EMME - collected STEM points going forward

Tuesday 16.August.2022

[note that there are other key documents req'd to understand these points]

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Two texts, one from Nature 2022, one from 2020

1. One of the must-read papers. This helps in understanding the scope and gravity of the situation.

https://www.nature.com/articles/s41558-022-01426-1.pdf

2. This is an early excerpt from a 2020 presentation and lecture series - from before COVID-19 emerged as a pandemic in China and then spread globally.

Impact of Environmental, Ecological, and Socioeconomic Changes in Early 21st Century on Viral and other Microbiological Disease, Epidemiology, Public Health Response and the Pharmaceutical Development Practices

We will show the underlying causes for why recent (2002+, particularly) epidemics and pandemics have decisively different characteristics that bear important, even critical, consequences for human health and social stability. In so doing we will show certain relationships active between such phenomena as viral mutation, new infectious vectors, novel routes and accelerations of transmission, higher virulence and the general-population disposition to more severe complications in personal and social health management for certain infectious diseases. We will show connectivity between hemifusion, endocytosis and other forms of viral entry, viral replication, consequent systemic over-reactions including cytokine storm inflammation, and also connectivity and common elements between these pathogenic processes and certain foundations for autoimmune reactions and related pathologies in signaling, communication and recognition that lead to autoimmune reactions and prolonged cellular component degradation in both neural and non-neural cellular types. We will describe how certain fundamental processes are biomolecular manifestations of a generalizable type of non-Turing computational paradigm, one which can be employed in both models, simulations and the design of corrective therapies, including pharmacological design and implementation, and also in an architecture for synthetic computation algorithms and machines designed and constructed along principles similar to those employed within the biology of viruses, bacteria, cells, and complex multi-celled organs and autonomous-behaving organisms.

Within this is clearly a well-defined place and pathway for the other research initiatives and projects which actually provide the foundations for what is going into these works – namely, everything concerning what we abbreviate as RTD, TBD, ICMC, and also GCM.

Specific "lead" paper and presentation --> -->

(This was a presentation at an online conference, Spring 2020)

Changes Afoot in the Kingdom: New Epidemiological Dynamics - the Confluence of Climate, Socieconomics, and Global Patterns upon Future Drug Discovery, Design, Testing, Trials and Implementation

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Abstract
Several very closely coupled behavioral changes on international, transcontinental and global scales have converged within recent decades, all of which involve greater movement, displacement and interfacing of different species of organisms which include humans, livestock breeding animals, and a variety of microorganisms that have high potential for infectious disease. These changes are closely coupled with population rise and density in close-habitation urban metropolis regions, greater affluence and resulting travel, both short-range frequent commuter distances and long-range commercial and leisure travel, especially by air. This set of changes in the underlying ecosystem and in socioeconomic patters can be linked to an increased variety and virulence within certain infectious disease agents. The overall changes are unpredicted and unexpected in most current models influencing healthcare planning and in particular public health including epidemiological management, that have emerged within the current two decades. These encompass and bring together mutual effects and often nonlinear impacts, attributable to the new dynamics of climate change, agriculture and food industry, transportation of good and movement of people, as well as interpersonal proximity, contact and exchange of personal physical media. The consequences are enormous for not only basic epidemiological models and response to epidemic and pandemic-potential infectious diseases, but also the fundamental models, systems, regulations and actual practices involved in drug research and discovery, design, testing and trials and product introduction and implementation within both institutional and private uses. We introduce some of the observed factors, relations and consequences, and we identify new pathways by which the medical establishment – public and private – including the pharmaceutical industry as a community – can more effectively prepare and establish the type of resilience necessary for reducing the personal and socioeconomic destructive impacts of epidemic and pandemic outbreaks, while simultaneously advancing the overall health of all segments and diversities of the global population.

Parallel Distributed Solution-Making that involves the General Public

EMME operates as a parallel distributed knowledge-making and solution-finding network that involves "everyday commonplace" things we all know and use on the internet, and the "general population" of people can be users and contributors. The meaning here is that all those people who are not scientists, programmers, doctors, nurses, and not working in any of the usual professional fields associated with the topics EMME is addressing, can in fact be helping to solve some critical problems in public health which come as a matter of course with the ways people use the internet today, as evidenced and witnessed by all the popular social networks.

Recall that EMME exists to accomplish data-gathering, information-making and knowledge-generating processes that are important to the mission goal of *minimizing the risks of emerging pandemic-potential diseases that are exacerbated and accelerated by climate change and related environmental dynamics*.

Let me paint a picture here of how EMME will be operating in as few as several months - keeping in mind that so much has been done already, including a vast amount on the STEM side, including hands-on r*eady-to-rock-n-roll* usable technology in the form of certain software tools.

Bear in mind that EMME is absolutely not a piece of software, not an "app" or set of apps, not "only" algorithms and software implementations, but there is the software side and that includes the internet and human-social-network side of things and it is (1) very important and (2) very unique to what EMME does.

I am going to describe something here and now that is not from the perspective of the scientists and researchers who are using EMME and its information for their express stated objectives, but from the perspective and activity of some of the people - potentially thousands and tens of thousands and more - who will be part of what we call EMMEnet - a global-reach, amorphous, asynchronous, parallel distributed network that is providing data which is being analyzed by synthetic intelligent agents and by humans working with them, for the purposes of EMME.

This here is something that by itself sets EMME apart from anything else underway in the world of environment, climate change, botany, zoology, zoonotics, virology, epidemiology, and public health.

These remarks here are not about the "main" science and tech within EMME, all of which is summarized in those other documents. Keep in mind that there is a formal system of environmental, climatic, and ecological monitoring going on - everything to do with data streaming in from satellites, from drones, from human and robotic assisted sensors, and from the data analytics going on with EMME algorithms.

We do not replace or supplant anything, but we have at our disposal the easy path to combining into EMME:

- massive, stochastic, asynchronous data collection that is coming from a large set of contributors and
- effective development of public health awareness, alertness, education and engagement

So - on to my brief "portrait" painting:

Everyone uses different apps on their phones and computers. SMS, email, and all those social media things - WhatsApp, Twitter, Telegram, Instagram, etc.

The "SHARE" icon is familiar to everyone.

Share a text, a photo, a video, whatever, with a friend or anyone.

Within the EMME world, people who have some level of exposure and training, which then propagates in its own way through social interactions, notice "something" that may be interesting and significant with respect to changes in the environment that are in EMME focus.

They may only notice something "unusual" and want to share it.

They may not know the significance - and neither may we, at first!!!

This sharing behavior is widely practiced, by millions, with all the usual social apps that people use in their daily lives. EMME is just adding to the list of things that people will notice and pay more attention to, with a bit of guidance, inspiration, education, and oh, yes, some special incentives (we'll get to that later and it does include such things as games, contests, prizes and awards!) - and to the lit of things that we want to come into the data streams of EMME's analytical engines.

The "something" (photo, text, video - some observation about vegetation, animals, bugs, climate, even to the explicit "extreme" (informationally speaking) about some symptoms of health or disease) gets shared, and it goes "into the hopper" of EMME's data analytics, the "engine" that is equipped with a population of intelligent agents all working to find if this is something relevant and if so, then in what useful way.

This is not "new". We and many others have been doing such things for decades, and in our team's case, it has a success track record which spans from elementary physics to the life sciences to counter-terrorism and national intelligence and security.

So, we know what we are doing and we certainly know what we are saying when we say,

EMME applies proven STEM to perform its tasks today.

This includes a very interesting thing from the computational perspective. We combine the benefits of the following (sorry for the brevity here, but all details can be explained later) in ways that nobody has done before, and which are not a question of "can they do it" but only "how soon can we all be part of this?!" - because it is so beneficial for all of the EMME purposes and also, for much more at **all the institutions that will be involved - America, Africa, Europe, and thereby the Whole World**.

We integrated four important things:

♦ Parallel Distributed Processing (where the parallelism is algorithmically essential for doing the task in any reasonable time and without huge wastes of time on "dead end" efforts - and this includes much of what gets called "machine learning and AI")

with

♦ Network Computing (e.g., BOINC - Berkeley Open Infrastructure for Network Computing; where a massively cumbersome task of usually number-crunching gets farmed out among thousands of processors across the internet (e.g., personal computers and even mobile phones) to divide-up the tasks that otherwise would take enormous amounts of time and energy on any single machine)

with

♦ Modeling and Simulation (that includes evaluating, in parallel again, massive numbers of possibilities, and among these, the generation of large amounts of simulated data - look-alikes and almost-likes - and again using well-established, proven, and even industry-accepted methods - in EMME's case we are not doing this with faces or text strings, but with configurations of climate, species movement and migration, micro-organism genomic variations, and human-ecosphere interactions)

with

♦ Social Networking and Communicating (that is widely, virtually universally, used by the whole population in not only the regions of EMME's initial focus but globally in all the places where EMME's concerns are real and demanding attention - and in ways that specific "academic research" programs cannot do effectively or even at all).

Initial Project Description (July 2022)

Initial project statement from 16.July.22 - there are points here expressed in other useful "intro" format.

Note that there are a few additional updates here as well from 15-16.August.

Environmental Monitoring of Species Migration & Mutation to Minimize Zoonotic Disease Epidemics

(abbreviated as “EMME”)

This project will produce a set of resources for use by many communities and agencies in addressing the challenge of emerging zoonotic diseases including novel variants not previously experienced within the human population. The project focuses upon certain geographic regions and ecosystems and populations, including human and human-contact animal species, where we believe that specific monitoring, including the use of a network model of multi-spectral sensors, and systematic data collection from humans (both “generally healthy” and those with certain diagnoses conditions), plus the application of advanced statistical and “machine learning’ models, can provide useful predictive knowledge about emergent diseases and their pathogens and vectors. The outcomes of this project are intended to serve the global public health community in reducing the threats of major epidemics and pandemics. Additional outcomes from the refined application and testing of innovative sensing and informatics analysis technology will benefit public health with respect to other diseases and disorders including non-infectious diseases, and the development of new mechanisms of public health education, hygiene and clinical care.

This project incorporates:

Environmental monitoring (integration of existing and ongoing data acquisition including computer-based data acquisition and simulation, and new data collection through targeted field studies, with employment of several new types of spectroscopy previously not available for consideration in these types of tasks).

This monitoring, both in the natural (urbanized, human-inhabited, and wild) environment, and through clinical testing of patients using mainly non-invasive and minimal-complexity techniques, is focused upon

Species Migration and Mutation
(principally examining what can be detected, measured, and also Inferred(!) about changes in habitat, population and inter-species relations involving a broad class of

Microorganisms; pathogen-types (including virus, bacteria, and micro-organism parasites)
and
Vectors; carrier-type (with respect to target microorganisms; both known and suspected/new-potential)

A central goal of the project is to establish a reliable set of procedures that will assist in earlier alerts and indicators that changes in the biosphere are leading to some probability levels of new distribution patterns for biothreat-capable organisms or their carriers.

By employing this type of system that will result from this project as a set of physical and informatic resources, plus the trained skillsets for using it, there will exist and progressively grow in accuracy and utility what we refer to as PHIBER, a basic population health informatics knowledge base. This involves compiling EHR-type medical data records that are also supplemented with extensive behavioral (lifestyle) and environmental data. This is a major challenge in the collection and in the determination of accuracy. Here is where several synthetic intelligence techniques can be applied, including those being used currently and expressly to simulate population health data and to perform error correction and completion-estimation within incomplete and irregular data.

The challenge, they key, and the cure to many studies within the etiology of different diseases and comorbidities including susceptibilities to infectious diseases of the types that emerge within the non-linearly changing environment is in accuracy of collection, reporting and assimilation of population health biometrics.

Within the overall project, given the evidence from many studies, especially in recent decades and even more so with the global experience of the COVID-19pandemic, there will also be a focus upon a class of disorders and diseases that appear to be closely linked with environmental factors and the changes within climate and the overall ecosystem for may human habitations, including water quality and the presence in air, water and other intake sources of different toxins which share in the emergence and intensification of what we term

NpC – neuro-cardio-autoimmune-inflammation.

