGATCGCACGCCCTCGTGCCTGGACGCATCATTCAAATTCTGCC	314
Sbjct	181	TGATAACTCGACGGATCGCACGCCCTGTGCCTGCACGCATCATTCAAATTCTGCC	240
Query	315	TATCAACTTCGATGGTAGGATAGTGGCTACTATGGTGGTACGGGTACGGAGAATTA	374
Sbjct	241	TATCAACTTCGATGGTAGGATAGTGGCTACCATGGTGGTACGGGTACGGAGAATTA	300
Query	375	GGGTTCGATTCCGAGAGGGAGGCTGAGAAACGGCTACCATCCAAGGAAGGCAGCAGG	434
Sbjct	301	GGGTTCGATTCCGAGAGGGAGGCTGAGAAACGGCTACCATCCAAGGAAGGCAGCAGG	360
Query	435	CGCGCAAATTACCAATCCTGACACGGGGAGGTAGTGACAATAAAACAAATCCGGCT	494
Sbjct	361	CGCGCAAATTACCAATCCTGACACGGGGAGGTAGTGACAATAAAACAAATCCGGCT	420
Query	495	CTTGAGTCTGGTAAATTGGAATGAGTACAATCTAAATCCCTAACGAGGATCCA	548
Sbjct	421	CTTGAGTCTGGTAAATTGGAATGAGTACAATCTAAATCCCTAACGAGGAGCCA	474

Score = 776 bits (420), Expect = 0.0
 Identities = 471/508 (93%), Gaps = 1/508 (0%)
 Strand=Plus/Plus

Query	896	ATAGTCAGAGG-TGAAATTCTGGATTATGAAAGACGAACAAC TCGAAAGCATTGCC	954
Sbjct	475	ATAGTCAGAGGCTGAAATTCTGGATTATGAAAGACGAACAACKCGAAAGCATTGCC	534
Query	955	AAGGATGTTTCAATTAACTAAGAACGAAAGTTGGGGCTCGAAGACGATCAGATAACCGTC	1014
Sbjct	535	AAGGATGTTTCAATTAACTAAGAACGAAAGTTGGGGATCGAAGACGATCAGATAACCGTC	594
Query	1015	CTAGTCTAACCATAAACGATGCCGACCAGGGATCAGTGGATGTTGCTTTAGGACTCCA	1074
Sbjct	595	CTAGTCTAACCATAAACGATGCCGACCAGGGATCGGTGATGTTGCTTACAGGACTCCG	654
Query	1075	CTGGCACCTTATGAGAAATCAAAGTTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTG	1134
Sbjct	655	CCGGCACCTTATGAGAAATCAAAGTTTGGGTTCCGGGGGAGTATGGNNNNNNNNNN	714
Query	1135	AAACTTAAGGAATTGACGGAAGGGCACCACCAAGGAGTGGAGCCTCGGCTTAATTGAC	1194
Sbjct	715	NNNNNNNNNNNAATTGACGGAAGGGCACCACCAAGGAGTGGAGNCCTCGGCTTAATTGAC	774
Query	1195	TCAACACGGGAAACTTACCAAGGTCAGACATAGTAAGGATTGACAGACTGAGAGCTTT	1254
Sbjct	775	TCAACACGGGAAACTTACCAAGGTCAGACATAGCAAGGATTGACAGACTGAGAGCTTT	834
Query	1255	TCTTGATTCTATGGGTGGTGGTCATGCCGTTCTAGTTGGTGGAGCGATTGTCTGGT	1314
Sbjct	835	TCTTGATTCTATGGGTGGTGGTCATGCCGTTCTAGTTGGTGGAGCGATTGTCTGGT	894
Query	1315	TAATTCCGTTAACGAAACGAGACCTCAGCCTGCTAAC TAGCTATGCCGAGGTATCCCTCCG	1374
Sbjct	895	TAATTCCGTTAACGAAACGAGACCTCAGCCTGCTAAC TAGCTACGTGGAGGTACTCCCTCA	954
Query	1375	CGGCCAGCTTCTTAGAGGGACTATGCC	1402
Sbjct	955	CGGCCAGCTTCTTAGAGGGACTATGCC	982

```
Score = 113 bits (61), Expect = 1e-28
Identities = 76/83 (92%), Gaps = 3/83 (4%)
Strand=Plus/Plus

Query 1654 TCCTACCGATTGAATGGTCCGGTGAAGTGTTCGGATCGCGGCACGTGGCGGTTCGCTG 1713
||||||| ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1244 TCCTACCGATTGAATGGTCCGGTGAAGTGTTCGGATCGCGGCACA-GGGCGGTTS-C-G 1300

Query 1714 CCGCGCACGTCGCGAGAAGTCCA 1736
||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 1301 CCGCGCACGTTGTGAGAAGTCCA 1323

Lambda      K      H
1.33     0.621    1.12

Gapped
Lambda      K      H
1.28     0.460    0.850

Effective search space used: 2298183

Matrix: blastn matrix 1 -2
Gap Penalties: Existence: 0, Extension: 2.5
```

