A Survey on LLM-Assisted Clinical Trial Recruitment

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Abstract

Clinical trials are designed in natural language and the task of matching them to patients, represented via both structured and unstructured textual data, benefits from knowledge aggregation and reasoning abilities of LLMs. LLMs with their ability to consolidate distributed knowledge hold the potential to build a more general solution than classical approaches that employ trial-specific heuristics. Yet, adoption of LLMs in critical domains, such as clinical research, comes with many challenges, such as, the availability of public benchmarks, the dimensions of evaluation and data sensitivity. In this survey, we contextualize emerging LLM-based approaches in clinical trial recruitment. We examine the main components of the clinical trial recruitment process, discuss existing challenges in adopting LLM technologies in clinical research and exciting future directions.

1 Introduction

Clinical trials evaluate the effects of an intervention on human health. Selecting the precise and required size of patient population is crucial for trial completion. According to various estimates, more than 50% of aborted clinical trials fail due to low accrual rates, and 80% of all clinical trials do not manage to recruit the required patient cohorts within the allotted time (Clinical Trials Arena, 2012; Williams et al., 2015; Pharmaceutical Technology, 2019). Although this trend has steadily declined over the past decade with the intensive use of technology-aided solutions, efficient patient recruitment remains the most crucial bottleneck in clinical trial research (Clinical Trials Arena, 2022). As electronic health records (EHRs) of patients become more accessible, clinical researchers adopt machine intelligence and develop explainable systems to correctly interpret model predictions (Murdoch and Detsky, 2013; Payrovnaziri et al., 2020; von Itzstein et al., 2021).

There has been a rapid development of methods leveraging LLMs for cohort retrieval and modeling (Fang et al., 2022; Tian et al., 2023; Park et al., 2024; Liu et al., 2025a; Wang et al., 2025), trial design (Reinisch et al., 2024; Curran et al., 2024; Bornet et al., 2025; Neehal et al., 2025), trial search (White et al., 2023; Rybinski et al., 2020), trial matching (Jin et al., 2024; Nievas et al., 2024; Wornow et al., 2025), trial outcomes and duration prediction (Reinisch et al., 2024; Yue et al., 2024a,b; Liu et al., 2025c), risk of bias assessment (Lai et al., 2024; Ji et al., 2025), and clinical trial results extraction (Lee et al., 2024), while the community catches up with recommended practices for responsible use of AI throughout the drug development process (Geraci et al., 2025).

Figure 1 shows the components in clinical trial recruitment, namely, data sourcing, information extraction, matching, and evaluation. An expert reviews several hundred patients per trial and can end up spending hours on one patient, hence incurring significant costs (Penberthy et al., 2012; Ni et al., 2015). Even simple automation using table queries and lexical searches saves between 165 hours to 1,329 hours of reviewing time when compared to manual evaluation (Penberthy et al., 2010). In the past, the patient recruitment process has seen relatively low adoption of the pretrained language models (He et al., 2020; Harrer, 2023; Lu et al., 2024). Generative LLMs serve as knowledge aggregators, and through their reasoning and instruction-following capabilities, they have revived research in the task of trial and patient matching (Jin et al., 2024; Nievas et al., 2024; Rybinski et al., 2024; Wornow et al., 2025).

Difference to Prior Work. Despite the rapidly evolving landscape of LLM technology, there is no prior work surveying this area. Gueguen et al. (2025) evaluate public trial matching tools and Layne et al. (2025) compare the efficacy of open

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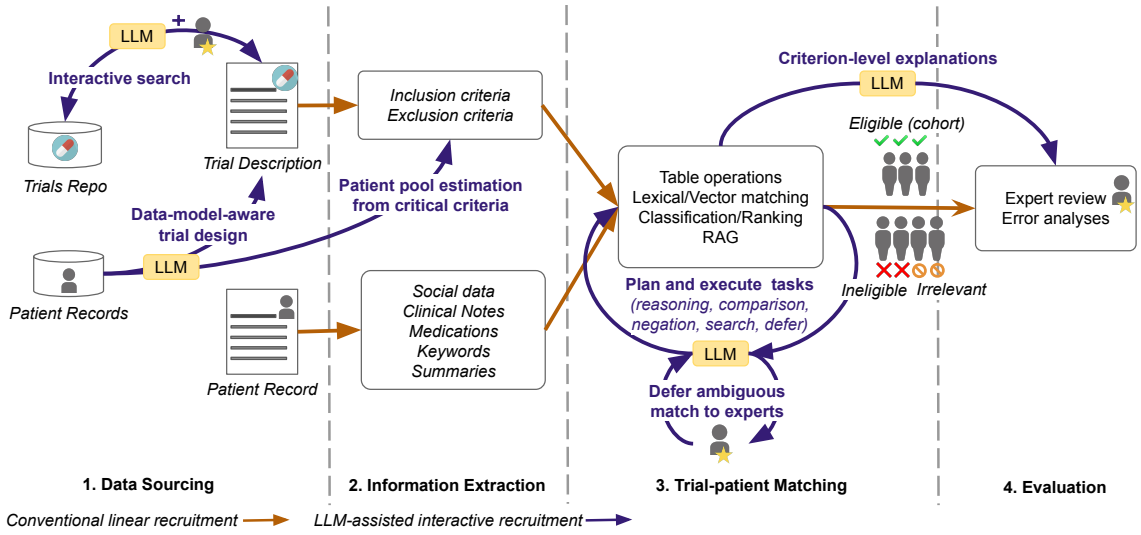

Figure 1: Components in a patient recruitment process: conventional linear flow (in orange) vs. our proposed LLM-assisted interactive flow (in purple).

and proprietary LLM-assisted trial and patient matching in oncology. Systematic reviews on this topic, bound by strict selection criteria and highly specific research question, do not capture the broad perspectives related to dataset challenges and evaluation beyond accuracy (Kim and Quintana, 2022; Idnay et al., 2022; Kantor and Morzy, 2024b; Chen et al., 2025) (See Appendix A). Although it provides an overview of LLM approaches used in clinical trial matching, Chen et al. (2025) only briefly discusses associated challenges and future work.

Our Contribution. We examine the main components of a trial recruitment process, presented in Figure 1. We formalize the problem of trial and patient matching. We analyze existing approaches via the tasks (classification vs. ranking), the directionality (trial-centric and patient-centric), the benchmarks used (longitudinal vs. short patient descriptions, single vs. multi-trial) and the evaluation metrics reported. We present a taxonomy of errors for a consistent evaluation of LLM-generated responses. We discuss the critical challenges associated with the use of LLMs in trial recruitment research. Finally, we present actionable steps towards interactive patient recruitment (illustrated in purple in Figure 1).