There are several conditions involving dysautonomia, arrhythmia of cardiovascular, gastrointestinal and other neuromuscular coordination, which appear to be linked to environmental intake of neuroactive substances and also certain infectious diseases with high neurological impact. Because those are on the rise, and more intense, especially with the novel emerging infectious and high-contagion diseases that we are examining (COVID-19 and PASC ("Long COVID") being a paradigm example), this project will this include data collection including diagnostic testing, and evaluation, of these NpC relations.

Overall, viewed as a whole, the work of this project will feed, support, help all other sectors of medicine and public health with achieving a Big Goal of reducing the incidence and impact of

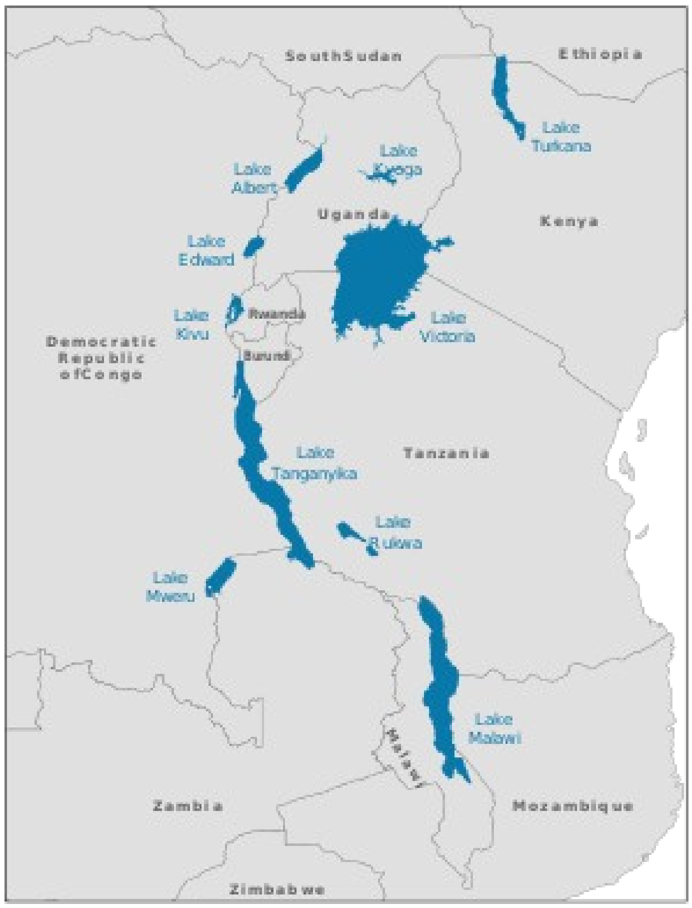
Minimizing Zoonotic Disease Epidemics
and
Neuromuscular atrophy and inflammatory conditions.

Our geo-focus, in terms of specific environmental areas:

[1] East Africa, near and around the Great Lakes there (as indicated by the figure below).
This is to-be-determined, but probably mostly around Lake Tanganyika and Lake Victoria.

Tanzania and Kenya sites – wild and urbanized - will be important, and not a problem for doing things. Uganda could be significant, also Mozambique, DRC, Zambia.

[2] Southern USA (and some specific reasons why for these, partly for the environment, the biosphere, the science, and partly because of a few institutions already focusing on the South).
Parts of Louisiana, Mississippi, Alabama, Florida, with particular attention to those geo-social regions that are known to already be affected by intrusive migration of species from tropical and equatorial regions, both through natural “wild” migration and by introduction through both unintentional and deliberate actions of invasive species.



[Added here - for Southeastern North America (15.Aug.22)] - Thinking mainly about wetlands, lowlands, freshwater areas, coastal regions, including those particularly subject to effects from large and intense storms such as hurricanes, in these USA states:

Virginia, North Carolina South Carolina, Georgia, Florida, Alabama, Mississippi, Louisiana, Texas.]

[Added here - for Tanzania (16.Aug.22)] -- Thinking about regions and towns which can be the starting-points for future fieldwork that involves physical on-the-ground visits and missions of doing activities with sensors and also collecting samples for analysis back in the university labs):

(in alphabetical order here for simplicity)

Arusha, Kahama, Kwanga, Mbeya,Mbinga, Mpanda, Mwanza, Rungwa.

It is all complex, really, because we are thinking and talking about areas to examine and monitor, not exclusively, but perhaps with special attention, pertaining to so many different factors:

- climate-change effects that are most significant upon vegetation and different animal movements
- increased human habitation and mixing of humans with normal "wild" species of plants and animals
- increased hunting of especially smaller species (this is one of the big problems in China, for instance)
- deforestation and other de-naturalization of the environment, including changes to bodies of water, both flowing or stagnant/swamp-like
- increased stagnant or slow-moving bodies of water, or increased drought

In both of the initial areas for physical, on-site close attention and fieldwork, we are not focused necessarily, certainly not only or mainly, upon wilderness regions, nor only upon human habitations, but upon those regions which are characterized by:

- being border zones, transition zones, crossover areas, for humans and the wild flora and fauna
- new influx of Change with respect to the biosphere, particularly regarding water, vegetation, human-introduced chemicals, pollutants, and waste (garbage)
- significantly increased or reduced traffic of all sorts (not only human)
- previous indications - proven or suspected - of the region being in some way involved in emergence of difference pathogens

[Resuming with original text from 16.July.22]
What will we actually DO, and what are we looking for – a recapitulation statement

[1]
Organize, include, assess, the tonnes of data already collected that can be pertinent, about species migration, mutations, changes; there is a lot connected with particularly these because of events in the past 20 years:

Ebola, Zika, Influenza, Coronavirus, Malaria, Hanta, Marburg, Cholera, Plague, Yellow fever, tick-borne diseases, Chagas (trypanosoma cruzi).

There is a huge amount of data out there, already and ongoing, but (a) nobody is integrating it into a systematic, coherent, easy-to-use form, and (b) a lot of data has missing parts, and (c) it is not yet being organized in a manner that can be easily accessed and used by a host of different users in local communities and "micro-social" frameworks. This is analogous to the challenges in the economic sector that have led, somewhat successfully, from a locally-often-inaccessible superstructure of macroeconomic institutions (establishing banks) to a micro-economy that provides the bridges and conduits from the macro institutions to the local communities.

[2]
Identify specific geo-regions that stand out as being worthwhile to monitor with close attention. We are still at the beginning stage of learning where to look, in which "haystacks" to expect that there can be which kinds of "needles" and how to develop appropriate algorithms for the different types of "haystacks" and "needles". This is about ecosystems and we can learn fast what we need from a few partners who are specialists. However, based upon the existing published literature and the work done worldwide over the past 30 years especially, much of it triggered by the global experiences with such diseases and their epidemics such as HIV, Ebola, Influenza, and now COVID-19, we do have a good headstart.

[3]
Identify the best ways to do such geo-specific monitoring that will be new and different in addition to whatever is already known and being done. The "newer" things to consider will be the types of sensors and detectors that can be employed using people just going around from place to place and also using drones, both airborne (UAV) and water (ASV). These include order-of-magnitude and broader-spectrum forms of spectroscopy that are now practical in terms of portability, use requirements, and cost for implementation. We believe that the use of such spectroscopic tools as photoacoustics, MEMS, CEBIT, and cascaded laser technologies, along with SIMOA (single-molecule analytics), combined with photographic and synthetic aperture radar, will provide a powerful, usable, economic and low-error method for answering the questions we face in this project. We also emphasize the power of the computational inference engines, the synthetic intelligence components. We can infer a lot for what we want to know, by using data about different species of flora and fauna that are not carriers (vectors) of disease organisms, per se, but good indicators that we sure ought to look in specific locations and look for specific convergences and other relations.

As a simple, crude example: migratory patterns involving deer and other ungulates (hoofed wild animals) and their predators and "symbiotic" species, can give us important pointers about various parasites and microorganisms. We don't need to sift painstakingly through the huge "haystacks" looking for hidden “needles”. *If* we can determine, for instance, that the needles got into the grass or hay when we were harvesting hay over where there is a lot of lavender growing… so then we look for the signs of the lavender leaves and flowers, and narrow down our search-spaces.

[4]
Integrating existing (and make some new) mechanisms for “pre”-epidemiological tracing and tracking (meaning: trying to trace and track indicators of risk and potential for various new “flash-fire” epidemics). Certain conditions of people including their lifestyle, their other prevalent diseases, their diets, can be pointers to where we should have a high-alert watch for the new “M&M” phenomena.

[5]
Public health education, starting with and using youth, students pre-university, the general public – and of course, with some incentives for them (this focus on internet, apps, also games and contests and prizes. This is where we bring in OASIS and the whole social-community-network of “COMEET” (communicate, collaborate, meet and make, educate, entertain and play, and trade) experiences with a “metaverse” type environment (something else in which we are involved).

Public information and dissemination of hygiene knowledge in basic and attractive methods is not only a goal of this project but a requirement for it to succeed. With the “Terra” social media environment as an Oasis-World that is a web “metaverse” – but one that is fundamentally different from many commercial offerings in this genre, because of being personalized and health-wellness-focused rather than as a vehicle for generating advertising revenue – we can literally reach the millions of people who need to be “enlisted” into both public health and hygiene practices and environmental observation and reporting. A spike of reports, regardless of predictable errors and even deliberate pseudo-facts, regarding changes in species activities, both flora and fauna, can provide our analytical algorithms and our team members with exactly the right trigger-alerts for activating the next steps which may be action involving human observers or robotic sensors or purely data analysis in a new perspective.

The biggest and best way to address the task of learning Early about new “M&M” is to have thousands and millions of “eyes” working for us as part of the “team”. We can do that if we can engage and energize People.

Brief Remarks on Information Security and Privacy

These are issues that will invariably arise because we are dealing with many types of data including at some point human health records (EHR, etc.) and also some of the data concerning physical and biological conditions and events may be considered private, proprietary, and otherwise in ways where there are concerns about specific attributes being kept secure.

We have worked in the past extensively with such issues in the medical world and in other sectors such as national intelligence and security. There are ample measures today for ensuring that privacy can be maintained where necessary. This enables us to think openly about doing information-technology tasks that involve the internet, cloud computing resources, and other forms of processing.

Homomorphic encryption (FHE, HEP) is well-known, refined, and now with advances in both software and especially in computational power, it is practical when necessary. Mutual information algorithms also can benefit and strengthen techniques such as FHE and HEP. The following brief excerpts (2017) give some information in this regard. This is not a central part of EMME work but it is good to know and especially for answering concerns by others including partners and sponsors. Note that the use of quantum entanglement theoretics, mentioned in the second abstract here, is being considered for future-stage application to some of the questions concerning migration and genetic mutation within species, particularly viral and bacterial microorganisms. This is where some advanced theoretical and experimental physics comes in to help in problems of epidemiology and zoonotic disease studies.

New methods for application of homomorphic encryption and inverse obfuscation to enhance real-time predictive analysis of anomalies, incidents and threats

Martin Joseph Dudziak PhD (principal investigator)

In spite of improvements in practical application of homomorphic encryption (FHE, HEP), there are challenges to using these methods for many applications involving very large data streams and problems involving diverse, competing relationships among often uncertain data elements. In particular these algorithms have been difficult to apply to real-time intensive operations aimed at detecting threats and indicators of threats pertinent to both combat and terrorism operations. Such operations typically require wide-spectrum data mining and cross-referencing within databases, and communication of partial-result data among both computation systems and human analysts in order to identify pertinent association and relationships that are worth further pursuit and “red-flagging.”

