

Big Data, Big Knowledge: Big Data for Personalized Healthcare

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Abstract—The idea that the purely phenomenological knowledge that we can extract by analyzing large amounts of data can be useful in healthcare seems to contradict the desire of VPH researchers to build detailed mechanistic models for individual patients. But in practice no model is ever entirely phenomenological or entirely mechanistic. We propose in this position paper that big data analytics can be successfully combined with VPH technologies to produce robust and effective *in silico* medicine solutions. In order to do this, big data technologies must be further developed to cope with some specific requirements that emerge from this application. Such requirements are: working with sensitive data; analytics of complex and heterogeneous data spaces, including nontextual information; distributed data management under security and performance constraints; specialized analytics to integrate bioinformatics and systems biology information with clinical observations at tissue, organ and organisms scales; and specialized analytics to define the “physiological envelope” during the daily life of each patient. These domain-specific requirements suggest a need for targeted funding, in which big data technologies for *in silico* medicine becomes the research priority.

Index Terms—Big data, healthcare, virtual physiological human.

I. INTRODUCTION

THE birth of big data, as a concept if not as a term, is usually associated with a META Group report by Doug Laney entitled “3-D Data Management: Controlling Data Volume, Velocity, and Variety” published in 2001 [1]. Further developments now suggest big data problems are identified by the so-called “5V”: volume (quantity of data), variety (data from different categories), velocity (fast generation of new data), veracity (quality of the data), and value (in the data) [2].

For a long time the development of big data technologies was inspired by business intelligence [3] and by big science (such as the Large Hadron Collider at CERN) [4]. But when in 2009 Google Flu, simply by analyzing Google queries, predicted flu-like illness rates as accurately as the CDC’s enormously complex and expensive monitoring network [5], some analysts started to claim that all problems of modern healthcare could be solved by big data [6].

In 2005, the term virtual physiological human (VPH) was introduced to indicate “a framework of methods and technologies that, once established, will make possible the collaborative

investigation of the human body as a single complex system” [7], [8]. The idea was quite simple:

- 1) To reduce the complexity of living organisms, we decompose them into parts (cells, tissues, organs, organ systems) and investigate one part in isolation from the others. This approach has produced, for example, the medical specialties, where the nephrologist looks only at your kidneys, and the dermatologist only at your skin; this makes it very difficult to cope with multiorgan or systemic diseases, to treat multiple diseases (so common in the ageing population), and in general to unravel systemic emergence due to genotype-phenotype interactions.
- 2) But if we can recompose with computer models all the data and all the knowledge we have obtained about each part, we can use simulations to investigate how these parts interact with one another, across space and time and across organ systems.

Though this may be conceptually simple, the VPH vision contains a tremendous challenge, namely, the development of mathematical models capable of accurately predicting what will happen to a biological system. To tackle this huge challenge, multifaceted research is necessary: around medical imaging and sensing technologies (to produce quantitative data about the patient’s anatomy and physiology) [9]–[11], data processing to extract from such data information that in some cases is not immediately available [12]–[14], biomedical modeling to capture the available knowledge into predictive simulations [15], [16], and computational science and engineering to run huge hypermodels (orchestrations of multiple models) under the operational conditions imposed by clinical usage [17]–[19]; see also the special issue entirely dedicated to multiscale modeling [20].

But the real challenge is the production of that mechanistic knowledge, quantitative, and defined over space, time and across multiple space-time scales, capable of being predictive with sufficient accuracy. After ten years of research this has produced a complex impact scenario in which a number of target applications, where such knowledge was already available, are now being tested clinically; some examples of VPH applications that reached the clinical assessment stage are:

- 1) The VPHOP consortium developed a multiscale modeling technology based on conventional diagnostic imaging methods that makes it possible, in a clinical setting, to predict for each patient the strength of their bones, how this strength is likely to change over time, and the probability that they will overload their bones during daily life. With these three predictions, the evaluation of the absolute risk of bone fracture in patients affected by osteoporosis will be much more accurate than any prediction based on

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external and indirect determinants, as it is in current clinical practice [21].

