EpiSeek

A literature search agent system for scientific questions

Designs

- Backend (Uvicorn) + Frontend (Vue 3)
- LLM Development Framework (LangChain)

Pipeline

- ❓ Accept text questions
- 🔎 Fetch relevant scientific papers
- 📝 Provide LLM-powered answer
- 💬 Interactive follow-up

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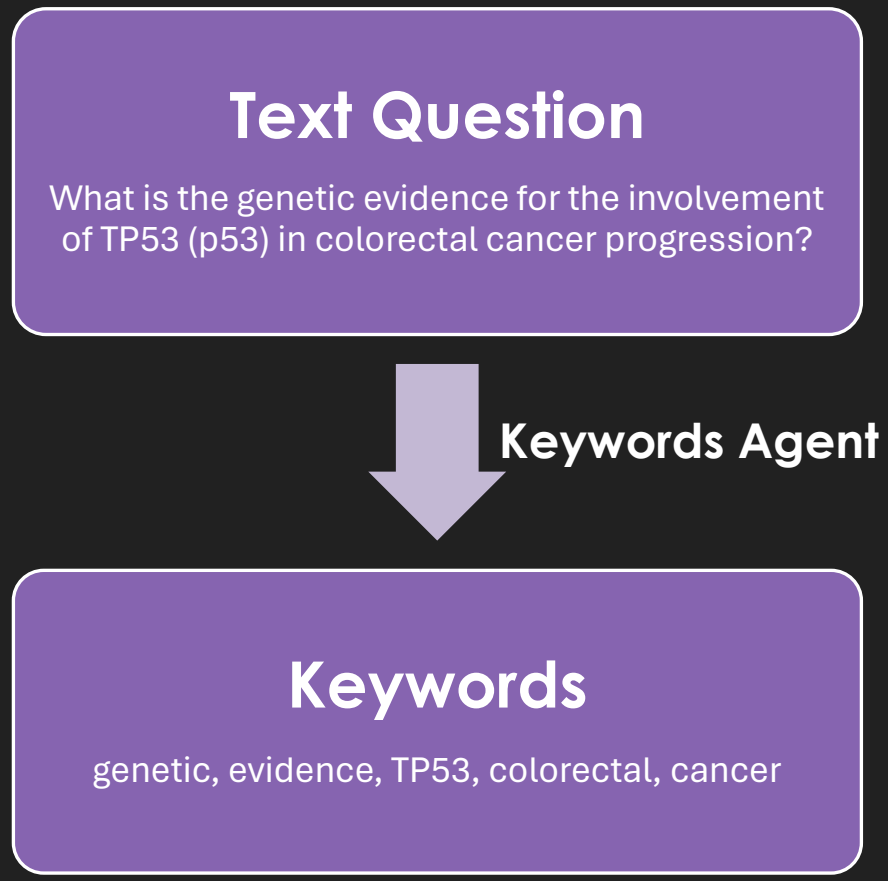

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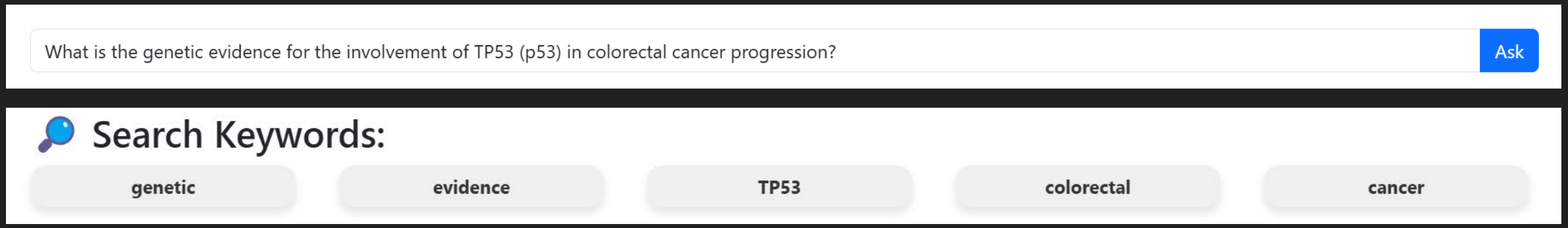
Keywords Agent

