

Comparing Traditional and Large Language Models For Extracting Breast and Endometrial Related Clinical Features From Electronic Health Records

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RWD31

Introduction



- In oncology, pathological features such as MMR instability and ER/PR receptor status are critical for identifying patients for specific medications or clinical trials.
- These **clinical features are often found exclusively in free-text reports** such as pathology reports, making them difficult to access or analyse in real-world evidence studies.
- **Large Language Models (LLMs) demonstrate promising potential** for extracting oncology markers from unstructured real-world data (RWD) at scale.
- Nonetheless, **concerns about accuracy and hallucinations** (misinterpretations) remain when comparing LLMs to domain-specific Natural Language Processing (NLP) models.

Methods



Dataset & Annotation:

- 2,151 individual reports were taken from a wider dataset of 77,693 fully-anonymised free-text pathology reports provided by Oxford University Hospital (min-max number of words per report: 6-3213 words; mean number of words per report: 341.7)
- Annotations were performed for 18 clinical features:
 - Endometrial cancer: FIGO stage, grade, p53, MMR, MLH1, MSH2, MSH6, PMS2, myometrial invasion, and lymphovascular invasion
 - Breast cancer: HER2, ER, and PR
 - Additional features: TNM staging (T, N, and M stages and edition used), blast cell percentage
- In total: 3,568 manual annotations incl. absence of clinical feature and different score (e.g. HER2 → positive/negative/not performed; Figo → 2a/2b/3a...)

Baseline models*:

BERT baseline models:

- Performance was compared against a **RoBERTa**, **BioBERT** as question-answering model (stage 1) and a **mpnet_v2⁵** model for stage 2. This sequence is the same for the **ArcTEX** model (right) for direct comparability of results.

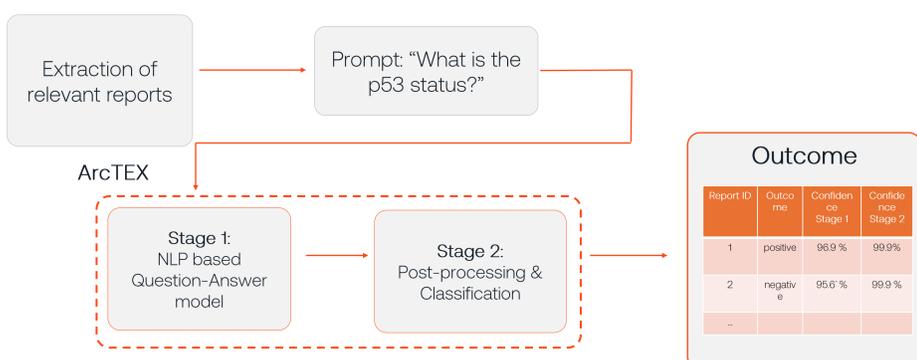
Large language models:

- Investigated LLMs: **Llama-2-7B**, **Llama-2-7B-chat**, **Llama-3-8B**, **Llama-3-8B-Instruct**
- Models were asked to provide the answer in a structured json (i.e.: {"HER2": "negative"})
- Multiple LLMs were optimised using the following techniques:
 - Prompt engineering (zero-shot, few-shot, role-based)
 - Unsupervised finetuning using low rank adaptation (LORA) using all available pathology reports⁶
- Example role-based prompt (i.e. "You are a pathologist identifying particular biomarkers of interest. You are asked the question '{question}'; regarding the following report: '{report}'. Please answer in the ...")

*All models accessed via HuggingFace platform

ArcTEX (Arcturis Text Enrichment and Extraction) model

- ArcTEX uses a two-stage process to extract and classify the results.
 - **Stage 1:** A finetuned BioBERT question-answering model extracts relevant text fragments from the report (i.e. "best described as wild-type")
 - **Stage 2:** A setfit classifier⁷ and further post-processing classifies these into a set of predefined classes. This steps ensures that the outcomes of ArcTEX are always free of personal identifiable information by design.
- Each stage generates a confidence score, allowing the end user to threshold the output and analyse model performance in handling a given dataset.



Evaluation:

- Test set was composed of 100 reports per clinical feature, split between 50 containing the feature and 50 without (n = 1800).
- The training set was composed of all remaining annotated reports with no overlap of the test set (n = 4714, average = 261.9 reports per marker). Reports, both with and without annotated clinical features were used for training and testing.

