



Gen Al-Powered Clinical Trials

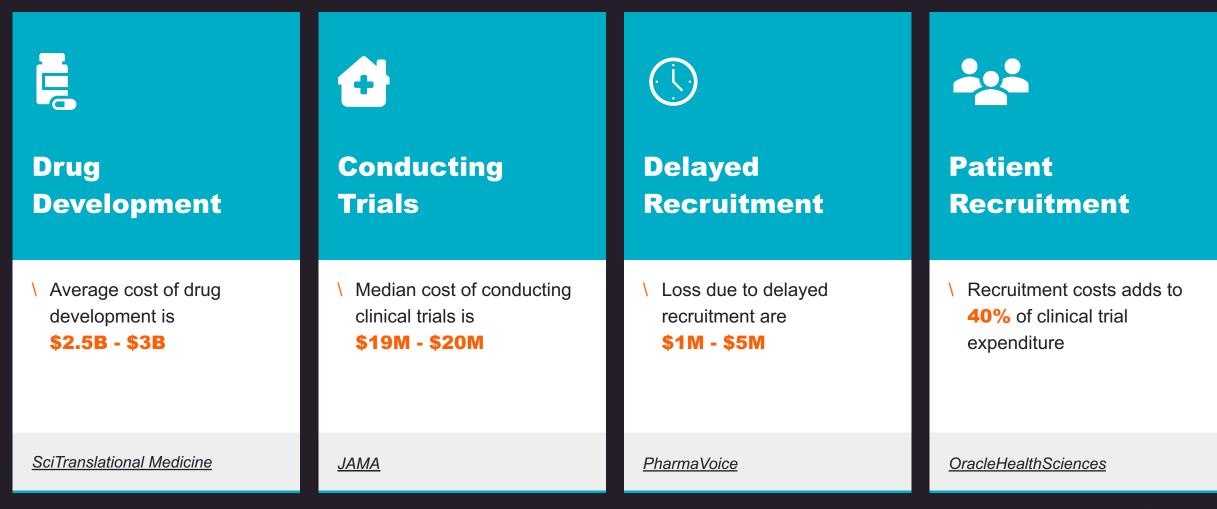
October 2023



Generative AI for Clinical Trials

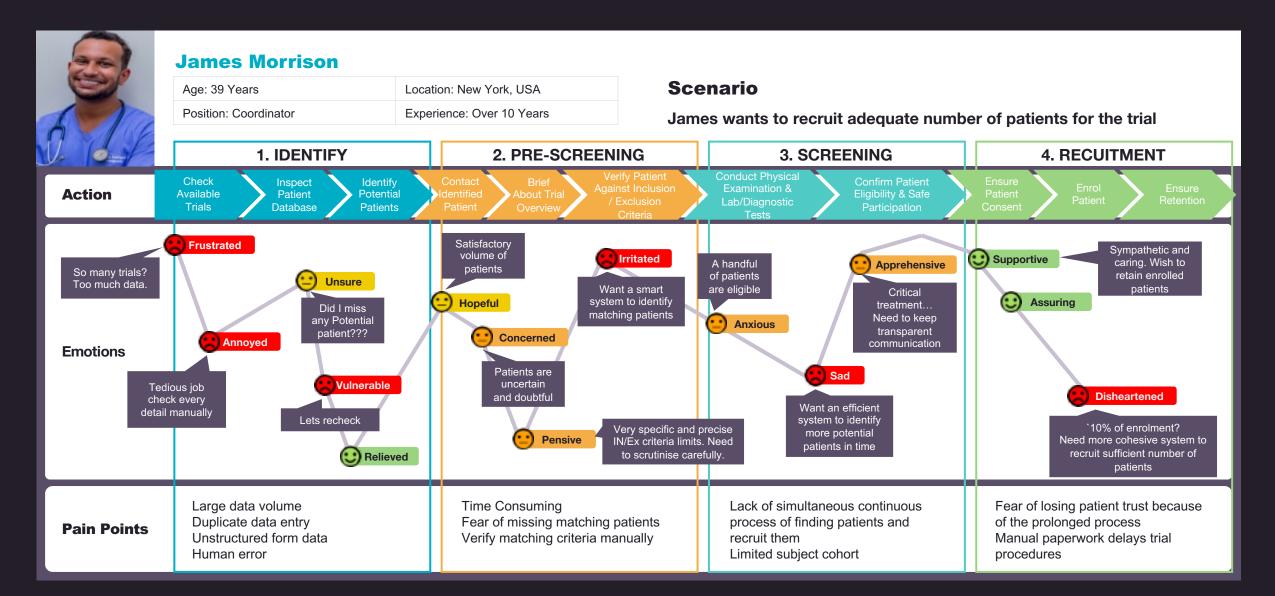
Current Landscape of Patient Recruitment in Clinical Trials