Methods drawn from diverse prior research and fielded application in sensor fusion, neurorestorative vision, volume reconstruction and stochastic monitoring, including work in CBRNE counterterrorism modeling (e.g., “NomadEyes” system), have shown promise in reducing search space requirements and the complexity of data model evaluations. Mutual information techniques, including work originating in medical imaging, are able to simplify requirements and processing time for referencing decrypted data sources. Construction of an overlay of hypothesis-pointer networks within the fully encrypted dataspace enables faster targeting of patterns of potential relevance and corroboration. The outcome is a highlighting of probabilities for relationships of interest between data components. This is a fundamentally new approach with geometrical, topological roots as opposed to classical inferencing, bayesian, and connectionist paradigms. These relationships are in turn analyzed for most-probable-fit matching with behavioral patterns abstracted from social and anthropological logics. The result can provide both qualitative and quantitative gains in detection of and reaction to dynamic, time-sensitive events affecting physical, financial, and information-sensitive outcomes.

HEP and biological system quantum entanglement for prediction of health trends and clinical outcomes

Martin Joseph Dudziak PhD (principal investigator)

Two sources of information derived from very large sources are integrated within a predictive engine. One source is constituted by historical, quantitative medical data derived from individual patient records and associated with specific individual identifiers. The second stream consists of parameters that are not linked to pathological conditions or indicators, but which consist of a mapping of bioelectromagnetic field strengths collected over extended periods of time, again derived from individual patients, but these are not directed associated with diagnostic determinants. The first stream is a patient-linked record of measurements and events with established empirical links to pathological conditions. The second stream provides patient-linked measurements that constitute a more theoretical and strongly epigenetic approach to health dispositions, disease management and pathogenic onsets. Both sources are linked with individual patients and thus concerns of information privacy must be addressed.

Correlations between these data collections form the basis for temporal predictions of medical anomaly and disease and such conditions can be the subject of extended health monitoring for individuals whose prognosis, on the basis of medical history, includes risks of certain diseases. Initially the focus of the study is directed at cardiovascular medicine but the basic model is applicable to other clinical specialties.

The use of fully homomorphic encryption processing (HEP) is to preserve privacy of the individuals in order that analysis can be performed upon encrypted patient data that remains encrypted. Individual data and projected health outcomes remain within the cybersecure domain of the health provider institution.

The role of system-level biological quantum entanglement (QBE) is in the mapping between quantitative measurements obtained by non-invasive monitoring (clinically comparable to EEG, EKG, EMG) and conditions such as myocardial infarction or atrial fibrillation. The theoretical basis is grounded in models of quantum entanglement among regional components of the central nervous system; this research includes hypothetical frameworks of epigenetic pathways, chreode dynamics, and extensions of Bohn-Hiley type quantum potential models.

Development of the fundamental QBE model is at a very early stage that requires substantial and diverse population data of the two types indicated. This process in turn requires means to work with such data in large-scale, open, “cloud” based computing platforms, and this undertaking requires a solution that meets the requirements of individual patient privacy. The result has been an application of HEP that can derive sufficient patterns of interest from encrypted patient data in order to apply the QBE algorithms. This overall model may be translated to serve other applications outside of the explicitly medical domain, such as in finance and security.

Several Points on Predictive Topological-Ordered Logic Maps and such

This is about what goes on inside the computational engine of EMME and what we term the ***sients*** - the intelligent agents. This is about analysis and prediction. These notes add to other material in both papers and presentations and in preliminary working documents within the EMME Project Team.

[1]

n-spaces and representation of environmental dynamics

Representation takes place in n-space surfaces, where data attributes are mapped in n-dimensions of information-space (i-space) (and there must be conversion functions for operating across different i-space coordinate systems).

What forms over time (from addition of details, meaning, observations) are features of interest that can be described as bubbles, holes, twists, knots, ripples, ridges, paths of movement that are translatable to spatial and temporal coordinate systems, for instance (in the case of EMME informatics).

There is obviously an algebra that can be created here to describe these transitions, these operations.

We are concerned with dynamical patterns of change, not fixed, static objects.

Human + machine analysis combined leads to discovery: "Look here, look there, it is a definite or a 'maybe', with some assignable probability", and then different hypotheses in the knowledge base can be evaluated (best in parallel), with pruning of the probability-tree as one rules out various hypotheses.

EMME and i-maps

These function like a geospatial map, providing a way to relate n-space surfaces with topological features (e.g., bubbles, holes, knots, twists, etc.) that can be noted, compared, and understood in a dynamic and moving (over time) fashion, and in relationship to one another. These relations can in some way be interpreted as causal, but it may be beneficial to explore a type of synchronicity logic (e.g., as explored by Jung and Pauli years ago).

We want to ask the question, in the context of EMME environmental and biological dynamics - how do certain knots, bubbles, and "pretzel" type twists (trefoil shapes) form, and where. We can even be less interested in "why" - the main thing is to be able to have an alert and "place a red pin or a green pin" on certain points in the EMME i-map.

When and when there is a pin placed onto the map, that is where there needs to be attention for further monitoring, and also for the public health system to engage and take early prophylactic action.

[2]

n-space configurations can be arbitrary, and therefor also the topologies that result, forming networks, graphs, that connect the points. Any "object" can be viewed and described from many perspectives and this arbitrariness is what allows cognitive reasoning to see some phenomena from very different perspectives until there may be a "match and fit" with something else that is recalled (from "memory").

In the brain this goes on constantly, and it is a type of GAN (generative adversarial network) process. Fitting, intersecting, reinforcing or diminishing reach other, cognitive objects will dominate and others become recessive, quiet, low-influence. Again, we bring up the "chreode" concept (C. H. Waddington and other early 20th century theoretical biologists) - over time certain paths of pattern detection and identification (classification) become strengthened, deepened, more dominant.

Choice of key attributes determines coordinates in the n-space and that determines the network and thus the topology. This originates in RTD theory and right in the heart of elementary particle physics, but it carries "forward and upward" in the evolving emergence of more complex form and structure, namely into chemistry and biology. It's just good to think that the reasons for why some things work the way they do in biology, and all the way into human brains and the "machine brains" that human brains design, has a foundation that rests in the fundamental way that matter emerged out of pure energy...

We are looking at how "gradient regions" ("GR") form over the "life" of the network into being increasingly distinct and "well-formed" - having distinct shapes within the n-space coordinate system. Ultimately there will be some type of contiguity among different GRs.

Challenge: How to connect the GRs that are defined around various node-points, in order to establish a satisfactory topology, a manifold that has continuity and no singularity holes. It must be continuous, unbroken, no cuts, no fold-overs. But this leads to a lot of questions:

- Why does that matter, really? Continuity, and no singularities?
- How to establish (prove) that such a property exists?
- What would it mean to have non-standard, non-smooth, non-continuous "manifolds"?
- What would such singularities "mean"? (in the context of an information-space, something where we have perhaps built a rich space of objects that derive from observations of phenomena in the world (example: environment, biology)?

[3]

[3.1]
Aiming toward a Geometry of Information (with questions on how the two Incompleteness Theorems relate to this)

We begin with topological structures such that the similarities among manifolds (knots, loops, bubbles, holes, etc.) map directly to different logics, semantics, "ideas" in the original sense (Gk, eidein, ἰδεῖν).

Novelty, change is expressible in topological transforms - stretch, twist, make holes, knots, bubbles.

Representation must (ought to) lead us from a logic of propositions to an algebra of geometry.

We easily and necessarily get involved in questions of infinity because there are infinite variations of representation. Any geometrical structure can be stretched, deformed, contorted - in an infinite number of ways. Without "cuts", and then, with "infinitely more variety", when there are "cuts" allowed. But these gets us right back to the problems faced by Cantor and others, and from the point of practical use of i-space and i-map concepts in computational problems that link with "real world applications" (e.g., EMME as one example). we can skip the infinities and limit ourselves, much as in conventional differential calculus and PDE.

How do different *"informational topoi"* interact with one another in the whole n-space? How can they combine and create/proceed in an "informational physics/chemistry/biology? by combining? This points to an algebraic representation and solutions. All of this can be represented in an SI "thinking machine" because fundamentally it is all expressible in number.

[3.2]
What can govern the choice of geometry for specific logics and semantics? Why one particular form or another, and how to govern the transformations from state (proceeds) A to state (process) B?

Consider examples of simple forms - circle, sphere, loo[p, torus, triangle, tetrahedron, moebius, trefoil, many types of knots, polyhedra, etc. Do we begin with something arbitrary or does it emerge, almost like the evolution of CDT (causal dynamical triangulation)? Consider all the work going on in mathematics now on the emergence of elementary forms from randomness, in basic number theory.

[3.3]
Each dimension in our i-space can refer to some range of values, assigned numerically, for representing gradients of some values associated with a spectrum that may be purely scalar or else vectors, tensors, associated with what originated (as data) as some qualitative values.

We want to say something like the following:
This geometrical object and its topological properties "maps" to these logical statements (propositions) and if we alter the logic, we alter the geometry, and vice versa. Then we can go further and "play" with the geometries of different objects and generate creative new information that may indicate *possibles* (which may not be possible in the "natural order", the world-as-it-is) and others that are possible and can be sought and found.

[3.4]
If we can represent a set of propositions that formulate some block of knowledge about X as a geometrical entity E in an n-space where each dimension represents some attributes of that entity E, as a topological structure defined by curves that establish its shape, its boundary-surface, then we can compare E with others of similar types and we can compare the curves making up E geometrically with other curves in other entities (~E), and we can look for similarities and differences of some meaning for understanding E and things like E and ~E.

Goal
Prove that any logical proposition p can be represented in a topological knot and that any operation on p can be performed in a manner that is topologically correct (i.e., no "cuts"), provided that such operation, resulting in true or false outcome, is semantically possible (feasible), thereby transforming the knot form into another that corresponds geometrically to that of the new statement p' after the operation.

[4]

Mathematical Issues that must be addressed and solved within the course of making "Topological Information Spaces and Maps" that can be useful in real-world applications.

Note that this does not mean that we cannot build things that work well, very well, and even better than what we have today in so-called AI and "machine learning", etc. The challenge is to do better, more powerfully, more accurately, more completely.

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Manners in which random or pseudo-random (weighted) connectivity within a space (let's keep it to 4d or even just 3-d for now) - dynamics that can behave in a manner akin to pressure, or superfluidity - can lead to defined and ordered (order-able) structures. Let's start with triangulation and then polytopes like tetrahedra. That's an underlying "basic problem" but it enters into not only one but four areas of system dynamics that concern me and others with me.

These dynamics (and more confusion in the topological and deep-algebraic aspects thereof) lead into the problems of how a collection of such "emergent" and "semi-stable" geometrical objects (manifolds of many knotty and gnarly sorts) influences each other, very collectively, very much with a combination of local-space behaviors and also Whole-to-the-Part influences. How the space as a whole, and some large region or subspace therein, influences, controls, constrains, what can be happening at the increasingly local scales. Metaphor here: How the sky as a whole influences the clouds that can form in some specific region. How the big cumulus cloud influences the emergence of condensation into rain droplets and the emergence of electrically charge regions. How the air in between the cloud and my backyard influences and controls the shape of the raindrops as they come down on my head..."

I mentioned, above, that all my questions and problems concern four areas of "system dynamics". These are four categories of dynamical relations between topological entities and "very large populations, networks, spaces filled with such"; they are, very roughly stated:

[1] (the first and underlying category) Proto-physics, emergence of particles - fermions and bosons - the fundamentals of the "Standard Model", from a flux-like, "pre-spacetime" superfluidic vacuum. But mathematically, we have a space that where points connect and structures emerge and disappear, but at some point (let's leave out "where" or "when"!), the structures are complex enough, steady enough, well-connected enough, that they have some stability in the sense of then influencing their "neighborhood".

Particles as manifolds, variants of toruses, with a lot of twists, but the main challenge here is that the local structures are intermittent manifestations of the whole. The blanket rolls, waves, folds, and ruffles, and in some regions, there are creases and clumpings...

