A Networked-based Approach for Modeling Team Performance and Efficiency

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ABSTRACT

Models of team behavior typically emphasize general group dynamics or the specific contributions of individual members representing different disciplines. The focus of such modeling is generally either sociological or psychological, depending on the modeling emphasis, but not both.

What is not typically addressed is modeling that accounts for both technical and sociocultural aspects of interactions between team members in the context of team activities and output. These two aspects together influence and guide team effort and either impede or expand the team's ability to achieve specified goals and objectives. Moreover, of prime importance, is that both technical capabilities and social/cultural aspects of interactions drive team communications and the exchange of information that leads to achievement of team goals.

The fundamental underlying assumption of this type of modeling is that teams, however conceived and constructed, operate under technical, organizational, and social constraints that can be represented by metaphors that have been used successfully for study in other disciplines. In this paper, we present epigenetic principles of biological cell and organism development and statistical mechanics principles of energy exchange and expenditure that are useful by analogy in characterizing team traits affecting team behavior, efficiency, and performance.

Keywords: Team behavior, epigenetics, statistical mechanics, entropy

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THE CHALLENGE OF NEW MODELS

With the development of new and increasingly powerful computational tools, there is the possibility that new simulations applied to old models will produce such improved results that there will be less incentive to search for alternative models. This paper, therefore, will focus on the modeling aspect of modeling and simulation (M&S). We propose an unusual epigenetic model (Fang et al., 2019; Gilbert, 2000; Goldberg et al., 2007; Kirk et al., 2015; Waddington, 1957) and suggest how it might provide a way that M&S could be applied to a class of problems that have not yet been widely analyzed. Specifically, we address team behavior, collaboration within teams, and team performance, all of which contribute to team-driven efficiency and innovation. We warn the reader that this model is still in an early stage of development, and is being used to suggest interesting directions to pursue for the application of appropriate models and simulations derived from those models.

Teams exhibit (at least) two forms of behavior, that we will call socially dominated and technically dominated. Socially dominated team behavior has been the subject, mathematically, of social network theory (Easley & Kleinberg, 2010), where it is argued that team members are "linked" (i.e., they interact) by social forces in a manner that reflects affinities based on interpersonal relations of one sort or another. Technically dominated behavior is concerned with linkages that may be imposed on team members, or develop between and among them, by their need to provide complementary skills or knowledge to solve certain types of problems. Work has been done (Moskowitz et al., 2015) to address network analysis of such teams and present metrics to assess their efficiency. The epigenetic model presented here is appropriate for analyzing both socially and technically dominated teams as well as their combinations.

Epigenetics (Waddington, 1957), in its original biological form, deals with the development of a living organism from conception to birth. It was proposed to answer the question of how cells in a multicellular organism, all with the same DNA instruction set, each reach different end states. The epigenetic model answers this question by hypothesizing that the same DNA molecule, when activated by different surrounding protein networks, can be guided to different fates. The attractiveness of an epigenetic model for collaboration in teams is that changes in network (team) structures provide a rich mechanism for modeling adaptive and rapid changes in team development and behavior. Genetic evolutionary models, in contrast to epigenetic developmental models, have been widely used in other areas. Such models, though, address mature organisms and random change driven by "natural selection", attributes rarely characteristic of team modeling. Genetic changes require some form of random mutation, which is relatively unlikely, so changes occur more slowly, and are not of interest in our modeling, since such random change processes can not only stifle rapid innovation but can actually reverse it (Colautti et al., 2010; Gomulkiewicz & Houle, 2009; Kirkpatrick et al., 1983). An important feature of the epigenetic model, aside from its avoidance of random events, is that the network (i.e., patterns of interaction), rather than the individual, becomes a basic unit of performance and innovation.

One of our assumptions is that interactions among team members provide the opportunity for the team to grow in expertise, insight, and performance. In a sense, it is not who is on the team that matters, it is the number of possible interactions between and among team members, i.e., team "entropy". To support (and validate) our modeling of team-based collaborative processes such as information exchange, learning, and problem solving, we require organizational (team) analogs of both DNA and the networks of "proteins" that signal, activate, and regulate the DNA. Table 1 lists model elements used in epigenetic and statistical modeling and their equivalents in our modeling of teams and organizations.

In established and innovative organizations, there are many networks (purchasing, legal, Research & Development (R&D), human resources, etc.) that signal and regulate various units of the organization (the organizational "genes")

and facilitate various cooperative and collaborative processes. It is important to identify these networks and to understand exactly how their mechanisms operate. It is of particular importance to develop a mapping of an organization's genome, the sum of its DNA arranged within and across the team or organization, and to characterize network activity in terms of the functioning of the 'organizational genome'.