Clinical trials play a critical role in drug development but often suffer because of **insufficient**, **inaccurate and expensive** patient recruitment process.



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Discover / User Journey – Clinical Trial Coordinator



Smart Trials — Generative AI Powered Cohort Identification

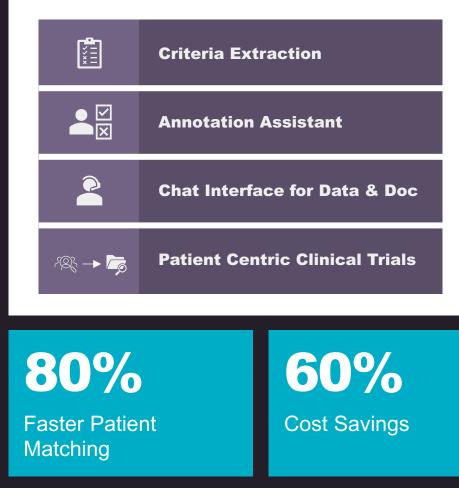
Current Landscape

Ę	Average cost of drug development is \$2.5B - \$3B
4	Median cost of conducting clinical trials is \$19M - \$20M
\bigcirc	Loss due to delayed recruitment range from \$1M - \$5M
	Recruitment costs adds to 40% of clinical trial expenditure

Benefits

- Reduce patient recruitment cost by 60%.
- Increase the clinical trial success rate by 30% using better cohort selection.
- Reduce annotation time by 50 60% for custom model creation to convert unstructured to structured data.

