Quasi-Independence, Homology and the Unity of Type: A Topological Theory of Characters

Günter P. Wagner

Department of Ecology and Evolutionary Biology
Yale University, New Haven, CT, USA

Peter F. Stadler

Institut für Theoretische Chemie und Molekulare Strukturbiologie
Universität Wien, Währingerstraße 17, A-1090 Wien, Austria

The Santa Fe Institute, 1399 Hyde Park Road, Santa Fe, NM 87501, USA

Phone: **43 1 4277-52737 Fax: **43 1 4277-52793
E-Mail: studla@tbi.univie.ac.at
URL: http://www.tbi.univie.ac.at/~studla

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Abstract. In this paper Lewontin's notion of "quasi-independence" of characters is formalized as the assumption that a region of the phenotype space can be represented by a product space of orthogonal factors. In this picture each character corresponds to a factor of a region of the phenotype space. We consider any region of the phenotype space that has a given factorization as a "type", i.e., as a set of phenotypes that share the same set of phenotypic characters. Using the notion of local factorizations we develop a theory of character identity based on the continuity of common factors among different regions of the phenotype space. We also consider the topological constraints on evolutionary transitions among regions with different regional factorizations, i.e., for the evolution of new types or body plans. It is shown that direct transition between different "types" is only possible if the transitional forms have all the characters that the ancestral and the derived types have and are thus compatible with the factorization of both types. Transitional forms thus have to go over a "complexity hump" where they have more quasi-independent characters than either the ancestral as well as the derived type. The only logical, but biologically unlikely, alternative is a "hopeful monster" that transforms in a single step from the ancestral type to the derived type. Topological considerations also suggest a new factor that may contribute to the evolutionary stability of "types." It is shown that if the type is decomposable into factors which are vertex irregular (i.e. have states that are more or less preferred in a random walk), the region of phenotypes representing the type contains islands of strongly preferred states. In other words types have a statistical tendency of retaining evolutionary trajectories within their interior and thus add to the evolutionary persistence of types.

Keywords: Quasi-Independence, Characters, Homology, Evolutionary Innovation, Body Plans, Generalized Topology, Product Spaces

1. Introduction

Evolutionary change results from the spontaneous generation of genetic variation and the fixation of variants in the population through natural selection and genetic drift. This basic assumption of the Neo-Darwinian model implies population genetics as a natural framework for studying the evolution of phenotypic adaptation, the evolution of gene sequences, and the process of speciation, see e.g. (Futuyma, 1998; Graur and Li, 2000).

Patterns of phenotypic evolution (Schlichting and Pigliucci, 1998), on the other hand, such as the punctuated mode (the partially discontinuous nature) of evolutionary change (Eldredge and Gould, 1972), developmental constraints or constraints to variation (nard Smith et al., 1985; Schwenk, 1995), innovation (Müller and Wagner, 1991), directionality in evolution, and phenotypic stability or homology are not adequately described by population genetics models. The reason is that before selection can determine the fate of a new phenotype, that phenotype must first be produced or "accessed" by means of variational mechanisms (Fontana and Buss, 1994). Phenotypes are not varied directly in a heritable fashion, but through genetic mutation and its consequences on development. The accessibility of a phenotype is therefore determined by the *genotype-phenotype map* which determines how phenotypes vary with genotypes (Lewontin, 1974; Wagner and Altenberg, 1996; Fontana and Schuster, 1998a). In a previous contributions it has been demonstrated that many of the recalcitrant phenomena in evolutionary biology, like punctuated innovation, developmental constraints, homology and irreversibility, can be understood as statements about the accessibility structure of the phenotype space (Fontana and Schuster, 1998a; Cupal et al., 2000; Stadler et al., 2001).

The motivation for emphasizing the central role of the genotype-phenotype map arose from studies in which RNA folding from sequences to secondary structures is used as a biophysically realistic, yet extremely simplified toy-model of a genotype-phenotype map. Simulated populations of replicating and mutating sequences under selection exhibit many phenomena known from organismal evolution: neutral drift, punctuated change, plasticity, environmental and genetic canalization, and the emergence of modularity, see e.g. (Fontana et al., 1989; Schuster et al., 1994; Huynen et al., 1996; Fontana and Schuster, 1998a,b; Ancel and Fontana, 2000). Laboratory experiments have also generated phenomena consistent with these patterns (Spiegelman, 1971; Lenski and Travisano, 1994; Szostak and Ellington, 1993).

The accessibility structure at the genotypic level is defined by the genetic operators such as mutation, homologous as well as non-homologous cross-over, gene duplication and gene-loss, and genomic rearrangements. In the simplest case of point-mutations only, accessibility arranges the sequences as graph. The vertices of this graph are the sequences; two sequences are connected by an edge if and only if they differ by a single point mutation. In the case of recombination a more complicated structure arises (Gitchoff and Wagner, 1996; Stadler and Stadler, 2002). The genotype-phenotype map translates genotypic accessibility into accessibility among phenotypes and therefore defines the structure of *phenotype space* (Fontana and Schuster, 1998a,b; Cupal et al., 2000). The important observation, as we shall see in the following, is that this translation is biased

and hence the source of asymmetries even if mutational mechanisms generate genetic variation at random. This is caused by the fact that the genotype-phenotype relation is strongly many-to-one and far from random.

