Explore — Impact of Computing Innovations Written Response Submission Template

Submission Requirements

2. Written Responses

Submit one PDF document in which you respond directly to each prompt. Clearly label your responses **2a–2e in order.** Your responses must provide evidence of the extensive knowledge you have developed about your chosen computing innovation and its impact(s). Write your responses so they would be understandable to someone who is not familiar with the computing innovation. Include citations, as applicable, within your written responses. **Your response to the first four prompts (2a–2d) combined must not exceed 700 words.**

Computational Artifact

2a. Provide information on your computing innovation and computational artifact.

- Name the computing innovation that is represented by your computational artifact.
- Describe the computing innovation's intended purpose and function.
- Describe how your computational artifact illustrates, represents or explains the computing innovation's intended purpose, its function or its effect.

(Approximately 100 words)

Insert response for 2a in the text box below.

My computational artifact represents the benefits of human genome sequencing. The human genome project uses highly distributed data acquisition and is in the process of converting to single-molecule sequencing technologies with much longer reads to handle the astronomical growth of the genomic big data. Once the human genome can be completely sequenced, we would be one step closer to preventing and curing genetic disorders[1], which is what is depicted by my artifact.

2b. Describe your development process, explicitly identifying the comput
techniques you used to create your artifact. Your description must be det
person unfamiliar with those tools and techniques will understand your process.

(Approximately 100 words)

Insert response for 2b in the text box below.

To create my computational artifact, I used Microsoft Word. First, I used the clipart on Microsoft Word to find and arrange 3 people outlines with two on top and one below. Second, I used Google to find a website that contained pictures of genetic disorders and copied and pasted the images below the lower person outline. I then inserted arrows from Microsoft Word to show the direction of gene flow[1]. I also inserted text boxes to explain how genome sequencing can affect this gene flow.

Computing Innovation

2c. Explain at least one beneficial effect and at least one harmful effect the computing innovation has had, or has the potential to have, on society, economy, or culture.

(Approximately 250 words)

Insert response for 2c in the text box below.

This computing innovation would benefit the medical field. Complete human genome sequencing would make pinpointing specific genes that cause disorders more efficient as well as more accurate. If we know the cause, finding the solution will come soon after. It would take us one step closer to altering specific genes to not only eliminate genetic disorders but also to make people healthier, smarter, and more attractive. Physical limitations would lift and humans would achieve better in their ideal bodies. One negative consequence is the possibility of data misuse[2]. If all of our genetic information is recorded, there is no guaranteeing that the information would remain private. It could perhaps affect employment and insurance rates in the future if a person's genes are flawed and the wrong people get a hold of the private information. In many ways, genetic information is much more explicit than social security numbers. Releasing such information to others is obviously risky.

2d. Using specific details, describe:

- The data your innovation uses.
- How the innovation consumes (as input), produces (as output), and/or transforms data.
- At least one data storage concern, data privacy concern, or data security concern directly related to the computing innovation.

(Approximately 250 words)

Insert response for 2d in the text box below.

The Human Genome Project uses approximately 1 zetta-base per year. The innovation acquires data from highly distributed sources such as universities, hospitals, and research laboratories. There are currently more than 2,500 sequencing instruments made by different manufacturers that are distributed throughout different nations.The resulting big data is distributed in units as a few genetic comparisons or gene sequences or as bulk downloads from from central repositories. To reduce the computing resources necessary for large-scale analysis of the data, cloud computing is used so that only small sections of code are uploaded and highly processed data are downloaded. The data for genomics is enormous, and it's estimated that up to 40 exabytes will be needed by 2050. Efficient data compression is one solution but decompression time is also a concern. The data is medically sensitive information and must be carefully guarded. Homomorphic encryption can be used to allow only certain groups to view the data, but it is currently too expensive[2].

References

2e. Provide a list of at least three online or print sources used to create your computational artifact and/or support your responses to the prompts provided in this performance task.

- At least two of the sources must have been created after the end of the previous academic year.
- For each online source, include the permanent URL. Identify the author, title, source, the date you retrieved the source, and, if possible, the date the reference was written or posted.
- For each print source, include the author, title of excerpt/article and magazine or book, page number(s), publisher, and date of publication.
- If you include an interview source, include the name of the person you interviewed, the date on which the interview occurred, and the person's position in the field.
- Include citations for the sources you used, and number each source accordingly.
- Each source must be relevant, credible, and easily accessed.

(Note: No word count limit for this answer)

Insert response for 2e in the text box below.

1. "FAQ About Genetic Disorders." Genome.gov, National Human Genome Research Institute (NHGRI), 10 Nov. 2015, www.genome.gov/19016930/faq-about-genetic-disorders/.
2. Stephens, Zachary D., et al. PLoS Biology, Public Library of Science, 7 July 2015, www.ncbi.nlm.nih.gov/pmc/articles/PMC4494865/.
3. "Top 10 Most Common Genetic Disorders." PositiveMed, PositiveMed, 31 Dec. 2017, positivemed.com/2014/03/24/10-common-genetic-disorders/.