

Large AI Models in Health Informatics: Applications, Challenges, and the Future

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Abstract— Large AI models, or foundation models, are models recently emerging with massive scales both parameter-wise and data-wise, the magnitudes of which often reach beyond billions. Once pretrained, large AI models demonstrate impressive performance in various downstream tasks. A concrete example is the recent debut of ChatGPT, whose capability has compelled people's imagination about the far-reaching influence that large AI models can have and their potential to transform different domains of our life. In health informatics, the advent of large AI models has brought new paradigms for the design of methodologies. The scale of multimodality data in the biomedical and health domain has been ever-expanding especially since the community embraced the era of deep learning, which provides the ground to develop, validate, and advance large AI models for breakthroughs in health-related areas. This article presents an up-to-date comprehensive review of large AI models, from background to their applications. We identify seven key sectors that large AI models are applicable and might have substantial influence, including 1) molecular biology and drug discovery; 2) medical diagnosis and decision-making; 3) medical imaging and vision; 4) medical informatics; 5) medical

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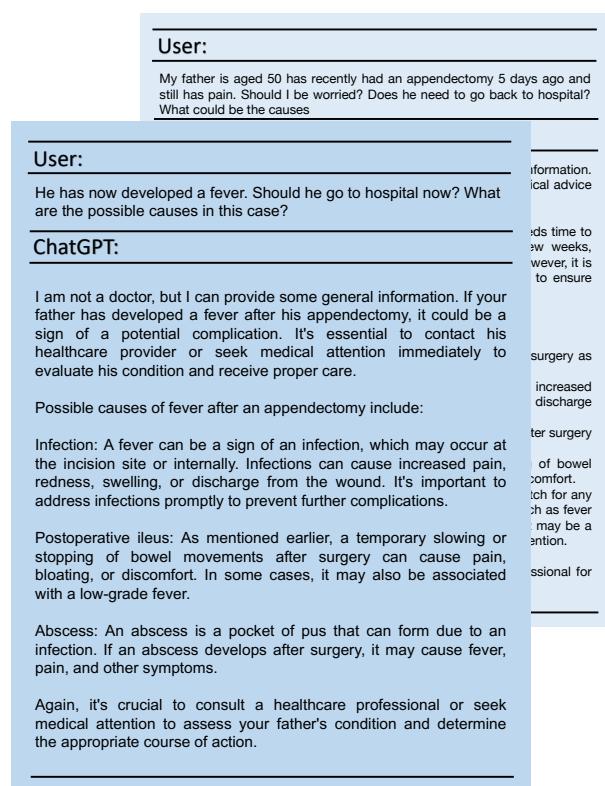


Fig. 1. We used ChatGPT (based on GPT-4) as a medical assistant, and queried it for medical advice. Its capability of recalling prior conversation and being able to contextualise a patient's past medical history shows its promising use in medical areas beyond being a simple symptom checker.

education; 6) public health; and 7) medical robotics. We examine their challenges in health informatics, followed by a critical discussion about potential future directions and pitfalls of large AI models in transforming the field of health informatics.

Index Terms—artificial intelligence; bioinformatics; biomedicine; deep learning; foundation model; health informatics; healthcare

I. INTRODUCTION

THE introduction of ChatGPT [1] has triggered a new wave of development and deployment of Large AI Models (LAMs) recently. Although groundbreaking, the AI

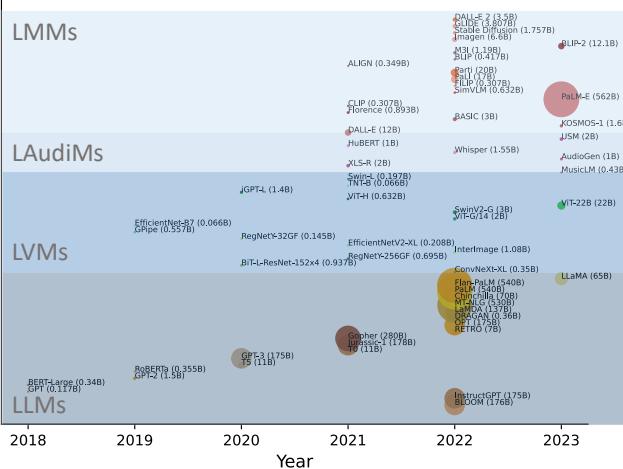


Fig. 2. An overview of general LAMs, presented with their number of parameters and the development timeline. The figure is divided into four sections, from bottom to top, each section showing 1) large language models (LLMs); 2) large vision models (LVMs); 3) large audio models (LAudiMs); and 4) large multi-modal models (LMMS). The sizes of the circles indicate the relative sizes of LAMs.

community has in fact started creating LAMs much earlier, and it was the seminal work that introduced the Transformer model [2] back in 2017 that accelerated the creation of LAMs.

The recent advances in data science and AI algorithms have endowed LAMs with strengthened *generative* and *reasoning* capabilities, significantly distinguishing them from early deep models. As shown in Fig. 1, we conversed with ChatGPT and queried it for medical advice, for which it responded with sound general medical knowledge, memory of prior conversation, and a proper level of prudence.

The LAMs that this article discusses are mainly foundation models [3]. However, this article also provides a retrospective of the recent LAMs that are not necessarily considered foundational at their current stage, but are seminal in advancing the future development of LAMs in the fields of biomedicine and health informatics.

Fig. 2 shows the timeline of the development of LAMs over the past five years. As shown in Fig. 2, the number of parameters of most LAMs reaches beyond billions. The sizes of LAMs developed in the natural language domain predominately outsize those of other domains.

One notable bottleneck of developing supervised medical and clinical AI models is that they require annotated data at scale for training a well-functioning model. However, such annotations have to be conducted by domain experts, which is often expensive and time-consuming. This causes the curation of large-scale medical and clinical data with high-quality annotations to be challenging. However, this might not be a bottleneck for LAMs, as they can leverage self-supervision and reinforcement learning in training, relieving the annotation burden and workload of creating large-scale annotated datasets. With the ever-increasing proliferation of medical internet of things such as pervasive wearable sensors, medical and clinical history such as electronic health records (EHRs), prevalent medical imaging for diagnoses such

as computed-tomography (CT) scans, the growing genomic sequence discovery, and more, the abundance of biomedical, clinical, and health data fosters the development of the next generation of AI models in the field, which are expected to have a large capacity for modeling the complexity and magnitude of health-related data, and actively engaging and assisting clinical and medical decision making.

Despite the homogeneity of the model architecture (current LAMs are primarily based on Transformer [2]), LAMs inherently are strong learners of heterogeneous data, which are common in the settings of biomedicine and healthcare. Fig. 3 shows common biomedical and healthcare data modalities. The multi-modal nature of biomedical and health data provides the natural and promising ground for fostering LAMs in this field.

Albeit inspirational, LAMs still face challenges and limitations, and the rapid rise of LAMs brings new opportunities as well as potential pitfalls. This article aims to provide an up-to-date comprehensive review of the recent development of LAMs, with a particular focus on their impacts on the biomedical and health informatics community. The remainder of this article is organized as follows: Section II describes the background of LAMs in general domains, such as natural language processing (NLP) and computer vision (CV); Section III discusses current progress and possible applications of LAMs in key sectors of health informatics; Section IV discusses challenges, limitations and risks of LAMs; Section V points out some potential future directions of advancing LAMs in health informatics, and Section VI concludes.

II. BACKGROUND OF LARGE AI MODELS

The burgeoning AI community has devoted much effort to developing large AI models (LAMs) in recent years by leveraging the massive influx of data and computational resources. Based on the pretraining data modality, this article categorizes the current LAMs into four types and defines them as follows:

- 1) Large Language Model (LLM): LLMs are pre-trained on language data and applied to language downstream tasks. Language in different settings can have different interpretations, e.g., protein is the language of life, and code is the language of computers.
- 2) Large Vision Model (LVM): LVMs are pre-trained on vision data and applied to vision downstream tasks.
- 3) Large Audio Model (LAudiM): LAudiMs are pre-trained on audio data and applied to audio downstream tasks.
- 4) Large Multi-modal Model (LMM): LMMs are pre-trained on multi-modal data, e.g., language and vision data, and applied to various single- or multi-modal downstream tasks.

This section provides an overview of the background of these four types of LAMs in general domains.

A. Large Language Models

The proposal of the Transformer architecture [2] heralds the start of developing large language models (LLMs) in the field of NLP. Since 2018, following the birth of GPT (Generative Pre-trained Transformer) [4] and BERT (Bidirectional Encoder

Representations from Transformers) [5], the development of LLMs has progressed rapidly.

Broadly speaking, the recent LLMs [6]–[20], have the following three distinct characteristics: 1) parameter-wise, the number of learnable parameters of an LLM can be easily scaled up to billions; 2) data-wise, a large volume of unlabelled data are used to pre-train an LLM, and the amount can often reach millions or billions if not more; 3) paradigm-wise, LLMs are first pre-trained often with non-supervised learning (e.g., masked language modeling [5] and next token prediction [21]), and then fine-tuned and adapted to various downstream tasks in which they are able to demonstrate impressive performance.

Recent advances reveal that LLMs are impressive zero-shot, one-shot, and few-shot learners. They are able to extract, summarize, translate, and generate textual information with only a few or even no prompt samples. Furthermore, LLMs manifest impressive reasoning capability, and this capability has been further strengthened recently with prompt engineering techniques such as Chain-of-Thought prompting [22].

As shown in Fig. 2, LLMs such as PaLM [8] have already contained 540 billion parameters, and there was an upsurge of the number of new LLMs in 2022, including the ChatGPT’s predecessor InstructGPT [14]. Despite the general consensus that scaling up the number of parameters and the amount of data will lead to improved performance, which leads to a dominant trend of developing LLMs often with billions of parameters and even trillions of data tokens (e.g., MT-NLG [10] was pre-trained with 270 billion tokens, and the training data of RETRO [23] had over 5 trillion tokens), there is currently no concerted agreement within the community that if this continuous growth of model and data size is optimal and necessary [6], [9].

To balance the data annotation cost and efficacy, as well as to train an LLM that can better align with human intent, researchers have commonly used reinforcement learning from human feedback (RLHF) [24] to develop LLMs that can exhibit desired behaviors. The core idea of (RLHF) [24] is to use human preference datasets to train a Reward Model (RM), which can predict the reward function and be optimized by RL algorithms (e.g. TRPO [25] or PPO [26]). The framework of RLHF has attracted much attention and become a key component of many LLMs, such as WebGPT [27], InstructGPT [14], Sparrow [28], and ChatGPT [1]. Recently, Susano Pinto *et al.* [29] have also investigated this reward optimization in vision tasks, which can possibly advance the development of future LVMs using RLHF. RLHF is also adopted in the recent LMM, GPT-4 [21].

B. Large Vision Models

It is a common practice in computer vision for better generalization to pre-train a model on a large-scale dataset and then fine-tune it on the target dataset [30]. We highlight that the new paradigm distinguishes from the old one in terms of the scale of the pre-training dataset and the method of pre-training. In recent years, the scale of vision dataset has grown up dramatically from millions to billions to enable larger-scale pretraining. ImageNet-1K [31] is a canonical, manually

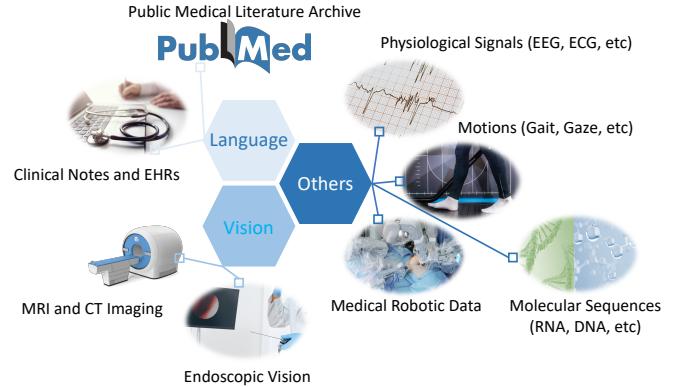


Fig. 3. Common data modalities in health informatics.

curated dataset with 1.28M images for visual pretraining. It is a subset of ImageNet-21K [32] (14M images), which has been so far the largest curated image dataset. Nevertheless, the prohibitive cost of curation severely hindered further scaling. To push the limit of the scale, several orders of magnitude larger datasets were collected with less or even no curation. JFT (300M [33], 3B [34] and 4B [35]) and IG (1B [36], 3.5B [37] and 3.6B [38]) are two most popular families of large datasets dedicated to visual pretraining. With the scale increasing, the quality of annotation is compromised and the availability of datasets is becoming limited.

Both supervised and unsupervised learning are popular pretraining paradigms in visual domain. The existing unsupervised pretraining methods can be categorized into three groups: autoregressive modeling, generative modeling, and contrastive learning. Autoregressive modeling trains the model to autoregressively predict the next pixel conditioned on the preceding ones [39]. Generative modeling trains the model to recover the original image based on its corrupted [40] or masked [41] variants. Contrastive learning trains the model to discriminate similar and/or dissimilar instances [42], [43].

Unlike NLP where transformers dominate, the canonical architecture of LVMs is either based on Convolutional Neural Networks (CNNs) or Vision Transformers (ViTs). They both demonstrate impressive yet close performance on many benchmarks [34], [44].

Since the introduction of AlexNet [45], scaling up CNNs has been a direction for visual recognition. Among many early attempts [46]–[49], ResNet [49], as a milestone of deep CNNs, proposed residual connection enabling top-down, direct, gradient flow to effectively train deep networks. Later, successive works refined the architectural design of ResNet manually [50], [51] and automatically [52], [53] for improved predictive performance. Given these high-performing baseline models, ideas such as scaling laws [54], [55], large-scale pretraining [36], [56] and efficient parallelism [57] were explored to scale them up regarding depth, width and input resolution. Latest models, such as ConvNeXt-XL [44] and InternImage [58], updated ResNets with ViTs components [59] and deformable convolution, respectively. They achieved state-of-the-art accuracy on ImageNet, and InternImage-H (1.08B parameters) is the largest CNN to date.

Vision Transformers have been actively researched recently. Early works ViT [60] and iGPT [39] transferred the transformer architectures [2], [20], respectively, from NLP to perform visual tasks with minimal modification. Several works were then proposed to better adapt NLP transformers to visual data. TNT [61] divided the image patches in ViT into smaller ones for fine-grained processing. Swin Transformer (SwinT) [59] proposed a shifted window mechanism to compute self-attention locally, for efficiency, yet allowing cross-window modeling for effectiveness. Recently, ViT-G/14 [34] and SwinV2-G [62] employed a set of training techniques to successfully scale ViT and SwinT models to 2B and 3B parameters, respectively. Latest, ViT-22B [35] further scaled ViTs to 22B parameters, the largest vision model to date, using an improved training recipe. We highlight that this scale greatly exceeds the current art of CNNs but is still smaller than many recent LLMs.

C. Large Audio Models

Recent advances in acoustics have also been influenced by the development of LAMs. W2v-BERT [63] and Wav2Vec [64] were trained on large amounts of unlabeled audio data, and their resulting representations can be used to enhance acoustic model training. AudioLM [65] employs a hierarchical approach to modeling audio sequences through a series of connected Transformer models. Hidden-Unit BERT (HuBERT) [66] (1B parameters) learns a combined acoustic and language model over the continuous inputs. As a large-scale model for cross-lingual speech representation learning, with up to 2B parameters, XLS-R [67] was trained on a vast corpus of publicly available speech audio (approximately half a million hours) in 128 diverse languages. MusicLM [68], Diffsound [69], and AudioGen [70] can generate high-fidelity music, sound, or audio from text descriptions. Trained on a vast and diverse collection of audio data, Whisper [71] (1.6B parameters) is able to tackle various tasks, such as language identification, speech recognition in multiple languages, and speech translation. Universal Speech Model (USM) [72] (with 2B parameters) demonstrates that leveraging a large unlabeled multilingual dataset for pre-training, followed by fine-tuning on a smaller labeled dataset, can facilitate the identification of under-represented languages. Overall, the application of LAMs to the field of acoustics has led to improvements in speech recognition, cross-lingual speech representation learning, and the generation of high-quality music and sound.

D. Large Multi-modal Models

Current research on large multi-modal models (LMMs) is mainly focused on two modalities: language and vision. Therefore, this section mainly discusses a particular type of LMM, i.e., large language-vision models (LLVMs).

Prior to the era of large models, language-vision data were dedicated to solving a specific task like image captioning [73]–[77] or visual question answering [76], [78]–[80] instead of pretraining large models. For most of them, the scale (thousands or millions) is relatively small and much behind the order of magnitude (billions) typical for pretraining modern large

models. Nevertheless, they usually provide richer, fine-grained annotations such as object localization. These extra signals can be explored to design alternative pretraining objectives [81] for potentially more efficient and/or effective learning. Later works [82]–[85] pushed the scale of public language-vision datasets to tens of millions, whereas the contemporary LLVMs were mostly pretrained on private datasets on the scale of (hundreds of) millions or billions [86]–[90]. To reproduce the result based on these private datasets, LAION-5B [91] was created with 2.3B data entries and, more importantly, available to the public.

Typical LLVMs adopt a dual-stream architecture. Raw input text and images are first processed separately by respective language and vision models to extract features. The features derived from different modalities are then fused into a unified representation through simple concatenation [86]–[88], [92] or an encoder mapping all features into a joint space [93]–[96]. The interaction between the paired text and images is then learned upon this representation to solve cross-modal tasks, such as visual question answering [87] and text-to-image generation [97]. Note that not all multi-modal systems follow this paradigm. For example, Visual ChatGPT [98] develops a prompt manager to bridge the communication between ChatGPT and a set of pre-trained LVMs.

To learn cross-modal representations, works such as CLIP [86], ALIGN [88], BASIC [89], Florence [87] and FILIP [94] were trained to match the extracted vision and language features in a contrastive manner. In contrast, SimVLM [99] and KOSMOS-1 [92] concatenated the features from different modalities into one single sequence and maximized the likelihood of the sequence autoregressively. Alternatively, FLAVA [93], BLIP [95] and M3I [96] pretrained models with multiple objectives. The overall objective can be composed of various learning tasks, like the aforementioned ones, on cross-modal representations [95], [96] or the same learning task on both cross-modal and uni-modal representations [93]. Their result suggested that different learning tasks can complement each other and regularizing uni-modal representations simultaneously can be beneficial. Furthermore, BLIP-2 [100], PaLI [90] and PaLM-E [101] (the largest LLVM to date with 562B parameters) improved the underlying image and language encoders for better performance. A simple strategy was scaling the image and language backbone models up. Latest released GPT-4 [21] extends its predecessor with the capability of processing visual input, and achieves human-level performance on various benchmarks.