Table 1. Epigenetic Modeling Analogs

Model element	Team analogy	Organization analogy
Cell/organism	The team	An enterprise consisting of organizational units
DNA/genes	The technical & social "instruction set" carried by each team member	Unit (e.g., R&D), having its set of policies, rules, assets: together, comprises the "instruction set" followed by the unit & its members.
Protein signaling networks	Groups/clusters of individuals on a team	Groups/clusters of organizational units
Signaling proteins	Team member inputs (technical, social) to team activity, problem solving, etc.	Unit technical, social outputs and interactions with other units
Network	The set of individual nodes and links comprising the structure of the team	The set of unit nodes and links arranged to form the structure of the organizations
Network nodes	Individual team members	Each organizational unit
Network links	Interactions between/among nodes	Interactions between/among nodes
Entropy	Measure of the number of interactions, or variations in interactions, between/among nodes	Measure of the number of interactions, or variations in, interactions between/among nodes

EPIGENETIC MODELING OF TEAM/GROUP PERFORMANCE

Epigenetic models are currently being used to understand complex diseases like diabetes, Alzheimer's, and cancer (West et al., 2012, referenced below) that originate in cellular developmental pathologies. We present instead an epigenetic model to describe the functioning of teams that are engaged in collaborative processes and that are also subject to pathologies. The model differentiates "developmental" activities by which a team solves a particular problem and develops a methodology using its internal collaborations, from the "Darwinian" genetic "evolutionary" processes by which the team's already developed methodology survives in some external competitive space. These two scales, epigenetic development and genetic evolution, are connected because characteristics of team performance selected for their fitness in the marketplace for the long term are ultimately assimilated into an organizational (genomic) structure that *subsequently* guides short time, stable operations. Waddington (1957) called an organism's stable development, which he wanted to explain, "homeorhesis". He proposed that an organism's DNA is sufficiently buffered by regulatory networks in the cell that many small variations accumulate yet remain "cryptic" or unexpressed. If the organism's surroundings during development are sufficiently perturbed, these cryptic variations can be expressed and may alter its fitness or produce pathologies. Waddington imagined epigenetics as a conceptual model in which developing organisms travel down a tilted "epigenetic landscape" (Figure 1) and find themselves guided by increasingly deeper, lower entropy (fewer available combinations between proteins and DNA) channels as their cells differentiate and stabilize in form and function. We suggest an analogous model for organizations or teams, where falling into differentiating channels of behavior may constrain innovation and limit finding novel approaches to new problems. Movement into these lower entropy channels is promoted by the "information" (negative entropy)

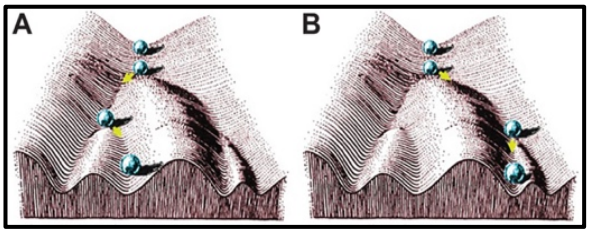

Figure 1. Waddington's developmental landscape diagram (Nobel, 2015)

provided by regulatory networks that control the behavior of groups of related "genes". Once their information content is utilized, these networks may be unable to sustain innovation (or the benefits of training); a revitalization may be needed in the form of new sources of entropy. We will suggest a possible use of game-play as a method for injecting entropy into an organization and avoiding entrapment by poor channels.

Genetics explains those processes by which mature organisms change over long periods of time yet retain a fitness for survival in their environments. We now understand these processes to be described by "natural selection", a combination of random changes in an organism, typically caused by mutations of its genetic material, accompanied by the necessity that these random changes be capable of survival in the environment. We shall be interested in modeling epigenetic processes that enable a team to function in its environment while it is actively solving a problem but in a developmental time frame (i.e., how does the team improve itself as it works on a particular problem) rather than a genetic time scale (e.g., how might the team become suited to solving other types of problems by changing its structure), with and without the benefit of random "mutations," which might be related to sudden breakthroughs, such as an unexpected "Eureka" moment. However, epigenetics relates precisely to those actions of the genome that can be changed without the long-term action of mutations and selection. Epigenetics deals with variations in what a genome can accomplish without actual changes in its DNA due to mutations, but as a result of the activities of complex networks of proteins that surround the un-mutated DNA and that regulate its behavior by activating its various genes in different combinations in response to intracellular and extracellular stimuli. In short, epigenetics is quite suitable to modeling "teamwork," rather than chance, but perhaps not so much for those brief "Eureka" moments or much longer time-scale evolutionary processes that require mutations of the DNA.

In epigenetics the DNA molecule and its immediate, protein-rich intracellular surroundings (called "cytokine") interact through a complex set of biochemical processes that have been treated mathematically using interacting networks (Liu et al., 2012). Here we use the broad mathematical definition of a network as a linked graph, a set of similar "nodes", which can represent virtually anything (e.g., team members in a training/educational environment, organizational units when looking at organizational performance or innovation), connected by "links," which signify interactions between the nodes (sociocultural, technical or both). Table 2 provides a generic example of team analogs of epigenetic modeling.

