

Genetic specification of recurrent neural networks: Initial thoughts

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Abstract – Computational Neuro-Genetic Modeling (CNGM) is discussed from the perspective of building Artificial Neural Network architectures starting with substantially pre-defined modules and processes (DNA-ANNs). This is equivalent to assuming that DNA code in a neuron can ultimately specify function, process and some level of data abstraction beyond the immediate role of genes to produce proteins or to regulate processes, and using that basis as a metaphor for DNA-ANNs. The potential advantages that might be derived from highly evolved, fine-grained hybrid genetic/connectionist systems, and some of the implementation challenges that they could present are discussed.

I. INTRODUCTION

ANNs were originally inspired by the search for ways to explain the functioning of the brain and to replicate its great computational powers (Anderson and Rosenfeld [1]). The brain will likely remain a source of inspiration and a far-off golden standard for very advanced computational capabilities for quite some time to come, so it is not surprising to see ANN research consider ways to incorporate new concepts from genetics, even if this is somewhat speculative at the current time.

Much of the focus of ANN research in the past has been on building connectionist architectures with various fixed activation functions for the nodes or neurons, using a variety of training approaches, and sometimes employing growth or pruning strategies to evolve a network structure. Often the objective has been to develop powerful general learning algorithms with somewhat specialized ANN architectures to tackle a broad class of problems, for example the ubiquitous Multi-Layer Perceptron (MLP) with backpropagation (Werbos [2], Parker [3], LeCunn [4], Rummelhardt, Hinton, McLelland [5]), Adaptive Resonance Theory (Carpenter and Grossberg [6]), and Self Organizing Maps (Kohonen [7]).

Evidence is rapidly accumulating that non-protein-coding DNA (npcDNA), sometimes in the past popularly referred to as "junk DNA", is not all simply waste coding interspersed between gene-coding regions (exons), but that it may have many very important roles in directing cellular processes beyond protein coding (Marcus [8]) and even beyond well-known regulatory functions (Mattick [9]). This is an exciting area of research for biology and neuroscience, and it will likely influence thinking in the humanities, cognitive

sciences and in Computational Intelligence. Several researchers are looking into how one might incorporate DNA-like capabilities into Artificial Neural Networks

(ANNs), or apply ANN methods to better understand and model the role of genetics in biological NNs. This work, currently described by Kasabov's phrase "Computational Neuro-Genetic Modeling" [10], is proceeding even though our knowledge of the biological processes is still in its infancy.

Work relating genetics and neuron or brain information processing is very broad, and is discussed in more detail in Section II.A. However, it is worthwhile to quickly list a few subjects:

- DNA as a memory molecule in early work (Crick and others [15] to [21]), although experiments haven't supported this;
- CNGMs as a means of modelling the the EEG signature of gene networks (Kasabov [11]);
- Ontogeny, or growth of the brain, and how genes can efficiently do this (Storjohann and Marcus [13]);
- Nature versus nurture – models of the relative importance of genetics and learning to retinotopic mappings (Thivierge [22]);

As a complement and contrast to the above work, this paper focuses on the genetic specification and operation of ANNs, simply referred to as DNA-ANNs, for which a core architecture and learning is pre-specified but the DNA-ANN may still learn and evolve over time in a variety of environments. The ultimate intent is to utilize a diverse combination of DNA-ANN architectures and learning methods such as mentioned in the second paragraph of this introduction. Additionally, there is some emphasis on recurrent neural networks in this paper (RNNs, referred to as DNA-RNNs when incorporating genetics).

Section II of this paper summarizes three key sources of inspiration for DNA-RNNs: genetics; computational models of neuron and brain function; and trends with ANNs. The sub-section on genetics overviews some advances in interpreting the diverse roles of DNA, and more specifically overviews current work on the DNA specification of the brain and the way in which it is structured and functions. Section III lists the benefits for ANNs that we hope to achieve by a similar pre-specification.

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II. INSPIRATION FOR DNA-ANNs

A. Inspiration from Genetics: beyond protein coding and regulation

1. DNA beyond genes and immediate regulatory function

Conventionally, "genes" might have been thought of as being "assembly language programming" for proteins, almost in a literal sense. This process involves finding the appropriate starting point on the DNA, culling out non-protein-coding sequences of mRNA (introns, part of npcDNA) from coding regions (exons) as indicated by spliceosomes. The mRNA is then used in ribosomes for the assembly of proteins. Occasionally, "decision points" occur in gene sequences that can result in different final proteins, depending on the regulatory function of a small component of npcDNA.

