# Networked buffering: a basic mechanism for distributed robustness in complex adaptive systems

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### 1. Abstract

This paper proposes a generic design principle for generating robust traits in complex systems that requires two basic conditions to be satisfied: 1) agents are versatile enough to perform more than one single functional role within a system and 2) agents are degenerate, i.e. there exists a partial overlap in the functional capabilities of agents. Our principle claim is formulated within the so-called *networked buffering hypothesis*. It outlines how degenerate systems may readily produce a distributed response to local perturbations and reciprocally how excess resources related to a single function can indirectly support multiple unrelated functions within a degenerate system. The conditions needed to achieve this buffering behavior are not demanding or rare, leading us to speculate that degeneracy may fundamentally underpin the distributed robustness that is prevalent within biological systems. We further argue that degenerate forms of distributed robustness may readily arise in other disciplines. For instance, it may allow for new insights into engineering design and strategic planning activities that occur under high uncertainty. We also speculate that the proposed hypothesis may explain recent breakthroughs in understanding the origins of resilience within complex ecosystems.

#### 2. Introduction

Robustness reflects an insensitivity in some functionality or measured state of a system to exposure to a variety of external environments or internal conditions. Robustness is observed whenever there exists a sufficient repertoire of actions to counter perturbations (requisite variety, [1]) and when a system "knows" what actions to take for each situation (requisite knowledge, [2]). In many complex adaptive systems (CAS), the actions of agents that make up the system are entirely based on interactions with their local environment, making these two requirements for robust behavior interrelated. When robustness is observed in such CAS, we generally refer to the system as being self-organized, i.e. stable properties spontaneously emerge *sans* centralized routines for matching actions and circumstances.

Many mechanisms that lead to robust properties have been distilled from the myriad contexts in which CAS, and particularly biological systems, are studied. For instance, robustness can form from loosely coupled feedback motifs in gene regulatory networks, from saturation effects that occur at high levels of flux in metabolic reactions, from spatial and temporal modularity in protein folding, from the functional redundancy in genes and metabolic pathways [3] [4], and from the stochasticity of dynamics occurring during multi-cellular development or within a single cell's interactome.

Although the mechanisms that lead to robustness are many and diverse, subtle commonalities can be found. Practically all mechanisms respond to perturbations through local interactions involving cooperation and competition amongst both similar as well as dissimilar components. The actions are rarely deterministically bijective (i.e. characterized by a 1:1 mapping between perturbation and response) and instead proceed through a concurrent stochastic process that in some circumstances is described as exploratory behavior [5].

This paper presents what is argued to be a new basic mechanism for achieving robustness. It arises in systems comprising degenerate agents and it is believed to be intimately related to several of the mechanisms just described.

### 3. Robustness through Diversity and Degeneracy

Degeneracy refers to conditions where there is a partial overlap in the functionalities of agents in a system. This means there are conditions where agents may by compensatory or functionally interchangeable. However, there are also

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<sup>&</sup>lt;sup>1</sup> Stochasticity enhances robustness but is not technically a mechanism for achieving it. Over time, stochasticity forces the states and structures of a system towards paths that are less sensitive to natural fluctuations and this provides "robustness for free" to any other congruent perturbations that were not previously observed.

conditions where the same agents are neither. Although degeneracy has at times been described as partial redundancy, these terms are often used with different meanings as is explained in Box 2.

On the surface, having similarities in the functions of agents provides robustness through a process that is intuitive and simple to understand. In particular, if there are many agents in a system that perform a particular service then the loss of one agent can be compensated for by others. The advantage of having diversity amongst functionally similar agents (i.e. only a partial structural and functional similarity) is also straightforward to see. If agents are somewhat different, they can exhibit different vulnerabilities: a perturbation or attack on the system is less likely to present a risk to all agents at once. This reasoning reflects common perceptions about the value of diversity in many contexts where CAS are found. For instance, it is analogous to what is described as response diversity in ecosystems [6] and it is conceptually similar to the advantages from ensemble approaches in machine learning or the use of diverse problem solvers in decision making [7]. In short, diversity is commonly viewed as advantageous because it can help a system to consistently reach and sustain desirable settings for a single system property by providing multiple distinct paths to a particular state. In accordance with this thinking, examples from many biological contexts have been given that illustrate degeneracy's positive influence on the stability of a single trait (e.g. see Box 1). Although this view of diversity is conceptually and practically useful in some circumstances, it is also simplistic and we believe insufficient for understanding how common types of diversity such as degeneracy can influence robustness.

