Leveraging Large Language Model for Populating OMOP Oncology CDM from the EHR : Feasibility Study & PRESENTER: Seng Chan You

INTRODUCTION

- The Oncology CDM Working Group developed ulletthe OMOP Oncology Extension to support the integration of cancer-specific information into the OMOP CDM.
- Despite these advancements, much of the lacksquarecancer-data in EHR remains in unstructured formats, making it challenging to utilize and standardize.
- language models (LLMs) Generative large \bullet promising solution to these present a challenges, by leveraging the in-context learning capabilities of LLMs.
- Among several candidate applications to validate feasibility, we focused on whether LLM-derived cancer data can be used to define cancer stage at diagnosis in accordance with updates to the AJCC staging system.

METHODS Data sources

- We obtained unstructured pathology and radiology reports for patients diagnosed with Hospital colorectal at Severance cancer between 2010 and 2023.
- A random sample of 1,000 individuals was

Prompt design

We interacted with GPT-40 via zero-shot prompting through the OpenAI API. A total of 20 reports were sampled to develop prompts to extract cancer data (Table 1). All output was compiled into a JSON format.

Evaluation

- We classified the cancer stage at diagnosis using based on the 8th edition of the AJCC TNM staging system. We compared the LLM-derived cancer stage at diagnosis with the TNM values retrieved from the EHRs database.
- Additionally, we defined the cancer stage using

In this study, we developed strategy to extract \bullet the cancer information from unstructured pathology and radiology reports of patients with colorectal cancer using state-of-the-art LLM.

selected for inclusion in the study. We used 1,579 radiology and 2,632 pathology reports documented within 30 days before or 120 days after initial cancer diagnosis.

both the 7th and 8th editions of the AJCC staging system and illustrated the changes in cancer stage, demonstrating the usefulness and of the LLM-derived flexibility cancer information.

Generative LLM can be used to populate Oncology CDM from the unstructured EHRs

Pathology rep						AJCC sta	aging fro	m EHR						
Category	Descriptor	Category	Descriptor			0	I	ПА	ШΒ	ПС	ШA	ШВ	ШС	
Feature	Size	Lymph node	Metastasis site		0 T	69	1	1	0	0	0	0	1	
	Histologic grade		Metastasis count		Т	2 1	234	7 116	0	0	0	3	0	
	Histologic type	Biomarkor	BRAF mutation		ΠВ	0	0	0	11	0	0	0	0	
	Location		KRAS mutation	AJCC	ПС	1	0	0	0	3	0	0	0	
	Procedure		Ki-67 index	staging	ША	0	1	0	0	0	18	0	0	
	Tumor status		MLH1	from LLM	ШВ	0	0	1	0	0	0	99	4	
Invasion	Depth of invasion		MSH2		ШС	0	0	0	0	0	0	1	14	
	Lymphovascular inva		MSH6		IVA	0	15	13	0	0	1	5	2	
	sion				IVB	0	1	2	1	0	0	0	0	
	Perineural invasion		Microsatellite instab ility	Figure 2. Com	paris	on of	0 TNM	5 stag	ing a	1 CCOr	0 ding	2 to the	² e AJC	
	Tumor budding		Mitotic count			TNM staging from AJCC 7th edition								
	Tumor deposits		NRAS mutation											
Margin	Basal margin		PMS2			0	I	ΠА	А П	В	ПС	ША	ШВ	
	Circumferential marg in	Other	Post treatment/Procedu		0 I	75 0	0 245	0 0	())	0 0	0 0	0 0	
	Distal margin		re status		ΠА	0	0	123	3 (C	0	0	0	
	Lateral margin			TNM	ΠВ	0	0	0	1	3	0	0	0	
	Proximal margin			staging	ПС	0	0	0	()	4	0	0	
	Resection margin			from	ША	0	0	0	()	0	19	0	
Radiology reports			AJCC 8th	ШB	0	0	0	()	0	0	105		
Feature	Tumor location			edition	ШС	0	0	0	()	0	0	0	
	Tumor status	_			IVA	0	0	0	(C	0	0	0	
	Size				IVB	0	0	0	()	0	0	0	
	JIZC				IVC	0	0	0	()	0	0	0	