- 2) More than 500 000 end-stage renal disease patients in Europe live on chronic intermittent haemodialysis treatment. A successful treatment critically depends on a well-functioning vascular access, a surgically created arterio-venous shunt used to connect the patient circulation to the artificial kidney. The ARCH project aimed to improve the outcome of vascular access creation and long-term function with an image-based, patient-specific computational modeling approach. ARCH developed patient-specific computational models for vascular surgery that makes possible to plan such surgery in advance on the basis of the patient's data, and obtain a prediction of the vascular access function outcome, allowing an optimization of the surgical procedure and a reduction of associated complications such as nonmaturation. A prospective study is currently running, coordinated by the Mario Negri Institute in Italy. Preliminary results on 63 patients confirm the efficacy of this technology [22].
- 3) Percutaneous coronary intervention (PCI) guided by fractional flow reserve (FFR) is superior to standard assessment alone to treat coronaries stenosis. FFR-guided PCI results in improved clinical outcomes, a reduction in the number of stents implanted, and reduced cost. However, currently FFR is used in few patients, because it is invasive and it requires special instrumentation. A less invasive FFR would be a valuable tool. The VirtuHeart project developed a patient-specific computer model that accurately predicts myocardial FFR from angiographic images alone, in patients with coronary artery disease. In a phase 1 study the methods showed an accuracy of 97%, when compared to standard FFR [23]. A similar approach, but based on computed tomography imaging, is even at a more advanced stage, having recently completed a phase 2 trial [24].

While these and some other VPH projects have reached the clinical assessment stage, quite a few other projects are still in the technological development, or preclinical assessment phase. But in some cases the mechanistic knowledge currently available simply turned out to be insufficient to develop clinically relevant models.

So it is perhaps not surprising that recently, especially in the area of personalized healthcare (so promising but so challenging) some people have started to advocate the use of big data technologies as an alternative approach, in order to reduce the complexity that developing a reliable, quantitative mechanistic knowledge involves.

This trend is fascinating from an epistemological point of view. The VPH was born around the need to overcome the limitations of a biology founded on the collection of a huge amount of observational data, frequently affected by considerable noise, and boxed into a radical reductionism that prevented most researchers from looking at anything bigger than a single cell [25], [26]. Suggesting that we revert to a phenomenological approach where a predictive model is supposed to emerge not from mechanistic theories but by only doing high-dimensional

big data analysis, may be perceived by some as a step toward that empiricism the VPH was created to overcome.

In the following, we will explain why the use of big data methods and technologies could actually empower and strengthen current VPH approaches, increasing considerably its chances of clinical impact in many “difficult” targets. But in order for that to happen, it is important that big data researchers are aware that when used in the context of computational biomedicine, big data methods need to cope with a number of hurdles that are specific to the domain. Only by developing a research agenda for big data in computational biomedicine can we hope to achieve this ambitious goal.

II. DOCTORS AND ENGINEERS: JOINED AT THE HIP

As engineers who have worked for many years in research hospitals, we recognize that clinical and engineering researchers share a similar mind-set. Both in traditional engineering and in medicine, the research domain is defined in terms of problem solving, not of knowledge discovery. The motto common to both disciplines is “whatever works.”

But there is a fundamental difference: Engineers usually deal with problems related to phenomena on which there is a large body of reliable knowledge from physics and chemistry. When a good reliable mechanistic theory is not available, engineers resort to empirical models, as far as they can solve the problem at hand. But when they do this, they are left with a sense of fragility and mistrust, and they try to replace them as soon as possible with theory-based mechanistic models, which are both predictive and explanatory.

Medical researchers deal with problems for which there is a much less well-established body of knowledge; in addition, this knowledge is frequently qualitative or semiquantitative, and obtained in highly controlled experiments quite removed from clinical reality, in order to tame the complexity involved. Thus, not surprisingly, many clinical researchers consider mechanistic models “too simple to be trusted,” and in general the whole idea of a mechanistic model is looked upon with suspicion.

But in the end “whatever works” remains the basic principle. In some VPH clinical target areas where we can prove convincingly that our mechanistic models can provide more accurate predictions than the epidemiology-based phenomenological models, the penetration into clinical practice is happening. On the other hand, when our mechanistic knowledge is insufficient, the predictive accuracy of our models is poor, and models based on empirical/statistical evidences are still preferred.

