Vision Language Model is NOT All You Need: Augmentation Strategies for Molecule Language Model

Namkyeong Lee, Siddhartha Laghuvarapu, Chanyoung Park, Jimeng Sun







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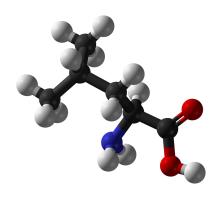




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BACKGROUND MOLECULE LANGUAGE MODELS



Molecule



Human language Description

Molecule Language Models

Understanding molecules in human language format

Major Research Direction

How to align molecules and their description better?

→ Mostly inspired by the recent VLM papers

BACKGROUND MOLECULE LANGUAGE MODELS



Aspirin is a commonly used drug for the treatment of pain and fever

Penicillin G Sodium is the sodium salt form of benzylpenicillin

CLIP-Style Pre-training

- Molecule and its corresponding description as a positive pair
- Descriptions of other molecules as negative pairs

Aligning the pairs in representation space

Molecule and its description to be close in representation space

Challenge 1. Limited Quantity of Molecule-Text Pair







Image



Text

Vision Language Model (VLM)

"Scale is Everything" view point

- → Massive amounts of crawled image-text pairs
- → Correlation between number of pairs and model performance







Molecule



Text

Molecule Language Model (MoLM)

Expensive wet-lab experiments are required for generating molecule-text pairs

Challenge 2. Different Expertise with Diverse Interests

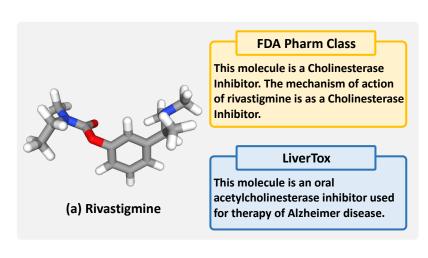


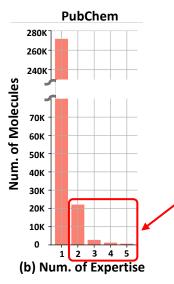
Largest molecule database

Over 94M molecules
From 1014 different data sources



Challenge 2. Different Expertise with Diverse Interests





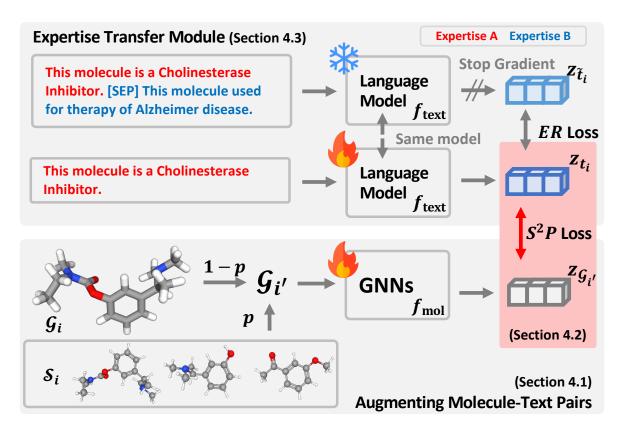
Specialized areas of experts

- → Typically restrict their knowledge to selective group of molecules
- → Numerous molecules have <u>missing expertise</u> across various experts

Only 27K Molecules out of 299K molecules have descriptions from multiple experts

Vision Language Model is NOT All You Need: Augmentation Strategies for Molecule Language Model

AMOLE: Augmenting molecule-text pair and transferring expertise between the molecules



Overall model architecture

Augmenting Molecule-Text Pairs

How to increase the number of molecule-text pairs?

Structural Similarity Preserving Loss

How to align augmented pairs more precisely?