Against a set of sequences

- BLAST is not limited to pairwise comparisons
 - in fact, pairwise is definitely not the default means of interaction
- We can compare the same sequence to a set of sequences
- In this case:
 - one query sequence (sequence of interest, our own)
 - 3167 subject sequences (a set of sequences from a bunch of other genes)
 - included the query sequence in the set of subject sequences
 - otherwise, just a standard BLAST

query	subject	%ident	length	#mismat	#gp_open	que_sta	que_end	sub_sta	sub_end	evaluate	score
18S_Abelia	18S_Abelia	100	1748	0	0	20	1767	20	1767	0	3229
18S_Abelia	18S_Acorus	96.41	474	16	1	76	548	1	474	0	785
18S_Abelia	18S_Acorus	92.72	508	36	1	896	1402	475	982	0	776
18S_Abelia	18S_Acorus	91.57	83	4	3	1654	1736	1244	1323	1.00E-28	113
18S_Abelia	18S_Aextoxicon	98.22	1741	31	0	24	1764	1	1741	0	3044
18S_Abelia	18S_Agave	97.3	1742	44	3	24	1763	1	1741	0	2955
18S_Abelia	18S_Ailanthus	98.09	1728	33	0	37	1764	1	1728	0	3009
18S_Abelia	18S_Alisma	95.91	1734	69	2	20	1751	10	1743	0	2808
18S_Abelia	18S_Alnus	97.15	1508	41	2	204	1710	3	1509	0	2545
18S_Abelia	18S_Amborella	96.04	1742	66	3	22	1761	1	1741	0	2832
18S_Abelia	18S_Angelica	98.51	1749	25	1	20	1767	17	1765	0	3085
18S_Abelia	18S_Anisophyllea	96.93	1106	33	1	24	1129	1	1105	0	1853
18S_Abelia	18S_Anisophyllea	97.7	609	13	1	1160	1767	1136	1744	0	1046
18S_Abelia	18S_Anisoptera	97.2	1747	46	3	23	1767	1	1746	0	2953
18S_Abelia	18S_Annona	95.23	1069	40	11	74	1141	39	1097	0	1681
18S_Abelia	18S_Aphanopetalum	97.71	1750	36	4	20	1767	2	1749	0	3009
18S_Abelia	18S_Arabidopsis	97.04	1046	29	2	723	1767	453	1497	0	1759
18S_Abelia	18S_Arabidopsis	96.4	444	13	3	20	462	20	461	0	728
18S_Abelia	18S_Aristolochia	93.32	449	16	5	91	539	1	435	0	652

