

COMPOSE: Cross-Modal Pseudo-Siamese Network for Patient Trial Matching

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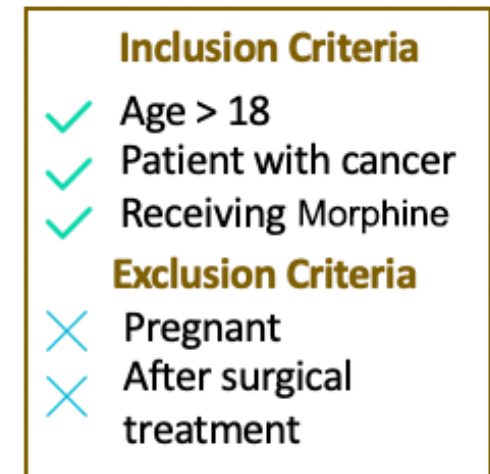
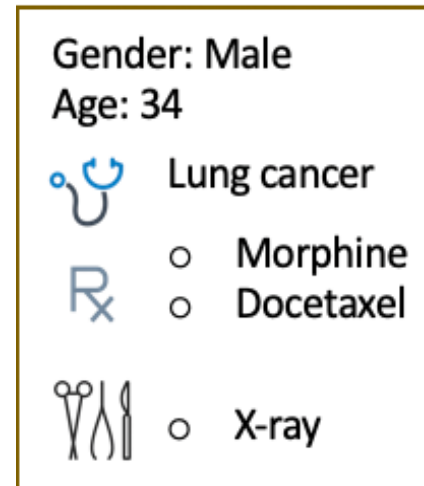
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Content

- **Clinical Background**
- **Challenges**
- **Method**
- **Experiment Results**

Clinical Background 1: What is patient trial matching?

- Electronic Health Records (EHR): A type of high-dimensional sequence data
 - Procedures
 - Diagnosis
 - Drugs
- Clinical trials: Unstructured text data
 - Inclusion Criteria
 - Exclusion Criteria



Clinical Background 2: Why automated patient trial matching is important?



Essential

Annual market over \$46 billion

Time Consuming

50% of trials delayed, 25% of cancer trials failed due to enrollment.

High Costs

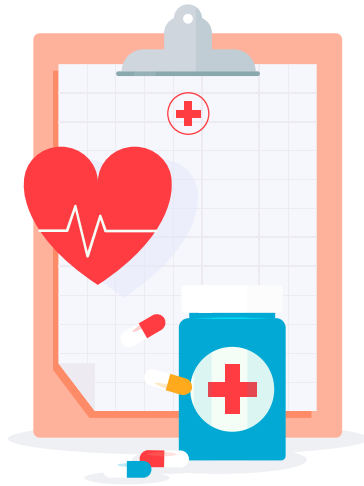
High recruitment cost: \$6000 to \$7500 per patient.

Content

- **Clinical Background**
- **Challenges**
 - Multi-granularity medical concept
 - Many-to-many relationship between patient and trials
 - Explicit inclusion/exclusion criteria handling
- **Method**
- **Experiment Results**

Challenge 1: Multi-granularity medical concept

- Eligibility criteria encode more general disease
- EHRs use more specific medical codes