Accessibility is an inherently topological notion. It does not come as a surprise, therefore, that the mathematical description of the phenotype space proposed by Stadler et al. (2001) is a generalized version of point set topology. It has been pointed out by Stadler and Stadler (2002) that accessibility in a natural way implies a weak notion of closure that turns out the a convenient starting point for the formal development of the theory that is given in section 4. The abstract description of phenotype spaces as objects that have even less *a priori* structure than topological spaces requires us to investigate the properties of each individual phenotype space before predictions are even conceivable. We may ask, for instance, whether there is a notion akin to "dimension" that can be related to the notion of *character* or *module*. This issue was partially explored by Stadler et al. (2001) in terms of a factorization of the space.

The motivation for the theory developed in this contribution is to obtain a mathematical language in which the origin of evolutionary novelties can be described and modeled. In the next section the problems associated with describing evolutionary novelties are discussed in order to motivate the present approach. After these conceptual preliminaries we provide an intuitive summary of the mathematical results as a guide to read the mathematical sections 4 and 5. In section 6 we return to an intuitive interpretation of the mathematical framework developed in this paper.

2. Conceptual Preliminaries

Population genetic theory is the basis for all major branches of evolutionary biology explaining the origin of adaptations, social behavior as well as the origin of species (Futuyma, 1998). For one class of evolutionary processes, however, population genetics has been surprisingly uninformative, i.e. the origin of evolutionary novelties (Wagner et al., 2000). Novelties are parts of a body plan that are neither homologous to an ancestral character nor serially homologous to another part of the body (Müller and Wagner, 1991). Various explanations have been given for that apparent limitation (Fontana and Buss, 1994; Gilbert, 2000; Wagner et al., 2000). One line of argumentation holds that the limited success of population genetic theory in dealing with evolutionary novelties is not due to an inherent conceptual limitation of the Neo-Darwinian theory of evolution. Rather it has been argued that the reason is conditional on the mathematical structure of population genetic theory (Shpak and Wagner, 2000). The variables of population genetic theory are genotype frequencies and derived quantities, like haplotype frequencies, allele frequencies and linkage disequilibria. The parameters of the theory are fitness values of genotypes and their derived variables, like additive effects etc, as well as parameters describing the transmission process: mutation and recombination rates, inbreeding coefficients and so on. In this mathematical picture the phenotype is excluded from consideration. For that simple reason questions about the evolution of phenotypic organization (novelties) can not even be stated as problems. Any information about the organization of the phenotype is implicitly given by the parameters and the structure of the equations describing changes in genotype frequencies.

Quantitative genetic theory is a branch of population genetics which does have a representation of the phenotype as a model variable, namely the state of quantitative attributes of the phenotype like body weight or clutch size. The objective of quantitative genetic theory is to predict the changes of the distribution of these quantitative attributes caused by mutation, recombination, inbreeding and selection (Bürger, 2000). This approach assumes that the processes modeled by the equations do not change the set of relevant attributes of the phenotype. In other words, it is assumed that the characters of a phenotype do not change. This assumption excludes any meaningful discussion of evolutionary novelties, which *per definitionem* are the addition of phenotypic characters to the body plan of the organism. Quantitative genetic theory predicts changes given an unchanging body plan, because the set of descriptors of the phenotype is not a variable in the mathematical language used.

This limitation of mathematical evolutionary theory can only be overcome if one finds a mathematical language in which the number and kind of phenotypic characters is not assumed a priory but is a result of an analysis of the model (Wagner and Laubichler, 2000; Shpak and Wagner, 2000; Stadler et al., 2001). We think that the theory of configuration spaces based on accessibility structures is such a language and we will use that language to achieve two goals: 1) to develop a mathematical character concept that allows the description of the origin and the loss of characters in evolutionary change, and 2) to clarify some elusive concepts like homology (i.e., character identity), body plans and innovation.

We think that the theory of configuration spaces is particularly well suited for this set of goals. Configuration spaces are defined on the bases of genetic operators which transform genotypes and phenotypes Reidys and Stadler (2002). As such they are rooted in the Neo-Darwinian insight that evolution results from the fixation of heritable variation produced by mutation and/or recombination. The theory of configuration spaces also does not make any a priori assumptions about the topological properties of the abstract spaces induced by mutation or other genetic operators. In contrast, quantitative genetic theory assumes that phenotypic evolution can adequately be described in a multi dimensional Euclidian space, with all its strong topological properties. No justification is usually given for that assumption. Configuration spaces also do not imply any assumptions about which parts of the organism are relevant characters. In fact there is not even a vocabulary in this theory that describes what a character is in a physical sense. All that is assumed is that there are organisms and that there are genetic processes that can transform the phenotypes of organism in some knowable fashion. Hence configuration spaces do not require us to make any ontic commitments on whether cells, genes or organs are the relevant units. All we assume is that organisms are transformed and that the rules of these transformation can be described in an abstract (pre-) topological space (Stadler et al., 2001).