- the BLAST of the sequence against itself starts at base 20
- any guesses why?

```
>18S_Abelia
NNNNNNNNNNNNNNNNNNNTAGTCATGCTTCTCAAAGATTAAGCCATGCATGTGAAGTATGAACATAATTCAAGACTGTGAAAC
TGCATGGCTCATTAAATCAGTTAGTTGTTGATGGTACCTGCTACTCGGATAACCGTAGTAACTCTAGGCTAATCGTCAA
CAAACCCGACTTCTGGAAGGATGCATTATTAGATAAAAGGTGACGCCGGCTCTGCCCTGCTGCATGATTGATAACTCG
ACGGATCGCACGCCCTCGGCCGGACGCATCATTCAAATTCTGCCCTACACTTCACTTGATGGTAGGATAGTGGCCTACTATGGT
GGTACGGGTGACGGAGAATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACACATCCAAGGAAGGCAGCGCGCAG
AATTACCAATCTGACACGGGAGGTAGTACAATAAAACAAATACCGGCTCTTGAGTCTGGAATTGGAATGAGTACAATCTA
AATCCCTAACGAGGATCCATTGGAGGGCAAGTCTGGTGCAGCAGCCGGTAATTCCAGCTCAATAGCTATATTAAAGTTGTTG
CAGTTAAAAGCTCGTAGTTGGACTTTGGGTTGGCTGGCGGTCCGGCTATCGGTGTGCAACGGCTGCTCGTCCCTCTGCCGG
ATGCGCTCTGGCTTAACCTGGTGGCTGTGCCCTCCGGCGCTTACTTTGAAGAAATTAGAGTGTCAAAGCAAGCCTACGCTCTG
GATACATTAGCATGGGATAACATCATAGGATTCCGGCTTATTACGTTGGCCTCGGGATGGAGTAATGATTAACAGGGACAGTGG
GGGCATTCTGATTTCATAGTCAGAGGTGAAATTCTGGATTATGAAAGACAACTGCGAAAGCATTGCAAGGATGTTTCT
TAATCAAGAACGAAAGTTGGGGCTCGAAGACGATCAGATACCGTCTTAGTCTCAACCATAACGATGCCGACCAGGGATCAGTGG
GTTGCTTTAGGACTCACTGGCACCTTATGAGAAATCAAAGTTGGGTTCCGGGGGAGTATGGTCGCAAGGCTGAAACTAAAG
GAATTGACGGAAGGGCACCACCAAGGAGTGGAGCTGCGGCTTAATTGACTCAACACGGGAAACTTACCAAGGTCCAGACATGTAAG
GATTGACAGACTGAGAGCTTTCTGATTCTATGGTGGTGGCATGGCGTTCTTAGTGGTGGAGCGATTGTCGGTTAACTC
CGTTAACGAAAGCAGACCTCAGCCTGTAACTAGCTATGCGGAGGTATCCCTCGCCGGCAGCTCTTAGAGGGACTATGCCCTTCAG
GCCACGGAAGTTGAGGCAATAACAGGCTGTGATGCCCTAGATGTTCTGGGCCGACGCGCGTACACTGATGATTCAACGAGCC
TATAGCCTGGCGACAGGCCGGAAATCTTGAATTCATGTGATGGGGTAGATCATTGAAATTGTTGGCTTAAACGAAGAA
TTCTAGTAAGCGCGAGTCATCAGCTCGCGTGAACGTCCTGCCCTTGTACACACCGCCCGCCTACCGATTGAATGGTC
CGGTGAAGTGGTCCGATCGCGCAGCTGGCGGTTGCTGCCGGCAGCTCGCAGAAGTCCACTGAACCTTACATTGAGAGGAAG
GAGAGTC
```

BLAST

- filter out repeats and less complex regions (this is different than FASTA)

```
>gi|195593191|gb|EU940837.1| Zea mays clone 1158441 mRNA sequence  
GTTCACATCATCCTGCAGGACTGCCTGAGGAGGGATCACACTGCCTCTCAGGCTTCAGTTAGTGCTTA  
TGGCGTTCTGTTAGAACCTGTATTGTATTCTGCTGGGAGCCTGAGTTCCATTCCGTGCAAAGATAAAAT  
CATGTGTGACGACACGTTGCAACAGCATTATGCTAAACTGCATTAATGATGATGCGTTGAGCTCCAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
ATTTTTTTTTTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAA
```

BLAST databases

- We can also search against a database
 - NR: non-redundant amino acid sequences
 - many many model organisms
 - BCT: bacterial sequences
 - ENV: environmental sequences
 - EST: expressed sequence tags
 - GSS: genome survey sequences
 - HTC: high throughput genomic sequencing
 - INV: invertebrate sequences
 - MAM: “other” mammal sequences
 - PAT: patent sequence
 - PLN: plant sequences
 - ROD: rodent sequences
 - PRI: primate sequences
 - VR: viral sequences
 - VRT: vertebrate sequences
- There are *more* (look for the ncbi ftp)

BLAST programs

- BLAST has different programs
 - **blastn**: nucleotide BLAST to other nucleotides
 - **blastp**: protein BLAST to protein sequences
 - **blastx**: translated nucleotides searching against a protein database
 - **tblastn**: proteins searching against translated nucleotide database
 - **tblastx**: translated nucleotides searching against translated nucleotide database
- There are many other specialized BLAST variants:
 - conserved domains
 - vector screening
 - MegaBLAST - essentially identical sequences
 - many specialized versions are just specific parameterizations of regular BLAST searches