CAS are typically made up of agents that influence the stability of more than just a single trait due to agents having a repertoire of distinct functional capabilities. For instance, gene products act as versatile building blocks that form complexes with many distinct targets. These complexes often have unique and non-trivial consequences inside or outside the cell. In the immune system, any single antigen receptor can bind with (i.e. recognize) many different ligands with different consequences for immune response. In gene regulation, each transcription factor can influence the expression of several different genes with distinct phenotypic effects. Within an entirely different domain, people in organizations are also versatile in the sense that they can take on distinct roles depending on who they are collaborating with and the current challenges confronting their group. More generally, the function an agent performs typically depends on the context in which it finds itself. By context, we are referring to the internal states of an agent and the demands or constraints placed on the agent by its environment. As illustrated further in Box 1, this contextual nature of an agent's function is a common feature of many biotic and abiotic systems and it is referred to hereafter as *functional plasticity*.

Because agents are generally limited in the number of functions they are able to perform over a period of time, tradeoffs naturally arise in the functions an agent performs in practice. These tradeoffs represent one of several causes of trait interdependence and they obscure the process by which diverse agents influence the stability of single traits. A second complicating factor is the ubiquitous presence of degeneracy. While one of an agent's functions may overlap with a particular set of agents in the system, another of its functions may overlap with an entirely distinct set of agents. Thus functionally related agents can have additional compensatory effects that are differentially related to other agents in the system. The resulting web of conditionally related compensatory effects further complicates the ways in which diverse agents contribute to the stability of individual traits with subsequent effects on overall system robustness.

### 4. The Networked Buffering Hypothesis

One aim of this paper is to show that when degeneracy and functional plasticity are present, narrowly focusing on the robustness of a single trait causes us to miss more systemic buffering that can emerge when the compensatory effects of degenerate agents are realized over many iterations of conditionally-activated interactions. We organize these arguments around what is referred to as the *networked buffering hypothesis* (NBH). The central tenets of our hypothesis are conceptually simple enough to explain using the diagrams in Figure 1.

First, consider a system comprised of a set of multi-functional agents. Each agent performs a finite number of tasks where the types of tasks performed are constrained by an agent's capabilities and the availability of tasks. In the diagrams in Figure 1, each agent is depicted by a pair of connected nodes. These node pairs represent two distinct tasks that an agent can perform. Nodes have also been grouped into clusters to indicate functional similarity. For instance, agents with nodes occupying the same cluster are said to be similar with respect to that task type. To be clear, task similarity implies that either agent can adequately perform a task of that type making them roughly interchangeable with respect to that task. In Figure 1d, we show what we call 'pure redundancy' or simply 'redundancy': similar agents are always functionally identical across all task types. In all other panels of Figure 1, similarities between agents only arise in a single task type meaning these agents have a partial similarity or 'degeneracy'.

Important differences in both the scale and the mechanisms for achieving robustness can be expected between the degenerate and redundant system classes. In Figure 1b, if more (agent) resources are needed in the bottom task group and excess resources are available in the top task group, then degeneracy between agents can allow agent resources to be reallocated from tasks where they are in excess to tasks where they are needed. This occurs through a sequence of context-

driven role reassignments as implied by the large arrows in the diagram – a process that is autonomous so long as agents are driven to complete unfulfilled tasks matching their functional repertoire.