Recently, LLVMs for text-to-image generation have also attracted much attention. DALL-E [97] and Parti [102] first learned a mapping from images to discrete tokens and then trained a transformer to autoregressively model the joint distribution over the concatenated image and text tokens. A different line of work combined LLVMs with diffusion models [103] to improve the generation quality. GLIDE [104] adopted CLIP as a classifier to steer the underlying diffusion models. unCLIP [105], a.k.a. DALL-E-2, Imagen [106] and Stable Diffusion [107] employed a pretrained LLM or LLVM to encode text into a sequence of embeddings and conditioned the diffusion process on these embeddings.

III. APPLICATIONS OF LARGE AI MODELS IN HEALTH INFORMATICS

In this section, we identify seven key sectors in which LAMs will have substantial influence and bring new paradigm shifts for tackling the problems and challenges in health informatics. The seven key sectors include 1) molecular biology and drug discovery; 2) medical diagnosis and decision-making; 3) medical imaging and vision; 4) medical informatics; 5) medical education; 6) public health; and 7) medical robotics. We summarize in Fig. 4 those LAMs that are identified in or can be applied to each corresponding sector, and illustrate in Fig. 5 various downstream applications and tasks in health informatics in which LAMs can play an important role.

A. Molecular Biology and Drug Discovery

1) Molecular Biology: Molecular biology studies the roles of biological macromolecules (e.g., DNA, RNA, protein) in life processes and describes various life activities and phenomena including the structure, function, and synthesis of molecules. Although many experimental attempts have been made on this topic over decades [108]–[110], they are still of high cost, long experiment cycle, and high production difficulty. For example, the number of experimentally determined protein structures stored in the protein data bank (PDB) hardly rivals that of known protein sequences. Efficient and accurate computational methods are therefore needed and can be used to accelerate the determination process. Due to the huge number of parameters and learning capacity, LAMs endow us with prospects to approach such a Herculean task. Especially, LLMs' outstanding representation learning ability has been employed to implicitly model the biological properties hidden in large-scale unlabeled data including RNA and protein sequences.

When it comes to the field of protein, starting from amino acid sequences, we can analyze the spatial structure of proteins and furthermore understand their functions, and mutual interactions. AlphaFold2 [111] pioneered leveraging the attention-based Transformer model [2] to predict protein structures. Specifically, they treated structure prediction as a 3D graph inference problem, where the network's inputs are pairwise features between residues, available templates, and multi-sequence alignment (MSA) embeddings. Especially, embeddings extracted from MSA can infer the evolutionary information between aligned sequences. Evoformer and structure modules were proposed to update the input representation and predict the final 3D structure, the whole process of which was recycled several times. Additionally, self-distillation and self-estimation were utilized on unlabeled data to improve prediction accuracy. Also based on MSA, RoseTTAFold [112] devised a 3-track neural network to exploit the interactions between sequence, distance map, and 3D coordinates concurrently. While previous works are well-established for single-chain protein prediction, AlphaFold-Multimer [113] extended AlphaFold to enable precise multi-chain protein complex prediction. Specifically, positional encoding was improved to encode chains, and multi-chain MSAs were paired based on species annotations and target sequence similarity.

Meanwhile, prohibitive computational resources (e.g., AlphaFold2 requires 128 TPU v3 for training) required for model training are barely accessible to many research communities. To reconcile this issue, Cheng *et al.* [114] reduced training and inference time and mitigated the severe memory consumption by scaling the model training on GPUs. HelixFold [115] reimplemented AlphaFold2 in a more efficient way using PaddlePaddle. On top of that, extensive efforts have been put into building open-source platforms and libraries, enabling protein structure prediction software more accessible to the public [116]–[119].

In spite of the groundbreaking endeavors aforementioned works have contributed, to achieving optimal prediction, they still heavily rely on MSAs and templates searched from genetic and structure databases, which is time-consuming. Instead, researchers managed to employ large-scale protein language models (PLMs) to learn co-evolution information in a self-supervised manner. PLMs learned the global relation and long-range dependencies of unaligned and unlabelled protein sequences and the learned representations can be transferred to benefit the downstream tasks (e.g., protein structure prediction). Rives *et al.* [120] proposed ESM-1b transformer (650M) which is trained on UniParc database [121] that comprises 86 billion amino acids. By studying representation space learned under self-supervision, they found the model learned to encode biochemical properties, biological variations, and remote homology of proteins. ProGen (1.2B) [122] utilized a conditional language model to provide controllable generation of protein sequences. By inputting desired tags (e.g., function, organism), ProGen can generate corresponding proteins such as enzymes with good functional activity. Elnaggar *et al.* [123] devised ProtT5-XXL (11B) which was first trained on BFD [124] and then fine-tuned on UniRef50 [125] to predict the secondary structure. ESMfold [126] scaled the number of model parameters up to 15B and observed a significant prediction improvement over AlphaFold2 and RoseTTAFold with considerably higher inference speed when MSAs and templates are unavailable. Similarly, from only the primary sequence input, OmegaFold [127] and RGN2 [128] can outperform MSA-based methods [111], [112], especially when predicting orphan proteins which are characterized by the paucity of homologous structure.

Moving beyond single-chain protein structure prediction, Chen *et al.* [129] utilized PLMs to enhance MSA-pairing and hence improve the accuracy of protein complex prediction. Instead of using single sequence input, MSA transformer [130] takes as input MSAs, which exploits the co-evolutionary signal across the protein family. In so doing, the model is capable of leveraging both covariance information and biological patterns of sequences learned during training. Some studies specialize in pre-trained antibody language models and elucidate that the learned embeddings can reveal antibody-specific information including immunogenicity, binding sites, structure, and function [131], [132]. Similarly, Yang *et al.* [133] applied the large-scale language model on single-cell RNA-seq data to capture mutual interactions between genes and facilitate downstream cell-type tasks (e.g., new cell type discovery).

In the context of RNA structure prediction, the number of

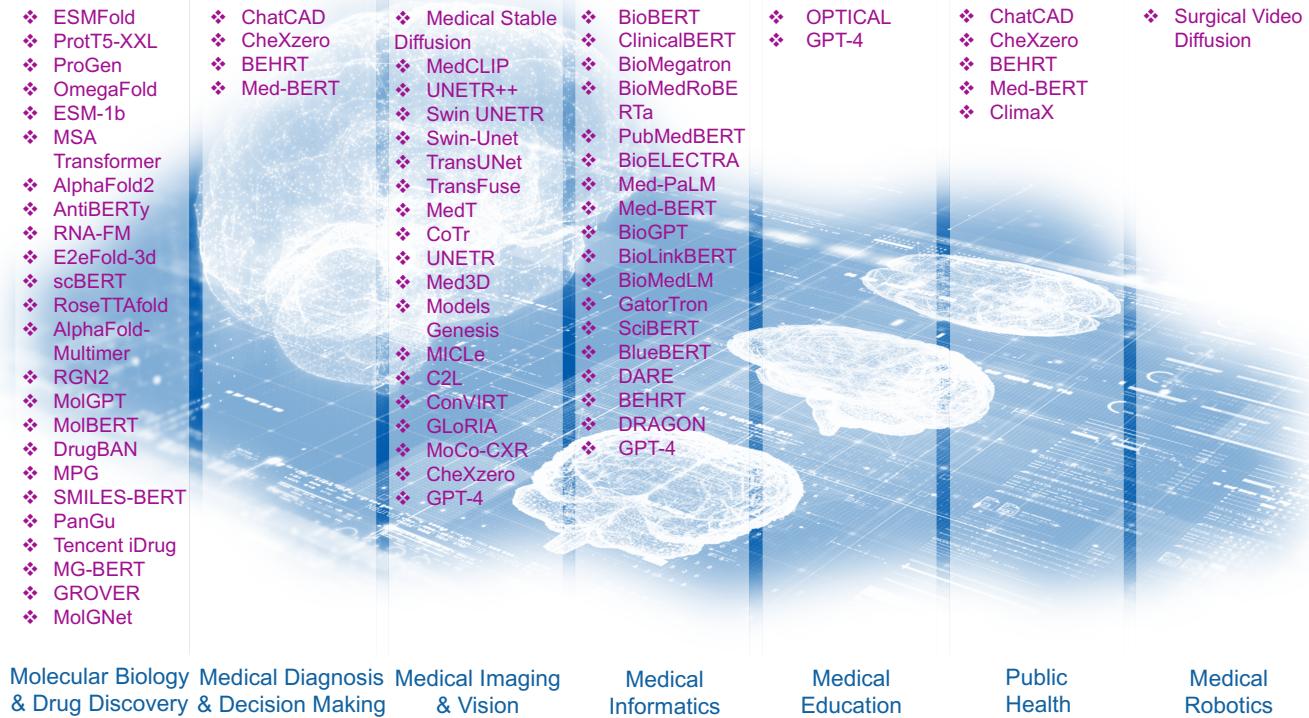


Fig. 4. A summary of current large AI models (LAMs) in biomedical and health informatics.

nonredundant 3D RNA structures stored in PDB is significantly less than that of protein structures, which hinders the accurate and generalizable prediction of RNA structure from sequence information using deep learning. To mitigate the severe unavailability of labeled RNA data, Chen et al. [134] proposed the RNA foundation model (RNA-FM), which learns evolutionary information implicitly from 23 million unlabeled ncRNA sequences [135], to facilitate multiple downstream tasks including RNA secondary structure prediction and 3D closeness prediction. Concretely, the model is enforced to predict the original nucleotide tokens from the masked ones and hence learn useful RNA representations. Furthermore, based on RNA-FM, Shen et al. [136] pioneered predicting 3D RNA structure directly.

Undoubtedly, these models are seminal and have reduced the time and cost of molecule structure prediction by a large margin. Thereby, this raises the question of whether AI can completely replace experimental methods such as Cryo-EM [108]. We deem that it still falls short from that point. Specifically, the advance of LAMs builds upon big data and large model capacity, which means their ability to predict unseen types of data could be problematic. For instance, [137] stated that AlphaFold can barely handle missense mutation on protein structure due to the lack of a corresponding dataset. Furthermore, how can we assess the quality of model prediction for unknown protein structures still remains unclear. In turn, these unverified protein structures cannot be applied to, for example, drug discovery. Therefore, protocols and metrics need to be established to assess their quality and potential impacts. There are mutual and complementary benefits between

LAMs and conventional experimental techniques. LAMs can be re-designed to predict the process of protein folding and reveal their mutual interactions so as to facilitate experimental methods. On the other hand, experimental information, such as some physical properties of molecules, can be leveraged by LAMs to further improve prediction performance, especially when dealing with rare data (e.g., orphan protein).

2) Drug Discovery: Novel drug discovery requires numerous iterative cycles of design, validation, screening, and optimization until a compound is found to be effective at the target site while meeting safety standards for humans [138]. Such complex, costly, and time-consuming flows may be accelerated by using LAMs. Recently, various transformer-based molecular property prediction techniques for drug discovery have been proposed including SMILES-BERT [139], SMILES Transformer [140], MolBERT [141] and AGBT [142] as the most popular representation of molecules is regarded as SMILES strings. Molecular Graphs are another representation of molecular property prediction introduced in GROVER [143]. With over 100 million parameters trained on 10 million unlabelled molecules data, GROVER is capable of acquiring abundant structural and semantic information about molecules for drug discovery. Apart from molecular property prediction, molecule generation is another fundamental task for drug discovery. Both MolGPT [144] and the accelerated Generative Model proposed by Yang et al. [145] used SMILES strings [146] as input for generation tasks. Treating molecular graph as input for molecule generation has been achieved in Molecule Chef [147] and de novo drug design [148]. Moreover, drug-target interaction (DTI) prediction, as an important component of

drug discovery, has also benefited from LAMs [149]–[151]. Previous research has mainly made contributions to drug discovery partially, thus the unified LAMs with whole-process optimization capabilities in drug discovery have started to be developed.

A typical representation learning framework that was trained on more than 700 million unlabeled molecules has been introduced by Chen *et al.* [152], which has the ability to automatically select the best model for a given task. In addition to this, Tencent iDrug [153] has developed an integrated AI platform for multi-functions including protein structure prediction, virtual screening, molecular generation as well as ADMET (absorption, distribution, metabolism, excretion, and toxicity) prediction. MolGNet [154], as a pre-trained model with 53 million parameters, has been integrated into the platform MPG [155] as a base module, which can be leveraged for multiple tasks, including molecular properties prediction, drug-drug interaction, and drug-target interaction. Zhang *et al.* [156] also proposed MG-BERT which was trained on sources from over 700 million unlabeled molecules. This method leveraged the advantages of self-supervised representation learning from LLMs where the local message-passing mechanism of GNN has been incorporated with a BERT model for precise and reliable prediction of drug features. The recent PanGu Drug Model [157], with a novel graph-to-sequence asymmetric structure, was trained on 1.7 billion data to learn the relationship between chemical structures and formula strings, similar to human cognitive transformation. Novel text-based representations instead of SMILES have been proposed so that the model was able to benefit from the structure of LLMs. DrugBAN [158] described the causality of the discoverable drugs and the initial one for accurate prediction and designed a solution to achieve generalization for drug-target pair discovery.

Although LAMs have shown competitive predictions for drug discovery, the current heterogeneous sources of data still lack the capacity to fulfill the emergency and rare requirements for clinical translation. The first yet comprehensive dataset (96 realized exemplar datasets) for AI drug discovery and corresponding benchmarks has been introduced recently [159], which may encourage more joint research from the medicine, chemistry and computer science communities to advance AI-based drug discovery. NVIDIA BioNeMo Service [160] has also recently released a highly integrated cloud service and framework to advance molecular biology and drug discovery.

B. Medical Diagnosis and Decision-making

As research has been carried out to improve the safety and strengthen the factual grounding of LAMs, it is foreseeable that LAMs will play a significant role in medical diagnosis and decision-making. A pilot study conducted by Kung *et al.* [161] revealed that ChatGPT was able to approach the passing performance of the US Medical Licensing Exam (USMLE), demonstrating sound knowledge spectrum and reasonable capabilities in bioethics, clinical reasoning, and medical management.

Medical diagnosis can also be automated and enhanced by LVMs, and other LMMs that incorporate visual modality

to offer more precise localization, recognition, detection, and segmentation of medical images, leading to better interpretation for diagnostic outcomes. For example, CheXzero [162], a zero-shot chest X-ray classifier, has recently demonstrated radiologist-level performance in classifying multiple pathologies which it never saw in its self-supervised learning process. An LMM that jointly learns from medical images and medical corpora can also provide medical diagnosis support by interpreting medical images for the clinicians [163].

Recently, ChatCAD [164], a framework that integrates multiple diagnostic networks with ChatGPT, demonstrated a potential use case of applying LLMs in computer-aided diagnosis (CAD) for medical images. By stratifying the decision-making process with specialized medical networks, and followed by an iteration of prompts based on the outcomes of those networks as the queries to an LLM for medical recommendations, the workflow of ChatCAD offers an insight into the integration of the LLMs that were pre-trained using a massive corpus, with the upstream specialized diagnostic networks for supporting medical diagnosis and decision-making.

Medical LAMs may also potentially produce a more reliable forecast of treatment outcomes and the future development of diseases using their strong reasoning capability. For example, Li *et al.* [165] proposed BEHRT, which is able to predict the most likely disease of a patient in his/her next visit by learning from a large archive of EHRs. Rasmy *et al.* [166] recently proposed Med-BERT, which was able to predict the heart failure of diabetic patients. The accurate prediction ability of these LLMs could benefit precision decision-making, provide clinical decision support, and better treatment recommendations for doctors in the future.

With the ubiquity of internet, medical LAMs can also offer remote diagnosis and medical consultation for people at home, providing people in need with more flexibility of medical consultation and diagnosis.

However, as Wang *et al.* [167] revealed, despite being informative, general LLMs such as ChatGPT actually are not definitive while responding to medical-related questions. This is also aligned with Jeblick *et al.*'s findings [168], which revealed that while asked to simplify radiological reports so that non-experts could also understand, ChatGPT sometimes would produce incorrect statements. Recently, Antaki *et al.* [169] also suggested that while the answers to general medical questions are generally sound, for specialized areas, such as neuro-ophthalmology and ophthalmic pathology, ChatGPT actually cannot produce reliable answers. As previously Gu *et al.* [170] indicated that LLMs pre-trained with medical corpora from scratch can exhibit better performance on medical tasks, for future development, it is promising to design a medical and clinical knowledgeable LAM with large amounts of unlabelled medical data so that the properly trained medical LAM can accurately interpret the current medical status and recall the medical history of a patient to automatically generate diagnostic report [171] for the patient, or generate more clinically sound responses for medical queries. We also envision that future diagnosis of complex diseases may also be conducted or assisted by a panel of clinical LAMs.

C. Medical Imaging and Vision

The adoption of medical imaging and vision techniques has vastly influenced the process of diagnosis and treatment of a patient. The wide use of magnetic resonance imaging (MRI), computed tomography (CT), positron emission tomography (PET), optical coherence tomography (OCT), and ultrasound also has produced a vast amount of multi-modal, multi-source, and multi-organ medical vision data to foster the development of medical vision LAMs.

Med3D [172], a heterogeneous 3D framework that enables pretraining on multi-domain medical vision datasets, shows strong generalization capabilities in downstream tasks, such as lung segmentation and pulmonary nodule classification. Models Genesis [173] has recently been proposed to boost 3D medical imaging with self-supervised learning, and yielded state-of-the-art performance on different 3D downstream applications. Google recently proposed MICLe [174], which utilizes self-supervised learning and shows robustness to distribution shift that is inherent in medical data. Contrastive learning has been a common choice in using self-supervised learning. Zhou et al. [175] proposed C2L, a self-supervised method that contrastively learns from 700k unlabelled radiographs for effective chest X-ray classification. ConvVIRT [176], a domain-agnostic approach that learns medical visual representations with paired diagnostic text, shows its contrastively learned visual representations lead to improved classification and retrieval accuracy. Similarly, GLoRIA [177] further adds the attention mechanism for contrastive learning of medical image and text pairs. MoCo-CXR [178] shows Momentum Contrast [43] pre-trained medical image representations can lead to better accuracy such as more accurate pleural effusion detection in many chest X-ray datasets. Many efforts have also been made to integrate the Transformer-based structure into models designed for medical vision, e.g., TransUNet [179], TransFuse [180], MedT [181], CoTr [182], and UNETR [183]. Swin-Unet [184] uses the hierarchical Swin Transformer [59] to construct a U-Net [185] structure for multi-organ and cardiac segmentation tasks, in which it outperforms the previous state-of-the-arts. Similarly, Swin UNETR [186] also leverages Swin Transformer for encoding features, and has validated the effectiveness of self-supervised pretraining of 3D medical images to tackle 3D medical segmentation challenges. UNETR++ [187] has recently been proposed, which balances the accuracy and efficiency of transformer-based structures for 3D medical segmentation. Sharing a similar paradigm of pre-training with self-supervision or basic architecture such as vision transformer, the above methods lay the foundation for fostering medical vision LAMs.