Table 2. Team Modeling Analogs – an Example

Model element	Team analogy
Cell/organism	The team, established & organized to pursue some objective
DNA/genes	The technical & sociocultural expertise, experience, attitudes, biases, etc., carried by each team member
Protein signaling networks	The technical & sociocultural pools of expertise available within the team to contribute explicitly to the team's objectives and activities, either by individuals or groups of like-minded team members (e.g., the team's 'experts' in a specific discipline, such as legal counsel).
Signaling proteins	Technical & sociocultural contributions expressed by team members to influence and drive team activities towards an end objective. to team activity, problem solving, etc.
Network	The set of team individuals (nodes) and their interaction links to other members. Taken together, makes up the structure of the team
Network nodes	Individual team members
Network links	Interactions between/among team members
Entropy	Measure of the number of interactions, or variations in interactions between/among nodes

These networks can include relations between the genes in the genome itself, as well as between the multitude of proteins within the surrounding cytokine that interact with those genes. Certain proteins activate, regulate and signal

different parts of the genome and trigger its responses to the effects of local cellular environment (i.e., temperature, pressure, chemical gradients, bio-chemical processes, etc.). Conditions within the cell can cause these networked processes to change and, when they do, the intra-cellular processes, induced by the activities of the networks and the DNA, will also change. In the following sections, we argue, metaphorically, that organizations/teams that support innovation and learning exhibit analogs of these networks. By identifying these analogs within a particular organization or team, we can (if we wish) isolate them, visualize their network structure, and address problems (pathologies) that are associated with them.

Epigenetic Analogs of Team Structure and Behavior

The set of all factors that can and do influence the functional relationship between the DNA molecule and its interacting networks of intra-cellular surroundings define possible states of the developing organism. Waddington imagined that these possible states could be considered as creating a quasi-continuum in the form of a two-dimensional surface, which he called the "epigenetic landscape" (Goldberg et al., 2007).

Waddington imagined this epigenetic landscape as being "tilted" and having progressively deepening and narrowing channels along which a developing organism was guided, as Figure 1 illustrates. He envisioned the process, metaphorically, as though a ball (the developing cell or organism) were rolling down the landscape, passing through its possible states, guided through the complex of channels under the action of a driving force like gravity.

The fate of a cell, its final differentiated form, depended upon the channel it happened to arrive at. Waddington had no hypothesis as to the nature of the guiding force that acted within the cell and played the role of gravity. There is still no universally agreed-upon hypothesis, so we take the position now being favored that the role of gravity is played by the entropy of the cellular network (Banerji et al., 2013), which can be thought of, in an oversimplified form, as the number of different configurations that the networks can have. The introduction of a fundamental role for entropy in epigenetic processes is important for our use of the model to describe team-based processes, since entropy can be correlated to multiple forms of variety, which is necessary for learning, invention, and innovation to occur. In the present model, the possible interactions between team members, or organizational units, will provide the variety. In a sense, it is not who is actually on the team that matters, it is the number of possible interactions between team members, and/or the structure of the organization within which the team functions. The idea is to obtain the best performance from a team that its members can produce. To generate epigenetic processes, the team needs the capacity to forge different interactions. Moskowitz (Moskowitz et al., 2015) suggests that the network structure's efficiency (team efficiency) is related to how well it can produce correlations between team members that are functioning independently.

Channel depth in the landscape plays an important role in stabilizing the development of an organism by ensuring that a few random mutations or pathological changes of the DNA or the networks of regulatory proteins would not cause the developing organism's structure to change radically. Actually, the channel does not "cause" the stability, it is a topological representation that the stability exists. In other words, once in a deepening channel, it would be difficult for the ball to roll up and over its surrounding walls and fall into a neighboring channel because the succession of states that the ball would have to pass through are biochemically difficult to achieve. Thus, the channel "provides" (actually, represents) direction, stability, and ultimate fate, all important factors in team-driven learning, problem-solving and innovation. A particular path taken by the ball as it rolls down the landscape is now termed a "developmental pathway". The actual biochemical mechanisms by which the pathway helps stabilize the organism's developmental process-flows, "homeorhesis", are to be interpreted as flow stability or process equilibrium. We shall suggest that some form of homeorhesis is required for maintaining team stability during a collaborative process, just as Waddington realized its consequences for organism stability during cellular differentiation. To be explicit, for teams, technical and social constraints are the analogs for the biochemical constraints that arise in cell development, as discussed below. Figure 2 provides a conceptual representation of the topology of a nominal team network. The upper and lower clusters represent two main sub-teams, with connections illustrating the possible technical and sociocultural connections among individual team members. Technical nodes are shown in red, sociocultural nodes in green. As among real teams and team members, some nodes are both technical and sociocultural connectors. Shown also are the varying numbers of connections each node has, representing possible pathways that promote team development. Links shown in yellow represent those nodes (connections among team members) that have significant impact on the entropy of the team as a whole. Actual modeling, a work in progress, is not part of this paper, but will be the subject of a next paper.