- LLM-powered
- Extract **5 most relevant keywords** from the question



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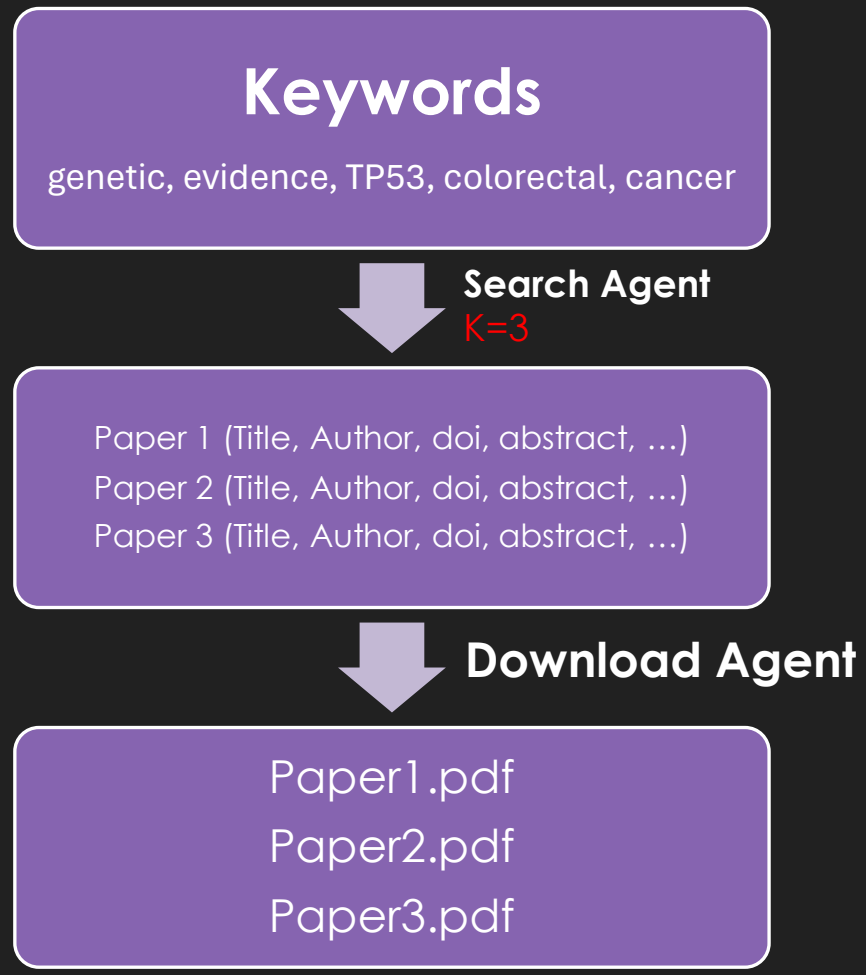