The true problem behind this story is the competition between two methods of modeling nature that are both effective in certain cases. Big data can help computational biomedicine to transform this competition into collaboration, significantly increasing the acceptance of VPH technologies in clinical practice.

III. BIG DATA VPH: AN EXAMPLE IN OSTEOPOROSIS

In order to illustrate this concept we will use as a guiding example the problem of predicting the risk of bone fracture in a woman affected by osteoporosis, a pathological reduction of her bone mineralized mass [27]. The goal is to develop predictors

that indicate whether the patient is likely to fracture over a given time (typically in the following ten years). If a fracture actually occurs in that period, this is the true value used to decide if the outcome prediction was right or wrong.

Because the primary manifestation of the disease is quite simple (reduction of the mineral density of the bone tissue) not surprisingly researchers found that when such mineral density could be accurately measured in the regions where the most disabling fractures occurred (hip and spine), such measurement was a predictor of the risk of fracture [28]. In controlled clinical trials, where patients are recruited to exclude all confounding factors, the bone mineral density (BMD) strongly correlated with the occurrence of hip fractures. Unfortunately, when BMD is used as a predictor, especially over randomized populations, the accuracy drops to 60–65% [29]. Given that fracture is a binary event, tossing a coin would give us 50%, so this is considered not good enough.

Epidemiologists run huge international, multicentre clinical trials where the fracture events are related to a number of observables; the data are then fitted with statistical models that provide phenomenological models capable of predicting the likelihood of fracture; the most famous, called FRAX, was developed by John Kanis at the University of Sheffield, U.K., and is considered by the World Health Organisation the reference tool to predict risk of fractures. The predictive accuracy of FRAX is comparable to that of BMD, but it seems more robust for randomised female cohorts [30].

In the VPHOP project, one of the flagship VPH projects funded by the Seventh Framework Program of the European Commission, we took a different approach: We developed a multiscale patient-specific model informed by medical imaging and wearable sensors, and used this model to predict the actual risk of fracture of the hip and at the spine, essentially simulating ten years of the patient's daily life [18]. The results of the first clinical assessment, published only a few weeks ago, suggest that the VPHOP approach could increase the predictive accuracy to 80–85% [31]. Significant but not dramatic: No information is available yet on the accuracy with fully randomized cohorts, although we expect the mechanistic model to be less sensitive to biases.

The goal of the VPHOP project was to replace FRAX; in doing this, the research consortium took a considerable risk, common to most VPH projects, when a radically new and complex technology aims to replace an established standard of care. The difficulty arises from the need to step into the unknown, with the outcome remaining unpredictable until the work is complete. In our opinion big data technologies could change this high-risk scenario, allowing a progressive approach to modeling where predictions are initially generated only using the available data, and then progressively *a priori* knowledge is introduced about the physiology and the specific disease, captured into mechanistic predictive models.

FRAX uses Poisson processes to define an epidemiological predictor for the risk of bone fracture in osteoporotic patients, which consider only the BMD and a few personal and clinical information on the patient [32]. It has already been proposed that this could be extended to include also data related to the

propensity to fall, such as stability tests, or wearable sensor recordings [33]. On the other hand, a vital piece of this puzzle is the ability of a patient's bone (as depicted in CT scan dataset) to withstand a given mechanical load without fracturing; this is something we can predict mechanistically with great accuracy [34]. The future are of technologies that make possible (and easy) to combine statistical, population-based knowledge with mechanistic, patient-specific knowledge; in the case at hand, we could keep a stochastic representation of the fall, and of the resulting load, and model mechanistically the fracture event in itself.

Can this example be considered a big data problem, in the light of the “5V” definition?