Figure 1. Overall performance of GPT-40 on classification of cancer stage

Pathology reports							ļ	AJCC sta	aging fro	m EHR						
Category	Descriptor	Category	Descriptor			0	I	ШΑ	ШΒ	ШС	ША	ШВ	ШС	IVA	IVB	IVC
Feature	Size		Metastasis site		0	69	1	1	0	0	0	0	1	3	0	0
	Histologic grade	Lymph node	Metastasis count		I 	2	234	7	0	0	0	1	0	0	1	0
	Histologic type		BRAF mutation		ША	1	1	116	1	0	0	3	0	1	0	0
	Location	Biomarker	KRAS mutation		пс	1	0	0	0	3	0	0	0	0	0	0
	Procedure		Ki-67 index	staging from LLM	ШA	0	1	0	0	0	18	0	0	0	0	0
	Tumor status		MLH1		ШВ	0	0	1	0	0	0	99	4	0	0	1
Invasion	Depth of invasion		MSH2		ШС	0	0	0	0	0	0	1	14	0	0	0
	Lymphovascular inva		MSH6		IVA	0	15	13	0	0	1	5	2	9	2	1
	sion				IVB	0	1	2	1	0	0	0	0	0	2	1
	Perineural invasion		Microsatellite instab		IVC	0	0	5	1	1	0	2	2	4	2	2
			ility	Figure 2 Comparison of TNIM staging according to the AICC editions												
	Tumor budding		Mitotic count					1 5145								
	Tumor deposits		NRAS mutation		TNM staging from AJCC 7th edition											
Margin	Basal margin		PMS2			0	I	ΠА	νП	B I	IC I	ШΑ	ШВ	ШС	IVA	IVB
	Circumferential marg in	Other	Post treatment/Procedu re status		0 I	75 0	0 245	0	()	0	0	0 0	0 0	0	0
	Distal margin				ПА	0	0	123	3 ()	0	0	0	0	0	0
	Lateral margin			ТММ	ΠВ	0	0	0	1	3	0	0	0	0	0	0
	Proximal margin			staging	ПС	0	0	0	()	4	0	0	0	0	0
	Resection margin			from	ША	0	0	0	()	0	19	0	0	0	0
Radiology reports			AJCC 8th	ШВ	0	0	0	()	0	0	105	0	0	0	
Feature	Tumor location			edition	ШС	0	0	0	()	0	0	0	15	0	0
					IVA	0	0	0	()	0	0	0	0	48	0
		_			IVB	0	0	0	()	0	0	0	0	0	7
	JIZE				IVC	0	0	0	()	0	0	0	0	10	9

RESULTS

- A total of 4,211 pathology and radiology reports
- A major difference between 7th and 8th edition By leveraging generative LLM, we will is that the inclusion of new stage involving
 - standardize the cancer-specific data from the

from 1,000 patients were analyzed.

- The agreement between LLM-derived AJCC stage and AJCC stage from structured EHRs is presented using confusion matrix in Figure 1. The overall accuracy of LLM-derived staging was 0.86. Cohen's Kappa was 0.82 (95%) confidence interval [CI], 0.78-0.85).
- Figure 2 shows the comparison of TNM staging \bullet groups according to the AJCC 7th and 8th edition.

peritoneal metastasis (stage IVC).

As a result, 19 patients, originally classified as stage IVA or IVB under the 7th edition, were reclassified as stage IVC.

CONCLUSION

- is ongoing study. Generative LLMs • This demonstrate feasibility in automating the extraction of structured cancer information from unstructured EHRs.
- This approach has the potential to construct well-fined resources for future research, reducing the workload of human experts.

EHR based on the OMOP Oncology Extension.

- Subin Kim^{1,2}, Jeong Eun Choi^{1,2}, Chang Jun Ko³, Seng Chan You^{1,2}
- ¹Dept. of Biomedical Systems Informatics, Yonsei University College of Medicine
 - ²Institute for Innovation in Digital Health Care, Yonsei University

³Dept. of Health Informatics and Biostatistics, Graduate School of Public Health, Yonsei University