However, for a long time researchers have suspected that the role of DNA goes much further than merely coding for proteins, that life was not merely a "combinatorial soup" (Mattick [9]) that coincidentally gave rise to the tremendously detailed, complex and specific anatomy and physiology of the cells and of entire organisms (Mattick [23], Ast [24], Eddy [25], Gibbs [26]).

Moreover, it was also clear that the "genes" of eukaryotic organisms (having cells with a nucleus as opposed to prokaryotic organisms with non-nuclear cells) account for only a small portion of the total DNA. For example, earlier estimates were that only ~1.5% of the 3.2 Giga base-pairs of amino acids in human DNA codes for proteins (less now, given the lower estimates of today's total gene counts!), and yet most DNA is transcribed to RNA! Furthermore, (Mattick [23]) points out that there is a poor relation between an organism's complexity and the number of protein-coding genes, but there is a more consistent relation between an organism's complexity and the amount of npcDNA. His description of the Cambrian period bio-complexity explosion (~1 Gy ago), and the rest of his analysis provide a substantial basis for going beyond the "central dogma of biology", that DNA only codes for genes and or their direct regulation. Highly complex architecture argues for the need or advantage and power of precise plans and "drawings" that are highly specific, either in the case of human buildings or biological systems.

The past expression "junk DNA" had perhaps conveyed the message that much of the DNA may simply be a wasteland of leftover code from past or modified needs, code resulting from replication errors, or code that served as a buffer to protect against certain types of error. While some of the npcDNA may have arisen by such mechanisms, the impression that much of it is "junk" could possibly be one of the great misnomers of scientific history. Furthermore, perhaps genes are merely the simplest and lowest level of coding on the DNA, just a starting point for much more powerful functionality and abstractions to be discovered. Changes in DNA or its expression can occur through mutation, crossover of genes (diploid cells and sexual

reproduction), and epigenetically (including cell differentiation). Epigenetic changes affect which sections of DNA are expressed by changes in the availability or in the "locking up" of sections of chromatin, the structures comprised of disk-like histones around which DNA sections are coiled. More recently, researchers are focusing on non-protein-coding RNA and micro-RNA. The latter consists of segments of RNA that can perhaps be as short as 15 to 35 base pairs, and are thought to play a role in regulating gene expression. The work of Kim, Krichevsky et.al. [27] focuses on the role of micro-RNA on neuron-related genetics, and shows that micro-RNA can play a gene-regulatory role by influencing spliceosome decision points.

2. DNA and the brain

[Minsky [30]]: *"The marvelous powers of the brain emerge not from any single, uniformly structured connectionist network but from highly evolved arrangements of smaller, specialized networks which are interconnected in very specific ways."*

Clearly, brain growth or ontogeny is a very highly ordered and directed process, and while there is a high degree of variability in comparing brains and brain function between individuals (based on anatomy, fMRI etc), there is also an extremely high degree of commonality and regularity. Strikingly similar adult human behavior by identical twins separated at birth and the theory of Universal Generative Grammar for linguistics (Chomsky [32]) are good examples of arguments for the pre-specification not just of "normal" anatomy and physiology, but of a great deal of "initial content" for the brain (data, functions, operating systems and likely far beyond that to use an admittedly poor metaphor from computing, but one that is easy to relate to). Steven Pinker's book "The blank slate" [34] summarizes a wide range of results, many of which have been known for a long time, that dispel the "blank slate" concept of the brain learning everything from scratch. The expression "blank slate" will be used often in this paper to contrast DNA-ANNs, which have at least some pre-specified initial content, with ANNs that only start to learn or evolve when presented with data.

Several researchers over time have proposed that DNA would have excellent characteristics as a "memory molecule", providing enormous information storage capabilities ([15]-[21]), but this could not be substantiated by experiments. However it should be noted that conventional genomics, which relates genes to proteins and regulatory functions, is vastly easier than trying to relate DNA coding to brain structure, function and information content, none of which can be directly measured in detail. That problem will get much worse as higher and higher levels of abstract brain function are addressed.