Objectives



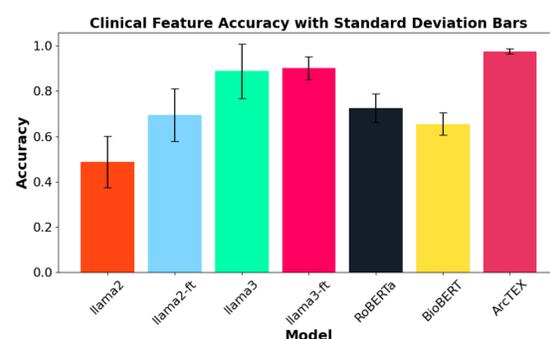
We have developed **ArcTEX (Arcturis Text Enrichment and Extraction)** model to support high-quality real-world evidence (RWE) studies by extracting oncology related features with high accuracy.

1. Compare ArcTEX to traditional NLP models (RoBERTa¹, BioBERT²) and general-purpose open-source LLMs (Llama2³ and Llama3⁴) to extract oncology markers from unstructured real-world data (RWD) at scale.
2. Compare the impact of different training schemes and optimisation strategies, including zero-shot learning, few-shot learning, and finetuning, and prompt engineering.

Results



- Figure shows results of specific LLMs and BERT based models. Llama labels have been shortened in figure and refer to:
 - Llama2: Llama-2-7B-chat, zero-shot, no further optimisation
 - Llama2-ft: Llama-2-7B-chat, role-based prompt and unsupervised finetuning
 - Llama3: Llama-3-8B-instruct, zero-shot, no further optimisation
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- All other LLMs and optimisation techniques were tested but resulted in lower accuracy compared to the best LLM models (results not shown here).



- **ArcTEX** demonstrates superior mean accuracy (98.66%) and lower variation (standard deviation = 1.1%) in comparison to the other models.

- The best-performing open-source LLM was **Llama-3-ft**, a Llama-3-8B-Instruct with role-based prompts and LORA finetuning, achieving a mean accuracy of 90.23% (standard deviation= 5.1%) across clinical markers

- The remaining models scored progressively lower scores with **RoBERTa** (mean: 72.44% / std: 9.70 %), **Llama2** (mean 69.54% / std: 11.6%), and **BioBERT** (mean: 67.67 % / std: 5.71%); all scoring less than 75% accuracy.
- Impact of optimisation of Llama3 model is low (comparison: llama3 vs. llama3-ft)
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Conclusions



- **ArcTEX demonstrates superior accuracy** and consistency in extracting clinical features from pathology reports, outperforming both BERT-based models and LLMs, even after fine-tuning.
- **Extensive fine-tuning is required for LLMs to match the accuracy** of domain-specific models (in particular for Llama2); zero- or few-shot prompting remains insufficient.
- Untrained LLMs often generate incorrect output formats, complicating result interpretation.
- Unlike LLMs, **ArcTEX also provides confidence scores** at each extraction step, offering deeper insights into how the extracted data can be effectively utilised.
- Both LLMs underperform compared to **ArcTEX**, highlighting the power of a model which is **computationally less expensive**, and **require less finetuning** to achieve the correct outputs. Furthermore, ArcTEX demonstrates superior accuracy with reduced deviation between clinical features compared to any comparable model.

