

Deep Learning, Genomics, and Precision Medicine

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Abstract

Abstract goes here.

Introduction

Biology and medicine are rapidly becoming data-intensive with respect to both research and practice. A recent comparison of genomics with social media, online videos and other data-intensive scientific disciplines suggested that the field of genomics alone would equal or surpass other fields in data generation and analysis within the next decade [1]. These data present new opportunities, but also new challenges. The data volume and complexity both indicate that automated algorithms will be needed to extract meaningful patterns and provide actionable knowledge allowing us to better treat, categorize, or study disease, all within data constrained and privacy critical environments.

Concurrent with this explosive growth in biomedical data, a new enthusiasm for a class of machine learning algorithms, known as deep learning, is revolutionizing image search. These architectures readily surpass previous best-in-class results, and computer scientists are now building many-layered neural networks from collections of millions of images. In a famous and early example, scientists from Google demonstrated that a neural network could learn to identify cats simply by watching online videos [2].

What if, more generally, deep learning could solve the challenges presented by the growth of data in biomedicine? Could these algorithms identify the "cats" hidden in our data - the patterns unknown to the researcher - and act on them? In this review, we examine whether deep learning's transformation of biomedical science is simply a matter of time or if there are unique challenges posed by biomedical data that render deep learning methods either more challenging or less fruitful to apply.

Defining deep learning

The term deep learning has come to refer to a collection of new techniques that, together, have demonstrated breakthrough gains over existing best-in-class algorithms across several fields. It is built on artificial neural networks, an idea that was first proposed in 1943 [3] as a model for how biological brains process information. Since then, interest in neural networks as computational models has waxed and waned several times. This history is interesting in its own right [4]. With the gains shown by techniques falling under the aegis of deep learning over alternative approaches, attention has shifted back to neural networks. Our focus is primarily on the downstream applications enabled by these advances.

Several important advances make the current surge of work done in this area possible. Easy-to-use software packages have brought the techniques of the field out of the specialist's toolkit to a broad community of computational scientists. With the growing attention focused on these methods, new techniques for fast training have enabled their application to larger datasets [5]. Dropout of nodes, edges and layers makes networks more robust, even when the number of parameters is very large. The growing popularity of the field has also led to a proliferation of neural network approaches, many of which are well suited for addressing distinct challenges. For example, neural networks structured as autoencoders or as adversarial networks require no labels and are now regularly used for unsupervised tasks. In this review, we do not exhaustively discuss the different types of deep neural network architectures. A recent book from Goodfellow et al [6] covers these in detail. Finally, the larger datasets now available are also well suited to fitting the many parameters that exist for deep neural networks.

The convergence of these factors currently makes deep learning extremely adaptable, and capable of addressing the nuanced differences of each domain to which it is applied. Many of the advances in deep learning were first developed for image analysis and text analysis, but the lessons learnt and techniques developed there can enable the construction of very powerful models specifically suited to the challenges presented by many domains. Neural networks, particularly deep ones, are a highly flexible representation capable of capturing many different types of features. Deep neural network approaches have demonstrated success from the game of Go [7] to quantum physics [8].

Will deep learning transform the study of human disease?

With this review, we set out to address the question: what would need to be true for deep learning to transform how we categorize, study, and treat individuals to maintain or restore health? We chose a high bar for "transform." Andrew Grove, the former CEO of Intel, coined the term Strategic Inflection Point to refer to a change in technologies or environment that requires a business to be fundamentally reshaped [9]. Here, we sought to identify whether deep learning was an innovation that would induce a strategic inflection point on the practice of biology or medicine. We structured the review with an eye towards the concept of precision medicine.

There are numerous examples where deep learning has been applied to biological problems and produced somewhat improved results, and there are numerous reviews that have focused on general applications of deep learning in biology [10–15]. We sought cases where deep learning was enabling researchers to solve challenges that were previously considered infeasible, or if it made difficult, tedious, and non-routine analyses routine.

In biomedical contexts, there are domain-specific considerations that influence how to best harness the power and flexibility of deep learning. Model interpretability can be critical. Understanding the patterns in data may be just as important as fitting the data. In addition, there are important and pressing questions about how to build networks that can efficiently represent the underlying structure and logic of the data. Domain experts can play important roles in designing networks to represent data appropriately, encoding the most salient prior knowledge and assessing success or failure. There is also great potential to create deep learning systems that are not intended to replace biologists and clinicians but rather cooperate with them, working to prioritize experiments or streamline tasks that do not require expert judgment.

Based on our guiding question, we focused on the application of deep learning to topics of biomedical importance. We divided the large range of topics into three broad classes: Disease and Patient Categorization, Fundamental Biological Study, and Patient Treatment. We briefly introduce the types of questions, approaches and data that are typical for each class in the application of deep learning.

Disease and Patient Categorization

A key challenge in biomedicine is the accurate classification of diseases and disease subtypes. In oncology, current "gold standard" approaches involve histology, requiring manual human expertise for quantification, or small panel of molecular markers, such as cell surface receptors or genes' expression. One example is the PAM50 approach to classifying breast cancer where the expression of 50 marker genes divides breast cancer patients into four subtypes. Significant heterogeneity still remains within these four subtypes [16,17]. Given the increasing wealth of molecular data available, a more comprehensive subtyping seems possible.

Several studies have used deep learning methods in order to better categorize breast cancer patients. For example, Tan et al. applied denoising autoencoders (DA), an unsupervised approach, in order to cluster breast cancer patients [18]. Ciresan et al. utilized convolutional neural networks (CNN) to count mitotic divisions in histological images; a feature that is highly correlated with disease outcome [19]. Despite these recent advances, a number of challenges exist in this area of research, such as the integration of disparate types of data, including electronic health records (EHR), imaging and histology data, and molecular omics data.

Fundamental Biological Study

Deep learning can be applied to answer more fundamental biological questions, and is especially suited to leveraging large amounts of data from high throughput omics studies. One classic biological problem where machine learning has been extensively applied is the prediction of molecular targets. Recent advances using deep learning have shown higher accuracy in determining molecular targets. For example, Lee et al. used deep recurrent neural networks (RNN) to predict gene targets of micro-RNAs [20]. Wang et al. used a residual CNN to predict protein-protein contact on a genome-wide scale [21]. Other biological questions that have been investigated include the prediction of protein secondary structure based on sequence data [22,23], recognition of functional genomic elements such as enhancers and promoters [24–26], predicting the deleterious effects of nucleotide polymorphisms [27], etc.

Patient Treatment

Although the application of deep learning to patient treatment is just beginning, we expect a dramatic increase in methods aiming to recommend patient treatment, predict treatment outcome, and guide future development of new therapies. Specifically, effort in this area aims to identify drug targets, identify drug interactions or predict drug response. One recent approach for predicting drug response is the use of protein structure to predict drug interactions and drug bioactivity through CNN [28]. Since CNNs leverage spatial relationships within the data, this particular deep learning framework is well suited to the problem. Drug repositioning is another active area of research. Aliper et al. used transcriptomic data to predict which drugs might be repurposed for other diseases through deep neural networks [29]. Similarly, it was shown that restricted Boltzmann machines (RBM) can be combined into deep belief networks (DBNs) to predict novel drug - target interactions and formulate drug repositioning hypotheses [30,31]. Finally, deep learning is also being successfully used to prioritize chemicals in the early stages of drug discovery for new targets [32].

Deep learning and patient categorization

In a healthcare setting, individuals are diagnosed with a disease or condition based on symptoms, the results of certain diagnostic tests, or other factors. Once diagnosed with a disease an individual might be assigned a stage based on another set of human-defined rules. While these rules are refined over time, the process is evolutionary rather than revolutionary.

We might imagine that deep learning or artificial intelligence methods could reinvent how individuals are categorized for healthcare. A deep neural network might identify entirely new categories of health or disease that are only present when data from multiple lab tests are integrated. As a potential example, consider the condition Latent Autoimmune Diabetes in Adults (LADA). The history of this disease classification is briefly reviewed in Stenström et al. [33].

Imagine that a deep neural network operating in the early 1980s had access to electronic health records with comprehensive clinical tests. It might have identified a subgroup of individuals with blood glucose levels that indicated diabetes as well as auto-antibodies, even though the individuals had never been diagnosed with type 1 diabetes - the autoimmune form of the disease that arises in young people. Such a neural network would be identifying patients with LADA. As no such computational approach existed, LADA was actually identified by Groop et al. [34]. However, this represents a potential hope of this area. Perhaps deep neural networks, by reevaluating data without the context of our assumptions, can reveal novel classes of treatable conditions.

Alternatively, imagine that a deep neural network is provided with clinical test results gleaned from electronic health records. Because physicians may order certain tests based on the diagnosis that they suspect a patient has, a deep neural network may learn to "diagnose" patients simply based on the tests that are ordered. For some objective function this may offer good performance (i.e. predicting an ICD code), even though it does not provide insight into the underlying disease beyond physician activity. This challenge is not unique to deep learning approaches; however, it is important for practitioners to be aware of these challenges and the possibility in this domain of constructing highly predictive classifiers of questionable actual utility.

Our goal in this section is to assess the extent to which deep learning is already contributing to the discovery of novel categories. Where it isn't, we focus on barriers to achieving these goals. We also highlight approaches that researchers are taking to address challenges within the field, particularly with regards to data availability and labeling.

Imaging applications in healthcare

One of the general areas where deep learning methods have had substantial success has been in image analysis. Applications in areas of medicine that use imaging extensively are also emerging. Mammography has been one area with numerous contributions [35–38]. In all of this work, the researchers must work around a specific challenge - the limited number of well annotated training images. To expand the number and diversity of images, the researchers have employed approaches where they employ adversarial examples [38] or first train towards human-created features before subsequent fine tuning [35]. The presence of a large bank of well-annotated mammography images would aid in the application of deep neural networks to this area. Though this strategy has not yet been employed in this domain, large collections of unlabeled images might first be used in an unsupervised context to construct high-quality feature detectors. Then the small number of labeled examples could be used for subsequent training. Similar strategies have been employed for EHR data where high-quality labeled examples are also difficult to obtain [39].

In addition to radiographic images, histology slides are also being analyzed with deep learning approaches. Ciresan et al. [19] developed one of the earliest examples, winning the 2012 International Conference on Pattern Recognition's Contest on Mitosis Detection while achieving human competitive accuracy. Their approach uses what has become a standard convolutional neural network architecture trained on public data. In more recent work, Wang et al. [40] analyzed stained slides to identify cancers within slides of lymph node slices. The approach provided a probability map for each slide. On this task a pathologist has about a 3% error rate. The pathologist did not produce any false positives, but did have a number of false negatives. Their algorithm had about twice the error rate of a pathologist. However, their algorithms errors were not strongly correlated with the pathologist. Theoretically, combining both could reduce the error rate to under 1%. In this area, these algorithms may be ready to incorporate into existing tools to aid pathologists. The authors' work suggests that this could reduce the false negative rate of such evaluations. This theme of an ensemble between deep learning algorithm and human expert may help overcome some of the challenges presented by data limitations.

One source of training examples with rich clinical annotations is the electronic health record. Recently Lee et al. [41] developed an approach to distinguish individuals with Age-related Macular Degeneration from control individuals. They extracted approximately 100,000 images from structured electronic health records, which they used to train and evaluate a deep neural network. Combining this data resource with standard deep learning techniques, the authors reach greater than 93% accuracy. One item that is important to note with regards to this work is that the authors used their test set for evaluating when training had concluded. In other domains, this has resulted in a minimal change in the estimated accuracy [42]. However, there is not yet a single accepted standard within the field of biomedical research for such evaluations. We recommend the use of an independent test set wherever it is feasible. Despite this minor limitation, the work clearly illustrates the potential that can be unlocked from images stored in electronic health records.

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Electronic health records

EHR data include substantial amounts of free text, which remains challenging to approach [43]. Often, researchers developing algorithms that perform well on specific tasks must design and implement domain-specific features [44].

These features capture unique aspects of the literature being processed. Deep learning methods are natural feature constructors. In recent work, the authors evaluated the extent to which deep learning methods could be applied on top of generic features for domain-specific concept extraction [45]. They found that performance was in line with, but did not exceed, existing state of the art methods. The deep learning method had performance lower than the best performing domain-specific method in their evaluation [45]. This highlights the challenge of predicting the eventual impact of deep learning on the field. This provides support that deep learning may impact the field by reducing the researcher time and cost required to develop specific solutions, but it may not lead to performance increases.

In recent work, Yoon et al.[46] analyzed simple features using deep neural networks and found that the patterns recognized by the algorithms could be re-used across tasks. Their aim was to analyze the free text portions of pathology reports to identify the primary site and laterality of tumors. The only features the authors supplied to the algorithms that they evaluated were unigrams and bigrams. These are the counts for single words and two-word combinations in a free text document. They subset the full set of words and word combinations to the 400 most commonly used ones. The machine learning algorithms that they employed (naïve Bayes, logistic regression, and deep neural networks) all performed relatively similarly on the task of identifying the primary site. However, when the authors evaluated the more challenging task, i.e. evaluating the laterality of each tumor, the deep neural network outperformed the other methods. Of particular interest, when the authors first trained a neural network to predict primary site and then repurposed those features as a component of a secondary neural network trained to predict laterality, the performance was higher than a laterality-trained neural network. This indicates a potential strength of deep methods. They can repurpose features across tasks, improving overall predictions as the field tackles new challenges. This approach is known as transfer learning (see Discussion).

Several authors have created reusable feature sets for medical terminologies using natural language processing (NLP) and neural embedding models, as popularized by Word2vec [47]. A goal of learning terminologies for different entities in the same vector space is to find relationships between different domains (e.g. drugs and the diseases they treat). It is difficult for us to provide a strong statement on the broad utility of these methods. Manuscripts in this area tend to compare algorithms applied to the same data but lack a comparison against overall best-practices for one or more tasks addressed by these methods. Techniques have been developed for free text medical notes [48], ICD and NDC, and claims data [49]. Methods for neural embeddings learned from electronic health records have at least some ability to predict disease-disease associations and implicate genes with a statistical association with a disease [50]. However, the evaluations performed did not differentiate between simple predictions (i.e. the same disease in different sites of the body) and non-intuitive ones. While promising, a lack of rigorous evaluations of the real-world utility of these kinds of features makes current contributions in this area difficult to evaluate. To examine the true utility, comparisons need to be performed against leading approaches (i.e. algorithms and data) as opposed to simply evaluating multiple algorithms on the same potentially limited dataset.

