Lab 3 GSI grading

GSI	feed	ba	ck

The respondent's email address (rebeccabarter@berkeley.edu) was recorded on submission of this form.

The name of the student whose paper you are grading *

Amy Ko

The student ID of the student whose paper you are grading *

24978168



Readability and grammar of written report (5 points) *

	1	2	3	4	5	
Difficult to read and/or poor grammar	0	\circ	0	0	•	Clearly written and excellent grammar

Level of written detail on comparison of R and C++ implementation and runtime (3 points) *

	0	1	2	3	
Did not write about a comparison of the R and C++ mplementation					Wrote a detailed comparison between the R and C++ implementations



Review the code written by the author. If you aren't sure of the correctness of the implementation, that's fine, just give a grade and say so in the comments.

Correctly coded the parallelization of k-means and pairwise similarity in R/C++ (3 points) *



Comments on implementation of parallelization or the similarity measure?

It was not obvious where to find your R implementation. I eventually found it in your .Rmd file, which is fine, but it might have been clearer to provide this as a function in a script separately.

Efficiency and practicality of R and C++ code (3 points) *



Suggestions for improving *efficiency* of R and/or C++ code *

C++ code and the R code that you did provide seems very reasonable :)

Does the	e author	satisfy	the foll	owing	code	readal	oility re	equirer	nents?	(3
points)										

Consistent spacing before and after variable assignment and addition symbols (" = ", " + "), and after commas (", ")							
✓ No line of code	✓ No line of code exceeds 80 characters						
✓ Consistent variable naming (words always separated by one of "_" or ".")							
Clarity of variable names (2 points) *							
	0	1	2				
variable names are unclear and meaningless (eg `df`, `x`, `data2`, etc)				variable names are helpful and unambiguous			
Quality of code of	comments (2 រុ	ooints) *					
	0	1	2				
there are almost no comments				the comments explain clearly what is being done and why			
Suggestions for improving *readability* of R code *							

Overall your code is very readable!

In the Rmd file there are a few places where spacing is inconsistent (e.g. the code on lines 160, 163 and 204).

Did the student provide all code necessary for recompiling their results AND report (note: you do not have to actually reproduce their report) (2 points) *

1 \			, ,	•	/ \
	0	1		2	
Incomplete code or no .Rnw/.Rmd file provided		C)		Everything was provided
Clarity of folder	structure (2	points) *			
	0	1		2	
The folder structure was very confusing)		It was clear what each file corresponded to and there were no surplus files floating around
Optional comm				- '-	lease provide
Figures Correctly produ	ıced Ben-Hur-	tvpe figure	s (3 poi	nts) *	
cocom, produ	0	1	2	3	
Did not provide a figure like Ben- Hur	0		0		Figures look correct
If the Ben-Hur f	igures do not	look corre	ct, what	is wrong?	

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Quality of Ben-H	ur Figure 3	replication	figures (3 p	oints) *	
	0	1	2	3	
Did not provide a figure like Ben- Hur	0				Provided clear and visually appealing figures
Discuss one (or figures *	more) thin	gs that you	liked about	the autho	r's Ben-Hur
Very nice and clear f	igures. I like t	hat you kept th	ne range consi	stent across	each of the
Discuss one (or Hur figures *	more) thin	gs that cou	ld be improv	ved for the	author's Ben-
I also prefer lines to replicate the paper :	-	ure 2, but I und	derstand that y	ou were tryir	ng to closely
Justification of o	conclusion	s drawn fro	m the Ben-H	lur-type fiເ	gures (3 points)
	0	1	2	3	
Did not write about any conclusions drawn from the figures					Clearly outlined interpretations of the figures and drew reasonable conclusions (e.g. found k = 3, or some other value, is the best and provides reasons why)

Comments on the conclusions and interpretations of the Ben-Hur type figures *

Very clearly explained.



Provide concluding comments

One or more things that you thought was well done overall *

Your report was excellently communicated and your code was very easy to read.

One or more things that could be improved upon overall *

Perhaps connecting back to the previous lab would have added a layer to your conclusions. Providing your R similarity function in its own R script would have been less ambiguous (your peer reviewers couldn't find it!)

Any other comments that you would like to add?

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