So, here is a bit of "Brownian motion" and connecting of dots that led to blobs. Or... better understood as knots, twists, vortices, and what I just call "pretzels" because they are not "knots" in the general topological sense, at least as I understand them.
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[2] (the second category) Cellular biology, boundary and border detection and measurement, and the consequences, for genetic expression within eukaryotic cells, for instance, that lead from the stem cell general-state to the vast differentiation of tissues and specific metabolic responses within different tissues that we see in the expanse of biology. This expanse, by the way, in our theoretical work, spans from viruses to bacteria to eukaryotic and multi-cellular organisms including those who develop brains and think and write about these matters...

Cells being informational engines that "measure" their topological boundaries, their surfaced, and what is "on the other side" of the membrane, the border. Then they react internally according to the code that is stored (genes), constantly influenced by "border sensing". This leads into several increasingly consistent and experimentally supported (now, finally) explanations (or at least, at this point, suggestive hypotheses) regarding virtually all aspects of normal and diseased metabolism, including implications for cancer, several autoimmune diseases, inflammatory response, and several neurological and cardiovascular conditions.

[3] (the third category) Neural processing, in the brain, as dynamic and somewhat holographic processes, where, to keep it simple albeit crude here, different perceptions and cognitive states - the "ideas" we form and reason/react with accordingly, are very much like the ancient Greeks first saw things and expressed in their language - namely - forms (ἰδέα - idea, "form, pattern," from ἰδεῖν - idein, "to see").

This has implications not only for biology and neurology, but for all aspects of pattern detection, recognition, evaluation, classification, and logical, inferential processes that I prefer to label collectively as "synthetic intelligence" but which in the vernacular is AI, machine learning, etc.

The challenge is in formulating a scientifically rigorous basic model of:

§ cognitive and semantic objects, and logical propositions - our "ideas" when in a strongly philosophical way I state, "I have an idea... I see in my mind... I believe this proposition..."

§ being represented, in the brain, and in any brain-like computing machine system that dares to go beyond the Church-Turing limitations of a computing machine (and thus, more like a cell or even a virus than any computers we know of today, including virtually all so-called "quantum computers"

§ by a variety, almost an infinity(!) of manifolds, which follow straightforward topological rules but where singularities and "Ricci cuts" and the likes of what Perelman and others before him were struggling to do since Poincare made his famous Conjecture, are allowed

§ and where these objects - knot-like, pretzel-like, multi-orb, multi-hole torii that interact among each other with a type of geometrically expressed set of rules that "are" the ways our thinking, our thoughts, interact in most cases - can be manipulated in a computational logic for a variety of tasks for constituting

knowledge representation
knowledge algebra
knowledge geometry

§ which can then be employed not only to store information in a machine that is not a biological brain but to operate upon all that information, to perform reasoning that includes imaginative, inventive, never-tried-or-thought-before reasoning.

Another metaphor here: a huge box filled with floating but invariably highly-connected blobs that look like toy molecules or things from KNEX or Lego, and tossing in some new blobs creates a variety of ripple effects that can cause combinations and changes to many of the others.

But in the brain, we assert, "The more one thinks (perceives, imagines, dreams, reasons) in certain patterns (styles, modes, channels of thinking), the more reinforced and rigid and dominant some of those become. Eventually, one can end up being a thinking machine, yes, still, but locked into memes, prejudices, predispositions, and automatic perceptual responses. We can see that in ourselves, and in the society around us...

The "Blue Brain" project, @ ETHZ, and some work going on (long-standing) in Israel and Italy and with a few other colleagues in USA, actually supports this, and finally, there is experimental evidence appearing...

[4] (the fourth category) Psychosocial, and more expansively, psychosocioeconomic, dynamics. How hives, swarms, flocks, schools, and societies behave in manners that can be effectively modeled - for value in prediction, in some forecasting, and (to be cautious here) in some ways of influence, by understanding the phenomena - the operators, the nodes in the network - as being these malleable, flexible, contortion-capable, but rule-following topological objects, these manifolds that can deform and reshape in many ways but maintaining integral manifold structure - unless and until such point as a singularity event is reached that, with enough energy, turns a "horn torus" into a ""dimpled sphere" or vice versa. That sort of thing.

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Now, continuing with some of those mathematical issues:

§1 In the broadest sense, measures, tools for determining maxima, minima, of curvatures in surfaces within some limits

§2 Conservation or average of properties like curvature, surface areas and volumes within some range or limits before what one must speak of as a singularity type of event or the need for a "cut"
§3 Minimums of distances between a hypothetical "center of gravity" that can be assigned to a topological object, or minimums of empty gap spaces in the context of a space-filling

§4 Ability to embed the object, the manifolds in target, inside a sphere or some polyhedron

§5 Measures of gradients, and changes that may be summed over a surface region, similar to grad-type functions in differential calculus, which indicate not just curvatures like + or - but something like a rate of expected change in the curvature in a portion of a manifold. "I am an ant crawling on the surface and the curvature is changing. I want to know when I am likely to start sliding off..."

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§6 Measures of similarity between different types of knots and twisted surfaces. How likely is type α to type β to types γ, δ, etc.?

§7 Measures of curvature, again, which could figure into "conservation of curvature" overall, within some manifold. A perfect sphere, call it 1, perfect flat surface, call it 0. But now I depress (compress) a region of my big ball. It has a smooth-bounded indentation. What can be said about the "sum" of all curvatures, in a manner like thinking of simple integrals, if the rest of that surface does not change (e.g., expand in compensation, as in a physical balloon, to the depression in one region) - or, alternatively, if that surface does change, like in the vase of most balloons?

§8 Is there a way to speak of "conservation of curvatures" in an object and what for can such information as this be useful? (I started on some papers about this, several years ago...)

§9 This is all pertaining to how objects can fit together in a space, in some "packing" sense, but also where it may be valuable to consider not the maximum packing of n spheres, for instance, in a given n-space, but to a certain "density" of the packing - maintaining, or maximizing, a certain "range" of values of objects within the defined space.

§10 So this enters into questions of how to measure proximity, closeness, points and regions of contact, including not just points but areas of the respective manifolds - shared surfaces, and shared volumes as well if we allow for things to intersect and "blend".

§11 How to express measures and ultimately rules governing how different manifolds can fit together and also change, "morph", into other types, by virtue of the contacts, and the sharings, and the "packings".

§12 Perhaps this is leading to questions about a topological equivalent or comparable to a ? Hamiltonian ? Lagrangian? Some measure of the overall state of a system composed of different topological objects that fill or form some connected network in given space.

§13 In the physics, and in the domain of knowledge representation, information modeling, all of this turns into questions about dynamically interacting networks of malleable, fittable, foldable, bendable manifolds that are filling some space either densely or sparsely.

§14 Ultimately this leads into measures, rules, and methods for what I term a "transmutation" - somehow, that word feels more fitting than simply "transformation". X is some type of spherical object that has been stretched twisted, and now it becomes distinctively different, perhaps still a ":sphere" in the formal sense, but radically different and almost, nearly, "only a singularity away" from "flipping into" being a torus. Or vice versa.

Once again, it bears restating - solving these questions is not a requirement for building a Seldon Prediction Engine that works very well, very cleanly, efficiently, accurately in a "good enough and better than what I think we have today in the general field". Gaps here in our maths and in the provability of certain theorems do not block us from building information spaces and i-maps that can do excellent work in applications (e.g., NpC, ASTRIC, EMME). It's just that I want to do Better than simply "good enough".

[5]

Topology of Pattern Recognition and Learning in Biological and Synthetic Intelligence

@ 02.may

In the brain we construct surfaces that represent objects and the objects are of a universe of various types, some pertaining to physical 3D/4D objects and others to entities that can be extraordinarily different from anything physical. These surfaces define dynamical activity among neurons in the cortex particularly. They are not surfaces bound as tissue boundaries but of electrochemical activity which is the form of cognitive processes. These pertain to what we know or assign as values to different attributes. We construct these objects and match them, map them, against others, looking for the best fits, and therein is how we recognize and classify patterns and proceed to build relations, associations, and inferences about the things in our world. These objects are in multiple dimensionalities, from 2 to n, but usually in the human brain we don't go much beyond 7 or 8. [refs to some papers by Tozzi, Peters, et al].

In SI (synthetic intelligence) we do much the same. But we can go much much higher in the dimensions and much broader and wider in the scope of making comparisons and tests for similarity between objects. With the aid of computational machines, we can go far beyond single-digit dimensions as appear to be the limiting cases for human cognition. We have no limits with the machine capabilities, only time to perform the computations.

06.june

Consider spatiotemporal paths of cognitive processing as following a type of DAG (directed acyclic graph). There is no backtracking, only moving forward in time. However, paths can lead from one node to many nodes and from many to one. Time is one dimension. The other dimensions are determined by the framework of action; in other words, spatial movement, or movement among conceptual structures defined by the attributes of those structures – in any case, a kind of n-dimensional space. [Refer to Peters, Tozzi, Oro, Deli and others re: capacity of human brain to work effectively in 5, 7, perhaps higher dimensions, and for things beyond the capacity of the brain, we have the additional tools of what we make to assist us – words, the logos, and logic, mathematics, geometry, and other forms, and the implements such as paper and pen, and now, computers and the knowledge-base penultimate of the web, the internet.]

Now let's think of the DAG-nets and how these can be considered as topological structures, as having boundaries, and internal-external surfaces, and regions. Including twists, loops, knots, everything that we can find in any topology.

Picture such constructs, arbitrarily – a set of knotted and twisted objects which are in an n-space, and for simplicity 3-space, and they represent cognitive processes and include the detection, identification, discrimination, recognition, classification acts with patterns, each of which has some semantic value in some context (but obviously not in all possible contexts!).

These constructs, these shapes, may be compared and combined with one another in an almost infinite variety of ways. Like taking knotted and twisted objects made of soft clay, and combining them, in ways that are following the rules for logical combinations – and this can be different from the usual way we think about topology, such as transforming one object into another shape without any cutting action – without any “surgery” – such as from a torus to a cup and vice versa, but as opposed to trying to change a sphere into a cup or torus, where cutting and splicing is required.

So within some Context of Cognition ($C_{og}C_{on}$), there are rules for how cognitive topological entities which include DAG-net actions (that give rise to their shapes) can be combined, at least easily, straightforwardly, and without “mayhem” operations. We may think of this as being like the rules of general thinking, both with respect to formal logic, yes, but also in a more general way. For instance, we have usual and typical ways that we think of how a horse can be transformed, visually, in our minds or on paper or in a graphics design program on a computer, into another type of horse, another type of the family Equidae, or even imaginatively with various members of the orders Artiodactyla (even-toed ungulates) or Perissodactyla (odd-toed ungulates). But it is more unusual, more challenging, more “work”, to transform a horse into a fish or turtle.

We must look strongly and heavily at imagination, fantasy, and error, in order to understand reasoning and “correct” thought processes. [note: I have been saying and writing this since the early 1980s.]

Think about how Morse theory and also other mathematics including Ramsey, Delaunay, Voronoi, can be applied to this type of matching and fitting between topological entities, looking for how two or more can either match as similar/identical or fit together in a “congruous and sensible” manner.

As certain topological forms get established in neutral processing, they become like *chreodes* are in the formation of stronger and more dominant pathways for neural excitation in the future. Shapes – topological entities – which define neutral activity over time but condensed in spatial configurations – become dominant so that in the future, when activity is nearly or approximately similar, then there is a “gravity” towards the strongest and most common pattern of dynamical activity, reinforcing it. Thus, the tendency to come up with a specific pattern over other possibilities gradually rises and rises and becomes stronger over time unless there are forces for keeping it separate, unique, different.

This is a type of “inverse chreode” in the sense that what we have is not a cutting of a pathway by which energy flows down a course, such as a sand hill, but a congealing and molding and sculpting of a multi-dimensional pattern of neural activity that acts like an object, a shape, to which other and newer activity will be pushed to fit-into and match-with --- unless there are stronger forces for keeping that as a separate and novel/different object.

The more some X is perceived as being a Y and not a Z, the more the class of X will widen and grow and more X will be perceived as Y and not Z. The gradual building of dispositions, trends, and patterns of classifying percepts into specific categories (types), over time. Apply this now to human psychology and interpersonal behavior!