Identifying consistent subgroups of individuals and individual health trajectories from clinical tests is also an active area of research. Approaches inspired by deep learning have been used for both unsupervised feature construction and supervised prediction. Early work by Lasko et al. [51], combined sparse autoencoders and Gaussian processes to distinguish gout from leukemia from uric acid sequences. Later work showed that unsupervised feature construction of many features via denoising autoencoder neural networks could dramatically reduce the number of labeled examples required for subsequent supervised analyses [39,52]. In addition, it pointed towards learned features being useful for subtyping within a single disease. In a concurrent large-scale analysis of EHR data from 700,000 patients, Miotto et al. [53] used a deep denoising autoencoder architecture applied to the number and co-occurrence of clinical events ("DeepPatient") to learn a representation of patients. The model was able to predict disease trajectories within one year with over 90% accuracy and patient-level predictions were improved by up to 15% when compared to other methods. Razavian et al. [54] used a set of 18 common lab tests to predict disease onset using both CNN and LSTM architectures and demonstrated improvement over baseline regression models. However, numerous challenges including data integration (patient demographics, family history, laboratory tests, text-based patient records, image analysis, genomic data) and better handling of streaming temporal data with many features, will need to be overcome before we can fully assess the potential of deep learning for this application area.

Still, recent work has also revealed domains in which deep networks have proven superior to traditional methods. Survival analysis models the time leading to an event of interest from a shared starting point, and in the context of EHR data, often associates these events to subject covariates. Exploring this relationship is difficult, however, given that EHR data types are often heterogeneous, covariates are often missing, and conventional approaches require the covariate-event relationship be linear and aligned to a specific starting point [55]. Early approaches, such as the Faraggi-Simon feed-forward network, aimed to relax the linearity assumption, but performance gains were lacking [56]. Katzman et al. in turn developed a deep implementation of the Faraggi-Simon network that, in addition to outperforming Cox regression, was capable of comparing the risk between a given pair of treatments, thus potentially acting as recommender system [57]. To overcome the remaining difficulties, researchers have turned to deep exponential families, a class of latent generative models that are constructed from any type of exponential family distributions [58]. The result was a deep survival analysis model capable of overcoming challenges posed by missing data and heterogeneous data types, while uncovering nonlinear relationships between covariates and failure time. They showed their model more accurately stratified patients as a function of disease risk score compared to the current clinical implementation.

There is a computational cost for these methods, however, when compared to traditional, non-network approaches. For the exponential family models, despite their scalability [59], an important question for the investigator is whether he or she is interested in estimates of posterior uncertainty. Given that these models are effectively Bayesian neural networks, much of their utility simplifies to whether a Bayesian approach is warranted for a given increase in computational cost. Moreover, as with all variational methods, future work must continue to explore just how well the posterior distributions are approximated, especially as model complexity increases [60].

Challenges and opportunities in patient categorization

Generating ground-truth labels can be expensive or impossible

A dearth of true labels is perhaps among the biggest obstacles for EHR-based analyses that employ machine learning. Popular deep learning (and machine learning) methods are often used to tackle classification tasks and thus require ground-truth labels for training. For EHRs this can mean that researchers must hire multiple clinicians to manually read and annotate individual patients' records through a process called chart review. This allows researchers to assign "true" labels, i.e. those that match our best available knowledge. Depending on the application, sometimes the features constructed by algorithms also need to be manually validated and interpreted by clinicians. This can be time consuming and expensive [61]. Because of these costs, much of this research, including the work cited in this review, skips the process of expert review. Clinicians' skepticism for research without expert review may greatly dampen their enthusiasm for the work and consequently reduce its impact. To date, even well-resourced large national consortia have been challenged by the task of acquiring enough expert-validated labeled data. For instance, in the eMERGE consortia and PheKB database [62], most samples with expert validation contain only 100 to 300 patients. These datasets are quite small, even for simple machine learning algorithms. The challenge is greater for deep learning models with many parameters. While unsupervised and semi-supervised approaches can help with small sample sizes, the field would benefit greatly from large collections of anonymized records in which a substantial number of records have undergone expert review. This challenge is not unique to EHR-based studies. Work on medical images, -omics data in applications for which detailed metadata are required, and other applications for which labels are costly to obtain will be hampered as long as abundant curated data are unavailable.

Successful approaches to date in this domain have sidestepped this challenge by making methodological choices that either reduce the need for labeled examples or that use transformations to training data to increase the number of times it can be used before overfitting occurs. For example, the unsupervised and semi-supervised methods that we've discussed reduce the need for labeled examples [52]. The anchor and learn framework [63] uses expert knowledge to identify high confidence observations from which labels can be inferred. The adversarial training example strategies that we've mentioned can reduce overfitting, if transformations are available that preserve the meaningful content of the data while transforming irrelevant features [38]. While adversarial training examples can be easily imagined for certain methods that operate on images, it's more challenging to figure out what an equivalent transformation would be for a patient's clinical test results. Consequently, it may be hard to employ adversarial training examples, not to be confused with generative adversarial neural networks, with other applications. Finally, approaches that transfer features can also help use valuable training data most efficiently. Rajkomar et al. trained a deep neural network using generic images before tuning using only radiology images [64]. Datasets that require many of the same types of features might be used for initial training, before fine tuning takes place with the more sparse biomedical examples. Though the analysis hasn't yet been attempted, it's possible that analogous strategies may be possible with electronic health records. For example, features learned from the electronic health record for one type of clinical test (e.g. a decrease over time in a lab value) may transfer across phenotypes.

Methods to accomplish more with little high-quality labeled data are also being applied in other domains and may also be adapted to this challenge, e.g. data programming [65]. In data programming, noisy automated labeling functions are integrated. Numerous writers have described data as the new oil [66,67]. The idea behind this metaphor is that data are available in large quantities, valuable once refined, and the underlying resource that will enable a data-driven revolution in how work is done. Contrasting with this perspective, Ratner, Bach, and Ré described labeled training data as "The New New Oil" [68]. In this framing, data are abundant and not a scarce resource. Instead, new approaches to solve problems arise when labeled training data become sufficient to enable them. Based on our review of research on deep learning methods to categorize disease, the latter framing rings true.

We expect improved methods for domains with limited data to play an important role if deep learning is going to transform how we categorize states of human health. We don't expect that deep learning methods will replace expert review. We expect them to complement expert review by allowing more efficient use of the costly practice of manual annotation.

Data sharing is hampered by standardization and privacy considerations

To construct the types of very large datasets that deep learning methods thrive on, we need robust sharing of large collections of data. This is in part a cultural challenge. We touch on this challenge in the Discussion section. Beyond the cultural hurdles around data sharing, there are also technological hurdles related to sharing individual health records or deep models built from such records. This subsection deals primarily with these challenges.

EHRs are designed chiefly for clinical, administrative and financial purposes, such as patient care, insurance and billing [69]. Research is at best a tertiary priority, presenting significant challenges to EHR-based research in general, and particularly to data intensive deep learning research. These difficulties can be grouped into three areas: local bias, wider standards and legal issues. Note these problems are not restricted to EHR but can also apply to any large biomedical dataset, e.g. clinical trial data.

Even within the same healthcare system, EHRs can be used differently [70,71]. Individual users have unique usage patterns, with different departments and different hospitals having different priorities which code patients and introduce missing data in a non-random fashion [72]. Patient data may be kept across several "silos" within a single health system. Even the most basic task of matching patients across systems can be challenging due to data entry issues [73]. The situation is further exacerbated by the ongoing introduction, evolution and migration of EHR systems, especially where reorganized and acquired healthcare facilities have to merge. As a result, EHR can be less complete and less objective than expected.

In the wider picture, standards for EHRs are many and evolving. Proprietary systems, indifferent and scattered use of health information standards and controlled terminologies makes combining and comparison of data across systems challenging [74,75]. Further diversity arises from variation in languages, healthcare practices and demographics. Merging EHR gathered in different systems (and even under different assumptions) is challenging [76].

Combining or replicating studies across systems thus requires controlling for both the above biases and dealing with mismatching standards. This has the practical effect of reducing cohort size, limiting statistical significance, preventing the detection of weak effects [77] and restricting the number of parameters that can be trained in a model. Further, rules-based algorithms have been popular in EHR-based research but because these are developed at a single institution and trained with a specific patient population they do not transfer easily to other populations [78]. For example, Wiley et al. [79] showed that warfarin dosing algorithms often under-perform in African Americans, illustrating that some of these issues are unresolved even at a treatment best practices level. Lack of standardization also makes it challenging for investigators skilled in deep learning to enter the field, as numerous data processing steps must be performed before algorithms are applied.

Finally, even if data were perfectly consistent and compatible across systems, attempts to share and combine EHR data face considerable legal and ethical barriers. Patient privacy can severely restrict the sharing and use of EHR [80]. Here again, standards are heterogeneous and evolving but often EHR data can often not be exported or even accessed directly for research purposes without appropriate consent. Once again, this has the effect of making data gathering more laborious, expansive and reducing sample size and study power.

Several technological solutions have been proposed in this direction, allowing access to sensitive data satisfying privacy and legal concerns. Software like DataShield [81] and ViPAR [82], although not EHR specific, allows querying and combining of datasets and calculation of summary statistics across remote sites by "taking the analysis to the data". The computation is carried out at the remote site. Conversely, the EH4CR project [75] allows analysis of private data by use of an inter-mediation layer that interprets remote queries across internal formats and datastores and returns the results in a de-identified standard form, thus giving real-time consistent but secure access. Continuous Analysis [83] can allow reproducible computing on private data. Using such techniques intermediate results can be automatically tracked and shared without sharing the original data. While none of these have been used in deep learning, the potential is there.

Even without sharing data, algorithms trained on confidential patient data may present security risks or accidentally allow for the exposure of individual level patient data. Tramer et al. [84] showed the ability to steal trained models via public APIs and Dwork and Roth [85] demonstrate the ability to expose individual level information from accurate answers in a machine learning model. Attackers can use similar attacks to find out if particular data instance was present in the original training set for the machine learning model [86] - in this case, whether a person's record was present. This presents a potential hazard for approaches that aim to generate data. Choi et al. propose generative adversarial neural networks as a tool to make sharable EHR data [87]; however, the authors didn't take steps to protect the model from such attacks.

There are approaches to protect models, but they pose their own challenges. Training algorithms in a differentially private manner provides a limited guarantee that an algorithm's output will be equally likely to occur regardless of the participation of any one individual. The limit is determined by a single parameter which provides a quantification of privacy. Simmons et al. [88] present the ability to perform GWASs in a differentially private manner and Abadi et al. [89] show the ability to train deep learning classifiers under the differential privacy framework. Federated learning [90] and secure aggregations [91–93] are complementary approaches that reinforce differential privacy. Both aim to maintain privacy by training deep learning models from decentralized data sources such as personal mobile devices without transferring actual training instances. This is becoming of increasing importance with the rapid growth of mobile health applications. However, the training process in these approaches places constraints on the algorithms used and can make fitting a model substantially more challenging. In our own experience it can be trivial to train a model without differential privacy, but quite difficult to train one within the differential privacy framework. The problem can be particularly pronounced with small sample sizes.

While none of these problems are insurmountable or restricted to deep learning, they present challenges that cannot be ignored. Technical evolution in EHRs and data standards will doubtless ease - although not solve - the problems of data sharing and merging. More problematic are the privacy issues. Those applying deep learning to the domain should consider the potential of inadvertently disclosing the participants identity. Techniques that enable training on data without sharing the raw data may have a part to play. Training within a differential privacy framework may often be warranted.

Discrimination and "right to an explanation" laws

In April 2016, the European Union adopted new rules regarding the use of personal information, the General Data Protection Regulation (GDPR) [94]. A component of these rules can be summed up by the phrase "right to an explanation". Those who use machine learning algorithms must be able to explain how a decision was reached. For example, a clinician treating a patient who is aided by a machine learning algorithm may be expected to explain decisions that use the patient's data. The new rules were designed to target categorization or recommendation systems, which inherently profile individuals. Such systems can do so in ways that are discriminatory and unlawful

TODO: @traversc citation needed.

As datasets become larger and more complex, we may begin to identify relationships in data that are important for human health but difficult to understand. The algorithms described in this review and others like them may become highly accurate and useful for various purposes, including within medical practice. However, to discover and avoid discriminatory applications it will be important to consider algorithm interpretability alongside accuracy. For example, if we train an algorithm to predict which drugs would be prescribed during a patient's visit to the doctor and there's an existing pattern of racial differences in prescription behavior

(TODO: @traversc - you can pick a different example but I think we need one - whichever one you think is most fully supported by the literature.), this pattern could become baked into the predictions made by the algorithm. Machine learning practitioners, and particularly those who use deep neural networks, which are challenging to interpret, must remain cognizant of this possibility and make every effort to prevent harm from discriminatory predictions.

To reach their potential in this domain, deep learning methods will need to be interpretable. Researchers need to consider the extent to which biases may be learned by the model and whether or not a model is sufficiently interpretable to identify biases. We discuss the challenge of model interpretability more completely in the discussion section.

Temporal Patient Trajectories

Traditionally, physician training programs justified long training hours by citing increased continuity of care and learning by following the progression of a disease over time, despite the known consequences of decreased mental and quality of life [95–98]. Yet, a common practice in EHR-based research is to take a point in time snapshot and convert patient data to a traditional vector for machine learning and statistical analysis. This results in significant signal losses as timing and order of events provide insight into a patient's disease and treatment. Efforts to account for the order of events have shown promise [99] but require exceedingly large patient sizes due to discrete combinatorial bucketing. Lasko et al. [51] used autoencoders on longitudinal sequences of serum urine acid measurements to identify population subtypes. More recently, deep learning has shown promise working with both sequences (Convolutional Neural Networks) [100] and the incorporation of past and current state (Recurrent Neural Networks, Long Short Term Memory Networks)[101]. This may be a particular area of opportunity for deep neural networks. The ability to discover relevant sequences of events from large number of trajectories requires powerful and flexible feature construction methods - an area at which deep neural networks tend to excel.