With the success of generative LAMs such as Stable Diffusion [107] in the general domain, which can generate realistic high-fidelity images with text descriptions, Chambon et al. [188] recently fine-tuned Stable Diffusion on medical data to generate synthetic chest X-ray images based on clinical descriptions. The encouraging generative capability of Stable Diffusion in the medical domain may inspire more future research on using generative LAMs to augment medical data that are conventionally hard to obtain.

MedCLIP [189] has recently been proposed, a contrastive learning framework for decoupled medical images and text, which demonstrated impressive zero-shot medical image classification accuracy. In particular, it yielded over 80% accuracy in detecting Covid-19 infection in a zero-shot setting.

Nevertheless, some compromises are also evident in medical vision LAMs. For example, the currently common practice of training LVMs and LMMs often limits the size of the medical images to shorten the training time and reduce the computational costs. The reduced size inevitably causes information loss, e.g., some small lesions that are critical for accurate recognition might be removed in a compressed downsampled medical image, whereas doctors could examine the original high-resolution image and spot these early-stage tumors. This may cause performance discrepancies between current medical vision LAMs and well-trained doctors.

LAMs are also transforming medical vision beyond clinical settings. For example, the recent GPT-4 [21] has been integrated to empower visual assistance, providing image-to-text interpretation for people with visual impairment [190].

D. Medical Informatics

In medical informatics, it has been a topic of long-standing interest to leverage large-scale medical information and signals to create AI models that can recognize, summarize, and generate medical and clinical content.

Over the past few years, with advances in the development of LLMs [5], [8], [17], and the abundance of EHRs as well as public medical text outlets such as PubMed¹, research has been carried out to design and propose BioLLMs. Since the introduction of BioBERT [191], a seminal BioLLM which outperformed previous state-of-the-art on various biomedical text mining tasks such as biomedical named entity recognition, many different BioLLMs that stem from their general LLM counterparts have been proposed, including Clinical-BERT [192], BioMegatron [193], BioMedRoBERTa [194], Med-BERT [195], BioELECTRA [196], PubMedBERT [170], BioLinkBERT [197], BioGPT [198], and Med-PaLM [199].

The recent GatorTron [200] model (8.9 billion parameters) pre-trained with de-identified clinical text (82 billion words) revealed that scaling up the size of clinical LLMs leads to improvements on different medical language tasks, and the improvements are more substantial for complex ones, such as medical question answering and inference. Previously, the PubMedBERT work [170] also revealed that instead of conducting continual pretraining from the checkpoint of an LLM pre-trained on the general-domain corpora, it is more favorable to conduct domain-specific pretraining from scratch (i.e., pretraining LLMs with biomedical corpora from scratch), which leads to remarkable improvements on medical language tasks. As LLMs start to show emergent abilities [201] with their size scaled up increasingly, Agrawal et al. [202] revealed that recent LLMs such as InstructGPT [14] and GPT-3 [17] can well extract clinical information in a few-shot setting despite being not explicitly trained for the clinical domain. Med-PaLM [199], a BioLLM with 540 billion parameters

¹<https://pubmed.ncbi.nlm.nih.gov/>

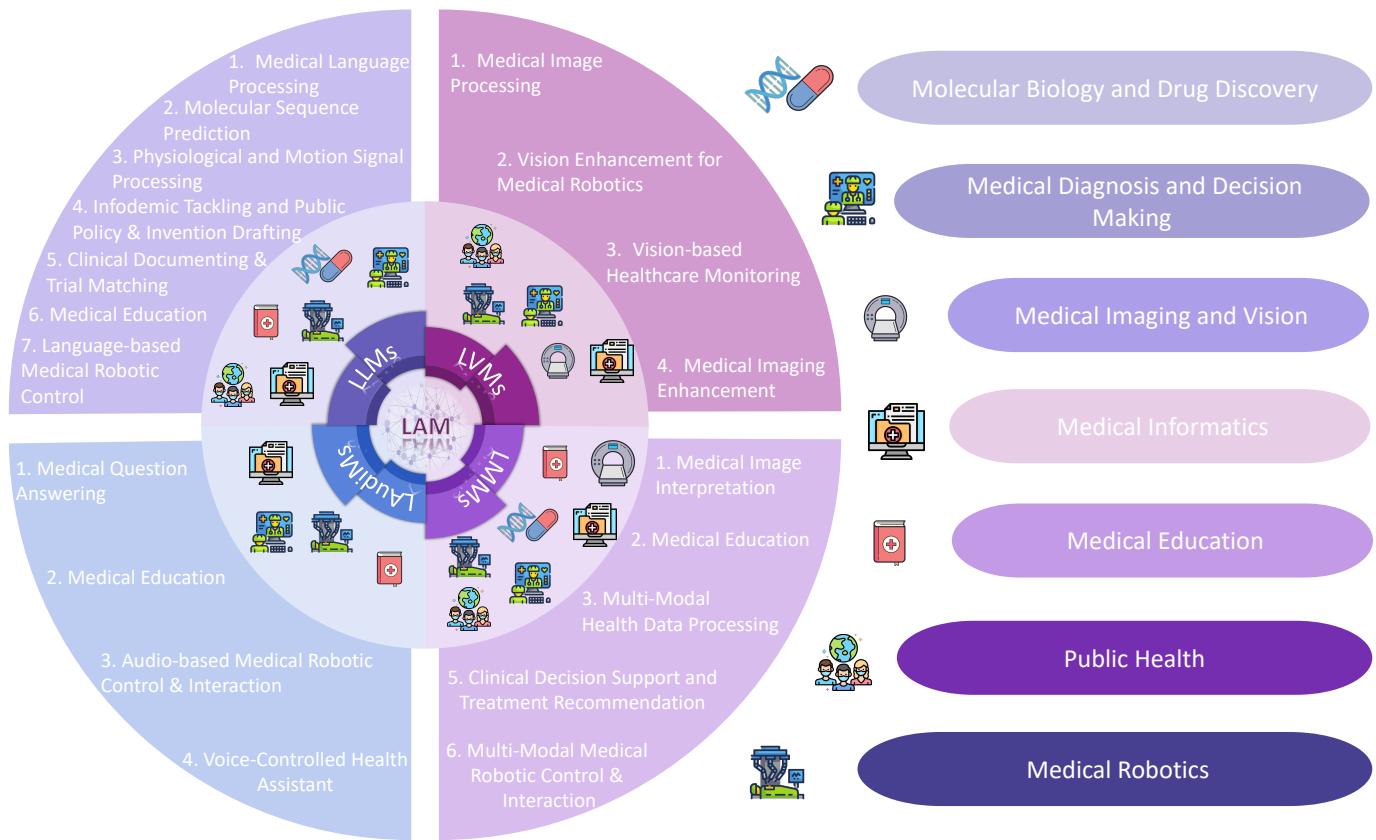


Fig. 5. Overview of the downstream applications and tasks of different large AI models (LAMs) in biomedical and health informatics.

generated by applying instruction prompt tuning on Flan-PaLM [7] (which exhibited state-of-the-art accuracy on Multi-MedQA [199]), demonstrated the ability to answer consumer medical questions that are comparable to the performance of clinicians. As prompt engineering has become a key technique for investigating and improving LLMs, Liévin *et al.* [203] have also applied various prompt engineering on recent GPT-3.5 series such as InstructGPT [14] to understand their abilities on medical question answering, and their results suggested that increasing Chain-of-Thoughts (CoTs) [22] per question can deliver better and more interpretable medical question responses.

The impressive performance of BioLLMs on medical language tasks shows their potential to be used to assist clinicians to process, interpret, and analyze clinical and medical data more efficiently, and also to vastly reduce the time that clinicians have to spend on documenting EHRs. BioLLMs can also assist the writing of prior authorizations for insurance purposes, accelerating treatment authorizations [204]. On the patient side, the zero-, one-, and few-shot learning capability of LLMs may enable them to provide personalized medical assistance based on the medical history of each individual patient. In addition, LLMs may also find them applicable in clinical trial matching. Based on candidates' demographics and medical history, a BioLLM may effectively generate eligible matching, which accelerates clinical trial recruitment and initiation. Patel and Lam [205] recently shed insight on the use of ChatGPT [1] to generate discharge summaries, which

could potentially relieve doctors from laborious writing and improve their clinical productivity.

E. Medical Education

It is likely that future medical education will also be influenced by LAMs, as research continues to strengthen their scientific grounding, sound reasoning, and creative generation.

The generative capability of ChatGPT may augment medical student learning and help them gain additional insights from AI-generated content as recently pointed out in [161]. A LAM with wide knowledge and social compliance can act as a companion learning assistant, answering medical questions promptly and explaining intricate terms and practices in simple sentences. For example, the recent GPT-4 model [21] can act as a Socratic tutor, leading a student step-by-step to find the answers by themselves, which is an important step towards practical adoption of LAMs in education as they can be steered to teach/assist students in a desired manner. The OPTICAL model proposed by Shue *et al.* [206] recently shows the feasibility of using LLMs to guide beginners to analyze bioinformatics data. The sentence paraphrasing abilities of LLMs such as ChatGPT may also help students with dyslexia [207] in their learning. However, concerns about the illegitimate uses of LAMs such as plagiarism are practical and should raise awareness. A pilot study conducted by Mitchell *et al.* [208] proposed a zero-shot detector named DetectGPT, which is able to distinguish human-written or LLM-generated text. This attempt may lead to more research into developing

reliable tools for verifying the content source and potentially countering the side effects of LAMs in education.

For medical education givers, LAMs can potentially create novel teaching and exam contents, and diversify the teaching formats and their presentation. Based on the history of medical study and outcomes, LAMs may also help design personalized and precise course materials for students in need. In addition, LAMs may also help deliver remote medical education, providing engaging learning experiences and opportunities for students living in resource-poor areas or from underprivileged families. In addition, LAMs can also serve as a grading and scoring system in medical education, e.g., grading the surgical skill of a surgeon operating a surgical robot.

In medical and clinical training such as nurse training, one can imagine a domain-knowledgeable LAM can act as an assistant or a trainer to supervise the training. For certain frequent and tedious routine medical training courses, human trainers tend to become less productive as training keeps repeating, and the quality of training delivery also varies among different human trainers. With a wide knowledge spectrum and responsive interactions, training delivered by a LAM can potentially be more engaging, productive, and the standard of training can be maintained as equal and of high quality.

F. Public Health

As the American epidemiologist Larry Brilliant said “*outbreaks are inevitable, but pandemics are optional*”, with the world gradually returning to normal after the Covid-19 pandemic, if there is one thing that the world has to reflect on, it is how we become prepared to prevent the next pandemic.

Based on past public policy and interventions to contain the spread of infectious diseases and the specific current situation, LLMs may help epidemiologists and policymakers to draft targeted public policies and recommend effective interventions. LLMs and other LAMs are also likely to be used to monitor, track, forecast, and analyze the progress of new outbreaks. As discussed in Section III-A, as LAMs have been actively researched in molecular biology and for drug discovery, they can potentially be used for the design of vaccine and drugs to treat and save people from new outbreaks. Furthermore, another potential usage of LAMs, as pointed out in [209], can be in precision triage and diagnosis, in which they could play a pivotal role as medical care workforce might be stretched when encountering a new outbreak. An important aspect of tackling an outbreak/epidemic is to handle misinformation. The study conducted by Chen et al. [210] revealed that from 21 January 2020 to 21 March 2020, Twitter produced over 72 million COVID-19-related tweets. If unverified media information proliferates at scale, it inevitably causes complications in tackling the outbreak. Although LAMs could be double-edged swords when it comes to misinformation, with gradually complete regulations and strengthened factual grounding of LAMs, they can be used to effectively identify misinformation and tackle public health infodemic.

Beyond their promising usage in preventing pandemics, LAMs are also an effective tool for solving other public health challenges, for example, providing large-scale dietary monitoring and assessment [211], [212] to tackle the growing *double*

burden of malnutrition [213] in many low- and middle-income countries, and demystifying and proposing new solutions for mental illnesses that are common in populations. Researchers have recently proposed ClimaX [214], a foundation model for forecasting weather and climate change. With its remarkable forecasting capability, LAMs such as ClimaX can advance our understanding of climate change and provide solutions to better address the global health issues posed by climate change.

G. Medical Robotics

From surgical robots that allow surgeons to perform precision minimally invasive surgery, to wearable robots that assist patients with health monitoring and rehabilitation, medical robotics has seen rapid growth and advances over the past few decades. Although the use of LAMs in medical robotics is nascent, it is foreseeable that they will have a significant impact on improving the vision, interaction, and autonomy of medical robotics at large.

1) Enhance Vision: The integration of LAMs into surgical robots has the potential to enhance both the 2D and 3D vision of these systems in surgery, e.g., improved segmentation of anatomical structures, and better 3D navigation to the targeted surgical site in neuro- and brain surgery [215]. In addition to online vision enhancement, LAMs can also potentially improve the offline workflow analysis of robotic surgery, and more accurately and objectively predict the likelihood of complications or successful outcomes, which help surgeons better plan and execute surgeries in the future. Furthermore, with their strong generative capabilities, LAMs can be used to generate and simulate surgical procedures, allowing surgeons to practice and refine their techniques before operating on a patient with real surgical robots. Beyond surgical robots, the perception of many companion and assistive robots can also be enhanced by LAMs, e.g., enabling a companion robot to better understand the patient’s emotion through accurate recognition of facial expressions [216], and enabling an assistive robot to offer safer and more natural blind navigation for visually impaired people [217].

2) Improve Interaction: LAMs may significantly improve the interactive capabilities of many rehabilitation and companion robots, by enabling them to recognize human emotions, gestures [218], and speech, and respond to high-level human language commands. This will be easier for patients undergoing rehabilitation to communicate and engage with their robotic assistants, improving their overall recovery experience. More intelligent LAMs may also better understand human intentions and create more human-like companionship, which could improve the overall quality of care for the elderly [219].

3) Increase Autonomy: In general robotic domains, Transformer architecture and associated advances in LAMs such as GPT [17] and BERT [5] have been applied to increase robotic autonomy [220]. Some recent research explores the application of LAM representation capabilities to robotics. For example, R3M [221] shows that visual representations derived from a large set of pretraining egocentric video data (Ego4D [222]) through video-language alignment can facilitate the learning

of skills for robotic manipulation tasks. MimicPlay [223] demonstrates that human-play data can enable data-efficient learning and help in learning latent plans. LLMs contain a wealth of semantic knowledge about the world [224], which in principle might be useful to robots aiming to act upon high-level, temporally extended instructions expressed in natural language. ChatGPT recently has been used to generate execution codes for robots based on natural language instructions, with an aim to transform robotic pipelines from the current *engineer in the loop* to the potential *user in the loop*, which can use high-level language commands to control and carry out robotic tasks [225]. With scaled-up capability, much work has proposed to use only one single LAM to conduct a diverse range of robotic tasks, demonstrating impressive adaptability and generalization skills [101], [226]–[231]. The progress made by these LAMs in general-purpose robotics may inspire the development of medical robotics towards higher autonomy.

Surgical robots with high levels of autonomy are capable to perform surgical tasks with little or even without human supervision, reducing the cognitive load of a surgeon during the operation [232]. To attain a high level of autonomy, a surgical robot must exhibit the ability to proficiently execute various surgical procedures while adapting to different operating environments [233]. Currently, there is an evident trend in medical research to pursue the augmentation of surgical robot autonomy with AI models [234], [235], [236].

However, most of the current research on surgical robot autonomy remains in level two, which only focuses on specific tasks instead of the whole procedure [237], [238]. The current trend in surgical robotics is to provide surgical strategies with preoperative data and adjust instrument movements based on real-time sensor feedback [237]. LAMs may help robots consistently maintain their performance while facing environmental changes or unexpected events with their strong adaptability and generalization capabilities. For example, in some abdominal surgeries, a LAM-based system can potentially better detect human respiratory motion, and adjust the instrument trajectory to avoid collision with organs, thereby minimizing the potential harm to patients. Additionally, this system may be utilized to transfer surgical proficiency across various surgical procedures, such as appendectomy and cholecystectomy, among others, with the ultimate objective of improving the overall surgical outcomes.

IV. CHALLENGES, LIMITATIONS, AND RISKS

Despite the promising outcome of LAMs, there remain many challenges and potential risks in developing and deploying LAMs in biomedical, clinical, and healthcare applications.

Compared to datasets used to pre-train LAMs in the general domain, as shown in Table I some current large datasets in health informatics are still relatively small. This is either because the annotation efforts are onerous, which hence restricts the scale of the labeled dataset, or because that particular type of data is in fact hard to obtain. For the former, as LAMs can use self-supervision to leverage unlabelled data, it may not be a hurdle for developing and advancing LAMs in the field, whereas for the latter case, it may not be intractable as

well, as LAMs show impressive zero- and few-shot learning capabilities, but more research needs to be conducted to verify the zero- and few-shot learning capabilities of LAMs in the medical and clinical settings.

Although the volume of unlabelled medical and health data is large, aggregating them and then curating datasets to pre-train LAMs still require proper handling of the underlying ethical, legal, safety, and privacy issues. In biomedical and healthcare scenarios, the robustness and fairness of LAMs are critical. Although the data-driven paradigm underpins the rapid invention of LAMs, biomedical and healthcare data inherently exhibit inequality. Current datasets for developing LAMs are biased against resource-poor countries and rare diseases, but the development will ultimately benefit them the most. This paradox poses challenges and requires continuous monitoring and efforts to ensure future medical LAMs will not develop biases (a recent study [269] revealed that ChatGPT can generate toxic, hazardous, biased contents). More importantly, LAMs such as ChatGPT are also vulnerable to adversarial attacks [167]. Robustifying LAMs against adversarial attacks requires even more data [270]. These, if not handled cautiously, pose potential risks such as reducing the credibility of LAMs in advising medical and clinical practitioners and the general public, and even more significant privacy issues such as a deployed LAM repeating back training data that potentially expose patient details.