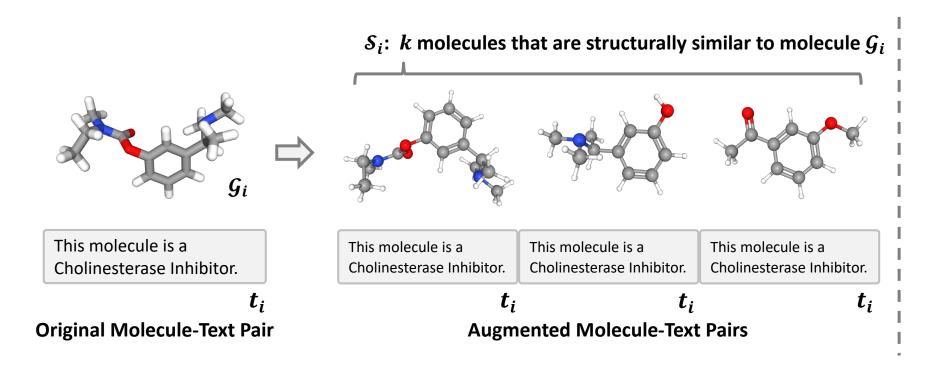
Expertise Transfer Module

How to transfer the expertise between molecules?

Augmenting Molecule-Text Pairs

Share textual descriptions among molecules with structural resemblances

→ "Structurally similar molecules tend to display analogous biological activities"



Tanimoto Similarity

$$s_{ij} = \frac{|\mathsf{fp}_i \cap \mathsf{fp}_j|}{|\mathsf{fp}_i| + |\mathsf{fp}_j| - |\mathsf{fp}_i \cap \mathsf{fp}_j|}$$

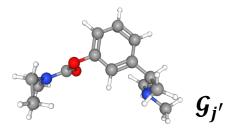
FP: Finger Print

Structural Similarity Preserving Loss

Shared description t_i is not specifically written for the molecules in S_i

- ightarrow Preserve structural similarity between ${\cal G}_i$ and ${\cal G}_{i'}$ in molecule-text joint space
- ightarrow The Tanimoto similarity between ${\cal G}_i$ and ${\cal G}_{i'}$ as a pseudo label for contrastive learning

Original Contrastive Learning

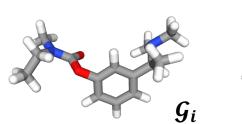


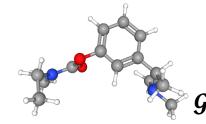
This molecule is a Cholinesterase Inhibitor.

 t_i

Label: 1 (Positive Pair) Label: 0 (Negative Pair)

Structural Similarity Preserving





This molecule is a Cholinesterase Inhibitor.

Label:
$$y_{ij'}^{t \to m} = \frac{\exp(s_{ij'}/\tau_1)}{\sum_{k'=1}^{N_{\text{batch}}} \exp(s_{ik'}/\tau_1)}$$

 s_{ij} : Tanimoto Similarity

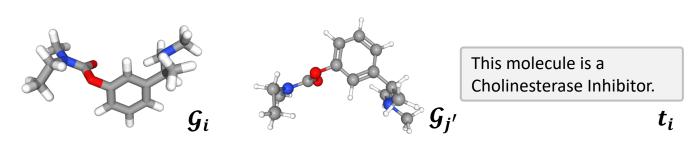
 t_i

Structural Similarity Preserving Loss

Shared description t_i is not specifically written for the molecules in S_i

- ightarrow Preserve structural similarity between ${\cal G}_i$ and ${\cal G}_{j'}$ in molecule-text joint space
- ightarrow The Tanimoto similarity between ${\cal G}_i$ and ${\cal G}_{i'}$ as a pseudo label for contrastive learning

Structural Similarity Preserving



Label:
$$y_{ij'}^{t \to m} = \frac{\exp(s_{ij'}/\tau_1)}{\sum_{k'=1}^{N_{\text{batch}}} \exp(s_{ik'}/\tau_1)}$$
 s_{ij} : Tanimoto Similarity