2 Background

Clinical Trial Recruitment. Also known as patient recruitment/enrollment/(pre-)screening, it is the process of matching patients (or a cohort) to a clinical trial via its eligibility criteria. Clinical trials have a dual nature, consisting of universal and trial-specific requirements, making it challenging to design generalized approaches (Idnay et al., 2023). This has traditionally resulted in linear trial-centric matching processes (illustrated in orange in Figure 1) with limited scope for interaction and feedback. Standard approaches have an initial data filter on structured EHRs followed by keyword matches and concept identification (Penberthy et al., 2010; Tun et al., 2023) or cohort-specific classifiers (Zhang and Demner-Fushman, 2017). Ni et al. (2015) represented both trials and patients as feature vectors supporting both trial and patient retrieval.

Biomedical NLP and LLMs. The biomedical NLP landscape is shifting from specialized pretrained language models, such as, BioBERT (Lee et al., 2020), BioLM (Lewis et al., 2020), PubmedBERT (Gu et al., 2021), BioGPT (Luo et al., 2022), MedCPT (Jin et al., 2023), among many others (Wang et al., 2023), towards instruction-following and chat-enabled LLMs (commonly termed generative AI), used as is (Nori et al., 2023; Kung et al., 2023) or fine-tuned for domain alignment, such as, Med-PaLM (Singhal et al., 2023), Med-Alpaca (Han et al., 2023) and LLaVA-Med (Li et al., 2023a). We point our reader to Thirunavukarasu et al. (2023) and Liu et al. (2025b) for further reading. The Journal of American Medical Informatics Association (JAMIA), which published 41 articles on biomedical health and LLMs in a focus issue, also observed this shift towards generative AI (Lu et al., 2024). They additionally report that the OpenAI (Achiam et al., 2023) family of proprietary

Search period	2019 - May 2025
Initial search pool *(135 SERPS, 9.8 results/SERP on average)*	1332
Excluded *(not related to trial and patient matching/duplicates)*	1207
Excluded *(full text not available / not a methodology, dataset, evaluation)*	98
Included	27
Included *(via citation network of Jin et al. (2024) and Wornow et al. (2025))*	25
Total included	52
Publication venues covered	27

Table 1: Survey Selection Protocol

models (GPT3.5/4 being the most common) is used much more often than open-sourced models (Touvron et al., 2023; Bai et al., 2023; Jiang et al., 2023). Dorfner et al. (2024) show that fine-tuning generative LLMs on the biomedical domain offers limited performance gain. Another study by Alber et al. (2025) shows that models are more prone to propagate medical misinformation encountered during fine-tuning despite performing well on benchmarks. Bedi et al. (2025) report that real patient data is used in less than 5% of the 519 biomedical studies using LLMs, and fairness, bias, uncertainty and deployment considerations are rarely assessed.

State of Adoption of NLP Advancements. Kantor and Morzy (2024b)'s study on adoption of AI for parsing eligibility criteria reports low adoption rates of generative AI, with BERT-based models being the most popular and generative models being used only since 2024. A systematic review of the role of NLP systems in patient recruitment in 2022 identified only 11 studies (Idnay et al., 2022). Heterogeneous outcomes, diverse results, a dependence on small retrospective data and a lack of common standardized benchmarks drive the gap in NLP research and their adoption in real-world settings (Idnay et al., 2024; Kantor and Morzy, 2024b). A study by Idnay et al. (2023), investigating how clinical researchers screened patients, highlights the challenges of universal and domain-specific nature of the eligibility criteria and makes recommendations to build interactive, flexible and transparent recruitment strategies. Interestingly, when Corbaux et al. (2024) categorize tools for oncological trial matching, they indicate that the automatic methods still fall in the research and development phase, yet to be commercially available.

3 Methodology

Given the interdisciplinary nature of the task and to reduce confirmation bias of known venues, we opted for a broad-scope search via Google Scholar. We queried with the keywords "clinical trial", "cohort discovery", "patient recruitment", "trial recruitment", "trial matching" in conjunction with "llm", "language model", "gpt" and inspected the first ten results pages, between the years 2019 and 2025 (both inclusive). We additionally used Jin et al. (2024) and Wornow et al. (2025) as seeds and recursively traced their citations to efficiently capture the evolution of predictive methods in this task. We finally included 52 papers in our survey of which 6 are from the arXiv and the rest span 27 venues in medical (e.g., JAMIA, Cureus, AMIA), computer science (r.g., TREC, SIGIR) and interdisciplinary (e.g., NEJM AI, Nature Communiations) publications. Table 1 provides details of the search protocol. We organized the papers into data sourcing (Section 4), information extraction and parsing (Section 5), trial and patient matching (Section 6) and evaluation (Section 7). Via our discussion on critical limitations in Section 8 and on promising directions towards interactive patient recruitment in Section 9, we provide a holistic discussion of the challenges of LLM-based trial recruitment pipelines and exciting future directions.

4 Data Sourcing: Public Benchmarks

We start with data sourcing, the first component of the recruitment pipeline (Figure 1). We analyze five trial and patient matching benchmarks.

- 2018 N2C2 Cohort Selection (Stubbs et al., 2019) for criterion-level eligibility prediction.[1]
- Koopman and Zuccon (2016) for ranking trials.
- Text REtrieval Conference Clinical Trial (TREC CT)[2] tracks 2021, 2022, 2023 for ranking trials.

Table 2 provides an overview of the benchmarks.

4.1 Trial Data

The TREC CT benchmarks and Koopman and Zuccon (2016) source the `ClinicalTrials.gov` reg-

[1]Currently unavailable as of 2024 Nov 6.

[2]Available at `https://www.trec-cds.org/`.

Task	Benchmark	Size	Eval. Metrics	Best Score	#P	LLM Usage (#P)
Cohort selection	2018 N2C2 (Stubbs et al., 2019)	#patients = 288 #records per patient = 2-5 #tokens/patient = 2711 #trials = 1 #criteria = 13	Micro-averaged: P, R, F1	0.91 micro F1	47	*(not applicable)*
Trial ranking	Koopman and Zuccon (2016)	#patient summaries (22 words avg) = 60 #patient description (78 words avg) = 60 #keywords (4.4 words avg) = 489 #trials = 204,855 #relevant matches = 685 #relevance judgments = 4000	MRR, P@5, adaptive precision	0.3 MRR $<$ 0.2 P@5	- †	*(not applicable)*
	TREC CT 2021 (Soboroff, 2021)*	#patient descriptions = 75 #trials = 375,580 #relevant matches = 5,570 #relevance judgments = 35,832	NDCG@10, P@10, MRR, R-Precision	0.71 NDCG@10 0.59 P@10 0.82 MRR 0.26 R-Precision	26	BERT-based keyword extraction (9) / query summarization (1), Transformer-based rankers (10)

	TREC CT 2022 (Roberts et al., 2022)	#patient descriptions = 50
		trials = 375,580
		#relevant matches = 3,949
		#relevance judgments = 35,394
			NDCG@10, P@10, MRR, R-Precision	0.61 NDCG@10
				0.50 P@10
				0.72 MRR
				0.32 R-Precision
					12	Query reformulation using BERT / sequence-to-sequence models (3), Transformer-based rankers (3)

	TREC CT 2023 (Rybinski et al., 2024)**	#patient tables = 40 #disease templates = 8 #trials = 451,538 #relevant matches = 11,963 #relevance judgments = 34,931	NDCG@10, P@10, MRR	0.81 NDCG@10 0.73 P@10 0.78 MRR	11	Query reformulation using LLMs (5), Transformer-based rankers (6), LLM prompt-based relevance prediction (4)

*Best scores are aggregated from the Appendix of the runs in the TREC Browser. †No participants, since this was not a challenge.
**Borrowed from (Rybinski et al., 2024) as TREC CT 2023 does not have a published track overview.