The next question is how one can use the information about the evolutionary process represented in a configuration space to define a biologically meaningful character concept. We propose that the most promising avenue is to start with Lewontin's notion of "quasi-independence." This concept was introduced by Lewontin (1978) to clarify the mechanistic assumptions underlying the adaptationist research program. Explaining a

character state as an adaptation caused by natural selection requires the assumption that the character state can be produced by mutation without significantly affecting the functionality and or structure of the rest of the body. This notion does not assume that genetic and mutational variation among characters is stochastically independent (i.e. is not correlated). All that is assumed is that genetic variation can be produced at not too low rate that natural selection can adjust one character without permanently altering other attributes of the phenotype. Hence we interpret the notion of quasi-independence as a statement about the topological properties of phenotypic configuration spaces. In (Stadler et al., 2001) we argued that quasi-independence is equivalent to local factorizability of the phenotypic configuration space. Local factorization means that the variational neighborhood of a phenotype can be described by the combination of character states, i.e. the coordinates of "dimensions" or factors. Characters which correspond to local factors have been called "structurally independent" (Stadler et al., 2001) to emphasize that this notion is our interpretation of Lewontin's concept rather than his original definition. The biological meaning of "locally factorizable" is that there are no variational limitations on realizing all possible combinations of character states. The range of phenotypes that can be described as a combination of states of a given set of character is of course limited. For instance it may be possible to describe all squirrel species by a combination of a character states of the set of "squirrel characters", but there is no such set of characters which would describe the phenotypic disparity of all metazoans. Therefore it was important to develop the mathematical concept of local factorization in (Stadler et al., 2001). In this paper the theory of local factorization is developed further and applied to the question of how character identity can be defined and how the evolution of novelties can be described within this framework.

3. Factorization of Phenotype Space: Non-technical Summary

In this section we give an intuitive preview of the results described in the mathematical part of this paper. Here we avoid many of the technical fine points that will be covered below and which will also be important for the biological interpretation of the results after the next section.

The notion of factorizability as a way to define characters and character identity can only be useful if it can be developed into a concept that can apply locally, i.e. to restricted parts of the configuration space. It is unlikely that there are any identifiable characters that apply to all living beings or even to reasonably large taxa, such a vertebrates or insects. There is no set of characters that would allow describing the organismal diversity as a combination of character states of this set of characters. Only within a limited range of phenotypic variation will we be able to identify quasi-independent characters that will give a reasonable framework for describing the variational tendencies of these characters. Hence critical for the present paper is the introduction of the notion of a local factorization.

The first step is to recognize that it is possible to restrict our attention to a smaller region Y within the whole phenotype space X, $Y \subset X$ and then may be find a factorizable part that embeds this subspace Y. Such a factorization can be called regional since it applies to a more limited region of the whole phenotype space. The smallest

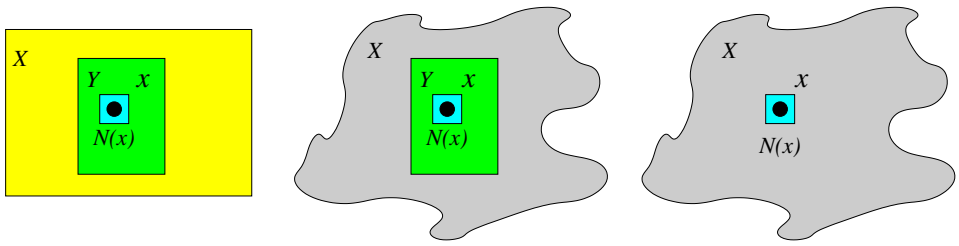

Figure 1. Global, regional, and local factors. If the entire phenotype space admits a factorization (r.h.s.) then each "rectangular" region, as well the vicinities of all its points are factorizable. The existence of a factorizable region (middle) implies that the vicinities of all interior points of this region decompose accordingly. Finally, a factorization might be possible only locally (l.h.s).

meaningful region to factorize is the factorization of the smallest neighborhood of a particular phenotype $x \in X$, also called the *vicinity of* x, $N(x)$. See Fig. 1. If it exists, we call the factorization of the vicinity of x the local factorization around x. The local factorization of x summarizes the variational degrees of freedom of the type x and is thus even experimentally operational.

The notion of local factorization is the basis for our topological approach to character definition, since it can be understood as an intrinsic dispositional (variational) property of the type x, say a certain phenotype. This notion also provides a connection between the local properties of phenotypes and the more global properties of the phenotype space. An important technical result is that any factorization of a finite space into parts that cannot factorized further is unique. This means that the identification of characters based on the variational degrees of freedom is entirely non-arbitrary.