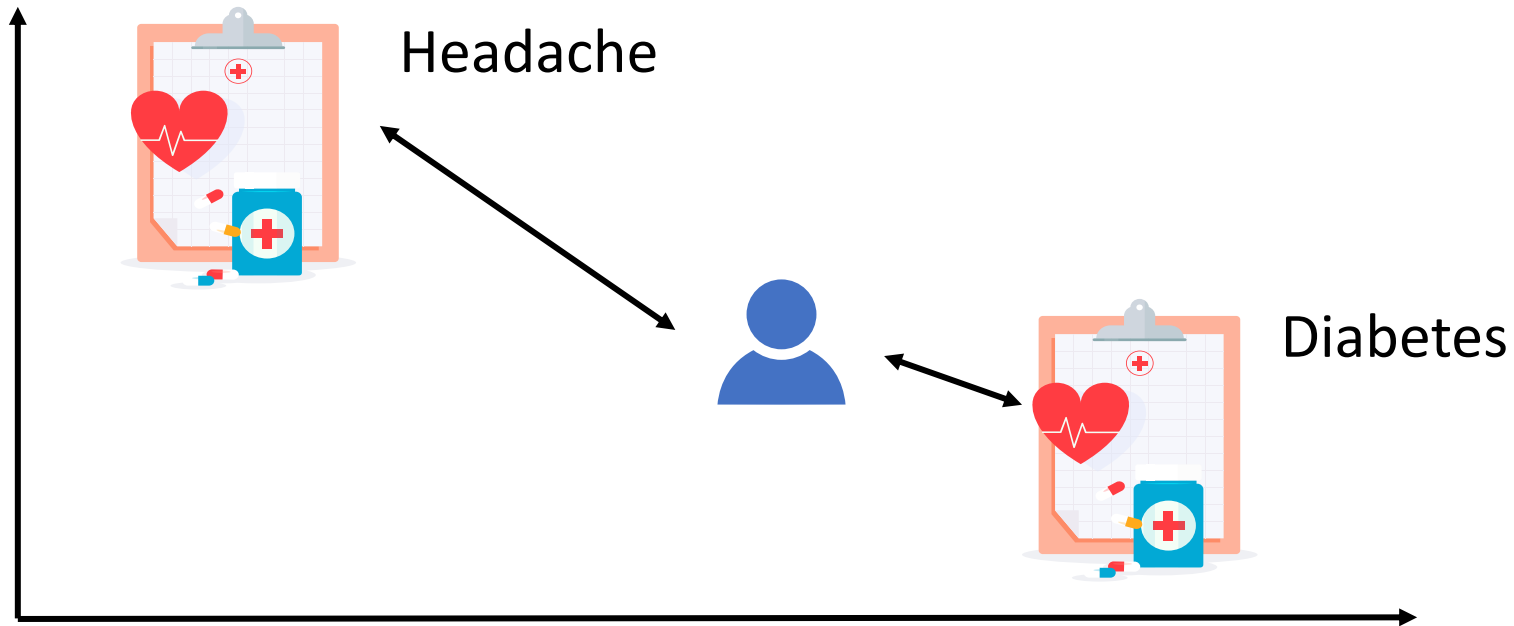


- ✓ Pleuropericardial adhesion
- ✓ Myocardial infraction
- ✓ Inflammatory cardiomyopathy

Trial of Cardiovascular Disesesases

Challenge 2: Many-to-many relationship between patients and trials

- Each patient may enroll in more than one trial and vice versa



- Align the patient embedding to different trial embeddings may confuse the embed function

Challenge 3: Explicit inclusion/exclusion criteria handling

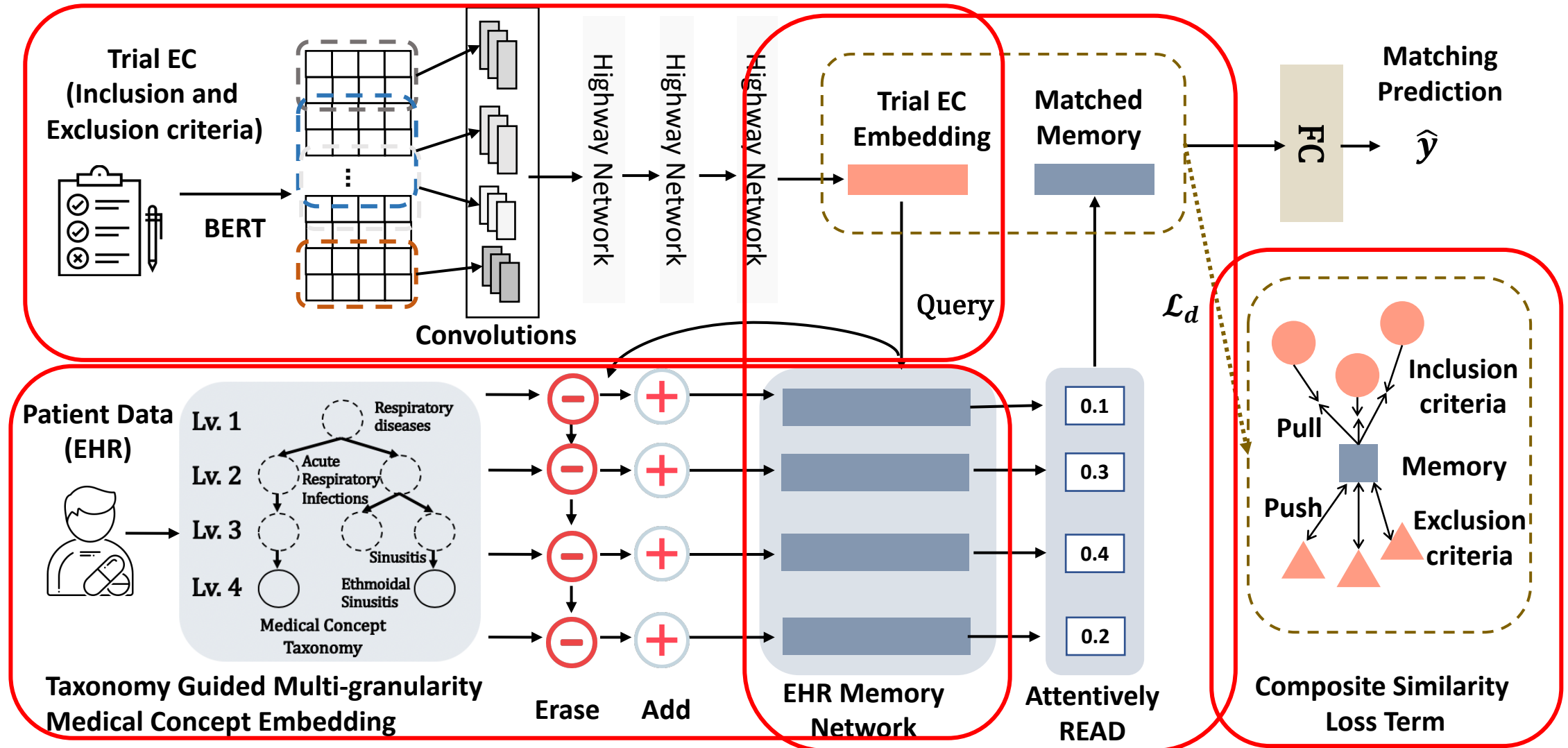
- Inclusion and Exclusion criteria describe desired and unwanted from the targeted patients