Marcus [8] convincingly argues that the mind is specified by genes in a manner that maximizes their information content. This occurs because the genes don't specify all of the details. More importantly they specify how structures are built and learn.

More recently, work by Michael Meaney and associates in Montreal ([35],[36]) have established strong evidence that epigenetic modifications may occur during the first week of a rat's life due to its mother's nurturing behavior, and that these epigenetically-based behavioral modifications can persist throughout the life of the rat. Furthermore, there is a high likelihood that this will be passed on to future generations (albeit there will presumably be a fresh influence due to each new generation of mothers). This is extremely interesting – not only does it provide a concrete example of epigenetically-driven changes in behavior, it also provides a basis for "Lamarckian heredity" of the mind whereby traits set during the life of an individual may be passed on, in contrast to the conventional "Mendelian heredity" for which the die is set at conception, and changes during an individual's life are not passed on other than through mutation, crossover, duplication of DNA code etc. Before being confident about the existence of Lamarckian heredity, the results would have to be confirmed over several generations of rats, and of course we would need experimental results for other examples as well, both behavioral and knowledge-related.

As mentioned in the introduction, given these growing indications of extensive genetic and epigenetic "pre-programming" of the brain, and possibly more direct "live" interactions between DNA, individual neurons and brain function, attempts at integrating gene-like capabilities into ANNs have begun. "Computational Neuro-Genetic Modeling" (CNGM) is perhaps best defined by the question posed by Kasabov [33]:

"Can they [CNGMs] facilitate the construction of [ANN] models that have flexible architectures, rapid trainability, adaptability to new environments, and the capacity to facilitate knowledge representation? How can we use these models to improve our understanding of the brain and to find cures for brain diseases?"

3) *Influence of brain function on DNA expression*

The whole "programming metaphor" for the DNA pre-specification and operation of the brain is hypothetical and only weakly indicated by experimental results. Much of the neurological experimental evidence is more suitable for establishing the "feedforward" influence of DNA on information content and processing. However, it is assumed in this paper for DNA-RNNs (artificial neural nets, not biological brains, but using biology as a metaphor and *vis-versa*) that the information content of the processing activities of a neuron or region of the brain can of itself influence npcDNA expression (a information "feedback" influence on selecting DNA code). There doesn't seem to be much direct evidence for that biologically, but it will be interesting to see if this theme emerges from experiments in the future.

Clearly organisms respond to their environment, and this involves a huge cascade of gene expression and regulation at every level of the organism, and one might argue that these could be more or less "fixed" responses. But learning in the

brain would require far more flexibility and rapidity of change than might exist or be allowable in most physiological responses. In a sense the immune system might provide an analogous example that must change very quickly to a rapidly changing external environment.

Meaney's results as discussed previously show behavioral changes in infant rats that are linked with epigenetic changes brought on by their mother's nurturing behavior, and that is at least a start. Extensive research has been carried out to model the role of hormones and more specifically neuromodulators (Doya, Dayan and Hasselmo [38]). But while this work models the influence of neuromodulators on the functioning of neurons or regions of the brain, it does not show specific mechanisms for the influence of information processing on DNA expression other than for physiological requirements.

B. Inspiration for DNA-ANNs from models of neurons, brain regions, and psychology

There has been a great deal of work over several decades on building ANN models of neurons, brain regions, sensory systems (olfactory by Freeman [40], Padgett [41] and their co-workers), motor systems (Grossberg [42]) and the effects of neuromodulators (Doya, Dayan and Hasselmo [38] as cited above). Furthermore, many general computational learning methods have been based on or inspired from the field of psychology (Hebbian learning, ART, Backpropagation, K series chaotic ANNs). It has been natural to think in terms of specialized neuron arrangements, "modules", connections, specialized regions of the brain, and whole-brain processes, the latter exemplified by major efforts to computationally model the whole brain [43].

There has also been a great deal of work on sensory and brain biomimetics and prosthesis (for example, retinal prosthetic work by groups led by Mark Humayun [45] and Eckhorn et al. [46], and a hippocampal prosthesis by Ted Berger's group [44]).

So what lessons or inspiration can we draw from neuron, brain, and psychology studies that can help us to develop DNA-ANNs? The short answer is that there will likely be a huge wealth of growth strategies, architectures, functions, and processes which should be directly relevant to DNA-ANNs, and the mind harbors capabilities that will continue to inspire research for a long time.

