Pairwise Alignment

Anything can align to anything...

BIOL 435/535: Bioinformatics January 25, 2021

With enough gaps, any sequence can be aligned to any other sequence

Seq1 - ABCNJROCLCRPM Seq2 - AJCJNRCKCRBP

With enough gaps, any sequence can be aligned to any other sequence

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Seq1 - ABCNJROCLCR-PM
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Seq2 - AJCJNR-CKCRBP-

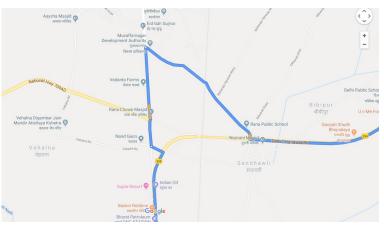
Seems reasonable...
but not systematic/repeatable

How best to align two sequences

- Global alignment
 - Best overall alignment from end-to-end



- Local alignment
 - Short regions of the sequences that have homology



Scoring alignments

Match

Mismatch

Gap

- Gap extension
 - One long gap is better than many short gaps

Construct scoring matrix starting at origin

 Trace path through scoring matrix by selecting local maximum (start at bottom right corner, end at origin)

Rules:

Start at origin at 0
Match (diagonal) = +1
Mismatch (diagonal) = 0
Gap (right or down) = -1

		Α	В	С	N	J	R	0	С	L	С	R	Р	M
	0													
Α														
J														
С														
J														
N														
R														
С														
К														
С														
R														
В														
Р														

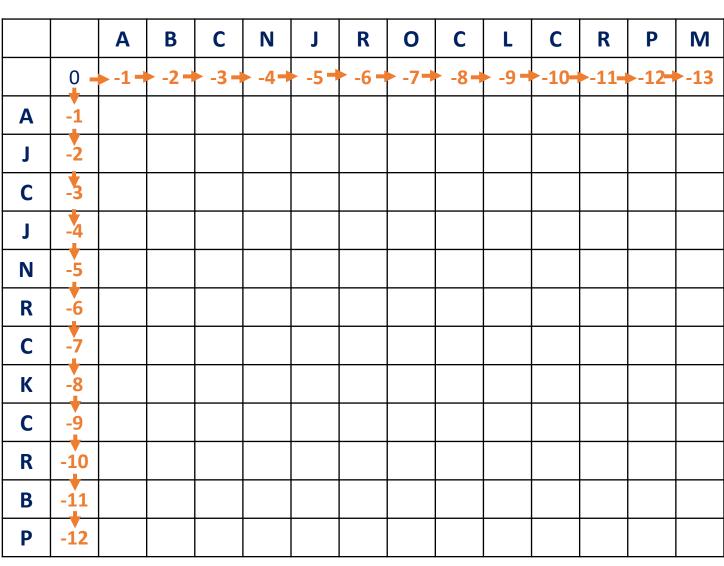
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		Α	В	С	N	J	R	0	С	L	С	R	P	M
	0 -	-1 →	-2 ◄	-3=	-4 →	-5 -	-6 -	-7→	-8 →	-9 -	-10	-11=	-12	-13
A	-1	1 -2 -2 1												
J	-2													
С	-3													
J	-4													
N	-5													
R	-6													
С	-7													
K	-8													
С	-9													
R	-10													
В	-11													
Р	-12													