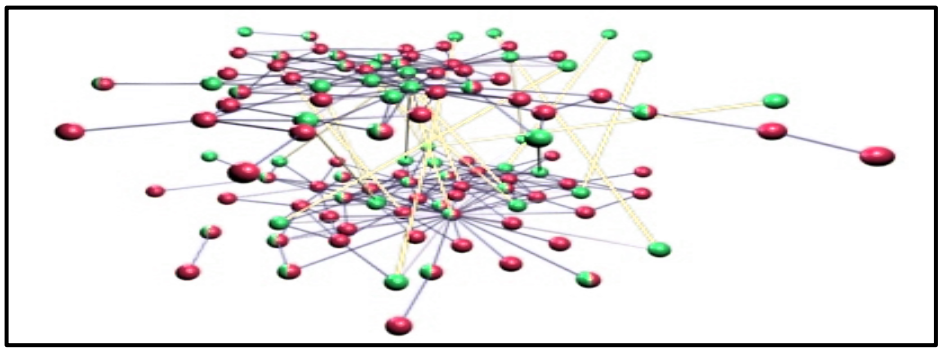

Figure 2. Illustration of team structure, showing technical (red) and sociocultural (green) nodes & links across a team consisting of 2 subteams

The Essence of Teamwork

Because channel formation in the epigenetic landscape helps to stabilize the organism against the effects of small perturbations or faults in the DNA or changes in the networks of its attendant proteins, it leads to what is called "cryptic genetic variation," which means that the cellular genome may include many cumulative factors that could potentially lead to variations in the organism, yet have not been expressed (i.e., they remained hidden, or "cryptic") because the particular pathway taken by the developing organism was defined by states that were stabilized against the expression of such individual variations. Although possible mutations of the cell were accumulating in the genome through small random variations in particular genes or gene clusters, or in defects in actions of the signaling proteins, combinations of other (non-pathological) genes and the activities of other signaling and regulating proteins could act in concert to "buffer" the genome and maintain the cell in a state of homeorhesis. Thus, a defective gene or protein could have its activities replaced by the concerted (i.e., networked) activities of other genes or proteins. The interconnected networks come to the collective rescue of "desired" cellular behavior by constructing an alternative path to achieve it. This is the essence of "teamwork". The same set of genes may act to achieve entirely different ends depending on the regulatory protein networks that are currently interacting with them.

STATISTICAL-THERMODYNAMICS MODELING VIEW OF GROUP PERFORMANCE

Entropy, Organizational Culture, and the Ergodic Hypothesis

In statistical thermodynamics, entropy is used as a measure of all possible system microstates (internal structure) that are consistent with its macrostate (external features). A fundamental hypothesis of statistical thermodynamics is the "equal *a priori* probabilities" of all microstates; every microstate that is consistent with the limitations of the macrostate has the same probability of making its appearance in a large ensemble of identical systems.

The principle of equal *a priori* probabilities can be violated if there is some underlying causal principle that forbids the appearance of some sets of microstates, even though they are in all other respects acceptable and consistent with their macrostates (Spielman, 2015). Such causal effects that forbid otherwise acceptable states from appearing are called constraints. Often constraints appear in the form of symmetries, which are typically geometric features of the underlying processes that cannot be violated. For example, the shape of the orbit of the moon about the earth could be anything, since the nature of space itself does not prevent movement in any direction. However, the geometrical nature of the Earth's gravitational attraction, which is spherically symmetric, limits the planar orbit of any isolated massive body about the Earth to be a conic section, which includes only hyperbolas, parabolas, ellipses, and circles.

In statistical thermodynamics, any initial distribution of molecular speeds in a closed container of identical gas molecules that is subjected to a fixed temperature environment is supposed to become "thermalized," and reach what is called a Maxwellian distribution of speeds that correspond to that temperature. If this does not occur, it may be supposed that some form of hidden symmetry or constraint prohibited that distribution of speeds from occurring. Suppose the gas molecules were in fact not identical, but were composed of two seemingly identical sets that differed in some way that prohibited one set of molecules from interacting with the other set. Then the resulting distribution might end

up as two independent, coexisting, but non-interacting Maxwellian distributions, each characterized by a different distribution of speeds but having the same temperature. This leads us to conclude that our reasonable expectations for the behavior of complex systems that are presumed to interact in some known way may not be met because some hidden symmetry or constraint prevents the interaction from occurring as expected. In human endeavors, we might hypothesize that cultural differences or social predilections, which are not necessarily openly expressed by the employees of an organization, might play the role of hidden constraints or symmetries that prevent the policies of the organization from being "thermalized" or distributed among the employees as would otherwise be expected.

As an example, when large numbers of industrial jobs were effectively sent overseas by the U.S. as part of globalization, it was expected that re-training would enable those displaced workers who lost their jobs to acquire new and higher-paying jobs so that the fruits of globalization would be distributed uniformly, in a sense "thermalized," with re-training playing the role of temperature. However, a host of "hidden constraints" – technical, educational, economic, and social - prevented this from happening, so that the distribution of wealth in the U.S. separated into several "Maxwellian" distributions, each characterized by a different income level, rather than a single one. Waddington's 'cryptic variations' may, in some sense, be maintained by hidden constraints within the cellular environment of the genome. These constraints may be a result of the workings of the protein networks. Similarly, in teams, cultural or other socially-driven differences can be manifest as either constraints, when they forbid some form of behavior, or as symmetries, when they render some seemingly diverse group "identical" in some way not otherwise obvious. These circumstances are neither good nor bad, they are simply part of the dynamics of a complex system that should be appreciated.