But some general observations are worth repeating here:

- Natural systems are rich, varied, dynamic and incredibly powerful at EVERY level – from the sub-neuron level up to the whole brain. It goes without saying that this is a massively parallel architecture, commonly with recurrent connections.
- There is a huge diversity and redundancy of structures, and spiking. Non-stationary dynamics seems to be a key characteristic.
- The growth process of the brain involves making seemingly random connections between neurons, and the die-off of a significant fraction of the initial neurons.

In spite of this, there is a regularity to the architecture of the brain and its subsystems: the brain is capable of highly reproducible performance for challenging problems in very noisy environments, even where there may be significant damage to many of the neurons involved (graceful degradation of performance).

- We likely have a long ways to go before we can properly identify and understand processes at higher levels of abstraction, even though current models are showing promise.

Ideally, a more general discussion of neural and brain models (ANNs) would be provided here, but only a few examples are listed below:

- Frontal cortex and basal ganglia circuits (Brown, Bulloch & Grossberg [42]);
- Multi-modular brain (Taylor [48]);
- Thalamo-cortical loops (Hecht-Nielsen [49]);
- Temporal sequences in frontal lobes (Taylor & Taylor [47]);
- Learning categories (Grossberg, Carpenter, Ersoy [50]); and
- Purkinje cell models (Dunin-Barkowski et.al. [51]).

The work of Storjammen and Marcus [13] is providing a first computational framework for the genetic specification of growth and end structure of "modules" that produce the right kind of functionality. Kasabov et al [10],[11] have worked on modelling the EEG signal characteristics of brain regions based on the kinetics of gene networks.

C. Inspirations for DNA-ANNs from trends with ANNs

This sub-section gives a very brief listing of selected trends in ANNs that are also a source of inspiration for Computational Neuro-Genetic Modelling (CNGM).

1) Diversity of approaches

As mentioned in the Introduction, there is a great diversity of ANN architectures and of approaches for their learning and evolution. The overall intent of DNA-ANNs as proposed in this paper is to make use of as many of the available ANN architectures and approaches as required or as possible.

2) Local, incremental learning approaches

Neural Gas Models [52][53] and Evolving Connectionist Systems (ECOS, Kasabov [54]) are examples of ANNs which have been designed to learn incrementally as new data is encountered. This may fit in well with DNA-ANNs, where a diverse population of substantially pre-specified DNA-ANNs could potentially be evolved in a more concise and effective manner.

3) Multi-phase NN Architecture: "Crystalline to Gaseous"

An interesting recent trend has been to generate substantially fixed weight neural networks for which only a small portion of the weights undergo changes during the learning phase, such as the Extreme Learning Machine (Huang [55],[56]) and Echo State Networks (Jaeger [57],[58]). Although there

are challenges and limitations (Prokhorov [63]), this provides some insight into how one might do even better by rapidly integrating and training DNA-ANN "modules" by pre-specifying architectures that allow the modules to be very rapidly and efficiently trained and evolved.

4) Networks, hierarchies of NNs:

There has been strong interest in building ensembles and hierarchies of many varieties of ANNs (Carpenter and Martens [60], Cuadros-Vargas and Romero [61]).

5) RNNs and Approximate Dynamic Programming (ADP)

RNNs are of particular relevance to the whole concept of DNA-ANNs, as they can handle dynamical systems well and they are an important tool for tackling high-level decision making and adaptation challenges such as Approximate Dynamic Programming (ADP) and control (Werbos [62], Prokhorov, Puskorius, Feldkamp [63], Venayagamoorthy [64], Si et.al. [65]). A recent paper (Santiago and Lendaris [66]) claims that RNNs can overcome a fundamental limitation of Artificial Intelligence (AI) – the "Frames Problem". This subject also leads into the theme of a recent workshop on achieving functional integration led by Hussain [67].

6) Signal processing and information theoretics

Signal processing techniques have been successfully applied to the difficult problem of training recurrent neural networks (RNNs) (Puskorius & Feldkamp [68],[69], Wan and van der Merwe [70]) in combination with the calculation of error derivatives for each node using Back Propagation Through Time (BPTT).