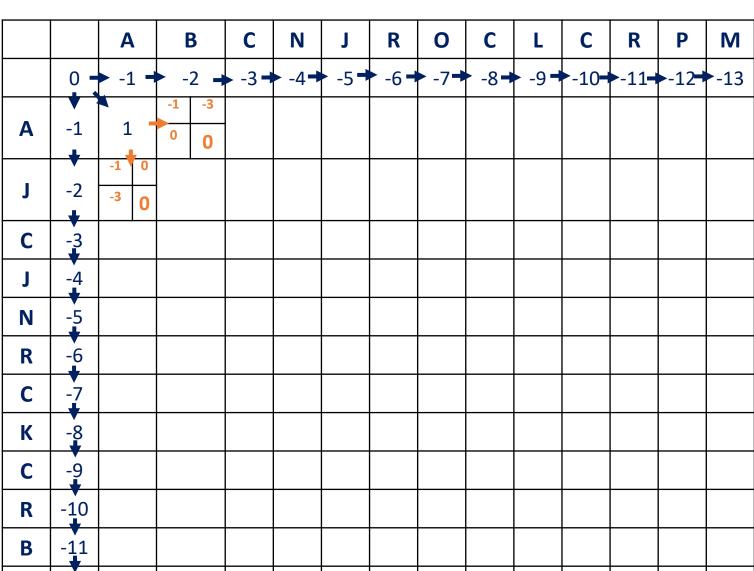
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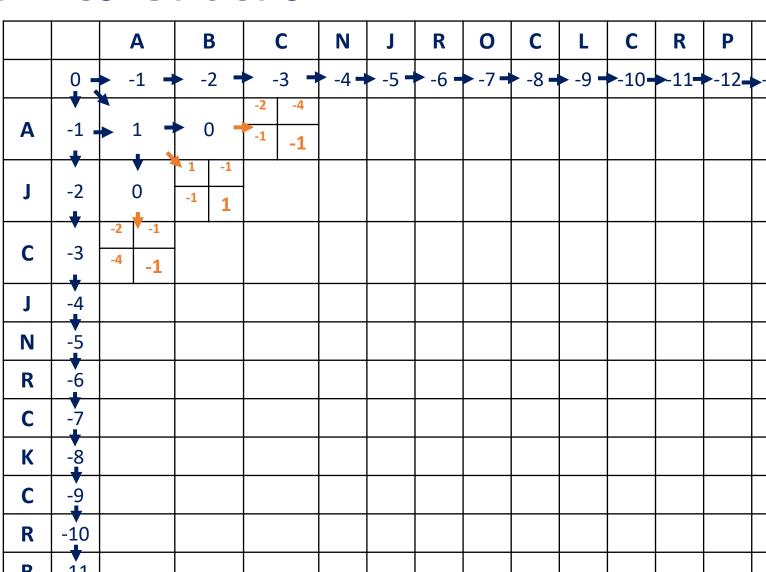
Rules:

Start at origin at o

Match (diagonal) = +1

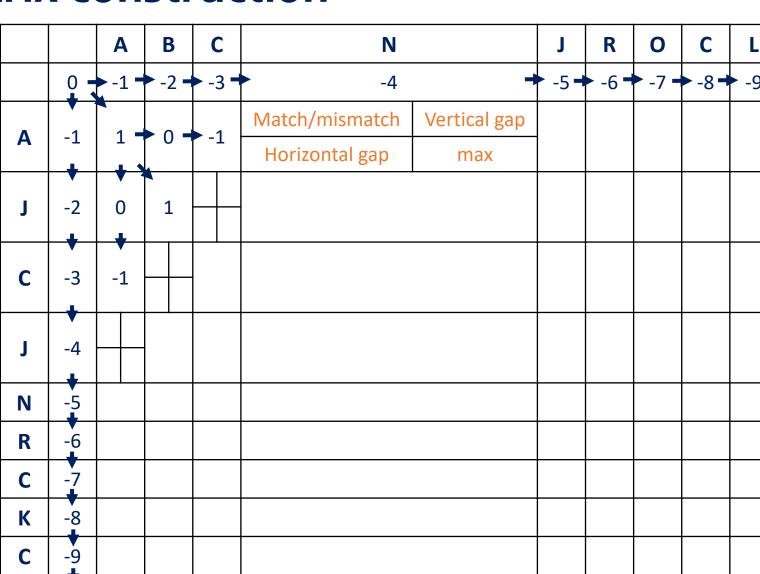
Mismatch (diagonal) = o

Gap (right or down) = -1



Rules:

Start at origin at 0
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Mismatch (diagonal) = 0
Gap (right or down) = -1