Inclusion criteria ← Age > 18 → Exclusion criteria

Content

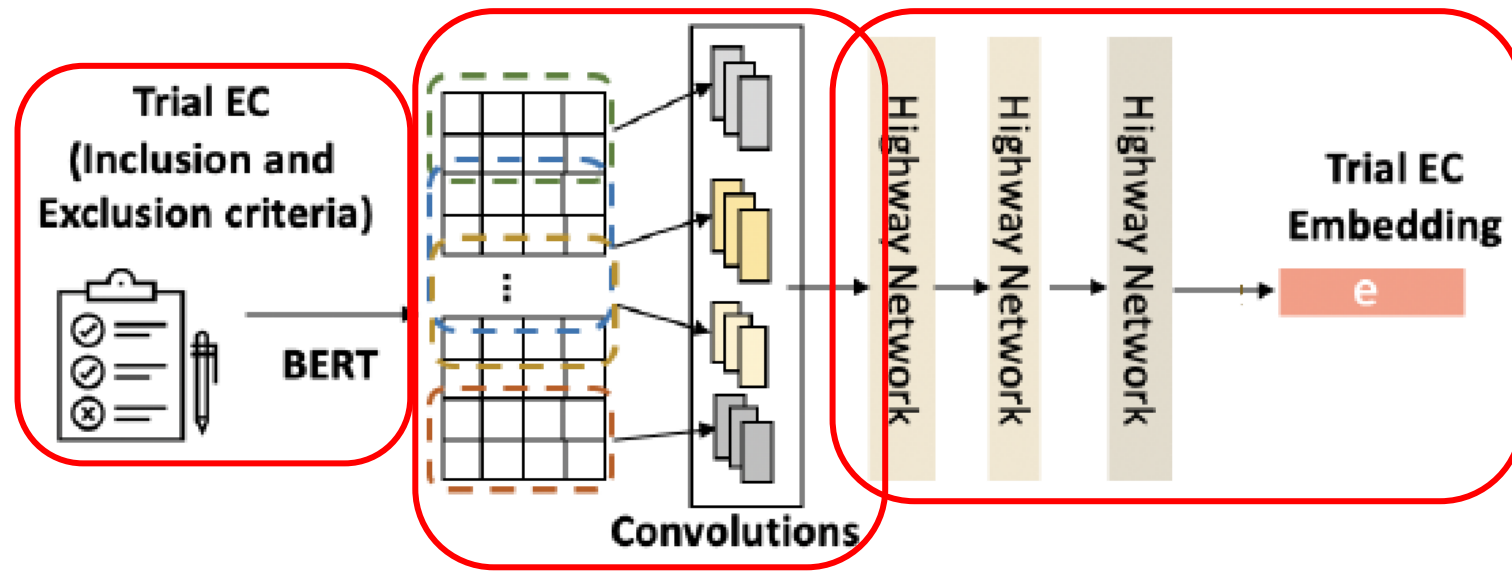
- Clinical Background
- Challenges
- **Method**
 - Trial eligibility criteria embedding
 - Taxonomy guided patient embedding
 - Attentional record alignment and dynamic matching
 - Explicit inclusion/exclusion criteria handling
- Experiment Results