For many researchers and institutions, the expensive computing infrastructure for developing and deploying LAMs is a practical major roadblock. Therefore, to create a sustainable ecosystem that fosters and docks future LAMs, which could benefit the medical and healthcare society at large, joint and collective efforts from researchers and policymakers are needed. Regulations for applying LAMs in medical and clinical settings should also be implemented, e.g., what level of autonomy should be endowed to LAMs to assist robotic surgery [232] and the accountability of the potential failures from medical LAMs.

The development of medical LAMs also faces transparency challenges. In the general domain, it is not uncommon to see many large-scale datasets that were used to pretrain LAMs remain closed source. The LAMs themselves are also restricted to limited access to outside researchers. These are expected to be more common in biomedical, clinical, and health domains, as the data are often expensive and under stricter scrutiny. Without transparency and more open-source efforts, the development of medical LAMs may only be a carnival and monopoly of a paucity of big companies and institutions.

V. FUTURE DIRECTIONS

As research continues to progress and advance the development of LAMs as well as further our understanding of their strengths and weaknesses, in this section, we discuss some potential research directions of LAMs and their future outlook in the field of biomedical and health informatics.

Currently, a large portion of medical LAM research is focused on language and vision. Other pervasive modalities

TABLE I
LARGE BIOMEDICAL, CLINICAL, AND HEALTH DATASETS

Dataset Name	Details	Data Modality	Task
PubMed Abstract [239]	a large archive of abstracts of biomedical literature	single	medical language processing
PubMed Central [240]	a large archive of full-text biomedical and life sciences literature	single	medical language processing
MIMIC-III [241]	53,423 distinct hospital admissions with detailed EHRs such as medications and physiologic signals	multiple	medical language processing
Clinical Practice Research Datalink [242]	11.3 million patients covering data on demographics, symptoms, diagnoses, therapies, etc	multiple	medical language processing
MIMIC-CXR [243]	65,379 patients, containing 377,110 chest X-ray images, and 227,835 radiology reports	multiple	medical language processing, medical vision
CheXpert [244]	65,240 patients, containing 224,316 chest radiographs	single	medical vision
PadChest [245]	67,000 patients, containing over 160,000 chest X-ray images	single	medical vision
MURA [246]	12,173 patients, containing over 40,561 multi-view radiographic images	single	medical vision
NIH Chest X-Rays [247]	30,000 patients, over 112,000 Chest X-ray images	single	medical vision
BRAX [248]	19,351 patients, 24,959 case studies, 40,967 Chest X-ray images with 14 radiological findings	multiple	medical vision
COVIDx [249]	13,870 patients containing COVID-19 positive cases, 13,975 CXR images	single	medical vision
Deep Lesion [250]	4,000 patients, 32,000 lesions CT images	single	medical vision
MedPix [251]	12,000 patients, 59,000 indexed and curated images	multiple	medical vision
TCIA [252]	an open-source archive containing millions of cancer images	multiple	medical vision
OCTA 500 [253]	500 patients, over 361,600 retinal scans	multiple	medical vision
Medical Segmentation Decathlon [254]	10 organs, 2,642 3D & 4D data of MRI, MR and CT modalities	multiple	medical vision
MedMNIST v2 [255]	708,069 2D images and 10,214 3D images	multiple	medical vision
Isic Archive [256]	23,000 multi-source dermatoscopic images	multiple	medical vision
UniParc [121]	250 million protein sequences, 86 billion amino acids	single	protein representation learning
UniProtKB [257]	an integrated database that contains various protein information with annotations	multiple	protein representation learning
UniRef100 [125]	200 million protein sequences, 80 billion amino acids	single	protein representation learning
UniRef90 [125]	similar sequences from UniRef100 clustered at 90% identity level	single	protein representation learning
UniRef50 [125]	similar sequences from UniRef100 clustered at 50% identity level	single	protein representation learning
Pfam [258]	18,259 protein families and 635 clans	single	protein representation learning
Big Fantastic Database [124]	2.1 billion protein sequences, 393 billion amino acids	single	protein representation learning
Observed Antibody Space [259]	558 million antibody sequences	single	antibody representation learning
PanglaoDB [260]	74 tissues with 1,126,580 cells	single	scRNA-seq representation learning
RNAcentral [135]	18 million ncRNA sequences and 13 million secondary (2D) structure	multiple	RNA representation learning
ChEMBL [261]	1,961,462 different compounds and 13,382 targets	single	drug discovery
ZINC20 [262]	1.4 billion compounds from 310 catalogs from 150 companies	single	drug discovery
DrugSpace2 [263]	12,443,292 different compounds	single	drug discovery
UniChem Database [264]	over 22 million compounds from 40 different datasets	single	drug discovery
PubChem [265]	114 million compounds, 302 million substances, 302 million bioactivities	multiple	drug discovery
BindingDB Dataset [266]	35 million literature, 42 million patents	multiple	drug discovery
DrugOOD Database [159]	contains 2,656,564 data of 8,982 proteins and 1,144,641 molecules	multiple	drug discovery
CMNPD [267]	a consortium of 96 datasets for AI drug discovery	multiple	drug discovery
Uni-Mol [268]	32,000 compounds, 3,400 organisms, 2,700 targets, 72,000 bioactivities	multiple	drug discovery
	19 million molecular, 210 million 3D molecular conformations	multiple	drug discovery
	3.2 million protein pockets	multiple	drug discovery

such as many tabular and time-series data including EEG and ECG are less explored. Speech is also an important avenue to explore, e.g., developing a medical LAudiM that can summarize recorded conversations into medical notes, which can save huge amounts of time in outpatient clinics. It is also worth future investigation on a wider range of medical and healthcare data modalities to potentially create a holistic LAM that can serve as the foundation for tackling various downstream tasks in this field.

Compared to data from the general domain, massive amounts can be aggregated to a central repository for LAM development. In biomedical, clinical, and health domains, data are often decentralized, and possessed by individual institutions and hospitals due to privacy and ethical issues. In light of this, future work can investigate the use of blockchain technologies and federated learning [271] to decentralize the development and deployment of LAMs for healthcare-related applications.

Inference budget becomes practical and more important for end users such as hospitals when it comes to the deployment of medical LAMs. Touvron et al. [6] recently suggested that it is possible to train smaller LAMs that retain competitive accuracy. Another potential way worth investigating is to use knowledge distillation [272] to transfer the capabilities of LAMs to smaller models.

Apart from accuracy, defining explicit evaluation metrics that can better measure the social and ethical compliance, and scientific and factual grounding of LAMs can advance and accelerate their practical applications in medical and health domains. For example, a clear passing threshold can be defined, and if LAMs are able to exceed the passing threshold, their strong reasoning and generative capabilities can potentially be leveraged to generate more medical data to either augment model training or further the understanding of, e.g., a particular disease.

The recent GeneTuring test [273] revealed that it is not uncommon for LLMs exhibiting AI hallucinations and the unawareness of its incapacity. RLHF might be a solution to strengthen the medical and factual grounding of biomedical and health LAMs. However, the current optimal policy of RLHF may lack security evaluation, which can not be directly applied to clinical experiments [274]. The use of RLHF also requires professional medical experts to curate the human preference dataset. For future work in this direction, joint efforts from clinical and RL experts are needed.

Prompt engineering which involves crafting effective prompts or inputs to guide a LAM's behavior has emerged as a key research direction for advancing LAMs. Similarly, prompt engineering in health informatics should involve the use of domain-specific prompts that reflect the relevant clinical

or medical knowledge. These prompts should be carefully crafted to reflect the nuances of the healthcare domain, and should be designed to guide a LAM toward accurate and clinically relevant predictions. Multi-modal prompts can be used to combine multiple sources of data, such as medical images and patient records, to guide a LAM's behavior. By using domain-specific, dataset-specific, interactive, and multi-modal prompts, healthcare providers can develop LAMs that are optimized for healthcare applications.

As discussed in Section IV, current LAMs still show different levels of vulnerability to adversarial attacks, how to increase their robustness and increase the interpretability and explainability [275] of their outputs remains an open question for future research.

VI. CONCLUSIONS

As opportunities always come with risks, the development and deployment of large AI models in biomedical and healthcare settings require more prudence. Joint efforts from domain experts and feedback from users are critical for the safe and ethical function of large AI models. Given the trajectories of AI model development and applications, large foundation AI models will soon have a significant influence on the field of biomedical and health informatics at large. With their wide knowledge spectrum and strengthened reasoning and generative capability, we conjecture that large medical AI models will assist and enable the delivery of precision healthcare, advance future medical discovery, provide innovative medical education, create productive clinical workflow, and many more beyond in this thriving field.

REFERENCES

- [1] OpenAI, “Chatgpt: Optimizing language models for dialogue,” 2022. [Online]. Available: <https://openai.com/blog/chatgpt/>
- [2] A. Vaswani, N. Shazeer, N. Parmar, J. Uszkoreit, L. Jones, A. N. Gomez, Ł. Kaiser, and I. Polosukhin, “Attention is all you need,” *Advances in neural information processing systems*, vol. 30, 2017.
- [3] R. Bommasani, D. A. Hudson, E. Adeli, R. Altman, S. Arora, S. von Arx, M. S. Bernstein, J. Bohg, A. Bosselut, E. Brunskill, E. Brynjolfsson, S. Buch, D. Card, R. Castellon, N. Chatterji, A. Chen, K. Creel, J. Q. Davis, D. Demszky, C. Donahue, M. Doumbouya, E. Durmus, S. Ermon, J. Etchemendy, K. Ethayarajah, L. Fei-Fei, C. Finn, T. Gale, L. Gillespie, K. Goel, N. Goodman, S. Grossman, N. Guha, T. Hashimoto, P. Henderson, J. Hewitt, D. E. Ho, J. Hong, K. Hsu, J. Huang, T. Icard, S. Jain, D. Jurafsky, P. Kalluri, S. Karamcheti, G. Keeling, F. Khani, O. Khattab, P. W. Koh, M. Krass, R. Krishna, R. Kuditipudi, A. Kumar, F. Ladhak, M. Lee, T. Lee, J. Leskovec, I. Levent, X. L. Li, X. Li, T. Ma, A. Malik, C. D. Manning, S. Mirchandani, E. Mitchell, Z. Munyikwa, S. Nair, A. Narayan, D. Narayanan, B. Newman, A. Nie, J. C. Niebles, H. Nilforoshan, J. Nyarko, G. Ogut, L. Orr, I. Papadimitriou, J. S. Park, C. Piech, E. Portelance, C. Potts, A. Raghunathan, R. Reich, H. Ren, F. Rong, Y. Roohani, C. Ruiz, J. Ryan, C. Ré, D. Sadigh, S. Sagawa, K. Santhanam, A. Shih, K. Srinivasan, A. Tamkin, R. Taori, A. W. Thomas, F. Tramèr, R. E. Wang, W. Wang, B. Wu, J. Wu, Y. Wu, S. M. Xie, M. Yasunaga, J. You, M. Zaharia, M. Zhang, T. Zhang, X. Zhang, Y. Zhang, L. Zheng, K. Zhou, and P. Liang, “On the Opportunities and Risks of Foundation Models,” Jul. 2022, arXiv:2108.07258 [cs]. [Online]. Available: <http://arxiv.org/abs/2108.07258>
- [4] A. Radford, K. Narasimhan, T. Salimans, I. Sutskever *et al.*, “Improving language understanding by generative pre-training,” 2018.
- [5] J. Devlin, M.-W. Chang, K. Lee, and K. Toutanova, “Bert: Pre-training of deep bidirectional transformers for language understanding,” *arXiv preprint arXiv:1810.04805*, 2018.
- [6] H. Touvron, T. Lavril, G. Izacard, X. Martinet, M.-A. Lachaux, T. Lacroix, B. Rozière, N. Goyal, E. Hambro, F. Azhar *et al.*, “Llama: Open and efficient foundation language models,” *arXiv preprint arXiv:2302.13971*, 2023.
- [7] H. W. Chung, L. Hou, S. Longpre, B. Zoph, Y. Tay, W. Fedus, E. Li, X. Wang, M. Dehghani, S. Brahma *et al.*, “Scaling instruction-finetuned language models,” *arXiv preprint arXiv:2210.11416*, 2022.
- [8] A. Chowdhery, S. Narang, J. Devlin, M. Bosma, G. Mishra, A. Roberts, P. Barham, H. W. Chung, C. Sutton, S. Gehrmann *et al.*, “Palm: Scaling language modeling with pathways,” *arXiv preprint arXiv:2204.02311*, 2022.
- [9] J. Hoffmann, S. Borgeaud, A. Mensch, E. Buchatskaya, T. Cai, E. Rutherford, D. d. L. Casas, L. A. Hendricks, J. Welbl, A. Clark *et al.*, “Training compute-optimal large language models,” *arXiv preprint arXiv:2203.15556*, 2022.
- [10] S. Smith, M. Patwary, B. Norick, P. LeGresley, S. Rajbhandari, J. Jasper, Z. Liu, S. Prabhumoye, G. Zerveas, V. Korthikanti *et al.*, “Using deepspeed and megatron to train megatron-turing nlg 530b, a large-scale generative language model,” *arXiv preprint arXiv:2201.11990*, 2022.
- [11] T. L. Scao, A. Fan, C. Akiki, E. Pavlick, S. Ilić, D. Hesslow, R. Castagné, A. S. Luccioni, F. Yvon, M. Gallé *et al.*, “Bloom: A 176b-parameter open-access multilingual language model,” *arXiv preprint arXiv:2211.05100*, 2022.
- [12] R. Thoppilan, D. De Freitas, J. Hall, N. Shazeer, A. Kulshreshtha, H.-T. Cheng, A. Jin, T. Bos, L. Baker, Y. Du *et al.*, “Lamda: Language models for dialog applications,” *arXiv preprint arXiv:2201.08239*, 2022.
- [13] S. Zhang, S. Roller, N. Goyal, M. Artetxe, M. Chen, S. Chen, C. Dewan, M. Diab, X. Li, X. V. Lin *et al.*, “Opt: Open pre-trained transformer language models,” *arXiv preprint arXiv:2205.01068*, 2022.
- [14] L. Ouyang, J. Wu, X. Jiang, D. Almeida, C. L. Wainwright, P. Mishkin, C. Zhang, S. Agarwal, K. Slama, A. Ray *et al.*, “Training language models to follow instructions with human feedback,” *arXiv preprint arXiv:2203.02155*, 2022.
- [15] J. W. Rae, S. Borgeaud, T. Cai, K. Millican, J. Hoffmann, F. Song, J. Aslanides, S. Henderson, R. Ring, S. Young *et al.*, “Scaling language models: Methods, analysis & insights from training gopher,” *arXiv preprint arXiv:2112.11446*, 2021.
- [16] V. Sanh, A. Webson, C. Raffel, S. H. Bach, L. Sutawika, Z. Alyafeai, A. Chaffin, A. Stiegler, T. L. Scao, A. Raja *et al.*, “Multitask prompted training enables zero-shot task generalization,” *arXiv preprint arXiv:2110.08207*, 2021.
- [17] T. Brown, B. Mann, N. Ryder, M. Subbiah, J. D. Kaplan, P. Dhariwal, A. Neelakantan, P. Shyam, G. Sastry, A. Askell *et al.*, “Language models are few-shot learners,” *Advances in neural information processing systems*, vol. 33, pp. 1877–1901, 2020.
- [18] C. Raffel, N. Shazeer, A. Roberts, K. Lee, S. Narang, M. Matena, Y. Zhou, W. Li, and P. J. Liu, “Exploring the limits of transfer learning with a unified text-to-text transformer,” *The Journal of Machine Learning Research*, vol. 21, no. 1, pp. 5485–5551, 2020.
- [19] Y. Liu, M. Ott, N. Goyal, J. Du, M. Joshi, D. Chen, O. Levy, M. Lewis, L. Zettlemoyer, and V. Stoyanov, “Roberta: A robustly optimized bert pretraining approach,” *arXiv preprint arXiv:1907.11692*, 2019.
- [20] A. Radford, J. Wu, R. Child, D. Luan, D. Amodei, I. Sutskever *et al.*, “Language models are unsupervised multitask learners,” *OpenAI blog*, vol. 1, no. 8, p. 9, 2019.
- [21] O. (2023), “Gpt-4 technical report,” *arXiv preprint arXiv:2303.08774*, 2023.
- [22] J. Wei, X. Wang, D. Schuurmans, M. Bosma, E. Chi, Q. Le, and D. Zhou, “Chain of thought prompting elicits reasoning in large language models,” *arXiv preprint arXiv:2201.11903*, 2022.
- [23] S. Borgeaud, A. Mensch, J. Hoffmann, T. Cai, E. Rutherford, K. Milligan, G. B. Van Den Driessche, J.-B. Lespiau, B. Damoc, A. Clark *et al.*, “Improving language models by retrieving from trillions of tokens,” in *International conference on machine learning*. PMLR, 2022, pp. 2206–2240.
- [24] P. F. Christiano, J. Leike, T. Brown, M. Martic, S. Legg, and D. Amodei, “Deep reinforcement learning from human preferences,” *Advances in neural information processing systems*, vol. 30, 2017.
- [25] J. Schulman, S. Levine, P. Abbeel, M. Jordan, and P. Moritz, “Trust region policy optimization,” in *International conference on machine learning*. PMLR, 2015, pp. 1889–1897.
- [26] J. Schulman, F. Wolski, P. Dhariwal, A. Radford, and O. Klimov, “Proximal policy optimization algorithms,” *arXiv preprint arXiv:1707.06347*, 2017.