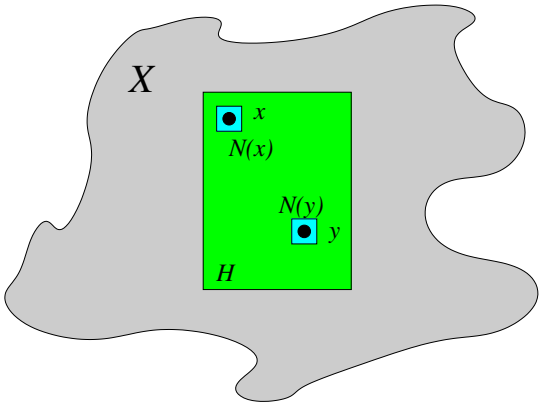

Figure 2. A regional factorization of H implies local factorizations at the interior points x and y that have all factors of H in common.

The next step is to clarify what it means, in the topological language, to say that two types x and y have the same characters, or in other words, have consistent local factorizations. Note that the vicinities of x and y do not need to overlap. Here we propose that the local factorizations of x and y are comparable (or consistent) if x and y

can be embedded in a subspace H that has a regional factorization $H_1 \times H_2 \times \cdots \times H_n$, Fig. 2. Factors in $N(x)$ and $N(y)$ are then comparable or equivalent if they project onto the same factors H_i of the regional factorization of H. In other words, embedding x and y into a regional factorization that encompasses both $N(x)$ and $N(y)$ allows one to used the regional factors to establish correspondences between the local factors $N_k(x)$ and $N_l(y)$.

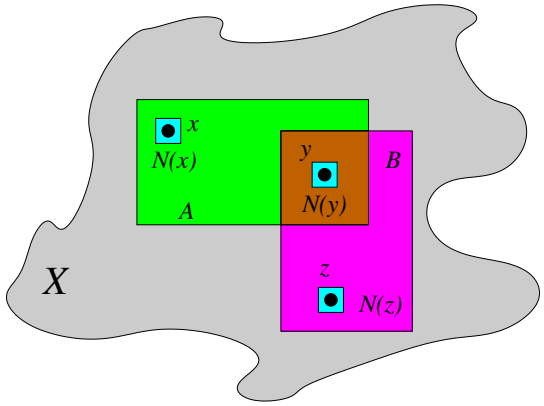

Figure 3. Suppose the factorizations in the regions A and B are such that the two resulting factorizations of the vicinity $N(z)$ have common factors. The corresponding factors also appear in the local factorizations around $N(x) \subset A$ and $N(y) \subset B$ and hence establish as (partial) correspondence between the factors of $N(x)$ and $N(y)$ even though x and y are not contained a common factorizable region.

This method of establishing correspondence between local factors (characters) requires that there is a region containing the two types which is in itself factorizable. Hence the reach of this method can be limited, if the phenotype space is complex and irregular. It is however possible to identify corresponding factors even between types which are not embedded in a factorizable region. To do this we have to introduce the notion of common factors of two overlapping but distinct factorizable regions, say A and B. Let us assume that the overlap of A and B contains a type y and its vicinity $N(y)$. Of course $N(y)$ is factorizable in this situation. Common factors of A and B are then those which correspond to the same factors or combination of factors of $N(z)$. Note that the two regions discussed in the previous paragraph do not need to be embedded into a larger regions which is factorizable. This affords us with the opportunity to establish the correspondence between two types, say x and z, which are not embedded in a regional factorization. All we need is a type y which shares common factors with x and y through regional factorizations that embed x and y, say A, and y and z, say B, Fig. 3. If A and B overlap and have common factors, these common factors can be used to establish a correspondence between some factors of x and z. This approach is similar to the method of local continuations through overlapping neighborhoods in functional analysis, Fig. 4.

The intuitive interpretation of the need for this construct is that there can be a character (i.e. a factor) which exists between quite different organisms, even if all or most of the other characters of the organisms are different. Because all the other characters

are different there is no region of the phenotype space that can be described with the same set of characters, i.e. there is no regional factorizable subspace that contains both types. But some of the characters still can be the same, like those of members from the same phylum, even though each class has a quite different decomposition of the body in addition to the shared factors. Hence the construction of local continuation is necessary to establish the correspondence of factors (characters) in organism that are not part of the same regional factorization.