NETWORK ENTROPY ANALOGS OF TEAM/GROUP BEHAVIOR

Entropy in Scientific and Technological Innovation

To support (and validate) an epigenetic model of collaborative processes, we require organizational or team analogs of both DNA and the networks of "proteins" that signal, activate and regulate the DNA. Table 1 is a partial mapping of the analogies drawn in the current state of our research. In a previous effort to describe the behavior of teams of inventors working on a patentable invention (Tavel & Markovits, 2017), an "innovation genotype" was constructed. This is a visual representation of the set of all technical competencies (gene analogs) that appear in an intellectual property (IP) portfolio. Corresponding "innovation networks" were also constructed, networks whose nodes are patented inventions and whose links are the inventors that have collaborated in their creation. This can be interpreted as that part of the regulatory network that is responsible for producing the visible evidence of innovation (i.e., patents) in an explicit form. In epigenetic studies of cellular processes, the question of whether or not certain biochemical processes have occurred is often answered by the presence or absence of biochemical metabolites or proteins that the cell would produce. An analogy between proteins and patented inventions exists for organizations whose creative output can be measured by the production of explicit knowledge, such as patented inventions, presentations, or publications generated by its personnel. Patents are generally considered a good metric for innovation (Atun et al., 2007). This past research treated the set of U.S. Patent and Trademark Office (USPTO) class codes, which are the different technologies recognized by the USPTO that can characterize the patents of an organization, as identifiable gene markers, and hypothesized that there should also exist the equivalent of a network of signaling proteins that activate the knowledge represented by separate codes (actually, the inventors who contribute their competencies to the patented inventions) so that a new innovation or innovative element can emerge (be expressed).

The emergence of a recognizable innovation (or problem solution) by an organization (or a team within the organization) may be associated with the adoption of a set of its inventions. This can be inferred from an approach to stability of a corresponding set of patents (i.e., filing new patents as older ones expire), implying the guidance of a Waddington-like channel. Early stages of an emerging innovation (or outlines of a problem solution) may be ill-defined, as made evident by many different class codes in its innovation genotype, so that an emerging industry may appear more like a broadly applicable and adaptive technology. This is a high entropy condition that might be called "technological promiscuity", since the term "promiscuity" in epigenetics refers to a cell that still has many options (channels available) because its entropy has not been depleted. The promiscuous technology will diffuse through different areas within organizations along shallow channels, allowing it to be easily adapted within the organization. Emerging industries, like Modeling and Simulation (M&S), often first appear as new technologies within individual companies or industries where they are applied as needed and developed by separate teams or task forces within those companies/industries.

As the strength of these identifiable techniques becomes recognized and made more broadly available through patents, journal articles, conferences, and even social media, separate companies (deep channels) may appear to provide these same services in a more differentiated fashion (low entropy states corresponding to fewer class codes in the patents). It should be noted, however, that the emergence of a new industry may signal a level of stability that is disadvantageous to the further development of the technology if it constrains the technology to remain within, for example, the applicable software provided by particular companies within the new industry.

The "signaling proteins" that enable small subsectors of technology to "merge" or act synergistically and lower their collective entropy include all the previous modes of explicit knowledge transfer such as patents, journal articles, delivered papers, and conference attendance/socialization. These modes operate both within and between industries/companies and between technical personnel and teams within an organization and within individuals themselves. Particular technologies may still maintain their original identities, and particular personnel may be retained and continue to contribute their competencies, but their areas of influence are enlarged by their applicability to a wider range of problems, and they may well require that new competencies form to support them in eco-system fashion. For example, the ability of biotechnology companies to develop innovative drugs (as opposed to combinations of pre-existing drugs) that target specific genetic defects requires the existence of other companies (a supportive eco-system) that can model molecular structure "in silico" and still other companies that can decode the genome and locate/edit the relevant genes. Once differentiated by deeper channels, these competencies are provided by their own industries, whereas they may have all been originally disseminated within a single company. We have seen this kind of differentiation in a genotype for Modeling and Simulation when studying genotypes in different U.S. states. For example, the M&S genotype in Michigan includes "genes" for the application of M&S to evaluating crashworthiness of vehicles. In a sense, a new channel has emerged that is fed by the entropy in the networks that transfer knowledge and skills within and between organizations. We consider this process a form of "speciation" where M&S develops as a range of species depending on the industries that use it. There is an almost viral aspect to M&S in that it "invades" an industry and harnesses the other technologies in it to expand its usefulness.

The Role of Entropy in Team Modeling

In Waddington's view, the topography of the epigenetic landscape, characterized by its tilt and channels, was the visualization of complex chemical signaling and regulating processes involving the intra-cellular proteins and the DNA they interact with. It is to be remembered that the detailed biochemical processes that occur within a developing organism have only metaphorical analogs within a team. Whereas specific proteins might bind to a gene in the DNA and thereby regulate its activity, we might envision scientists or engineers with different areas of technical competence providing support (binding) to each other when some particular intransigent problem needed a solution or a "workaround".