Similarity in representation space

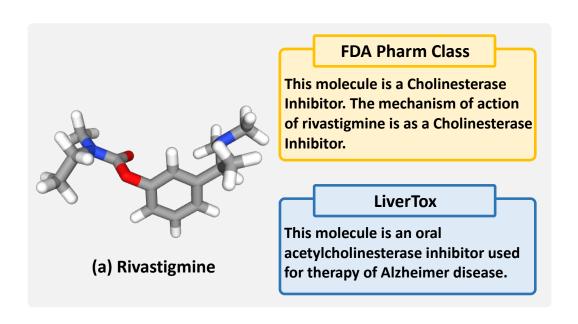
$$\hat{y}_{ij'}^{t \rightarrow m} = \frac{\exp(\text{sim}(z_{t_i}, z_{\mathcal{G}_{j'}})/\tau_2)}{\sum_{k'=1}^{N_{\text{batch}}} \exp(\text{sim}(z_{t_i}, z_{\mathcal{G}_{k'}})/\tau_2)}$$

Structural Similarity Preserving (S2P) Loss

$$\mathcal{L}_{S^2P}^{t \to m} = -\frac{1}{N_{Batch}} \sum_{i=1}^{N_{batch}} \sum_{j'=1}^{N_{batch}} y_{ij'}^{t \to m} \log \hat{y}_{ij'}^{t \to m}$$

Expertise Transfer Module

Transferring the expertise gained from molecules with extensive description to those with less description



"Different areas of expertise are interrelated"

Cholinesterase inhibitor

Improve communication between nerve cells by increasing levels of Acetylcholine in the nervous system

→ Can be therapy of Alzheimer disease

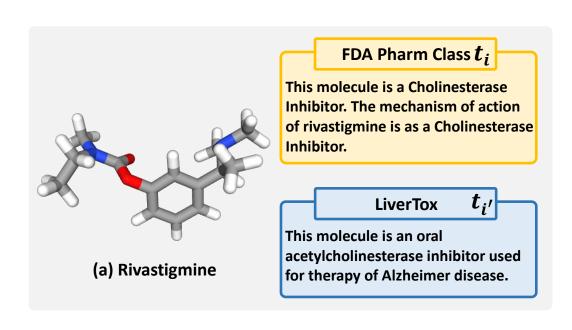
FDA Pharm Classes



LiverTox

Expertise Transfer Module

Transferring the expertise gained from molecules with extensive description to those with less description

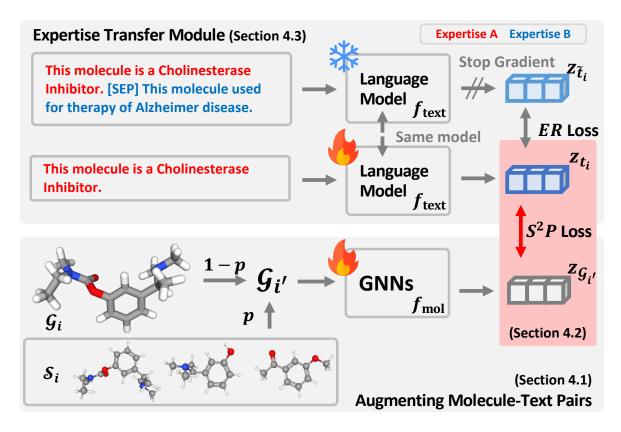


Expertise Reconstruction (ER) Loss

Reconstruction target \widetilde{t}_i by concatenating two descriptions $\widetilde{t}_i = t_i$ [SEP] $t_{i'}$

$$\mathcal{L}_{ER} = -\frac{1}{N_{Batch}} \sum_{i=1}^{N_{batch}} \|f_{\text{text}}(t_i) - \text{SG}(f_{\text{text}}(\tilde{t}_i))\|_2^2$$

Model behaves as if there exists extensive expertise available, enabling reliable predictions even with lack of detailed description