- [27] R. Nakano, J. Hilton, S. Balaji, J. Wu, L. Ouyang, C. Kim, C. Hesse, S. Jain, V. Kosaraju, W. Saunders *et al.*, “Webgpt: Browser-assisted question-answering with human feedback,” *arXiv preprint arXiv:2112.09332*, 2021.
- [28] A. Glaese, N. McAleese, M. Trebacz, J. Aslanides, V. Firoiu, T. Ewalds, M. Rauh, L. Weidinger, M. Chadwick, P. Thacker *et al.*, “Improving alignment of dialogue agents via targeted human judgements,” *arXiv preprint arXiv:2209.14375*, 2022.
- [29] A. Susano Pinto, A. Kolesnikov, Y. Shi, L. Beyer, and X. Zhai, “Tuning computer vision models with task rewards,” *arXiv e-prints*, pp. arXiv-2302, 2023.
- [30] J. Yosinski, J. Clune, Y. Bengio, and H. Lipson, “How transferable are features in deep neural networks?” *Advances in neural information processing systems*, vol. 27, 2014.
- [31] J. Deng, W. Dong, R. Socher, L.-J. Li, K. Li, and L. Fei-Fei, “Imagenet: A large-scale hierarchical image database,” in *2009 IEEE conference on computer vision and pattern recognition*. Ieee, 2009, pp. 248–255.
- [32] T. Ridnik, E. Ben-Baruch, A. Noy, and L. Zelnik-Manor, “Imagenet-21k pretraining for the masses,” in *Thirty-fifth Conference on Neural Information Processing Systems Datasets and Benchmarks Track (Round 1)*.
- [33] C. Sun, A. Shrivastava, S. Singh, and A. Gupta, “Revisiting unreasonable effectiveness of data in deep learning era,” in *Proceedings of the IEEE international conference on computer vision*, 2017, pp. 843–852.
- [34] X. Zhai, A. Kolesnikov, N. Houlsby, and L. Beyer, “Scaling vision transformers,” in *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, 2022, pp. 12 104–12 113.
- [35] M. Dehghani, J. Djolonga, B. Mustafa, P. Padlewski, J. Heek, J. Gilmer, A. Steiner, M. Caron, R. Geirhos, I. M. Alabdulmohsin, R. Jenatton, L. Beyer, M. Tschannen, A. Arnab, X. Wang, C. Riquelme, M. Minderer, J. Puigcerver, U. Evcı, M. Kumar, S. van Steenkiste, G. F. Elsayed, A. Mahendran, F. Yu, A. Oliver, F. Huot, J. Bastings, M. Collier, A. A. Gritsenko, V. Birodkar, C. N. Vasconcelos, Y. Tay, T. Mensink, A. Kolesnikov, F. Pavetić, D. Tran, T. Kipf, M. Luvcić, X. Zhai, D. Keysers, J. Harmsen, and N. Houlsby, “Scaling vision transformers to 22 billion parameters,” *ArXiv*, vol. abs/2302.05442, 2023.
- [36] P. Goyal, M. Caron, B. Lefauze, M. Xu, P. Wang, V. Pai, M. Singh, V. Liptchinsky, I. Misra, A. Joulin *et al.*, “Self-supervised pretraining of visual features in the wild,” *arXiv preprint arXiv:2103.01988*, 2021.
- [37] D. Mahajan, R. Girshick, V. Ramanathan, K. He, M. Paluri, Y. Li, A. Bharambe, and L. Van Der Maaten, “Exploring the limits of weakly supervised pretraining,” in *Proceedings of the European conference on computer vision (ECCV)*, 2018, pp. 181–196.
- [38] M. Singh, L. Gustafson, A. Adcock, V. de Freitas Reis, B. Gedik, R. P. Kosaraju, D. Mahajan, R. Girshick, P. Dollár, and L. Van Der Maaten, “Revisiting weakly supervised pre-training of visual perception models,” in *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, 2022, pp. 804–814.
- [39] M. Chen, A. Radford, R. Child, J. Wu, H. Jun, D. Luan, and I. Sutskever, “Generative Pretraining From Pixels,” in *Proceedings of the 37th International Conference on Machine Learning*. PMLR, Nov. 2020, pp. 1691–1703, iSSN: 2640-3498. [Online]. Available: <https://proceedings.mlr.press/v119/chen20s.html>
- [40] H. Chen, Y. Wang, T. Guo, C. Xu, Y. Deng, Z. Liu, S. Ma, C. Xu, C. Xu, and W. Gao, “Pre-trained image processing transformer,” in *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, 2021, pp. 12 299–12 310.
- [41] K. He, X. Chen, S. Xie, Y. Li, P. Dollár, and R. Girshick, “Masked Autoencoders Are Scalable Vision Learners,” 2022, pp. 16 000–16 009. [Online]. Available: https://openaccess.thecvf.com/content/CVPR2022/html/He_Masked_Autoencoders_Are_Scalable_Vision_Learners.CVPR_2022.paper.html
- [42] T. Chen, S. Kornblith, M. Norouzi, and G. Hinton, “A simple framework for contrastive learning of visual representations,” in *International conference on machine learning*. PMLR, 2020, pp. 1597–1607.
- [43] K. He, H. Fan, Y. Wu, S. Xie, and R. Girshick, “Momentum contrast for unsupervised visual representation learning,” in *Proceedings of the IEEE/CVF conference on computer vision and pattern recognition*, 2020, pp. 9729–9738.
- [44] Z. Liu, H. Mao, C.-Y. Wu, C. Feichtenhofer, T. Darrell, and S. Xie, “A convnet for the 2020s,” in *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, 2022, pp. 11 976–11 986.
- [45] A. Krizhevsky, I. Sutskever, and G. E. Hinton, “Imagenet classification with deep convolutional neural networks,” *Communications of the ACM*, vol. 60, no. 6, pp. 84–90, 2017.
- [46] K. Simonyan and A. Zisserman, “Very deep convolutional networks for large-scale image recognition,” *arXiv preprint arXiv:1409.1556*, 2014.
- [47] C. Szegedy, W. Liu, Y. Jia, P. Sermanet, S. Reed, D. Anguelov, D. Erhan, V. Vanhoucke, and A. Rabinovich, “Going deeper with convolutions,” in *Proceedings of the IEEE conference on computer vision and pattern recognition*, 2015, pp. 1–9.
- [48] K. He, X. Zhang, S. Ren, and J. Sun, “Delving deep into rectifiers: Surpassing human-level performance on imagenet classification,” in *Proceedings of the IEEE international conference on computer vision*, 2015, pp. 1026–1034.
- [49] —, “Deep residual learning for image recognition,” in *Proceedings of the IEEE conference on computer vision and pattern recognition*, 2016, pp. 770–778.
- [50] —, “Identity mappings in deep residual networks,” in *Computer Vision–ECCV 2016: 14th European Conference, Amsterdam, The Netherlands, October 11–14, 2016, Proceedings, Part IV 14*. Springer, 2016, pp. 630–645.
- [51] S. Xie, R. Girshick, P. Dollár, Z. Tu, and K. He, “Aggregated residual transformations for deep neural networks,” in *Proceedings of the IEEE conference on computer vision and pattern recognition*, 2017, pp. 1492–1500.
- [52] B. Zoph, V. Vasudevan, J. Shlens, and Q. V. Le, “Learning transferable architectures for scalable image recognition,” in *Proceedings of the IEEE conference on computer vision and pattern recognition*, 2018, pp. 8697–8710.
- [53] I. Radosavovic, R. P. Kosaraju, R. Girshick, K. He, and P. Dollár, “Designing network design spaces,” in *Proceedings of the IEEE/CVF conference on computer vision and pattern recognition*, 2020, pp. 10 428–10 436.
- [54] M. Tan and Q. Le, “Efficientnet: Rethinking model scaling for convolutional neural networks,” in *International conference on machine learning*. PMLR, 2019, pp. 6105–6114.
- [55] —, “Efficientnetv2: Smaller models and faster training,” in *International conference on machine learning*. PMLR, 2021, pp. 10 096–10 106.
- [56] A. Kolesnikov, L. Beyer, X. Zhai, J. Puigcerver, J. Yung, S. Gelly, and N. Houlsby, “Big transfer (bit): General visual representation learning,” in *Computer Vision–ECCV 2020: 16th European Conference, Glasgow, UK, August 23–28, 2020, Proceedings, Part V 16*. Springer, 2020, pp. 491–507.
- [57] Y. Huang, Y. Cheng, A. Bapna, O. Firat, D. Chen, M. Chen, H. Lee, J. Ngiam, Q. V. Le, Y. Wu *et al.*, “Gpipe: Efficient training of giant neural networks using pipeline parallelism,” *Advances in neural information processing systems*, vol. 32, 2019.
- [58] W. Wang, J. Dai, Z. Chen, Z. Huang, Z. Li, X. Zhu, X. Hu, T. Lu, L. Lu, H. Li *et al.*, “Internimage: Exploring large-scale vision foundation models with deformable convolutions,” *arXiv preprint arXiv:2211.05778*, 2022.
- [59] Z. Liu, Y. Lin, Y. Cao, H. Hu, Y. Wei, Z. Zhang, S. Lin, and B. Guo, “Swin transformer: Hierarchical vision transformer using shifted windows,” in *Proceedings of the IEEE/CVF international conference on computer vision*, 2021, pp. 10 012–10 022.
- [60] A. Dosovitskiy, L. Beyer, A. Kolesnikov, D. Weissenborn, X. Zhai, T. Unterthiner, M. Dehghani, M. Minderer, G. Heigold, S. Gelly, J. Uszkoreit, and N. Houlsby, “An Image is Worth 16x16 Words: Transformers for Image Recognition at Scale,” 2021. [Online]. Available: https://openreview.net/forum?id=YicbFdNTTy&utm_campaign=f86497ed3a-EMAIL_CAMPAIGN_2019.04.24.03.18.COPY_01&utm_medium=email&utm_source=Deep%20Learning%20Weekly&utm_term=0_384567b42d-f86497ed3a-72965345
- [61] K. Han, A. Xiao, E. Wu, J. Guo, C. Xu, and Y. Wang, “Transformer in Transformer,” in *Advances in Neural Information Processing Systems*, vol. 34. Curran Associates, Inc., 2021, pp. 15 908–15 919. [Online]. Available: <https://proceedings.neurips.cc/paper/2021/hash/854d9fcfa60b4bd07f9bb215d59ef5561-Abstract.html>
- [62] Z. Liu, H. Hu, Y. Lin, Z. Yao, Z. Xie, Y. Wei, J. Ning, Y. Cao, Z. Zhang, L. Dong, F. Wei, and B. Guo, “Swin Transformer V2: Scaling Up Capacity and Resolution,” 2022, pp. 12 009–12 019. [Online]. Available: https://openaccess.thecvf.com/content/CVPR2022/html/Liu_Swin_Transformer_V2_Scaling_Up_Capacity_and_Resolution_CVPR_2022.paper.html
- [63] Y.-A. Chung, Y. Zhang, W. Han, C.-C. Chiu, J. Qin, R. Pang, and Y. Wu, “W2v-bert: Combining contrastive learning and masked language modeling for self-supervised speech pre-training,” in *2021 IEEE Automatic Speech Recognition and Understanding Workshop (ASRU)*. IEEE, 2021, pp. 244–250.

- [64] S. Schneider, A. Baevski, R. Collobert, and M. Auli, “wav2vec: Unsupervised pre-training for speech recognition,” *arXiv preprint arXiv:1904.05862*, 2019.
- [65] Z. Borsos, R. Marinier, D. Vincent, E. Kharitonov, O. Pietquin, M. Sharifi, O. Teboul, D. Grangier, M. Tagliasacchi, and N. Zeghidour, “Audioml: a language modeling approach to audio generation,” *arXiv preprint arXiv:2209.03143*, 2022.
- [66] W.-N. Hsu, B. Bolte, Y.-H. H. Tsai, K. Lakhota, R. Salakhutdinov, and A. Mohamed, “Hubert: Self-supervised speech representation learning by masked prediction of hidden units,” *IEEE/ACM Transactions on Audio, Speech, and Language Processing*, vol. 29, pp. 3451–3460, 2021.
- [67] A. Babu, C. Wang, A. Tjandra, K. Lakhota, Q. Xu, N. Goyal, K. Singh, P. von Platen, Y. Saraf, J. Pino *et al.*, “Xls-r: Self-supervised cross-lingual speech representation learning at scale,” *arXiv preprint arXiv:2111.09296*, 2021.
- [68] A. Agostinelli, T. I. Denk, Z. Borsos, J. Engel, M. Verzetti, A. Caillon, Q. Huang, A. Jansen, A. Roberts, M. Tagliasacchi *et al.*, “Musiclm: Generating music from text,” *arXiv preprint arXiv:2301.11325*, 2023.
- [69] D. Yang, J. Yu, H. Wang, W. Wang, C. Weng, Y. Zou, and D. Y. Diffsound, “Discrete diffusion model for text-to-sound generation,” *arXiv preprint arXiv:2207.09983*, vol. 2, 2022.
- [70] F. Kreuk, G. Synnaeve, A. Polyak, U. Singer, A. Défossez, J. Copet, D. Parikh, Y. Taigman, and Y. Adi, “Audiongen: Textually guided audio generation,” in *The Eleventh International Conference on Learning Representations*, 2023. [Online]. Available: <https://openreview.net/forum?id=CYK7RfcOzQ4>
- [71] A. Radford, J. W. Kim, T. Xu, G. Brockman, C. McLeavey, and I. Sutskever, “Robust speech recognition via large-scale weak supervision,” *arXiv preprint arXiv:2212.04356*, 2022.
- [72] Y. Zhang, W. Han, J. Qin, Y. Wang, A. Bapna, Z. Chen, N. Chen, B. Li, V. Axelrod, G. Wang *et al.*, “Google usm: Scaling automatic speech recognition beyond 100 languages,” *arXiv preprint arXiv:2303.01037*, 2023.
- [73] V. Ordonez, G. Kulkarni, and T. Berg, “Im2Text: Describing Images Using 1 Million Captioned Photographs,” in *Advances in Neural Information Processing Systems*, vol. 24. Curran Associates, Inc., 2011. [Online]. Available: <https://papers.nips.cc/paper/2011/hash/5dd9db5e033da9c6fb5ba83c7a7ebea9-Abstract.html>
- [74] P. Young, A. Lai, M. Hodosh, and J. Hockenmaier, “From image descriptions to visual denotations: New similarity metrics for semantic inference over event descriptions,” *Transactions of the Association for Computational Linguistics*, vol. 2, pp. 67–78, Feb. 2014. [Online]. Available: https://doi.org/10.1162/tacl_a.00166
- [75] X. Chen, H. Fang, T.-Y. Lin, R. Vedantam, S. Gupta, P. Dollar, and C. L. Zitnick, “Microsoft COCO Captions: Data Collection and Evaluation Server,” Apr. 2015, *arXiv:1504.00325* [cs]. [Online]. Available: <http://arxiv.org/abs/1504.00325>
- [76] R. Krishna, Y. Zhu, O. Groth, J. Johnson, K. Hata, J. Kravitz, S. Chen, Y. Kalantidis, L.-J. Li, D. A. Shamma, M. S. Bernstein, and L. Fei-Fei, “Visual Genome: Connecting Language and Vision Using Crowdsourced Dense Image Annotations,” *International Journal of Computer Vision*, vol. 123, no. 1, pp. 32–73, May 2017. [Online]. Available: <https://doi.org/10.1007/s11263-016-0981-7>
- [77] P. Sharma, N. Ding, S. Goodman, and R. Soricut, “Conceptual Captions: A Cleaned, Hypernymed, Image Alt-text Dataset For Automatic Image Captioning,” in *Proceedings of the 56th Annual Meeting of the Association for Computational Linguistics (Volume 1: Long Papers)*. Melbourne, Australia: Association for Computational Linguistics, Jul. 2018, pp. 2556–2565. [Online]. Available: <https://aclanthology.org/P18-1238>
- [78] Y. Zhu, O. Groth, M. Bernstein, and L. Fei-Fei, “Visual7W: Grounded Question Answering in Images,” 2016, pp. 4995–5004. [Online]. Available: https://openaccess.thecvf.com/content_cvpr_2016/html/Zhu_Visual7W_Grounded_Question_CVPR_2016_paper.html
- [79] D. A. Hudson and C. D. Manning, “GQA: A New Dataset for Real-World Visual Reasoning and Compositional Question Answering,” 2019, pp. 6700–6709. [Online]. Available: https://openaccess.thecvf.com/content_CVPR_2019/html/Hudson_GQA_A_New_Dataset_for_Real-World_Visual_Reasoning_and_Compositional_CVPR_2019_paper.html
- [80] Y. Goyal, T. Khot, A. Agrawal, D. Summers-Stay, D. Batra, and D. Parikh, “Making the V in VQA Matter: Elevating the Role of Image Understanding in Visual Question Answering,” *International Journal of Computer Vision*, vol. 127, no. 4, pp. 398–414, Apr. 2019. [Online]. Available: <https://doi.org/10.1007/s11263-018-1116-0>
- [81] L. H. Li, P. Zhang, H. Zhang, J. Yang, C. Li, Y. Zhong, L. Wang, L. Yuan, L. Zhang, J.-N. Hwang, K.-W. Chang, and J. Gao, “Grounded Language-Image Pre-Training,” 2022, pp. 10965–10975. [Online]. Available: https://openaccess.thecvf.com/content/CVPR2022/html/Li-Grounded_Language-Image_Pre-Training.CVPR_2022_paper.html
- [82] B. Thomee, D. A. Shamma, G. Friedland, B. Elizalde, K. Ni, D. Poland, D. Borth, and L.-J. Li, “YFCC100M: the new data in multimedia research,” *Communications of the ACM*, vol. 59, no. 2, pp. 64–73, Jan. 2016. [Online]. Available: <https://doi.org/10.1145/2812802>
- [83] S. Changpinyo, P. Sharma, N. Ding, and R. Soricut, “Conceptual 12M: Pushing Web-Scale Image-Text Pre-Training To Recognize Long-Tail Visual Concepts,” 2021, pp. 3558–3568. [Online]. Available: https://openaccess.thecvf.com/content/CVPR2021/html/Changpinyo_Conceptual_12M_Pushing_Web-Scale_Image-Text_Pre-Training_To_Recognize_Long-Tail_Visual_CVPR_2021_paper.html
- [84] K. Srinivasan, K. Raman, J. Chen, M. Bendersky, and M. Najork, “WIT: Wikipedia-based Image Text Dataset for Multimodal Multilingual Machine Learning,” in *Proceedings of the 44th International ACM SIGIR Conference on Research and Development in Information Retrieval*, ser. SIGIR ’21. New York, NY, USA: Association for Computing Machinery, Jul. 2021, pp. 2443–2449. [Online]. Available: <https://doi.org/10.1145/3404835.3463257>
- [85] K. Desai, G. Kaul, Z. T. Aysola, and J. Johnson, “RedCaps: Web-curated image-text data created by the people, for the people,” Jan. 2022. [Online]. Available: <https://openreview.net/forum?id=VjJxBiI9zh>
- [86] A. Radford, J. W. Kim, C. Hallacy, A. Ramesh, G. Goh, S. Agarwal, G. Sastry, A. Askell, P. Mishkin, J. Clark, G. Krueger, and I. Sutskever, “Learning Transferable Visual Models From Natural Language Supervision,” in *Proceedings of the 38th International Conference on Machine Learning*. PMLR, Jul. 2021, pp. 8748–8763, iSSN: 2640-3498. [Online]. Available: <https://proceedings.mlr.press/v139/radford21a.html>
- [87] L. Yuan, D. Chen, Y.-L. Chen, N. Codella, X. Dai, J. Gao, H. Hu, X. Huang, B. Li, C. Li, C. Liu, M. Liu, Z. Liu, Y. Lu, Y. Shi, L. Wang, J. Wang, B. Xiao, Z. Xiao, J. Yang, M. Zeng, L. Zhou, and P. Zhang, “Florence: A New Foundation Model for Computer Vision,” Nov. 2021, *arXiv:2111.11432* [cs]. [Online]. Available: <http://arxiv.org/abs/2111.11432>
- [88] C. Jia, Y. Yang, Y. Xia, Y.-T. Chen, Z. Parekh, H. Pham, Q. Le, Y.-H. Sung, Z. Li, and T. Duerig, “Scaling Up Visual and Vision-Language Representation Learning With Noisy Text Supervision,” in *Proceedings of the 38th International Conference on Machine Learning*. PMLR, Jul. 2021, pp. 4904–4916, iSSN: 2640-3498. [Online]. Available: <https://proceedings.mlr.press/v139/jia21b.html>
- [89] H. Pham, Z. Dai, G. Ghiasi, K. Kawaguchi, H. Liu, A. W. Yu, J. Yu, Y.-T. Chen, M.-T. Luong, Y. Wu *et al.*, “Combined scaling for open-vocabulary image classification,” *arXiv e-prints*, pp. arXiv–2111, 2021.
- [90] X. Chen, X. Wang, S. Changpinyo, A. Piergiovanni, P. Padlewski, D. Salz, S. Goodman, A. Grycner, B. Mustafa, L. Beyer *et al.*, “Pali: A jointly-scaled multilingual language-image model,” *arXiv preprint arXiv:2209.06794*, 2022.
- [91] C. Schuhmann, R. Beaumont, R. Vencu, C. W. Gordon, R. Wightman, M. Cherti, T. Coombes, A. Katta, C. Mullis, M. Wortsman, P. Schramowski, S. R. Kundurthy, K. Crowson, L. Schmidt, R. Kaczmarczyk, and J. Jitsev, “LAION-5B: An open large-scale dataset for training next generation image-text models,” Oct. 2022. [Online]. Available: <https://openreview.net/forum?id=M3Y74vmsMcY>
- [92] S. Huang, L. Dong, W. Wang, Y. Hao, S. Singhal, S. Ma, T. Lv, L. Cui, O. K. Mohammed, B. Patra, Q. Liu, K. Aggarwal, Z. Chi, J. Bjorck, V. Chaudhary, S. Som, X. Song, and F. Wei, “Language Is Not All You Need: Aligning Perception with Language Models,” Mar. 2023, *arXiv:2302.14045* [cs]. [Online]. Available: <http://arxiv.org/abs/2302.14045>
- [93] A. Singh, R. Hu, V. Goswami, G. Couairon, W. Galuba, M. Rohrbach, and D. Kiela, “FLAVA: A Foundational Language and Vision Alignment Model,” 2022, pp. 15638–15650. [Online]. Available: https://openaccess.thecvf.com/content/CVPR2022/html/Singh_FLAVA_A_Foundational_Language_and_Vision_Alignment_Model_CVPR_2022_paper.html
- [94] L. Yao, R. Huang, L. Hou, G. Lu, M. Niu, H. Xu, X. Liang, Z. Li, X. Jiang, and C. Xu, “FILIP: Fine-grained Interactive Language-Image Pre-Training,” Jan. 2022. [Online]. Available: <https://openreview.net/forum?id=cpDhesEDC2>
- [95] J. Li, D. Li, C. Xiong, and S. Hoi, “BLIP: Bootstrapping Language-Image Pre-training for Unified Vision-Language Understanding and Generation,” in *Proceedings of the 39th International Conference on*