Recently there have been attempts to characterize ensembles of cells based on particular processes whose genome signaling network is known, by arranging them by networks and assigning to the networks a form of "entropy," which is a measure of statistical variety in an ensemble (West et al., 2012; Banerji et al., 2013). In this approach there is no causally predictable behavior of a single cell, rather it is the statistical behavior of an ensemble of cells that is determined. This entropic/statistical analysis, which requires detailed biochemical knowledge of the interactions between proteins and DNA within those cells, suggests that cells such as stem cells and certain cancer cells, that are initially undifferentiated with many options for future development of possible signaling pathways (a condition called "pluripotency"), have a high network entropy and sit in a broad shallow channel, whereas cells that have already been differentiated (e.g., have become nerve cells, blood cells, or skin cells) have a lower network entropy and sit in a narrow, deeper channel. Methods have been described in the literature for calculating the entropy changes in such processes (West et al., 2012), which would be related to the average rate at which information in signal flow over the network is degraded or rendered uncertain by loss of network structure. Thus, when an undifferentiated cell (or an ensemble of such cells) with high network entropy becomes differentiated, leading to an ensemble with lower network entropy and lower probability of meaningful new developments, the entropy loss can be ascribed to the activation of many different signaling pathways which then are no longer available and are lost to future interactions. A particularly illustrative example of this approach (West et al., 2012) describes research in which differential network entropy analysis was applied to reveal cancer system hallmarks, demonstrating association of cancer cell networks with high entropy.

The activation of these pathways implies a loss of uncertainty, given the smaller number of pathways that remain and can still be activated. Thus, a loss of entropy by the ensemble describing the entire network-based system occurs. In the team-driven processes of invention or innovation, each step taken by the team along a particular direction may lead to the impossibility (or extreme difficulty) of retracement and/or the investigation of alternative steps that might have been taken (Takahashi, 2012). In our modeling, this is a depletion of useful entropy. This is the conundrum of grasping for "low hanging fruit," or the basis of the class of what are called "greedy algorithms" that are used to search for optimal solutions of certain types of equations, but get trapped by poorer solutions or "local minima". Kirkpatrick (Kirkpatrick et al., 1983) developed a search algorithm called "simulated annealing" which sought to discover optimal solutions to certain combinatorial problems by randomly generating sequences of possible solutions, typically accepting those that were improvements but, with a certain probability, also accepting solutions that were poorer. The poorer solutions were used as seeds for a new series of solutions and so on. The application of such an approach within the context of the epigenetic model, might provide a virtual mechanism (i.e., a simulation) to move a developing cell out of its channel by effectively giving it a booster-shot of entropy. We will propose a game-based methodology that might perform a similar task for innovating teams.

Entropy Flow Analogs in Team Processes

It has been suggested that intracellular network entropy flows are related to the tilt of Waddington's epigenetic landscape (Balter, 2015; Liu et al., 2012, Takahashi, 2012). Loss of entropy is associated with loss of height, motion down the sloping landscape, and the ultimate capture by a deep channel. This is analogous to a loss of gravitational potential energy when a real boulder rolls, or water flows, down a hillside. We might say that network entropy is to network-based epigenetic processes what potential energy is to dynamic or mechanistic processes. When a cell is relatively undifferentiated (as is a stem cell) but is developing towards a possible differentiated form (e.g., as a blood cell), many signaling pathways are available and the cell's fate is uncertain. Such a "promiscuous" cell has high entropy as measured by the availability of signaling pathways. As the cell moves towards low entropy as a result of network-based protein/genome signaling and activation interactions that lead to the loss of potentially active proteins (recall that these interactions may result from a protein bonding to a DNA site and being lost to further activity), there is a corresponding loss of future options. The channel becomes deeper and narrower, and (metaphorically) the cell finds it increasingly difficult to rise out of the channel to sample other channels, so it becomes correspondingly increasingly stable. It must be remembered that "signaling" by a protein is a biochemical process that typically requires chemical bonding of the protein to a site in the DNA. Thus, the protein is effectively removed from its network, and the entropy of the network system is reduced. However, the cell may still harbor "cryptic" variations waiting for the proper perturbation or local environmental change for them to be expressed. Perhaps such variations will be capable of expression in future generations of the same cell's development, if those generations exist in a different environment.

MODELING GROUP BEHAVIOR

"Entropy-Driven" Team Behaviors and Processes

Within the cell, several types of networks active in epigenetic processes have been identified and characterized. For example, in the cell, different genes in the genome must be instructed when to "do their thing" so to speak. Most genes do not act as individuals, but act in concert with other genes that may have different locations on the genome. To initiate some concerted gene activity, proteins present in the cell send signals to the involved genes by combining with them chemically through chemical bonds. When a protein bonds with a gene, it may stimulate the gene to perform some biochemical action or it may inhibit the gene from performing some action. The result of the protein-instigated gene activity leads to the "expression" of certain additional proteins that are necessary for further gene activity in the cell to occur and, in particular, for the cell to continue along certain developmental lines. The expressed proteins govern the metabolic components of the gene activity and give evidence that the activity has occurred. If the metabolites are not found, it may be inferred that the activity did not occur. We discussed above a particular genomic analogy that we call the "innovation genotype". This structure is characterized by the aggregate of technical specialties expressed by an organization through its intellectual property (IP) portfolio, i.e., its patents. For organizations that measure innovation with patenting, this structure provides a meaningful analog to that portion of a genome that relates to the construction, storage, and use of knowledge.