- 1) *Volume*: This is probably the big data criterion that current VPH research fits least well. Although the community wishes to exploit the vast entirety of clinical data records, often there is simply not the level of detail, or depth, that supports the association of parameters in the mechanistic models with the data in the clinical record. The datasets that support these analyses are often very expensive to acquire, and currently the penetration is limited. Nevertheless, this is an important area of research, in which the VPH community could learn from, and exploit, existing technology from the big data community.
- 2) *Variety*: The variety is very high. In the example at hand we would have clinical data, data from medical imaging, data from wearable sensors, lab exams, and simulation results. This would include both structured and nonstructured data, with 3-D imaging posing specific problems of data treatment such as automated voxel classification (see as examples [35]–[37]).
- 3) *Velocity*: Osteoporosis is a chronic condition; as such all patients are expected to undergo a full specialist control every two years, where the totality of the examinations is repeated. Regarding growth rate: If to this we add that the ageing of the population is constantly increasing the number of patients affected, we face growth rates in the order of 55–60% every year.
- 4) *Veracity*: Here there is a big divide between clinical research and clinical practice. While data collected as part of clinical studies are in general of good quality, clinical practice tends to generate low quality data. This is due in part to the extreme pressure medical professionals face, but also to a lack of “data value” culture; most medical professionals see the logging of data a bureaucratic need and a waste of time that distracts them from the care of their patients.
- 5) *Value*: The *potential* value associated with these data is very high. The cost of osteoporosis, including pharmacological intervention in the EU in 2010 was estimated at €37 billion [38]. Moreover, in general, healthcare expenditure in most developed countries is astronomical: the 2013/2014 budget for NHS England was £95.6 billion, with an increase over the previous year of 2.6%, at a time when all public services in the UK are facing hard cuts. In OECD countries, we spend on average USD\$3395 per year per inhabitant in healthcare (source: OECD 2011).

But the *real* value of big data analytics in healthcare still remains to be proven. We believe this is largely due to the need for much more sophisticated analytics, which incorporate *a priori* knowledge of pathophysiology; this is exactly what the VPH has to offer to big data analytics in healthcare.

IV. FROM DATA TO THEORY: A CONTINUUM

Modern big data technologies make it possible in a short time to analyze a large collection of data from thousands of patients, identify clusters and correlations, and develop predictive models using statistical or machine-learning modeling techniques [39], [40]. In this new context it would be feasible to take all the data collected in all past epidemiology studies - for example, those used to develop FRAX - and continue to enrich them with new studies where not only new patients are added, but different types of information are collected.

Another mechanism that in principle very high-throughput technologies make viable for exploration is the normalization of digital medical images to conventional space-time reference systems, using elastic registration methods [41]–[43], followed by the treatment of the quantities expressed by each voxel value in the image as independent data quanta. The voxel values of the scan then become another medical dataset, potentially to be correlated with average blood pressure, body weight, age, or any other clinical information.

Using statistical modeling or machine learning techniques we may obtain good predictors valid for the range of the datasets analyzed; if a database contains outcome observables for a subset of patients, we will be able to compute automatically the accuracy of such a predictor. Typically the result of this process would be a potential clinical tool with known accuracy; in some cases the result would provide a predictive accuracy sufficient for clinical purposes, in others a higher accuracy might be desirable.

In some cases there is need for an explanatory theory, which answers the “how” question, and which may be used in a wider context than that a statistical model normally is. As a second step, one could use the correlation identified by the empirical modeling to elaborate possible mechanistic theories. Given that the available mechanistic knowledge is quite incomplete, in many cases we will be able to express a mathematical model only for a part of the process to be modeled; various “grey-box” modeling methods have been developed in the last few years that allow one to combine partial mechanistic knowledge with phenomenological modeling [44].

The last step is where physiology, biochemistry, biomechanics, and biophysics mechanistic models are used. These models contain a large amount of validated knowledge, and require only a relatively small amount of patient-specific data to be properly identified.

In many cases these mechanistic models are extremely expensive in terms of computational cost; therefore input-output sets of these models may also be stored in a data repository in order to identify reduced-order models (also referred as “surrogate” models and “meta-models”) that accurately replace a

computationally expensive model with a cheaper/faster simulation [45]. Experimental design methods are used to choose the input and output parameters or variables with which to run the mechanistic model in order to generate the meta-model’s state space description of the input-output relations—which is often replaced with a piecewise partial least-squares regression approximation [46]. Another approach is to use Nonlinear AutoRegressive Moving Average model with eXogenous inputs in the framework of nonlinear systems identification [47].