LLM based workbench tools for Clinical Trials

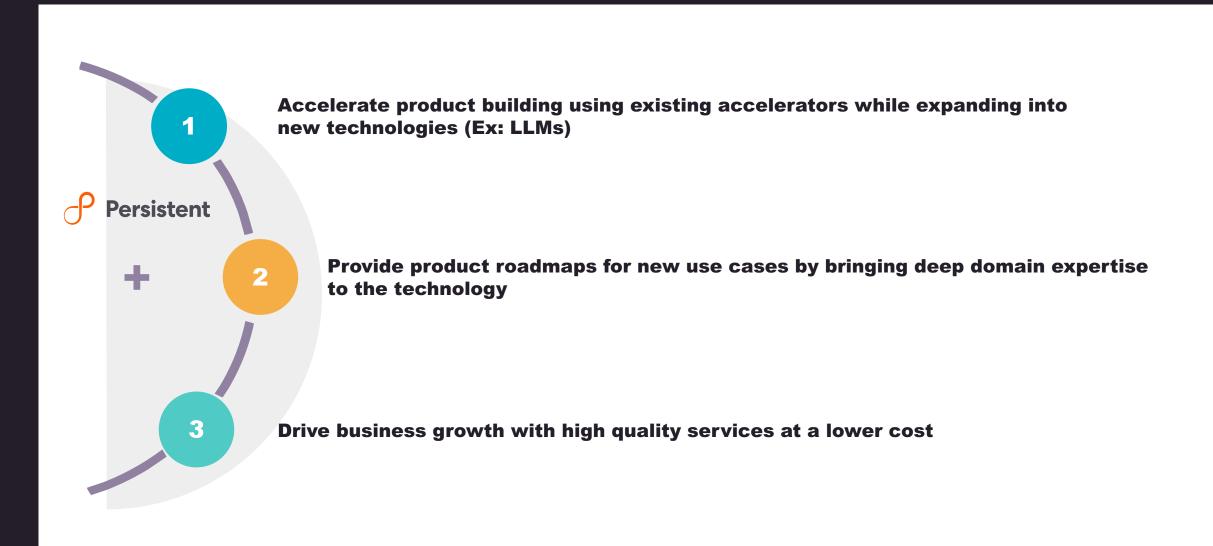


Large Language Model based tools to accelerate clinical trials

Annotator Assist	Chat Protocol	Protocol Assist		
Tool to warm-start annotations of protocol documents for extracting eligibility criteria	An efficient BOT to "chat" with protocol document for clinical trails	 Generates a baseline editable template for clinical trials 		
 Uses LLM's to auto annotate eligibility criteria from protocol documents 	 LLM techniques such as chaining and embeddings are used to make chats senseful 	 Uses NLP techniques like text clustering, summarization, natural language generation 		
\ Helps to reduce 50% - 60% of overall time required for annotations	 Takes queries in natural language, does semantic search to provide most accurate answer while staying within boundaries of the document 	 Gives head-start in creating the protocol document for clinical trials by providing baseline content 		
The LLM based annotated data is verified by SME and can be used to train local models for better criteria	Real time answers saving time to browse hundreds of pages	Reduces the time taken to write a clinical trial protocol document		