Method Overview: COMPOSE



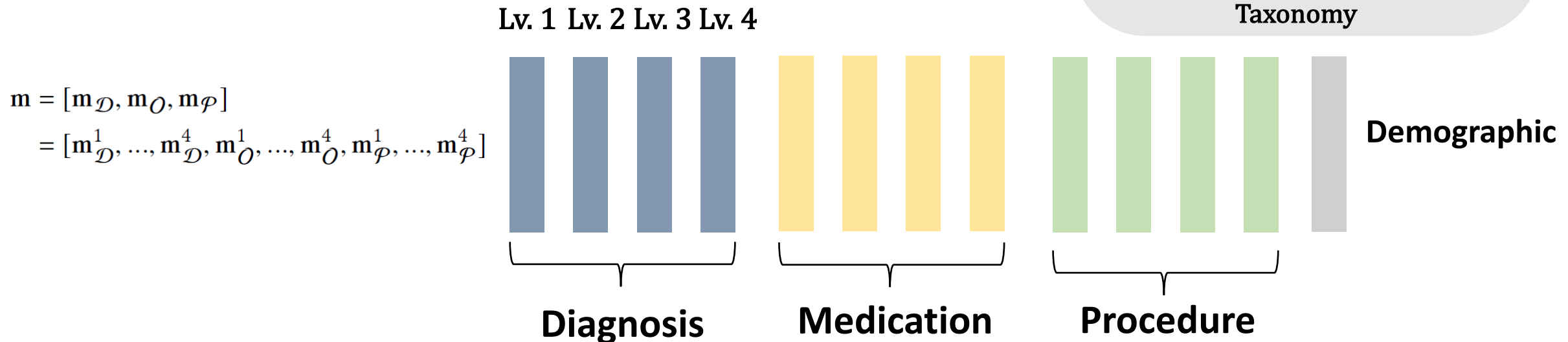
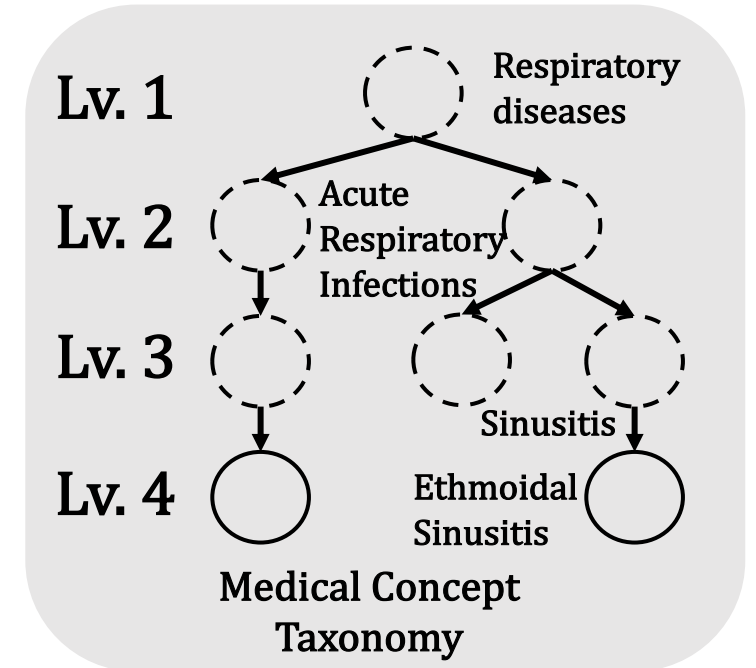
Method: Trial eligibility criteria embedding

- Use BERT to learn contextual embeddings for EC sentence $[w_1, \dots, w_N]$
 $\tilde{c} = [\tilde{w}_1, \dots, \tilde{w}_N] = \text{BERT}([w_1, \dots, w_N])$
- Use different kernel sizes to capture different granularity semantics
 $x = [\text{Conv}(\tilde{c}, k_1), \text{Conv}(\tilde{c}, k_2), \text{Conv}(\tilde{c}, k_3), \text{Conv}(\tilde{c}, k_4)]$
- Use highway network and max pooling to obtain the final EC embedding
 $u = \sigma(\text{Conv}(x, k))$
 $v = u \cdot \text{Conv}(x, k) + x \cdot (1 - u)$
 $e = \text{MaxPool}(v)$



Method: Taxonomy guided patient embedding

- Use medical concept taxonomy to divide each concept into four levels
 - the Uniform System of Classification (USC)
- Three memory networks to store diagnosis, medications and procedures



Method: Taxonomy guided patient embedding

- Augment medical codes with textual description:

- Code 692.9 -> “Contact dermatitis and other eczema”