Final Model Training Loss

$$\mathcal{L} = \mathcal{L}_{S^2P} + \alpha \cdot \mathcal{L}_{ER}$$

Overall model architecture

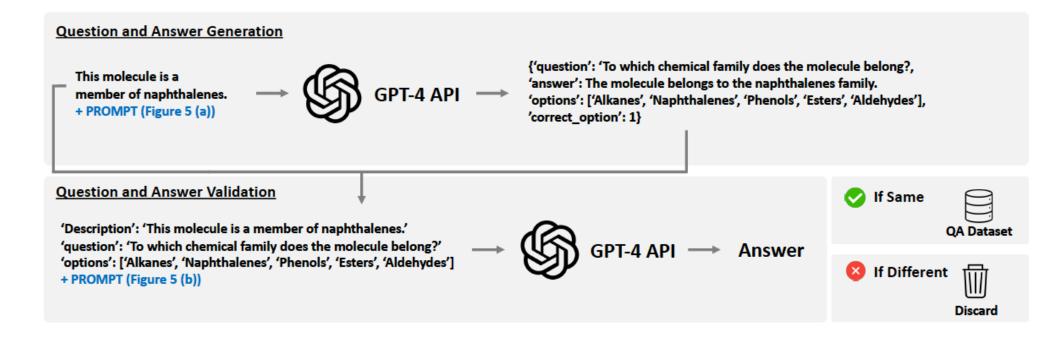
EXPERIMENTS ZERO-SHOT QUESTION AND ANSWERING

Task description

Given molecule and question, choose the correct answer from the options

Dataset Generation

Instruct GPT-4 to generate multiple-choice question comprising five options, all derived from the given textual description



EXPERIMENTS ZERO-SHOT QUESTION AND ANSWERING

Task description

Given molecule and question, choose the correct answer from the options

Original Description

This molecule is a member of naphthalenes

GPT-Generated Questions

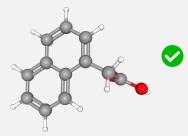
To which Chemical Family does the molecule belong?

GPT-Generated Options

[Alkanes, Naphtalenes, Phenols, Esters, Aldehydes]

Formulate QA Task as Retrieval Task

"Harder version of Retrieval Tasks"



To which chemical family does the molecule belong? Alkanes
To which chemical family does the molecule belong? Naphtalenes
To which chemical family does the molecule belong? Phenols
To which chemical family does the molecule belong? Esters
To which chemical family does the molecule belong? Aldehydes

		S	MILES	Graph			
	MolT5	BioT5	KV-PLM	Molecule STM	MoMu	Molecule STM	AMOLE
Descr.	24.84	27.54	30.07	36.11	38.31	37.97	39.26
Pharma.	22.49	27.03	26.68	29.60	29.85	29.52	31.58

Observations

AMOLE consistently outperforms baseline models

- → Extract more intricate information from the slight variations
- → Attribute to its ability in inferencing related expertise!

EXPERIMENTS ZERO-SHOT VIRTUAL SCREENING

Virtual Screening

Computational technique to search large libraries of compounds quickly to identify the compounds most likely to have desired properties

Task description

Model's proficiency in virtual screening drugs by supplying a textual description of a desired property Two distinct descriptions for each property: Abstractive and Detailed

Dataset	Textual Description					
HIA	Human intestinal absorption (HIA)					
	The molecule is positive w.r.t. a property that is defined as 'the ability of the body to be absorbed from the human gastrointestinal system into the bloodstream of the human body'					
Pgp Inhibition	P-glycoprotein Inhibition					
	This molecule is known to inhibit P-glycoprotein, which is an ABC transporter protein involved in intestinal absorption, drug metabolism, and brain penetration, and its inhibition can seriously alter a drug's bioavailability and safety.					
DILI	Inducing liver injury					
	This molecule induces liver injury that is most commonly caused by Amoxicillin clavulanate isoniazid, and nonsteroidal anti-inflammatory drugs.					
VDR	Vitamin D receptor					
	This molecule is active w.r.t. Vitamin D receptor. The best pharmacophore hypothesis contains one hydrogen bond acceptor (A), one hydrogen bond donor (D) and two hydrophobic regions (H).					