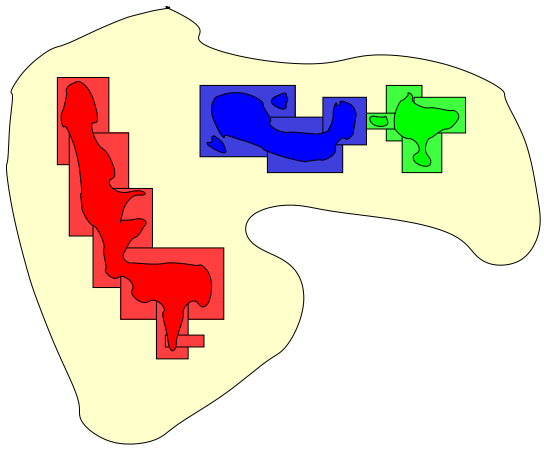

Figure 4. The correspondence between factors can be extended further through a series of regional factorization, defining the subset on which a factor exists as the interior of the union of all the overlapping factorizable regions.

An interesting consequence of the notion of overlapping regional factorizations is a result about the dimensionality of the local neighborhoods in the overlap of the regional factorizations. Since the local factorization in an overlap between two regional factorizations has to be compatible with either factorization the dimensionality in the region of overlap has to be at least as high and in most cases higher than in either of the two region. In particular we show below that the dimensionality of every local factorization in the interior of the overlap of A and B has to be

$$\dim N(x) = \dim A + \dim B - \phi(A, B)$$

where $\phi(A, B)$ is the number of common factors of the regions A and B. This fact will have interesting consequences for evolution of new types, i.e. the evolution from one area of regional factorization to another. This is a situation which pertains to the evolutionary origin of new characters and types of body organization.

In the following two sections we develop the mathematical framework. We start with the axioms of generalized topological spaces and briefly show how genetic operators such as mutation and recombination give rise to such abstract spaces in a natural way. After introducing the basic constructs of subspace, quotient space, and product space we consider the global, regional, and local versions of factorizability and their relationships. In section 5 we specialize our framework to finite sets. In this setting the Unique Prime Factor Theorem (Imrich and Klavžar, 2000) holds, which is a prerequisite for the "continuation results" mentioned above.

4. Generalized Topological Spaces

4.1. Genetic Operators. The abstract description of recombination spaces is pioneered in (Gitchoff and Wagner, 1996; Stadler and Wagner, 1998; Stadler et al., 2000). It is based on the notion of the *recombination function* $\mathcal{R} : X \times X \to \mathcal{P}(X)$ assigning to each pair of parents x and y the *recombination set* $\mathcal{R}(x, y)$ introduced by Gitchoff and Wagner (1996) as the set of all all their potential offsprings. Recombination in general satisfies two axioms:

(X1) $\{x, y\} \in \mathcal{R}(x, y)$,
(X2) $\mathcal{R}(x, y) = \mathcal{R}(y, x)$.

Condition (X1) states that replication may occur without recombination, and (X2) means that the role of the parents is exchangeable. Often a third condition

(X3) $\mathcal{R}(x, x) = \{x\}$

is assumed. Note that (X3) is not satisfied by models of unequal crossover (Shpak and Wagner, 2000; Stadler et al., 2002). Functions $\mathcal{R} : X \times X \to \mathcal{P}(X)$ satisfying (X1), (X2), and (X3) were considered recently as so-called *transit functions* (Changat et al., 2001) and as *P-structures*, with a focus on algebraic properties, in (Stadler and Wagner, 1998; Stadler et al., 2000). A *closure operator* associated with a recombination function was introduced by Gitchoff and Wagner (1996) as

$$\mathsf{cl}(A) = \bigcup_{x,y \in A} \mathcal{R}(x, y) \tag{1}$$

The situation is much simpler in the case of mutation. Following the spirit of the Gitchoff-Wagner closure function we define $\mathsf{cl}(A)$ as the set of all mutations that can be obtained from a set A in a single step.

The abstract notion of assigning a "closure" $\mathsf{cl}(A)$ to every subset A of the set of types X is the starting point of our formal development. In general, we may think of $\mathsf{cl}(A)$ as the set of all types that can be produced from a "population" in a single step.

4.2. Closure and Neighborhood. Let $\mathsf{cl} : \mathcal{P}(X) \to \mathcal{P}(X)$ be a set-valued set function which we call the *closure function*. Its conjugate is the *interior function* $\mathsf{int} : \mathcal{X} \to \mathcal{X}$ defined by

$$\mathsf{int}(A) = X \setminus \mathsf{cl}(X \setminus A)\,. \tag{2}$$

The *neighborhood function* $\mathcal{N} : X \to \mathcal{P}(\mathcal{P}(X))$ is defined by

$$\mathcal{N}(x) = \{N \subseteq X | x \in \mathsf{int}(N)\} \tag{3}$$

It is not hard to show that closure, interior, and neighborhood can be used to define each other. For example, given the neighborhood function $\mathcal{N}$, the closure function is obtained as

$$x \in \mathsf{cl}(A) \iff (X \setminus A) \notin \mathcal{N}(x) \tag{4}$$

The most commonly assumed properties of closure function, or equivalently, neighborhood functions are summarized in Table 1. The equivalence of closure and neighborhood versions of these conditions is well-known, see e.g. (Gastl and Hammer, 1967). We say that (X, cl) is an *isotone space* if (K0) and (K1) is satisfied. If in addition (K2) holds