III. WHAT MIGHT WE HOPE TO ACHIEVE WITH DNA-ANNs?

How **might** the incorporation of DNA-like capabilities into ANNs benefit their design, learning, evolution and function? For the sake of brevity, potential benefits are listed below with a minimum of explanations, but keep in mind that any advantage of DNA-ANNs over other ANNs remains to be demonstrated. Note that many of the points raised in Section II provide background for the DNA-ANN wish lists below.

A. "Starting with the right answer"

Starting with the right answer, or approximately the right structure, function, processes and network pre-training, is the most obvious potential advantage of pre-specified DNA-ANNs. In general we of course don't know the answer before we start, but a good guess can go a long way towards finding a good solution quickly.

- Evolution has a very long time to develop extremely powerful methods – and perhaps "true learning" requires evolutionary processes (Fogel [74]). It may be too much to ask that "excellent, real-time" ANNs arise

quickly from "blank slate" ANNs that have no training and an inappropriate structure, while DNA-ANNs will naturally possess a diverse "toolbox" of proven solutions to a wide variety of problems. Obviously a desirable characteristic of DNA-ANNs would be the automatic evolution of new capabilities over time, including novel strategies and principles in both general and specialized domains.

- In essence, we can take advantage of "societal/ species experience" across time and environments well beyond an individual's own experience.
- The evolution of stable systems of complex modules may greatly facilitate their application, interpretation and the extraction of meaning from their connections and behavior when modeling a system. This type of "interpretability" may help contribute to building robust, effective systems of ANNs and hybrid systems involving ANNs. There are also several related issues:
 - Small-world universal function approximation – what is the smallest set of ANNs, of various functional capabilities (general to specific), that is sufficient to solve most of the problems in a domain of interest? Are there general design principles for deriving a reduced set (something like design and analysis patterns for software development ([76],[77],[78]))?
 - False confidence in good fits - This is the converse situation whereby models of sufficiently complex systems may tend to become "small-world universal function approximators", and while these may fit data extremely well, there may not be a strong assurance that the model is conceptually well founded. In any case, one hope is that DNA-ANNs will have the property of developing "sensible" models for problems, models that minimize the chances of arriving at "wild" or phenomenologically erroneous solutions.
- Reiterating the point above in another way, we are looking for the [evolution, emergence] of [enduring, robust, powerful] representations of [risks, processes, situations, systems, data]. We are hoping to simultaneously achieve goals that may appear to be conflicting when "learning from the blank slate":
 - excellent AND fast;
 - richness of representation and understanding AND with only a minimum of input data and environmental situations.
- We can avoid an excessive reliance on general, powerful learning methods, and base learning more on the capabilities and power of a long evolutionary heritage that is pre-programmed (including very general & powerful learning methods).
- The brain and modern computers have huge a memory space and processing capacity. Take advantage of this! This means that we are not restricted to a small set of tools, nor to a single learning theory/method. That doesn't mean that very general powerful learning methods aren't important or that they won't be commonly used, it's just that there is no reason to be constrained to a small subset of approaches where

highly specialised solutions work much better.

B. Higher levels of abstraction

Following on with the concept of rich representations as discussed above, what we would also like to achieve, and expect to be present with DNA-ANNs, are ever-evolving, higher and higher level abstractions of the environments we encounter and the toolsets that we are using.

- Abductive reasoning (reasoning by simili and metaphor versus inductive, deductive and transductive logic) - Reasoning by simili or metaphor (pattern matching and beyond) could be one of the more important learning methods at higher levels of abstraction. This kind of reasoning would facilitate problem solving and innovation through restructuring existing solutions for different problems. Furthermore, a rich DNA-RNN environment with "lessons from the past" is essential for this. Is abductive reasoning actually more common and powerful than inductive and deductive logic, especially after an ANN or individual gains experience and wisdom?
- Meaning - Perhaps by defining and identifying relatively-common modules with well known characteristics, it will become easier to describe the functioning of ANNs to predict their behaviors for different problem domains, and therefore to visualize how to build completely new modules and systems. This is related to the concept of "logic is an emergent property" for complex systems (a term borrowed from a similar phrase for semantics).
- Symbolic logic – Symbolic logic immediately comes to mind as being a natural extension from abductive reasoning. When does symbolic (rule or belief based) reasoning take precedence, and is this related to the degree of abstraction? (see also Healy et.al [84])
- Coherence – For DNA-ANN modules which "fit together" with other modules, subsection A above ("Starting with the right answer") also infers that they would "co-evolve". That doesn't mean that all new modules have to fit with many others – a "stand-alone" module might legitimately lack coherence with other modules yet still serve a purpose well.
- Systems-level tools - While concepts and toolsets move to higher levels of abstraction and complexity, we might expect the need for systems-level approaches to building and operating that complexity. Which of the conventional IT tools will apply, and how will these have to evolve? For example:
 - design/ analysis patterns – as mentioned in Sub-section A above ;
 - global brain model projects may illustrate these challenges [43].
- Problem decomposition and modularisation seems to be a "natural" way to analyze complex systems. DNA-RNNs should help this (see "abductive reasoning" and "logic is an emergent property" immediately above in Sub-section II.B and which relate directly to this).
- Ockham's razor [75] (all other things being equal, take the simplest explanation) is a natural for ensembles of