Table 2: Overview of the public trial and patient matching benchmarks. #P is the number of participating teams. LLM usage (#P) tracks the number of participants using LLMs that we could verify from the proceedings.

istry. Meanwhile, the N2C2 benchmark focuses on a single trial. ClinicalTrials.gov is one of the largest online databases of clinical studies submitted by investigators from over 200 countries. As of June 2025, it lists more than 400,000 clinical trials, thousands of which are active. The euclinicaltrials.eu is another public online registry comprising over 50,000 trials from the European Union of which, 7000 are active. Every trial comprises a study description, eligibility criteria and study plan among other details. All the LLM-based methods we analyze use the ClinicalTrials.gov registry and one additionally uses EudraCT, the internal database a subset of which is publicly available via the EU Clinical Trials Registry (refer Table 5 in Appendix).

4.2 Patient Data

The N2C2 benchmark contains 288 de-identified longitudinal records of patients. The trial ranking benchmarks use up to 75 synthetic patient profiles, comprising keywords defining cohorts in (Koopman and Zuccon, 2016), short textual patient descriptions: 75 in TREC CT 2021 and 50 in TREC CT 2022, and 40 questionnaire templates in TREC CT 2023. The MIMIC database (Johnson et al., 2016, 2020) is the largest anonymized public database of structured and unstructured data of 299,712 patients. While this dataset is popular for training biomedical LLMs (as mentioned in Section 2), it is not used in any of the five benchmarks, possibly due to significant challenges in obtaining eligibility labels on this scale. Of the 20 LLM-based methods reported in Table 5, 15 used one of the benchmarks from Table 2, 2 used synthetic patient profiles (EHR) made publicly available, 3 used private patient data: 2 clinical notes and 1 structured patient data.

4.3 Annotated Labels

Two medical experts annotated 3,744 criterion-level labels in the N2C2 benchmark. The TREC CT annotations were created by pooling the top-k results from all participating teams. Medical experts manually annotated this pool of trial and patient matches (Koopman and Zuccon, 2016; Soboroff, 2021; Roberts et al., 2022). Out of a total of 35,394 pooled trial and patient matches in the 2022 edition, 11% were judged as *eligible*, 9% as *ineligible* and 80% as *not relevant* with an average of 700 trials judged per patient (Roberts et al., 2022). The relevance judgments were more balanced between the three labels (Rybinski et al., 2024) in TREC CT 2023. All benchmarks depend on manual anno-

tation from experts, which is time-consuming and challenging to scale (Kim and Quintana, 2022).

5 Information Extraction and Parsing

Extraction of medical entities evolved from a combination of rule-based heuristics and feature-based supervised sequence labeling models (Kang et al., 2017; Yuan et al., 2019) via embedding-based neural models (Khan et al., 2019; Tseo et al., 2020) to transformer-based pretrained models and generative AI (Liu et al., 2021c; Zeng et al., 2020; Tian et al., 2021; Li et al., 2022; Murcia et al., 2024; Kantor and Morzy, 2024a). Datta et al. (2024) use disease-specific prompting to extract structured information about entities and its attributes from criteria text. Gao et al. (2020); Zhang et al. (2020) and Theodorou et al. (2023) use BERT-based embeddings to encode eligibility criteria and patient data. Patient data converted to search queries, via reformulation and expansion using LLMs, are particularly effective in trial retrieval (Peikos et al., 2023; Rybinski et al., 2024; Peikos et al., 2024; Jin et al., 2024). Yuan et al. (2019); Tian et al. (2023); Park et al. (2024); Mugambi et al. (2024) and Ziletti and D'Ambrosi (2025) use semantic parsing to translate eligibility criteria into logical forms ready for querying structured patient databases.

6 Trial and Patient Matching

6.1 Formalization

Given sets of inclusion and exclusion criteria (C_{inc}, C_{exc}) from a trial and a set of patient data, P, we formalize the trial and patient matching problem, M, to predict one of the labels *Ineligible (Inel.)*, *Irrelevant (Irr.)* or *Eligible (Eli.)* by aggregating criterion-level binary matches $M'(c, P)$.

$$M(C_{inc}, C_{exc}, P) = \begin{cases} \textit{Inel.}, & \exists c \in C_{exc}, M'(c, P) \\ \textit{Irr.}, & \exists c \in C_{inc}, \neg M'(c, P) \\ \textit{Eli.}, & \neg(\textit{Inel.} \vee \textit{Irr.}) \end{cases} \quad (1)$$

This induces a priority, such that, a patient satisfying any exclusion criteria becomes ineligible, regardless of inclusion criteria matches. Section 6.2 explores the task at varying levels of granularity, starting from criterion-level via trial-level predictions to trial ranking. Criterion-level binary decisions become too restrictive, such that one unmet criterion M' due to lack of data can render the entire match M as ineligible. In such cases, where missing information is expected, ranking trials is a feasible first step. Just ranking trials is insufficient as it does not provide the degree of criteria coverage. In Section 8, we elaborate on the importance of formalization and its effects on trial-level aggregation.

Classical	LLM-based
! Direction-specific approaches, applicable to a set of trials or a cohort	* Direction-agnostic criteria- & trial-level prediction
! Trial-specific heuristics: filters and features	* Generalizable across trials
! Evaluated on private patient data	* Public benchmarks more common

Table 3: Differences between classical and LLM-based trial matching approaches.

Despite the task in Equation 1 being direction-agnostic, there exist two directional approaches to tackle the matching problem, mainly due to data availability. First is the **trial-centric** approach, taken by a trial investigator, that matches longitudinal patient records to a specific trial. The 2018 N2C2 cohort selection is a trial-centric benchmark with criterion-level predictions. Alternatively, a **patient-centric** approach, taken by a patient or their healthcare provider, matches relevant trials from a trial registry to a short description of the patient. Koopman and Zuccon (2016) and the TREC CT 2021, 2022, and 2023 are patient-centric benchmarks for ranking trials.

6.2 LLM-based Approaches

Unlike classical approaches (Penberthy et al., 2010; Ni et al., 2015; Zhang and Demner-Fushman, 2017; Yuan et al., 2019; Tun et al., 2023), LLM-based approaches do not rely on trial-specific heuristics. Table 3 lists the primary differences between the classical and LLM-based approaches (see Appendix C for a full comparison). We group the LLM-based approaches by the granularity of the matches, starting with criterion-level prediction via trial-level prediction to trial ranking. While criterion- and trial-level predictions are direction-agnostic, trial ranking is a patient-centric task. With enough patients, we could evaluate patient ranking, similar to the bidirectional implementation in Ni et al. (2015)'s work, though this has not yet been addressed.

