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Introduction to Generative AI with AWS
Project Documentation Report

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Complete the answers to the questions below to complete your project report. Create a PDF of the completed document and submit the PDF with your project.

Question	Your answer:
Step 2: Domain Choice What domain did you choose to fine-tune the Meta Llama 2 7B model on? Choices: 1. Financial 2. Healthcare 3. IT	Healthcare
Step 3: Model Evaluation Section What was the response of the model to your domain-specific input in the **model_evaluation.ipynb file**?	For the input: "Myeloid neoplasms and acute leukemias derive from" The model response was: "`myeloid progenitors. These leukemias are classified according to the WHO classification of tumors of the hematopoietic and lymphoid tissues. The WHO classification of tumors of the hematopoietic and lymphoid tissues is a compreh`" For the input: "Genomic characterization is essential for" Th model response was: "`understanding the molecular mechanisms of the disease and for developing new treatment strategies.`

	Several studies have reported that genetic variants in genes associated with the inflammatory pathway are associated with susceptibility to PFPS. For example, the gene encoding the TNF-alpha receptor” For the input: “Certain germline disorders may be associated with” The model response was: “increased risk of developing malignant or benign tumors in the breast. Germline mutations in the BRCA1 and BRCA2 genes are associated with an increased risk of developing breast cancer in both women and men. The lifetime risk of breast cancer for women with BRCA1 mut” For the input: “In contrast to targeted approaches, genome-wide sequencing” The model response was: “can identify many potentially important genes. Genome-wide association studies (GWAS) have been successful in identifying genes that affect susceptibility to a range of human diseases, including type 2 diabetes and cardiovascular disease. However, the power of GWAS is”
Step 4: Fine-Tuning Section After fine-tuning the model, what was the response of the model to your domain-specific input in the **model_finetuning.ipynb file**?	After fine tuning the model, the responses seem to be more domain specific. For the first input: “Myeloid neoplasms and acute leukemias derive from” The model response was: “” For the input: “Genomic characterization is essential for” Th model response was: “myeloid progenitor cells that undergo

	clonal expansion and differentiation. These neoplasms may be characterized by the presen ce of immunophenotypic markers, such as CD33, CD13, CD34, CD117, CD11b, CD" For the input: "Genomic characterization is essential for" Th model response was: "the discovery of new biomarkers in the field of personalized medicine. Genomic characterization is also important for the deve lopment of new biomarkers for clinical and epidemiological studies. The goal of this course is to provide an introduction to the genomic characterization of biomarkers" For the input: "Certain germline disorders may be associated with" The model response was: "increased risk of malignancies in the child. In these cases, the child is at increased risk for malignancies, but the absolute risk is very low. Children with NF1 have a 1% to 2% risk of developing malignancies. In addition, there is an" For the input: "In contrast to targeted approaches, genome-wide sequencing" The model response was: "of human tumors has revealed that somatic mutations are a major driver of cancer. In this study, we analyzed the somatic mutation profile of 248 primary and metastatic tumors from 18 different cancer types and found that the majority of

	mutations were non-recurrent.”