

A Novel Approach to Matching Patients to Clinical Trials Using the OMOP Common Data Model

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Background

Clinical trials are essential for the development of new treatments but they often struggle to identify, match, and recruit the right patients in an efficient manner.¹ This is especially true for underserved populations where limited access to clinical trials may result in health disparities, inequities, and outcomes of care.² The DISRUPT project, a collaborative effort which includes Mount Sinai, Columbia University, and the Albert Einstein College of Medicine, funded by 'Stand Up to Cancer' program aims to disrupt the current practice of identifying and matching patients to clinical trials by making cancer clinical trials an easy and accessible choice for every patient.³ One key objective of this project is the computable components of matching a patient's clinical biomarker data in an electronic health record to the specific inclusion and exclusion criteria of clinical trials available from multiple sources, in as real-time fashion as possible, at scale.

The OMOP-CDM serves as the format for storing patient level data necessary for matching patients to trial information. DISRUPT utilizes a phased approach of 1) obtaining the oncology clinical trial information from the NCI-C TRP API and parsing the relevant inclusion information through an innovative PARSER application, 2) screening for pertinent patient information from existing patient populations via SCREENER application that connects to OMOP-CDM and natural language processing to sift through clinical notes and free text reports, 2) matching potential trials with eligible patients using a MATCHER process. The screening of patients was accomplished using a combination of querying for discrete criteria as well as regular expression queries against clinical text.

This project intends to show how Albert Einstein's NLP infrastructure (ElasTex™), which is based on APACHE cTAKES and Elastic Search, and integrates directly with Atlas cohort management functionality can be embedded into the DISRUPT pipeline and provide an end-to-end patient screening and matching process for clinical trials using OMOP-CDM, Atlas and NLP functionality.

Methods

We implemented the DISRUPT pipeline and tested the pipeline end-to-end to establish a baseline. We focused on the screener codebase and identified the specific endpoints that would need to be integrated to ELasTex™ and Atlas cohort functionality.

The code in the SCREENER was modified to remove the DISRUPT workflow of regular expression queries and directly query OMOP-CDM and NLP queries via ELasTex™ to obtain pertinent patient biomarker data. All patients screened and matched via this integrated query platform are published as Atlas cohorts for downstream characterization, and recruitment.