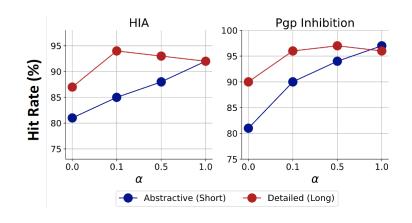
Procedure

- 1. Obtain the representation of textual description of the desired property
- 2. Top 100 molecules that are closest to the textual representation
- 3. Calculate the hit ratio (%)

EXPERIMENTS ZERO-SHOT VIRTUAL SCREENING

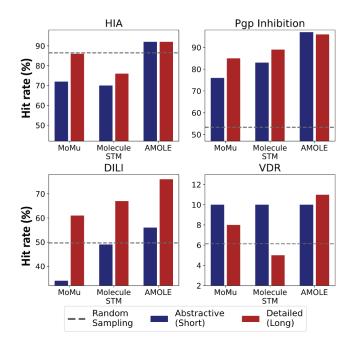
Virtual Screening

Computational technique to search large libraries of compounds quickly to identify the compounds most likely to have desired properties



Task description

Model's proficiency in virtual screening drugs by supplying a textual description of a desired property Two distinct descriptions for each property: Abstractive and Detailed



Observations

AMOLE shows notably robust performance compared to the baseline methods

- → Regardless of whether the description is abstractive or detailed
- → Attribute to Expertise Transfer module, which equips the model with the ability to deduce related information even when only a abstract level of detail is provided

Sensitivity Analysis

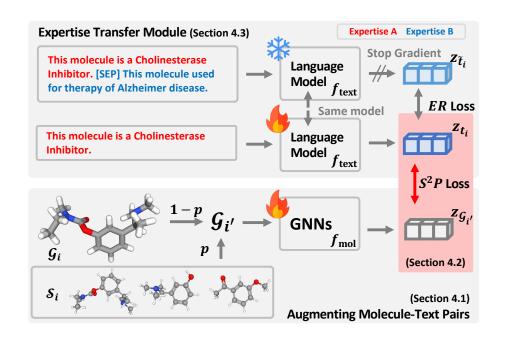
Detailed Prompt: Consistent Model Performance

Abstractive Prompt: Significantly varies according to the choice of α

- \rightarrow As α increases, AMOLE's effectiveness improves
- → Expertise transfer module effectively allows the model to infer related information

CONCLUSION

In this paper, we propose training strategies for molecule language model



Augmenting Molecule-Text Pairs

Share the textual descriptions among molecules with structural resemblances

Structural Similarity Preserving Loss

Preserve molecules' structural similarity in molecule-text joint space

Expertise Transfer Module

Transferring the expertise gained from molecules with extensive descriptions to those with less description

Extensive experiments

- demonstrate the efficacy of AMOLE in grasping the nuances of molecules and their textual descriptions
- Highlight promising applicability for practical use in the drug discovery process

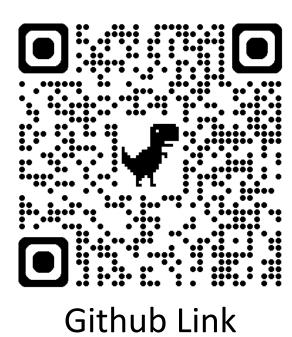
THANK YOU!

[Full Paper] https://arxiv.org/pdf/2407.09043

[Source Code] https://github.com/Namkyeong/AMOLE

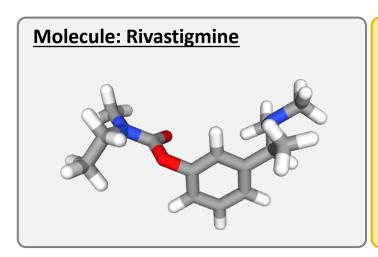
[Author Email] namkyeong96@kaist.ac.kr





APPENDIX

Challenge 2. Different Expertise with Diverse Interests



FDA Pharm Classes

Main Interest

Approved indication of an active moiety that scientifically valid and clinically meaningful

Description for Rivastigmine

This molecule is a Cholinesterase Inhibitor.

The mechanism of action of rivastigmine is as a Cholinesterase Inhibitor.