Web BLAST example

 **BLAST®** Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

► NCBIBLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)

New DELTA-BLAST, a more sensitive protein-protein search [Go](#)

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

<input type="checkbox"/> Human	<input type="checkbox"/> Oryza sativa	<input type="checkbox"/> Gallus gallus
<input type="checkbox"/> Mouse	<input type="checkbox"/> Bos taurus	<input type="checkbox"/> Pan troglodytes
<input type="checkbox"/> Rat	<input type="checkbox"/> Danio rerio	<input type="checkbox"/> Microbes
<input type="checkbox"/> Arabidopsis thaliana	<input type="checkbox"/> Drosophila melanogaster	<input type="checkbox"/> Apis mellifera

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a nucleotide database using a nucleotide query <i>Algorithms:</i> blastn, megablast, discontiguous megablast
protein blast	Search protein database using a protein query <i>Algorithms:</i> blastp, psi-blast, phi-blast, delta-blast
blastx	Search protein database using a translated nucleotide query
tblastn	Search translated nucleotide database using a protein query
tblastx	Search translated nucleotide database using a translated nucleotide query

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ blastn suite Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

Enter Query Sequence

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) Query subrange [?](#)

From
To

Or, upload file No file chosen [?](#)

Job Title
Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

Choose Search Set

Database Human genomic + transcript Mouse genomic + transcript Others (nr etc.);
 [?](#)

Organism [Optional](#) Enter organism name or id—completions will be suggested Exclude [+](#)
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude [Optional](#) Models (XM/XP) Uncultured/environmental sample sequences

Entrez Query [Optional](#)
Enter an Entrez query to limit search [?](#)

Program Selection

Optimize for Highly similar sequences (megablast)
 More dissimilar sequences (discontiguous megablast)
 Somewhat similar sequences (blastn)
Choose a BLAST algorithm [?](#)

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ blastn suite Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

From
To

>18S_Abelia
NNNNNNNNNNNNNNNNNNNNNTAGTCATATGCTCTCAAAGATTAAAGCCATCCATGTGA
AGTATGAACTTACAGACTGAAACTGGCAATGGCTCATTAATCAGTTAGTTGTTG
ATGCTACCTGCTACTCGGATAACCCTAGTAATTCTAGACGCTAATACGTCCAACACCCGA
CTTCTGGAGGGATCCATTAGATAAAAGTCGACCGGGCTCTGCCGTTGCTGGAT

Or, upload file No file chosen

Job Title
Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database Human genomic + transcript Mouse genomic + transcript Others (nr etc.):

Organism Enter organism name or id—completions will be suggested Exclude

Optional Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude Models (XM/XP) Uncultured/environmental sample sequences

Optional Entrez Query
Enter an Entrez query to limit search

Program Selection

Optimize for Highly similar sequences (megablast)
 More dissimilar sequences (discontiguous megablast)
 Somewhat similar sequences (blast)

BLAST Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)
 Show results in a new window

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: 11

Max matches in a query range: 0

Scoring Parameters

Match/Mismatch Scores: 2,-3

Gap Costs: Existence: 5 Extension: 2

Filters and Masking

Filter: Low complexity regions
 Species-specific repeats for: Homo sapiens (Human)

Mask: Mask for lookup table only
 Mask lower case letters

BLAST Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)
 Show results in a new window

18S_Abelia

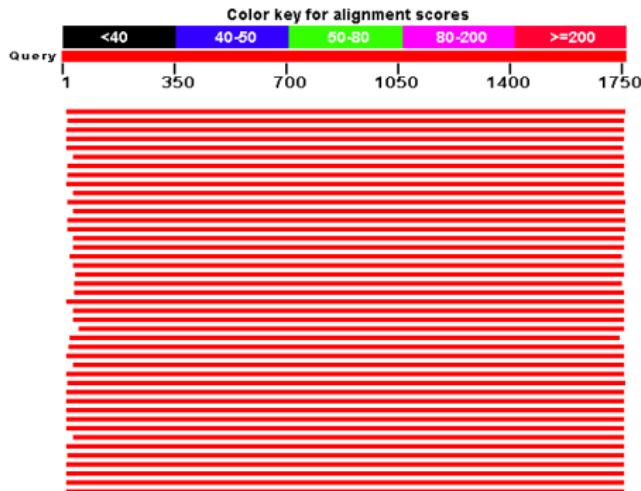
Query ID Icl|27385
Description 18S_Abelia
Molecule type nucleic acid
Query Length 1767

