

Criteria	Ratings				
Section 1: Explain the use of the global alignment programs provided	Excellent	Good	Acceptable	Needs Improvement	Not Done
	Describes what they would expect the scoring matrix (a) to look like and why. Can identify the traceback matrix (d) and explain how it is used. Discusses why this is a good alignment and provides reasoning for this. Includes the potential number of alignments (1,352,078). Discussed the way that changing the weights of the mismatch and gap penalty change the alignment score and alignment.	Declares that this is what they expect with no explanations for the scoring matrix (a). Can identify the traceback matrix (d). Discusses why this is a good alignment. Includes the potential number of alignments (1,352,078). Identified that changing the weights of the mismatch and gap penalty change the alignment score and alignment.	Declares that this is what they expect with no explanations for the scoring matrix (a). Can identify the traceback matrix (d). Identifies that this is a good alignment. Includes the potential number of alignments as a calculation but not the final number. Identified that changing the weights of the mismatch and gap penalty change the alignment score and alignment.	Declares that this is what they expect with no explanations for the scoring matrix (a). Cannot identify the traceback matrix (d). Does not identify this is a good alignment. Includes an incorrect potential number of alignments. Does not identify that changing the weights of the mismatch and gap penalty change the alignment score and alignment.	At least 2 questions not answered.
Section 2: Perform alignment on mRNA sequences.	Excellent	Good	Acceptable	Needs Improvement	Not Done
	Is able to successfully run R program and edit to	Is able to successfully run R program and edit to	Is able to successfully run R program and edit to	Is not able to successfully run R program and edit to	At least 2 questions not answered.

Reason from alignment scores about similarity.	<p>determine the differences between the various RNAs. Identifies the size of matrix a (number of bases seq1x number of bases seq2), 627x631. Explains why. Alignment score should be 175 if using M=1, X=-2, g=-5. Potential alignments are HUGE (too large for Excel to calculate). Explain why so large. If using default scores, human HBB is closer to mouse HBB than human HBA. Discusses that the alignment score is lower for human HBB to HBA than human HBB to mouse HBA. Depending on the values they use, they may get different answers.</p>	<p>determine the differences between the various RNAs. Identifies the size of matrix a (number of bases seq1x number of bases seq2), 627x631. Alignment score should be 175 M=1, X=-2, g=-5. (With built in scores. If they have changed this might be different.) Potential alignments are HUGE (too large for Excel to calculate). If using default scores, human HBB is closer to mouse HBB than human HBA. Discusses that the alignment score is lower for human HBB to HBA than human HBB to mouse HBA. Depending on the values they use, they may get different answers.</p>	<p>determine the differences between the various RNAs. Identifies the size of matrix a (number of bases seq1x number of bases seq2), 627x631. Provides an alignment score but doesn't specify the penalties used to achieve it. Just says they can't calculate it. Identifies that mouse is closer, but doesn't provide an accurate reason for why. Depending on the values they use, they may get different answers. They should identify one pair. Does not describe why this pair is the best. Provides an image of the alignment of at least one of the RNAs with another.</p>	<p>determine the differences between the various RNAs. Incorrectly identifies the size of matrix a (number of bases seq1x number of bases seq2), 627x631. Provides an alignment score but doesn't specify the penalties used to achieve it. Just says they can't calculate it. Incorrectly identifies that HBA is closer. Depending on the values they use, they may get different answers. They should identify one pair. Does not describe why this pair is the best. Does not provide an image of the alignment of at least one of the RNAs with another.</p>	
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	They should identify one pair and discuss why they think they are the most similar (highest edit distance score). Provides an image of the alignment of at least one of the RNAs with another.	They should identify one pair and identify that this pair has the highest edit distance. Provides an image of the alignment of at least one of the RNAs with another.			
Section 3: Understand and explain use of local alignment and difference between local and global alignments	Excellent	Good	Acceptable	Needs Improvement	Not Done
	Is able to successfully run R program and edit to determine the differences between the RNA and genome. Discusses how the alignment doesn't align the exons well, as one would like for an RNA → genome alignment. Describes a method to make the alignment better, either local alignment, or using an additional type of penalty, gap	Is able to successfully run R program and edit to determine the differences between the RNA and genome. Discusses that the alignment doesn't align well. Doesn't identify that it's because it's not aligning exons properly. Describes a method to make the alignment better, either local alignment, or using an additional type of penalty, gap	Is able to successfully run R program and edit to determine the differences between the RNA and genome. Discusses that the alignment doesn't align well. Doesn't identify that it's because it's not aligning exons properly. Describes a method to make the alignment better, either local alignment, or using an additional type of penalty, gap	Is unable to successfully run R program and edit to determine the differences between the RNA and genome. Doesn't think the alignment is bad. Can not identify that exons should be identified. Identifies that a local alignment would be better. They do not edit the R program to make a 4 th option, 0. The program doesn't run.	Does not attempt to edit R program.