$$\tilde{g}_t = \text{MaxPool}(\text{BERT}([w_1, \dots, w_L]))$$

- Update memories at each visit

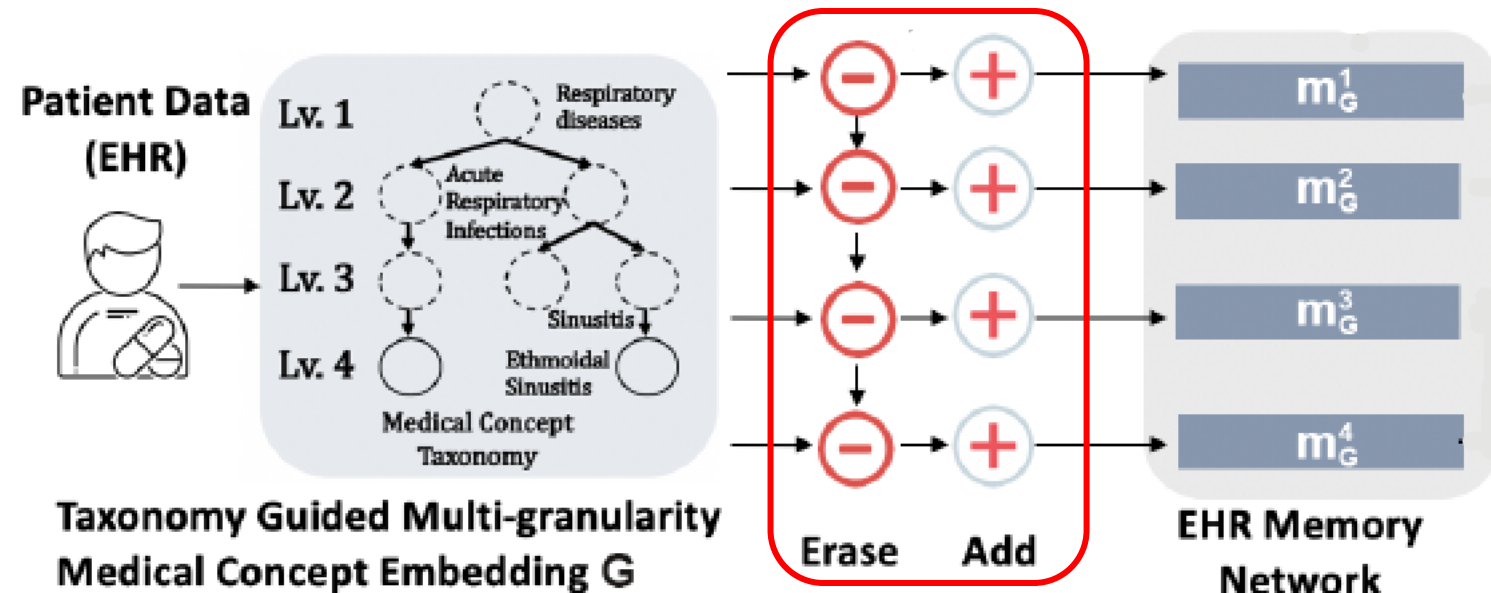
- Erase-followed-by-add:

$$\text{erase}_t = \sigma(W_e \tilde{g}_t^k + b_e),$$

$$\text{add}_t = \tanh(W_a \tilde{g}_t^k + b_a)$$

- Update slot:

$$m_G^k \leftarrow m_G^k \odot (1 - \text{erase}_t) + \text{add}_t$$

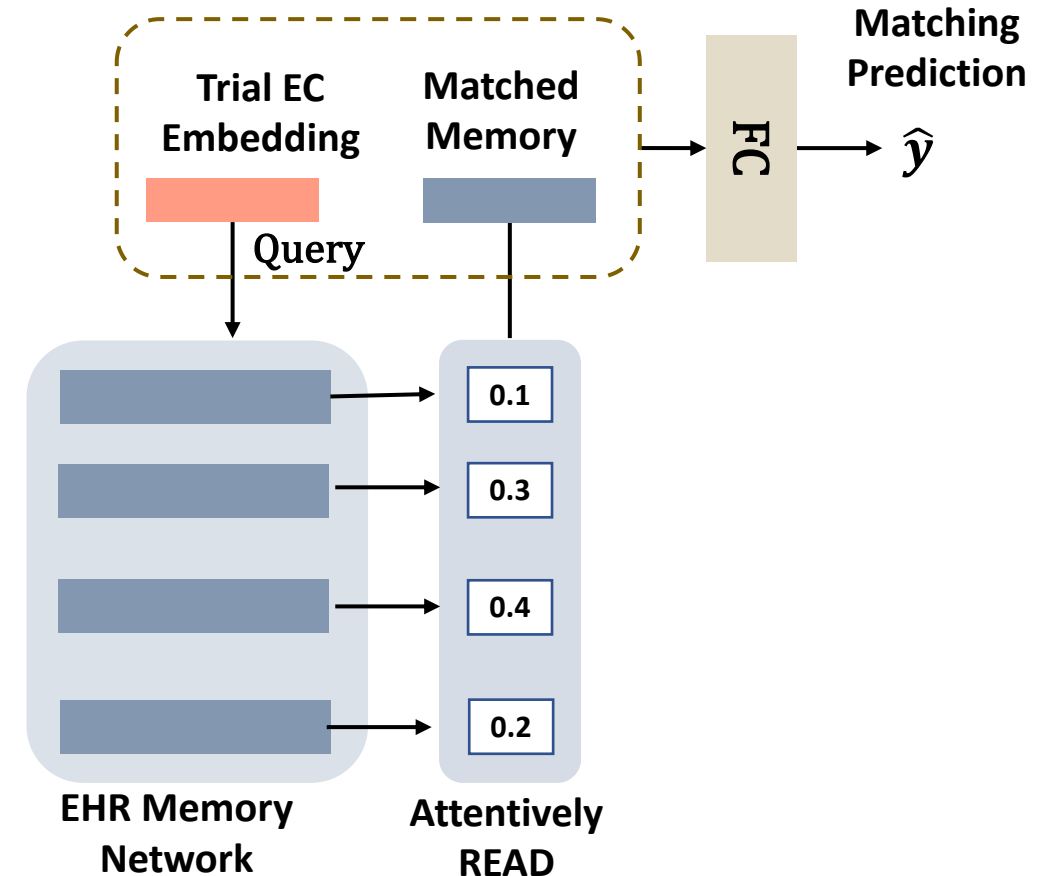


Method: Attentional record alignment and dynamic matching

- Let each EC correspond to the sub-memories
- Attentional matching
 - Trial EC embedding -> Query
 - Matched memory -> Response

$$a_{k,G} = \frac{\exp(\mathbf{m}_G^k \mathbf{T} \text{MLP}(\mathbf{e}))}{\sum_{x \in \{\mathcal{D}, \mathcal{O}, \mathcal{P}\}} \sum_{i=1}^4 \exp(\mathbf{m}_x^i \mathbf{T} \text{MLP}(\mathbf{e}))}$$

$$\tilde{\mathbf{m}} = \sum_{x \in \{\mathcal{D}, \mathcal{O}, \mathcal{P}\}} \sum_{i=1}^4 a_{i,x} \mathbf{m}_x^i$$



Method: Explicit inclusion/exclusion criteria handling

- Classification loss:

$$\mathcal{L}_c = -(\mathbf{y}^T \log(\hat{\mathbf{y}}) + (1 - \mathbf{y})^T \log(1 - \hat{\mathbf{y}}))$$

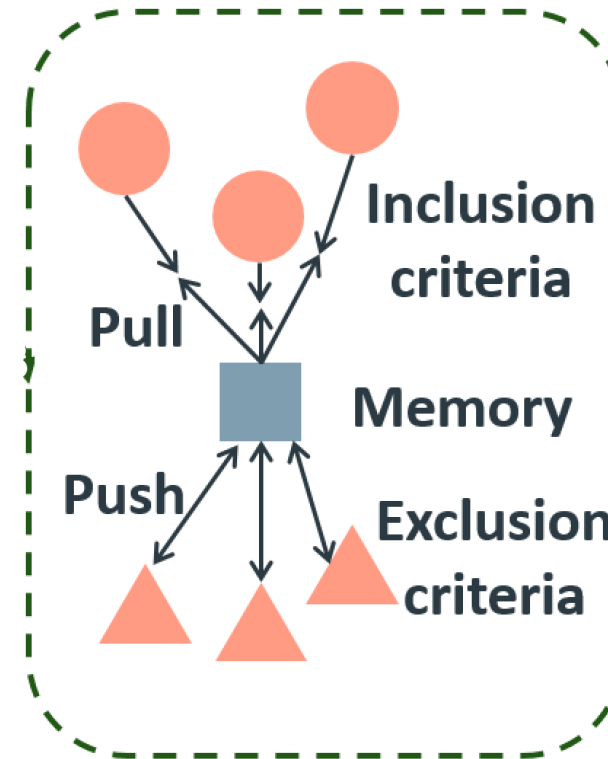
- Inclusion/Exclusion loss:

$$\mathcal{L}_d = \begin{cases} \underline{1 - d(e, \tilde{\mathbf{m}}_I)}, & \text{if } e \text{ is } e_I \\ \underline{\max(0, d(e, \tilde{\mathbf{m}}_E) - \alpha)}, & \text{if } e \text{ is } e_E \end{cases}$$

-> 0 **>= α**

- Final loss:

$$\mathcal{L} = \mathcal{L}_c + \mathcal{L}_d$$



**Composite Similarity
Loss Term**

Content

- Background & Motivation
- Problem Formulation
- Insights
- Solution
- **Experiment**
 - Patient trial matching
 - Discussions
 - Case studies

Experiment

- **Dataset**

- Clinical trial data

- 590 trials from publicly available data source (clinicaltrials.gov)
 - 12,445 criteria-level EC statements

- Patient EHR data

- 83,371 patients from 2002 to 2018

Experiment: Patient trial matching

- Outperforms all baseline models across both trial level and criteria level matching in all evaluation metrics.
- 24.3% higher accuracy for trial level matching
- 8.8% higher accuracy and 4.7% higher AUROC for criteria level matching