This illustrates a basic process by which resources related to one type of function can support unrelated functions and it is a common feature of the systems listed in Table 1. In fact, conditional interoperability is so common within some domains that many domain experts would view this as an entirely unremarkable feature. What is not commonly appreciated however is that the number of distinct paths by which reallocation of resources is possible can potentially be enormous in highly degenerate systems, depending on where resources are needed and where they are in excess (see additional arrows in Figure 1c). Conversely, this also implies that it is theoretically possible for excess agent resources related to one task to indirectly support a number of other tasks, thereby increasing the effective versatility of any single buffer (seen if we reversed the flow of arrows in Figure 1c). Moreover, because buffers in a degenerate system are partially related, the stability of any trait is potentially the result of a distributed response within the system. For instance, resource availability can arise through an aggregated response from several of the paths in Figure 1c. In short, excess resources related to a single function can be used in a highly versatile manner. Although interoperability of agents may be localized, at the system level extra resources can offer huge reconfiguration opportunities.

These basic attributes are not feasible in systems composed of purely redundant agents (Figure 1d). Without a partial overlap in capabilities, agents in the same functional groups can only support each other and, conversely, excess resources cannot support unrelated tasks outside the group. Buffers are thus localized. In the particular example illustrated in Figure 1d, agent resources are always tied to one of two types of tasks. Although this ensures certain levels of resources will always remain available within a given group, it also means they are far less likely to be utilized when resource requirements vary, thereby reducing resource efficiency. In other words, resource buffers in purely redundant systems are isolated from each other, limiting how versatile the system can be in reconfiguring these resources. In fact, every type of variability in task requirements needs a matching realization of redundancies. If broad reconfigurations are required (e.g. due to a volatile environment) then these limitations will adversely affect system robustness. Although such statements are not surprising and follow directly from the diagrams in Figure 1, they are not trivial either because the sum of agent capabilities within the redundant and degenerate systems are identical.

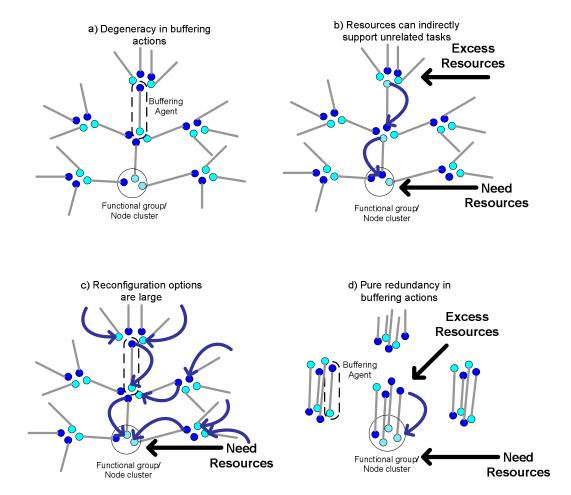


Figure 1: Conceptual models of a buffering network. a) Degeneracy in multi-functional agents; b) pathway for reconfiguring resources; c) reconfiguration options are potentially large; and, d) redundant system buffers cannot support broad resource reconfiguration options.

### 5. Evidence in Support of NBH

There is a long-standing interest in the origins of robustness and resilience within CAS in general and biological systems in particular. Although considerable progress has been made in understanding constraint/deconstraint processes in biology [5], a full account of biological robustness remains elusive. The extent to which degeneracy can fill this knowledge gap is unknown, however we outline several reasons why degeneracy might play a vital role in facilitating biological robustness.

#### The omnipresence of degeneracy in biological CAS

Stability under variable conditions is a defining attribute of biology at all scales. Any mechanism that broadly contributes to such stability must be as ubiquitous as the robust traits it accounts for. Although many mechanisms studied in the literature (such as those mentioned in the Introduction) are broadly observed, few are as pervasive as degeneracy. In fact, degeneracy is readily seen throughout molecular, genetic, and cellular levels in biology [4]. As argued in Box 1, it is readily observed in other CAS including human organizations, human-engineered systems, and ecosystems.

If degeneracy broadly accounts for biological robustness then it should be intimately related to many mechanisms discussed in the literature. One prominent example where this occurs is the relationship between degeneracy and feedback regulation. For example, regulation in metabolic reactions and gene expression involves control over the sequences of interactions that occur in the 'omic' network. This control is mostly enacted by a process of competitive exclusion within the first interaction step in a pathway (e.g. first metabolite in a reaction pathway or the initial binding of RNA polymerase prior to gene transcription). Except in the case where competition occurs amongst identical molecules, this inhibition-based regulatory process is only possible due to degeneracy in the affinity of molecular species. Even autoregulation requires the existence of degeneracy between reactants and products.