	extension. They correctly edit the R program to make a 4 th option, 0. The program runs.	extension. They correctly edit the R program to make a 4 th option, 0. The program runs.	extension. They edit the R program to make a 4 th option, 0. The program doesn't run.		
Section 4: Multiple Sequence Alignment with Bioconductor	Excellent	Good	Acceptable	Needs Improvement	Not Done
	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than mine and identifies that the clear exon/intron boundaries without random matches between the RNA in intronic regions is why it's better. Identifies that the local alignment only provides an alignment of the last exon with the DNA as it's the exon with the highest score. They provide images of the multiple sequence alignment of both	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than mine and identifies that the clear exon/intron boundaries without random matches between the RNA in intronic regions is why it's better. Identifies that the local alignment only provides an alignment of ONE of the exons with the DNA. They provide images of the multiple sequence alignment of both the HBBs and the HBX data. They also	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than mine and identifies that the clear exon/intron boundaries without random matches between the RNA in intronic regions is why it's better. Identifies that the local alignment only provides an alignment of part of the RNA with the DNA. They provide a dendrogram and identify that most hemoglobins are more similar to the same type than	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than without explanation of why it's better. Identifies that the local alignment only provides an alignment of part of the RNA with the DNA. They do not provide a dendrogram. They identify that most hemoglobins are more similar to the same type than those from the same organism. Indicate an incorrect	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than without explanation of why it's better. No description or explanation of the local alignment. They do not provide a dendrogram. They identify that most hemoglobins are more similar to the same type than those from the same organism. Indicate an incorrect evolutionary explanation. No next step given

	<p>the HBBs and the HBX data. They also provide a dendrogram and identify that most hemoglobins are more similar to the same type than those from the same organism. Indicates that this means these genes diverged, evolutionarily before these species diverged, so these gene duplication and evolution vents happened before speciation. They provide a reasonable next step.</p>	<p>provide a dendrogram and identify that most hemoglobins are more similar to the same type than those from the same organism. Indicates that this means these genes diverged, evolutionarily before these species diverged. They provide a reasonable next step.</p>	<p>those from the same organism. Indicates that this means these genes diverged, evolutionarily before these species diverged. They provide a reasonable next step.</p>	<p>evolutionary explanation. No next step given</p>	
Section 5: Use BLAST.	Excellent	Good	Acceptable	Needs Improvement	Not Done
Reason from BLAST results about similarity and evolution.	<p>Identifies 4 closely related sequences that are not the same sequence. They have some discussion about how similar they are. They identify at</p>	<p>Identifies 4 closely related sequences that are not the same sequence. They have some discussion about how similar they are. They identify at</p>	<p>Identifies 4 closely related sequences that are not the same sequence. They have NO discussion about how similar they are. They identify at</p>	<p>Identifies less than 4 closely related sequences that are not the same sequence. They have NO discussion about how similar they are. They</p>	<p>Does not complete one of the elements of this section.</p>

	least beta, delta, epsilon (1&2), gamma (1&2), beta pseudogene, alpha (1&2), theta, mu, and zeta. There should be an alignment of these and an image of either the alignment or the dendrogram, or both.	least 6 of the hemoglobins. There should be an alignment of these and an image of either the alignment or the dendrogram, or both.	least 6 of the hemoglobins. There should be an alignment of these , but no image of the dendrogram or alignment is given.	identify at least 4 of the hemoglobins. No alignment is indicated	
Well written and clear	Excellent	Acceptable		Needs Improvement	
	Answers to each section written in paragraph form. Clearly written and easy to understand.	Answers to each section written mainly in paragraph form. Mostly clearly written and easy to understand.		Answers to each section written in bullet form. Difficult to understand.	
Extra Credit	Excellent	Part Way		Doesn't work	
	R program runs and generates local alignment(s) for regions that align	R program doesn't run, but in reading through it, looks like it would work, but has bugs.		Doesn't make sense or isn't attempted.	