Table 1. Axioms for Generalized Closure Spaces

	closure	neighborhood
(K0)	$\mathsf{cl}(\emptyset) = \emptyset$	$X \in \mathcal{N}(x)$
(K1) isotone	$A \subseteq B \implies \mathsf{cl}(A) \subseteq \mathsf{cl}(B)$ $\mathsf{cl}(A \cap B) \subseteq \mathsf{cl}(A) \cap \mathsf{cl}(B)$ $\mathsf{cl}(A) \cup \mathsf{cl}(B) \subseteq \mathsf{cl}(A \cup B)$	$N \in \mathcal{N}(x)\,, N \subseteq N' \implies N' \in \mathcal{N}(x)$
(K2) expansive	$A \subseteq \mathsf{cl}(A)$	$N \in \mathcal{N}(x) \Rightarrow x \in N$
(K3) sub-linear	$\mathsf{cl}(A \cup B) \subseteq \mathsf{cl}(A) \cup \mathsf{cl}(B)$	$N', N'' \in \mathcal{N}(x) \implies N' \cap N'' \in \mathcal{N}(x)$
(K4) idempotent	$\mathsf{cl}(\mathsf{cl}(A)) = \mathsf{cl}(A)$	$N \in \mathcal{N}(x) \iff \mathsf{int}(N) \in \mathcal{N}(x)$

then (X, cl) is a *neighborhood space*. Neighborhood spaces satisfying (K3) are the *pre-topological spaces* studied in detail by Čech (1966). Finally, a pretopological space with idempotent closure is a *topological space* in the usual sense. If (K1) holds then equ.(4) is equivalent to the more common expression (Day, 1944, Thm.3.1,Cor.3.2)

$$\mathsf{cl}(A) = \{x \in X | \forall N \in \mathcal{N}(x) : A \cap N \neq \emptyset\} \tag{5}$$

Since the mutants of each parent are independent of the rest of the population we have

$$\mathsf{cl}(A) = \bigcup_{x \in A} \mathsf{cl}(\{x\}) \tag{6}$$

in the case of mutation. This condition is equivalent to (K1) and (K3) in finite sets. We assume that replication without mutation is possible, thus $x \in \mathsf{cl}(\{x\})$ and hence $A \in \mathsf{cl}(A)$, i.e., (K2) holds. The validity of (K0) is assumed by definition. It follows that mutation defines a pretopology on the genotype space, see (Stadler et al., 2001).

The case of recombination is dealt with in some more detail in (Stadler and Stadler, 2002). We have

Theorem 1. *The closure space* (X, cl) *arising from any recombination function* $\mathcal{R}$ *for which* (X1) *and* (X2) *hold, satisfies* (K0), (K1), *and* (K2).

Condition (X3) is then equivalent to $\mathsf{cl}(\{x\}) = \{x\}$, i.e., the well-known (T1)-separation axiom.

Consider a genotype-phenotype map $\Phi : (V, \mathsf{cl}) \to X$ from the genotype space (V, cl), which we describe as a generalized closure space with closure function cl into a set of phenotypes X. The GP-map Φ defines a closure function on X such that $y \in c(B)$ means "phenotype y is accessible from the collection B of phenotypes". Is is argued at length by Fontana and Schuster (1998a); Stadler et al. (2001) that this construction is meaningful because the pre-images $\Phi^{-1}(y) = \{v \in V | \Phi(v) = y\}$ from extensive neutral networks. If we assume that b' is accessible from b iff there is a pair of genotypes v and v' with $b = \Phi(v)$ and $b' = \Phi(v)$ that are accessible in genotype space obtain the so-called induced closure or accessibility closure

$$c^*(B) = \Phi(\mathsf{cl}\big(\Phi^{-1}(B)\big)) \tag{7}$$

on the phenotype space X. The other extreme, where we require accessibility from every genotype, is known as *shadow topology* (Stadler et al., 2001). A useful closure structure on the phenotype space will in general be finer than the accessibility closure and coarser than the shadow closure. We emphasize that the entire discussion in this contribution is independent of the details of the definition of the closure function on the phenotype space. It will be sufficient to assume that a closure function exists that reflects the mutual accessibilities of phenotypes.

4.3. Neighborhood Spaces. In this section we collect some basic facts on neighborhood space that will be used throughout the mathematical parts of this contribution. The theory of neighborhood spaces directly generalizes the theory of topological spaces. Additional information of neighborhood spaces can be found in the work of Day (1944); Hammer (1962); Gastl and Hammer (1967); Gniłka (1994). For a detailed account of separation axioms in neighborhood spaces we refer to (Stadler and Stadler, 2001).

4.3.1. *Subspaces.* The notion of a subspace in the topological context should not be confused with subspaces of vector spaces. In the topological context, a subspace of X is simply an arbitrary subset that inherits its structure from X.