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Search Agent

- Using the API of Semantic Scholar
- Download PDF with open access

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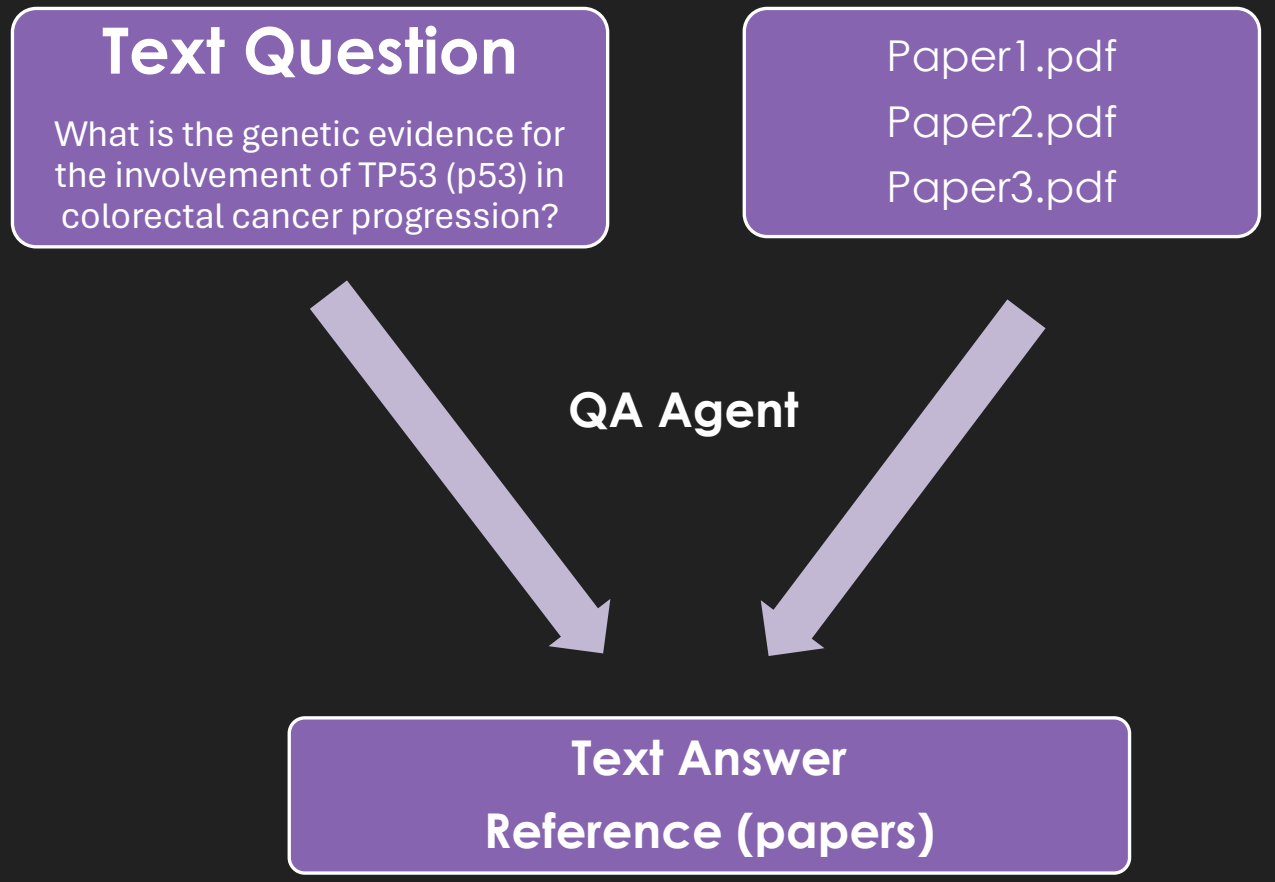

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QA Agent

- LLM-powered
- Use PyPDF2.PdfReader to read PDFs
- Chunk papers to fix the context of LLM
- Session history for follow-up

Pipeline

2. Genetic polymorphisms in TP53, nonsteroidal anti-inflammatory drugs and the risk of colorectal cancer: evidence for gene–environment interaction?

   Year: 2007

   Authors: ["Xianglin Tan", "A. Nieters", "M. Hoffmeister", "L. Beckmann", "H. Brenner", "J. Chang-Claude"]

   Abstract: Objective Substantial evidence indicates that nonsteroidal anti-inflammatory drugs protect against colorectal cancer by altering cell cycle progression and/or inducing apoptosis, whereas p53 protein is crucial to maintaining cell-cycle arrest and regulating DNA repair, differentiation, and apoptosis. Genetic variants in TP53 gene might therefore influence colorectal cancer risk and modify the effects of nonsteroidal anti-inflammatory drugs. We assessed the association of TP53 Arg72Pro and p53PIN3 polymorphisms with colorectal cancer risk and their possible interaction with nonsteroidal anti-inflammatory drug use. Methods We included 467 cases and 563 controls from a population-based case–control study. Multivariate logistic regression analysis was used to estimate the association between genotypes, environmental exposures and colorectal cancer risk, adjusting for potential confounders. Results Odds ratios of colorectal cancer were 0.75 (95% confidence interval, 0.57–0.99) for TP53 72Pro carriers compared with those homozygous for the TP53 72Arg allele and 0.78 (95% confidence interval, 0.58–1.05) for p53PIN3 A2 carriers compared with p53PIN3 A1A1. Risks differed by nonsteroidal anti-inflammatory drug use. For both investigated TP53 polymorphisms, we found that the colorectal cancer risk associated with regular nonsteroidal anti-inflammatory drug use was statistically significantly modified by the TP53 genotype (P values for interaction=0.049 and 0.034, respectively), whereby a substantial protective effect of nonsteroidal anti-inflammatory drug use was observed for homozygous carriers of the 72Arg allele and of the PIN3 A1 allele (odds ratio 0.44; 95% confidence interval, 0.30–0.65 and odds ratio, 0.45; 95% confidence interval, 0.31–0.65). The interaction between nonsteroidal anti-inflammatory drugs and TP53 genetic polymorphisms was confirmed by haplotype analysis. Conclusions These data suggest that the TP53 genotype may modify the influence of nonsteroidal anti-inflammatory drug use on the risk of colorectal cancer. A direct proof of functional analysis is warranted to confirm these findings.