How is deep learning used to study basic biological processes in a manner that may provide future insights into human disease?

The (awkward) placeholder section title is intended to help define the scope. We do not want this section to become a miscellaneous collection of everything that does not fit in Categorize and Treat.

One proposal is that we organize this roughly by what is being predicted, which will generally correspond to the types of data being used. For each sub-section we can quickly introduce the prediction problem and cite some examples of the relevance to disease. Hypothetically, if we had an algorithm that produced perfect predictions on the task, what would we learn and how could those predictions be used?

Existing reviews could be mentioned briefly.

It may not fit here, but there could be a general discussion of why different neural network architectures are particularly well-suited for different types of input data. For example, CNNs and RNNs for 1-dimensional data are used in several categories below.

A few suggestions for sub-sections follow. Some of these could be left out because our goal is not an exhaustive enumeration of methods. Some are important areas of biology, but there may not be much deep learning- specific

content to present. Others may be important areas where we lack expertise, in which case we may acknowledge the application area but not dive into merits or weaknesses of individual methods.

TODO: dropped signaling subsection, decide whether to discuss in intro and why it has received less attention, @rmjDc5rm as example

Gene expression

Gene expression measurements characterize the abundance of many thousands of RNA transcripts within a given organism, tissue, or cell. This characterization can represent the underlying state of the given system and can be used to study heterogeneity across samples as well as how the system reacts to perturbation. While gene expression measurements have been traditionally made by quantitative polymerase chain reaction (qPCR), low throughput fluorescence based methods, and microarray technologies, the field has shifted in recent years to primarily performing RNA sequencing (RNA-seq) to catalog whole transcriptomes. As such next generation sequencing technologies continue to fall in price and rise in throughput, applying deep learning to study gene expression data is likely to make training deep models more feasible. With increased modeling ability, deep learning approaches are likely to grow in popularity and lead to novel biological insights.

Already several deep learning approaches have been applied to gene expression data with varying aims. For instance, many researchers have applied unsupervised deep learning models to extract meaningful representations of gene modules or sample clusters. Denoising autoencoders have been used to cluster yeast expression microarrays into known modules representing cell cycle processes [102] and also to stratify yeast strains based on chemical and mutational perturbations [103]. Shallow (one hidden layer) denoising autoencoders have also been fruitful in extracting biological insight from thousands of *Pseudomonas aeruginosa* experiments [104,105] and in aggregating features relevant to specific breast cancer subtypes [18]. These unsupervised approaches applied to gene expression data are powerful methods for aggregating features and identifying gene signatures that may otherwise be overlooked by alternative methods. An additional benefit of unsupervised approaches is that ground truth labels, which are often difficult to acquire or are incorrect, are nonessential. However, careful interpretation must be performed regarding how the genes are aggregated into features. Precisely attributing node activations to specific biological functions risks over-interpreting models and can lead to incorrect conclusions.

Alternatively, deep learning approaches are also being applied to gene expression prediction tasks. For example, a deep neural network with three hidden layers outperformed linear regression in inferring the expression of over 20,000 target genes based on a representative, well-connected set of about 1,000 landmark genes [106]. However, while the deep learning model outperformed already existing algorithms in nearly every scenario, the model still displayed poor performance. The paper was also limited by computational bottlenecks that required data to be split randomly into two distinct models and trained separately. It is unclear how much performance would have increased if not for computational restrictions. Furthermore, a convolutional neural network applied to histone modifications, termed DeepChrome, [107] was shown to predict gene expression output. DeepChrome greatly improved high or low expression prediction accuracy over existing methods. Deep learning applied to epigenetic data for gene expression inference is a promising approach to study gene regulation. Deep learning approaches have also been applied to study cancer gene expression data with goals of identifying subtypes of patients with different molecular features and clinical manifestations [108]. In the study, the authors combine RBMs to integrate gene expression, DNA methylation, and miRNA data and use the constructed features in search of ovarian cancer subtypes. While the aforementioned approaches are promising, many convert gene expression measurements to categorical or binary variables thus ablating many complex gene expression signatures present in intermediate and relative numbers.

Deep learning applied to gene expression data is in its infancy but the future is bright. Many hypotheses can now be interrogated because of increasing amounts of data and new developing technologies. For example, there is a growing appreciation for the large impact of disease heterogeneity on research and treatment strategies for disease. New technologies are being developed, such as single cell RNA-seq and high throughput fluorescence based imaging that are good matches for deep learning. Concurrently, deep learning methods are being developed to address novel problems such as adjusting for batch effects in single-cell RNA-seq data [109]. Moreover, deep learning is already well established in the image processing community, so the marriage of fluorescence based imaging techniques and deep learning is natural. These technologies are growing in popularity and will provide increasingly novel perspectives with respect to how cellular heterogeneity impacts gene expression coordination within a sample. In general, as the flow of gene expression data increases, and techniques to integrate heterogeneous genomic measurements made on the same samples are enhanced, the quality and types of questions deep learning can address is poised to improve.

Splicing

Pre-mRNA transcripts can be spliced into different isoforms by retaining or skipping subsets of exons, or including parts of introns. This alternative splicing provides cells with enormous spatiotemporal flexibility to generate multiple distinct proteins from a single gene. Splicing is catalyzed by small nuclear RNAs (snRNAs) and spliceosomal proteins, which detect sequence motifs such as splice sites and exon sequence enhancers and silencers (ESE and ESS). Various RNA-binding proteins and noncoding RNAs can bias these reactions by altering binding affinities, blocking splice sites, or sequestering splicing factors. This remarkable complexity unfortunately lends itself to defects that underlie many diseases [110]. For instance, in Becker muscular dystrophy, a point mutation in dystrophin creates an ESS that induces

skipping of exon 31. A recent study found that quantitative trait loci (QTLs) that affect splicing in lymphoblastoid cell lines are enriched within risk loci for schizophrenia, multiple sclerosis and other immune diseases, implicating mis-splicing as a much more widespread feature of human pathologies than previously thought [111].

Sequencing studies routinely return thousands of unannotated variants. Which cause functional changes in splicing, and if so, how? Prediction of a “splicing code” has been a holy grail over the past decade. Initial machine learning approaches used a naive Bayes model and a 2-layer Bayesian neural network with thousands of hand-derived sequence-based features to predict the probability of exon skipping [112,113]. With the advent of deep learning, more complex models were built that provided better predictive accuracy [114,115]. Importantly, these new approaches can take in not only genomic features, but also tissue identity and CLIP-seq measurements of interactions between splicing factors and RNA, which all improve predictive accuracy.

The massive improvement seen with deep learning seems to stem from hidden layers being able to create new higher-order “features”, whereas earlier approaches often assumed independence of features and were unable to generalize. Higher-order understanding is especially important in splicing, which depends not only on the primary sequence, but also local RNA structure, tissue identity, splicing factor binding, and other currently unknown factors — all of which interact in complex, incompletely characterized ways. With new tools to interpret these meta-features, a major focus of current deep learning research, we will soon have the ability to extract a more nuanced biological understanding of splicing — perhaps by interrogating informative hidden nodes within neural networks that take in tissue type as part of the input, or by building separate networks for each tissue type and looking for common versus distinctive nodes [116].

A parallel effort has been to use more data with simpler models. An exhaustive study using readouts of splicing for millions of synthetic intronic sequences was able to describe motifs that influence the strength of alternative splice sites [117]. Interestingly, they built a simple linear model using hexamer motif frequencies that successfully generalized to exon skipping: in a limited analysis using SNPs from three genes, it predicted exon skipping with three times the accuracy of Xiong et al.’s framework. This case is instructive in that clever sources of data, not just more powerful models, can lead to novel insights.

We already understand how mis-splicing of a single gene can cause diseases such as Duchenne muscular dystrophy. The challenge now is to uncover how alternative splicing genome-wide gives rise to or is involved in complex, non-Mendelian diseases such as autism, schizophrenia, Type 1 diabetes, and multiple sclerosis [118]. As a proof of concept, Xiong et al. [114] sequenced five ASD and 12 control samples, each with an average of 42,000 rare variants, and identified 19 genes with neural functions that are mis-spliced. Deep learning will allow scientists and clinicians to rapidly profile thousands of unannotated variants for functional effects on splicing and nominate candidates for further investigation. Moreover, these nonlinear algorithms can deconvolve the effects of multiple variants on a single splice event without the need to perform combinatorial *in vitro* experiments.

Our end goal is to predict an individual’s tissue-specific, exon-specific splicing patterns from their genome sequence and other measurements. Knowing exactly which genes are mis-spliced in each tissue could enable a new branch of precision diagnostics that also stratifies patients and suggests targeted therapies to correct splicing defects. A continued focus on interpreting the “black box” of deep neural networks, along with integrating more comprehensive and diverse data sources, will likely provide the path forward to a better understanding of the basic determinants of splicing and its links to complex disease, which will lead to novel diagnostics and therapeutics.

Transcription factors and RNA-binding proteins

Transcription Factor and RNA-binding proteins are key components for gene regulation, making them very important to understand for higher level biological processes. While high-throughput sequencing techniques such as chromatin immunoprecipitation and massively parallel DNA sequencing (ChIP-seq) have been able to accurately identify binding regions for DNA and RNA proteins, these experiments are both time consuming and expensive. In addition, the sequencing methods do not provide any sort of analysis on the proteins which would lead to a better understanding of the underlying process. Thus, there is a need to computationally predict and understand these binding regions *de novo* from sequences.

Transcription factors

Transcription factors (TFs) are regulatory proteins that bind to certain locations on a DNA sequence and control the rate of mRNA production. ChIP-seq and related technologies are able to identify highly likely binding sites for a certain TF, and databases such as ENCODE [119] have provided ChIP-seq data for hundreds of different TFs across many laboratories. However, ChIP-seq experiments are expensive and time consuming. Since the data that scientists have discovered is available, *in silico* methods to predict binding sites are of great interest, thus eliminating the need to do new ChIP-seq experiments every time analysis is done on a new sequence.

In order to computationally predict transcription factor binding sites (TFBSs) on a DNA sequence, researchers initially used consensus sequences and position weight matrices to match against a test sequence [120]. Simple neural network classifiers were then proposed to differentiate positive and negative binding sites but did not show significant improvements over the weight matrix matching methods [121]. Later, SVM techniques outperformed the generative

methods by using k-mer features [122,123], but string kernel based SVM systems are limited by expensive computational cost proportional to the number of training and testing sequences. More recently, [124] showed that convolutional neural network models could achieve state of the art results on the TFBS task and are scalable to a large number of genomic sequences.

Since the work by [124] was published, there have been a multitude of deep learning works on the TFBS task. Due to the motif-driven nature of the TFBS task, most architectures have been convolutional-based, as summarized in [125]. [126] introduced several new convolutional and recurrent neural network models for predicting TFBSs, which showed improvements over other deep learning models on the dataset from [124]. While many models for TFBS prediction resemble computer vision and natural language processing (NLP) tasks, it is important to note that DNA sequence tasks are fundamentally different than NLP tasks, and thus the models should be adapted from traditional deep learning models in order to account for such differences. For example, motifs may appear in either strand of a DNA sequence, resulting in two different forms of the motif (forward and reverse complement) due to complementary base pairing. To handle this issue, [127] created a convolutional model which can find motifs in both directions. Since deep learning for protein binding prediction is still in early stages, we expect to see an increase in domain-specific architectures for this task.

Deep learning models have shown great accuracy on TFBS prediction, but the results are not fully convincing for several reasons. First, ChIP-seq experiments give a continuous value of binding likelihood at a certain location based on many experiments at that location in DNA. Based on these values, the TFBS task is usually converted into a binary classification task based on a certain threshold of the ChIP-seq value. However, the ChIP-seq values are often noisy, resulting in a target class that may be incorrect dependent on the defined threshold. Converting the task into a binary classification isn't completely accurate since the model may give a high probability of a binding site, but the ChIP-seq binding signal may be just barely over the binary classification threshold, resulting in potential false positive (or the signal may be just below the threshold, resulting in potential false negatives).

Second, most datasets for TFBS prediction are separated by TF, requiring a separate model for each TF (i.e. binary classification on each TF sub-dataset). In reality, there may be multiple TFs binding at the same location and TF binding may be dependent on other TFs, thus requiring both a dataset which gives all TF binding values at every location as well as a multi-task model. [124] use multiple TFs at once, but TF binding prediction is an intermediate step for predicting effects of noncoding variants in their model, so TFBS prediction is not heavily analyzed.

A third issue is that it is unclear exactly how to include non-binding or "negative" sites in the datasets. Since the number of positive binding sites of a particular TF is relatively small with respect to the total number of base-pairs in DNA, we must choose a small subset of the total non-binding sites, resulting in some sort of bias over all of the actual negative sites. Regardless of the negative site selection, most datasets evenly balance the positive and negative binding sites and report auROC for the metric. This is very misleading in a task where the binding sites are very unevenly balanced in the real world (see Discussion). Thus, we need datasets which more accurately model real TFBS data.

At the model level, while deep learning models have shown that it is possible to automatically extract features for TFBS prediction at the sequence level, these basic models cannot predict the binding on new unseen cell types or conditions. Since ChIP-seq experiments have been performed on only a small subset of cell lines, these prediction models are not of use for new or rare cell lines. To handle this issue and create models which can be used across cell lines, there are several options. The most prominent would be to introduce a multimodal model that, in addition to sequence data, incorporates cell-line specific features such as chromatin accessibility, DNA methylation, or gene expression. Without cell-specific features, the other option is to use domain adaptation methods where we train our model on a source cell type and use unsupervised feature extraction methods to predict on a target cell type. [116] predicts binding in new cell type-TF pairs, but the cell types must be in the training set for other TFs besides the target TF. A more general domain transfer model across cell types would be more useful.