Definition 2. *Let (X, cl) be a neighborhood space and let $Y \subseteq X$. We say that (Y, c_Y) is a subspace of (X, cl) if $c_Y(A) = \mathsf{cl}(A) \cap Y$ for all $A \subseteq Y$.*

We will sometimes use the notation $Y \Subset X$. It follows directly from the definition that the restriction map $(Y, c_Y) \to (X, \mathsf{cl}) : x \mapsto x$ is continuous. Furthermore, the relative interior is

$$\mathrm{int}_Y(A) = Y \cap \mathsf{int}(A \cup (X \setminus Y)) \tag{8}$$

and the neighborhood systems in (Y, c_Y) are given by

$$\mathcal{N}_Y(x) = \{N \cap Y | N \in \mathcal{N}(x)\} \tag{9}$$

This can be seen e.g. following the lines of (Čech, 1966, 17.A).

4.3.2. *Product Spaces.* Products of neighborhood spaces will play a crucial role in our discussion.

Definition 3. *Let (X_1, c_1) and (X_2, c_2) be two isotonic closure spaces. Then the product space $(X_1 \times X_2, c_1 \times c_2)$ is defined by means of the neighborhood system $\mathcal{N}(x_1, x_2)$, where*

$$N \in \mathcal{N}(x_1, x_2) \iff \exists N_1 \in \mathcal{N}_1(x_1) \text{ and } N_2 \in \mathcal{N}_2(x_2) \text{ such that } N_1 \times N_2 \subseteq N \tag{10}$$

For sets of the form $A_1 \times A_2$ this translates to a simple formula for the product closure in isotonic spaces, see also (Gniłka, 1994, Thm.8.1)

$$\mathsf{cl}(A_1 \times A_2) = c_1(A_1) \times c_2(A_2) \tag{11}$$

If (X_1, c_1) and (X_2, c_2) satisfy (K2), (K3), or (K4), respectively, so does their product.

4.3.3. *Quotient Spaces.* Let $\mathbb{P}$ be a partition of X and denote by $[x]$ the class of $\mathbb{P}$ to which x belongs. The function $\chi_{\mathbb{P}} : X \to X/\mathbb{P}$, $x \mapsto [x]$ is called the *canonical map* from X to $X/\mathbb{P}$. We use the abbreviation $[A] = \chi_{\mathbb{P}}(A)$.

Definition 4. *Let (X, cl) be an isotone space and $\mathbb{P}$ be a partition of X. Then the* quotient space $X/\mathbb{P}$ *is the isotone space on the set $X/\mathbb{P}$ that has*

$$\mathcal{B}([x]) = \big\{[N] \big| N \in \mathcal{N}(x') \text{ for all } x' \in [x]\big\} \tag{12}$$

as a basis of the neighborhood system of $[x]$.

It follows that equ.(12) defines the finest structure on $X/\mathbb{P}$ such that $\chi_{\mathbb{P}}$ is continuous. (For all $[x]$ and all $M \in \mathcal{M}([x])$ we need that for each $x' \in [x]$ there is $N_{x'} \in \mathcal{N}(x')$ such that $[N] \subseteq M$, i.e., $\bigcup_{x' \in [x]} [N_{x'}] = \left[\bigcup_{x' \in [x]} N_{x'}\right] \subseteq M$. The argument is then essentially the same as in (Fischer, 1959).)

4.4. The Factorization Theorem. Throughout this contribution we will be concerned with criteria under which a given isotonic space can be represented as a product of other non-trivial neighborhood spaces.

Definition 5. *An isotone space (X, cl) is* factorizable *if there are non-trivial spaces (X_1, c_1) and (X_2, c_2) such that $(X, \mathsf{cl}) \simeq (X_1, c_1) \times (X_2, c_2)$.*

Before we derive a characterization of factorizability we need a few more definitions:

A pair of partitions $\mathbb{P}_1$ and $\mathbb{P}_2$, with canonical maps $\chi_{\mathbb{P}_1}(x) = [x]_1$ and $\chi_{\mathbb{P}_2}(x) = [x]_2$, is *orthogonally complementary* if for all $x \in X$ holds $[x]_1 \cap [x]_2 = \{x\}$. Furthermore, given X and a pair of partitions $\mathbb{P}_1$ and $\mathbb{P}_2$ of X we introduce the map

$$\imath : X \to X/\mathbb{P}_1 \times X/\mathbb{P}_2,\ x \mapsto \imath(x) = ([x]_1, [x]_2) \tag{13}$$

which defines the coordinate representation of $x \in X$ for the product of the quotient space.

By construction $\imath$ is continuous. It is not hard to verify that $\imath$ is invertible if and only if $\mathbb{P}_1$ and $\mathbb{P}_2$ are orthogonally complementary, see (Stadler et al., 2001) for a more detailed discussion. It follows that X is factorizable if $\imath^{-1}$ is continuous (in which case $\imath$ is an isomorphism between X and $X/\mathbb{P}_1 \times X/\mathbb{P}_2$, and neither $\mathbb{P}_1$ nor $\mathbb{P}_2$ is the discrete partition (in which case neither $X/\mathbb{P}_1$ nor $X/\mathbb{P}_2$ consists of a single point.