- Machine Learning.* PMLR, Jun. 2022, pp. 12 888–12 900, iSSN: 2640-3498. [Online]. Available: <https://proceedings.mlr.press/v162/li22n.html>
- [96] W. Su, X. Zhu, C. Tao, L. Lu, B. Li, G. Huang, Y. Qiao, X. Wang, J. Zhou, and J. Dai, “Towards All-in-one Pre-training via Maximizing Multi-modal Mutual Information,” Nov. 2022, arXiv:2211.09807 [cs]. [Online]. Available: <http://arxiv.org/abs/2211.09807>
- [97] A. Ramesh, M. Pavlov, G. Goh, S. Gray, C. Voss, A. Radford, M. Chen, and I. Sutskever, “Zero-Shot Text-to-Image Generation,” in *Proceedings of the 38th International Conference on Machine Learning.* PMLR, Jul. 2021, pp. 8821–8831, iSSN: 2640-3498. [Online]. Available: <https://proceedings.mlr.press/v139/ramesh21a.html>
- [98] C. Wu, S. Yin, W. Qi, X. Wang, Z. Tang, and N. Duan, “Visual chatgpt: Talking, drawing and editing with visual foundation models,” *arXiv preprint arXiv:2303.04671*, 2023.
- [99] Z. Wang, J. Yu, A. W. Yu, Z. Dai, Y. Tsvetkov, and Y. Cao, “SimVLM: Simple Visual Language Model Pretraining with Weak Supervision,” Jan. 2022. [Online]. Available: <https://openreview.net/forum?id=GURhfTuf3>
- [100] J. Li, D. Li, S. Savarese, and S. Hoi, “BLIP-2: Bootstrapping Language-Image Pre-training with Frozen Image Encoders and Large Language Models,” Jan. 2023, arXiv:2301.12597 [cs]. [Online]. Available: <http://arxiv.org/abs/2301.12597>
- [101] D. Driess, F. Xia, M. S. M. Sajjadi, C. Lynch, A. Chowdhery, B. Ichter, A. Wahid, J. Tompson, Q. Vuong, T. Yu, W. Huang, Y. Chebotar, P. Serbanet, D. Duckworth, S. Levine, V. Vanhoucke, K. Hausman, M. Toussaint, K. Greff, A. Zeng, I. Mordatch, and P. Florence, “Palm-e: An embodied multimodal language model,” in *arXiv preprint arXiv:2303.03378*, 2023.
- [102] J. Yu, Y. Xu, J. Y. Koh, T. Luong, G. Baid, Z. Wang, V. Vasudevan, A. Ku, Y. Yang, B. K. Ayan *et al.*, “Scaling autoregressive models for content-rich text-to-image generation,” *Transactions on Machine Learning Research*, 2022.
- [103] F.-A. Croitoru, V. Hondu, R. T. Ionescu, and M. Shah, “Diffusion models in vision: A survey,” *arXiv preprint arXiv:2209.04747*, 2022.
- [104] A. Q. Nichol, P. Dhariwal, A. Ramesh, P. Shyam, P. Mishkin, B. McGrew, I. Sutskever, and M. Chen, “Glide: Towards photorealistic image generation and editing with text-guided diffusion models,” in *International Conference on Machine Learning.* PMLR, 2022, pp. 16 784–16 804.
- [105] A. Ramesh, P. Dhariwal, A. Nichol, C. Chu, and M. Chen, “Hierarchical text-conditional image generation with clip latents,” *arXiv preprint arXiv:2204.06125*, 2022.
- [106] C. Saharia, W. Chan, S. Saxena, L. Li, J. Whang, E. Denton, S. K. S. Ghasemipour, R. Gontijo-Lopes, B. K. Ayan, T. Salimans *et al.*, “Photorealistic text-to-image diffusion models with deep language understanding,” in *Advances in Neural Information Processing Systems*, 2022.
- [107] R. Rombach, A. Blattmann, D. Lorenz, P. Esser, and B. Ommer, “High-resolution image synthesis with latent diffusion models,” 2021.
- [108] X.-C. Bai, G. McMullan, and S. H. Scheres, “How cryo-em is revolutionizing structural biology,” *Trends in biochemical sciences*, vol. 40, no. 1, pp. 49–57, 2015.
- [109] K. Wüthrich, “The way to nmr structures of proteins,” *Nature structural biology*, vol. 8, no. 11, pp. 923–925, 2001.
- [110] J. M. Grimes, D. R. Hall, A. W. Ashton, G. Evans, R. L. Owen, A. Wagner, K. E. McAuley, F. von Delft, A. M. Orville, T. Sorensen *et al.*, “Where is crystallography going?” *Acta Crystallographica Section D: Structural Biology*, vol. 74, no. 2, pp. 152–166, 2018.
- [111] J. Jumper, R. Evans, A. Pritzel, T. Green, M. Figurnov, O. Ronneberger, K. Tunyasuvunakool, R. Bates, A. Žídek, A. Potapenko *et al.*, “Highly accurate protein structure prediction with alphafold,” *Nature*, vol. 596, no. 7873, pp. 583–589, 2021.
- [112] M. Baek, F. DiMaio, I. Anishchenko, J. Dauparas, S. Ovchinnikov, G. R. Lee, J. Wang, Q. Cong, L. N. Kinch, R. D. Schaeffer *et al.*, “Accurate prediction of protein structures and interactions using a three-track neural network,” *Science*, vol. 373, no. 6557, pp. 871–876, 2021.
- [113] R. Evans, M. O’Neill, A. Pritzel, N. Antropova, A. Senior, T. Green, A. Žídek, R. Bates, S. Blackwell, J. Yim *et al.*, “Protein complex prediction with alphafold-multimer,” *BioRxiv*, pp. 2021–10, 2021.
- [114] S. Cheng, R. Wu, Z. Yu, B. Li, X. Zhang, J. Peng, and Y. You, “Fastfold: reducing alphafold training time from 11 days to 67 hours,” *arXiv preprint arXiv:2203.00854*, 2022.
- [115] G. Wang, X. Fang, Z. Wu, Y. Liu, Y. Xue, Y. Xiang, D. Yu, F. Wang, and Y. Ma, “Helixfold: An efficient implementation of alphafold2 using paddlepaddle,” *arXiv preprint arXiv:2207.05477*, 2022.
- [116] Z. Li, X. Liu, W. Chen, F. Shen, H. Bi, G. Ke, and L. Zhang, “Unifold: an open-source platform for developing protein folding models beyond alphafold,” *BioRxiv*, pp. 2022–08, 2022.
- [117] G. Ahdriz, N. Bouatta, S. Kadyan, Q. Xia, W. Gerecke, T. J. O’Donnell, D. Berenberg, I. Fisk, N. Zanichelli, B. Zhang *et al.*, “Openfold: Retraining alphafold2 yields new insights into its learning mechanisms and capacity for generalization,” *BioRxiv*, pp. 2022–11, 2022.
- [118] A. Villegas-Morcillo, L. Robinson, A. Flajolet, and T. D. Barrett, “Manyfold: an efficient and flexible library for training and validating protein folding models,” *Bioinformatics*, vol. 39, no. 1, p. btac773, 2023.
- [119] M. Mirdita, K. Schütze, Y. Moriwaki, L. Heo, S. Ovchinnikov, and M. Steinegger, “Colabfold: making protein folding accessible to all,” *Nature methods*, vol. 19, no. 6, pp. 679–682, 2022.
- [120] A. Rives, J. Meier, T. Sercu, S. Goyal, Z. Lin, J. Liu, D. Guo, M. Ott, C. L. Zitnick, J. Ma *et al.*, “Biological structure and function emerge from scaling unsupervised learning to 250 million protein sequences,” *Proceedings of the National Academy of Sciences*, vol. 118, no. 15, p. e2016239118, 2021.
- [121] U. Consortium, “The universal protein resource (uniprot),” *Nucleic acids research*, vol. 36, no. suppl.1, pp. D190–D195, 2007.
- [122] A. Madani, B. McCann, N. Naik, N. S. Keskar, N. Anand, R. R. Eguchi, P.-S. Huang, and R. Socher, “Progen: Language modeling for protein generation,” *arXiv preprint arXiv:2004.03497*, 2020.
- [123] A. Elnaggar, M. Heinzinger, C. Dallago, G. Rehwavi, W. Yu, L. Jones, T. Gibbs, T. Feher, C. Angerer, M. Steinegger, D. Bhowmik, and B. Rost, “Protrans: Towards cracking the language of life’s code through self-supervised deep learning and high performance computing,” *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. PP, pp. 1–1, 07 2021.
- [124] M. Steinegger and J. Söding, “Clustering huge protein sequence sets in linear time,” *Nature communications*, vol. 9, no. 1, p. 2542, 2018.
- [125] B. E. Suzek, Y. Wang, H. Huang, P. B. McGarvey, C. H. Wu, and U. Consortium, “Uniref clusters: a comprehensive and scalable alternative for improving sequence similarity searches,” *Bioinformatics*, vol. 31, no. 6, pp. 926–932, 2015.
- [126] Z. Lin, H. Akin, R. Rao, B. Hie, Z. Zhu, W. Lu, A. dos Santos Costa, M. Fazel-Zarandi, T. Sercu, S. Candido *et al.*, “Language models of protein sequences at the scale of evolution enable accurate structure prediction,” *BioRxiv*, 2022.
- [127] R. Wu, F. Ding, R. Wang, R. Shen, X. Zhang, S. Luo, C. Su, Z. Wu, Q. Xie, B. Berger *et al.*, “High-resolution de novo structure prediction from primary sequence,” *BioRxiv*, pp. 2022–07, 2022.
- [128] R. Chowdhury, N. Bouatta, S. Biswas, C. Floristean, A. Kharkar, K. Roy, C. Rochereau, G. Ahdriz, J. Zhang, G. M. Church *et al.*, “Single-sequence protein structure prediction using a language model and deep learning,” *Nature Biotechnology*, vol. 40, no. 11, pp. 1617–1623, 2022.
- [129] B. Chen, Z. Xie, J. Qiu, Z. Ye, J. Xu, and J. Tang, “Improved the protein complex prediction with protein language models,” *BioRxiv*, pp. 2022–09, 2022.
- [130] R. M. Rao, J. Liu, R. Verkuil, J. Meier, J. Canny, P. Abbeel, T. Sercu, and A. Rives, “Msa transformer,” in *International Conference on Machine Learning.* PMLR, 2021, pp. 8844–8856.
- [131] J. A. Ruffolo, J. J. Gray, and J. Sulam, “Deciphering antibody affinity maturation with language models and weakly supervised learning,” *arXiv preprint arXiv:2112.07782*, 2021.
- [132] Y. Wang, X. Gong, S. Li, B. Yang, Y. Sun, C. Shi, H. Li, Y. Wang, C. Yang, and L. Song, “xtrimoabfold: Improving antibody structure prediction without multiple sequence alignments,” *arXiv preprint arXiv:2212.00735*, 2022.
- [133] F. Yang, W. Wang, F. Wang, Y. Fang, D. Tang, J. Huang, H. Lu, and J. Yao, “scbert as a large-scale pretrained deep language model for cell type annotation of single-cell rna-seq data,” *Nature Machine Intelligence*, vol. 4, no. 10, pp. 852–866, 2022.
- [134] J. Chen, Z. Hu, S. Sun, Q. Tan, Y. Wang, Q. Yu, L. Zong, L. Hong, J. Xiao, T. Shen *et al.*, “Interpretable rna foundation model from unannotated data for highly accurate rna structure and function predictions,” *BioRxiv*, pp. 2022–08, 2022.
- [135] “Rnacentral 2021: secondary structure integration, improved sequence search and new member databases,” *Nucleic acids research*, vol. 49, no. D1, pp. D212–D220, 2021.
- [136] T. Shen, Z. Hu, Z. Peng, J. Chen, P. Xiong, L. Hong, L. Zheng, Y. Wang, I. King, S. Wang *et al.*, “E2efold-3d: End-to-end deep learning method for accurate de novo rna 3d structure prediction,” *arXiv preprint arXiv:2207.01586*, 2022.