Criterion-Level Prediction. Here, methods utilize the reasoning capability of LLMs to obtain ratio-

nale and other context data in addition to the eligibility label. Hamer et al. (2023) use 1-shot prompt, where given the patient profile and the eligibility criteria, the LLM first labels each criterion as either being applicable to the patient or not, followed by a list of rationales and finally, the eligibility labels for the applicable criteria. Unlu et al. (2024); Beattie et al. (2024) and Wornow et al. (2025) chunk longitudinal patient data and store them as vector embeddings. They prompt LLMs with criteria and relevant patient data chunks under zero-shot setting, with Beattie et al. (2024) providing expert criterion-level strategy and Wornow et al. (2025) providing criteria modifications in the prompts.

Unlu et al. (2024) generate only the decision label from GPT4 and Beattie et al. (2024) and (Wornow et al., 2025) generate criterion-level JSON objects, comprising the criteria label, the eligibility label and a rationale among other context. Both work with proprietary OpenAI models (GPT-3.5 and GPT-4) and Wornow et al. (2025) additionally used open-sourced Llama (Jiang et al., 2023) and Mixtral models (Jiang et al., 2024). Ferber et al. (2024) prompt GPT-4o to generate criterion-level boolean predictions to be reviewed by experts.

Trial-Level Prediction. Wong et al. (2023) used GPT3.5 and GPT4 to extract and structure eligibility criteria into logical expression to be matched locally with structured patient information. Yuan et al. (2023) use LLMs to augment eligibility criteria and pass the BERT-based embeddings of these criteria and patient data through a fully connected classification layer to predict patient-criterion eligibility. The classifier and embedding models are trained jointly on classification loss and a contrastive loss function derived from Equation 1.

Trial Ranking. These methods formulate effective queries, retrieve trials and re-rank them. Query processing involve generating sentence queries from patient descriptions using a fine-tuned T5 model (Pradeep et al., 2022) or zero-shot LLM prompts (Saeidi et al., 2023; Kusa et al., 2023b), generating patient descriptions from trial data via 1-shot LLM prompts (Zhuang et al., 2023), generating noSQL queries via LLMs (Ferber et al., 2024), using LLMs to reformulate and expand queries (Rybinski et al., 2024; Peikos et al., 2024; Datta et al., 2025), and using LLMs to extract keywords (Jullien et al., 2024; Jin et al., 2024; Nievas et al., 2024).

Next comes retrieval, using embeddings similarity (Lahiri et al., 2023; Richmond and Deshpande, 2023; Saeidi et al., 2023; Ferber et al., 2024; Saeidi, 2025) or a multi-stage retrieval with neural re-rankers (Zhuang et al., 2023; Rybinski and Karimi, 2023; Rybinski et al., 2024; Jin et al., 2024; Datta et al., 2025). Some re-rank the top trials using GPT models (Zhuang et al., 2023; Rybinski et al., 2024; Datta et al., 2025), some prompt LLMs for relevance labels (Pradeep et al., 2022), while others prompt LLMs to generate trial- or criterion-level eligibility labels (Rybinski et al., 2024; Peikos, 2023; Jin et al., 2024; Nievas et al., 2024; Jullien et al., 2024). Criterion-level labels are then aggregated using set-based reasoning mechanisms (Jullien et al., 2024), variations of the matching Equation 1 (Jin et al., 2024; Nievas et al., 2024; Saeidi, 2025), and by prompting LLMs (Jin et al., 2024).

7 Evaluation

Standard metrics, such as, precision, recall, F1, normalized discounted cumulative gains (NDCG@k) and mean reciprocal rank (MRR) are popular metrics used by the benchmarks (Table 2). When we compare the different systems side by side (see Table 5 in Appendix) the lack of standardized reporting becomes apparent. Five of the eight (62.5%) methods that tackle criterion-level and trial-level eligibility prediction introduce their own datasets of which three use private patient data.

In the criterion-level prediction task, 3 of the six reported methods use the N2C2 benchmark, namely, Beattie et al. (2024); Wornow et al. (2025) and Saeidi (2025). Even between these three methods, comparison is difficult, since Beattie et al. (2024) report their best results on a subset of the benchmark, and Saeidi (2025) report the performance averaged on N2C2 and TREC CT 2023.

13 of the 14 methods for trial ranking use the TREC CT benchmarks of which 9 evaluate their performance on the 2023 edition, 5 on the 2022 edition and 5 on the 2021 edition. The remaining method ran evaluations on their own dataset of 51 synthetic EHR profiles and 15 trials. 2 methods for trial ranking ran additional evaluations on the SIGIR benchmark.

7.1 Evaluation Beyond Accuracy

Some methods evaluate justification quality of the LLMs via manual evaluation, but differ in the subsets evaluated and the metrics used (Jin et al., 2024; Nievas et al., 2024; Wornow et al., 2025). Notably, researchers in the medical domain have stressed the

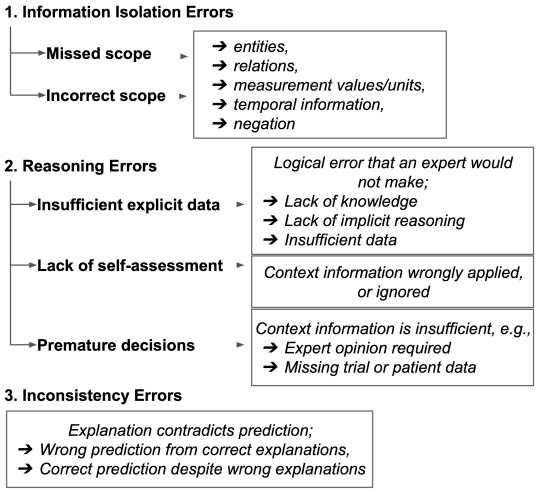

Figure 2: Taxonomy of errors in LLM-generations.

lack of consistent benchmark data, primarily, due to the dependence on manual review which also restricts the size of the data (Kim and Quintana, 2022; Kantor and Morzy, 2024b).

Rybinski et al. (2024) report query latency, with GPT models having 15 times higher latency (47.8s) compared to smaller pre-trained models for a 12% increase in NDCG@10. Wornow et al. (2025) report the cost per patient in terms of money (up to 11.88$), API calls (up to 57) and token used (up to 103,000). Both Hamer et al. (2023) and Jin et al. (2024) report a workload reduction, from a 90% reduction in the criteria to be screened by Harrer (2023) to a 42.6% reduction in screening time by Jin et al. (2024), when using LLM-generated predictions and explanations.

A broader audit on faithfulness of the explanations, logical completeness of the explanations with respect to the criteria, handling missing information, robustness to counterfactuals, uncertainty and bias is lacking in the current methods.