ANNs, and applies very well to the DNA-ANN concept:

- use algorithms/ theories where appropriate (constant, linear, gentle non-linear, strong non-linear, chaotic, discontinuous);
- extend to the next level of complexity when necessary; and
- step up into complexity for the purposes of generalization to cover a greater portion of the problem domain.

C. Rapid training, learning and evolution

Many researchers are looking for orders of magnitude faster training while still generating accurate/ robust solutions. Local learning methods have contributed to this (Kasabov ECOS), and recent examples include "Extreme Learning Machines" (Guang-Bin Huang et.al. [55][56]) and "Echo State Networks" (Jaeger [58] and Prokhorov [59]) as described in Section II.C.3 above. Of course, fast specialized modules can always be combined with powerful general learning techniques for unusual/ difficult problems, where more time will be required to learn/ evolve.

- The clear preference is for training time to almost disappear if quality solutions can still be generated – in other words we should be targeting one-shot learning where that is possible!! And how do we know when this should be possible?
- Rapid reconfiguration of DNA-ANN modules – a capability to rapidly rearrange them along “high likelihood solutions” arrangements would be desirable. In the limit, dynamic structures would allow DNA-ANNs to switch and evolve in real time! If that "easy approach" doesn't work then a longer term, more exhaustive evolution may be required.
- Data (delivery mechanism) – DNA-ANNs offer a unique opportunity – that code segments can identify data (DNA or RNA code keys physically bring data and destination together!), and "data" can drive code and architecture. A mental picture is that of RNA transcription, where chunks of micro-RNA and introns are shed off, and can potentially work in parallel as interacting code and data. Perhaps there is something that can be done with a "computational soup" (This is reminiscent of Stuart Kauffman's work [79], however, whereas Kauffman spoke of the benefits of being at the edge of chaos, current research is showing the benefits of being fully chaotic).
- Recurrent Neural Networks (RNNs) are especially difficult to train, and benefits here may be of greatest value.

D. Quality of solutions/ models

Hopefully, DNA-ANNs will provide the robustness, reliability, and accuracy of solutions that have evolved over a broad range of real-world situations encountered over evolutionary times ("tried and true"). This bears some relationship to Subsection B above as it leads into "bigger picture", better solutions that simultaneously address other

needs, threats and opportunities that may be associated with the immediate objective in mind. However, achieving this with DNA-ANN modules will likely be harder than for most of the specialized ANNs currently used.

- Plasticity versus stability - This classical challenge for ANNs is to retain what is learned, while training on new data. Many ANNs have addressed this problem, but in a sense DNA-ANNs may be the penultimate solution, if the learning is closely related to pre-specified "content"!
- Resistance to the effects of damage and disease - DNA-ANNs should have regenerative capabilities, at least for their pre-specified components. And while ANNs have always been recognized for their amazing robustness, DNA-ANNs could take this to quite a different level. Lamarckian heredity makes this even more interesting! If cortical neurons can be "reborn", that clearly would provide an AMAZING plasticity of the brain! However epigenetic changes won't be sufficient unless they can be communicated from "experienced" to new neurons. See Section II.A.2 for comments on Lamarckian heredity.

E. Resource utilization

Because of their "hybrid symbolic/ connectionist" nature, DNA-ANNs may offer some unique opportunities for the efficient and effective utilization of "brain resources".