If degeneracy were absent then the regulatory processes in biology would become highly fragile to genetic and environmental perturbations. In particular, only one type of molecular species could be responsible for each type of control action, and the removal of that species could not be directly compensated for by others. Under these conditions, change in function mutations to non-redundant protein-coding genes would likely result in changes to one or more traits. In other words, mutational robustness would be greatly reduced and cryptic genetic variation would not be observed in natural populations.

#### Degenerate robustness through local and distributed responses

More than half of all mutational robustness in genes is believed to be the result of distributed actions and not genetic redundancy [8]. Although a similar analysis of the origins of robustness has not taken place for other biological contexts, there is plenty of anecdotal evidence to support the claim that both local functional redundancy and distributed forms of robustness are prevalent in biology.

Degeneracy may play a prominent role in both sources of robustness. Prior studies have already presented considerable evidence of degeneracy's positive influence on single trait stability through localized compensatory effects, or what is more often described as functional redundancy [4]. On the other hand, our principle claim in this paper is that degeneracy can also contribute to systemic forms of robustness through distributed compensatory actions.

To evaluate these claims, we investigate the sources of robustness (localized and distributed) in degenerate models of genome:proteome (G:P) mappings that were previously studied in [9]. In the previous study (Figure 2a), degenerate systems were found to be more robust than purely redundant ones, with the difference becoming larger between the system classes as they were subjected to increasingly larger perturbations, i.e. loss of function mutations. The same study also measured the number of distinct null mutation combinations under which a system could remain viable (defined in that study as *versatility*) and found that degenerate systems were also more robust with respect to this measurement. Importantly, this robustness improvement became more pronounced as the size of the systems increased (Figure 2b). With the sum of functional capabilities kept identical between the degenerate and redundant system classes, it follows that the observed differences in robustness were a consequence of different organizational properties of the gene products.

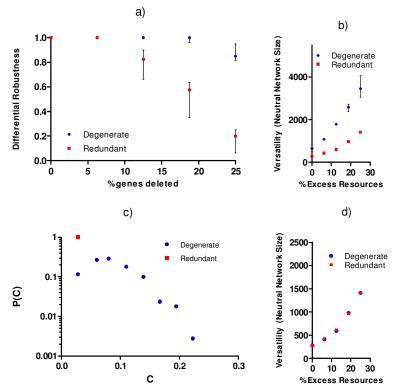


Figure 2: Local and distributed sources of robustness in redundant and degenerate genome:proteome models. a) Differential robustness is measured as the proportion of (mutated) conditions where the system phenotype remains unchanged versus number of null mutations. b) Versatility-robustness is measured as the number of null mutation combinations ("neutral network size") where the phenotype remains unchanged for different levels of initial excess gene product resources, i.e. different system sizes. Results shown in panels a-b are taken from [9]. c) Frequency distribution (of panel b experiments with %excess resources = 0) for the number of distinct gene products that change their function. d) Versatility results when gene products can only change their functional contribution immediately after a perturbation.

Here, we show that this enhanced robustness originates from distributed compensatory effects in the degenerate systems. First, in Figure 2d we repeat the experiments used to derive the results in Figure 2b, except in this case each system only responds to perturbations through local actions. More precisely, only genes that share some functional similarity to the mutated gene are permitted to change and thus participate in the system's response to that mutation. Changes to genes (state changes) are reflected by the time spent in interactions between gene products and target ligands. By adding this constraint to the simulation, it eliminates any possibility that distributed compensatory pathways can be active in either system (see [9] for experiment details).

The robustness of the purely redundant systems is found to remain unchanged compared with the results in Figure 2b while the robustness of degenerate systems degraded to values that are undistinguishable from the redundant system results. Comparing the two sets of experiments, we find that roughly half of the total robustness that is observable in the degenerate genome:proteome models in [9] originates from non-local actions.