While neural architectures are rapidly changing and producing better results, it is clear that deep learning can be efficiently and effectively used to do functional prediction on the genome given raw data.

Accurately predicting transcription factors computationally is useful, but it is also important to understand how these computational models make their predictions. To handle this, several papers have focused on understanding machine learning models [124,126,128]. [124] was the first to introduce a visualization method for a deep learning model on the TFBS task, and they did so by visualizing the learned convolution filters which were informative for the model's prediction of a specific sample. However, this approach was specific to visualizing certain samples fed through their particular model. [126] introduced a suite of state-of-the-art deep learning models and new visualizations techniques for a more in-depth analysis of TFBSs. Furthermore, [128] introduced an advanced visualization method and toolbox for analyzing possible TFBS sequences. [124] also introduced mutation maps, where they could easily mutate, add, or delete base pairs in a sequence and see how the model changed its prediction. This is something that would be very time consuming in a lab setting, but easy to simulate using their model. Visualization techniques on deep learning models are important because they can provide new insights on regulatory mechanisms and can lead biologists to test and verify in a lab setting, leading to new biomedical knowledge. Since the "linguistics" of DNA are unclear, interpretability of models is crucial to pushing our understanding forward.

TODO: cut RNA-binding proteins from above section, refer to representative papers

Promoters, enhancers, and related epigenomic tasks

TODO: There's inevitably a lot of overlap between this and the transcription binding section. Maybe in the long term think about restructuring to one big "r

Identification of promoters and other cis-regulatory elements (CREs) presents an obvious use case for deep learning. Transcriptional control is undoubtedly a vital - and early - part of the regulation of gene expression. An abundance of sequence and associated functional data (e.g. ENCODE, ExAC) exists across species. At the same time, studies of gene regulation have often focused on the protein (binding) rather than promoter level [129], perhaps due to the ill-defined nature of CREs. A promoter itself can be seen as an assemblage of "active" binding sites for transcription factors interspersed by less-characterized and perhaps functionally silent spacer regions. However, the sequence signals that control the start and stop of transcription and translation are still not well understood, compounded by incomplete understanding of alternative transcripts and the context for these alternatives. Sequence similarity is poor even between functionally correlated genes. While homologs might be studied for insight, they may not exist or may be just as poorly characterized.

Recognizing enhancers presents additional challenges. Enhancers may be up to 1 Mbp upstream or downstream from the target promoter, on either strand, even within the introns of other genes [130]. They do not necessarily operate on the nearest gene and may in fact effect multiple genes. Their activity is frequently tissue- or context-specific. A substantial fraction of enhancers displays modest or no conservation across species. There is no universal enhancer sequence signal or marker for enhancers, and some literature suggests that enhancers and promoters may be just categories along a spectrum [131]. One study [132] even showed that only 33% of predicted regulatory regions could be validated, while a class of "weak" predicted enhancers were strong drivers of expression. Yet there is growing evidence for their vast ubiquity, making them possibly the predominant functional non-coding element. Thus, identifying enhancers is critical yet the search space is embarrassingly large.

While prior (non-deep learning) approaches have made steady improvements on promoter prediction, there is little consensus on the best approach and performance is poor. Typically algorithms will recognize only half of all promoters, with an accompanying high false positive rate [133]. Methods with better sensitivity generally do so at the cost of poorer specificity. Conventional identification of enhancers has leaned heavily on simple conservation or laborious experimental techniques, with only moderate sensitivity and specificity. For example, while chromatin accessibility has often been used for identifying enhancers, this also "recognizes" a wide variety of other functional elements, like promoters, silencers and repressors.

The complex nature of CREs (and our ignorance as to what are the important features of them) therefore seems a good subject for deep learning approaches. Indeed, neural networks were used for promoter recognition as early as 1996, albeit with mixed results [134]. Since then, there have been much work in applying deep learning to this area, although little in the way of comparative studies or reviews. We will therefore focus on a few recent characteristic studies to outline the state of the art and extant problems.

Most broadly, Kelley et al. [135] trained CNNs on DNA accessibility datasets, getting a marked improvement on previous methods, albeit still with a high false positive rate. (Note as above, using DNA accessibility conflates enhancers with other functional sites.) This study also featured a useful interpretability approach (analogous to *in silico* mutagenesis [136]) introducing known protein binding motifs into sequences and measuring the change in predicted accessibility.

Umarov et al. [137] demonstrated the use of Convolutional Neural Networks in recognizing promoter sequences, achieving markedly better performance than conventional methods (sensitivity and specificity exceeding 90%). While some results were achieved over bacterial promoters (which are considerably simpler in structure), surprisingly roughly similar performance was found for human promoters. This work also included a promising and simple method for interpretability (randomly substituting bases in a recognized promoter region, then checking for a change in recognition) that would be useful to exploit more widely.

Xu et al. [138] applied CNNs to the detection of enhancers, achieving incremental improvements in specificity and sensitivity over previous SVM-based approach, and markedly better performance for cell-specific enhancers. A massive improvement in speed was also achieved. Additionally, they compared the performance of different CNN architectures, finding that while layers for batch normalization improved performance, surprisingly deeper architectures decreased performance.

Singh et al. [139] also used batch normalization, approaching the problem of predicting enhancer-promoter interactions from solely the sequence and location of putative enhancers and promoters in a particular cell type. Performance was comparative to state of the art conventional techniques that used the whole gamut of full functional genomic and non-sequence data.

Given the conflation between different CREs, the study of Li et al. [140] is particularly interesting. They used a feed-forward neural network to distinguish classes of CREs and activity states. Active enhancers and promoters could be easily distinguished, as could active and inactive elements. Perhaps unsurprisingly, it was difficult to distinguish

between inactive enhancers and promoters. They also investigated the power of sequence features to drive classification, finding that beyond CpG islands, few were useful.

In summary, deep learning is a promising approach for identifying CREs, able to interrogate sequence features that are complex and ill-understood, already offering marked improvements on the prior state of the art. However, the exact methodology is up for debate and needs examination and more comparative study. Work needs to be done in understanding the best architecture to be used. Further concern surrounds the training data. CNNs require a large training set to avoid over-fitting, yet in many cases we do not have a large "gold standard" dataset to train against. Further more, the quality and meaning of training data needs to be closely considered, given that a "promoter" or "enhancer" may only be putative or dependent on the experimental method or context of identification. Else we risk building detectors not for CREs but putative CREs. The best model of negative sample needs also to be considered, as does the problem of imbalanced data. In a sentence, these methods can only be as good as their training data. Finally, interpretability is a problem but one that appears to be solvable given empirical approaches.

TODO: discuss enhancer-promoter and enhancer-target prediction

Micro-RNA binding

Prediction of microRNAs (miRNAs) in the genome as well as miRNA targets is of great interest, as they are critical components of gene regulatory networks and are often conserved across great evolutionary distance [141,142]. While many machine learning algorithms have been applied to solve these prediction tasks, they currently require extensive feature selection and optimization. For instance, one of the most widely adopted tools for miRNA target prediction, TargetScan, trained multiple linear regression models on 14 hand-curated features including structural accessibility of the target site on the mRNA, the degree of site conservation, and predicted thermodynamic stability of the miRNA:mRNA complex [143]. Some of these features, including structural accessibility, are imperfect or empirically derived. In addition, current algorithms suffer from low specificity [144].

As in other applications, deep learning promises to achieve equal or better performance in predictive tasks by automatically engineering complex features to minimize an objective function. Two recently published tools use different recurrent neural network-based architectures to perform miRNA and target prediction with solely sequence data as input [144,145]. Though the results are preliminary and still based on a validation set rather than a completely independent test set, they were able to predict microRNA target sites with 15-25% higher specificity and sensitivity than TargetScan. Excitingly, these tools seem to show that RNNs can accurately align sequences and predict bulges, mismatches, and wobble base pairing without requiring the user to input secondary structure predictions or thermodynamic calculations.

Further incremental advances in neural-network approaches for miRNA and target prediction will likely be sufficient to meet the current needs of systems biologists and other researchers, who use prediction tools mainly to nominate candidates that are then tested experimentally. Similar to other applications, the major contribution of deep learning will be to deliver deep insights into the biology of miRNA targeting as we learn to interrogate the hidden nodes within neural networks.

Protein secondary and tertiary structure

Proteins play fundamental roles in all biological processes including the maintenance of cellular integrity, metabolism, transcription/translation, and cell-cell communication. Complete description of protein structures and functions is a fundamental step towards understanding biological life and also highly relevant in the development of therapeutics and drugs. UniProt currently has about 94 millions of protein sequences. Even if we remove redundancy at 50% sequence identity level, UniProt still has about 20 millions of protein sequences. However, fewer than 100,000 proteins have experimentally-solved structures in Protein Data Bank (PDB). As a result, computational structure prediction is essential for a majority number of protein sequences. However, predicting protein 3D structures from sequence alone is very challenging, especially when similar solved structures (called templates) are not available in PDB. In the past decades, various computational methods have been developed to predict protein structure from different aspects, including prediction of secondary structure, torsion angles, solvent accessibility, inter-residue contact map, disorder regions and side-chain packing.

Machine learning is extensively applied to predict protein structures and some success has been achieved. For example, secondary structure can be predicted with about 80% of 3-state (i.e., Q3) accuracy by a neural network method PSIPRED [146]. Starting from 2012, deep learning has been gradually introduced to protein structure prediction. The adopted deep learning models include deep belief network, LSTM(long short-term memory), deep convolutional neural networks (DCNN) and deep convolutional neural fields[23,147]. Here we focus on deep learning methods for two representative sub-problems: secondary structure prediction and contact map prediction. Secondary structure refers to local conformation of a sequence segment while a contact map contains information of global conformation. Secondary structure prediction is a basic problem and almost an essential module of any protein structure prediction package. It has also been used as sequence labeling benchmark in the machine learning community. Contact prediction is much more challenging than secondary structure prediction, but it has a much larger impact on tertiary structure prediction. In recent years, contact prediction has made good progress and its accuracy has been significantly improved [148–151].

Protein secondary structure can exhibit three different states (alpha helix, beta strand and loop regions) or eight finer-grained states. More methods are developed to predict 3-state secondary structure than 8-state. A predictor is typically evaluated by 3-state (i.e., Q3) and 8-state (i.e., Q8) accuracy, respectively. Qi et al. developed a multi-task deep learning method to simultaneously predict several local structure properties including secondary structures [152]. Spencer, Eickholt and Cheng predicted secondary structure using deep belief networks [22]. Heffernan and Zhou et al. developed an iterative deep learning framework to simultaneously predict secondary structure, backbone torsion angles and solvent accessibility [153]. However, none of these deep learning methods achieved significant improvement over PSIPRED [154] in terms of Q3 accuracy. In 2014, Zhou and Troyanskaya demonstrated that they could improve Q8 accuracy over a shallow learning architecture conditional neural fields [155] by using a deep supervised and convolutional generative stochastic network [156], but did not report any results in terms of Q3 accuracy. In 2016 Wang and Xu et al. developed a deep convolutional neural fields (DeepCNF) model that can significantly improve secondary structure prediction in terms of both Q3 and Q8 accuracy [23]. DeepCNF possibly is the first that reports Q3 accuracy of 84-85%, much higher than the 80% accuracy maintained by PSIPRED for more than 10 years. It is also reported that DeepCNF can improve prediction of solvent accessibility and disorder regions [147]. This improvement may be mainly due to the introduction of convolutional neural fields to capture long-range sequential information, which is important for beta strand prediction. Nevertheless, improving secondary structure prediction from 80% to 84-85% is unlikely to result in a similar amount of improvement in tertiary structure prediction since secondary structure mainly reflects coarse-grained local conformation of a protein structure.

Protein contact prediction and contact-assisted folding (i.e., folding proteins using predicted contacts as restraints) represents a promising new direction for ab initio folding of proteins without good templates in PDB. Evolutionary coupling analysis (ECA) is an effective contact prediction method for some proteins with a very large number (>1000) of sequence homologs [151], but ECA fares poorly for proteins without many sequence homologs. Since (soluble) proteins with many sequence homologs are likely to have a good template in PDB, to make contact-assisted folding practically useful for ab initio folding, it is essential to predict accurate contacts for proteins without many sequence homologs. By combining ECA with a few other protein features, shallow neural network-based methods such as MetaPSICOV [149] and CoinDCA-NN [157] have shown some advantage over ECA for proteins with a small number of sequence homologs, but their accuracy is still not very good. In recent years, deep learning methods have been explored for contact prediction. For example, Di Lena et al. introduced a deep spatio-temporal neural network (up to 100 layers) that utilizes both spatial and temporal features to predict protein contacts [158]. Eickholt and Cheng combined deep belief networks and boosting techniques to predict protein contacts [159] and trained deep networks by layer-wise unsupervised learning followed by fine-tuning of the entire network. Skwark and Elofsson et al. developed an iterative deep learning technique for contact prediction by stacking a series of Random Forests [160]. However, blindly tested in the well-known CASP competitions, these methods did not show any advantage over MetaPSICOV [149], a method using two cascaded neural networks. Very recently, Wang and Xu et al. proposed a novel deep learning method RaptorX-Contact [148] that can significantly improve contact prediction over MetaPSICOV especially for proteins without many sequence homologs. RaptorX-Contact employs a network architecture formed by one 1D residual neural network and one 2D residual neural network. Blindly tested in the latest CASP competition (i.e., CASP12 [161]), RaptorX-Contact is ranked first in terms of the total F1 score (a widely-used performance metric) on free-modeling targets as well as the whole set of targets. In the CASP12 test, the group ranked second also employed a deep learning method. Even MetaPSICOV, which ranked third in CASP12, employed more and wider hidden layers than its old version. Wang and Xu et al. have also demonstrated in another blind test CAMEO (which can be interpreted as a fully-automated CASP) [162] that their predicted contacts can help fold quite a few proteins with a novel fold and only 65-330 sequence homologs and that their method also works well on membrane protein contact prediction even if trained mostly by non-membrane proteins. In fact, most of the top 10 contact prediction groups in CASP12 employed some kind of deep learning techniques. The RaptorX-Contact method performed better mainly due to introduction of residual neural networks and exploiting contact occurrence patterns by simultaneous prediction of all the contacts in a single protein. It is still possible to further improve contact prediction by studying new deep network architectures. However, current methods fail when proteins in question have almost no sequence homologs. It is unclear if there is an effective way to deal with this type of proteins or not except waiting for more sequence homologs. Finally, the deep learning methods summarized above also apply to interfacial contact prediction of a protein complex, but may be less effective since on average protein complexes have fewer sequence homologs.