LiverTox

Main Interest

Injury attributable to prescription and nonprescription medications

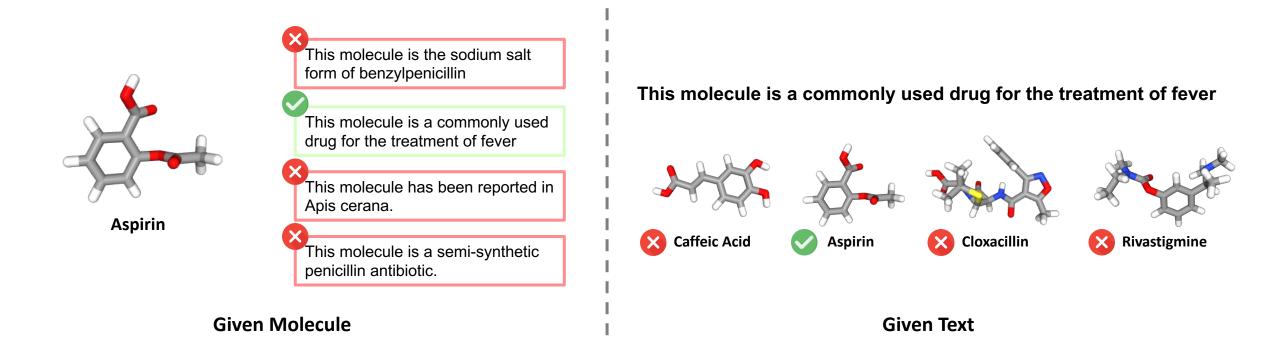
Description for Rivastigmine

This molecule is an oral acetylcholinesterase inhibitor used for therapy of Alzheimer disease.

EXPERIMENTS ZERO-SHOT CROSS-MODAL RETRIEVAL

Task description

Choosing an appropriate description from several alternatives for a specific molecule (Given Molecule) or retrieving the molecule that aligns with particular description (Given Text)



EXPERIMENTS ZERO-SHOT CROSS-MODAL RETRIEVAL

Task description

Choosing an appropriate description from several alternatives for a specific molecule (Given Molecule) or retrieving the molecule that aligns with particular description (Given Text)

	SMILES	Graph	Given Molecule @ 20			Given Text @ 20		
	SWILLS		Descr.	Pharma.	ATC	Descr.	Pharma.	ATC
Single Encode	er							
MolT5	✓	Х	5.06	6.80	6.48	6.66	6.02	6.10
MOITS			(0.44)	(0.28)	(0.25)	(2.02)	(0.57)	(0.09)
BioT5	✓	×	6.47	7.42	7.71	6.02	7.36	6.78
D1013			(0.13)	(0.52)	(0.16)	(0.42)	(0.13)	(0.45)
ZZZDIM	✓	×	42.28	36.84	30.21	45.64	37.93	33.22
KV-PLM			(3.29)	(0.53)	(0.40)	(2.51)	(0.62)	(0.40)
Separate Enco	oder							
MoMu	×	✓	97.39	77.82	51.34	96.84	77.05	47.68
MOMU			(0.19)	(0.54)	(0.37)	(0.17)	(0.28)	(0.34)
MoleculeSTM	✓	×	96.70	77.28	52.36	96.22	75.01	50.01
Molecules I M			(0.35)	(0.94)	(0.29)	(0.29)	(0.49)	(0.40)
M - 1 1 - CTM	x 1	✓	95.87	79.21	52.70	95.82	77.15	48.54
MoleculeSTM			(1.87)	(0.75)	(0.75)	(0.37)	(0.74)	(0.49)
AMOLE	Х	✓	96.48	81.46	54.76	97.20	80.11	51.47
AMOLE			(2.94)	(0.60)	(0.57)	(0.26)	(0.42)	(0.56)

Observations

- MoMu (Random augmentation of molecules) exhibit the lowest performance
- → Random augmentation of molecules can generate the molecules that are chemically invalid
- → Even worse than MoleculeSTM (No augmentation of molecules)
- AMOLE achieves the best results in five out of six datasets
- Performance gap widens with increasingly challenging tasks (Description < Pharm < ATC)