3. **The Cytokine Network in Colorectal Cancer: Implications for New Treatment Strategies**

   Year: 2022

   Authors: ["H. Braumüller", "Bernhard Mauerer", "Johanna Andris", "C. Berlin", "T. Wieder", "R. Kesselring"]

   Abstract: Colorectal cancer (CRC) is one of the most frequent tumor entities worldwide with only limited therapeutic options. CRC is not only a genetic disease with several mutations in specific oncogenes and/or tumor suppressor genes such as APC, KRAS, PIC3CA, BRAF, SMAD4 or TP53 but also a multifactorial disease including environmental factors. Cancer cells communicate with their environment mostly via soluble factors such as cytokines, chemokines or growth factors to generate a favorable tumor microenvironment (TME). The TME, a heterogeneous population of differentiated and progenitor cells, plays a critical role in regulating tumor development, growth, invasion, metastasis and therapy resistance. In this context, cytokines from cancer cells and cells of the TME influence each other, eliciting an inflammatory milieu that can either enhance or suppress tumor growth and metastasis. Additionally, several lines of evidence exist that the composition of the microbiota regulates inflammatory processes, controlled by cytokine secretion, that play a role in carcinogenesis and tumor progression. In this review, we discuss the cytokine networks between cancer cells and the TME and microbiome in colorectal cancer and the related treatment strategies, with the goal to discuss cytokine-mediated strategies that could overcome the common therapeutic resistance of CRC tumors.

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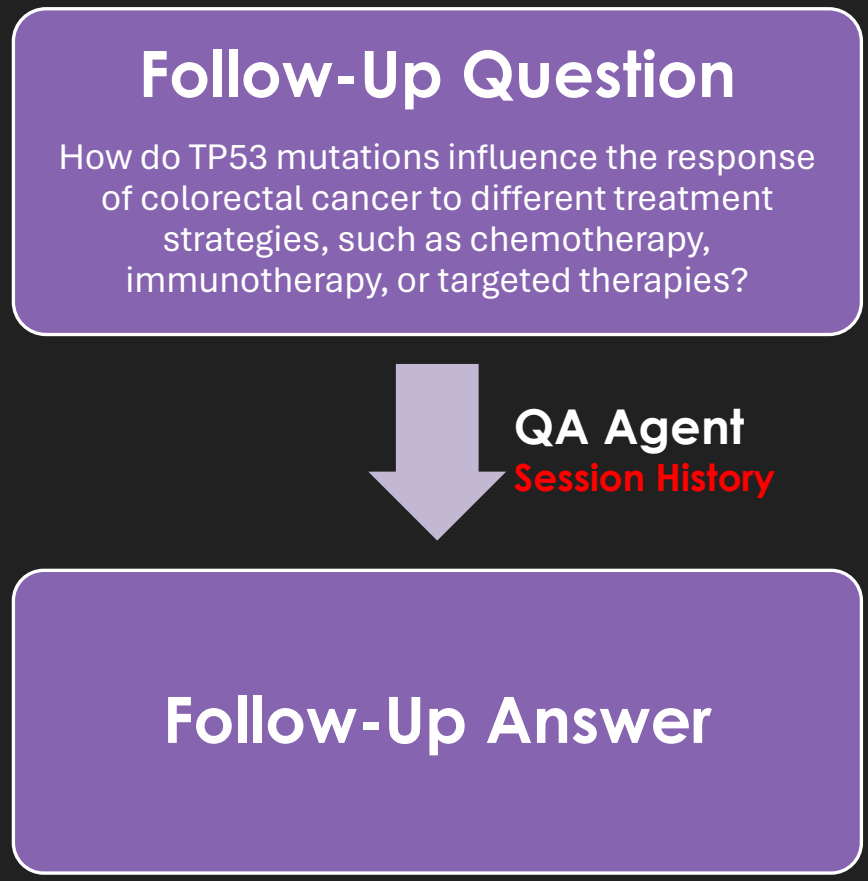