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.28+ [► Citation](#)

Other reports: [► Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Graphic Summary**Distribution of 100 Blast Hits on the Query Sequence** ⓘ

Mouse over to see the define, click to show alignments



Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Max ident	Accession
<input type="checkbox"/>	Abelia triflora 18S rRNA gene	3153	3153	98%	0.0	100%	AJ236004.1
<input type="checkbox"/>	Scabiosa sp. Albach 39 18S rRNA gene	3126	3126	98%	0.0	99%	AJ236006.1
<input type="checkbox"/>	Dipsacus asperoides isolate JianShi 18S ribosomal RNA gene, partial sequence	3124	3124	98%	0.0	99%	GU166826.1
<input type="checkbox"/>	Dipsacus asperoides isolate EnShi YuTangBa 18S ribosomal RNA gene, partial sequence	3124	3124	98%	0.0	99%	GU166824.1
<input type="checkbox"/>	Dipsacus asperoides isolate BaDong 18S ribosomal RNA gene, partial sequence	3113	3113	98%	0.0	99%	GQ806564.1
<input type="checkbox"/>	Dipelta yunnanensis 18S ribosomal RNA gene, partial sequence	3103	3103	97%	0.0	99%	GQ983567.1
<input type="checkbox"/>	Viburnum acerifolia 18S rRNA gene	3101	3101	98%	0.0	99%	AJ236007.1
<input type="checkbox"/>	Sambucus ebulus 18S rRNA gene	3099	3099	98%	0.0	99%	AJ236005.1
<input type="checkbox"/>	Lonicera maackii 18S ribosomal RNA gene, complete sequence	3099	3099	98%	0.0	99%	U66701.1
<input type="checkbox"/>	Patrinia triloba 18S ribosomal RNA gene, partial sequence	3097	3097	97%	0.0	99%	GQ983572.1
<input type="checkbox"/>	Valeriana officinalis 18S rRNA gene	3095	3095	98%	0.0	99%	AJ236003.1
<input type="checkbox"/>	Triplostegia glandulifera 18S ribosomal RNA gene, partial sequence	3088	3088	97%	0.0	99%	GQ983577.1
<input type="checkbox"/>	Griselinia lucida 18S ribosomal RNA gene, complete sequence	3088	3088	98%	0.0	99%	AF206922.1
<input type="checkbox"/>	Griselinia littoralis 18S rRNA gene	3088	3088	98%	0.0	99%	AJ236000.1
<input type="checkbox"/>	Morina longifolia 18S ribosomal RNA gene, partial sequence	3085	3085	97%	0.0	99%	GQ983569.1
<input type="checkbox"/>	Dipsacus asperoides isolate EnShi ShuangHe 18S ribosomal RNA gene, partial sequence	3083	3083	97%	0.0	99%	GU166825.1
<input type="checkbox"/>	Dipsacus sp. Jansen 931 18S ribosomal RNA gene, partial sequence	3081	3081	97%	0.0	99%	U43150.1
<input type="checkbox"/>	Diervilla sessilifolia 18S ribosomal RNA gene, partial sequence	3079	3079	97%	0.0	99%	GQ983566.1

Alignments

[Download](#) [GenBank](#) [Graphics](#)
[▼ Next](#) [▲ Previous](#) [Descriptions](#)