Remember that these objects, these topological structures, are dynamic, not static, and they are not in 3D and not in 4D but in multiple higher dimensions. However, observing the brain, such as thru fMRI, we will see things in a 3D+time manner. How to bridge things to the higher dimensionality of the cognitive relations?

This challenge is one in thinking about how biological brains operate to recognize patterns, to make associations and those propositional, linguistic and formally symbolic expressions we know as logic, as inferences, but also it is a challenge - with similarities but also differences - in how we can do similar functions in non-biological "brains"; i.e., in a synthetic intelligence machine.

The two realms are supportive, neither exclusive nor locked-in-step together. Both can be paths to each other, in the sense that the more we can learn about the biological neural networks using topological structures and orderings, the more we can hoipe to achieve with synthetic neural networks, and vice versa.

[6]

Comments from recent work (2020-2021) on emergence and social spread of particular diseases

We can work toward developing a formalism, and ultimately a set of equations, to employ with in a model that can be used for evaluating real-world data that is collected from observations, and for evaluating simulations including alternatives that can vary strikingly from the apparent path-forward given by the observations. Of course, these are very rough sketches, only notes pointing in some new direction.

[3.1] Assertion: Within recent decades there has been an emergence of more numerous and more frequent epidemic/pandemic-potential diseases which share certain general characteristics in common with respect to their epidemiology:

• more frequent variations (by genetic mutation) from the general classes of microbes that were commonly known and experienced in disease-outbreaks, in past decades and further back in history (specifically looking at influenza, ebola, coronavirus in particular)

• novel circumstances of emergence as infectious diseases within the human population, with some of the novelty involving geographic location and vectors within animal species

• rapidity of transmission throughout human populations on a trans-continental and planetary-wide scale, reaching “far corners of the globe” on an unprecedented scale.

We can refer to this as the Emergence Modulation (EM) and we can further state that this has three principal components, as previously enumerated – accelerated variations (V), novel emergence (E), and rapid transmission (T).

[3.2] Assertion: There are multiple factors contributing as initiators of to this phenomenon (“Emergence Modulation”, EM) and these involve not one but potentially all of the following, and we attempt to isolate some "targets" for quantification that can come from examination of the data streams that are being collected, and some new types which need to be examined:

❚ Massive changes in the entire ecosystem of the planet due to the combined action of:
• climate changes, by both natural and human-accelerated causes

• environmental changes of natural origins both climate-related and non-climate-related

• environmental changes caused directly by humans through inhabitation including dense urbanization, deforestation, mining, changes to lakes, rivers, wetlands, estuaries, and man-made reservoirs and other water processes, and other similar changes. This includes the massive planetary-wide human occupation of vast regions of land that had always been "natural and wild" or certainly "rural" (e.g., farmlands) and definitely not densely urbanized. We call this the Ecosystem Change Factor (ECF).

❚ Forced dislocation and consequent movement (and cases of species extinction or increases of species populations) of many animal and plant species. We call this the Species Movement Factor (SMF).

❚ Massive increases in certain animal populations and primarily in very concentrated geographic regions of the planet, due to human habitation, cultivation of livestock, increase of garbage and waste products, and other human activities (e.g., cattle, sheep, pigs, poultry, rats). We can call this the Animal Species Change Factor (SCF).

❚ The simple fact of a massive human population (now approaching nearly 8 billion), arguably more than double of what many experts consider to be an optimal maximum number of humans for the planet, and with most of this population growth being in an intensely accelerated period of time (post-1950) and in specific geographic regions (densely urbanized regions of several parts of the world characterized by proximity to formerly wild/rural regions in which many animal and plant species had previously been living relatively undisturbed for time immemorial. We can call this the Overpopulation Factor (OPF).

❚ Rapid acceleration in a short period of time (post-1950 and in particular post-1990) of massive travel by large and mixed-population groups of humans and human-associated objects (cargo) - (much of which is either of a biological nature in terms of materials or suitable for serving as a medium for the transport of small animal species and virtually any types of microbes) - through daily commuting and long-distance (trans-continental and inter-continental) travel. We can call this the Travel and Transport Factor (TTF).

❚ Massive and in many cases excessive and inappropriate use of antibiotic medicines and antimicrobial substances used on the human body and in materials and environments of contact with the body or in the general environment of habitation (including preparations of foods; e.g., processed foods). We can call this the Antibiotics Factor (AF).

❚ Significant changes in the hygiene habits of very large segments of the human population, particularly during the time since @ 1950, whereby there is the threefold "contradictory" phenomena of:
• more general hygiene (e.g., in-home toilets, showers, more frequent bathing, laundry, etc.)
• dramatically less hygiene through public contact by often vast numbers of different people with common-contact objects (e.g., handrails, doorknobs, metro train and bus seats, and other surfaces (especially) in high-traffic locations.
• dramatically less exposure by the majority of the population to "natural and normal dirt"; i.e., materials that are rich in microbe content and beneficial for developing general immune strength for an

environment characterized by many different types of microbes, particularly viral and bacterial. We can call this the Hygiene Factor (HF).

❚ Massive changes within the human population in sexual habits including three principal elements:
• significant increases in sexually transmitted diseases (STD) within the overall population
• statistically significant changes in sexual practices including uses of condoms and other devices and forms of apparel (which are often stored in non-optimal conditions regarding hygiene and which are typically hand-held during preparation and use)
• statistically significant increases, among certain population elements, in the numbers of different sexual partners and specifically from widely varying geographic, genetic, dietary (foods and drinks consumed and in what methods, again bringing in matters of hygiene but also (potential) parasite exposure antibiotic resistance) types of individuals, and also where significant-distance travel by one or both partners is involved prior to the sex activities (thereby adding to varying exposure to different contagious agents). We can call this the Sexual Habits Factor (SHF).

❚ Massive increase in the consumption of "prepared foods" that involve factory production, containerization, multiple forms of transport, freezing or refrigeration, significant and repetitive changes in geographic location during transport, delivery and retail stocking, significant handling during purchase and at-home storage and preparations, and the use of multiple synthetic ingredients that include specifically antimicrobial and antibiotic substances as well as other artificial and non-nutritional ingredients. We can call this the Processed Food Factor (PFF).

❚ Significant respiratory intake of chemicals (including microplastics) that adversely affect the nasallaryngeal-pulmonary tract in terms of inflammation and reduce the capabilities of that system for effective countering of ingested microbial organisms. We can call this the Adverse Respiration Factor (ADF).

❚ An effectively "zero strength" system of social mechanics on a planetary scale for minimizing epidemic and pandemic contagion risk through social distancing, lockdowns, quarantines, and basic separation of all population elements from interfacing and co-mingling during a sufficient period of time to reduce the risks of transmission for such diseases that can be spread from person to person. We can call this the Social Distancing Factor (SDF).

[3.3] Assertion: No one of the "factor" items presented here is being argued as a "primary" factor by itself. Each of these "factors" contributes to the risk of there being new viral, bacterial and parasitical agents capable of and leading to rapid, unforeseen and potentially large-scale transmission within the human population. All contribute in different ways to the problems of easy, swift-moving and even uncontrollable pandemics by novel and often rapidly mutation infectious diseases for which there may be no prior medicines or vaccines, and for which a rapid response (as seen with COVID-19) will be required. None of these "factors" can be easily, or in any practical manner, be addressed completely, or even significantly, without a seemingly impossible set of psychosocioeconomic changes on a planetary scale. However, by being aware of these factors and then, as a planetary society - demonstrating far more unity and cohesion than we have seen during the 2020-present period with respect to COVID-19 - deciding to do something to address all of these, together, logically and simultaneously, we do stand some chance as a human species of reducing some of the challenges ahead for our species.

[3.4] Assertion: There may be a way to consider all of the aforementioned Factors as parameters within some set of equations which can be employed to construct useful models for the Emergence Modulation (EM) and its V, E and T components. Such a model may be usable for making predictions regarding future epidemiological events including the geographic prediction of transmission and mutation events. However, it is not clear that any such models will be able to have a significant impact on the progression of future large-scale epidemics and pandemics, due to the observed phenomena of human resistance to effective countermeasures of prevention and protection, including measures of hygiene, vaccination and social distancing. Such models may help in response and for some minimization of undesirable effects (infections, deaths), but they cannot be expected to be very useful without massively different practices by the human population.

[3.5] Assertion: There will be more novel microbes, particularly among viruses, which are the most challenging of microorganisms to combat in terms of both public health practices and therapeutic medicines. There will be increasing difficulty to “catch” new variants before they commence to spread in human populations. There will be increased challenges due to climate change and the environmental consequences which will include more species migrations and adaptations to different environments. There will be increased challenges due to socioeconomic factors including those that can be expected due to upcoming and unavoidable climate-related and population-related environmental dynamics.

[3.6] Closing Comment: The COVID-19 experience has been a major “wake-up-and-recognize-things” process affecting all of human society. It was not the first in modern times. We have had a few strong early warnings with H1N1 influenza and with a few other influenza variants during the past decade (several avian flus). We have had major wake-ups with SARS- and MERS, and with Ebola. Very little was done to develop necessary changes in the society, within most nations, especially those variously characterized as “Western” and “affluent”. There will be other forms of the Emergence Modulation (EM) and it is unavoidable that some of the accelerated variations (V), novel emergence (E), and rapid transmission (T) processes will result in microbes (ore than likely, viruses) that have very high transmission and very high lethality (e.g., similar to MERS or some of the avian influenzas).

[7]

This has application in the mathematics even though it may seem far removed from the EMME theme.

Topological Solitonic Networks, Conservation of Curvature and Virtual Qubits

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Abstract

Topological solitonic structures giving rise to stable and semi-stable toroidal structures occuring as minimal energy configurations, are examined as elements within a (3+1) spacetime where summations of curvature and rates of curvature variation spanning a closed system constitute a "conservation of curvature" Ͼ. The underlying theoretical framework derives from investigations into the emergence of particles including all known types, fermionic and bosonic, within the Standard Model and the derivation of these structures involves a representation of nonlinear field interactions in the formalism of solitonic networks which describe topological changes within a fundamentally particle-free spacetime matrix. The stability of nodes defining interactions (collisions) in a simple four-dimensional spacetime within such networks is presented as the dynamic function giving rise to stable and semi-stable formations ("tensegritons", τ) with the properties of particulate matter in the physical universe and the utility for construction of synthetic "virtual" particles within a computational environment. In such an environment, transitions in energy states among such tensegriton nodes τ will be propagated to other nodes in the closed system (e.g., "qubit array") in a manner that preserves the topological Ͼ including through the introduction of system noise within such a computational array, thereby addressing certain critical concerns in the design and operation of quantum-entanglement based trans-Turing computing machines.

[8]

This has application in the mathematics even though it may seem far removed from the EMME theme.

An investigation into a class of three-dimensional soliton behavior of two general cases, closed-system sets and open-system networks, such that the resulting interactions produce a torus effect. This is further explored as a basis for interpretation of particle phenomenology within physics in general and specifically within a New Standard Model that interprets both conventional or "light" matter plus so-named "dark" matter as toroidal phenomena emerging from a singular energy field (so-named "dark energy").

Irrespective of implications and argumentation relative to particle physics, the notion of a stable toroidal structure deriving from one 3D solitonic expression or as a consequence of interaction (collision) among multiple 3D solitons offers some interesting prospects within mathermatics and theoretical physics, with possible relevance as well to the field of quantum computing and quantum information systems.

[9]

This has application ito EMME because it refers to underlying architecture within Seldon, the "Prediction Engine" software that ultimately, in a later phase, is what processes the massive data streams coming in.

We abbreviate the population-space as POP and the behavior-space as ATT (for "Attributes" - they are PSED types, but for simplicity, "ATT").