As further evidence of distributed robustness in degenerate G:P mappings, we use the same conditions as in Figure 2b except now we systematically introduce single loss of function mutations and record the number of distinct gene products that change state. In the probability distributions in Figure 2c, the redundant systems display localized responses as expected while the degenerate systems respond to a disturbance with both small and large numbers of distinct gene products.

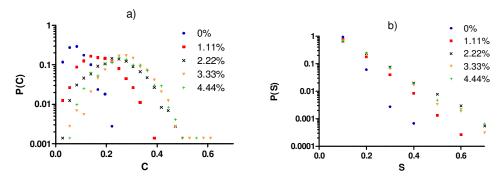


Figure 3 Probability distributions for a) the proportion of distinct gene products that that change state (C) and b) the magnitude of change in gene products (S). Experiments are shown for degenerate G:P mappings using the same conditions as in Figure 2b, but with the following modifications: 1) perturbations to the system are of single null mutations only and 2) systems are initialized with different amounts of excess resources (% excess indicated by data set label).

As small amounts of excess resources are added to degenerate systems (Figure 3a), single null mutations tend to invoke responses in a larger number of distinct gene products while robustly maintaining system traits, i.e. system responses become more distributed while remaining phenotypically cryptic. In measuring the magnitude of state changes for individual gene products, we find the vast majority of changes occurring are consistently small across experiments, although larger state changes become increasingly likely when excess resources are introduced (Figure 3b). The effect from adding excess resources saturates quickly and shows little additional influence on system properties (C and S) for excess resources > 2%.

Individually varying other parameters of the model such as the maximum rate of gene expression [2, 30], the size of the genetic system [10, 100], or the level of gene multi-functionality [2, 4] did not alter the basic findings reported here. Thus for the degenerate G:P mappings studied in [9], we find that distributed responses play an important role in conferring mutational robustness towards single null mutations. Although experimental conditions differ in some respects from the analysis of single gene knockouts in *S. cerevisiae* [8], both studies find evidence that the mutational robustness of genetic systems is predominantly a consequence of distributed effects. Here we have further shown that this distributed robustness is facilitated by the presence of degeneracy.

### 6. Discussion

The redundancy model in Figure 1 reflects a logical decomposition of structure that is encouraged in most human planning/design activities. While there are many circumstances where redundancy is beneficial, there are others where we now anticipate it will be detrimental. Redundancy can afford economies of scale and provide transparency, which can allow a system to be more amenable to manipulation by boundedly rational managers. When systems or subsystems operate within a well-controlled and predictable environment with few degrees of freedom, redundancy/decomposition design principles are known to be efficient AND effective. However, when variability in conditions is large or when conditions can change unexpectedly, pure redundancy will not provide a system with the flexibility needed to adapt and prevent system failure. We propose that under these circumstances, degeneracy design principles could be vital to achieving robustness.

The potential significance of this conclusion is underscored by the scope of problems where robustness in a volatile environment is important. Indeed, such problems are embedded within some of the most pressing social, ecological, and economic challenges facing our world. For instance, in a world of broad international alliances, it is important to develop collaborative security networks that are versatile enough to deal with future unanticipated threats. Within increasingly volatile markets, particularly those sensitive to technological innovation, an organization's survival depends on its ability to rapidly adapt in response to new unexpected opportunities.

In a world experiencing unprecedented environmental regime shifts brought about due to changes in our global climate, it is vital to understand what enables ecosystems to be resilient. Ecology theory and decades of simulation experiments have concluded that increasing complexity (increasing number of species, number of species interactions) should destabilize an ecosystem, while empirical evidence suggests complexity and robustness are positively correlated. In an important breakthrough study, Kondoh [10] has demonstrated that this paradox is resolved in models when two general conditions are observed: i) species are functionally plastic in resource consumption; what is referred to in the study as adaptive foraging and ii) potential connectivity in the food web is high. However, because higher connectivity also increases the number of pairs of degenerate species, these findings indirectly suggest that degeneracy and functional plasticity facilitate robustness in complex ecosystems. Despite rich domain differences, we contend there are fundamental similarities in how the organizational properties of CAS can facilitate flexibility and resilience within a volatile environment.