7.2 Taxonomy of LLM Errors

Since there is no one accepted taxonomy of errors, we often come across inconsistent and semantically overlapping categories of errors in LLM generated explanations. For e.g., *incorrect reasoning* and *lack of knowledge* are recognized as independent error types by Jin et al. (2024); Hamer et al. (2023); Nievas et al. (2024), even though the latter often leads to the former (full list in Appendix B). In the proposal by Liévin et al. (2024), reasoning errors are separate from reading comprehension, even though the instances of incorrect reading comprehension occur when the model ignores contextual information and *"reasons"* using its learned knowledge. Here, we identify where errors occur and break them down further by an identifiable source of the error (see Figure 2).

Information Isolation Errors. These are errors in information extraction from patient data or trial criteria falls. This includes ***missed*** or ***incorrect*** NER, measurements (numeric or unit), temporal scopes and negations. LLMs are good at recognizing entities and measurements, but still struggle with negations (Nievas et al., 2024).

Reasoning Errors. An error in the explanations provided by LLMs falls into this category. The most common source is ***insufficient explicit data***, which occurs when LLMs fail to draw logical conclusions from given data, while a human expert can. This stems from previously unseen data (*"lack of knowledge"*) or the inability to recall prior information (*"lack of implicit reasoning"*) or the inability to infer from context (*"insufficient data"*). The second source of reasoning errors is ***lack of self-assessment***. The LLM contradicts explicit information in the prompt. The error occurs when knowledge is wrongly recalled or knowledge is correctly recalled, but contextual information is not applied, resulting in wrong reasoning. This is often referred to as *"incorrect knowledge"*. The third source are ***premature decisions*** made by an LLM when the criterion or patient data is ambiguous and it is necessary to defer to an expert opinion.

Inconsistency Errors. Generating explanations to arrive at final answers unlock LLM's reasoning capacities (Wei et al., 2022). Even so, the explanation and the prediction can be inconsistent. LLMs may predict incorrectly despite correct explanation (reported as explanation-output mismatch in Nievas et al. (2024)). The opposite situation, when a prediction is correct despite an incorrect explanation, is more difficult to identify without human evaluation of automated verification checks. Wornow et al. (2025) report between 3%-8% of incorrect or partially correct justifications despite the LLM making a correct eligibility prediction. This shortcut, similar to cognitive biases in humans, hints towards a bias that the model picked up during training. Both cases negatively impact transparency and accountability of the matching system.

8 Discussion

Annotated Corpora and their Size. Despite attempts to structure clinical trials (Chen et al.,

2022), finding similar trials and analyzing systematic failure cases is notoriously difficult (Rybinski et al., 2020; White et al., 2023). Criterion-level annotations require significant manual annotations, thereby limiting the size of the corpus. For instance, Chia Kury et al. (2020) and LCT (Dobbins et al., 2022), are manually annotated corpora of 1000 trials each, while supervised annotators such as, EliIE (Kang et al., 2017) and Criteria2Query (Yuan et al., 2019), require expensive manual labels (230 disease-specific clinical trials in this case). Eligibility labels on real patient data from real enrollment status, necessary to discount reviewer bias, are only available on a small-scale, if at all, due to the trade-off between scale and privacy (Kim and Quintana, 2022). The systems thus evaluated on private retrospective data (Wong et al., 2023; Yuan et al., 2023; Unlu et al., 2024) cannot be transparently compared. Kantor and Morzy (2024b) stress on standardized benchmarks as the dependence on manual evaluation hinders meta-analyses and comparison between different studies. Public annotations, such as the TREC CT tracks have an average of 700 trial annotations per patient for less than 100 patients, while the N2C2 has only a few thousands of criterion-level annotations. Jointly, the major public corpora, e.g., *ClinicalTrials.gov* and *MIMIC* datasets, present an opportunity to build on the proposal by Kim and Quintana (2022) to generate large-scale data using automated methods.

Dimensions of Evaluation. In Section 7 we see that the majority of methods focus on model accuracy, corroborating the result from Bedi et al. (2025), which reports that more than 95% of studies use accuracy as the primary dimension of evaluation, while fairness, bias and uncertainty are measured less frequently. Omar et al. (2024) reviewed 27 clinical trials evaluating LLMs in healthcare also found the accuracy and reliability standards for LLM use to be undefined. Further results from Nemati et al. (2025), who benchmarked the annotation ability of LLMs across 9 performance metrics, show that while LLMs consistently score high on precision, recall and F1 (lowest being 0.8), their scores highly vary on semantic similarity, factual consistency, relevance, fluency, consistency and coherence (ranging from 0.1 to 0.9) highlighting the need for multiple dimensions of evaluation.

Formalization. Equation 1 highlights the importance of aggregation and priority. Surprisingly, very few works explicitly formalize the matching task. This lack of formalization coincides with an absence of aggregation strategies for trial-level predictions (Hamer et al., 2023; Wornow et al., 2025; Unlu et al., 2024) and others. Formalization guides Yuan et al. (2023) to design a loss function that accounts for the contrastive requirements of inclusion and exclusion criteria, and Jullien et al. (2024) and Saeidi (2025) to define re-ranking scores.

Societal Impact. Recent research measured distinct bias in disease diagnosis across gender, age and disease in popular LLM models (GPT4, ChatGPT and Qwen) (Zhao et al., 2024b) and found that GPT4 tends to stereotype demographic presentations when generating diagnoses (Zack et al., 2024). Alber et al. (2025) show that LLMs are prone to making medical misjudgments by replacing just 0.001% of the training data with medical misinformation. All LLM-based systems, except the trial ranking models, are evaluated on a few disease-specific trials (see Table 5 in Appendix C), the largest being 146 trials, covering 10 cancer types, evaluated by Hamer et al. (2023), making the generalizability of LLMs across diseases unclear. In addition to generalizability tests across diseases, we recommend risk and bias assessments on demographic slices (Benkirane et al., 2025).

Data Sensitivity. Several methods deploy GPT models on Azure AI to comply with privacy regulations (Unlu et al., 2024; Wong et al., 2023; Wornow et al., 2025). Yet, processing patient data with LLMs raises serious ethical challenges due to lack of HIPAA compliance (Edemekong et al., 2024). As already discussed, creating large-scale realistic patient records while protecting their privacy is particularly challenging. We recommend locally deploying open-sourced models or set up a Business Associate Agreement (BAA) with cloud API providers for HIPAA compliance. There is interest in generating synthetic data, as digital twins of patients, with limited access to real patient data as a viable privacy protected alternative (Das et al., 2023; Wang et al., 2024).

Core Limitations of LLMs. According to Harrer (2023) the core limitations affecting LLM adoption are **unfiltered pre-training**, which does not differentiate between facts, opinions, or misinformation; **lack of self-assessment**, where a model generates invalid but syntactically and semantically coherent sentences; **non-determinism**: where surface-form prompt variations lead to drastic changes in the output and repeatability is not guaranteed under

consistent input conditions; and, **knowledge recall**: where updating outdated data or injecting new information requires expensive retraining since the mechanisms of memory in LLMs are not well understood. These limitations pose a direct challenge to the transparency and accountability principles of AI for health laid down by the World Health Organization (Guidance, 2021).

