UDACITY

Introduction to Generative AI with AWS

Project Documentation Report

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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	2. Healthcare
Step 3: Model Evaluation Section What was the response of the model to your domain-specific input in the **model_evaluation.ipynb file**?	Myeloid neoplasms and acute leukemias derive from > a common precursor cell, the myeloid progenitor cell. The common myeloid progenitor cell is a self renewing multipotent cell that gives rise to the granulocyte, monocyte, and erythroid lineages. In addition to these three lineages, ========== Genomic characterization is essential for > the design of effective strategies to control the disease. Bacterial vaginosis (BV) is the most common vaginal infection in women of reproductive age. It is caused by an imbalance in the vaginal microbiota, with an increase in the ana ========== Certain germline disorders may be associated with

	> increased risk of developing multiple endocrine neoplasia. The most common of these is familial multiple endocrine neoplasia type 2A (MEN 2A), which is caused by mutations in the RET proto-oncogene (10). MEN 2A is character ========== In contrast to targeted approaches, genome-wide sequencing > of the virus provides a comprehensive picture of the viral population and can identify viral variants that are more likely to be transmitted. The first step in genome sequencing is to obtain a viral sample from the patient. This can be done by obtaining a nasopharyngeal swab ==========
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**?	Myeloid neoplasms and acute leukemias derive from > [{'generated_text': ' a common progenitor, the multipotent myeloid progenitor cell (MPC).1,2 MPCs give rise to granulocytes, monocytes, and erythrocytes, and also to cells that differentiate along the dendritic cell (DC) line'}] ========== Genomic characterization is essential for > [{'generated_text': ' the development of targeted therapies for cancer. Genome-wide association studies (GWAS) have identified genetic markers that are associated with cancer risk. However, the majority of the identified markers do not have a direct effect on cancer, but rather they are markers for common genetic variants that do influence'}]

	========== ===== Certain germline disorders may be associated with > [{'generated_text': ' an increased risk of developing a second primary cancer. These associations are based on a small number of studies, and the evidence is considered of low quality.\nThe risk of a second primary cancer in patients with a known germline mutation is usually estimated from the rate of second primary cancers in the general population.'}] ========== ===== In contrast to targeted approaches, genome-wide sequencing > [{'generated_text': ' has the potential to identify a wide range of mutations in the genome, including those that may be relevant to the development of drug resistance. These approaches are being applied to clinical samples in an effort to identify genetic factors that may influence the development of drug resistance.\nDNA sequencing has the potential to'}] ========== =====