- [137] G. R. Buel and K. J. Walters, "Can alphafold2 predict the impact of missense mutations on structure?" *Nature Structural & Molecular Biology*, vol. 29, no. 1, pp. 1–2, 2022.
- [138] T. Burki, "A new paradigm for drug development," *The Lancet Digital Health*, vol. 2, no. 5, pp. e226–e227, 2020.
- [139] S. Wang, Y. Guo, Y. Wang, H. Sun, and J. Huang, "Smiles-bert: large scale unsupervised pre-training for molecular property prediction," in *Proceedings of the 10th ACM international conference on bioinformatics, computational biology and health informatics, 2019*, pp. 429–436.
- [140] S. Honda, S. Shi, and H. R. Ueda, "Smiles transformer: Pre-trained molecular fingerprint for low data drug discovery," *arXiv preprint arXiv:1911.04738*, 2019.
- [141] B. Fabian, T. Edlich, H. Gaspar, M. Segler, J. Meyers, M. Fiscato, and M. Ahmed, "Molecular representation learning with language models and domain-relevant auxiliary tasks," *arXiv preprint arXiv:2011.13230*, 2020.
- [142] D. Chen, K. Gao, D. D. Nguyen, X. Chen, Y. Jiang, G.-W. Wei, and F. Pan, "Algebraic graph-assisted bidirectional transformers for molecular property prediction," *Nature communications*, vol. 12, no. 1, p. 3521, 2021.
- [143] Y. Rong, Y. Bian, T. Xu, W. Xie, Y. Wei, W. Huang, and J. Huang, "Self-supervised graph transformer on large-scale molecular data," *Advances in Neural Information Processing Systems*, vol. 33, pp. 12 559–12 571, 2020.
- [144] V. Bagal, R. Aggarwal, P. Vinod, and U. D. Priyakumar, "Molgpt: molecular generation using a transformer-decoder model," *Journal of Chemical Information and Modeling*, vol. 62, no. 9, pp. 2064–2076, 2021.
- [145] L. Yang, G. Yang, Z. Bing, Y. Tian, Y. Niu, L. Huang, and L. Yang, "Transformer-based generative model accelerating the development of novel braf inhibitors," *ACS omega*, vol. 6, no. 49, pp. 33 864–33 873, 2021.
- [146] S. Honda, S. Shi, and H. R. Ueda, "Smiles transformer: Pre-trained molecular fingerprint for low data drug discovery," *arXiv preprint arXiv:1911.04738*, 2019.
- [147] J. Bradshaw, B. Paige, M. J. Kusner, M. Segler, and J. M. Hernández-Lobato, "A model to search for synthesizable molecules," *Advances in Neural Information Processing Systems*, vol. 32, 2019.
- [148] D. Grechishnikova, "Transformer neural network for protein-specific de novo drug generation as a machine translation problem," *Scientific reports*, vol. 11, no. 1, pp. 1–13, 2021.
- [149] I. Lee, J. Keum, and H. Nam, "Deepconv-dti: Prediction of drug-target interactions via deep learning with convolution on protein sequences," *PLoS computational biology*, vol. 15, no. 6, p. e1007129, 2019.
- [150] T. Nguyen, H. Le, T. P. Quinn, T. Nguyen, T. D. Le, and S. Venkatesh, "Graphdta: predicting drug–target binding affinity with graph neural networks," *Bioinformatics*, vol. 37, no. 8, pp. 1140–1147, 2021.
- [151] K. Huang, C. Xiao, L. M. Glass, and J. Sun, "Moltrans: molecular interaction transformer for drug–target interaction prediction," *Bioinformatics*, vol. 37, no. 6, pp. 830–836, 2021.
- [152] D. Chen, J. Zheng, G.-W. Wei, and F. Pan, "Extracting predictive representations from hundreds of millions of molecules," *The journal of physical chemistry letters*, vol. 12, no. 44, pp. 10 793–10 801, 2021.
- [153] G. Xiong, Z. Wu, J. Yi, L. Fu, Z. Yang, C. Hsieh, M. Yin, X. Zeng, C. Wu, A. Lu *et al.*, "Admetlab 2.0: an integrated online platform for accurate and comprehensive predictions of admet properties," *Nucleic Acids Research*, vol. 49, no. W1, pp. W5–W14, 2021.
- [154] P. Li, J. Wang, Y. Qiao, H. Chen, Y. Yu, X. Yao, P. Gao, G. Xie, and S. Song, "Learn molecular representations from large-scale unlabeled molecules for drug discovery," *arXiv preprint arXiv:2012.11175*, 2020.
- [155] ——, "An effective self-supervised framework for learning expressive molecular global representations to drug discovery," *Briefings in Bioinformatics*, vol. 22, no. 6, p. bbab109, 2021.
- [156] X.-C. Zhang, C.-K. Wu, Z.-J. Yang, Z.-X. Wu, J.-C. Yi, C.-Y. Hsieh, T.-J. Hou, and D.-S. Cao, "Mg-bert: leveraging unsupervised atomic representation learning for molecular property prediction," *Briefings in bioinformatics*, vol. 22, no. 6, p. bbab152, 2021.
- [157] X. Lin, C. Xu, Z. Xiong, X. Zhang, N. Ni, B. Ni, J. Chang, R. Pan, Z. Wang, F. Yu *et al.*, "Pangu drug model: learn a molecule like a human," *bioRxiv*, pp. 2022–03, 2022.
- [158] P. Bai, F. Miljković, B. John, and H. Lu, "Interpretable bilinear attention network with domain adaptation improves drug–target prediction," *Nature Machine Intelligence*, pp. 1–11, 2023.
- [159] Y. Ji, L. Zhang, J. Wu, B. Wu, L.-K. Huang, T. Xu, Y. Rong, L. Li, J. Ren, D. Xue, H. Lai, S. Xu, J. Feng, W. Liu, P. Luo, S. Zhou, J. Huang, P. Zhao, and Y. Bian, "DrugOOD: Out-of-Distribution (OOD) Dataset Curator and Benchmark for AI-aided Drug Discovery – A Focus on Affinity Prediction Problems with Noise Annotations," *arXiv e-prints*, p. arXiv:2201.09637, Jan. 2022.
- [160] N. Corporation, "Bionemo," 2023, accessed on Month Day, Year. [Online]. Available: <https://www.nvidia.com/en-us/gpu-cloud/bionemo/>
- [161] T. H. Kung, M. Cheatham, A. Medenilla, C. Sillos, L. De Leon, C. Elepaño, M. Madriaga, R. Aggabao, G. Diaz-Candido, J. Maningo *et al.*, "Performance of chatgpt on usmle: Potential for ai-assisted medical education using large language models," *PLOS Digital Health*, vol. 2, no. 2, p. e0000198, 2023.
- [162] E. Tiu, E. Talius, P. Patel, C. P. Langlotz, A. Y. Ng, and P. Rajpurkar, "Expert-level detection of pathologies from unannotated chest x-ray images via self-supervised learning," *Nature Biomedical Engineering*, pp. 1–8, 2022.
- [163] Z. Chen, Y. Du, J. Hu, Y. Liu, G. Li, X. Wan, and T.-H. Chang, "Multi-modal masked autoencoders for medical vision-and-language pre-training," in *Medical Image Computing and Computer Assisted Intervention-MICCAI 2022: 25th International Conference, Singapore, September 18–22, 2022, Proceedings, Part V*. Springer, 2022, pp. 679–689.
- [164] S. Wang, Z. Zhao, X. Ouyang, Q. Wang, and D. Shen, "Chatcad: Interactive computer-aided diagnosis on medical image using large language models," *arXiv preprint arXiv:2302.07257*, 2023.
- [165] Y. Li, S. Rao, J. R. A. Solares, A. Hassaine, R. Ramakrishnan, D. Canoy, Y. Zhu, K. Rahimi, and G. Salimi-Khorshidi, "Behrt: transformer for electronic health records," *Scientific reports*, vol. 10, no. 1, pp. 1–12, 2020.
- [166] L. Rasmy, Y. Xiang, Z. Xie, C. Tao, and D. Zhi, "Med-bert: pretrained contextualized embeddings on large-scale structured electronic health records for disease prediction," *NPJ digital medicine*, vol. 4, no. 1, p. 86, 2021.
- [167] J. Wang, X. Hu, W. Hou, H. Chen, R. Zheng, Y. Wang, L. Yang, H. Huang, W. Ye, X. Geng *et al.*, "On the robustness of chatgpt: An adversarial and out-of-distribution perspective," *arXiv preprint arXiv:2302.12095*, 2023.
- [168] K. Jeblick, B. Schachtner, J. Dexl, A. Mittermeier, A. T. Stüber, J. Topalis, T. Weber, P. Wesp, B. Sabel, J. Riecke *et al.*, "Chatgpt makes medicine easy to swallow: An exploratory case study on simplified radiology reports," *arXiv preprint arXiv:2212.14882*, 2022.
- [169] F. Antaki, S. Touma, D. Milad, J. El-Khoury, and R. Duval, "Evaluating the performance of chatgpt in ophthalmology: An analysis of its successes and shortcomings," *medRxiv*, pp. 2023–01, 2023.
- [170] Y. Gu, R. Tinn, H. Cheng, M. Lucas, N. Usuyama, X. Liu, T. Naumann, J. Gao, and H. Poon, "Domain-specific language model pretraining for biomedical natural language processing," *ACM Transactions on Computing for Healthcare (HEALTH)*, vol. 3, no. 1, pp. 1–23, 2021.
- [171] V. Ramesh, N. A. Chi, and P. Rajpurkar, "Improving radiology report generation systems by removing hallucinated references to non-existent priors," in *Machine Learning for Health*. PMLR, 2022, pp. 456–473.
- [172] S. Chen, K. Ma, and Y. Zheng, "Med3d: Transfer learning for 3d medical image analysis," *arXiv preprint arXiv:1904.00625*, 2019.
- [173] Z. Zhou, V. Sodha, M. M. Rahman Siddiquee, R. Feng, N. Tajbakhsh, M. B. Gotway, and J. Liang, "Models genesis: Generic autodidactic models for 3d medical image analysis," in *Medical Image Computing and Computer Assisted Intervention-MICCAI 2019: 22nd International Conference, Shenzhen, China, October 13–17, 2019, Proceedings, Part IV 22*. Springer, 2019, pp. 384–393.
- [174] S. Azizi, B. Mustafa, F. Ryan, Z. Beaver, J. Freyberg, J. Deaton, A. Loh, A. Karthikesalingam, S. Kornblith, T. Chen *et al.*, "Big self-supervised models advance medical image classification," in *Proceedings of the IEEE/CVF International Conference on Computer Vision*, 2021, pp. 3478–3488.
- [175] H.-Y. Zhou, S. Yu, C. Bian, Y. Hu, K. Ma, and Y. Zheng, "Comparing to learn: Surpassing imagenet pretraining on radiographs by comparing image representations," in *Medical Image Computing and Computer Assisted Intervention-MICCAI 2020: 23rd International Conference, Lima, Peru, October 4–8, 2020, Proceedings, Part I 23*. Springer, 2020, pp. 398–407.
- [176] Y. Zhang, H. Jiang, Y. Miura, C. D. Manning, and C. P. Langlotz, "Contrastive learning of medical visual representations from paired images and text," in *Machine Learning for Healthcare Conference*. PMLR, 2022, pp. 2–25.
- [177] S.-C. Huang, L. Shen, M. P. Lungren, and S. Yeung, "Gloria: A multimodal global-local representation learning framework for label-efficient medical image recognition," in *Proceedings of the IEEE/CVF International Conference on Computer Vision*, 2021, pp. 3942–3951.
- [178] H. Sowrirajan, J. Yang, A. Y. Ng, and P. Rajpurkar, "Moco pretraining

- improves representation and transferability of chest x-ray models," in *Medical Imaging with Deep Learning*. PMLR, 2021, pp. 728–744.
- [179] J. Chen, Y. Lu, Q. Yu, X. Luo, E. Adeli, Y. Wang, L. Lu, A. L. Yuille, and Y. Zhou, "Transunet: Transformers make strong encoders for medical image segmentation," *arXiv preprint arXiv:2102.04306*, 2021.
- [180] Y. Zhang, H. Liu, and Q. Hu, "Transfuse: Fusing transformers and cnns for medical image segmentation," in *Medical Image Computing and Computer Assisted Intervention—MICCAI 2021: 24th International Conference, Strasbourg, France, September 27–October 1, 2021, Proceedings, Part I 24*. Springer, 2021, pp. 14–24.
- [181] J. M. J. Valanarasu, P. Oza, I. Hacihaliloglu, and V. M. Patel, "Medical transformer: Gated axial-attention for medical image segmentation," in *Medical Image Computing and Computer Assisted Intervention—MICCAI 2021: 24th International Conference, Strasbourg, France, September 27–October 1, 2021, Proceedings, Part I 24*. Springer, 2021, pp. 36–46.
- [182] Y. Xie, J. Zhang, C. Shen, and Y. Xia, "Cotr: Efficiently bridging cnn and transformer for 3d medical image segmentation," in *Medical Image Computing and Computer Assisted Intervention—MICCAI 2021: 24th International Conference, Strasbourg, France, September 27–October 1, 2021, Proceedings, Part III 24*. Springer, 2021, pp. 171–180.
- [183] A. Hatamizadeh, Y. Tang, V. Nath, D. Yang, A. Myronenko, B. Landman, H. R. Roth, and D. Xu, "Unetr: Transformers for 3d medical image segmentation," in *Proceedings of the IEEE/CVF winter conference on applications of computer vision*, 2022, pp. 574–584.
- [184] H. Cao, Y. Wang, J. Chen, D. Jiang, X. Zhang, Q. Tian, and M. Wang, "Swin-unet: Unet-like pure transformer for medical image segmentation," in *Computer Vision—ECCV 2022 Workshops: Tel Aviv, Israel, October 23–27, 2022, Proceedings, Part III*. Springer, 2023, pp. 205–218.
- [185] O. Ronneberger, P. Fischer, and T. Brox, "U-net: Convolutional networks for biomedical image segmentation," in *Medical Image Computing and Computer-Assisted Intervention—MICCAI 2015: 18th International Conference, Munich, Germany, October 5–9, 2015, Proceedings, Part III 18*. Springer, 2015, pp. 234–241.
- [186] Y. Tang, D. Yang, W. Li, H. R. Roth, B. Landman, D. Xu, V. Nath, and A. Hatamizadeh, "Self-supervised pre-training of swin transformers for 3d medical image analysis," in *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, 2022, pp. 20730–20740.
- [187] A. Shaker, M. Maaz, H. Rasheed, S. Khan, M.-H. Yang, and F. S. Khan, "Unetr++: Delving into efficient and accurate 3d medical image segmentation," *arXiv preprint arXiv:2212.04497*, 2022.
- [188] P. Chambon, C. Bluelthgen, C. P. Langlotz, and A. Chaudhari, "Adapting pretrained vision-language foundational models to medical imaging domains," *arXiv preprint arXiv:2210.04133*, 2022.
- [189] Z. Wang, Z. Wu, D. Agarwal, and J. Sun, "Medclip: Contrastive learning from unpaired medical images and text," *arXiv preprint arXiv:2210.10163*, 2022.
- [190] "Be my eyes," 2023. [Online]. Available: <https://www.bemyeyes.com/>
- [191] J. Lee, W. Yoon, S. Kim, D. Kim, S. Kim, C. H. So, and J. Kang, "Biobert: a pre-trained biomedical language representation model for biomedical text mining," *Bioinformatics*, vol. 36, no. 4, pp. 1234–1240, 2020.
- [192] E. Alsentzer, J. R. Murphy, W. Boag, W.-H. Weng, D. Jin, T. Naumann, and M. McDermott, "Publicly available clinical bert embeddings," *arXiv preprint arXiv:1904.03323*, 2019.
- [193] H.-C. Shin, Y. Zhang, E. Bakhturina, R. Puri, M. Patwary, M. Shoeybi, and R. Mani, "Biomegatron: Larger biomedical domain language model," *arXiv preprint arXiv:2010.06060*, 2020.
- [194] S. Gururangan, A. Marasović, S. Swayamdipta, K. Lo, I. Beltagy, D. Downey, and N. A. Smith, "Don't stop pretraining: Adapt language models to domains and tasks," *arXiv preprint arXiv:2004.10964*, 2020.
- [195] L. Rasmy, Y. Xiang, Z. Xie, C. Tao, and D. Zhi, "Med-bert: pretrained contextualized embeddings on large-scale structured electronic health records for disease prediction," *NPJ digital medicine*, vol. 4, no. 1, p. 86, 2021.
- [196] K. raj Kanakarajan, B. Kundumani, and M. Sankarasubbu, "Bioelectra: pretrained biomedical text encoder using discriminators," in *Proceedings of the 20th Workshop on Biomedical Language Processing*, 2021, pp. 143–154.
- [197] M. Yasunaga, J. Leskovec, and P. Liang, "Linkbert: Pretraining language models with document links," *arXiv preprint arXiv:2203.15827*, 2022.
- [198] R. Luo, L. Sun, Y. Xia, T. Qin, S. Zhang, H. Poon, and T.-Y. Liu, "Biogpt: generative pre-trained transformer for biomedical text generation and mining," *Briefings in Bioinformatics*, vol. 23, no. 6, 2022.
- [199] K. Singhal, S. Azizi, T. Tu, S. S. Mahdavi, J. Wei, H. W. Chung, N. Scales, A. Tanwani, H. Cole-Lewis, S. Pfohl *et al.*, "Large language models encode clinical knowledge," *arXiv preprint arXiv:2212.13138*, 2022.
- [200] X. Yang, A. Chen, N. PourNejatian, H. C. Shin, K. E. Smith, C. Parisien, C. Compas, C. Martin, A. B. Costa, M. G. Flores *et al.*, "A large language model for electronic health records," *npj Digital Medicine*, vol. 5, no. 1, p. 194, 2022.
- [201] J. Wei, Y. Tay, R. Bommasani, C. Raffel, B. Zoph, S. Borgeaud, D. Yogatama, M. Bosma, D. Zhou, D. Metzler *et al.*, "Emergent abilities of large language models," *arXiv preprint arXiv:2206.07682*, 2022.
- [202] M. Agrawal, S. Hegselmann, H. Lang, Y. Kim, and D. Sontag, "Large language models are few-shot clinical information extractors," *arXiv preprint arXiv:2205.12689*, 2022.
- [203] V. Liévin, C. E. Hother, and O. Winther, "Can large language models reason about medical questions?" *arXiv preprint arXiv:2207.08143*, 2022.
- [204] "Fairway health - process prior authorization faster," 2023. [Online]. Available: <https://www.ycombinator.com/launches/IHu-fairway-health-process-prior-authorization-faster>
- [205] S. B. Patel and K. Lam, "Chatgpt: the future of discharge summaries?" *The Lancet Digital Health*, 2023.
- [206] E. Shue, L. Liu, B. Li, Z. Feng, X. Li, and G. Hu, "Empowering beginners in bioinformatics with chatgpt," *bioRxiv*, pp. 2023–03, 2023.
- [207] H. Dai, Z. Liu, W. Liao, X. Huang, Z. Wu, L. Zhao, W. Liu, N. Liu, S. Li, D. Zhu *et al.*, "Chataug: Leveraging chatgpt for text data augmentation," *arXiv preprint arXiv:2302.13007*, 2023.
- [208] E. Mitchell, Y. Lee, A. Khazatsky, C. D. Manning, and C. Finn, "Detectgpt: Zero-shot machine-generated text detection using probability curvature," *arXiv preprint arXiv:2301.11305*, 2023.
- [209] D. M. Korngiebel and S. D. Mooney, "Considering the possibilities and pitfalls of generative pre-trained transformer 3 (gpt-3) in healthcare delivery," *NPJ Digital Medicine*, vol. 4, no. 1, p. 93, 2021.
- [210] E. Chen, K. Lerman, E. Ferrara *et al.*, "Tracking social media discourse about the covid-19 pandemic: Development of a public coronavirus twitter data set," *JMIR public health and surveillance*, vol. 6, no. 2, p. e19273, 2020.
- [211] J. Peng, P. Shi, J. Qiu, X. Ju, F. P.-W. Lo, X. Gu, W. Jia, T. Baranowski, M. Steiner-Asiedu, A. K. Anderson *et al.*, "Clustering egocentric images in passive dietary monitoring with self-supervised learning," in *2022 IEEE-EMBS International Conference on Biomedical and Health Informatics (BHI)*. IEEE, 2022, pp. 01–04.
- [212] J. Qiu, F. P.-W. Lo, X. Gu, M. L. Jobarteh, W. Jia, T. Baranowski, M. Steiner-Asiedu, A. K. Anderson, M. A. McCrory, E. Sazonov, M. Sun, G. Frost, and B. Lo, "Egocentric image captioning for privacy-preserved passive dietary intake monitoring," *IEEE Transactions on Cybernetics*, 2023.
- [213] B. M. Popkin, C. Corvalan, and L. M. Grummer-Strawn, "Dynamics of the double burden of malnutrition and the changing nutrition reality," *The Lancet*, 2019.
- [214] T. Nguyen, J. Brandstetter, A. Kapoor, J. K. Gupta, and A. Grover, "Climax: A foundation model for weather and climate," *arXiv preprint arXiv:2301.10343*, 2023.
- [215] R. Secoli, E. Matheson, M. Pinzi, S. Galvan, A. Donder, T. Watts, M. Riva, D. D. Zani, L. Bello, and F. Rodriguez y Baena, "Modular robotic platform for precision neurosurgery with a bio-inspired needle: System overview and first in-vivo deployment," *Plos one*, vol. 17, no. 10, p. e0275686, 2022.
- [216] G. D'Onofrio, L. Fiorini, A. Sorrentino, S. Russo, F. Ciccone, F. Giuliani, D. Sancarlo, and F. Cavallo, "Emotion recognizing by a robotic solution initiative (emotive project)," *Sensors*, vol. 22, no. 8, p. 2861, 2022.
- [217] J. Qiu, L. Chen, X. Gu, F. P.-W. Lo, Y.-Y. Tsai, J. Sun, J. Liu, and B. Lo, "Egocentric human trajectory forecasting with a wearable camera and multi-modal fusion," *IEEE Robotics and Automation Letters*, vol. 7, no. 4, pp. 8799–8806, 2022.
- [218] J. Sun, B. Zhou, M. J. Black, and A. Chandrasekaran, "Locate: End-to-end localization of actions in 3d with transformers," *arXiv preprint arXiv:2203.10719*, 2022.
- [219] P. Asgharian, A. M. Panchea, and F. Ferland, "A review on the use of mobile service robots in elderly care," *Robotics*, vol. 11, no. 6, p. 127, 2022.