In Section 7, we discuss how knowledge recall and lack of self-assessment surface through reasoning errors. Ways to mitigate non-determinism could include model robustness evaluations to prompt modifications and model settings like temperature and decoding strategies. Using domain-specific LLMs (Singhal et al., 2023), grounding LLMs with external knowledge (Alber et al., 2025), and verifying LLM reasoning could be useful in handling unfiltered pre-training from affecting inference time decision-making

9 Future Directions

As interest in LLMs orchestrating an end-to-end pipeline and incorporating human interactions is gaining more attention (Gao et al., 2024; Qiu et al., 2024), we focus on four promising directions.

Trial Search. Past trials that share a target population are important for designing new trials, recruiting patients, systematic reviews and meta-analyses. This problem has seen little activity since clustering using lexical features (Hao et al., 2014). Newer search methods include constructing a clinical trial knowledge graph Chen et al. (2022), searching via patient EHRs (Wu et al., 2018) and designing features for similarity matchingSun et al. (2022). Jullien et al. (2023) use textual entailment in LLMs to find trials that match short descriptions. However, these models falter on inferences that require numerical reasoning and could not surpass a BM25 baseline for ranking evidence.

Interactive Trial Design. LLM agents have the potential of bridging the semantic gap between eligibility criteria and patient data by suggesting data models underlying patient data for structuring eligibility criteria early on. This collaborative idea is not new (Luo et al., 2013), yet, designing eligibility criteria is a big challenge and has been handled post-hoc by optionally considering patient data models (Kang et al., 2017; Sun and Loparo, 2019; Liu et al., 2021a; Dasgupta et al., 2020). Small patient pools, which ultimately affect the successful completion of a trial, are often the result of restrictive criteria (Clinical Trials Arena, 2022). LLMs can improve trial design by identifying restrictive criteria for trial investigators to relax them and create larger patient pools, especially for trials tackling diseases with a high mortality rate (Liu et al., 2021b).

Collaborative Trial Planning. Liu et al. (2025c) propose an iterative feature discovery model using LLM agents for interpretable trial outcome prediction. Markey et al. (2025) showed promising results on content relevance and suitability of trial protocols generated using LLMs, with room for improvement in logical reasoning and provenance. Similar to Shi et al. (2024), who propose collaboration of agents for knowledge-augmentation and reasoning, LLM agents can identify and distribute tasks and aggregate them to a final result. Another important operation is learning to defer to experts (Mozannar and Sontag, 2020), which can separate operable criteria, such as those that require tabular operations (e.g., via structured queries) or reasoning (temporal, numerical, negation), from criteria that require expert feedback.

Explainable Matches. Explaining black-box LLM predictions in human-understandable form is very challenging (Zhao et al., 2024a) and in clinical trial matches, this is limited to chain-of-thought generations, which is only one of the many facets of explainability (Nauta et al., 2023; Bodria et al., 2023; Chen and Eickhoff, 2024). Consistency and completeness checks, logical component matches, robustness tests on negative, numeric and temporal logic can greatly improve the reliability of guided explanations. Wong et al. (2023), for instance, could potentially explain eligibility via logical component (mis)matches. We hope that the error taxonomy discussed in Section 7.2 assists in systematic evaluation of explanations.

10 Conclusion

The task of clinical trial recruitment, that matches patients to a clinical trial via its participation eligibility criteria, benefits from knowledge aggregation and reasoning abilities of LLMs. In this survey, we critically examine the evolving role of LLM technologies in clinical research. We analyze the main components in a clinical trial recruitment process and provide a modern perspective on the challenges in adopting LLMs to clinical research, such as the benchmarks used, the dimensions of evaluation and data sensitivity. We hope that this serves as a valuable resource for future research.

11 Limitations

This survey focuses on the role of advances in NLP in the critical domain of clinical trial recruitment. Given that this is a rapidly evolving field, we have made our best effort to include a comprehensive view of available resources and methods. It is possible that more sophisticated methods using the latest technology already exist (e.g., in the form of proprietary products), but are not yet made public or are only available as abstracts, as is common in some medical communities, for example, the Annual Meeting of the American Society of Clinical Oncology (ASCO). Clinical trial and patient matching involves sensitive data, and is therefore vulnerable to dual-use risk, which must be challenged and debated by experts on ethics, governance, and technology. Such extensive discussion is out of the scope of this work, but we point our readers to dedicated research on these topics (Braun, 2021; Li et al., 2023b).

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A Systematic Reviews versus Surveys

A systematic review is a common practice in the medical research community, with standardized reporting guidelines (Moher et al., 2009; Page et al., 2021). This guideline has a checklist of required items in the title, abstract, introduction, methods, results, discussion and other information that every study needs to fulfil. These studies are bound by strict inclusion and exclusion criteria applied to the scientific literature considered for any assessment. This rigor is necessary in evidence-based analysis of a specific research question. A survey is more flexible and provides a board coverage of the topic being discussed. For instance, the guidelines for writing surveys in our community as outlined by ACM Computing Surveys, TACL and ARR aim to draw perspectives on an evolving topic of interest.

ACM Computing Surveys (long paper). A paper that summarizes and organizes recent research results in a novel way that integrates and adds understanding to work in the field. A survey article assumes a general knowledge of the area; it emphasizes the classification of the existing literature, developing a perspective on the area, and evaluating trends.

TACL (excerpt). They should thus not simply be a descriptive enumeration of the contents of papers, but draw broad themes and (importantly) provide new insights on the topic. These insights should be major contributions of the submission.

ARR (note). all papers are expected to include reviews of related literature. This category is meant for the papers that go beyond that, e.g. in scope or in establishing new interdisciplinary connections.

B Reported Error Types

In the following we illustrate the the error distributions by percentages as reported by previous studies.

Errors reported in (Jin et al., 2024) supplementary:
- Incorrect reasoning: 30.7%
- Lack of medical knowledge: 15.4%
- Ambiguous label definition: 26.9%
- other errors: 26.9% (self-conflicting)

Errors reported in (Hamer et al., 2023):
- Incorrect reading: 6.5%
- Insufficient knowledge: 2.2%
- Incorrect reasoning: 91.3%

Errors reported in (Nievas et al., 2024):
- Lack of knowledge 55%
- Implicit criteria 15%
- Wrong reasoning
- Accurate reasoning, wrong decision
- Lack of restraint when expert opinion is needed
- Negated criteria error

C Trial and Patient Matching Systems

Table 4 gives an overview of all the classical systems in covered in this survey by their direction of approach, method, source data characteristics and limitations. Table 5 covers all the LLM-based systems discussed in this survey by their task, method, data source characteristics and limitations. We notice the shift in the availability of patient sources towards public data in the LLM-based approaches. We also notice a shift towards trial ranking due to publicly available data.