extraction

Accelerate your clinical trials by partnering with Persistent

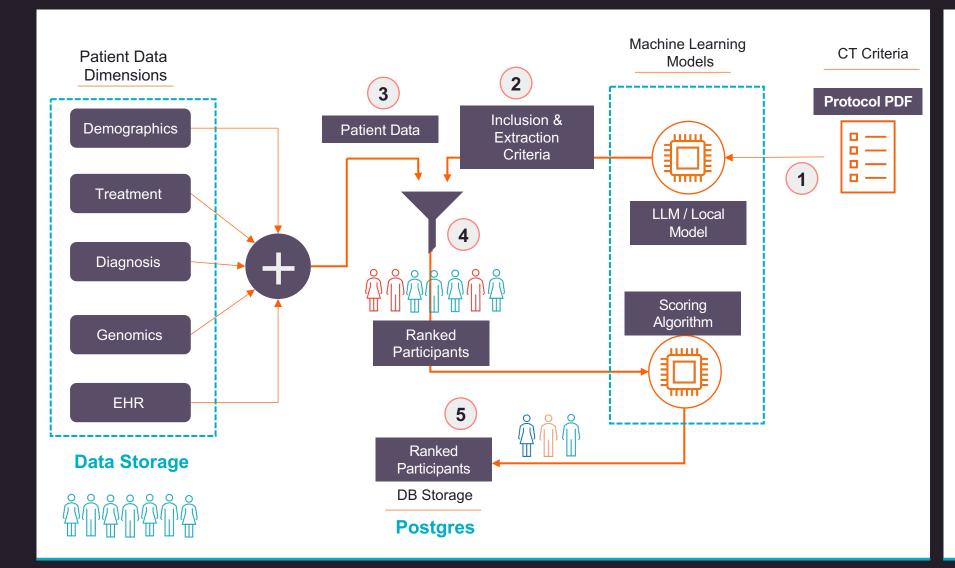


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                          "May we ask for a goo rating ?",
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                                  {text: 'Not now', anPress: () ⇒ {
                                       In Reset the timer n
                                        Cache.set('ratingPromptTimer', __mod())
```

Technical details

Oncology CT High Level Architecture Diagram

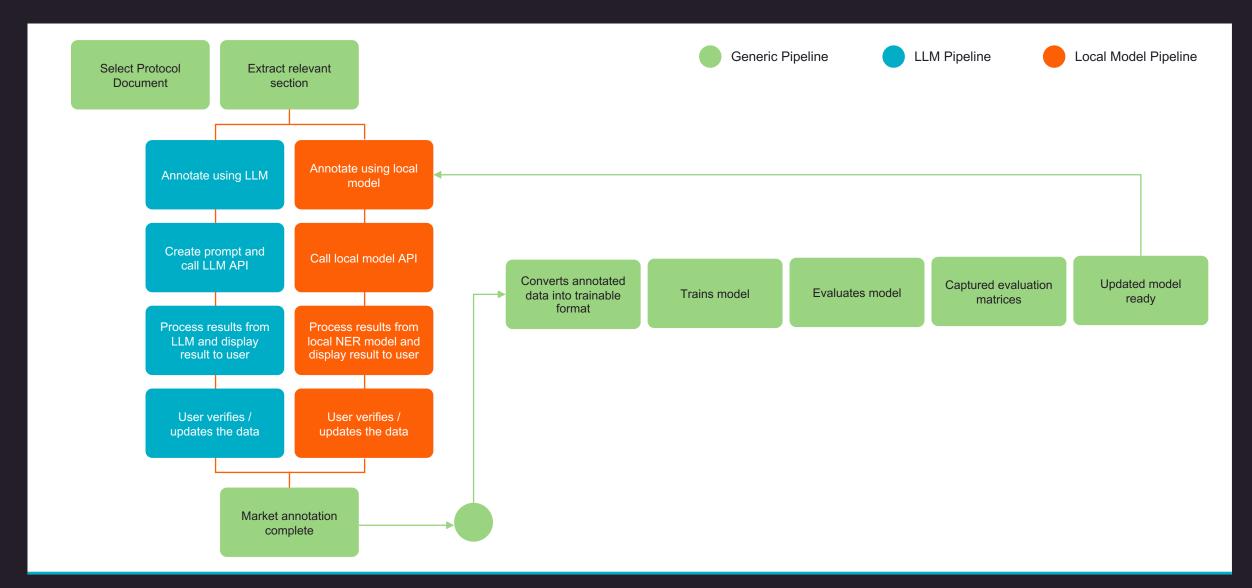


- 1. Inclusion and exclusion criteria are extracted from the protocol document
- 2. The criteria are passed to NER model (LLM / local model) to extract key entities
- 3. Patient data set is filtered based on the extracted key entities
- 4. The filter returns those patients which are eligible for the clinical trials
- 5. The scoring model will rank the patients based on who will benefit the most from clinical trial

Need for annotation: protocol documents annotations can be time consuming

- Varied tools for annotation
- Idea: use of LLM's to fast-track the annotations !
- Were conscious of cost factor and IP while calling API's
- Tool to warm-start annotations of protocol documents for extracting eligibility criteria
- Uses LLM's to auto annotate eligibility criteria from protocol documents
- Helps to reduce 50% 60% of overall time required for annotations
- The LLM based annotated data is verified by SME and can be used to train local models for better criteria extraction

Annotator Assist: Fast-pace your annotations [2]



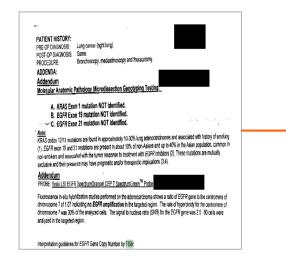
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Fast Tracking Annotations using Large Language Models (LLMs)

Example Pathology Text Reports

Challenges	Solutions
 Need for manual annotation by specialists Pathology report annotations are tedious & time consuming Data privacy and Security concerns 	 Building reliable models for faster & accurate annotations of huge datasets Developing proprietary solution that can toggle between LLM API's and locally trained NLP Model