It is interesting to note that no real model is ever fully “white-box.” In all cases, some phenomenological modeling is required to define the interaction of the portion of reality under investigation with the rest of the universe. If we accept that a model describes a process at a certain characteristic space-time scale, everything that happens at any scale larger or smaller than that must also be accounted for phenomenologically. Thus, it is possible to imagine a complex process being modeled as an orchestration of submodels, each predicting a part of the process (for example at different scales), and we can expect that, while initially all submodels will be phenomenological, more and more will progressively include some mechanistic knowledge.

The idea of a progressive increase of the explanatory content of a hypermodel is not fundamentally new; other domains of science already pursued the approach described here. But in the context of computational biomedicine this is an approach used only incidentally, and not as a systematic strategy for the progressive refinement of clinical predictors.

V. BIG DATA FOR COMPUTATIONAL BIOMEDICINE: REQUIREMENTS

In a complex scenario such as the one described above, are the currently available technologies sufficient to cope with this application context?

The brief answer is no. A number of shortcomings that need to be addressed before big data technologies can be effectively and extensively used in computational biomedicine. Here we list five of the most important.

A. Confidential Data

The majority of big data applications deal with data that do not refer to an individual person. This does not exclude the possibility that their aggregated information content might not be socially sensitive, but very rarely is it possible to reconnect such content to the identity of an individual.

In the cases where sensitive data are involved, it is usually possible to collect and analyze the data at a single location; so this becomes a problem of computer security; within the secure box, the treatment of the data is identical to that of nonsensitive data.

Healthcare poses some peculiar problems in this area. First, all medical data are highly sensitive, and in many developed countries are considered legally owned by the patient, and the healthcare provider is required to respect patient confidentiality. The European parliament is currently involved in a complex debate about data protection legislation, where the need for

individual confidentiality can be in conflict with the needs of society [48].

Second, in order to be useful for diagnosis, prognosis or treatment planning purposes the data analytics results must in most cases be relinked to the identity of the patient. This implies that the clinical data cannot be fully and irreversibly anonymized before leaving the hospital, but requires complex pseudoanonymization procedures. Normally the clinical data are pseudoanonymized so as to ensure a certain k -anonymity [49], which is considered legally and ethically acceptable. But when the data are, as part of big data mash-ups, relinked to other data, for example from social networks or other public sources, there is a risk that the k -anonymity of the mash-up can be drastically reduced. Specific algorithms need to be developed that prevent such data aggregation when the k -anonymity could drop below the required level.

B. Big Data: Big Size or Big Complexity?

Consider two data collections:

- 1) In one case, we have 500 TB of log data from a popular web site: a huge list of text strings, typically encoding 7–10 pieces of information for transaction.
- 2) In the other, we have a full VPHOP dataset for 100 patients, a total of 1 TB; for each patient, we have 122 textual information items that encode the clinical data, three medical imaging datasets of different types, 100 signal files from wearable sensors, a neuromuscular dynamics output database, an organ-level model with the results, and a tissue-scale model with the predictions of bone remodeling over ten years. This is a typical VPH data folder; some applications require even more complex data spaces.

Which one of these two data collections should be considered big data? We suggest that the idea held by some funding agencies, that the only worthwhile applications are those targeting data collections over a certain size, trivializes the problem of big data analytics. While the legacy role of big data analysis is the examination of large amounts of scarcely complex data, the future lies in the analysis of complex data, eventually even in smaller amounts.

C. Integrating Bioinformatics, Systems Biology, and Phenomics Data

Genomics and postgenomics technologies produce very large amounts of raw data about the complex biochemical processes that regulate each living organism; nowadays a single deep-sequencing dataset can exceed 1 TB [50]. More recently, we have started to see the generation of “deep phenotyping” data, where biochemical, imaging, and sensing technologies are used to quantify complex phenotypical traits and link them to the genetic information [51]. These data are processed with specialised big data analytics techniques, which come from bioinformatics, but recently there is growing interest in building mechanistic models of how the many species present inside a cell interact along complex biochemical pathways. Because of the complexity and the redundancy involved, linking this very large body of mechanistic knowledge to the higher-order cell-cell and cell-

tissue interactions remains very difficult, primarily for the data analytics problems it involves. But when this is possible, genomics research results finally link to clinically relevant pathological signs, observed at tissue, organ, and organism scales, opening the door to a true systems medicine.