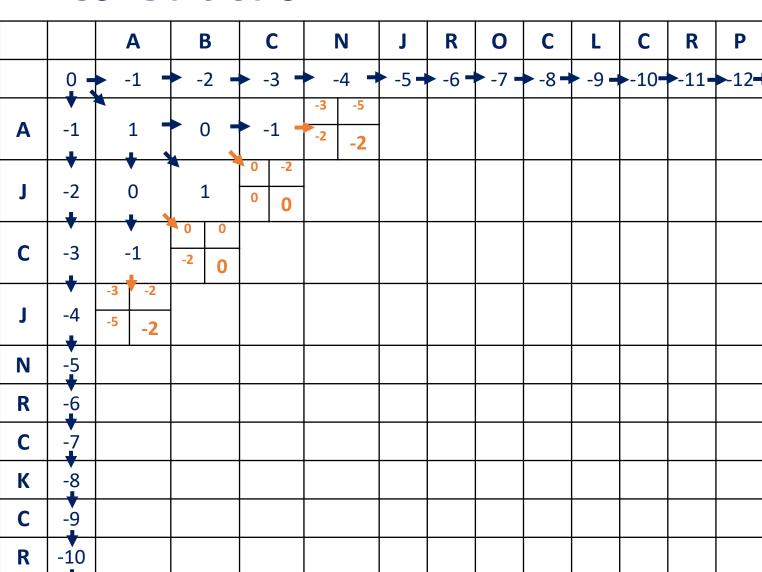
Rules:

Start at origin at 0

Match (diagonal) = +1

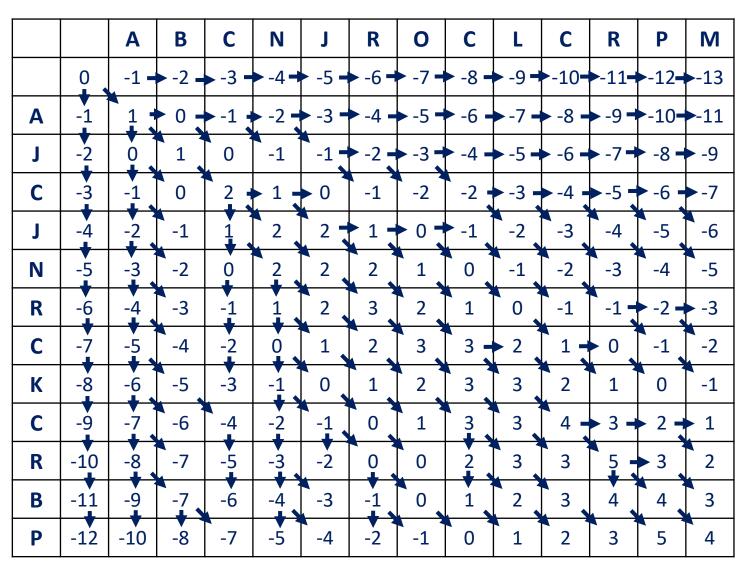
Mismatch (diagonal) = 0

Gap (right or down) = -1

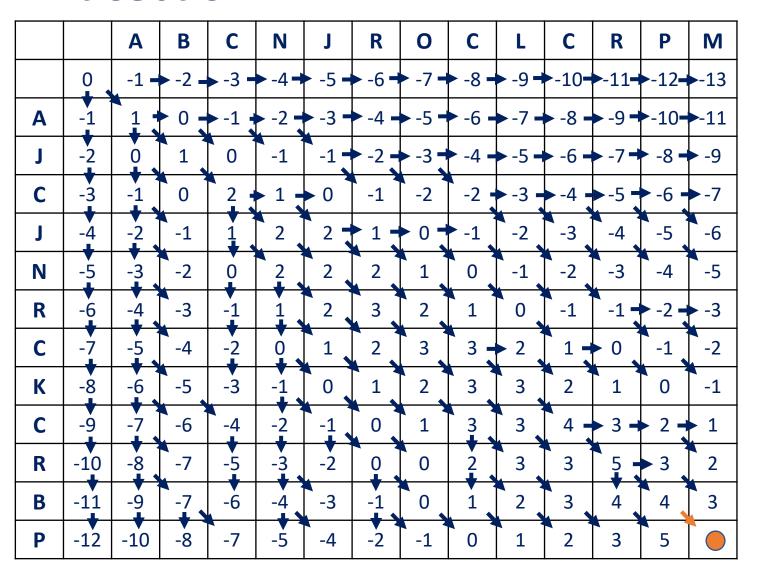


Rules:

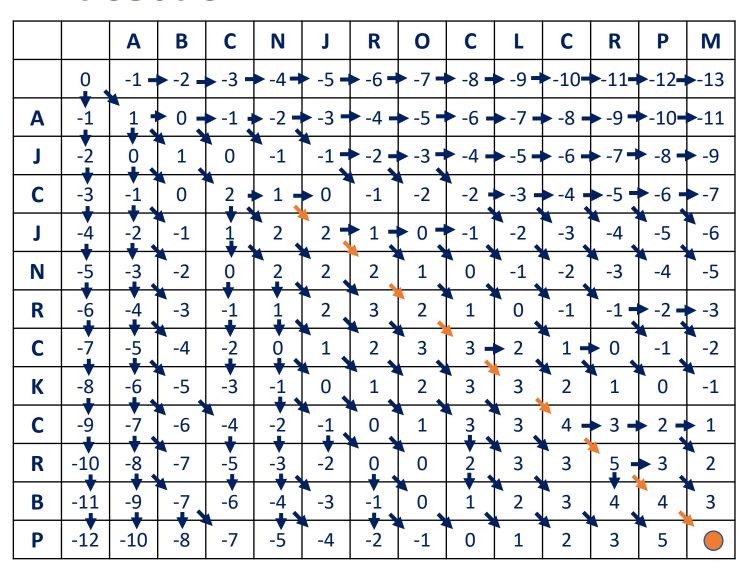
Start at origin at 0
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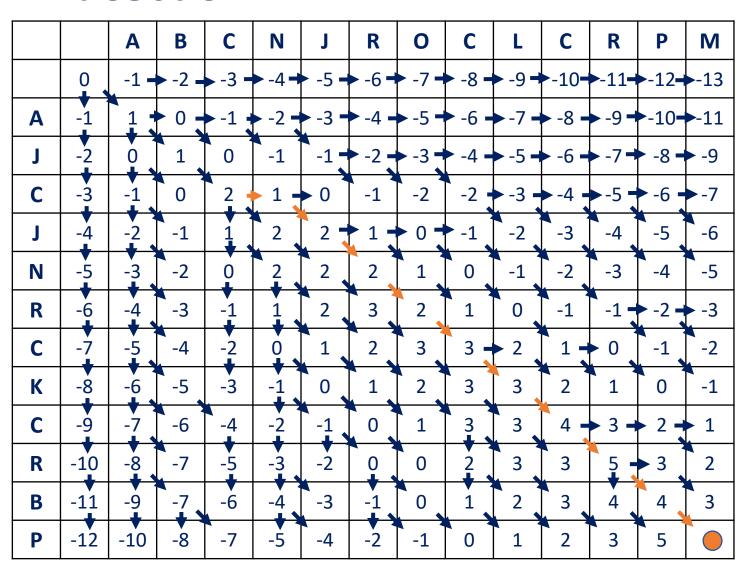
Rules:



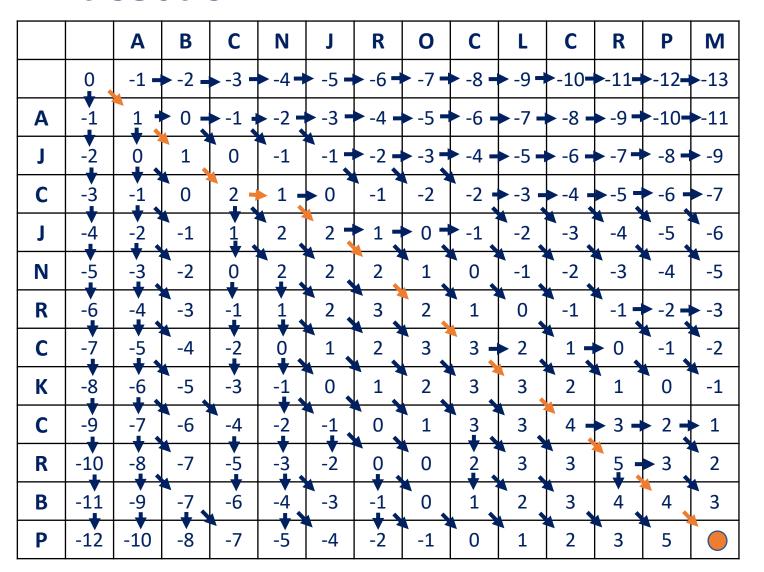
Rules:



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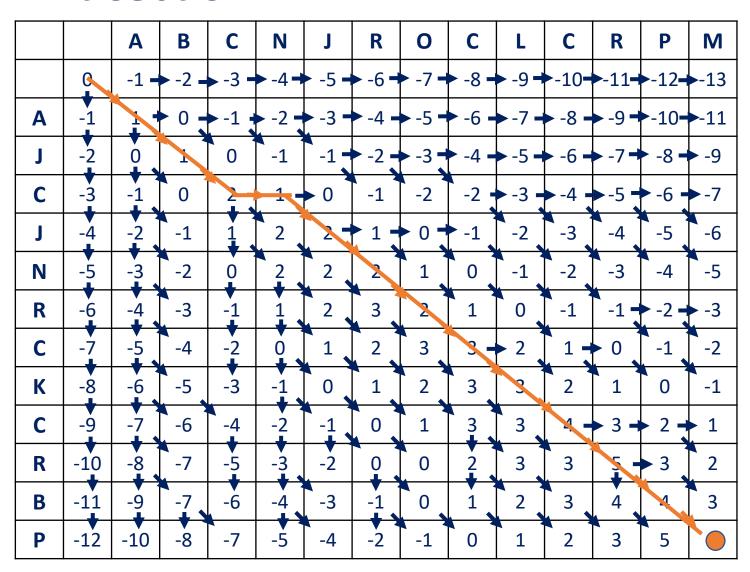
Rules:



Rules:

Start at bottom right corner, proceed through highest scoring path at each cell, (tie goes to the diagonal)

ABCNJROCLCRPM
AJC-JNRCKCRBP



Smith & Waterman Local Pairwise Alignment

 Construct scoring matrix (no negative numbers, lowest cell score possible is o)

• Trace path through scoring matrix by selecting local maximum (start at global high score, trace toward origin until hitting a o)

Smith & Waterman Local Pairwise Alignment Traceback

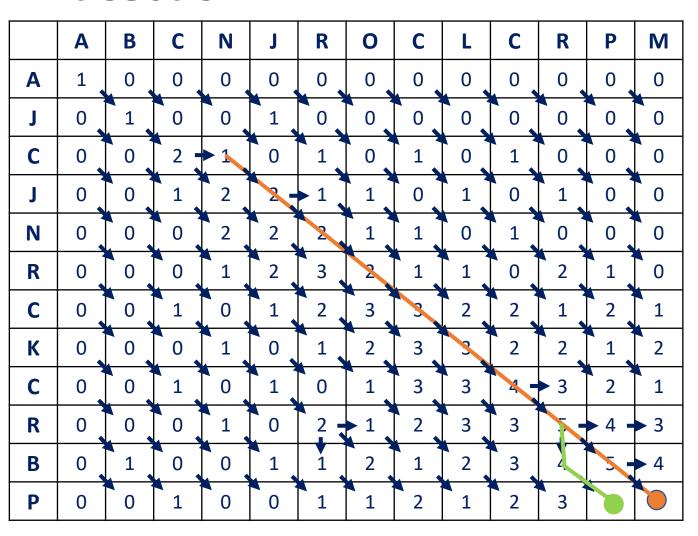
Rules:

Start at highest score, proceed through highest scoring path at each cell, (through the source from each cell), until you hit a o

NJROCLCRPM CJNRCKCRBP

or

NJROCLCR-P CJNRCKCRBP



Practice Run! Go to GitHub page, download activity ppt

Next up: Multiple Sequence Alignment

Download MEGA

Homework #2 will be posted this afternoon

Please read: Needleman & Wunsch 1970, Smith & Waterman 1981