Morphological phenotypes

A field poised for dramatic revolution by deep learning is bioimage analysis. Thus far, the primary use of deep learning for biological images has been for segmentation - that is, for the identification of biologically relevant structures in images such as nuclei, infected cells, or vasculature, in fluorescence or even brightfield channels [163]. Once so-called regions of interest have been identified, it is often straightforward to measure biological properties of interest, such as fluorescence intensities, textures, and sizes. Given the dramatic successes of deep learning in biological imaging, we simply refer to articles that review recent advancements [12,163,164]. We believe deep learning will become a commonplace tool for biological image segmentation once user-friendly tools exist.

We anticipate an additional kind of paradigm shift in bioimaging that will be brought about by deep learning: what if images of biological samples, from simple cell cultures to three-dimensional organoids and tissue samples, could be mined for much more extensive biologically meaningful information than is currently standard? For example, a recent

study demonstrated the ability to predict lineage fate in hematopoietic cells up to three generations in advance of differentiation [165]. In biomedical research, by far the most common paradigm is for biologists to decide in advance what feature to measure in images from their assay system. But images of cells contain a wide variety of quantitative information, and deep learning may just be the tool to extract it. Although classical methods of segmentation and feature extraction can produce hundreds of metrics per cell in an image, deep learning is unconstrained by human intuition and can in theory extract more subtle features. Already, there is evidence deep learning can surpass the efficacy of classical methods [166], even using generic deep convolutional networks trained on natural images [167], known as transfer learning.

The impact of further improvements on biomedicine could be enormous. Comparing cell population morphologies using conventional methods of segmentation and feature extraction has already proven useful for functionally annotating genes and alleles, identifying the cellular target of small molecules, and identifying disease-specific phenotypes suitable for drug screening [168–170]. Deep learning would bring to these new kinds of experiments - known as image-based profiling or morphological profiling - a higher degree of accuracy, stemming from the freedom from human-tuned feature extraction strategies.

TODO: Make sure that at the end we clearly emphasize our excitement around unsupervised uses.

Single-cell

Single-cell methods are generating extreme excitement as biologists recognize the vast heterogeneity within unicellular species and between cells of the same tissue type in the same organism [171]. For instance, tumor cells and neurons can both harbor extensive somatic variation [172]. Understanding single-cell diversity in all its dimensions — genetic, epigenetic, transcriptomic, proteomic, morphologic, and metabolic — is key if precision medicine is to be targeted not only to a specific individual, but also to specific pathological subsets of cells. Single-cell methods also promise to uncover a wealth of new biological knowledge. A sufficiently large population of single cells will have enough representative “snapshots” to recreate timelines of rapid biological processes. If tracking processes over time is not the limiting factor, single cell techniques can provide maximal resolution compared to averaging across all cells in bulk tissue, enabling the study of transcriptional bursting with single-cell FISH or the heterogeneity of epigenetic patterns with single-cell Hi-C or ATAC-seq [173,174].

However, large challenges exist in studying single cells. Relatively few cells can be assayed at once using current droplet, imaging, or microwell technologies, and low-abundance molecules or modifications may not be detected by chance in a phenomenon known as dropout. To solve this problem, Angermueller et al. [175] trained a neural network to predict the presence or absence of methylation of a specific CpG site in single cells based on surrounding methylation signal and underlying DNA sequence, achieving several percentage points of improvement compared to random forests or deep networks trained only on CpG or sequence information. Similar deep learning methods have been applied to impute low-resolution ChIP-seq signal from bulk tissue with great success, and they could easily be adapted to single cell data [116,176].

Examining populations of single cells can reveal biologically meaningful subsets of cells as well as their underlying gene regulatory networks [177]. Unfortunately, machine learning generally struggles with unbalanced data — when there are many more inputs of class 1 than class 2 — because prediction accuracy is usually evaluated over the entire dataset. To tackle this challenge, Arvaniti et al. [178] classified healthy and cancer cells expressing 25 markers by using the most discriminative filters from a CNN trained on the data as a linear classifier. They achieved an impressive precision of 50% to 90% with 80% recall on cells where the subset percentage ranged from 0.1 to 1%, which significantly outperformed logistic regression and distance-based outlier detection methods. However, they did not benchmark against random forests, which tend to be better with unbalanced data, or against the neural network itself, and their data was fairly low dimensional. Future work will be needed to establish the utility of deep learning in cell subset identification, but the stunning improvements in image classification over the past 5 years [179] suggest that this goal will be achievable.

The sheer quantity of “omic” information that can be obtained from each cell, as well as the number of cells in each dataset, uniquely position single-cell data to benefit from deep learning. In the future, lineage tracing could be revolutionized by using autoencoders to reduce the feature space of transcriptomic or variant data followed by algorithms to learn optimal cell differentiation trajectories [180], or by feeding cell morphology and movement into neural networks [165]. Reinforcement learning algorithms [7] could be trained on the evolutionary dynamics of cancer cells or bacterial cells undergoing selection pressure and reveal whether patterns of adaptation are random or deterministic, allowing us to develop therapeutic strategies that forestall resistance. It will be exciting to see the creative applications of deep learning to single-cell biology that emerge over the next few years.

TODO: <https://github.com/greenelab/deep-review/issues/153>

Metagenomics

TODO: Add reference tags to this section Metagenomics (which refers to the study of genetic material, 16S rRNA and/or whole-genome shotgun DNA, from microbial communities) has revolutionized the study of micro-scale ecosystems within us and around us. There is increasing literature of applying machine learning in general to metagenomic analysis. In the

late 2000's, a plethora of machine learning methods were applied to classifying DNA sequencing reads to the thousands of species within a sample. An important problem is genome assembly from these mixed-organism samples. And to do that, the organisms should be "binned" before assembling. Binning methods began with many k-mer techniques [181] and then delved into other clustering algorithms, such as self-organizing maps (SOM)[182]. Then came the taxonomic classification problem, with researchers naturally using BLAST [183], followed by other machine learning techniques such as SVMs [184], naive Bayesian classifiers [185], etc. to classify each read. Then, researchers began to use techniques that could be used to estimate relative abundances of an entire sample, instead of the precise but painstakingly slow read-by-read classification. Relative abundance estimators (a.k.a diversity profilers) are MetaPhlan [186], (WGS)Quikr [187], and some configurations of tools like OneCodex[188] and LMAT [189]. While one cannot identify which reads were mapped back to an organism using relative abundance estimators, they can be useful for faster comparative and other downstream analyses. Newer methods hope to classify reads and estimate relative abundances at faster rates [190] and as of this writing, there are more than 70 metagenomic taxonomic classifiers in existence. Besides binning and classification of species, there is functional identification and annotation of sequence reads [191,192]. However, the focus on taxonomic/functional annotation is just the first step. Once organisms are identified, there is the interest in understanding the interrelationship between these organisms and host/environment phenotypes [193]. One of the first attempts was a survey of supervised classification methods for microbes->phenotype classification [194], followed by similar studies that are more massive in scale[195,196]. There have been techniques that bypass the taxonomic classification step altogether [197], (sequence composition to phenotype classification). Also, researchers have looked into how feature selection can improve classification [196,198], and techniques have been proposed that are classifier-independent [199,200].

So, how have neural networks (NNs) been of use? Most neural networks are being used for short sequence->taxa/function classification, where there is a lot of data for training (and thus suitable for NNs). Neural networks have been applied successfully to gene annotation (e.g. Orphelia [201] and FragGeneScan [202]), which usually has plenty of training examples. Representations (similar to Word2Vec [47] in natural language processing) for protein family classification has been introduced and classified with a skip-gram neural network [203]. Recurrent neural networks show good performance for homology and protein family identification [204,205]. Interestingly, Hochreiter, who invented Long Short Term Memory, delved into homology/protein family classification in 2007, and therefore, deep learning is deeply rooted in functional classification methods.

One of the first techniques of "de novo" genome binning used self-organizing maps, a type of NN[182]. Essinger et al. use ART, a neural network algorithm called Adaptive Resonance Theory, to cluster similar genomic fragments and showed that it has better performance than K-means. However, other methods based on interpolated Markov models [206] have performed better than these early genome bidders. Also, neural networks can be slow, and therefore, have had limited use for reference-based taxonomic classification, with TAC-ELM [207] being the only NN-based algorithm to taxonomically classify massive amounts of metagenomic data. Also, neural networks can fail to perform if there are not enough training examples, which is the case with taxonomic classification (since only ~10% of estimated species have been sequenced). An initial study shows that deep neural networks have been successfully applied to taxonomic classification of 16S rRNA genes, with convolutional networks provide about 10% accuracy genus-level improvement over RNNs and even random forests [208]. However, this study performed 10-fold cross-validation on 3000 sequences in total.

Due to the traditionally small numbers of metagenomic samples in studies, neural network uses for classifying phenotype from microbial composition are just beginning. A standard MLP was able to classify wound severity from microbial species present in the wound [209]. Recently, multi-layer, recurrent networks (and convolutional networks) have been applied to microbiome genotype-phenotype, with Ditzler et al. being the first to associate soil samples with pH level using multi-layer perceptrons, deep-belief networks, and recursive neural networks (RNNs) [210]. Besides classifying the samples appropriately, Ditzler shows that internal phylogenetic tree nodes inferred by the networks are appropriate features representing low/high pH, which can provide additional useful information and new features for future metagenomic sample comparison. Also, an initial study has show promise of these networks for diagnosing disease [211].

There are still a lot of challenges with applying deep neural networks to metagenomics problems. They are not ideal for microbial/functional composition->phenotype classification because most studies contain tens of samples (~20->40) and hundreds/thousands of features (aka species). Such underdetermined/ill-conditioned problems are still a challenge for deep neural networks that require many more training examples than features to sufficiently converge the weights on the hidden layers. Also, due to convergence issues (slowness and instability due to large neural networks modeling very large datasets [212]), taxonomic classification of reads from whole genome sequencing seems out of reach at the moment for deep neural networks -- due to only thousands of full-sequenced genomes as compared to hundreds of thousands of 16S rRNA sequences available for training.

However, because recurrent neural networks are showing success for base-calling (and thus removing the large error in the measurement of a pore's current signal) for the relatively new Oxford Nanopore sequencer [213], there is hope that the process of denoising->organism/function classification can be combined into one step in using powerful LSTM's. LSTM's are working miracles in raw speech signal->meaning translation [214], and combining steps in metagenomics are not out of the question. For example, metagenomic assembly usually requires binning then assembly, but could deep neural nets accomplish both tasks in one network? Does functional/taxonomic classification need to be separate

processes? The largest potential in deep learning is to learn "everything" in one complex network, with a plethora of labeled (reference) data and unlabeled (microbiome experiments) examples.

Sequencing and variant calling

While we have so far discussed the role of deep learning in analyzing genomic data, deep learning approaches can also substantially improve our ability to obtain the genomic data itself. We will discuss two specific challenges: calling SNPs (single nucleotide polymorphisms) and indels (insertions and deletions) with high specificity and sensitivity, and improving the accuracy of new types of data such as nanopore sequencing. These two tasks are critical for studying rare variation, allele-specific transcription and translation, and splice site mutations, among others. In the clinical realm, sequencing of rare tumor clones and other genetic diseases will require accurate calling of SNP and indels.

Current methods achieve relatively high (>99%) precision at 90% recall for SNPs and indel calls from Illumina short-read data [215], yet this leaves a large number of potentially clinically significant remaining false positives and false negatives. These methods have so far relied on experts to build probabilistic models that reliably separate signal from noise. However, this process is time consuming and, more importantly, fundamentally limited by how well we understand and can model the factors that contribute to noise. Recently, two groups have applied deep learning to construct data-driven and, therefore, unbiased noise models. One of these models, DeepVariant, leverages Inception, a neural network trained for image classification by Google Brain, by encoding reads around a candidate SNP as a 221x100 bitmap image, where each column is a nucleotide and each row is a read from the sample library [215]. The top 5 rows represent the reference, and the bottom 95 rows represent randomly sampled reads that overlap the candidate variant. Each RGBA (red/green/blue/alpha) image pixel encodes the base (A, C, T, G) as a different R value, quality score as a G value, strand as a B value, and variation from the reference as the alpha value. The neural network outputs genotype probabilities for each candidate variant. They were able to achieve better performance than GATK, a leading genotype caller, even when GATK was given information about population variation for each candidate variant. Another method, still in its infancy, hand-developed 642 features for each candidate variant and fed these vectors into a fully connected deep neural network [216]. Unfortunately, this feature set required at least 15 iterations of software development to fine-tune, which will likely not be generalizable.

Going forward, we believe that variant calling will benefit more from optimizing neural network architectures than from developing features by hand. An interesting and informative next step would be to rigorously test whether encoding raw sequence and quality data as an image, tensor, or some other mixed format produces the best variant calls. Because many of the latest neural network architectures (ResNet, Inception, Xception, and others) are already optimized for and pre-trained on generic, large-scale image datasets [217], encoding genomic data as images could prove to be a generally effective, and efficient, strategy.

In limited experiments, DeepVariant was robust to sequencing depth, read length, and even species [215]. However, a model built on Illumina data, for instance, may not be applicable to PacBio long-read data or MinION nanopore data, which have vastly different specificity and sensitivity profiles and signal-to-noise characteristics. Recently, Boza et al. used bidirectional recurrent neural networks to infer the *E. coli* sequence from MinION nanopore electric current data with 2% higher per-base accuracy than the proprietary hidden Markov model-based algorithm Metrichor (86% to 88%) [213]. Unfortunately, training any neural network requires a large amount of data, which is often not available for new sequencing technologies. To circumvent this, one very preliminary study simulated mutations and spiked them into somatic and germline RNA-seq data, then trained and tested a neural network on simulated paired RNA-seq and exome sequencing data [218]. However, because this model was not subsequently tested on ground-truth datasets, it is unclear whether simulation can produce sufficiently realistic data to produce reliable models.