- [220] L. Chen, K. Lu, A. Rajeswaran, K. Lee, A. Grover, M. Laskin, P. Abbeel, A. Srinivas, and I. Mordatch, "Decision transformer: Reinforcement learning via sequence modeling," *Advances in neural information processing systems*, vol. 34, pp. 15 084–15 097, 2021.
- [221] S. Nair, A. Rajeswaran, V. Kumar, C. Finn, and A. Gupta, "R3m: A universal visual representation for robot manipulation," *CoRL*, 2022.
- [222] K. Grauman, A. Westbury, E. Byrne, Z. Chavis, A. Furnari, R. Girdhar, J. Hamburger, H. Jiang, M. Liu, X. Liu *et al.*, "Ego4d: Around the world in 3,000 hours of egocentric video," in *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, 2022, pp. 18 995–19 012.
- [223] C. Wang, L. Fan, J. Sun, R. Zhang, L. Feifei, D. Xu, Y. Zhu, and A. Anandkumar, "Mimicplay: Long-horizon imitation learning by watching human play," *ArXiv*, 2022.
- [224] J. Sun, D.-A. Huang, B. Lu, Y.-H. Liu, B. Zhou, and A. Garg, "Plate: Visually-grounded planning with transformers in procedural tasks," *IEEE Robotics and Automation Letters*, vol. 7, no. 2, pp. 4924–4930, 2022.
- [225] S. Vemprala, R. Bonatti, A. Bucker, and A. Kapoor, "Chatgpt for robotics: Design principles and model abilities," Microsoft, Tech. Rep. MSR-TR-2023-8, February 2023. [Online]. Available: <https://www.microsoft.com/en-us/research/publication/chatgpt-for-robotics-design-principles-and-model-abilities/>
- [226] S. Reed, K. Zolna, E. Parisotto, S. G. Colmenarejo, A. Novikov, G. Barth-maron, M. Giménez, Y. Sulsky, J. Kay, J. T. Springenberg, T. Eccles, J. Bruce, A. Razavi, A. Edwards, N. Heess, Y. Chen, R. Hadsell, O. Vinyals, M. Bordbar, and N. de Freitas, "A generalist agent," *Transactions on Machine Learning Research*, 2022, featured Certification. [Online]. Available: <https://openreview.net/forum?id=1ikK0kHjvj>
- [227] M. Shridhar, L. Manuelli, and D. Fox, "Cliprot: What and where pathways for robotic manipulation," in *Conference on Robot Learning*. PMLR, 2022, pp. 894–906.
- [228] —, "Perceiver-actor: A multi-task transformer for robotic manipulation," *arXiv preprint arXiv:2209.05451*, 2022.
- [229] M. Ahn, A. Brohan, N. Brown, Y. Chebotar, O. Cortes, B. David, C. Finn, C. Fu, K. Gopalakrishnan, K. Hausman, A. Herzog, D. Ho, J. Hsu, J. Ibarz, B. Ichter, A. Irpan, E. Jang, R. J. Ruano, K. Jeffrey, S. Jesmonth, N. Joshi, R. Julian, D. Kalashnikov, Y. Kuang, K.-H. Lee, S. Levine, Y. Lu, L. Luu, C. Parada, P. Pastor, J. Quiambao, K. Rao, J. Rettinghouse, D. Reyes, P. Sermanet, N. Sievers, C. Tan, A. Toshev, V. Vanhoucke, F. Xia, T. Xiao, P. Xu, S. Xu, M. Yan, and A. Zeng, "Do as i can and not as i say: Grounding language in robotic affordances," in *arXiv preprint arXiv:2204.01691*, 2022.
- [230] Y. Jiang, A. Gupta, Z. Zhang, G. Wang, Y. Dou, Y. Chen, L. Fei-Fei, A. Anandkumar, Y. Zhu, and L. Fan, "Vima: General robot manipulation with multimodal prompts," *arXiv preprint arXiv:2210.03094*, 2022.
- [231] A. Brohan, N. Brown, J. Carbajal, Y. Chebotar, J. Dabis, C. Finn, K. Gopalakrishnan, K. Hausman, A. Herzog, J. Hsu *et al.*, "Rt-1: Robotics transformer for real-world control at scale," *arXiv preprint arXiv:2212.06817*, 2022.
- [232] G.-Z. Yang, J. Cambias, K. Cleary, E. Daimler, J. Drake, P. E. Dupont, N. Hata, P. Kazanzides, S. Martel, R. V. Patel *et al.*, "Medical robotics—regulatory, ethical, and legal considerations for increasing levels of autonomy," *Science Robotics*, vol. 2, no. 4, 2017.
- [233] M. Yip and N. Das, "Robot autonomy for surgery," in *The Encyclopedia of MEDICAL ROBOTICS: Volume 1 Minimally Invasive Surgical Robotics*. World Scientific, 2019, pp. 281–313.
- [234] M. Ginesi, D. Meli, A. Roberti, N. Sansonetto, and P. Fiorini, "Autonomous task planning and situation awareness in robotic surgery," in *2020 IEEE/RSJ International Conference on Intelligent Robots and Systems (IROS)*, 2020, pp. 3144–3150.
- [235] C. Shin, P. W. Ferguson, S. A. Pedram, J. Ma, E. P. Dutson, and J. Rosen, "Autonomous tissue manipulation via surgical robot using learning based model predictive control," in *2019 International Conference on Robotics and Automation (ICRA)*, 2019, pp. 3875–3881.
- [236] H. Saeidi, J. D. Opfermann, M. Kam, S. Wei, S. Léonard, M. H. Hsieh, J. U. Kang, and A. Krieger, "Autonomous robotic laparoscopic surgery for intestinal anastomosis," *Science robotics*, vol. 7, no. 62, p. eabj2908, 2022.
- [237] P. E. Dupont, B. J. Nelson, M. Goldfarb, B. Hannaford, A. Menciassi, M. K. O'Malley, N. Simaan, P. Valdastri, and G.-Z. Yang, "A decade retrospective of medical robotics research from 2010 to 2020," *Science Robotics*, vol. 6, no. 60, p. eabi8017, 2021.
- [238] R. Zhang, J. Chen, Z. Wang, Z. Yang, Y. Ren, P. Shi, J. Calo, K. Lam, S. Purkayastha, and B. Lo, "A step towards conditional autonomy - robotic appendectomy," *IEEE Robotics and Automation Letters*, vol. 8, no. 5, pp. 2429–2436, 2023.
- [239] "Pubmed abstract," 2023. [Online]. Available: <https://pubmed.ncbi.nlm.nih.gov/download/>
- [240] "Pubmed central," 2023. [Online]. Available: <https://www.ncbi.nlm.nih.gov/pmc/>
- [241] A. E. Johnson, T. J. Pollard, L. Shen, L.-w. H. Lehman, M. Feng, M. Ghassemi, B. Moody, P. Szolovits, L. Anthony Celi, and R. G. Mark, "Mimic-iii, a freely accessible critical care database," *Scientific data*, vol. 3, no. 1, pp. 1–9, 2016.
- [242] E. Herrett, A. M. Gallagher, K. Bhaskaran, H. Forbes, R. Mathur, T. Van Staa, and L. Smeeth, "Data resource profile: clinical practice research datalink (cprd)," *International journal of epidemiology*, vol. 44, no. 3, pp. 827–836, 2015.
- [243] A. E. Johnson, T. J. Pollard, S. J. Berkowitz, N. R. Greenbaum, M. P. Lungren, C.-y. Deng, R. G. Mark, and S. Horng, "Mimic-cxr, a de-identified publicly available database of chest radiographs with free-text reports," *Scientific data*, vol. 6, no. 1, p. 317, 2019.
- [244] J. Irvin, P. Rajpurkar, M. Ko, Y. Yu, S. Ciurea-Ilcus, C. Chute, H. Marklund, B. Haghgoo, R. Ball, K. Shpanskaya *et al.*, "Chexpert: A large chest radiograph dataset with uncertainty labels and expert comparison," in *Proceedings of the AAAI conference on artificial intelligence*, vol. 33, no. 01, 2019, pp. 590–597.
- [245] A. Bustos, A. Pertusa, J.-M. Salinas, and M. de la Iglesia-Vayá, "Padchest: A large chest x-ray image dataset with multi-label annotated reports," *Medical image analysis*, vol. 66, p. 101797, 2020.
- [246] P. Rajpurkar, J. Irvin, A. Bagul, D. Ding, T. Duan, H. Mehta, B. Yang, K. Zhu, D. Laird, R. L. Ball *et al.*, "Mura: Large dataset for abnormality detection in musculoskeletal radiographs," *arXiv preprint arXiv:1712.06957*, 2017.
- [247] N. I. of Health Chest X-Ray Dataset, "Nih chest x-rays," 2018, accessed on Month Day, Year. [Online]. Available: <https://www.kaggle.com/datasets/nih-chest-xrays/data>
- [248] E. P. Reis, J. P. de Paiva, M. C. da Silva, G. A. Ribeiro, V. F. Paiva, L. Bulgarelli, H. M. Lee, P. V. Santos, V. M. Brito, L. T. Amaral *et al.*, "Brax, brazilian labeled chest x-ray dataset," *Scientific Data*, vol. 9, no. 1, p. 487, 2022.
- [249] L. Wang, Z. Q. Lin, and A. Wong, "Covid-net: A tailored deep convolutional neural network design for detection of covid-19 cases from chest x-ray images," *Scientific reports*, vol. 10, no. 1, pp. 1–12, 2020.
- [250] K. Yan, X. Wang, L. Lu, and R. M. Summers, "Deeplesion: automated mining of large-scale lesion annotations and universal lesion detection with deep learning," *Journal of medical imaging*, vol. 5, no. 3, pp. 036 501–036 501, 2018.
- [251] N. L. of Midecine, "The national library of medicine presents medpix," unknown, accessed on Month Day, Year. [Online]. Available: <https://medpix.nlm.nih.gov/home>
- [252] K. Clark, B. Vendt, K. Smith, J. Freymann, J. Kirby, P. Koppel, S. Moore, S. Phillips, D. Maffitt, M. Pringle *et al.*, "The cancer imaging archive (tcia): maintaining and operating a public information repository," *Journal of digital imaging*, vol. 26, pp. 1045–1057, 2013.
- [253] M. Li, Y. Zhang, Z. Ji, K. Xie, S. Yuan, Q. Liu, and Q. Chen, "Ipnv-v2 and octa-500: Methodology and dataset for retinal image segmentation," *arXiv preprint arXiv:2012.07261*, 2020.
- [254] M. Antonelli, A. Reinke, S. Bakas, K. Farahani, A. Kopp-Schneider, B. A. Landman, G. Litjens, B. Menze, O. Ronneberger, R. M. Summers *et al.*, "The medical segmentation decathlon," *Nature communications*, vol. 13, no. 1, p. 4128, 2022.
- [255] J. Yang, R. Shi, D. Wei, Z. Liu, L. Zhao, B. Ke, H. Pfister, and B. Ni, "Medmnist v2-a large-scale lightweight benchmark for 2d and 3d biomedical image classification," *Scientific Data*, vol. 10, no. 1, p. 41, 2023.
- [256] P. Tschandl, C. Rosendahl, and H. Kittler, "The ham10000 dataset, a large collection of multi-source dermatoscopic images of common pigmented skin lesions," *Scientific data*, vol. 5, no. 1, pp. 1–9, 2018.
- [257] U. Consortium *et al.*, "Uniprot: the universal protein knowledgebase," *Nucleic acids research*, vol. 46, no. 5, p. 2699, 2018.
- [258] J. Mistry, S. Chuguransky, L. Williams, M. Qureshi, G. A. Salazar, E. L. Sonnhammer, S. C. Tosatto, L. Paladin, S. Raj, L. J. Richardson *et al.*, "Pfam: The protein families database in 2021," *Nucleic acids research*, vol. 49, no. D1, pp. D412–D419, 2021.
- [259] A. Kovatsuk, J. Leem, S. Kelm, J. Snowden, C. M. Deane, and K. Krawczyk, "Observed antibody space: a resource for data mining next-generation sequencing of antibody repertoires," *The Journal of Immunology*, vol. 201, no. 8, pp. 2502–2509, 2018.

- [260] O. Franzén, L.-M. Gan, and J. L. Björkegren, “Panglaodb: a web server for exploration of mouse and human single-cell rna sequencing data,” *Database*, vol. 2019, 2019.
- [261] A. Gaulton, L. J. Bellis, A. P. Bento, J. Chambers, M. Davies, A. Hersey, Y. Light, S. McGlinchey, D. Michalovich, B. Al-Lazikani *et al.*, “Chembl: a large-scale bioactivity database for drug discovery,” *Nucleic acids research*, vol. 40, no. D1, pp. D1100–D1107, 2012.
- [262] J. J. Irwin, K. G. Tang, J. Young, C. Dandarchuluun, B. R. Wong, M. Khurelbaatar, Y. S. Moroz, J. Mayfield, and R. A. Sayle, “Zinc20—a free ultralarge-scale chemical database for ligand discovery,” *Journal of chemical information and modeling*, vol. 60, no. 12, pp. 6065–6073, 2020.
- [263] T. Yang, Z. Li, Y. Chen, D. Feng, G. Wang, Z. Fu, X. Ding, X. Tan, J. Zhao, X. Luo *et al.*, “Drugspacex: a large screenable and synthetically tractable database extending drug space,” *Nucleic acids research*, vol. 49, no. D1, pp. D1170–D1178, 2021.
- [264] J. Chambers, M. Davies, A. Gaulton, A. Hersey, S. Velankar, R. Petryszak, J. Hastings, L. Bellis, S. McGlinchey, and J. P. Overington, “Unichem: a unified chemical structure cross-referencing and identifier tracking system,” *Journal of cheminformatics*, vol. 5, no. 1, p. 3, 2013.
- [265] S. Kim, J. Chen, T. Cheng, A. Gindulyte, J. He, S. He, Q. Li, B. A. Shoemaker, P. A. Thiessen, B. Yu *et al.*, “Pubchem 2019 update: improved access to chemical data,” *Nucleic acids research*, vol. 47, no. D1, pp. D1102–D1109, 2019.
- [266] M. Yazdani-Jahromi, N. Yousefi, A. Tayebi, E. Kolanthai, C. J. Neal, S. Seal, and O. O. Garibay, “Attentionstidti: an interpretable graph-based model for drug-target interaction prediction using nlp sentence-level relation classification,” *Briefings in Bioinformatics*, vol. 23, no. 4, p. bbac272, 2022.
- [267] C. Lyu, T. Chen, B. Qiang, N. Liu, H. Wang, L. Zhang, and Z. Liu, “Cmnpd: a comprehensive marine natural products database towards facilitating drug discovery from the ocean,” *Nucleic Acids Research*, vol. 49, no. D1, pp. D509–D515, 2021.
- [268] G. Zhou, Z. Gao, Q. Ding, H. Zheng, H. Xu, Z. Wei, L. Zhang, and G. Ke, “Uni-mol: A universal 3d molecular representation learning framework,” in *The Eleventh International Conference on Learning Representations*, 2023. [Online]. Available: <https://openreview.net/forum?id=6K2RM6wVqKu>
- [269] T. Y. Zhuo, Y. Huang, C. Chen, and Z. Xing, “Exploring ai ethics of chatgpt: A diagnostic analysis,” *arXiv preprint arXiv:2301.12867*, 2023.
- [270] L. Li and M. W. Spratling, “Data augmentation alone can improve adversarial training,” in *The Eleventh International Conference on Learning Representations*, 2023. [Online]. Available: <https://openreview.net/forum?id=y4uc4NtFWaq>
- [271] Q. Dou, T. Y. So, M. Jiang, Q. Liu, V. Vardhanabuti, G. Kaassis, Z. Li, W. Si, H. H. Lee, K. Yu *et al.*, “Federated deep learning for detecting covid-19 lung abnormalities in ct: a privacy-preserving multinational validation study,” *NPJ digital medicine*, vol. 4, no. 1, p. 60, 2021.
- [272] D. Qin, J.-J. Bu, Z. Liu, X. Shen, S. Zhou, J.-J. Gu, Z.-H. Wang, L. Wu, and H.-F. Dai, “Efficient medical image segmentation based on knowledge distillation,” *IEEE Transactions on Medical Imaging*, vol. 40, no. 12, pp. 3820–3831, 2021.
- [273] W. Hou and Z. Ji, “Geneturing tests gpt models in genomics,” *bioRxiv*, pp. 2023–03, 2023.
- [274] C. Yu, J. Liu, S. Nemati, and G. Yin, “Reinforcement learning in healthcare: A survey,” *ACM Computing Surveys (CSUR)*, vol. 55, no. 1, pp. 1–36, 2021.
- [275] A. Carusi, P. D. Winter, I. Armstrong, F. Ciravegna, D. G. Kiely, A. Lawrie, H. Lu, I. Sabroe, and A. Swift, “Medical artificial intelligence is as much social as it is technological,” *Nature Machine Intelligence*, pp. 1–3, 2023.