Sample Pathology Report



User review for extracted entities

Final Extracted entities

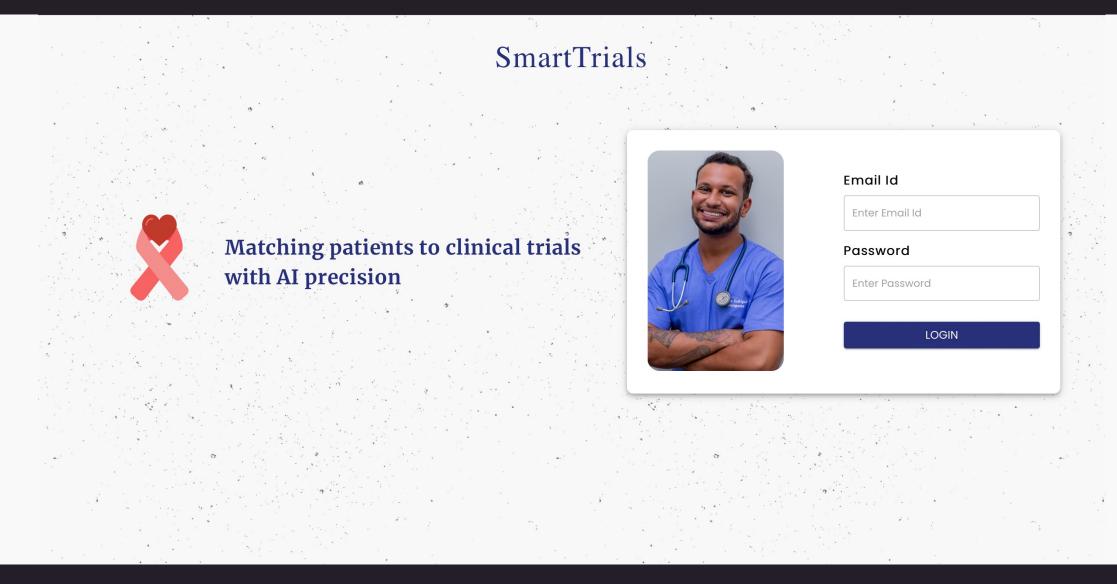
EXTRACT ENTITIES		E SAVE TO DB
(1) EGFR exon 19 and 21 mutations are present in about 10% of <u>non-AS(ans</u> and up to 40 y, In the <u>AS(an</u> population, common " nosmok.rs and associated with the tumor r•• <u>pon</u> •• to treatment with EGFR inhibitors (2). These mutations are <u>mutually</u>	Tumor size	2.5cm 0.6cm
, ~~~~ codon 12/13 mutations ate found in approximately 10-30% lung <u>adenocarcinomas a-d. associat-d</u> with <u>his-ory</u> of smokin <u>9</u>	Pathology stage	T2N0Mx
B. EGFR Exon 19 mutation NOT identified • •c~~c. <u>EGFRExon</u> 21 mutation NOT identified.		EGFR Exon 21 mutation EGFR amplification
A. KRAS Exon 1 mutation NOT identified.	Genomic Biomarkers	KRAS Exon 1 mutation EGFR Exon 19 mutation
PROCEDURE: Bronchoscopy. mediastinoscopy and thoracotomy.	Cancer type	Non small cell lung cancer
PRE-OP DIAGNOSIS: Lung <u>c.ancer</u> (right lung). <u>Same.POST-OP</u> DIAGNOSIS:	Cancer subtype	Invasive moderately differentiated adenocarcinoma Typical carcinoid
Patient Ehr	Label Assay type	Entities FISH



Demo Screenshots



Demo— OncoClinician / Clinical Trial Coordinator



Demo - Chat with your data

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•	🗜 Your de	latabase consists of 1846 lung cancer patients		
4	- Tour or	atabase consists of fore fourier patients		
ø				
	Table			
	Text			
	Pie Chart			
	Bar Chart	Type Something	>	
	Line Chart			

Demo – Convert Unstructured data – Structured data using GenAl

Persistent LLM Annotator Assist v0.1

List of (available documents (45):	Q		Upload Document:	G	LLM annotation: <mark>80 mins</mark> Manual annotation: <mark>280 mins</mark>	
	Study of Atezolizumab in Combination W CT02657434	ANNOTATE 📡			•	Model: Davinci	•
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	Study of Erlotinib in Participants Wit CT01667562	ANNOTATE 📡	OR	ANNOTATE USING LLM		02542293	0
	Study of Atezolizumab (MPDL3280A) Comp CT02409342	ANNOTATE 📡				03164616	0
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