Method development for interpreting new types of sequencing data has historically taken two steps: first, easily implemented hard cutoffs that prioritize specificity over sensitivity, then expert development of probabilistic models with hand-developed inputs [218]. We anticipate that these steps will be replaced by deep learning, which will infer features simply by its ability to optimize a complex model against data.

The impact of deep learning in treating disease and developing new treatments

TODO: write Treat intro TODO: Add representative papers about Modeling Metabolism and Chemical Reactivity

Categorizing patients for clinical decision making

There has been sustained interest in applying deep learning to clinical decision making for over two decades. In 1996, Tu [219] compared the effectiveness of artificial neural networks and logistic regression, questioning whether deep learning would replace traditional statistical methods for predicting medical outcomes such as myocardial infarction [220] or mortality [221]. He posited that while neural networks have several advantages in representational power, the difficulties in interpretation may limit clinical applications. In 2006, Lisboa and Taktak [222] examined the use of artificial neural networks in medical journals, concluding that neural networks provided an increase in benefit to healthcare relative to traditional screening methods in 21 of 27 studies.

While significant progress has been made in developing deep learning methods for diagnosis, it is not clear that these methods have yet transformed clinical decision making. The difficulty in applying deep learning to clinical decision making represents a challenge common to many deep learning applications: it is much easier to predict an outcome than to suggest an action to change the outcome. Several attempts at recasting the clinical decision making problem into a prediction problem (i.e. prediction of which treatment will most improve the patient's health) have accurately predicted prescription habits, but technical and medical challenges remain for clinical adoption. In particular, remaining challenges include actionable interpretability of deep learning models, fitting deep models to limited and heterogeneous data, and integrating complex predictive models into a dynamic clinical environment.

A critical challenge in moving from prediction to treatment recommendations is the necessity to establish a causal relationship for a recommendation. Causal inference is often framed in terms of counterfactual question [223]. Johansson et al [224] use deep neural networks to create representation models for covariates that capture nonlinear effects and show significant performance improvements over existing models. In a less formal approach, Kale et al [225] first create a deep neural network to model clinical time series and then analyze the relationship of the hidden features to the output using a causal approach.

Applications

Trajectory Prediction for Treatment

A common application for deep learning techniques in this domain is to leverage the temporal structure of healthcare records. As previously discussed, many studies [226–229] have used deep recurrent networks to categorize patients but most stop short of suggesting clinical decisions. Nemati et al [230] used deep reinforcement learning to optimize a heparin dosing policy for intensive care patients. However, because the ideal dosing policy is unknown, the model's predictions must be evaluated on counter-factual data. This represents a common challenge when bridging the gap between research and clinical practice: because the ground-truth is unknown, researchers struggle to evaluate model predictions in the absence of interventional data, but clinical application is unlikely until the model has been shown to be effective. The impressive applications of deep reinforcement learning to other domains [7] have relied on knowledge of the underlying processes (e.g. the rules of the game). Some models have been developed for targeted medical problems [231], but a generalized engine is beyond current capabilities. Further development of the rules underlying biological processes could unleash deep learning methods that are currently hampered by the difficulties of counter-factual inference.

Efficient Clinical trials

A clinical task to deep learning which has been more successfully applied is the assignment of patients to clinical trials. Ithapu et al [232] used a randomized denoising autoencoder to learn a multimodal imaging marker that predicts future cognitive and neural decline from positron emission tomography (PET), amyloid florbetapir PET, and structural magnetic resonance imaging. By accurately predicting which cases will progress to dementia, they were able to efficiently assign patients to a clinical trial and reduced the required sample sizes by a factor of five. Similarly, Artemov et al [233] applied deep learning to predict which clinical trials were likely to fail and which were likely to succeed. By predicting the side effects and pathway activations of each drug, and then translating these activations to a success probability, their deep learning-based approach was able to significantly outperform a random forest classifier trained on gene expression changes. These approaches suggest promising directions to improve the efficiency of clinical trials and accelerate drug development.

Challenges

Actionable Interpretability

A common challenge in many applied deep learning problems is the consideration of deep learning models as uninterpretable "black boxes". Without human- intelligible reasoning for the model's predictions, it is difficult to trust the model. This presents a major challenge for the risk-averse task of clinical decision making. As described above, there has been some work to directly assign treatment plans without interpretability; however, the removal of human experts from the decision-making loop make the models difficult to integrate with clinical practice. To alleviate this challenge, several studies have attempted to create more interpretable deep models, either specifically for healthcare or as a general procedure for deep learning. Further work in interpreting predictions and understanding the knowledge learned by deep neural networks seem necessary for transformative impact in clinical practice. Interpretability in deep learning is reviewed more extensively in the Discussion.

Integrating Deep Learning with Clinical Practice

As deep learning models are difficult to interpret, many current models have been designed to replace aspects of clinical practice rather than to assist trained clinicians. This makes it difficult to integrate deep learning with clinical decision making. In addition, the challenges that physicians face are largely similar to those faced by machine learning models. For a given patient, the number of possible diseases is very large, with a long tail of rare diseases.

Furthermore, patients are highly heterogeneous and may present with very different signs and symptoms for the same disease. Physicians are experienced in treating patients with common diseases, but rare diseases are extremely challenging. Unfortunately, machine learning methods also struggle for rare diseases. Because deep learning models are data-intensive, directly applying current deep learning models to diagnose patients with rare diseases would require prohibitively large datasets. Focused effort in reducing the data requirements of deep learning by integrating pre-existing knowledge or compiling large datasets of patient records may unlock the power of deep learning for clinical practice.

Drug repositioning

Drug repositioning (or repurposing) is an attractive option for delivering new drugs to the market because of the high costs and failure rates associated with more traditional drug discovery approaches [234,235]. A decade ago, the concept of the Connectivity Map [236] had a sizeable impact on the field: reverse matching disease gene expression signatures with a large set of reference compound profiles allowed to formulate repurposing hypothesis at scale using a simple non-parametric test. Since then, several advanced computational methods have been applied to formulate and validate drug repositioning hypotheses [237–239]. Using supervised learning and collaborative filtering to tackle this type of problems is proving successful in different scenarios, especially when coupling disease or compound omic data with topological information from protein-protein or protein-compound interaction networks [240–242].

Menden et al [243] used a shallow neural network to predict sensitivity of cancer cell lines to drug treatment using both cell line and drug features, opening the door to precision medicine and drug repositioning opportunities in cancer. More recently, Aliper et al [29] used gene- and pathway-level drug perturbation transcriptional profiles from the Library of Network-Based Cellular Signatures (LINCS) [244] to train a fully connected deep neural network able to predict drug therapeutic uses and indications. By using confusion matrices and leveraging misclassification, the authors formulate a number of interesting hypotheses, including repurposing cardiovascular drugs such as otenzepad and pinacidil for neurological disorders.

Drug repositioning can also be approached by attempting to predict novel drug-target interactions and then repurposing the drug for the associated indication [245,246]. Wang et al [247] devised a pairwise input neural network with two hidden layers that takes two inputs, a drug and a target binding site, and predicts whether they interact. Wang et al [30] trained individual RBMs for each target in a drug-target interaction network and used these models to predict novel interactions pointing to new indications for existing drugs. Wen et al. [31] extended this concept to deep learning by creating a DBN of stacked RBMs called DeepDTIs, which is able to predict interactions on the basis of chemical structure and protein sequence features.

Drug repositioning appears to be an obvious candidate for the development of deep learning applications both because of the large amount of high-dimensional data available and because of the complexity of the question being asked. However, what is perhaps the most promising piece of work in this space [29] is more a proof of concept than a real-world hypothesis-generation tool; notably, deep learning was used to predict drug indications but not for the actual repositioning. At present, some of the most popular state-of-the-art methods for signature-based drug repurposing [248] do not use predictive modelling. While this might change in the future, we believe that a mature and production-ready framework where deep learning is directly applied to the problem of drug repositioning is currently missing.

Ligand-Based Prediction of Bioactivity

In the biomedical domain, high-throughput chemical screening aims to improve therapeutic options over a long term horizon [249] TODO: add another general screening reference. The objective is to discover which small molecules (also referred to as chemical compounds or ligands) effectively and specifically affect the activity of a target, such as a kinase, protein-protein interaction, or broader cellular phenotype.

TODO: clarify desired outputs, what will be done with the top-ranked hits, one vs multiple hits, abandoning lead compounds This screening process can serve as the first step in the long drug discovery pipeline, where novel chemicals are pursued for their ability to inhibit or enhance disease-relevant biological mechanisms. The appeal of machine learning in this domain is the need to improve the efficiency of the initial high-throughput screens such that sufficient candidate active compounds can be identified without exhaustively screening libraries of hundreds of thousands or millions of chemicals.

TODO: is the sufficient number target dependent? This task has been treated as a classification, regression, and ranking problem. In reality, it does not fit neatly into any of those categories. An ideal algorithm will rank a sufficient number of active compounds before the inactives, but the rankings of actives relative to other actives and inactives to other inactives is less important [250]. TODO: can improve this first attempt at an intro by reviewing more existing literature on the topic

TODO: check which other existing reviews should be referenced

We primarily focus on ligand-based approaches that train on chemicals' features without requiring knowledge of the target, as opposed to alternative strategies that use target features such as the protein structure TODO: add examples. Chemical features may be represented as a list of molecular descriptors such as molecular weight, atom counts, charge representations, summaries of atom-atom relationships in the molecular graph, and more sophisticated derived properties [251]. Alternatively, chemicals can be characterized with the fingerprint bit vectors, textual strings, or novel learned representations described below. Neural networks have a long history in this domain [32]

TODO: can add additional references besides this review, and the 2012 Merck Molecular Activity Challenge on Kaggle generated

substantial excitement about the potential for high-parameter deep learning approaches. The winning submission was an ensemble that included a multitask multilayer perceptron network [252], and the Merck sponsors noted drastic improvements over a random forest (RF) baseline, remarking "we have seldom seen any method in the past 10 years that could consistently outperform RF by such a margin" [253]. Subsequent work explored the effects of jointly modeling far more targets than the Merck challenge [254,255], with [255] showing that the benefits of multitask networks had not yet saturated even with 259 targets. Although a deep learning approach, DeepTox [256], was also the overall winner of another competition, the Toxicology in the 21st Century (Tox21) Data Challenge, it did not dominate alternative methods as thoroughly as in other domains. DeepTox was the top performer on 9 of 15 targets and highly competitive with the top performer on the others. However, for many targets there was little separation between the top two or three methods. A reliance on AUC ROC TODO: define here? for the evaluation (see Discussion) further hinders the ability to declare Tox21 as an outright success for deep learning.

In retrospect, the nuanced Tox21 performance may be more reflective of the practical challenges encountered in ligand-based chemical screening than the extreme enthusiasm generated by the Merck competition. A study of 22 absorption distribution, metabolism, excretion, and toxicity (ADMET) tasks demonstrated that there are limitations to multitask transfer learning that are in part a consequence of the degree to which tasks are related [257]. Some of the ADMET datasets showed far superior performance in multitask models of only the 22 ADMET tasks relative to more expansive multitask networks that included over 500 less-similar tasks.

TODO: also has a good discussion of information leakage in cross validation, include that in the Discussion section In addition, training datasets encountered in practical applications may be tiny relative to what is available in public datasets and organized competitions. A study of BACE-1 inhibitors included only 1547 compounds [258]. Machine learning models were able to train on this limited dataset, but overfitting was a challenge and the differences between random forests and a deep neural were negligible, especially in the classification setting. Overfitting is still a problem in larger chemical screening datasets with tens or hundreds of thousands of compounds because the number of active compounds can be very small, on the order of 0.1% or 1% of all tested chemicals for a typical target TODO: verify those estimates. This is consistent with the strong performance of low-parameter neural networks that emphasize compound-compound similarity, such as influence-relevance voter, [250,259] instead of predicting compound activity directly from chemical features.

TODO: include recent DeepChem IRV benchmarks?

Much of the recent excitement in this domain has come from what could be considered a creative experimentation phase, in which deep learning has offered novel possibilities for feature representation and modeling of chemical compounds. A molecular graph, where atoms are nodes and bonds are edges, is a natural way to represent a chemical structure. Traditional machine learning approaches relied on preprocessing the graph into a feature vector, such as a fixed-width bit vector fingerprint [260]. An overly simplistic but approximately correct view of these fingerprints is that each bit represents the presence of absence of a particular chemical substructure in the molecular graph. Modern neural networks can operate directly on the molecular graph as input. Duvenaud et al [261] generalized standard circular fingerprints by substituting discrete operations in the fingerprinting algorithm with operations in a neural network, producing a real-valued feature vector instead of a bit vector. Other approaches offer trainable networks that can in theory learn chemical feature representations that are optimized for a particular prediction task. Lusci et al adapted recursive neural networks for directed acyclic graphs for undirected molecular graphs by creating an ensemble of directed graphs in which one atom is selected as the root node [262]. A single feature vector is obtained by summing over all feature vectors for all directed graphs in the ensemble. Graph convolutions on undirected molecular graphs have eliminated the need to enumerate artificial directed graphs, learning feature vectors for atoms that are a function of the properties of neighboring atoms and local regions on the molecular graph [263,264].

Advances in chemical representation learning have not been limited to graph-based neural networks. The simplified molecular-input line-entry system (SMILES) is a standard way to transform a chemical into string-based representation. A SMILES-to-SMILES autoencoder learns a continuous latent feature space for chemicals [265].