### 7. Conclusions

This paper introduces what is argued to be a new mechanism for generating robustness in complex adaptive systems that arises due to a partial overlap in the functional roles of multi-functional agents; a system property also known in biology as degeneracy. There are many biological examples where degeneracy is already known to provide robustness through the local actions of functionally redundant components. Here however we have presented a conceptual model showing how degenerate agents can readily form a buffering network whereby agents can indirectly support many functionally dissimilar tasks. These distributed compensatory effects result in greater versatility and robustness: characteristics with obvious relevance to systems operating in highly variable environments.

Recent studies of genome-proteome models have found degenerate systems to be exceptionally robust in comparison to those without degeneracy. Expanding on these results, we have tested some of the claims of the buffering network hypothesis and determined that the enhanced robustness in degenerate genome:proteome mappings is in fact a consequence of distributed (non-local) compensatory effects that are not observable when robustness is achieved using only pure redundancy. Moreover, the proportion of local versus non-local sources of robustness within the degenerate models shows little sensitivity to scaling and appears compatible with biological data on mutational robustness.

### Box1: Degeneracy in biotic and abiotic systems

In biology, degeneracy refers to conditions where the functions or capabilities of components overlap partially. In a review by Edelman and Gally [4], numerous examples are used to demonstrate the prevalence of degeneracy throughout biology. It is pervasive in proteins of every functional class (e.g. enzymatic, structural, or regulatory) [11] and is readily observed in ontogenesis (see page 14 in [12]), the nervous system [13] and cell signalling (crosstalk). In the particular case of proteins, it is also now known that partial functional similarities can arise even without any obvious similarities in sequence or structure [14].

Degeneracy and associated properties like functional plasticity are also prevalent in other biotic and abiotic systems, such as those listed below in Table 1. For instance, in transportation fleets the vehicles are often interchangeable but only for certain tasks. Multi-functional force elements within a defence force structure also can exhibit an overlap in capabilities but only within certain missions or scenarios. In an organization, people often have overlapping job descriptions and are able to take on some functions that are not readily achieved by others that technically have the same job. In the food webs of complex ecosystems, species within similar trophic levels have a partial overlap in resource competition. Resource conditions ultimately determine whether competition will occur or whether the two species will forage for distinct resources [10].

Table 1: Systems where agents are multifunctional and have functions that can partially overlap with other agents. We speculate that degeneracy may be able to have a systemic effect on robustness within each of these domains.

Agent	System	Environment	Control	Agent Tasks
Vehicle type	Transportation	Transportation	Command and	Transporting
	Fleet	Network	Control	goods, pax
Force element	Defence Force Structure	Future Scenarios	Strategic Planning	Missions
Person	Organization	Marketplace	Management	Job Roles
Demes	Ecosystem	Physical	Self-organized	Resource usage
		Environment		and creation
Gene Products	Interactome	Cell	Self-organized and	Energetic and
			evolved	sterric interactions
Antigen	Immune System	Antibodies and	Immune learning	Recognizing
	-	host proteins		foreign proteins

Degeneracy has become increasingly appreciated for its role in trait stability, as was noted in [15] and more thoroughly discussed in [4]. For instance, gene families can encode for diverse proteins with many distinctive roles yet sometimes these proteins can compensate for each other during lost or suppressed gene expression, as seen in the developmental roles of the adhesins gene family in *A. Saccharomyces* [16]. At higher scales, resources are often metabolized by a number of distinct compensatory pathways that are effectively interchangeable for certain metabolites even though the total effects of each pathway are not identical.

More generally, when agents are degenerate some functions will overlap meaning that the influence an agent has in the system could alternatively be enacted by other agents, groups of agents, or pathways. This functional redundancy within a specified context provides the basis for both competition and collaboration amongst agents and in many circumstances can contribute to the stability of individual traits (cf. [4]).