Direction	Method	Patient Source	Trial Source	Metrics (Best)	Limitations
Trial-centric	Penberthy et al. (2010) Discrete-data filter and sub-word matching	**Availability**: Private **Size** 282-2,112 **Mode**: text, tables **Additional annotation**: expert review	**Availability**: public (1); unknown (4) **Size**: 5 **Type**: Specific	Yield (% cross trials): 17.2 to 73.8 Efficiency (ratio manual to automated screening time): 0.8 to 19.4	Manually coded eligibility criteria. String similarity for keyword search.
	Yuan et al. (2019) (Criteria2Query) NL to structured queries Information extraction, normalization Mapping to pre-defined cohort templates	No patient data	**Availability**: Public* **Size**: 10 **Type**: Varying **Additional annotation**: 125 criteria sentence, 215 entities, 34 relations, 137 negations, 20 attributes	F1 (NER): 0.79 F1 (RE): 0.80 Accuracy (across tasks): 0.51 to 0.98	Disease-specific NER. Query templates cannot deal with missing attributes. Entity normalization into a small set of 2000 concepts.
	Tun et al. (2023) Rule-based filters Similarity scores per criteria as features to a classifier	**Availability**: Private **Size**: 40,000 **Mode**: text, tables **Additional annotation**: 109 patients labels	**Availability**: Unknown **Size**: 1 **Type**: Specific	Sensitivity (across models): 0.4 to 1.0 Precision (across models): 0.23 to 0.78	Limited to a single trial Rules-based models have high sensitivity (1.0) and low precision (0.23). Hybrid classifier makes a good sensitivity and precision trade-off, but is not robust to criterion changes.
	Ni et al. (2015) Discrete-data filter Index trial and patient bag-of-words vectors Return top vector matches for a trial	**Availability**: Private **Size**: 215 **Mode**: text, tables **Additional annotation**: historical match, expert review	**Availability**: Public* **Size**: 55 **Type**: Specific	Workload reduction: 85% Precision: 12.5% Specificity: 89.9%	Majority of false positives due to lack of semantic knowledge
Patient-centric	Ni et al. (2015) Return top vector matches for a patient	*(same as previous row)*		Workload reduction: 54.7% to 92.8% Precision: 4% to 35.7& Specificity: 65.5% to 95.5%	Majority of false positives due to lack of semantic knowledge
	Zhang and Demner-Fushman (2017) Bag-of-words feature vector SVM classifier	No patient data	**Availability**: Public* **Size**: 2461 **Type**: 891 Specific; 1570 Varying **Additional annotation**: Trial labels	Precision: 0.90 Recall: 0.86 F2: 0.87	Cohort-specific model No real patient data considered Closest to keyword search (trials to cohort)

* Public source for clinical trials: https://clinicalTrials.gov

Table 4: Overview of classical systems covered in this survey: direction, methods, data sources and limitations.

Task	Method	Patient Source	Trial Source	Metrics (Best)	Limitations
Criterion-level prediction	Hamer et al. (2023) 1-shot prompt to LLM for criteria level prediction with explanation	**Availability**: Public (synthetic patient profile) **Size**: 10 **Mode**: Short text **Type**: Specific	**Availability**: Mixed (clinicalTrials.gov, EudraCT*) **Size**: 146 clinical trials **Type**: Specific **Additional Annotation**: Expert review	Criterion-level accuracy: 72% Trial-level precision: 0.71 Trial-level recall: 0.5 Workload reduction: 90% Stochasticity of precision / recall (10 runs): 0.03 / 0.02 SD	Majority of criterion-level errors due to incorrect reasoning (91%) which also occur for true positives
	Unlu et al. (2024) RAG approach	**Availability**: Private **Size**: 3,000 **Mode**: Textual clinical notes	**Availability**: Public** **Size**: 1 **Type**: Specific	Accuracy: 0.92 Correlation coeff: 0.81 Precision: 98.1% Recall: 92.3% Specificity: 93.9%	RAG pipeline evaluated on a single trial.
	Ferber et al. (2024) Sequential GPT-4o requests to create structured query to trial DB; remove irrelevant trials; and make criterion-wise boolean predictions	**Availability**: Public **Size**: 51 **Mode**: EHR	**Availability**: Public** **Size**: 15 **Type**: Specific	Trial Recall: 93.3% Accuracy: 92.7% to 97.8%	Refined evaluation with updated human judgment risks circular evaluation via target leakage or confirmation bias.
	Beattie et al. (2024) RAG approach with criterion-specific guidance prompts	**Availability**: Public (2018 N2C2: Cohort Selection)		Accuracy: 0.86 Sensitivity: 0.86 Specificity: 0.90 Precision: 0.87 Micro F1: 0.85	Best performance metrics is obtained on test subset (40 of 182). Expert guidance requires manual expertise for every criterion.
	Wornow et al. (2025) Zero-shot RAG approach with criteria modifications	**Availability**: Public (2018 N2C2: Cohort Selection)		Precision: 0.91 Recall: 0.92 Overall macro-F1: 0.81 Overall micro-F1: 0.93 Cost / patient: 0.87 USD to 11.88 USD API calls / patient: 1 to 57 Tokens (10^3) / patient: 8 to 103	67% of incorrect decision had correct reasoning indicating potential shortcuts taken by LLMs. Best strategy ICAN is 10 times more expensive than the least expensive strategy ACAN.
	Saeidi (2025) Few-shot LLM prompts with fine-tuned BERT-based concept embeddings of patient and criteria to predict binary eligibility labels.	**Availability**: Public (2018 N2C2: Cohort Selection)		Precision: 0.92 Recall: 0.93 Macro-F1: 0.83 Micro-F1: 0.94	Reported metrics are combined across N2C2 and TREC datasets which tackle different tasks. No ablation on components: concept matching, prompt design, fine-tuning embedding models

