

EHA-6002: AI-Driven Structuring of Eligibility Criteria to Enhance Patient Recruitment in Multiple Myeloma Clinical Trials

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BACKGROUND

Patient recruitment in clinical trials remains a significant challenge, particularly in hematologic malignancies such as multiple myeloma (MM). Complex and often inconsistent eligibility criteria hinder both patients and clinicians from identifying suitable studies. Despite the increasing number of clinical trials, many patients struggle to find appropriate trials due to these barriers.^{1,2} To address this issue, we present an AI-driven approach designed to systematically label clinical trials and extract structured eligibility criteria, thereby enhancing the efficiency of patient-trial matching.

AIMS

This study aimed to develop and validate an AI-based system for the extraction and standardization of eligibility criteria in MM clinical trials, with a focus on improving recruitment strategies. Our objectives included evaluating the accuracy and efficiency of eligibility classification and assessing the practical implementation of structured criteria in clinical settings.

ACKNOWLEDGMENTS

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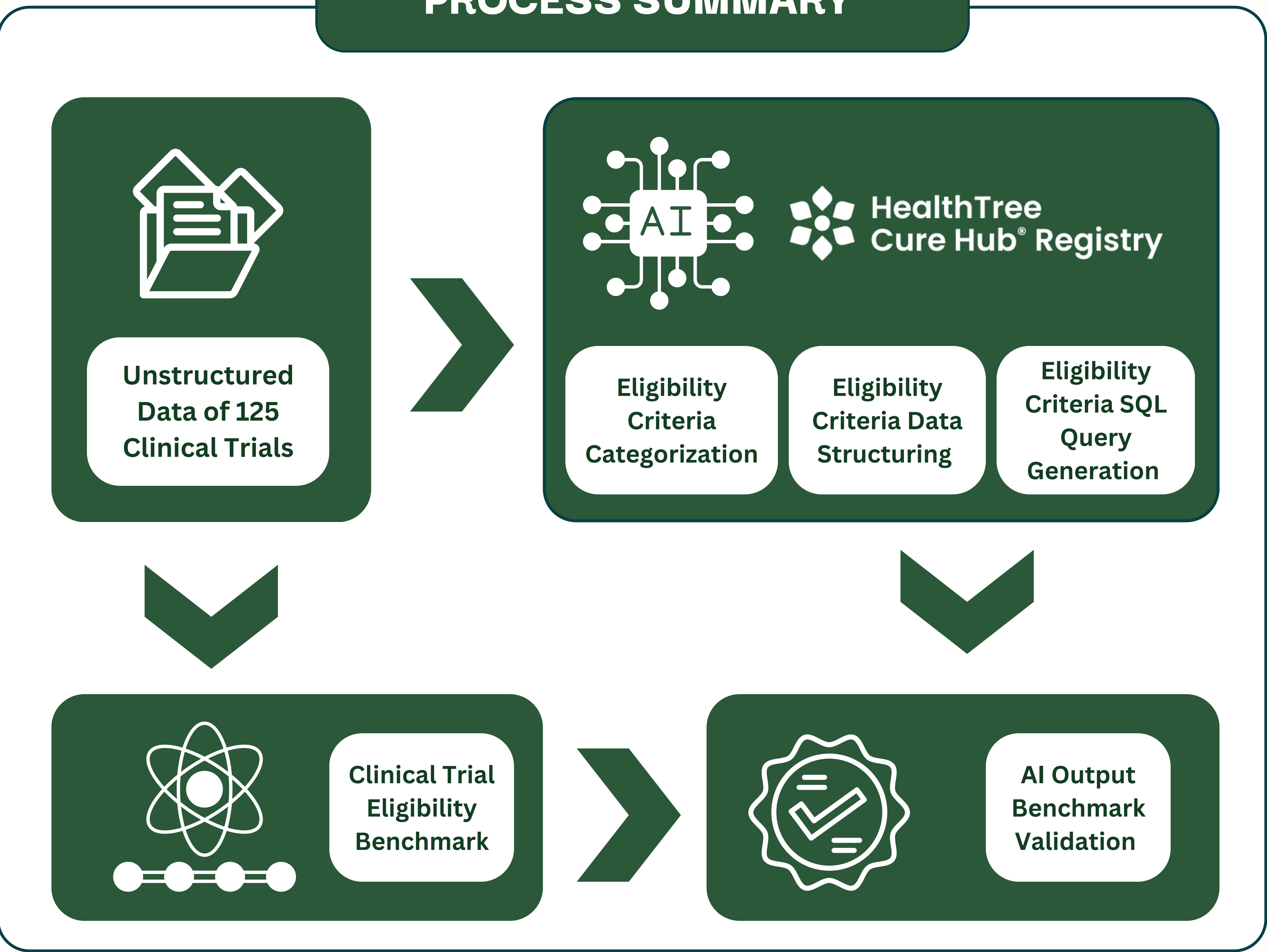
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METHODOLOGY

A dataset of 125 multiple myeloma clinical trials was manually labeled, identifying 2,571 eligibility criteria categorized into 103 unique rule types. Using a hybrid AI approach with OpenAI's o1 model, we developed a pipeline to standardize eligibility rules into structured SQL queries for direct comparison with patient data in the HealthTree Cure Hub Registry. The system extracted and validated key criteria, including Eastern Cooperative Oncology Group (ECOG) performance status and age-related eligibility, using vector search techniques and cosine similarity scoring. Extracted rules were structured with numerical values and logical operators and validated against human-abstracted benchmarks.

PROCESS SUMMARY



RESULTS

Our AI-driven approach demonstrated high accuracy in extracting key eligibility criteria, achieving **97.7% precision for Eastern Cooperative Oncology Group (ECOG) performance status** and **94% precision for age-related criteria**. The structured dataset and AI model significantly improve the automation of trial matching, facilitating efficient identification of eligible patients.

CONCLUSION

For patients who hear the devastating words, “There are no more options,” AI-driven, automated clinical trial matching—enabled by electronic health record transferability—can offer renewed hope. Standardizing eligibility criteria through AI-driven extraction and structured query generation has the potential to optimize patient-trial matching in multiple myeloma. By integrating structured trial data with real-world patient registries, this approach enhances recruitment efficiency, ultimately accelerating clinical trial enrollment and access to novel therapies. Thus future research will focus on expanding the labeled dataset and further refining AI-driven rule extraction and validation methods, thereby enhancing the practical implementation of this technology in clinical trials.

REFERENCES

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