Injecting "Entropy" into a Team or Organization

One way of testing the epigenetic model of team-driven innovation is to investigate its implications for releasing a mature, already differentiated organization or team from a deep, low entropy channel (a rut) that may have stifled creativity or contributed to an unhealthy or inappropriate culture. A possible method of doing this is by injecting positive entropy into the team (or corporate network), thereby simulating the tilting of Waddington's landscape and introducing the possibility of the team retracing its steps. The network entropy expresses the combination of diversity of organizational genetic structure (pluripotency) and the possibilities of the various signaling and activation proteins (promiscuity). Enhancing network activity properly can produce a genetic expression of traits, possibly exposing cryptic variations and enabling their expression, that would be favorable to the success of the team as an organism and could cause (or allow) switching between different channels and help discover an optimal channel. Certainly, one way of increasing entropy is by insertion of new genes (individual expertise, or, for an organization, a unit's new policy or rules, or an added unit) or by inducing mutations of already present genes. This might be done by "inserting" subject-matter experts, or additional organizational units, as consultants (analogous to gene editing) rather than by creating a complete sub-organization (adding a gene or group of genes, effectively creating recombinant DNA). We will, instead, inject entropy in the spirit of epigenetics by modifying the protein signaling mechanisms already within the organization. Injection of entropy in this way could be accomplished "virtually" by establishing a gaming environment that simulates a protein interaction network.

Injecting "Entropy" Through Gaming

If, for the sake of argument, we consider different structural components of the organization (e.g., divisions, groups, etc.) that are responsible for its activities as the analogs of gene/protein networks, then the injection of entropy could be accomplished by the addition of a protein-like signaling or regulating mechanism that would couple presently uncoupled genes. Entropy, in the form of network structure, would reside in this new mechanism and could then be dissipated as the mechanism interacted with the genetic material. Stated differently, this is the equivalent of getting different parts – units – of the organization to work together more effectively, each still using their present skills, or, alternatively to do work on their own, but using a different methodology introduced to them by the disconnected "genes', e.g., different personnel in different divisions. Note that this approach can work for both "social entropy", where problems are arising because of poor social "chemistry", and "technical entropy," where problems arise as a result of poor skill-set matches. Organisms are often resilient because of their ability to substitute different regulatory proteins or different genes to recover the activities that other genes and proteins fail to supply as a result of some defect or pathology. For organizations, by equipping them to use different activity pathways, or to re-wire network "nodes and links" to accomplish what others were meant to do, we increase their resilience.

It is our contention that this can be done virtually, through game-playing. For example, suppose gene "a", representing an organizational component (a divisional activity or personnel competency) that "expresses" a method of solving problem set P_a (i.e., that solves a particular set of problems in its own particular way), is told to present one of its problems, p_a, to gene "b", an organizational component that is presently working within the domain of problem set P_b. Gene "b" is then challenged to solve problem p_a using its "b" methodology, which may be completely unrelated to problems in the P_a problem set. Thus, the problem itself, by its game-implemented passage between genes "a" and "b", serves as a signaling protein to activate gene "b" to express a solution to a problem normally solved by gene "a". This cross-expression represents "mixing entropy" (the addition of new elements into a previous mixture) added to the system, because the system now has the potential for performing a new set of operations, which would not have been considered in the absence of this "game." Thus, gene "b", using its own methodology, is now "working" on a problem typically relegated to gene "a". It doesn't matter if the "a" and "b" genes are totally different (e.g., hull design and turbine design in a naval lab), what is important is the cross-fertilization of ideas and the subsequent increase of network entropy by a virtual re-wiring process. In a certain sense, this is the virtualization of sending individual people to conferences, but now it is "sending" one gene to another via a signaling protein (the "protein" being the problem itself). This generates a challenge unlike that found at a conference, which is much more of a passive environment and, therefore, carries less mixing entropy.

Further, this kind of entropy injecting could be carried out entirely within a game-playing environment, where the game players (representing the organizational genes) are presented with a challenge through the game structure. So, as the game is played, the "simulated" epigenetic processes are creating increased entropy, which, by analogy, is tilting the epigenetic landscape so that new channels become available, thereby effectively lowering the barriers to channel switching. Note, the game mechanism itself is losing entropy (as it plays itself out) while the players, considered as

part of a global network, are gaining entropy by acquiring new possibilities created by the game. There are games that could be structured to perform this type of process. An example is "MMOWGLI" (Massively Multiplayer Online War Game Leveraging the Internet), a game developed by the US Navy for problem solving exercises.

