Thesis proposal

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Introduction/Background

Drug discovery—the process by which a potential new medicine is identified—is a complex process that encompasses the intersection of several fields (such as biology, statistics, chemistry or pharmacology). The entire process is a long and costly endeavor, with a typical time-frame of 10 to 20 years till market release and an estimated cost between 2 and 3 billion USD [Schneider, 2019, Scannell et al., 2012]. With just a small quantity of the initially identified compounds actually becoming an approved medicine—only 1 out of 10 000 synthesized molecules gets market approval one day. Many of these dropouts happening at the early stages of the entire pipeline.

It exists, then, a need for better mechanisms for detecting better candidates. One of the most promising directions is to improve the *in-silico* methods—computational simulations are relatively cheap and quick run that makes them an interesting solution. *In-silico* simulations then cover two main aspects: **predictive modelling**, meaning modeling the dynamics of the human body—such that any effect relevant to the drug or the disease will be captured by it—and **generative modelling**, i.e. methods to generate good candidates which, in part, means methods that are effective at exploring the vast space of possible compounds, estimated to be on the order of 10^{60}[Reymond et al., 2012]. Several computational approaches have been used over the years, from modeling molecular dynamics simulations to data-driven statistical methods [Hung and Chen, 2014, Kuhn et al., 2016]. Recently deep learning (DL) has shown signs to be a potential game-changer [Dargan et al., 2019].

DL has been able to capitalize on the exponential growth of data and the higher availability of computational resources. DL has had remarkable success in computer vision (CV) [Guo et al., 2016] and natural language processing (NLP) [Young et al., 2018], and has become the go-to solution for any problem in these two fields. For instance, in the case of CV, where we deal with images, a key element of any architecture's success was the use of convolutional layers—one will mostly observe convolutional neural networks (CNNs) when analyzing the state of the art in CV—which introduces a structural a prior based on the structure of the data[Fukushima, 1980, LeCun, 1989, Ulyanov D., Vedaldi A., 2018]. A similar case can be made for NLP. When we deal with biological and molecular data, it exists a challenge and an opportunity on how to deal with this intrinsic structure, i.e. leveraging the knowledge that they are graphs. Efforts in generalizing the convolution operator on non-euclidian structures have given rise to graph convolutional neural networks (GCNNs)[Wu et al., 2019]. GCNNs, then, pose an oportunity to drug discovery due to their capacity to deal natively with graph data[Sun et al., 2019].

Another of the big challenges is to unify all the aspects of drug-discovery and be able to incorporate all the relevant biological information when designing possible candidate molecules. An initial success story on that line is a recent paper [Zhavoronkov et al., 2019] where the authors describe a deep learning method by which they are able to discover, synthesize, and test in an animal model, inhibitors of discoidin domain receptor 1 (DDR1)—a kinase implicated in fibrosis—in less than two months.

Those promising results, albeit encouraging, are just the tip of the iceberg. There is still a long way until a model can satisfactorily capture the biological complexity of an arbitrary target and produce promising candidates. On top of that, there is an added dimension, as such model should account for the variability from patient to patient and be able to generate a molecule that accommodates for all the genotypic and phenotypic variants or generate different candidates for each of the genetic populations of interest. That is especially important for hypercomplex diseases; for example in cancer where a genotypically heterogeneous cancer population may appear within a single patient [Boland and Yurgelun, 2017]. So the same variant effects arise

inside a dynamic ecosystem, where a drug that just targets a subpopulation may lead to an evolutionary pressure complicating further the treatment outlook [Enriquez-Navas et al., 2015].

There is then a great need to develop models that can be conditioned based on a large set of biological factors and meaningfully account for these variations when generating a compound or/and evaluating a compound's effect when administered. What is, in other words, the need for the wider adoption of precision medicine.

Last of all, in a more holistic view, it is of interest to develop multi-scale models that capture system complexity at different levels. For instance, a model that can learn protein-compound interactions—commonly known as the docking problem—while at the same time use this information to predict effects of the introduction of the compound on the larger protein-protein interaction (PPI) network[Sun et al., 2019].

Aim & Methods

The aim of this thesis will be two-fold. One the one side, analyze how the explicit use of GCNNs may open new opportunities when dealing with biological and chemical data. On the other side, explore how modeling the biology at different levels (e.g. molecular structure v.s. molecular interaction network) may help create better models. Furthermore, evaluate how these different scales may be integrated.

This precise work will be focused on exploring all these concepts in the context of designing anti-cancer drugs. The work will be done in collaboration with the Computational Systems Biology group at IBM Research (Zurich), which is currently focused on individualized pediatric cure (iPC). As such, an end goal of this project is for the end results of it to help in that effort, for instance in contributing to the ongoing research in neuroblastoma.

As mentioned previously, the idea of using GCNNs for drug discovery is not a new one in the literature [Sun et al., 2019]. My project will build upon those ideas presented in the literature, expand them and test their feasibility by implementing them into a wider framework for drug design [Born et al., 2019]. In that context, two main areas of application appear. One of them is to re-design the generative model, for instance by reframing the variational autoencoders, used for molecule generation, to architectures that operate over graphs [Simonovsky and Komodakis, 2018, Li et al., 2018a, Li et al., 2018b]. The second area is to find better ways to asses the activity of these molecules, and in a wider context, assess their relevance as drug candidates, i.e. improve the predictive model. In the concrete case of the mentioned framework, it is done by using a critic network [Manica et al., 2019]. This can be expanded on a set of different fronts: using structural data instead of SMILES[1] [Li et al., 2017, Do et al., 2019], by using GCNNs over PPI networks, like STRING[2], in a manner that allows for the use all the information available[Oskooei et al., 2019, Wang et al., 2019], or by introducing particular scores (rewards) based in the interaction of the compound to certain targets [Yingkai Gao et al., 2018, Zhavoronkov et al., 2019] or the combination of the compound with other drugs [Zitnik et al., 2018]—a common practice in patients with cancer. All these possible changes on the critic model would apply at different abstraction levels. That opens the door to seek for ways to integrate the representations learnt at those different stages [Ying et al., 2018, Ma and Zhang, 2019, Huang et al., 2019]. On top of that information extracted from here could be then leveraged on the drug generation part of the framework.

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[1] http://opensmiles.org/

[2] https://string-db.org/

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