Fundamental Functions (FF)
The fundamental functions (FF) of the PE are employed for all context-specific functions (CF) – applications - that may be constructed as targeted inquiries and forecasts using the PE. For instance, a user may want to know how a segment of the population will react to the introduction of a new type of brand, a new product, and under certain socioeconomic conditions. These are all context-specific, contextual functions.

[1] Present-Active
Given a subset of ATT elements, find the subset of POP that lists, in some ordering, those members of the POP which exhibit those ATT. You have some behaviors and dispositions. You want to find who within a subset of the POP exhibits these the most, the best, or the least, etc.

[2] Present-Dominant
Given a subset of the POP, find the subset(s) of the ATT that dominate, that are the present most dominant within that POP subset. What characterizes this collection of POP members in terms of their ATT.

[3] Future-Reactive
What-If. Change the environment of the world in which the POP live and operate. This is reflected in changes within data associated with POP members and with rules, patterns, heuristics, and other governing factors influencing the relationships between POP members and different ATT elements. Now run [1] and see how these POP members will be in contrast to original/actual [1].

[4] Future-Dominant
What-If. Change the environment of the world in which the POP live and operate. This is similar to [3]. Now run [2] and see how these POP members will be in contrast to original/actual [2].

[5] Evolve
Given a subset of ATT elements, and a subset of POP, generate a simulation that allows for interaction between POP and ATT elements in order to determine causal relationships and to forecast future outcomes. This "fifth element" of the FF is the most complex and does requires not only the prior four FF to be well-established but that there is a history of the operation of the PE using those four other FF, thereby building up additional meta-information that can be used in this class of functions.

[10]

This is relevant because it links with the genomic examinations that need to be done in the search for risks and probabilities of mutation within wild and pre-epidemic forms of certain pathogens, particular viruses, and in how we can plan ahead for methods of mitigating different infectious viruses - such as with the VESID approach undertaken with respect to SARS-CoV-2.

Topological Information Processes in Viral-Host Interaction and Membrane Penetration: common natural biocomputation processes underlying certain contagious and autoimmune diseases and adaptive mutation

M Dudziak, E Deli, R Roman, O Ori

Abstract
A model incorporating principles of topological order and efficiency shows utility for demonstration of a mechanism present in both viral entries for certain agents including coronavirus, influenza and filovirus types such as ebola, and also in non-infectious disorders and diseases associated with autoimmune reactions, particularly within the brain and central nervous system. This process can be described as a type of natural biocomputation involving extensive molecular surfaces. It appears to fit with observations of surface protein changes within viral envelopes and primary structures involved in entry to target host cells, and it involves an iterative changes within viral protein conformation and surface topography that can be associated with underlying mutations within the viral strain. Similar processes appear to be present in the phenomenologically distinct and non-viral initial inflammatory stages of neurons affecting axons, both myelin sheaths and interior microtubule chains, leading to neuronal degeneration that triggers subsequent normative engagement of the immune system response. The apparent computational process is similar to certain non-Turing quantum computing models and leads to consideration of an underlying common mechanism within certain biological structures that involves the interaction among non-smooth manifolds and the optimization of surface-fitting that is consistent with Ricci Flow models for deformation and maintainability of topological consistency.

[11]

This is for background re: the synthetic intelligence ("sient") components.

Brain is not a Turing Machine and AI is a limit-case of adaptive logic

M Dudziak, E Deli

Abstract
Thermodynamics is a rapidly changing field that promises the development of novel techniques and applications. The brain's synaptic network displays a topological character, which is related to psychology. Cortical activation compresses information and builds an evoked potential. The frequencies of the brain's evoked cycle reflect the energy need of synaptic changes. Deep learning can also be divided into phases that consist of compression of information and relaxation, which culminates in representation. Just as backpropagation in current neural networks, feedback loops in the brain improve performance. The brain's biggest loop is the evoked cycle. It is centered on the resting state, which is maintained by self-regulation. Self-

regulation is an essential quality of neural systems that perform computations with thermodynamic efficiency in orders of magnitude greater than current supercomputers. Subjective perception of stimulus is an appropriate Fourier transform of the input. The resulting temporal organization orients the mental world orthogonally to the physical environment. Temporal orientation allows biological systems to form memory, learning, and evolution. As material systems observe the principle of least action when moving in space, intelligent systems might balance their action repertoire between the past and the future. Thus, generalization is a type of memory that boosts the ability to handle future challenges. The resting state permits the gradual evolution of the system in time and engenders the brain's temporal orientation. In a temporal system, quantum phenomena such as, entanglement forms in time and therefore is resistant to spatial disturbance. The later quality is perhaps the most essential advantage of brain-like quantum systems. A self-regulating system herein that can change and learn in response to the environment, and it may be suitable as the evolvable elements for future for thermodynamic computers.

[12]

This nmaterial is here because it pertains to foundations of the topological information maps that can be employed within Seldon and the SI analytics of the EMME data streams.

Topological Representation of System State Spaces and Geometric Mapping and Computation with Topological Information Resonance (As a Fundamental Process in Nature)

DRAFT NOTES DRAFT NOTES

M J Dudziak

Abstract (and main points) –
This is just a summary of what is going into this, aiming toward a proof of [1] or [2]:

[1] Any system, no matter how complex or uncertain, can be at least partially modeled (such that its main behaviors can be controlled and predicted – and this in some provable way, that it can be done so) through a <u>topological representation</u> that assigns system parameters to the following types of entities within an arbitrary and unique-to-the-system geometrical object which comprises a closed manifold and closed network in n dimensions:

- vertices (points)
- edges (lines)
- angles between vertices and lines
- functions specifying relations between 2 or more parameters which can be represented geometrically

Let S be any system, and m(S) be such a model. Let p[i] be any parameter within S that is contained within m(S). Let p[i] → g[i] denote the mapping of some parameter set to a geometrical set.

The model m(S) is that topological representation. Is it unique; i.e., only one possible m(S) for a given S? Probably not; there should be many possibilities. Some will be more accurate, more complete/comprehensive, than others. Is a given m(S) unique to only one S? Probably so.

[1.1] Any m(S) will under any circumstances of change remain within the same general topological class. In other words, however it changes, it stays within its topological type/class. If it is a certain polyhedron, it remains that polyhedron, howsoever distorted it may become.

[2] Can it be a Proof – in a manner that is not only consistent with but perhaps follows the logic of Gödel in his two principal "incompleteness" theorems – that there are systems – and ways to identify them – such that they CANNOT be modeled completely – "complete" in a rigorous sense, again with reference to Gödel – and that no combination of state-space parameters, no computational model, can be sufficiently certain as to cover all potential catastrophic-function aspects of the state-space? This is important to achieve, in order to show that something based upon alternative methods (e.g., [1], and incorporating randomization and stochastic approximation) is a satisfying and achievable alternative.

[3] Mapping of topologies – building upon [1], this addresses how to approximate a model that can be more reliable, even though "incomplete" – for systems that fall into the category addressed by [2].

The objective is to have a machine that can accept as input different models which consist of topologies and rules for transformations, and then this machine can undergo modifications which change its state and thus its topology, and these changes can be used to predict changes in the corresponding parts of the original model. This machine must be able to adapt to many different models m(S). So its architecture must not be dependent upon any S or m(S).

[3.1] Any model m(S) has a defined topology and rules for operations (transformations). This may be mapped to another topology T that possesses different rules of operations, regardless of the system S for which m(S) is a model.

[3.2] Based upon the choice of T, there can be a correspondence between m(S) and T such that changes to T can in turn be mapped back to m(S).

[3.3] The "model of a model" (T) has the ability to change its topology in response to signals that may be electronically induced and controlled, such as with proteins that will change conformation in certain ways.

[3.4] Changes in T can be interpreted as changes in m(S) and from m(S) there can be interpretations made regarding system S.

So there need to be some constraints about how both source and destination are defined. For example, a sphere will not map to a torus or vice versa. But a closed space will map to another closed space of the same general type. A sphere to a sphere, a torus to a torus, etc.

> But about spheres and torii, we must consider that where R = radius from center to center of the ring and r = radius of the ring
>
> > R>r torus is regular type ("donut")
> >
> > R= r is horn type, with only narrow line in the middle but this is a real separation between the surfaces!
> >
> > R < r = spindle type, gradually approaching a sphere as R approaches 0.
> >
> > So in a way the two are convertible, although not in the "pure" topological sense. Somehow this is significant, as long as we keep that distinction in mind.

(What about purely 2D surfaces on which everything is mapped as points in the 3rd dimension?

So each representation is a type of landscape, but all on some flat base.)

This is a very important point. Some system S will evolve over time, and its model m(S) will change, and its topology will change according to the functions governing m(S). But that is all unique to how m(S) is defined. How can we compute using a topological information resonance (TIR) method the changes, similarities, bifurcations, catastrophes, all sorts of variations in m(S)? This is different from classical methods – we compute values of different functions, numerically, with some formulae, and after all the numeric calculations, we see what m(S) may be, and we make some conclusions, etc.

Instead, we want to map the (significant) features of m(S) to another topological framework tcp which is a physical structure that can be manipulated electromechanically/chemically so that its geometry changes over time, in a way that indicates how S will change over time. We want to create a configuration for tcp such that it reflects m(S) and the changes we introduce to tcp will be analogous to those that occur within system S.

[from the earlier draft of this document, from @ 8.July.18]

[4] Consider a molecular array T that can be configured in a variety of specific geometries, almost like a set of "snake-cube" toys can be bent in different arrangements. This can be a 2D array with all the chains running laterally.

Model m(S) is mapped as a topology onto T. This is the initial state of T, corresponding to some initial state of m(S). Now T must evolve in a manner that corresponds to m(S). We have a set of functions governing all the possible changes to the parameter components of m(S). That comes from the analysis of S which resulted in m(S). But now we need to map those functions from m(S) to functions operating on the corresponding elements in T.

So we have an n-dimensional space and p parameters and potentially p! functions (combinations or permutations here?), and it is mapped to a 2-d space, with p or fewer parameters, and some subset (smaller) of functions.

We need to develop a correspondence between m(S) and T – an "information resonance" - such that changes in T, generated by the ways that T can be modulated and transformed, will either:

- reflect known or projected changes in m(S), which can be translated into functions within T, or
- be functions in T that can be translated into behaviors in m(S)

The key for having something that can actually work on a variety of NP-Hard problems, true XCS, is in having a T that can physically change its structure, its conformation, in ways that will be completely mappable to the model m(S). Thus, when T changes in some unforeseen and novel way, it will be clear how the changed T reflects how m(S) can or did change.

[5] How to construct T so that it can be used as described in [4]? Consider this approach. The case is made for a T that is a TCP – a topological computing process(or), and the novel computation model is TIR (topological information resonance).

A **topo-cell** is composed of one layer of the active molecular structure (AM) and an interface grid (IG) that can deliver electrical current to specific coordinates which each have contact with the AM. The AM may be strands or strings or chords of a protein-polymer conjugate, for instance. The AM is in contact with the IG such that there are points in the IG which can conduct signals to and from the AM. The AM will change its topology in the course of TIR computation through one of n possible configuration changes in the AM at different points – these points correspond to the coordinates in the interface grid IG. *Initially we ignore everything about quantum entanglement (QE) and coherence of QE elements within AM, and between multiple topo-cells, although we definitely allow for and predict the existence of such.*

> Note about TCP and GCM:
> Note that the TCP – topological computing processor – is composed of one or multiple topo-cells plus other logic, some of which is to interface the TCP with the rest of the GCM. The GCM is composed of one or more TCP plus other computing processors, including (classical, conventional) Turing-machine types.
>
> So the overall architecture of the GCM, analogous to how in most conventional computers there is D/A and A/D and various “central” processing elements (all digital), has the following:
> TCP units, interfacing with conventional microprocessors and other digital electronics, which in turn has interfaces with the analog world.

Let's allow for the present that there are the following possible configuration changes in the AM of any topo-cell, at any given IG point. There will be prescribed reactions to a signal delivered at the IG. For now let us assume that these are simple.