TODO: connect to related EHR paper TODO: autoencoder doesn't fit cleanly with supervised methods, revisit organization after adding GANs In this learned continuous space is it possible to train some types of supervised learning algorithms or interpolate between continuous representations of chemicals in a manner that is not possible with discrete (e.g. bit vector or string) features. A drawback is that not all SMILES strings produced by the autoencoder's decoder correspond to valid chemical structures. TODO: could mention GANs here Altae-Tran et al developed a one-shot learning network[264] to address the reality that most practical chemical screening studies are unable to provide the thousands or millions of training compounds that are needed to train larger multitask networks. Using graph convolutions to featurize chemicals, the network learns an embedding from compounds into a continuous feature space such that compounds with similar activities in a set of training tasks have similar embeddings. The approach is evaluated in an extremely challenging setting where the embedding is learned from a subset of prediction tasks (e.g. activity assays for individual proteins) and only one to ten labeled examples are provided as training data on a new task. On Tox21 targets, even when trained with *one* task-specific active compound and *one* inactive compound, the model is able to generalize reasonably well because it has learned an informative embedding function from the related tasks. Random forests, which cannot take advantage of the related training tasks, trained in the same setting are only slightly better than a random classifier. Despite the success on Tox21, performance on MUV datasets, which contains assays designed to be challenging for chemical informatics algorithms, is considerably worse. The authors also demonstrate the limitations of transfer learning as embeddings learned from the Tox21 assays have little utility for a drug adverse reaction dataset.

These novel, learned chemical feature representations may prove to be essential for accurately predicting why some compounds with similar structures yield similar target effects and others produce drastically different results. Currently, these methods are enticing but do not necessarily outperform classic approaches by a large margin. The neural fingerprints [261] were narrowly beaten by regression using traditional circular fingerprints on a drug efficacy prediction task (but were superior for predicting solubility or photovoltaic efficiency). Graph convolutions [263] performed comparably to a multitask network using standard fingerprints and slightly better than the neural fingerprints [261] on the drug efficacy task but were slightly worse than the influence-relevance voter method on an HIV dataset. [250].

TODO: there are also problems with some papers using ROC primarily for benchmarking, which skews results and makes it hard to assess absolute p

We remain optimistic for the potential of deep learning and specifically representation learning in this domain and propose that rigorous benchmarking on broad and diverse prediction tasks will be as important as novel neural network architectures and expanded public datasets to advance the state of the art and convincingly demonstrate superiority over traditional cheminformatics techniques. Fortunately, there has recently been significant progress in this direction. The DeepChem software [264,266] and MoleculeNet benchmarking suite [267] built upon it contain chemical bioactivity and toxicity prediction datasets, multiple compound featurization approaches including graph convolutions, and various machine learning algorithms ranging from standard baselines like logistic regression and random forests to recent neural network architectures. Independent research groups have already contributed additional datasets and prediction algorithms to DeepChem, and adoption of common benchmarking evaluation metrics, datasets, and baseline algorithms has the potential to establish the practical utility of deep learning in chemical bioactivity prediction and lower the barrier to entry for machine learning researchers without biochemistry expertise.

One open question in ligand-based screening pertains to the benefits and limitations of transfer learning. Multitask neural networks have shown the advantages of jointly modeling many targets [254,255]. Other studies have shown the limitations of transfer learning when the prediction tasks are insufficiently related [257,264]. This has important implications for representation learning. The typical approach of improving deep learning models by expanding the dataset size may not be applicable if only "related" tasks are beneficial, especially because task-task relatedness is ill-defined. The massive chemical state space will also influence the development of unsupervised representation learning methods [265]. Future work will establish whether it is better to train on massive collections of diverse compounds, drug-like small molecules, or specialized subsets.

TODO: other papers to add such as generative models

TODO: relationship to traditional docking (some networks include docking scores), deep learning with structure (e.g. [Z7fd0BYf; @bNBiliTt; @17Ya

TODO: analogies to other domains where deep learning can capture the behavior of complex physics (e.g. quantum physics example)?

TODO: link to drug repurposing section above, DeepDTIs uses ECFPs as features for its 1412 compounds and protein sequence composition (PSCs

Discussion

Despite the disparate data types and scientific goals in the learning tasks covered above, several challenges are broadly important for deep learning in the biomedical domain. We present factors that may impede further progress, initial steps that have been taken to address them, and suggested research practices to overcome these obstacles.

Evaluation

What are the challenges in evaluating deep learning models that are specific to this domain? This can include a discussion of ROC versus precision-recall curves for the imbalanced classes often encountered in biomedical datasets. It could also mention alternative metrics that are used in specific sub-areas such as enrichment factors in virtual screening. A lack of true gold standard data for some problems complicates both training and evaluation. Confidence-weighted labels are valuable when available.

Is progress in some biomedical areas slowed when new predictions (e.g. from generative models) cannot be assessed by any human expert and require experimental testing? For example, contrast a painting or song generated by a GAN versus a novel chemical compound. Related is the idea that on some tasks (e.g. the recent wave of deep learning versus MD image classification papers) it is easy to tell when deep learning has produced a breakthrough because human-level performance is an impressive baseline. In many tasks we reviewed, human-level performance is irrelevant.

TODO: draft coming May 4 or 5

Interpretation

As the challenge of interpretability is common across many domains, there is significant interest in developing generic procedures for knowledge extraction from deep models. Ribeiro et al [268] focus on interpreting individual predictions rather than interpreting the model. By fitting simple linear models to mimic the predictions of the deep learning model in a small neighborhood of a data sample, they generated an interpretable model for each prediction. While this procedure can provide interpretable models for each sample, it is unclear whether these interpretable models are reliable.

Theoretical guarantees on the curvature of the predictions of deep learning models are not known, and it is unclear whether predictions from deep learning models are robust to sample noise. Toward quantifying the uncertainty of predictions, there has been a renewed interest in confidence intervals for deep neural networks. Early work from Chrysosouris et al [269] provided confidence intervals under the assumption of normally distributed error. However, Nguyen et al [270] showed that the confidence of convolutional neural networks is not reliable; they can output confidence scores over 99.99% even for samples that are purely noise. Recently, Fong and Vedaldi [271] provided a framework for understanding black box algorithms by perturbing input data.

For domain-specific models, we previously described approaches for the interpretation and visualization of neural networks that predict transcription factor binding [124,126,128]. Other studies have primarily focused on integrating attention mechanisms with the neural networks. Attention mechanisms dynamically weight the importance the neural network gives to each feature. By inspecting the attention weights for a particular sample, a practitioner can identify the important features for a particular prediction. Choi et al [272] inverted the typical architecture of recurrent neural networks to improve interpretability. In particular, they only used recurrent connections in the attention generating procedure, leaving the hidden state directly connected to the input variables. In the clinical domain, this model was able to produce accurate diagnoses in which the contribution of previous hospital visits could be directly interpreted. Choi et al [273] later extended this work to take into account the structure of disease ontologies and found that the concepts represented by the model were aligned with medical knowledge. Che et al [274] introduced a knowledge-distillation approach which used gradient boosted trees to learn interpretable healthcare features from trained deep models.

Data limitations

A lack of large-scale, high-quality, labeled training data has impacted deep learning in nearly all applications we have discussed, from healthcare to genomics to drug discovery. The challenges of training complex, high-parameter neural networks from few examples are obvious, but uncertainty in the labels of training instances can be just as problematic. In genomics, for example, labeled data may be derived from an experimental assay that has known and unknown technical artifacts, biases, and error profiles. It is possible to weight training examples or construct Bayesian models to account for uncertainty or non-independence in the data. For example, Park et al. [275] estimated shared non-biological signal between datasets to correct for non-independence related to assay platform or other factors in a Bayesian integration of many datasets. However, such techniques are rarely placed front and center in the description of methods, so these steps may be overlooked.

For some types of data, especially images, it is straightforward to augment training datasets by splitting one labeled example into multiple examples. An image can easily be rotated, flipped, or translated and retain its label [37]. 3D MRI and 4D fMRI (with time as a dimension) data can be decomposed into sets of 2D images [276]. This greatly expands the number of training examples in domains where only hundreds of subjects are available but artificially treats images from the same volume as independent instances and sacrifices the structure inherent in the data. CellCnn trains a model to recognize rare cell populations in single-cell data by creating training instances that consist of random subsets of cells that are randomly sampled with replacement from the full dataset [178].

Simulated or semi-synthetic training data has also been employed in multiple biomedical domains.

TODO: simulated data: #5 #99 #293, maybe #117 and #197. There is a counter-example from drug discovery to include as well that is related to #55

Multimodal, multi-task, and transfer learning, discussed in detail below, can also combat data limitations to some degree. There are also emerging network architectures, such as Diet Networks for high-dimensional SNP data [277]. Diet Networks use multiple networks to drastically reduce the number of free parameters by first flipping the problem and training a network to predict parameters (weights) for each input (SNP) to learn a feature embedding. This embedding (i.e. PCA, per class histograms, or a Word2vec [47] generalization) can be learned directly from the input data or can take advantage of other datasets or domain knowledge. Additionally, in this task, the features are the examples, an important fact when it is typical to have 500k+ SNPs and only a few thousand patients. Finally, this embedding is of a much lower dimension, allowing for a large reduction in the number of free parameters. In the example given, the authors reduced the number of free parameters from 30 million to 50 thousand, a factor of 600.

Hardware limitations and scaling

Efficiently scaling deep learning is challenging, and there is a high computational cost (e.g., time, memory, energy) associated with training neural networks and using them for classification. As such, neural networks have only recently found widespread use [278].

Many have sought to curb the costs of deep learning, with methods ranging from the very applied (e.g., reduced numerical precision [279–282]) to the exotic and theoretic (e.g., training small networks to mimic large networks and ensembles [283,284]). The largest gains in efficiency have come from computation with graphics processing units (GPUs) [278,285–289], which excel at the matrix and vector operations so central to deep learning. The massively parallel nature of GPUs allows additional optimizations, such as accelerated mini-batch gradient descent [286,287,290,291]. However, GPUs also have a limited quantity of memory, making it difficult to implement networks of significant size and complexity on a single GPU or machine [285,292]. This restriction has sometimes forced computational biologists to use workarounds or limit the size of an analysis. For example, Chen et al. [106] aimed to

infer the expression level of all genes with a single neural network, but due to memory restrictions they randomly partitioned genes into two halves and analyzed each separately. In other cases, researchers limited the size of their neural network [21,265]. Some have also chosen to use slower CPU implementations rather than sacrifice network size or performance [293].

Steady improvements in GPU hardware may alleviate this issue somewhat, but it is not clear whether they can occur quickly enough to keep up with the growing amount of available biological data or increasing network sizes. Much has been done to minimize the memory requirements of neural networks [279–283,294,295], but there is also growing interest in specialized hardware, such as field-programmable gate arrays (FPGAs) [289,296] and application-specific integrated circuits (ASICs). Specialized hardware promises improvements in deep learning at reduced time, energy, and memory [289]. Logically, there is less software for highly specialized hardware [296], and it could be a difficult investment for those not solely interested in deep learning. However, it is likely that such options will find increased support as they become a more popular platform for deep learning and general computation.

Distributed computing is a general solution to intense computational requirements, and has enabled many large-scale deep learning efforts. Early approaches to distributed computation [297,298] were not suitable for deep learning [299], but significant progress has been made. There now exist a number of algorithms [281,299,300], tools [301–303], and high-level libraries [304,305] for deep learning in a distributed environment, and it is possible to train very complex networks with limited infrastructure [306]. Besides handling very large networks, distributed or parallelized approaches offer other advantages, such as improved ensembling [307] or accelerated hyperparameter optimization [308,309].

Cloud computing, which has already seen adoption in genomics [310], could facilitate easier sharing of the large datasets common to biology [311,312], and may be key to scaling deep learning. Cloud computing affords researchers significant flexibility, and enables the use of specialized hardware (e.g., FPGAs, ASICs, GPUs) without significant investment. With such flexibility, it could be easier to address the different challenges associated with the multitudinous layers and architectures available [313]. Though many are reluctant to store sensitive data (e.g., patient electronic health records) in the cloud, secure/regulation-compliant cloud services do exist [314].

Data, code, and model sharing

A robust culture of data, code, and model sharing would do much to speed advances in this domain. The cultural barriers of data sharing in particular are perhaps best captured by the implications of using the term "research parasite" to describe scientists who use data from other researchers [315]. In short, a field that honors only discoveries and not the hard work of generating useful data will have difficulty encouraging scientists to share their hard-won data. Unfortunately, it's precisely those data that would help to power deep learning in the domain. Efforts are underway to recognize those who promote an ecosystem of rigorous sharing and analysis [316].

The sharing of high-quality, labeled datasets will be especially valuable. In addition, researchers who invest time to preprocess datasets to be suitable for deep learning can make the preprocessing code (e.g., Basset [135] and variationanalysis [216]) and cleaned data (e.g., MoleculeNet [267]) publicly available to catalyze further research. However, there are complex privacy and legal issues involved in sharing patient data that cannot be ignored. Furthermore, in some domains, some of the best training data has been generated privately, for example, high-throughput chemical screening data at pharmaceutical companies. One perspective is that there is little expectation or incentive for this private data to be shared. However, data are not inherently valuable. Instead, the insights that we glean from them are where the value lies. Private companies may establish a competitive advantage by releasing sufficient data for improved methods to be developed.

Code sharing and open source licensing is essential for continued progress in this domain. We strongly advocate following established best practices for sharing source code, archiving code in repositories that generate digital object identifiers, and open licensing [317] regardless of the minimal requirements, or lack thereof, set by journals, conferences, or preprint servers. In addition, it is important for authors to share not only code for their core models but also scripts and code used for data cleaning (see above) and hyperparameter optimization. These improve reproducibility and serve as documentation of the detailed decisions that impact model performance but may not be exhaustively captured in a manuscript's methods text.

Because many deep learning models are often built using one of several popular deep learning frameworks, it is also possible to directly share trained predictive models. The availability of pre-trained models can accelerate research, with image classifiers as an apt example. A pre-trained neural network can be quickly fine-tuned on new data and used in transfer learning, both discussed below. Taking this idea to the extreme, genomic data has been artificially encoded as images in order to benefit from pre-trained image classifiers [215]. "Model zoos", collections of pre-trained models, are not yet common in biomedical domains but have started to appear in genomics applications [175,318]. Sharing models for patient data requires great care because deep learning models can be attacked to identify examples used in training. We discuss this issue as well as recent techniques to mitigate these concerns in the patient categorization section.

