Cognition and Neurocomputation

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Cognition and Neurocomputation is a subject that can be thought of either as a narrow specialty area of neuroscience, psychology and psychiatry or egotistically even the main area of which those other subjects are sub-areas. The underlying principle of the subject is that the emergence of the phenomenon of human cognition is approachable and even explainable as the natural emergence of a *macro*-phenomenon from an extensive *micro*-phenomenon in analogy as, for example, classical Newtonian physics can explain the motions of planets.

Historically when there is a break-through in neurocomputation there are attempts to explain cognitive effects by analogy. Such was the case 70 years ago with the McCullough-Pitts neuron and simple neural networks, 60 years ago with the Perceptron, 40 years ago with neural networks and backpropagation, and now during the past 10 years with *deep neural networks*. Usually these "explanations" are somewhat naïve from a cognitive viewpoint and can occasionally be even a bit embarrassing. It is fair to say that the explanations of cognitive behavior directly from the neurocomputation model has not yet been an overwhelming success.

Nonetheless, great advances have occurred; an example is the work of McClelland et al. [14]. Here the lesson is that when one can see the produced model and the human model as two instances of a common mechanism, where the *interpretation* of the mechanism can be completely different in each. The simpler the artificial model is then results in the largest strengthening of belief in the correctness of the mechanism in the human. For good examples, see McClelland et al. [14] and Peleg, Hazan et al. [13].

As a subject, we see that Neurocomputation and Cognition has at least three main components, "Cognition", "Neuro" and "Computation". "Cognition" can be thought of as (i) the *goal*, that is, neurocomputation is there to *explain* by computational means human cognitive abilities, or alternatively (ii) as the *source,* being taken as a well-known strong

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human ability, and then trying to abstract from it artificial reproductions of it, which can be used for "practical" tasks. In both cases, the "Neuro" part indicates that the successful artificial construct should be an *emergent* property of many neurons, either artificial or natural. The precise choice of the model of the basic neuron and the basic method of modifying the model (e.g. weights, or architecture) reflect the "Computational" constraints. On the one hand, to emphasize the explanatory effect of the model, it should be as simple as possible in implementing the abstractions of the components of the theory. On the other hand, if the implementation is mainly for using the abstraction from the cognitive source for a practical device, one can diverge from the biological principles as needed.

In recent years, with the "deep learning revolution" (and actually prior to it) [1] it has become clear that the emergence requirement indicates that these neurocomputational models are often driven by "learning" from sample data. From this point of view, each model after learning is a statistical representation of the data. In general, more complex ("deep", "convolutional", "recurrent" and so on) models seem to have an ability to represent more complex data distributions. This richness in representation seems to be more comprehensive than standard statistics, and perhaps should be thought of as the statistics of our time. However, this richness comes with a price–these new statistics are dependent on having sufficient data. (Occasionally, other "tricks" or methodologies are used to somewhat compensate for this lack of data (e.g. drop-out or transfer learning) and to avoid what is commonly known as the "overfitting" phenomena.)

This is particularly important for many of the cognitive modeling tasks, wherein the data is usually collected by conduction of complex neurophysiological experiments resulting in relatively small and high dimensional data sets. This problem is usually called the *curse-of-dimensionality* [2] or a *small-n-large-p* [3]. For example, a typical fMRI experiment will contain less than 100 participants (i.e. data-points), having at least 30 min with 2 s sampling rate per participant. Thus, in this case, assuming each fMRI scan contains 40,000 voxels and the raw dimensionality of a single data point is 36×10^6.

Looked at in this way, the listed papers in this collection can also be seen as essentially dealing with the problem of computational approaches to biomarker discovery. In this collection of works, biomarkers could be defined generally as bits of *measurable* information whose presence alone, or in a combination with other measures, is indicative of some phenomenon. However, these biomarkers can sometimes be problematical in the neurocomputation setting, as these discovered biomarkers, while statistically indicative can be difficult or impossible to interpret. That is, the direct techniques can be very good in classification or predictive analysis, but more lacking in explanatory ability. On the other hand, the flexibility of the artificial neural modeling allows the possibility of testing neurophysiologically based connectivity hypotheses in a controlled setting. Observing this hypothesis in the artificial setting adds (or denies) support to the theory.

These are just some of the issues struggled with and arising in work in this field. In this collection of articles, we see many of these issues confronted in different settings.

This issue grew out of a special session on Cognition and Neurocomputation organized by Larry Manevitz, Alex Frid and Bernadette Ribeiro as part of the IJCNN/WCII 2018 meeting in Rio de Janeiro. Some of these papers are substantial expansions of work presented there while others are completely new papers. All of the papers presented here have undergone the usual stiff reviewing process of AMAI. Below we give a brief summary of the issues to which each paper relates.