IG signals that can be transmitted to the AM at specific coordinates:

> -1, 0, +1, and what these can be are a negative spike, nothing, and a positive spike.

What the AM can do may be more complex in response to receiving these signals:

Helical-twist CCW	Helical-twist CW	No change	
Fold up	Fold down	Fold left	Fold right

[6] Mapping from m(S) into TCP.
For every feature within the m(S) there is some combination of the TCP alphabet of conformational changes. Any action performed within the m(S) is translated into either a sequence or a parallel combination of TCP alphabet elements that will be associated with one or more points in the IG.

The 2D TCP (with raised surface, thus a fractal type of 2.x D) reflects/shows by its topology, what is in the more complex and harder/impossible to visualize higher-dimensional m(S).

Changes made to the TCP, acting upon its surface the changes in the m(S), will reflect the general state and course of the m(S).

Changes made directly to the TCP, such as introducing changes to the topology through the IG in to the AM structure, can indicate significant (or insignificant) variations that could be in the m(S). Thus, one needs to be able to backtrack or perform inversely the steps that would be in the m(S) for the kinds of changes seen in the AM.

For instance, use some sequence a-a-c-d-e-h-g-d-a-a and run this across several nodes in the IG. The result is a new conformation of the AM. Suppose it looks particularly interesting, from pos or neg perspectives with respect to the system S. Suppose the AM resembles some other surface which pertains to some similar model m(s') and some system S'. So, now, let's see what operations in the m(S) in terms of its topology would have mapped to that sequence a-a-c-d-e-h-g-d-a-a in the AM within the TCP.

We could have one or perhaps multiple operations that result in the same AM sequence. We then evaluate what those would be like, for system S, and we can study carefully how S would move into such states as indicated by the m(S) in such a state that is represented by the AM in the TCP.

[7] New material, started on 9.July, 11:30 am
What this all comes down is is the following:

[7.1] Any system can have at least one multidimensional topological model mt(S) (formerly just called m(S) in preceding notes). This model can be (a) suitable for control and prediction which represents everything required, sufficiently, in the state-space dynamics, and (b) represented in a topological form, as some geometrical object with functions that govern the change of the structure of this topology. It is not necessarily only vertices, edges and faces, and not only 3D, and not only a polyhedron.

[7.2] Any system S may have multiple mt(S) but each mt(S) will be specific and uniquely for that S.

[7.3] This model mt(S) can in turn be be mapped purely as a geometrical operation – as a projection - into a "surface model" ms(S) which has an exact correspondence with the mt(S). This is a 3D model consisting of a 2D array, a grid, such that there is a third dimension of variation in the geometry – thus, a surface of deformations (twists, folds, bends) in an otherwise smooth grid. (Visually, it would look like a rugged surface of hills, valleys, flat regions, rough regions, and various twists and turns at the grid points in the array.) The claim here is that this surface will accurately be a mapping of the higher-dimensional mt(S).

As the mt(S) may change in the course of "running" or "executing" the model, for control/prediction of system S, and the topology of that 3D or 3D+ geometrical object changes, so will the surface of the corresponding ms(S) change – for instance, it may develop new hills, peaks, valleys, pools, flat areas, even singularities, and thinking of the surface as being a grid of lines (strings, threads, chords, chains), which correspond to molecular chains that implement this ms(S), these threads will change in their orientations with twists, folds, bends, and this leads to a distinctive rugged surface that it is claimed is a unique mapping of the original model mt(S).

[7.3] The ms(S) is implemented in a physical structure, the TCP topo-cell. The material making up the grid-array of configurable molecular chains (active material/molecular-structure; AM) is controlled in its conformational changes by signals applied to specific intersection points in the interface grid (IG) which in turn connects to electronics that generate those signals.

The ms(S) changes according to an algorithm that is based upon the mt(S) which translates the positions of points (parameters) in the mT(S) and values for functions relating different parameters of the mt(S) into operations that can be performed with the AM via signals delivered via the IG. These operations will alter the surface of the ms(S) through twists, folds, bends, and no-ops (no changes) at these IG points.

[7.4] However, there will be variations that may not be predictable because of quantum scale behaviors within the AM array. This means that the AM can take on a variety of different configurations in response to the actions of the signals applied, which in turn originate from the parameters and functions of the mt(S).
This means that the ms(S) can vary in its conformational changes, in unpredictable ways. Each such configuration that actually results can be an indicator of what might be the case in the behavior of the mt(S) and thus the system S.

Potentially there can be millions or billions of variant configurations. Some will tend to dominate. There will be a statistical way of measuring these variations. This will be significant is making estimates about which are more possible and significant. From these, one then needs to go back to what the changes would be in the mt(S) and thus in the system S.

The whole idea is to generate, using the ms(S), a huge number of variations in the surface conformations, employing the conformational quantum effects and variations in the substrate material, the molecluar chains making up the AM, in order to generate a large number of different possibilities for how the system's parameters could behave, and then to begin to select those few that will actually be possbly relevant in the real system S.

[7.5] The resulting dynamic surfaces of the ms(S) reflect in a reduced dimensionality (2D array with fractal-like third dimension of hills, valleys, etc.) the behavior of the mt(S). The claim here is that this surface will be an indicator of changes within the original system S being modeled. As the surface of the ms(S) changes, this reflects changes in the more complex S. These changes in the ms(S) surface are observable (measurable) by applying some current through the IG that will result in a set of values for all the intersection points – thus, a 2D array that describes the topography of the surface.

[7.6] Furthermore, the measured maps of the ms(S) can be captured by other means, such as using AFM type principles, using a laser to scan the entire grid surface, and this data is saved as a digtal array that describes that surface. This can ten be compared, rapidly, with a large number of other known patterns, as a means of making comparisons with either empirically observed system S behaviors, or other ms(S) conformations, which cold indicate something of interest relevant to the behavior of the current S, on the basis of these other maps which are from other models of S or from entirely other systems.

The result is that there can be a set of “maps of interest” which can be the subject of frther computational analysis to determine if there are some similar conditions, similar trends, in a given system behavior, which are similar to some others, in a positive or negative sense. All of this is for having better and faster methods for generating possible system configurations that can then be analyzed using more classical numerical computation.

At the heart of this is the QUANTUM BEHAVIORS within the ACTIVE MOLECULAR STRUCTURE (AM) which will generate many variations in the overall outcome of the ms(S) – these many variations will include many irrelevant and "impossible" variations in terms of what the mt(S) and the underlying system S can possibly be, but these im-possibilities can be quickly ruled ot numerically. The result is that there will be some subset of the ms(S) surface conformation variations that is "realistic" for consideration. These are the ones that will merit further analysis using the Turing-machine components of the GCM – not the TCP (which consists of the topo-cell with its AM and IG) but conventional numerical processor(s) – and these resources could include the use of QTC (quantum Turing computer) devices, if the computational demand and their capability warrants such use, but otherwise it will be conventional, classical computing with ALU and FPU logic.

[x] Generalizations beyond fundamental physics and biology - to information and computation science

In principle, if a topological model m(S) can be constructed for any system S, including at the molecular, atomic, and subatomic levels, then that m(S) can be mapped to a topology in a TCP. That (call it tcp(S)) can be programmed to change its configuration and the behavior of its topological changes, and any given specific states, can be mapped back to the m(S) and indicate what will happen or what should be done to specific parameters of S, as modeled in m(S), in order to have the desired or predicted results.

[Other points from the same notebook]

x-4.2 – Multiple, repeated twisting leads to topologies resembling explicit knot-making and any type of repeated knot-making gradually approaches the topology of a highly deformed sphere. But within such structures is a massive amount of information stored in each twist, each fold, each knot, within the overall structure. This could be a path for knowledge representation but more specifically for representing different parameters of a complex system space and the ways that they are both known to change and suspected of possibly changing, in the cases of those parameters that are too uncertain to be adequately measured or predicted by classical means.

x-4.3 Our human brain receives 3D information and rebuilds it all in a 2D array of neurons, but this is then used to general cognitive models of 3D objects.

Arguably, the "world out there" is 4D space (plus time, as a "5th" dimension). And that gets "captured as snapshots" of 3D frames, just as a photograph is a 2D representation of something we call "3D." But that information which comes into the eyes, gets transformed into signals that end up in a 2D array of neurons, and it from the changes and interactions and comparisons between all those 2D representations, that the cognitive elements of the brain generate models called "3D." And then further processing can allow the brain to create models of 4D spaces, and even models that have more than 4D. [See work by A. Tozzi and J. Peters on fMRI and Hypersphere models of the brain]

x-4.4 What can be learned from PERSPECTIVE? This refers to the contrast between *linear perspective* (the typical way we think, and also what is typical in "Western" art, developed in the renaissance in Italy), and *reverse perspective* (e.g., what is more common in Byzantine and Russian ikon painting).

[Here, I have been lead more and deeper into the mathematical and art theory work of the great Pavel Florensky:
Imaginary numbers in Geometry (.Мнимости в геометрии. Расширение области двухмерных образов геометрии.) devoted to the geometrical interpretation of Albert Einstein's theory of relativity. But Florensky goes much farther and deeper than contemporary mechanistic, reductionist science.

We can look at a scene that is in a “reverse perspective” and our brains rearrange things so that it appears in the natural perspective! This is not only interesting – it points to how our brains are able to transform one system of parameters into another. And this does not take a lot of “calculation” in the process!

[13]

A new approach to Ricci Flow in developing a topological ordering that implies internal teleology governing emergence of order and structure in complex systems including biological organisms

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[new version begun 03.May.2019]

Abstract
Is the Ricci Flow much more than a very interesting mathematical tour de force which is vitally important within general relativity as well as formal topology? The examination of more general interpretations of entropy and complexity within systems leads to a concept of geometric information flow that optimizes in order to maintain consistency of both the entropic and negentropic processes. A system may exhibit increased turbulence and chaos as a necessary component of increasing organization that locally preserves information and increases order that enables successive stages of such behavior. Such a system can be shown to lead to an increase of topological information that is preserved over the course of many turbulent phases including catastrophic disorder phases. This behavior can be seen as a different type of Ricci Flow that is useful in examining the complexity-phase transition mechanisms that lead to self-replication within molecular structures and consequently in multi-molecular structures given the attribute of “life, itself”.

[14]

Remarks on the Seldon Prediction Engine and how it works for attaining objectives in personal and public health and wellness

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How Synthetic Intelligence coupled with Massive Data enables more efficient and productive medicine

mjd_28apr22

Introduction

Prediction of dispositions, trends and expected behavior is practical and achievable when there is a sufficiently large and diverse stream of data coupled with an analytical engine capable of using that data. The Seldon Prediction Engine is such a computational engine, applicable to different domains and it employs large and multifarious data streams, originating from multiple sources including social communication and networking platforms.

The initial focus of using Seldon is upon personal and public health and wellness. Among the sources of data are those involving information sharing among a very large and diverse population through different internet platforms – the commonly used popular ones and also one that is designed for enabling people in areas of lifestyle that enhance their health and wellness. This is the OASIS communication platform (instantiated as an Oasis "world" and known as "Terra"). The missions of a Seldon analytical environment can be many, but in this initial focus of use it is directed at the challenge of how to learn more about the likely behaviors of many people, taken as population groupings, in order to derive useful information for use by those people and their medical providers in attaining and sustaining better health and avoiding a variety of adversities that include chronic and debilitating disorders and acute diseases such as viral and bacterial infections.

In developing this type of predictive application, there is an important factor of personal privacy and non-intrusiveness. Specifically, the methods employed by the Seldon architecture do not depend upon, nor do they require, specific personal identifier information, in order to construct predictive outcomes about health conditions and dispositions for types, groups, classes of people. Thus, privacy and anonymity is preserved. The aim of the analytics is to provide estimates about observable attributes which can be noticed by both individuals and health providers, in such a manner that is conducive, supportive, and desirable for people to accept and to act upon, rather than to attempt to identify specifics about any individuals. Thus, our emphasis is upon modeling of characteristic traits which are derived from observing and studying very large sets of data linked with the behaviors of very large populations, and thereby deriving observable qualities that can be sought and identified, by individuals themselves and by their health providers.