DeepChem [264,266,267] and DragoNN [318] exemplify the benefits of sharing code under an open source license and pre-trained models. DeepChem, which targets drug discovery and quantum chemistry, has actively encouraged and received community contributions of learning algorithms and benchmarking datasets. As a consequence, it now

supports of a large suite of machine learning approaches, both deep learning and competing strategies, that can be run on diverse test cases. This realistic, continual evaluation will play a critical role in assessing which techniques are most promising for chemical screening and drug discovery. Like formal, organized challenges such as the ENCODE-DREAM *in vivo* Transcription Factor Binding Site Prediction Challenge[319], TODO: placeholder URL until the pre-print is available DeepChem provides a forum for the fair, critical evaluations that are not always conducted in individual methodological papers, which can be biased toward favoring a new proposed algorithm. DragoNN, Deep Regulatory Genomic Neural Networks, offers not only code and a model zoo but also a detailed tutorial and partner package for simulating training data. These resources, especially the ability to simulate datasets that are sufficiently complex to demonstrate the challenges of training neural networks but small enough to train quickly on a CPU, are important for (human) training and attracting machine learning researchers to problems in genomics and healthcare. We have even included DragoNN and hands-on model training into the curriculum of a graduate student course.

Multimodal, multi-task, and transfer learning

As discussed above, the fact that biomedical datasets often contain a limited number of instances or labels can be a cause of poor performance of machine learning algorithms. When trained on such datasets, deep learning models are particularly prone to overfitting due to their high representational power. However, transfer learning techniques also known as domain adaptation enable transfer of extracted patterns between different datasets and even domains. This approach can be described in a 2-step process: (1) training a model for the base task, and (2) reusing the trained model for the target problem in hand. The first step allows a model to take advantage of larger amount of data, labels, or both, to extract better feature representations. Transferring learnt features in deep neural networks improves performance compared to randomly initialized features even when pre-training and target sets are dissimilar. However, transferability of features decreases as the distance between the base task and target task increases [320].

In image analysis, previous examples of deep transfer learning applications proved large scale natural image sets[321] to be useful for pre-training models that can then serve as generic feature extractors applied to various types of biological images [14,167,322,323]. More recently, deep learning models trained to predict protein sub-cellular localization successfully performed predictions for proteins not originally present in the training set [324]. Moreover, in this type of task, learnt features performed reasonably well even when applied to images obtained using different fluorescent labels, imaging techniques, and different cell types [325]. However, there are no established theoretical guarantees for feature transferability between distant domains such as natural images and various modalities of biological imaging. Because learnt patterns are represented in deep neural networks in a layer-wise hierarchical fashion, this issue is usually addressed by fixing an empirically chosen number of layers that preserve generic characteristics of both training and target datasets. Then, the model is fine-tuned by re-training multiple networks' top layers on the specific dataset in order to re-learn domain-specific high level concepts. For example, see fine-tuning for radiology image classification [64]. Fine-tuning on specific biological datasets enables more focused predictions. The Basset package [135] for prediction of functional activities from DNA sequences was shown to rapidly learn and accurately predict on new data by leveraging a model pre-trained on available public data. To simulate this scenario, authors put aside 15 of 164 cell type datasets and trained the Basset model on the remaining 149 datasets. Then, they fine-tuned the model with one training pass of each of the remaining datasets and achieved results close to the model trained on all 164 datasets together. In another example, Min et al. [138] demonstrated how training on the experimentally validated FANTOM5 permissive enhancer dataset followed by fine-tuning on ENCODE enhancer datasets improved cell type-specific predictions, outperforming state-of-the-art results.

Multimodal learning is related to transfer learning. It assumes simultaneous learning from various types of inputs, such as images and text. It allows capture of features that describe common concepts across input modalities. Generative graphical models like restricted Boltzmann machines (RBM) and their stacked versions, deep Boltzmann machines (DBM), and deep belief networks (DBN), demonstrate successful extraction of more informative features for one modality (images or video) when jointly learnt with other modalities (audio or text) [326]. Deep graphical models such as DBNs are considered to be well suited for multimodal learning tasks since they learn a joint probability distribution from inputs. They can be pre-trained in an unsupervised fashion on large unlabeled data and then fine-tuned on a smaller number of labeled examples. When labels are available, convolutional neural networks (CNN) are ubiquitously used since they can be trained end-to-end with backpropagation and demonstrate state-of-the-art performance in many discriminative tasks [14]. Jha et al. [115] showed that an integrated training approach delivers better performance compared to individual networks. They compared a number of feed-forward architectures trained on RNA-seq data with and without an additional set of CLIP-seq, knockdown, and over-expression based input features. Results showed that the integrative deep model generalized well for combined data, offering large performance improvement for alternative splicing event estimation. Chaudhary et al. [327] trained a deep autoencoder model jointly on RNA-seq, miRNA-seq, and methylation data from TCGA to predict survival subgroups of hepatocellular carcinoma patients. This multimodal approach that treated different omics as different modalities outperformed both traditional methods (PCA) and single-omic models. Interestingly, multi-omic model performance did not improve when combined with clinical information, suggesting that the model was able to capture redundant contributions of clinical features through their correlated genomic features. Chen et al. [328] used deep belief networks to learn phosphorylation states of a common set of signaling proteins in primary cultured bronchial cells collected from rats and humans treated with distinct stimuli. By interpreting species as different modalities representing similar high-level concepts, they showed that DBNs were able to capture cross-species representation of signaling mechanisms in response to a common stimuli. Another application

used DBNs for joint unsupervised feature learning from cancer datasets containing gene expression, DNA methylation, and miRNA expression data [108]. This approach allowed for the capture of intrinsic relationships in different modalities and for better clustering performance over conventional k-means based methods. Multimodal learning with CNNs is usually implemented as a collection of individual networks in which each learns representations from single data type. These individual representations are further concatenated before or within fully-connected layers. FIDDLE [329] is an example of multimodal CNNs that represents an ensemble of individual networks that take as inputs a number of genomic datasets, including NET-seq, MNase-seq, ChIP-seq, RNA-seq, and raw DNA sequence to predict Transcription Start Site-seq (TSS-seq) outputs. The combined model radically improves performance over separately trained datatype-specific networks, suggesting that it learns the synergistic relationship between datasets.

Multi-task learning (MTL) is an approach related to transfer learning. In an MTL framework a model co-learns a number of tasks simultaneously such that features are shared across them. DeepSEA framework [124] implemented a multi-task joint learning of diverse chromatin factors sharing predictive features from raw DNA sequence. This allowed, for example, a sequence feature that is effective in recognizing binding of a specific TF to be simultaneously used by another predictor for a physically interacting TF. Similarly, TFImpute [116], a CNN-RNN architecture learned information shared across transcription factors and cell lines to predict cell-specific TF binding for TF-cell line combinations based on only a small fraction (4%) of the combinations using available ChIP-seq data. On multiple test sets that excluded specific TFs and cell lines, TFImpute showed comparable or superior performance compared to the state-of-the-art. Yoon et al. [46], previously discussed in the section on Electronic Health Records, demonstrated that predicting the primary cancer site from the cancer pathology reports together with its laterality substantially improved the performance for the latter task, suggesting that MTL can effectively leverage the commonality between two tasks using a shared representation. A number of studies previously mentioned in the section on developing new treatments employed multi-task learning approach to predict a large number of compound and target interactions for drug discovery [252,255] and drug toxicity prediction [256,330]. Kearnes et al. [257] did a systematic comparison of single-task and multi-task deep models on a set of industrial ADMET datasets. They confirmed that multi-task learning can improve performance over single-task models. They further showed that smaller datasets tend to benefit more from multitask learning than larger datasets. Results emphasized that multitask effects are highly dataset-dependent, suggesting the use of dataset-specific models to maximize overall performance.

MTL approach is complementary to multimodal and transfer learning. All three techniques can be used together in the same model. For example, Zhang et al. [322] combined deep model-based transfer and multi-task learning for cross-domain image annotation. One could imagine extending that approach to multimodal inputs as well. Common characteristic of these methods lies in better generalization of extracted features by leveraging relationships between information in provided in inputs and task objectives, represented at various hierarchical levels of abstraction in a deep learning model structure.

Despite demonstrated improvements, transfer learning approaches also pose a number of challenges. As mentioned above, there are no theoretically sound principles for pre-training and fine-tuning. Most best practice recommendations are heuristic and have to take into account additional hyper-parameters that depend on specific deep architectures, sizes of pre-training and target datasets, and similarity of domains. However, similarity of datasets and domains in transfer learning and relatedness of tasks in MTL are difficult to access. Most current studies address these limitations by empirical evaluation of the model using established best practices or heuristics and cross-validation. Unfortunately, negative results are typically left out and not presented in the final study publications. Results by Rajkomar et al. [64] showed that a deep CNN trained on natural images can boost radiology image classification performance. However, due to differences in imaging domains, target task required either re-training the initial model from scratch with special pre-processing or fine-tuning of the whole network on radiographs with heavy data augmentation to avoid overfitting. Exclusively fine-tuning top layers led to much lower validation accuracy (81.4 vs 99.5). Fine-tuning procedure for the discussed Basset model pre-trained on data from different cell types required no more than one training pass. Otherwise, the model started overfitting new data [135]. DeepChem successfully improved results for low-data drug discovery with one-shot learning for related tasks. However, it demonstrated clear limitations to cross-task generalization across unrelated tasks in one-shot models, specifically nuclear receptor assays and patient adverse reactions [264].

Overall, multimodal, multi-task and transfer learning strategies demonstrate high potential for many biomedical applications that are otherwise limited by data volume and presence of labels. However, these methods not only inherit most methodological issues from natural image, text, and audio domains, but also pose new challenges, specific to biological data. Making negative results, source code, and pre-trained models publicly available helps to accelerate progress in this direction. However, there are privacy considerations for models trained on sensitive data, such as patient-related information (see Data sharing section). Thus, there is a compelling need for the development of privacy-preserving transfer learning algorithms, such as Private Aggregation of Teacher Ensembles (PATE-G) [93], that can leverage publicly available data. We suggest that these types of models deserve deeper investigation to establish sound theoretical guarantees and best practices and determine limits for the transferability of features between various closely related and distant learning tasks.

Conclusions

Deep learning-based methods now match or surpass the previous state of the art in a diverse array of tasks in patient and disease categorization, fundamental biological study, genomics, and treatment development. Returning to our central question: given this rapid progress, has deep learning transformed the study of human disease? Though the answer is highly dependent on the specific domain and problem being addressed, we conclude that deep learning has not *yet* realized its transformative potential or induced a strategic inflection point. Despite its dominance over competing machine learning approaches in many of the areas reviewed here and quantitative improvements in predictive performance, deep learning has not yet definitively "solved" those problems.

As an analogy, consider recent progress in conversational speech recognition. Since 2009 there have been drastic performance improvements, with error rates dropping from more than 20% to less than 6% [331] and finally approaching or exceeding human performance in the past year [332,333] TODO: need better source for this error trajectory. The phenomenal improvements on benchmark datasets are undeniable, but halving the error rate on these benchmarks did not fundamentally transform the domain. Widespread adoption of conversational speech technologies will require not only improvements over baseline methods but truly solving the problem, in this case exceeding human-level performance, as well as convincing users to embrace the technology [331]. We see parallels to the healthcare domain, where achieving the full potential of deep learning will require outstanding predictive performance as well as acceptance and adoption by biologists and clinicians.

Some of the areas we have discussed are closer to surpassing this lofty bar than others, generally those that are more similar to the non-biomedical tasks that are now monopolized by deep learning. In medical imaging, diabetic retinopathy [334], diabetic macular edema [334], tuberculosis [335], and skin lesion [336] classifiers are highly accurate and comparable to clinician performance in the latter case.

In other domains, perfect accuracy will not be required because deep learning will be used primarily to prioritize experiments and assist discovery. For example, in chemical screening for drug discovery, a deep learning system that successfully identifies dozens or hundreds of target-specific, active small molecules from a massive search space would have immense practical value even if its overall precision is modest. In medical imaging, deep learning can point an expert to the most challenging cases that require manual review [335], though the risk of false negatives must be addressed.

Conversely, the most challenging tasks may be those in which predictions are used directly for downstream modeling or decision-making, especially in the clinic. As an example, errors in a predicted protein contact map could be amplified if that contact map is used directly for 3D structure prediction. In addition, the stochasticity and complexity of biological systems implies that for some problems, for instance, predicting gene regulation in disease, perfect accuracy will be unattainable.

Even if deep learning in biology and healthcare is not yet transformative today, we are extremely optimistic about its future. Given how rapidly deep learning is evolving, its full potential in biomedicine has not been explored. We have highlighted numerous challenges beyond improving training and predictive accuracy, such as preserving patient privacy and interpreting models. Ongoing research has begun to address these problems and shown they are not insurmountable. Deep learning offers the flexibility to model data in its most natural form, for example, longer DNA sequences instead of k-mers for transcription factor binding prediction and molecular graphs instead of pre-computed bit vectors for drug discovery. These flexible input feature representations have spurred creative modeling approaches that would be infeasible with other machine learning techniques. Unsupervised methods are currently less-developed than their supervised counterparts, but they may have the most potential. When deep learning algorithms can summarize very large collections of input data into interpretable models that spur scientists to ask questions that they didn't know to ask, it will be clear that deep learning has transformed biology and medicine.

Author contributions

TODO: not sure if it should go here, but somewhere we should talk about how we wrote this thing, since it is still somewhat unconventional to have a
We recognized that writing a review on a rapidly developing area in a manner that allowed us to provide a forward-looking perspective on diverse approaches and biological problems would require expertise from across computational biology and medicine. We created an open repository on the GitHub version control system and engaged with numerous authors from papers within and outside of the area. Paper review was conducted in the open by # individuals, and the manuscript was drafted in a series of commits from # authors. Individuals who met the ICJME standards of authorship are included as authors. These were individuals who contributed to the review of the literature; drafted the manuscript or provided substantial critical revisions; approved the final manuscript draft; and agreed to be accountable in all aspects of the work. Individuals who did not contribute in one or more of these ways, but who did participate, are acknowledged at the end of the manuscript.

TODO: update after finalizing discussion in #369

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