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Task	Method	Patient Source	Trial Source	Metrics (Best)	Limitations
Trial-level prediction	Wong et al. (2023) Few-shot prompts to LLM to generate structured forms of eligibility criteria using provided templates	**Availability**: Private **Size**: Unknown **Mode**: Structured **Additional Annotation**: 523 trial and patient historical labels; 68,485 trial and patient new labels	**Availability**: Public** **Size**: 53 **Type**: Specific	Recall (historical data): 76.8% Precision: 0.88 Recall: 67.3 F1: 76.1	Clinical Trial eligibility limited to the first 40 lines. Trial-level performance is very low (F1 score range:[29.6-48])
	Yuan et al. (2023) Prompt LLMs to reformulate eligibility criteria Train patient and criterion encoders contrastively on inclusion and exclusion criteria to predict trial-level match	**Availability**: Private **Size**: 825 **Mode**: Longitudinal text records	**Availability**: Public** **Size**: 6 **Type**: Specific **Additional Annotation**: 100,000 criterion-patient labels	Criterion-level: Precision: 0.96 Recall: 0.86 F1: 0.91 Trial-level: Precision: 0.80 Recall: 0.83 F1: 0.81	Criterion-level performance metrics 10 points higher than trial-level performance. High variance between different trials: F1 range: 0.48 - 0.98, even with trials concerning the same condition. Data separation methods for testing generalizability is unknown.
Trial ranking	Pradeep et al. (2022) Synthesize queries for initial trial retrieval. Fine-tune T5 to generate relevance label based on patient description and trial data	**Availability**: Public (TREC CT 2021)		NDCG@10: 0.71 P@10: 0.59 RR: 0.81	Zero-shot relevance ranking is only slightly better than BM25 with synthetic queries. Model prediction is difficult to interpret as signals come from trial condition, description and criteria.
	Zhuang et al. (2023) Hybrid sparse-dense retriever for top-1000. Cross-encoder re-ranker GPT4 for top-20 re-rank	**Availability**: Public (TREC CT 2023)		TREC CT 2022: P@10: 0.56 R@1000: 0.65 NDCG@10: 0.65 TREC CT 2023: P@10: 0.51 R@1000: 0.38 NDCG@10: 0.73	Precision (0.51) and recall (0.38) on TREC CT is very low. Validation on textual patient note does not transfer well to testing on structured patient note
	Embedding cosine similarity of patient and trial embeddings obtained using GPT Richmond and Deshpande (2023).	**Availability**: Public (TREC CT 2023)		MAP: 0.02	Direct embeddings of entire patient and trial documents are ineffective.
	Embedding cosine similarity of patient and trial embeddings obtained using Sentence Transformer by Lahiri et al. (2023).	**Availability**: Public (TREC CT 2023)		NDCG@10: 0.03 P@10: 0.09 MAP@10 and R@10 < 0.01	Direct embeddings of entire patient and trial documents are ineffective.

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Task	Method	Patient Source	Trial Source	Metrics (Best)	Limitations
	Kusa et al. (2023b) Sentence query formulation using GPT-3.5. Query enrichment using Kusa et al. (2023a). Trial-level prediction of re-ranked pairs using GPT-3.5.	**Availability**: Public (TREC CT 2023)		NDCG@10: 0.68 P@10: 0.58 RR: 0.65	Zero-shot LLM prompts provide marginal improvement over neural rerankers
	Peikos (2023) Utilize GPT3.5 to obtain trial-level labels for final re-ranking on top of lexical and neural re-rankers	**Availability**: Public (TREC CT 2023)		NDCG@10: 0.65 P@10: 0.44 RR: 0.58	Query processing is template-based and excludes negative information.
	Ferber et al. (2024) No-SQL query formulation from patient EHR using GPT-4o for initial retrieval, followed by vector embedding re-ranking.	**Availability**: Public **Size**: 51 **Mode**: EHR	**Availability**: Public** **Size**: 15 **Type**: Specific The authors consider an initial pool of 105,600 trials of which only 15 are annotated at trial- and criterion-level	%age of trials recalled at top-10: 93.3%	Refined evaluation with updated human judgment risks circular evaluation via target leakage or confirmation bias. Performance metrics used is very different to standard accuracy, precision and recall metrics.
	Rybinski and Karimi (2023) Multi-stage retriever with fine-tuned GPT3.5-turbo	**Availability**: Public (TREC CT 2021, 2022, 2023)		TREC CT 2023: NDCG@10: 0.73 P@10: 0.52 RR: 0.66	
	Rybinski et al. (2024) Multi-stage retriever using GPT3.5/GPT4 LLM-based relevance scoring and filtering Chain-of-thought (CoT) prompts with GPT4	**Availability**: Public (TREC CT 2021, 2022, 2023)		TREC CT 2023: NDCG@10: 0.78 P@10: 0.69 RR: 0.84	High latency of GPT4 trade-off for the performance boost Gains over (Rybinski and Karimi, 2023) is mainly due to reranker used (TCRR) Additional marginal gains via CoT of the larger GPT4 model.
	Jullien et al. (2024) LLM-guided basic attribute extraction for trial retrieval and filtering. Criterion-level LLM predictions fed to set-reasoning-based re-rank scoring functions.	**Availability**: Public (TREC CT 2022)		NDCG@10: 0.69 P@10: 0.73 P@25: 0.63 MRR: 0.86	LLMs underperform in exclusion criteria labeling.

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Task	Method	Patient Source	Trial Source	Metrics (Best)	Limitations
	Jin et al. (2024) (TrialGPT) Hybrid trial filtering with BM25 and MedCPT (Jin et al., 2023) Criterion-level LLM prediction aggregated to trial scores	**Availability**: Public (Koopman and Zuccon (2016), TREC CT 2021, 2022) **Additional annotation**: 1,015 criterion-patient labels		NDCG@10: 0.72 P@10: 0.66 AUROC (Excluding): 0.79 Time savings: 42.6% Reasoning correctness: 87.8% correct, 9.7% partially correct, 2.6% incorrect	The overall metric that averages over NDCG, P@10 and AUROC is meaningless Retrieval on prefiltered could bias results to be more favorable Longitudinal patient data not tested LLM aggregation assumes LLMs perform mathematical reasoning
	Nievas et al. (2024) Extends (Jin et al., 2024) to open-source LLMs	*(same as Jin et al. (2024))* **Additional annotation:** Patient sentence supporting eligibility label 500 criteria labels on: eligibility and difficulty.		NDCG@10: 66.3 P@10: 58.8 AUROC: 65.2 AURPC: 65.15 Implicit criterion-level accuracy (CLA): 68.7 Explicit CLA: 59.9 Win-rate: 68.9% Faithfulness (P/R/F1): *Exact scores not reported*.	Significantly high fine-tuning costs Reported aggregated score over metrics that span precision, recall, accuracy and AUC is meaningless.
	Datta et al. (2025) (Patient2Trial) Lexical retrievers use LLM generated query expansion. LLM predicts trial-level label and a criterion-level rationale with a matching score. Final ranking based on matching score.	**Availability**: Public (TREC CT 2023)		NDCG@10: 0.81 NDCG@30: 0.82 P@10: 0.73 P@30: 0.73 MRR: 0.78 Bpref: 0.30 P-precision: 0.24	Trials prefiltered by disorder-specific keywords. Manually curated disorder-specific instructions. Model predicted trial-level label is not evaluated
	Saeidi et al. (2023); Saeidi (2025) Embed patients and trials to concept vector space. Use variations of Equation 1 to compute relevance scores.	**Availability**: Public (TREC CT 2023)		Precision: 0.92 Recall: 0.93 Macro-F1: 0.83 Micro-F1: 0.94	Reported metrics are combined across N2C2 and TREC datasets. No direct connection between criterion-level LLM predictions and trial-level embeddings-based relevance score computations

* *EudraCT (European Union Drug Regulating Authorities Clinical Trials) is the European clinical trials database (EudraCT).*
** *Public source for clinical trials:* `clinicalTrials.gov`.

Table 5: Overview of LLM-based systems covered in this survey: tasks, methods, data sources used and limitations.