	Model	Accuracy
Baselines	LSTM+GloVe	0.4294±0.010
	LSTM+BERT	0.5460±0.008
	Criteria2Query	0.6147±-
	DeepEnroll	0.6737±0.021
Reduced	COMPOSE-MN	0.7833±0.011
	COMPOSE-Highway	0.8102±0.009
	COMPOSE- \mathcal{L}_1	0.8212±0.010
Proposed	COMPOSE	0.8373±0.012

	Model	Accuracy	AUROC	AUPRC
Baselines	LSTM+GloVe	0.722±0.010	0.789±0.009	0.784±0.009
	LSTM+BERT	0.834±0.008	0.845±0.007	0.840±0.007
	DeepEnroll	0.869±0.012	0.936±0.013	0.947±0.011
Reduced	COMPOSE-MN	0.899±0.012	0.955±0.013	0.960±0.010
	COMPOSE-Highway	0.912±0.007	0.965±0.007	0.967±0.009
	COMPOSE- \mathcal{L}_d	0.939±0.010	0.976±0.009	0.973±0.007
Proposed	COMPOSE	0.945±0.008	0.980±0.007	0.979±0.008

Discussion: Varying length of patient record

- How COMPOSE performs in matching trials with patients who have short or long records?
 - Short (1 visit), Medium (2-3 visits), Long (≥ 4 visits)
- COMPOSE have robust performance

Model	Short	Medium	Long
LSTM+GloVe	0.4906	0.4328	0.0000
LSTM+BERT	0.5484	0.5512	0.5338
Criteria2Query	0.6833	0.5989	0.5172
DeepEnroll	0.6779	0.6797	0.6443
COMPOSE	0.8420	0.8389	0.8350

Discussion: Varying disease types

- How COMPOSE performs on different types of diseases?
 - Chronic, Oncology, Rare diseases
- Achieves 77.3% higher accuracy for chronic diseases
- Most baseline models fail to match correct patients for oncology and rare diseases

Model	Chronic Diseases	Oncology	Rare Diseases
LSTM+GloVe	0.1793	0.0000	0.0000
LSTM+BERT	0.2062	0.0000	0.0000
Criteria2Query	0.5103	0.2722	0.2292
DeepEnroll	0.3345	0.0000	0.0000
COMPOSE	0.5931	0.6370	0.6875

Discussion: Varying trial phases

- How COMPOSE performs on different phases?
 - Phase I, II, III
- 155% higher accuracy for phase I trials
- 19% higher accuracy for phase II trials
- 27% higher accuracy for phase III trials

Model	Phase I	Phase II	Phase III
LSTM+GloVe	0.0008	0.5865	0.3743
LSTM+BERT	0.0025	0.6045	0.4862
Criteria2Query	0.3025	0.6433	0.5870
DeepEnroll	0.2034	0.7493	0.6329
COMPOSE	0.5189	0.8939	0.8005

Discussion: Varying threshold of matching

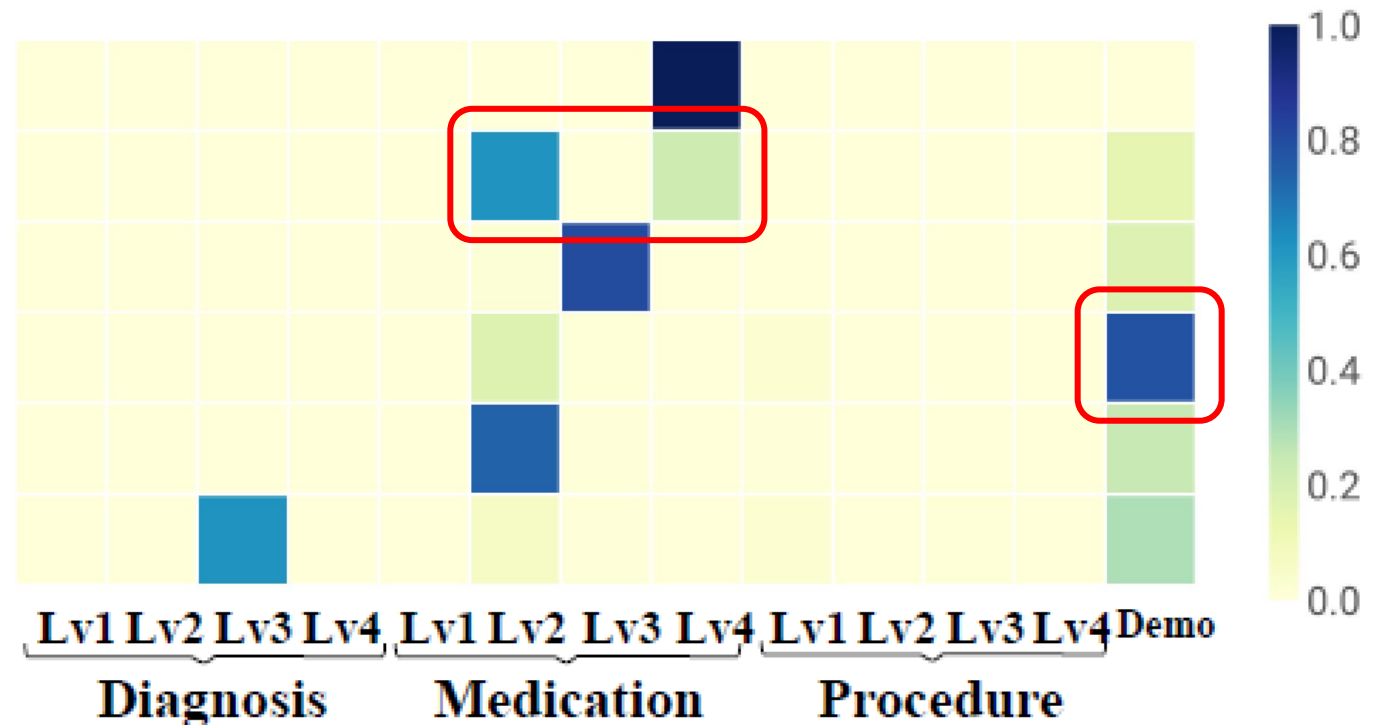
- Some inclusion or exclusion criteria can be too strict to prevent finding patients
- How COMPOSE performs on varying thresholds?
 - 70%, 80%, 90%
- COMPOSE have robust performance under all thresholds