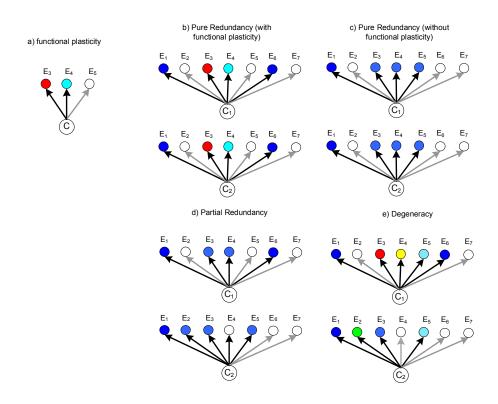
## Box2: Degeneracy, Redundancy, and Partial Redundancy

Redundancy and degeneracy are two design principles that both contribute to the robustness of biological systems [4] [8]. Redundancy is an easily recognizable design principle that is prevalent in both biological and man-made systems. Here, redundancy means 'redundancy of parts' and refers to the coexistence of identical components with identical functionality (i.e. isomorphic and isofunctional). In information theory, redundancy refers to the repetition of messages, which is important for reducing transmission errors. Redundancy is also a common feature of engineered or planned systems where it provides robustness against variations of a very specific type ('more of the same' variations). For example, redundant parts can substitute for others that malfunction or fail, or augment output when demand for a particular output increases.

Degeneracy differs from pure redundancy because similarities in the functional response of components are not observed for all conditions (see Figure 4d). In the literature, degeneracy has at times been referred to as functional redundancy or partial redundancy, however the definitions provided for these terms rarely capture the full meaning of degeneracy intended here or implied in [4] [13].

The definition of degeneracy we use requires degenerate components to be multi-functional, with the function performed at any given time being dependent on the context; a behavior we label as *functional plasticity*. Thus for degeneracy to be present, some (but not all) functions related to a component or module must also be observable in others, i.e. a partial and conditional similarity in the repertoire of functional responses (see Figure 4). In contrast, partial redundancy is often used to describe the conditional similarity in functional responses for components capable of only a single function (see Figure 4c). This is analogous to the definition of response diversity within ecosystems [6]<sup>2</sup> and is conceptually similar to ensemble approaches in machine learning.

Functional plasticity is necessary to create the buffering networks discussed in Section 4 and for the enhanced evolvability observed in [17] [9]. However this requirement is not as demanding as it may at first seem. Functional plasticity is common in biological systems and occurs for most cited examples of degeneracy in [4]. Gene products such as proteins typically act like versatile building blocks, performing different functions that depend on the complex a protein forms with other gene products or other targets in its environment[18] [19]. In contrast to earlier ideas that there was one gene for each trait, gene products are now know to have multiple non-trivial interactions with other "targets", i.e. in the interactome [20] [21] and these are rarely correlated in time [22]. The alternative, where a gene's functions are all performed within the same context (referred to as "party hubs" in [22]), is known to be considerably less common in biology.



<sup>&</sup>lt;sup>2</sup> Response diversity is defined as the range of reactions to environmental change among species contributing to the same ecosystem function.

Figure 4 Illustration of degeneracy and related concepts. Components (C) within a system have a functionality that depends on their context (E) and can be functionally active (filled nodes) or inactive (clear nodes). When a component exhibits qualitatively different functions (indicated by node color) that depend on the context, we refer to that component as being functionally plastic (panel a). Pure redundancy occurs when two components have identical functions in every context (panels b and c). Partial redundancy is a term often used to describe two components with a single (but same) function whose activation depends on the context in different ways (panel d). Degeneracy describes components that are functionally plastic and where the functions are similar in some situations but different in others (panel e).