This aids in maintaining personal privacy and an environment of non-intrusiveness, which is very important for the interactive process to proceed in a positive manner. The model does not aim to generate predictions about individual persons a, b or c, but about types of persons X, Y or Z. The resulting information can be used in different ways spanning from medical research including pharmaceutical discovery to public health education and patient-provider dialog in order to most effectively attain results in healthcare and lifestyle that provide optimal benefits for individuals and thereby the society as a whole.

Our focus with Seldon and data acquisition sources such as the Oasis social communication environment and PHIBER (Population Health Informatics Biomedical Equity Resource) 1 is – among the broader objectives of improved communication, collaboration, entertainment and other positive interpersonal experiences - to improve the diagnostics, therapeutics, and outcomes for individuals and for populations in many types of disorders and diseases. We focus upon health conditions which are often (historically, statistically) addressed only after progressed development, with often serious consequences including comorbidities and death, or in the case of transmissible diseases, contagion spread within the general population. This is a large subset of medical pathologies that makes up a large component of healthcare burdens in terms of personal disabilities and dysfunction, and also in terms of healthcare budgets and financial burdens to the entire society.

Technology

There are two major computational tasks that are essential for addressing these problems. Both of these benefit from mature information technologies that are widely employed in other applications which are in wide use
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currently, including a vast array of image and text processing that is employed in a very similar use-context, namely that of large populations of diverse users within social networks.

One task can be summarized as data correction, restoration and completion. Examples include: noisy, fuzzy images such as faces, text characters (alphanumeric) and text content (semantics). Algorithms and implemented functions including VAE (Variant Auto-Encoder) networks are among the most powerful and well-developed tools for performing such tasks. Noisy signal data is "cleaned up", missing elements are restored, and the basis is the use of neural network algorithms that have been trained on similar datasets.

The second major task can be summarized as data generation, modification, and replication. Examples include: creating novel faces, bodies, movements, of humans, animals, plants, or novel text content, based upon existing images, text, and other data objects. Algorithms and implemented functions including GAN (Generalized Adversarial Network) networks are among the most powerful and well-developed tools for performing such tasks. From examples used in the training sets, new samples that are characteristic of certain types can be generated. This is now widely used in media such as in special effects for movies to create representative human-like or animal-like faces, gestures, crowds, for instance.

An example of how these algorithms are employed in contemporary imaging applications can be found in Figures 1, 2 and 3 (see Appendix) as well as several papers in the References section. It is worth well to reflect upon the successful applications of these algorithms (and others including Bayesian probabilistic networks and other forms of "supervised" and "unsupervised" neural networks, and also formal symbolic logic systems) to applications that are seemingly very different and unrelated, such as imaging and text/language understanding and tasks of both correction and modification/improvisation.

The rationale for this assertion is that these methods – first developed in very abstract areas of research and then applied to signal processing and later image manipulations - can be applied to exactly the tasks faced in several closely related medical and healthcare domains. The same general classes of algorithms can be applied to other data types where the features are different from visual or linguistic 1 Formerly referred to as PHEBR (Population Health Equity Bioinformatics Resource); the name change is intended to make this more amendable and acceptable in the "mainstream" world of communications and media. The acronym even has a potentially useful phonetic quality – "PHIBER" as in "fiber" types, but rather, components of models such as can describe medically-relevant attributes. The Seldon (Prediction) Engine is a suite of tools for extracting future-value information which derive from datasets that originate from very large sampling populations. Seldon employs such algorithms as VAE and GAN along with others, all in the service of performing similar functions of data correction/restoration/completion and generation/modification/replication. References [7] and [9] below provide two papers of significance in this regard of using algorithms such as GAN for medical applications beyond imaging, and including in the synthesis of electronic health records (EHR).

The applications of the architecture and system that comprise Seldon are not only varied but multitudinous. However, at the present time, the primary direction for use of Seldon is in the broad domain of health and wellness, spanning physiology and psychology, for an open population of people. The value of such masses of data for Seldon and for applications concerning health and wellness are in the ability, using such algorithms as VAE, GAN and others, to make classifications and estimates regarding a variety of physiological and psychological states, dispositions, trends, and possible future conditions. This information does not pinpoint specific individual cases but likely patterns of behavior and measurable qualities, which can be useful to individuals and their care-providers.

What is unique and new is that Seldon is not directing its attention to such constructs as faces, bodies, alphanumeric characters, signal patterns (e.g., radar, sonar), or semantic content of texts, but to other collections of attributes within data streams that may very likely include a large variety of data types including text, facial expressions, gestures, and other media. These data streams, typically from social networking platforms, are exchanged by people in a variety of personal and social communication contexts. Furthermore, most of the data exchanges are not in the context of anything specific to health or medicine but in dialogs, postings, and remarks that are explicitly not related to health and overall wellness. This is important, valuable, for gathering the type of data which an analytical system such as Seldon can employ to derive deeper insight into health conditions that are not easily obtainable, even through person-to-person dialog (e.g., between a patient and provider) or through quantifiable measurements (standard bioinformatics).

Attributes that Matter

Now let us consider what we need to accomplish with:

• very large databases that have huge amounts of data which is ◦ not specific to health concerns ◦ not quantitative ◦ rough, fuzzy, noisy and even contradictory ◦ largely consisting of data about lifestyles and activities that may not directly pertain to health but from which inferences can be made

• and the challenge of using such information – in combination with specific medical data in quantitative form (statistical types, as well as data provided by some individuals directly)

• in order to generate useful information for predicting future health patterns and outcomes for large numbers of people, mainly on the basis of the lifestyle data, including much that pertains to levels of stress and other psychophysiological factors which are contributors to various disorders and diseases (especially of the "NpC" type; e.g., dysautonomic, arrhythmic, autoimmune)

• in a manner that can be used by both individuals and families, and their healthcare providers, to achieve better outcomes for all, ultimately through a combination of self-care and the processes of improved, more knowledgeable patient-provider communications

What are some of the significant attributes that can be processed in this manner? What can we gain from the social communications between people of the sort that are common on many current social networks and in the Oasis environment in particular? Our challenge is to obtain certain types of data which can be used within inferential and pattern-recognition processes.

[15]

Disruption of Autonomic Control Functions through Informational Storm Events Triggered by Chronic Sustained Stressor Agents

We examine the balance between sympathetic and parasympathic control networks and the effects of deregulation brought on by chaotic signal conflict and a "double bind" bifurcation syndrome, contributing to noise and informational heat dissipation. This complex of conflicting and negating signal action compounds a signal weakness effect that operates at the level of energy transfer propagated as biosolitons through protein chains, in turn affecting adversely protein conformational dynamics and the geometrical behavior of DNA helical structures within protein sheaths. Further, we explore the role of both neurochemical and bioelectromagnetic stressor agents as the principal class of factors responsible for the mechanics of such neurosystem disruption.

We introduce an explanation for the biophysics by which such stressors directly and adversely affect biosoliton signal propagation in proteins and nucleic acids, demonstrating a causal path from such stressors (both external stimuli and internal psychological triggers) to what can be termed "informational storms" within the autonomic neural networks. Such storms, analogous to cytokine storms within the context of infectious disease, encode and reinforce cycles of behavior including the emergence of chronic positive feedback loops related to the informational storm events and signal weakness effects.

We explore how these cyclical, "chreode-like" formative processes thereby create and reinforce epigenetic effects of activation and deactivation for particular immediate-early expression genes that are centrally responsible for control of both FF (fight-or-flight) and RR (relaxation response) systemic behaviors, principally through regulation of cortisol and DHEA metabolism and homeostasis. We further argue that the long-term deregulation and loss of efficient signaling, and the positive feedback loops that result, is a strong model for explanation of the neurodynamics involved in a number of disorders of the autonomic nervous system, leading to significant pathologies of the cardiovascular, gastrointestinal and endocrine systems.

We claim that a combination of psychological and physiological behaviors, supported by appropriate pharmacological agents but strongly resting upon techniques including exercises to develop conscious control of several generally-considered autonomic functions, can lead to long-term control that dampens and subdues the signal weakness and informational storm phenomena sufficiently to reverse the observed positive feedback loops and create an effective pathway to reduce the overall dysautonomic behaviors.

[16]

Reflexive Topological Dynamics and the Basis of Topological Limits and Bounds of Structural Deformation and Morphological Change

Martin Dudziak, Ottorino Ori

Comments in advance:

[1] This probably should be two or even more papers. But perhaps it starts out as one, and then there will be splits into different specific areas. The aim here is to have one or at most two papers that provide a suitable foundation for going further into at least two areas where theory can be applied to well-defined need-areas in industries that are stable and capable of supporting further research. We want to show as theoretical results some X which will clearly bring benefits to some Y that people and the society need and where those needs and benefits are understood by enough people.

[2] I see two such application areas – medicine (specifically virology, VESID), and geological exploration and discovery (specifically, mining for metals). These may seem very far apart, and in some ways, this is true, but when it comes to topological stressors, strains, and efficiencies of transformation operations, this is where there is more unity.

Now some generalized claims, and then some ideas about the structure of an initial paper along these lines.

Claims:

[1] Given a complete and closed topological surface (2D? 3D? - which may represent symbolically, informationally, a non-physical set of data that has been mapped to such a topology), there is a mapping that can represent the whole as a unique unitary entity. This mapping (M), perhaps represented as a formal set of numbers (not as just one number), sufficiently represents the Whole and not just any one segment of the manifolds that make up the whole topological structure. This M controls (limits, constrains) the variations by which any given subset of that surface – any delimitable (bounded, finite) portion – can be modified, deformed, changed in its shape.

The shape of the Whole controls what can be done (changed) to any portion (part). The information in M, about the Whole, governs any changes within the parts (down to some limit point in scale, something to be determined and defined).

We can term this as the principle of wholism – the whole controls the parts and how they can change and still be a contiguous part of that same whole, and without destroying that categorizable, definable "essential characteristic" of the Whole. (Something here reminds me of eigenvalues, eigenvectors...)

The next claim is very pertinent to problems like VESID and can potentially explain why certain objects, such as viruses, have the shapes that they do. But this second claim, I will also suggest, is important in geology and the dynamics – the flows and possible changes in shape - of geological regions such as in crust and upper mantle, etc.

[2] A given structure, which may be composed of many elements, can be represented as a continuous, closed topological entity. From the parts, as long as they are connected, we can say that one can move (e.g., a pointer, like a pencil) from one segment to another to another and eventually connect all segments. We can then make transformations of shape for the given structure and these changes will, we can assert, be reflected in some dynamic changes within some, if not all, of the component parts. For example, consider a simple ball, a virus, an organ system in the body, or something much larger, such as a large 3D segment of the Earth's crust or mantle. Such a volumetric object must follow certain rules by which it can transform its shape, and making changes in one part will make changes in 1 or more other parts, just like pushing down on a soft ball will make deformations in other regions. These rules are governed by the physics and chemistry of the materials that compose the object (volume, region). If the object has a complex multi-part geometry, then the changes will be reflec5ted in a variety of ways, but we can assert that there will be some changes affecting everything, somehow.

There are regions, and especially at borders and joins between polyhedral (polytopic) and polygonal segments, where there is some measure of efficiency in terms of the level of energy needed to change one structure into another, to make a break or preserve a join. We can measure some type of stress or strain that exists where one segment of the object joins another, and these regions, whether they are treated as lines or areas or volumes, will all express some change, some dynamics, when the object-as-a-whole is being manipulated, or when one region of the object is directly affected (i.e., there will be consequences for the other regions). Indeed, many parts (segments, regions) may appear to be unaffected, to have "zero" (join-stress, etc.), but actually, the claim is made here, even those regions in a "real world" object (using a virus and a geological flow formation as two examples) which seem to have "zero" change, really do have something changing, and it may be not evident unless specific measurements (molecular or larger scales) are made.

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