Model	70% Matching	80% Matching	90% Matching
LSTM+GloVe	0.6218	0.5862	0.5057
LSTM+BERT	0.7231	0.6861	0.6238
DeepEnroll	0.8225	0.7963	0.7422
COMPOSE	0.9334	0.9193	0.8915

Case study: Attention weights on memory slots

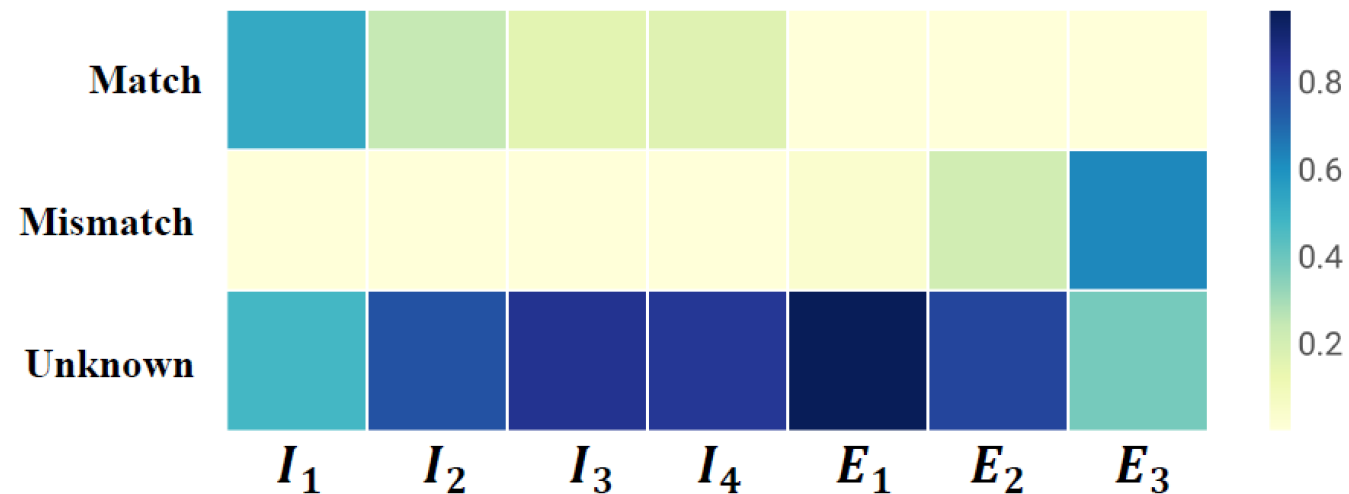
- A trial on Cabozantinib which treats grade IV astrocytic tumors

1. received temozolomide therapy
2. receiving warfarin (or other coumarin derivatives)
3. acute intracranial/intratumoral hemorrhage.
4. pregnant or breast-feeding
5. serious intercurrent illness
6. inherited bleeding diathesis or coagulopathy



Case study: Failed case

- A trial for *Early Stage Non-Small Cell Lung Cancer*
- I2: Lung function capacity capable of tolerating the proposed lung surgery
- I3: Eastern Cooperative Oncology Group (ECOG) Performance Status of 0-1
- I4: Available tissue of primary lung tumor



Thank you!

COMPOSE: Cross-Modal Pseudo-Siamese Network for Patient Trial Matching

<https://github.com/v1xerunt/COMPOSE>

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