Assessing Quality of a Large Language Model (LLM)-Derived Prostate Cancer (PC) Real-World Dataset: An Application of the Validation of Accuracy for LLM/ML-Extracted Information and Data (VALID) Framework

MSR65

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Background

- The VALID Framework assesses LLM-derived real-world data (RWD) quality across three dimensions: variable-level metrics, verification checks, and replication analyses[1]
- This study applied VALID to a novel, LLM-derived PC dataset to determine suitability for generating real-world evidence (RWE)

Methods

- **Data source:** All cases of PC spanning non-metastatic through mCRPC setting from the US-based, electronic health record-derived, deidentified Flatiron Health Research Database.[2] LLM-derived data (n=385,566) were compared to human abstracted metastatic PC dataset (n=29,471)
- **Variables:** LLMs extracted clinically meaningful characteristics, including initial/metastatic diagnosis, castration-resistant PC (CRPC) or hormone-sensitive PC (HSPC) status, and treatment information. As a reference standard, the same variables were curated via expert human abstraction
- **Statistical methods:** The three dimensions of VALID were used as tools to assess LLM-derived data quality:
  - Variable-level metrics: The test set underwent double abstraction. F1 scores were calculated using Abstractor 2 as the reference standard for both Abstractor 1 and the LLM. The Delta F1 (LLM performance minus abstractor-to-abstractor agreement) was evaluated to assess whether the LLM achieved human-level performance
  - Verification checks: Verification checks assessed how often patients received >1 metastatic hormone-sensitive prostate cancer (mHSPC) line of therapy (LOT) in both the LLM-derived dataset and the expert human abstracted dataset
  - Replication analyses: Replication assessed real-world overall survival (rwOS) in two LOT defined cohorts—1L androgen receptor pathway inhibitor (ARPI) in metastatic CRPC (mCRPC) setting and 2L poly (ADP-ribose) polymerase inhibitors (PARPi) in mCRPC setting—in both the LLM-derived dataset and the human-abstracted dataset using the Kaplan-Meier (KM) method. Median rwOS was calculated and compared across datasets
- **Study cohorts:**
  - For Variable-level metrics, test sets of 349-500 patients were doubly abstracted to assess abstractor vs abstractor performance
  - For verification checks and replication analysis, an expert-human abstracted metastatic PC dataset was compared to an LLM-extracted prostate cancer dataset

Results

- Variable-level metrics:

Variable name	Delta F1 score (LLM – abstraction)
Initial diagnosis date	- 2.10%
Metastatic diagnosis date	- 2.11%
CRPC/HSPC status	- 0.52 %

- Verification checks:
  - In the LLM-derived dataset, the percentage of patients with >1 mHSPC LOT was 3.3% higher in the LLM-extracted dataset compared to the expert human-abstracted dataset
- Replication:
  - Median survival time (months, 95% CI) for patients with 1L mCRPC ARPI is similar in the LLM-extracted (25.3, 24.9-25.8) and expert human-abstracted (24.4, 23.7-25.1) datasets **(Figure 1)**
  - Median survival time (months, 95% CI) for patients with 2L mCRPC PARPi is similar in the LLM-extracted (15.8, 13.9-17.2) and expert human-abstracted (15.9, 14.5-17.8) datasets **(Figure 2)**

Figure 1. rwOS in 1L mCRPC ARPI-treated patients

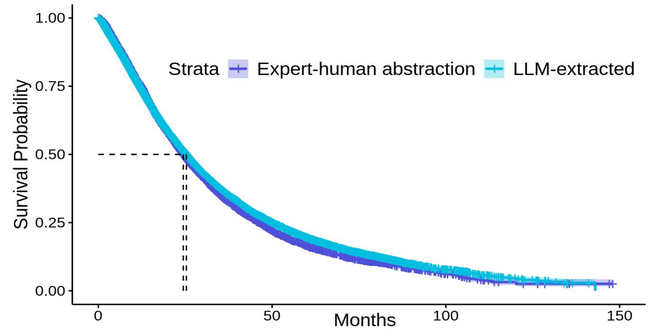
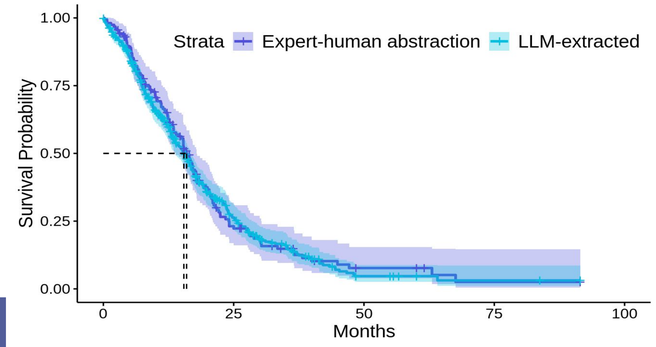


Figure 2. rwOS in 2L mCRPC PARP inhibitor-treated patients



The **VALID Framework** provided an approach that ensures **LLM-extracted RWD** can generate **fit-for-purpose RWE** in PC

Future Directions

- The VALID framework demonstrated fit-for-purpose performance across evaluated endpoints and populations. Future work will focus on scaling application and further standardizing evaluation across diverse real-world use cases

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References

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