CONCLUSION

Powerful new methods for simulation are being driven by advances in computation. However, this shouldn't let us lose sight of the importance of developing new models as well. The modeling approach presented in this paper adapts two successful models, one new (epigenetics) and one old (statistical mechanics), to model group performance, at either the team or organizational level. We treat either as a living organism, making use of the fact that ultimately all living systems must obey the laws of physics and biology. The innovation presented is to also incorporate analogs of team and organizational entropy to the modeling of learning and training modalities used to drive performance.

Although it is tempting to suggest that a poorly functioning team or organization may be running out of energy, it is argued here that it is more likely running out of entropy. Focusing on team aspects of entropy, in either its Shannon form as information or reduction of uncertainty, or in its statistical thermodynamic form, as variety, enables modeling and visualization to see how to re-invigorate team behavior and performance by forming new links and emphasizing team topology.

Waddington's epigenetic landscape is employed as a non-computational way of visualizing team development, providing a schema to model a team and make use of the concepts presented to see how changes in team structure and team interactions can affect a team's development. The game-play example illustrates a possible process for modeling and analyzing aspects of team interactions, and for investigating effects of changes to team composition, individual skills, and/or injection of new knowledge or technology. It is our intention to extend this research to produce computational models embodying the entropy, epigenetics, and adaptations of statistical mechanics concepts introduced here.

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REFERENCES

Atun, R.A., Harvey, I., & Wild, J. (2007). Innovation, Patents and Economic Growth. *International Journal of Innovation Management*, *vol. 11, No. 2*, pp. 279-297.

Balter, M. (2015). Can epigenetics explain homosexuality puzzle?. *Science*, *vol. 350, Issue 6257*, pp. 148.

Banerji, C., Miranda-Saavedra, D., Severini, S., Widschwendter, M., Enver, T., Zhou, J., & Teschendorff, A. (2013). Cellular network entropy as the energy potential in Waddington's differentiation landscape. *Science Reports*, *vol. 3*. 3039 DOI: 10.1038/srep03039

Colautti, R., Eckert, C., & Barrett, S. (2010). Evolutionary constraints on adaptive evolution during range expansion in an invasive plant. 277. *Proceedings of the Royal Society B*. https://doi.org/10.1098/rspb.2009.2231

Easley, D., & Kleinberg, J. (2010). *Networks Crowds and Markets*: *Reasoning aboit a Highly Connected World.* Cambridge University Press.

Fang, X., Kruse, K., Lu, T., & Wang, J. (2019). Nonequilibrium physics in biology. *Reviews of Modern Physics*, *Vol. 91*, No. 4, Oct.-Dec. 2019, p. 045004.

Gilbert, S. F. (2000). Diachronic Biology Meets Evo-Devo: C. H. Waddington's Approach to Evolutionary Developmental Biology. *American Zoology., 40:729-737*.

Goldberg, A. D., Allis, C.D., & Bernstein, E. (2007). Epigenetics: A Landscape Takes Shape. Elsevier Inc. *Cell* 128, p. 635.

Gomulkiewicz, R., & Houle D. (2009). Demographic and Genetic Constraints on Evolution. *The American Naturalist*, *Vol. 194*, no. 6, December 2009. pp. e219-e229.

Kirk, P. D. W., Babtie, A.C., & Stumpf, M. P. H. (2015). Systems biology (un)certainties. *Science, vol. 350,* pp. 386-388.

Kirkpatrick, S., Gelatt Jr., C.D., & Vecchi, M.P. (1983). Optimization by Simulated Annealing. *Science*, *vol. 220, no. 4598*, pp. 671-680.

Liu, Z.P., Wang, Y., Zhang, X.S., & Chen, L. (2012). Network-based analysis of complex diseases. *The Institute of Engineering and Technology (IET) Systems. Biology., vol. 6, Issue. 1,* pp. 22-33. Available via www.ietdl.org.

Moskowitz, I. S., Lawless, W., Hyden, P., & Mittu, R. (2015). A Network Science Approach to Entropy and Training. *2015 AAAI Spring Symposium,* pp. 44-51.

Nobel, D. (2015). Conrad Waddington and the origin of epigenetics. *Journal of Experimental Biology*, *vol.218,* pp. 816-818.

Spielman, I. B. (2015). Assembling a complex quantum ensemble. *Science, vol. 348, Issue 6231,* pp. 185-186.

Takahashi, K, (2012). Cellular reprogramming-lowering gravity on Waddington's epigenetic landscape. *Journal of Cell Science* 125, pp. 2553-2560 DOI: 10.1242/jcs.084822

Tavel, M. & D. Markovits. (2017). A Genetic Model of the Development of Modeling & Simulation. *Proceedings of the 2017 Interservice/Industry Simulation & Education Conference (I/ITSEC), December 2017*.

Waddington, C. H. (1957). *The Strategy of the Genes; a Discussion of Some Aspects of Theoretical Biology*. Allen and Unwin, London.

West, J., Bianconi, G, Severini, S., & Teschendorff, A. (2012). Differential network entropy reveals cancer system hallmarks. *Scientific Reports 2, 802.* https://doi.org/10.1038/srep00802