- Perhaps biological neurons cannot fire too long due to energetic, ion, neurotransmitter and other physiological demands, with the consequences that:
 - they must rotate tasks to have competitive system performance, and to minimize downtime; and
 - the "spacially wandering" processing of tasks would lead to qualitatively different computational capabilities.
- Share/ swap/ rotate tasks – Taking the previous insight further, it's easy to imagine the advantage of "migrating computations" in a biological NN. But the capability of doing "wandering computations" will itself give rise to new capabilities:
 - This will help to balance workload across the brain, allowing a restoration of ions, energy, and neurotransmitters, and a period of rest for neurons.
 - Individual neurons don't have to operate at maximum power for long periods of time even though the problem or its solution may actually require that a constant high output be provided.
 - There could result a tremendous robustness of the brain's capabilities as these will be realitively insensitive to local neuronal damage, disease and dysfunction.
- Functional overloading – having multiple functionalities share the same NN module will clearly yield an efficiency of resources. But as hinted in sub-sections above it may possibly lead to some kind of "morphing" evolutionary process towards more powerful learning, architectures and abstraction.
 - Functional overloading – reminds one of the effects of neuro-modulators (Kenji Doya [38][39]) and

- gene networks (Kasabov [10],[11]), including a capacity for meta learning.
- Beyond merely "switching" between functionalities, the same NN module could simultaneously be part of many different "models" and processes.
- The ability to handle variable object inputs and problem types should be a characteristic that arises from functional overloading.
- DNA code overloading - This is not the same as functional overloading for an ANN module as discussed in the previous point, but instead refers to the potential re-use of DNA coding for different purposes in different neurons, or for different computational processes in the same neuron.
 - Given that there are 3.2 Gbp (base pairs) of amino acids in the human DNA – for any "program" of length x bp, what is the probability of finding the code on an individual's genome (assuming that there is some way of accessing all code on the genome). Clearly this relates to the length of x , given that the probability is 1.0 for one "legitimate" bp, and pretty well zero for $x = \text{length of the individual's entire genome}$.
 - For code of "moderate length" (say 100,000 bps), there is probably a reasonable chance of finding code very close to that being sought, but that may have a few errors. So could "errors" result simply because of the convenience of using an approximate sequence of code, rather than from any change in the code or its expression?
 - DNA code overloading provides for a way of "re-interpreting DNA" for a completely different application.

F. Non-linear dynamical systems modeling and control

This author feels that RNNs, and especially those for control and Approximate Dynamic Programming, are a particularly important class of ANNs for which real advantages of DNA-RNNs must eventually be shown. Merely using DNA-ANNs as a pre-specification for ANNs is fine, but it doesn't give much more than simply what has already happened – many researchers over time creating highly specific and effective ANNs through a variety of approaches, and that activity will certainly continue. But the power of RNNs may be currently limited by the difficulties with training, evolving and applying them, and if DNA-RNNs, together with many other approaches to this challenge, could make substantive contributions in this area, then perhaps not only will it help with the implementation of current RNNs, but it may also contribute to the development of much more powerful RNNs.

- Dynamic transitions and performance in non-stationary environments – Given that RNNs and their ensembles are characterised by recurrent feedback, how can one rapidly evolve systems that are robust with respect to non-stationary environments where changes may cascade in an unstable fashion through the RNN? DNA-RNN modules offer an opportunity to implement

"self-muting" or "self-stabilizing" mechanisms to reduce these problems, or conversely, to promote instability when that is required. Examples of issues in this area include:

- Dynamic transitions during learning/evolution and control actions - Current RNNs already learn how to do this quite well (as previously cited Puskorius and Feldkamp [68],[69], Wan and van der Merwe [70]), plus Kozma and Meyers [82]). Naturally, it would be preferable that cycling through DNA-RNN modules would be possible in real time.
- Searching problem/solution state space – It may be desirable to "destabilize" ANNs to cycle through possible approaches to solving problems. An example might be chaotic searches through weight-space as a means of "parameter adjustment", or cycling through many modules of a very diverse set of DNA-RNNs, wherein each of these ensemble-architectures is effective for different classes of problems. And if there isn't an easy solution on hand, then building new "pre-configured ensemble-architectures" should be a capability of DNA-RNNs. This provides a "strategic" capability for DNA-RNNs, in that completely new approaches/ techniques/ concepts would arise, as might be appropriate for Approximate Dynamic Programming (ADP). Evolutionary theory, particle swarms, and chaos theory are examples of techniques for implementing searches that are at least partially randomized, and these can be used in combination with each other or in conjunction with gradient-based methods like BPTT.
- Variable object inputs/ problem types - as with functional overloading, it would be a useful capability if DNA-ANNs were designed to be able to use a different number of inputs, a variety of input "types" and missing data. Actually, that capability may be essential in many real-world situations, and its the sort of thing that is difficult to do in a general sense starting from a "blank slate".
- Instability-breaking – Is it possible to "break through" the Lyapunov and Slotine [83] criteria for stability constraints simply because the "behavior" of a DNA-RNN isn't "fixed"? Can DNA-RNNs "quench" unstable control responses to provide stable short-term dynamics that enhance learning speeds and response times? (Obviously, switching control strategies is an option).
- Ultimately, to use software programming analogies, perhaps what we are looking for are "strategies, design patterns, evolutionary principles, system engineering principles" to copy, create, and evolve DNA-RNN modules, and that these strategies would be provided as part of the "DNA code". What are the principles and means of more effectively evolving infrastructure and processes for meta-or-abstract level data / functions/ and processes?

V. CONCLUSION

The chief potential advantage of DNA-ANNs may be the ease and rapidity of evolving and training robust modules (genetically pre-specified core of DNA-ANN ensembles, and ensembles of ensembles, with a capability for further learning and evolution) for very diverse and non-stationary environments. There may be an especially important role for DNA-RNNs in controls and Approximate Dynamic Programming. However, many of these capabilities could easily be part of an RNN design package for an "RNN ensemble design engineer", so it's not clear if the incorporation of "DNA" into ANNs will really add much beyond the "hand-crafted evolution" that has always occurred with human scientific and engineering endeavors.

Clearly, approaches to specifying DNA-ANN modules are the second priority, drawing from a rich population of existing ANNs (general and highly specialized), and creating/ evolving new compact modules and means for their integration. To be really useful, means are required of evolving large-scale DNA-ANN modules over a very large and diverse population of benchmark problems.

There is also a critical need to better understand the meaning of, and to find appropriate tools for, evolving and training modules at higher and higher levels of abstraction (meta-levels) – one can't help thinking that at some point this transitions into the symbolics of Artificial Intelligence (AI).

Finally, the overall vision of this paper is on the retention of a vast set of DNA-ANN tools and methods because reliable and robust approaches to highly varied problems will likely require a rich environment of evolved, proven tools, very much as implied by Minsky's quote in Section II.A.2. The issue becomes not one of finding a "grand unified field theory" of problem solving at this very early stage of the development of ANNs, but to evolve effective ways of coordinating a variety of these DNA-ANN methodologies to work together at different levels of abstraction.

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planned in this area within the Canadian federal government at this time.

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- C. Hung, "A Constructive Self-Organising Model for A Non-Stationary Environment"
 - M. Dittenbach, A.s Rauber, "Constructive/Hierarchical Self-Organizing Maps"
 - J. Pakkanen, E. Oja, "Analyzing large data sets efficiently with The Evolving Tree"

- E. Cuadros-Vargas, R.A.F. Romero, "The SAM-SOM and MAM-SOM Families"
 - A.T-W. Chan, J S-Y. Lee, "Anomaly Detection with the Growing Hierarchical Self Organising Map"
 - V. Baier, "Motion Processing and Prediction With a Hierarchical RSOM based Model"
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- M. de Kamps, "Large scale brain simulations are not a technical problem"
 - Iversen, N.K. Taylor, K. Brown, "Integrating Neural Network Strategies for Discrimination, Recognition and Clustering"
 - V. Eliashberg, "The ULC Project"
 - X. Gu, "Integrate Different Neural Models Using Double Channels of Pulse Coupled Neural Network"
 - L.A. Coward, "Practical Architecture Limits on Complex Learning Systems"
 - W.J. Puma-Villanueva, G.B. Bezerra, C.A. M. Lima, F.J. Von Zuben, "Improving Support Vector Clustering with Ensembles"
 - T.S. Hussain, "Explicit Learning Relationships within Neural Systems"
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