Pipeline

Follow-up Questions:

Question: How do TP53 mutations influence the response of colorectal cancer to different treatment strategies, such as chemotherapy, immunotherapy, or targeted therapies?
Answer: TP53 mutations in colorectal cancer (CRC) influence treatment responses in several ways: 1. **Chemotherapy**: TP53 mutations are often associated with resistance to certain chemotherapeutic agents. The loss of p53 function can impair the ability of cancer cells to undergo apoptosis in response to DNA-damaging drugs, leading to reduced efficacy of treatments like 5-fluorouracil and oxaliplatin. 2. **Immunotherapy**: TP53 mutations can affect the tumor microenvironment and immune evasion mechanisms. Tumors with TP53 mutations may have altered antigen presentation, which can impact the effectiveness of immune checkpoint inhibitors. However, some studies suggest that TP53 mutations may also lead to increased neoantigen load, potentially enhancing responses to immunotherapy. 3. **Targeted Therapies**: The presence of TP53 mutations can complicate the effectiveness of targeted therapies. For instance, tumors with TP53 mutations may exhibit altered signaling pathways that can lead to resistance against therapies targeting specific oncogenes or pathways, such as those involving KRAS or the Wnt signaling pathway. Overall, TP53 mutations are associated with poorer treatment outcomes and can necessitate alternative therapeutic strategies or combination therapies to improve efficacy.

Question: How do different types of TP53 mutations (e.g., missense vs. nonsense mutations) impact the prognosis and treatment resistance in colorectal cancer?
Answer: Different types of TP53 mutations can significantly impact prognosis and treatment resistance in colorectal cancer (CRC): 1. **Missense Mutations**: These mutations often result in the production of a mutant p53 protein that retains some functional activity. The specific effects can vary based on the mutation's location and the resulting protein conformation. Generally, missense mutations are associated with a poorer prognosis compared to wild-type TP53, as they can lead to altered cell cycle regulation and increased tumor aggressiveness. They may also contribute to resistance against chemotherapy and targeted therapies due to the altered signaling pathways. 2. **Nonsense Mutations**: These mutations lead to the production of truncated p53 proteins that lack functional domains necessary for tumor suppression. Nonsense mutations typically result in a complete loss of p53 function, which is associated with a more aggressive tumor phenotype and worse overall prognosis. Tumors with nonsense mutations are often more resistant to treatments that rely on p53-mediated apoptosis, such as certain chemotherapies. In summary, missense mutations may confer some functional activity and variability in treatment response, while nonsense mutations generally lead to complete loss of function, resulting in poorer prognosis and increased treatment resistance.

Ask a follow-up question... Ask

Details

Front End

query, followUpQuery, result, followUpHistory,
loading, followUpLoading, ask, askFollowUp, topK

Result: keywords, papers, answer, …

Back End

Details

- API
  - /ask: GET
    - Initial question: (**question**: encoded text, **top_k**: int, **follow_up=false**: boolean)
    - Follow-up question: (**question**: encoded text, **follow_up=true**: boolean)

Challenges

- Continue from the previous conversation
  - Solution: Use a dict to store session histories with session ID
- Token limit exceeded
  - Solution: Have to chunk the text by token_limit=4,096 to fit the 8,192 token context window of GPT-4o-mini
- Paper access denied
  - Use abstract instead

Further Improvement

- Markdown formatting for answers
- Pop-up Notifications
- More types of error handling

Live Demo

- http://localhost:5173/