Abelia triflora 18S rRNA gene

Sequence ID: [embAJ236004.1](#) Length: 1767 Number of Matches: 1

Related Information

Range 1: 20 to 1767 [GenBank](#) [Graphics](#)
[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
				Plus/Plus
3153 bits(3496)	0.0	1748/1748(100%)	0/1748(0%)	
Query 20		GTAGTCATATGCTTGTCTCAAAGATAAACCATGCATGGTGAACTATGAACTAATTCAAGA		79
Sbjct 20		CTAGTCATATGCTTGTCTCAAAGATAAACCATGCATGGTGAACTATGAACTAATTCAAGA		79
Query 80		CTGTGAAACTCGGAATGGCTCAATTAAATCAGTTATAGTTTGTGTGATGGTACCTGCTACT		139
Sbjct 80		CTGTGAAACTCGGAATGGCTCAATTAAATCAGTTATAGTTTGTGTGATGGTACCTGCTACT		139
Query 140		CGGATAACCGTAGTAACTCTAGAGCTTAATCCTGCAAAACACCCGACTCTCGAAAGGGA		199
Sbjct 140		CGGATAACCGTAGTAACTCTAGAGCTTAATCCTGCAAAACACCCGACTCTCGAAAGGGA		199
Query 200		TGCAATTAAATAGATAAAAGGTGACGGCGGCCCTGTGCCCTTGTGTGGATGATTCTATGATA		259
Sbjct 200		TGCAATTAAATAGATAAAAGGTGACGGCGGCCCTGTGCCCTTGTGTGGATGATTCTATGATA		259
Query 260		ACTCGACGGATCGCACGGCCCTGTGCCGGGACGGCATCATCAAATTCTGCCCTATCA		319
Sbjct 260		ACTCGACGGATCGCACGGCCCTGTGCCGGGACGGCATCATCAAATTCTGCCCTATCA		319
Query 320		ACTTTCGATGCTAGGATAGTGGCTACTATGGTGGTGACGGGTGACGGAGAATTAGGGTT		379
Sbjct 320		ACTTTCGATGCTAGGATAGTGGCTACTATGGTGGTGACGGGTGACGGAGAATTAGGGTT		379
Query 380		CGATTCGGAGAGGGAGGCCTGAGAAAAGGCCTACCATCATAAGGAAGGCAGCAGGCCGC		439
Sbjct 380		CGATTCGGAGAGGGAGGCCTGAGAAAAGGCCTACCATCATAAGGAAGGCAGCAGGCCGC		439
Query 440		AAATTACCCAATCTGACACGGGGAGGTAGTGACAATAAAACAAATACGGGCTTTG		499
Sbjct 440		AAATTACCCAATCTGACACGGGGAGGTAGTGACAATAAAACAAATACGGGCTTTG		499

Other reports: [▼ Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#)

Search Parameters	
Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Database	
Posted date	Apr 22, 2013 2:26 PM
Number of letters	48,635,782,348
Number of sequences	25,407,946
Entrez query	none

Karin-Altschul statistics		
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics	
Length adjustment	37
Effective length of query	1730
Effective length of database	47695688346
Effective search space	82513540838580
Effective search space used	82513540838580

DNA vs. Protein

- Should you use **blastn** or **blastp**?

DNA vs. Protein

- Should you use blastn or blastp?
- Four potential nucleotides $\{A, C, G, T\}$ and therefore four potential states
- There are 22 amino acids states (including stops)
- blastp should be more sensitive than blastn (larger state space
→ lower chance of a random hit)
- If sequences are highly similar, DNA works well
- If no translated sequences available, DNA is required
 - intergenic spacers
 - RNA genes

Is homology a quantitative measure?

- Can anything be “90% homologous”?

Homology is a boolean term (with quantitative support measures)

- nothing is “90% homologous”
 - things are either homologous or not
 - there are no “degrees” of homology
 - there may be a degree of your support for homology
- statistical significance depends on the size of the alignments and the database
 - E -value increases as database gets bigger
 - more chance for a random hit
 - E -value decreases as alignments get longer
 - more significant the longer the alignment

Sequence similarity can suggest homology

- (1) significant alignment over (2) the majority of the length of both sequences → strongly suggests homology
- homologous sequences do not always produce significant alignments (!)
- regions with low complexity (but that are not cleaned out by initial steps in BLAST) can produce significant alignments with virtually no homology

Pease and Smith. 2016. *Briefings in Bioinformatics*.

So what are the “rules” for determining homology?

- (There are no easy or standarized rules)
- Nucleotides
 - Some have suggested that sequence identity $> 70\%$ is the standard for homology
 - E -values of 10^{-6} or less = nope
- Proteins
 - sequence identity $> 25\%$ has been suggested
 - E -values of 10^{-3} or less = hmm... nope
- You must verify and thoroughly explore your own dataset.
- In a high-throughput large-scale analysis, there will be a (inescapable) margin of error

Conclusions and Questions

- Can pairwise sequence alignment address your question?
 - Are there any homologous sequences?
 - Are a set of sequences I have homologous?
- What questions are not approachable?
 - What are the **relationships** among these sequences?
 - Is there shared **function** with this sequence?
- Which database should you search?
- Which program should you run?
 - When possible, it is best to search protein databases
 - Use NR and general GenBank for exploration or specific queries,
 - Best to narrow down to a smaller database, if possible
- Be critical of your results! (quality control, basic metrics)