D. Where are the Data?

In big data research, the data are usually stored and organised in order to maximize the efficiency of the data analytics process. In the scenario described here, however, it is possible that parts of the simulation workflow require special hardware, or can be run only on certain computers because of licence limitations. Thus, one ends up trading the needs of the data analytics part with those of the VPH simulation part, always ending up with a suboptimal solution.

In such complex simulation scenarios, data management becomes part of the simulation process; clever methods must be developed to replicate/store certain portions of the data within organisations and at locations that maximize the performance of the overall simulation.

E. Physiological Envelope and the Predictive Avatar

In the last decade, there has been a great deal of interest in the generation and analysis of patient-specific models. Enormous progress has been made in the integration of image processing and engineering analysis, with many applications in healthcare across the spectrum from orthopaedics to cardiovascular systems and often multiscale models of disease processes, including cancer, are included in these analyses. Very efficient methods, and associated workflows, have been developed that support the generation of patient-specific anatomical models based on exquisite three and four-dimensional medical images [52], [53]. The major challenge now is to use these models to predict acute and longer-term physiological and biological changes that will occur under the progression of disease and under candidate interventions, whether pharmacological or surgical. There is a wealth of data in the clinical record that could support this, but its transformation into relevant information is enormously difficult.

All engineering models of human organ systems, whether focused on structural or fluid flow applications, require not only the geometry (the anatomy) but also constitutive equations and boundary conditions. The biomedical engineering community is only beginning to learn how to perform truly personalized analysis, in which these parameters are all based on individual physiology. There are many challenges around the interpretation of the data that is collected in the course of routine clinical investigation, or indeed assembled in the Electronic Health Record or Personal Health Records. Is it possible to predict the threat or challenge conditions (e.g., limits of blood pressure, flow waveforms, joint loads), and their frequency or duration, from the data that is collected? How can the physiological envelope of the individual be described and characterized? How many analyses need to be done to characterize the effect of the physiological envelope on the progression of disease or on the effectiveness of treatment? How are these analyses best formulated

and executed computationally? How is information on disease interpreted in terms of physiology? As an example, how (quantitatively) should we adapt a patient-specific multiscale model of coronary artery disease to reflect the likelihood that a diabetic patient has impaired coronary microcirculation? At a more generic level, how can the priors (in terms of physical relationships) that are available from engineering analysis be integrated into machine learning operations in the context of digital healthcare, or alternatively how can machine learning be used to characterize the physiological envelope to support meaningful diagnostic and prognostic patient-specific analyses? For a simple example, consider material properties: Arteries stiffen as an individual ages, but diseases such as moyamoya syndrome can also dramatically affect arterial stiffness; how should models be modified to take into account such incidental data entries in the patient record?

VI. CONCLUSION

Although sometimes overhyped, big data technologies do have great potential in the domain of computational biomedicine, but their development should take place in combination with other modeling strategies, and not in competition. This will minimize the risk of research investments, and will ensure a constant improvement of *in silico* medicine, favoring its clinical adoption.

We have described five major problems that we believe need to be tackled in order to have an effective integration of big data analytics and VPH modeling in healthcare. For some of these problems there is already an intense on-going research activity, which is comforting.

For many years the high-performance computing world was afflicted by a one-size-fits-all mentality that prevented many research domains from fully exploiting the potential of these technologies; more recently the promotion of centres of excellence, etc., targeting specific application domains, demonstrates that the original strategy was a mistake, and that technological research must be conducted at least in part in the context of each application domain.

It is very important that the big data research community does not repeat the same mistake. While there is clearly an important research space examining the fundamental methods and technologies for big data analytics, it is vital to acknowledge that it is also necessary to fund domain-targeted research that allows specialized solutions to be developed for specific applications. Healthcare, in general, and computational biomedicine, in particular, seems a natural candidate for this.

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Authors’ photographs and biographies not available at the time of publication.