### 8. References

- [1] W. R. Ashby, An introduction to cybernetics: Methuen London, 1964.
- [2] F. Heylighen and C. Joslyn, "Cybernetics and second order cybernetics," *Encyclopedia of physical science & technology*, vol. 4, pp. 155-170, 2001.
- [3] H. W. Ma and A. P. Zeng, "The connectivity structure, giant strong component and centrality of metabolic networks," *Bioinformatics*, vol. 19, pp. 1423-1430, 2003.
- [4] G. M. Edelman and J. A. Gally, "Degeneracy and complexity in biological systems," *Proceedings of the National Academy of Sciences, USA*, p. 231499798, 2001.
- [5] M. Kirschner and J. Gerhart, "Evolvability," Proceedings of the National Academy of Sciences, USA, vol. 95, pp. 8420-8427, 1998.
- [6] T. Elmqvist, C. Folke, M. Nystrom, G. Peterson, J. Bengtsson, B. Walker, and J. Norberg, "Response diversity, ecosystem change, and resilience," *Frontiers in Ecology and the Environment*, vol. 1, pp. 488-494, 2003.
- [7] L. Hong and S. E. Page, "Groups of diverse problem solvers can outperform groups of high-ability problem solvers," *Proceedings of the National Academy of Sciences*, vol. 101, pp. 16385-16389, 2004.
- [8] A. Wagner, "Distributed robustness versus redundancy as causes of mutational robustness," *BioEssays*, vol. 27, pp. 176-188, 2005.
- [9] J. M. Whitacre and A. Bender, "Degeneracy: a design principle for achieving robustness and evolvability," *Journal of Theoretical Biology, (Accepted Nov, 2009)*, 2009.
- [10] M. Kondoh, "Foraging adaptation and the relationship between food-web complexity and stability," *Science*, vol. 299, p. 1388, 2003.
- [11] A. Wagner, "The role of population size, pleiotropy and fitness effects of mutations in the evolution of overlapping gene functions," *Genetics*, vol. 154, pp. 1389-1401, 2000.
- [12] S. A. Newman, "Generic physical mechanisms of tissue morphogenesis: A common basis for development and evolution," *Journal of Evolutionary Biology*, vol. 7, pp. 467-488, 1994.
- [13] G. Tononi, O. Sporns, and G. M. Edelman, "Measures of degeneracy and redundancy in biological networks," *Proceedings of the National Academy of Sciences, USA*, vol. 96, pp. 3257-3262, 1999.
- [14] D. Petrey and B. Honig, "Is protein classification necessary? Toward alternative approaches to function annotation," *Current Opinion in Structural Biology*, vol. 19, pp. 363-368, 2009.
- [15] J. M. Whitacre, "Degeneracy: a link between evolvability, robustness and complexity in biological systems," *Journal of Theoretical Biology (submitted October 2009)*.
- [16] B. Guo, C. A. Styles, Q. Feng, and G. R. Fink, "A Saccharomyces gene family involved in invasive growth, cell-cell adhesion, and mating," *Proceedings of the National Academy of Sciences, USA*, p. 220420397, 2000.
- [17] J. M. Whitacre and A. Bender, "Degenerate neutrality creates evolvable fitness landscapes," in *WorldComp-2009* Las Vegas, Nevada, USA, 2009.
- [18] A. C. Gavin, P. Aloy, P. Grandi, R. Krause, M. Boesche, M. Marzioch, C. Rau, L. J. Jensen, S. Bastuck, and B. Dümpelfeld, "Proteome survey reveals modularity of the yeast cell machinery," *Nature*, vol. 440, pp. 631-636, 2006.
- [19] R. Krause, C. von Mering, P. Bork, and T. Dandekar, "Shared components of protein complexes-versatile building blocks or biochemical artefacts?," *BioEssays*, vol. 26, pp. 1333-1343, 2004.
- [20] N. N. Batada, T. Reguly, A. Breitkreutz, L. Boucher, B. J. Breitkreutz, L. D. Hurst, and M. Tyers, "Stratus not altocumulus: a new view of the yeast protein interaction network," *PLoS Biol*, vol. 4, p. e317, 2006.
- [21] N. N. Batada, T. Reguly, A. Breitkreutz, L. Boucher, B. J. Breitkreutz, L. D. Hurst, and M. Tyers, "Still stratus not altocumulus: further evidence against the date/party hub distinction," *PLoS Biol*, vol. 5, p. e154, 2007.
- [22] J. D. J. Han, N. Bertin, T. Hao, D. S. Goldberg, G. F. Berriz, L. V. Zhang, D. Dupuy, A. J. M. Walhout, M. E. Cusick, and F. P. Roth, "Evidence for dynamically organized modularity in the yeast protein–protein interaction network," *Nature*, vol. 430, pp. 88-93, 2004.