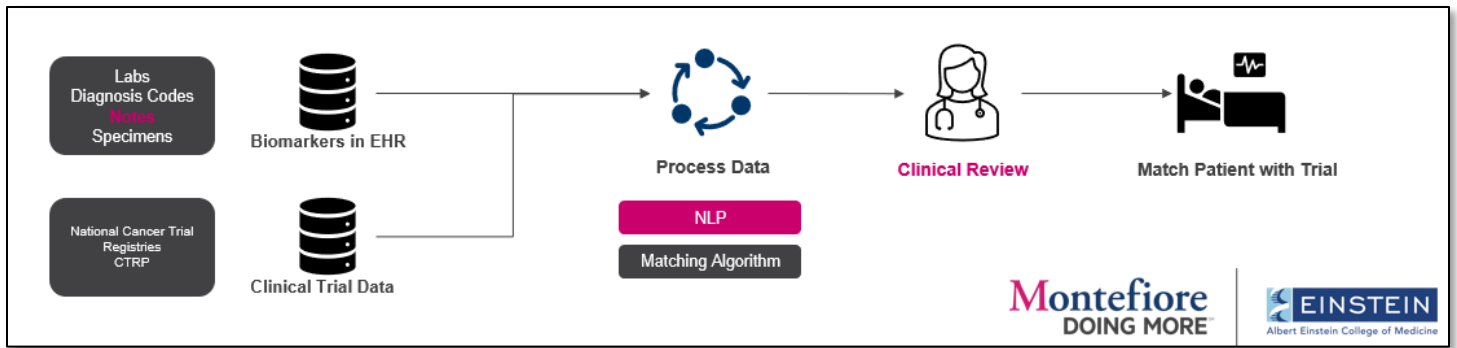


Figure 1: Description of Clinical Trial Matching Workflow

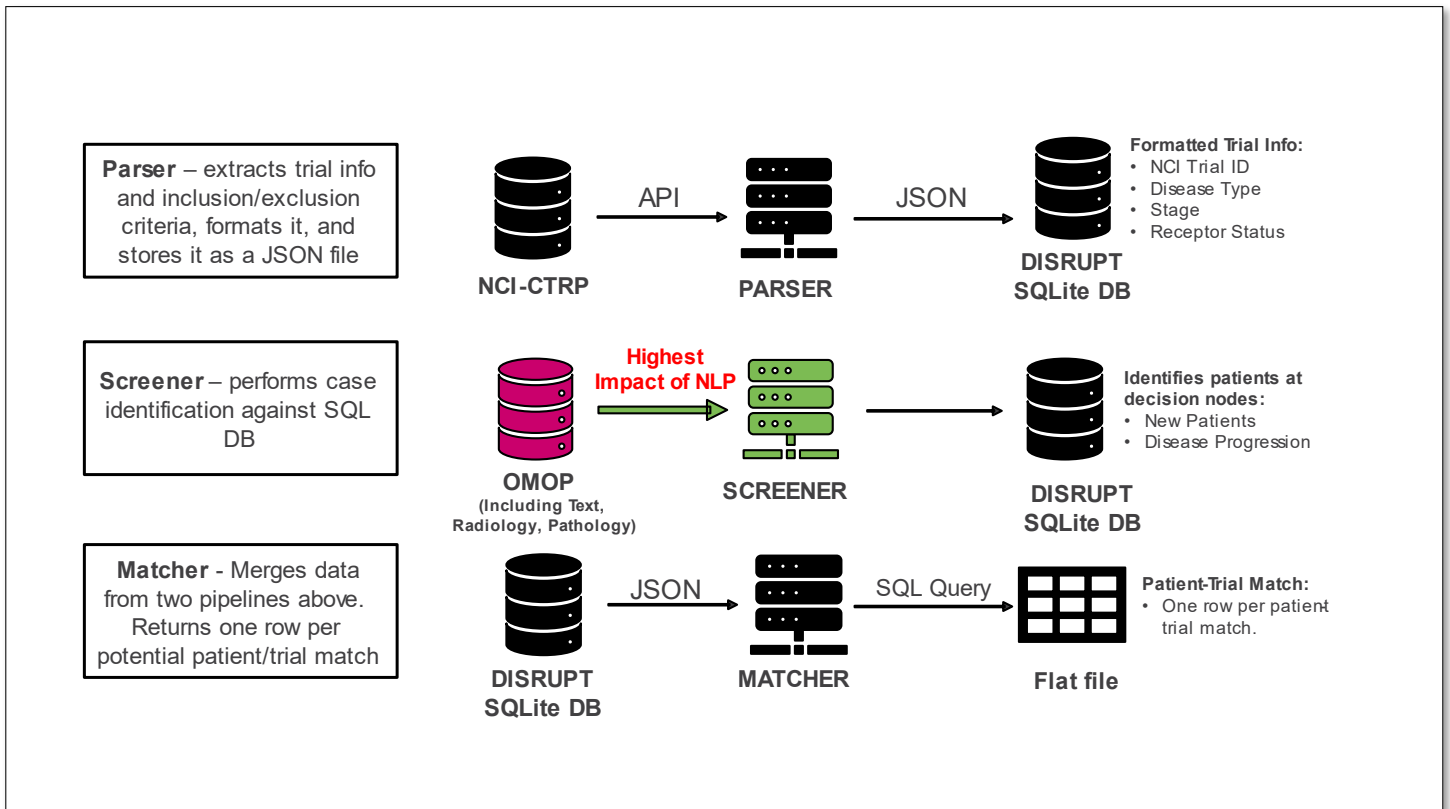


Figure 2: DISRUPT Data Pipeline

Results

We have implemented our NLP-enabled approach in Montefiore health-system’s DISRUPT pipeline. We have found that this integrated approach can efficiently identify eligible patients and believe our approach can scale equitable access to clinical trial recruitment process.

Conclusion

We believe that DISRUPT has the potential to make a significant impact on the recruitment of patients for clinical trials. By improving the efficiency of clinical trial recruitment, we can help to ensure that more patients have access to new treatments and that new treatments can be developed more quickly.

References:

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