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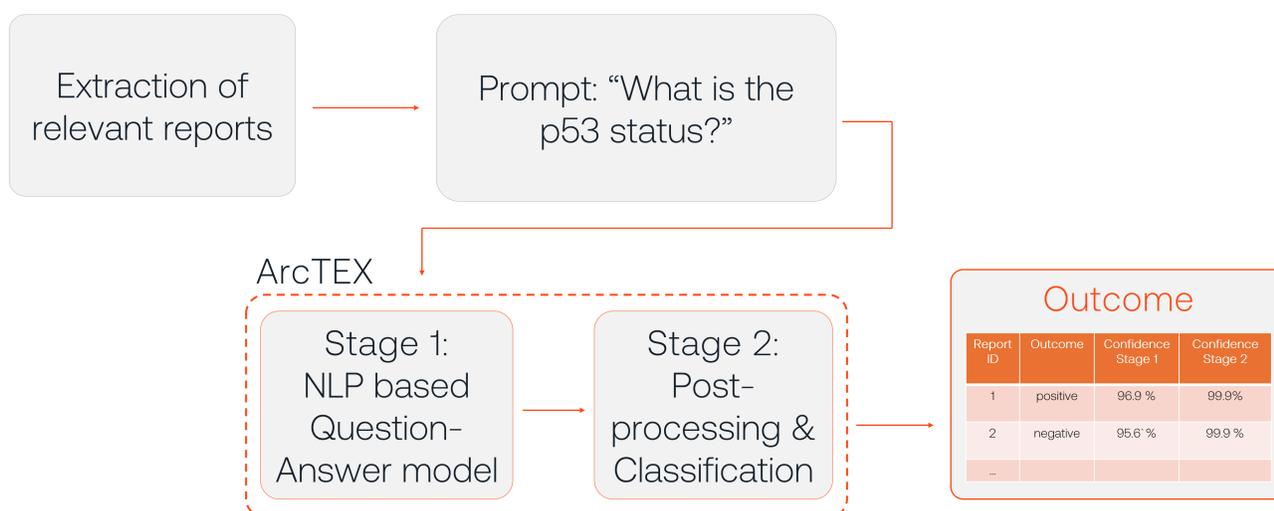
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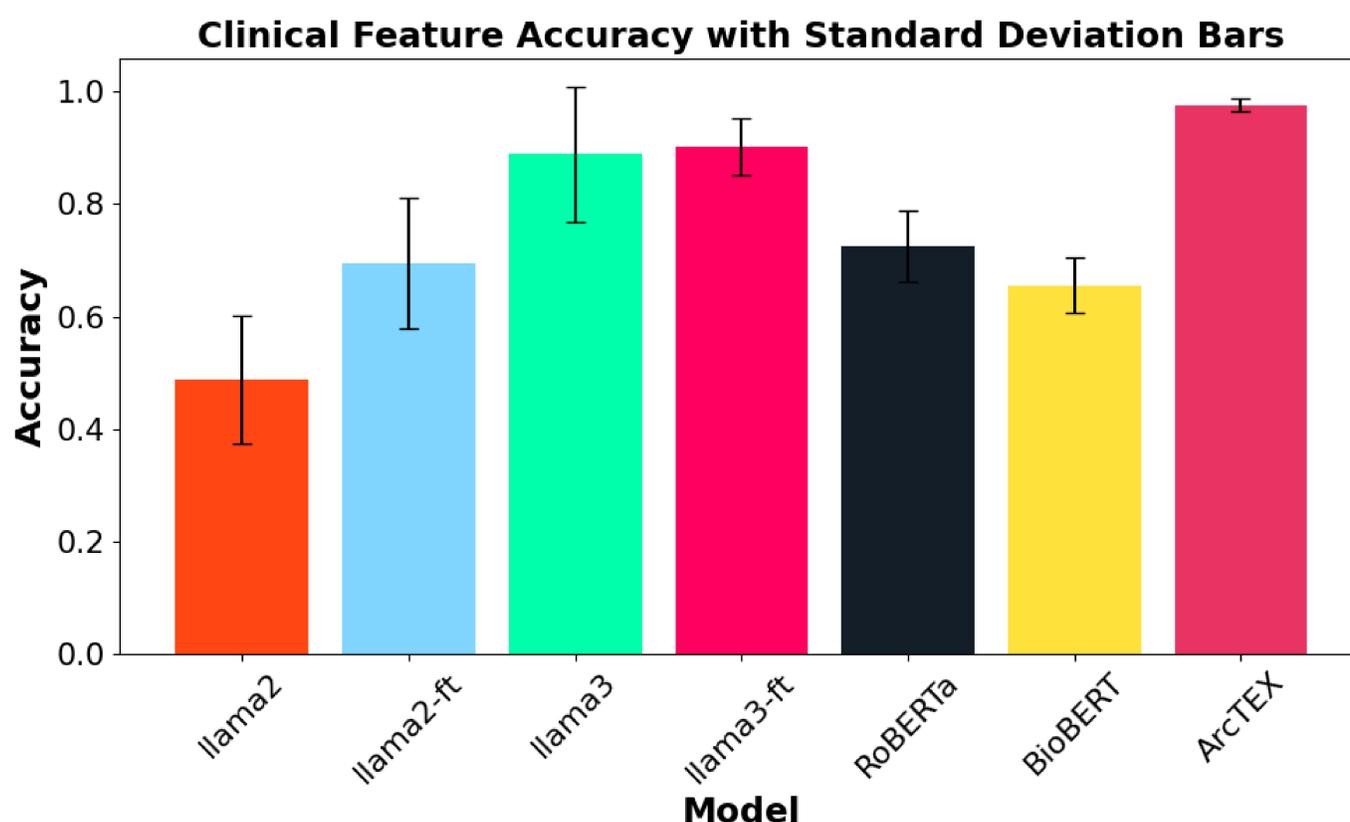
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