Analyzing cognitive processes from complex neuro-physiologically based data: some lessons by Alex Frid and Larry M. Manevitz [4] considers in varying settings, the application

and adaptation of machine learning techniques specifically to a variety of cognitive tasks. These include memory retrieval, discovery of biological markers in the speech signal for Parkinson Disease differential diagnosis (i.e. to level of progression of the disease), biological markers and classification for Dyslexia diagnosis, visual classification, grammatical identification during reading) over a variety of biological signals (EEG, ERP, voice signal, fMRI). One of the main "lessons" is that the relative paucity of data (almost always the case in human cognitive data) to make subtle distinctions from data can be overcome by emphasizing both the feature selection and the fusion methods or combining the information from the chosen features.

The machine learning methodologies adaptations put forth include a novel ("expansion-projection") deep autoencoder architecture, the generation of an artificial exhaustive dictionary of potential responses to stimuli, adapting a convolution deep neural network to the one dimensional raw speech signal (and automatic discovery of "standard" signal processing filters), and boosting methods to find multivariate combinations of univariate chosen features.

The next paper, *Data-driven Koopman operator approach for computational neuroscience* by Natasza Marrouch, Joanna Slawinska, Dimitrios Giannakis and Heather L. Read [5], deals with a specific representation of the EEG data, The show that the use of a "Koopman" operator on the EEG data (instead of a FFT or Wavelet, for example) can result in a representation that is good for presenting mechanisms that underlie natural spatial and temporal coordination of neural activities across various brain areas and during different steps of cognitive processing.

The two papers *Deep learning models for brain machine interfaces* by Lachezar Bozhkov and Petia Georgieva [6] and *Human-In-The-Loop active learning* via *brain computer interface* by Eitan Netzer and Amir B. Geva [7] are interested in Brain-Computer Interfaces, however from quite different approaches. The first paper's main approach to obtaining a quality user-independent encoding of brain-motor encoding is to use a stacked autoencoder, with each level trained separately. They show how to balance the accuracy/generalizability conundrum (over different users) in their setting. The second paper shows how one can add a human supervisor to the loop of learning by combining the appropriate choice of a clustering algorithm and then selection of an appropriate labeling request to the human. That is, the system requests a useful new label implementing the concept of "active learning". Although used here to make a human in the loop feasible, this concept of clustering and then requesting a label for an indicative member of the cluster can be adapted to other mechanisms as well.

Learning non-convex abstract concepts with regulated activation networks by R. Sharma, B. Ribeiro, A. M. Pinto, and F. A. Cardoso [8] deals with an interesting methodology (called Regulated Activation Networks [9]) appropriate to growing a representation for an arbitrary "concept". Here the authors distinguish between "convex" and "non-convex" representations. Given n-dimensional data, they define the basic concepts as being n-dimensional balls chosen, for example, as clusters, and then develop a way to combine clusters in this space, based on similarity of the centroids of the clusters. The number of such concepts (both "convex" and "non-convex") are learned from the data; with a heuristic cut-off methodology. The system is automatic, unlike the Netzer-Geva [7] paper in this issue. They show how this method can be thought of as analogous to human concept building and apply it to a variety of data bases.

The paper *Lattice map spiking neural networks* (*LM-SNNs*) *for clustering and classifying image data* by H. Hazan, D. J. Saunders, D. T. Sanghavi, H. Siegelmann, and R. Kozma [10] is the latest in a series of works exploring the importance of computational advantage of adding additional biological features to complex artificial neural networks. In particular, in this

work, the basic artificial model (McCullogh-Pitts) of a neuron is replaced by the computationally more complex (but still simple from the neuroscience perspective) spiking neurons in a lattice map. Moreover, the authors explore biologically related adaptations such as inhibition schedules in global STDP and selective mechanisms in the neurons. Amongst the results is an adaptation of self-organizing maps, and showing a reduction of computational resources needed as compared to comparable deep neural networks in a different topological setting.

The final paper *Classifying the valence of autobiographical memories from fMRI data* [11] by Alex Frid, Noberto Eiji Nawa and Larry M. Manevitz investigates how to classify from fMRI data freely retrieved autobiographical memories as to their valence (i.e. "happy" versus "sad" memories). The method used is a combination of strong univariate feature selection together with a boosting algorithm. It is interesting to note that in the paper of Ando and Nawa [12], the authors (who designed the clever experiment and gathered the data), tried an opposite philosophy of using most of the brain features (under the assumption that memory retrieval is very dispersed in the brain) and did indeed show that such autobiographical retrieval can be distinguished from other cognitive tasks (specifically counting backwards). On the other hand, they could not make the delicate distinguishment of valence. Since that work was on the same data set as in this paper, this gives an indication of the importance of matching the appropriate statistical learning methodology to the problem.

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