The product of the quotient spaces has a basis of its neighborhood system that is of the form $[N']_1 \times [N'']_2$ with $N' \in \mathcal{N}([x]_1)$ and $N'' \in \mathcal{N}([x]_2)$. Furthermore, we have $\imath(A) \subseteq [A]_1 \times [A]_2$ for all sets $A \subseteq X$. Factorizability thus requires in particular that $\imath(N)$ is a neighborhood in the product space for all $N \in \mathcal{N}(x)$. This condition can be rewritten as a condition on neighborhoods in (X, cl) and we obtain

Theorem 6. *An isotone space (X, cl) is factorizable if and only if a there is a pair of non-trivial orthogonally complementary partitions $\mathbb{P}_1$ and $\mathbb{P}_2$ such that the neighborhood systems satisfy the following "rectangle condition":*

$$\forall N \in \mathcal{N}(x)\, \exists N', N'' \in \mathcal{N}(x) :\ [N']_1 \times [N'']_2 \subseteq \imath(N)\,. \tag{14}$$

In pretopological spaces the rectangle condition simplifies because of the "filter property" (K3) of neighborhoods: For any two neighborhoods N' and N'' of x, their intersection $N' \cap N'' = N'''$ is again a neighborhood. Thus we can replace N' and N'' by the same neighborhood N''' in equ.(14) and find the following stronger version of the rectangle condition:

$$\forall N \in \mathcal{N}(x)\, \exists N' \in \mathcal{N}(x) :\ [N']_1 \times [N']_2 \subseteq \imath(N)\,. \tag{15}$$

4.5. Local Factorization. It was argued already by Stadler et al. (2001) that it may be unlikely that the space of all possible phenotypes will be factorizable as a whole. A local theory of factorization is thus desirable. We start with a simple but useful technical

Lemma 7. *Suppose* (X, cl) *has a factorization* $(X, \mathsf{cl}) \simeq (X_1, c^1) \times (X_2, c^2)$*, let* $Y_1 \subseteq X_1$*,* $Y_2 \subseteq X_2$*, and* $Y = Y_1 \times Y_2$*. Then* $(Y_1, c^1_{Y_1}) \times (Y_2, c^2_{Y^2}) \simeq (Y, c_Y)$ *is a subspace of* (X, cl)*.*

Proof. The neighborhoods of $y = (y_1, y_2) \in Y$ are the sets $N \cap (Y_1 \times Y_2)$ for all $N \in \mathcal{N}(y)$. This set-system has a basis of the form $(N_1 \times N_2) \cap (Y_1 \times Y_2) = (N_1 \cap Y_1) \times (N_2 \cap Y_2)$ where $N_1 \in \mathcal{N}(y_1)$ and $N_2 \in \mathcal{N}(y_2)$. On the other hand, $N_i \cap Y_i$, $i = 1, 2$ are (by construction) a basis of the neighborhood systems on the subspaces $(Y_i, c^i_{Y_i})$. □

Lemma 7 allows us to transfer a factorization down to all its "rectangular" subspaces. In particular, we already know that the neighborhood system of each point has a basis of rectangular neighborhoods by equ.(14). This suggests to consider a local version of factorizability (Stadler et al., 2001):

Definition 8. (X, cl) *is* locally factorizable *in* $x \in X$ *provided for each neighborhood* $N' \in \mathcal{N}(x)$ *there is a neighborhood* $N \subseteq N'$ *such that the subspace* (N, c_N) *is factorizable.*

Suppose $Y \Subset X$ has a factorization into subspaces Y_1 and Y_2. Of course such a *regional* factorization does not imply that the entire space X is factorizable. However, we have the following

Lemma 9. *Let* (Y, c_Y) *be a subspace of* (X, cl) *that is factorizable with the two factors* Y_1 *and* Y_2*. Suppose* $x \in \mathsf{int}(Y)$ *and such that* $\{x_i\} \notin \mathcal{N}_{Y_i}(x_i)$ *for* $i = 1, 2$*, where* (x_1, x_2) *is the coordinate representation of* x*. Then* (X, cl) *is locally factorizable at* x*.*

Proof. By construction the subspace (Y, c_Y) is factorizable at x. Since $x \in \mathsf{int}(Y)$ there is a neighborhood $N \in \mathcal{N}(x)$ (w.r.t. X) that is contained in Y and that is of the form $N' \times N''$ with $N' \neq \{x_1\}$ and $N'' \neq \{x_2\}$. □

We can summarize the results of this section as follows: If $X = X_1 \times X_2$ is a global factorization, then every rectangular subspace $Y = Y_1 \times Y_2$ has a regional factorization. The existence of a regional factorization of some subspace $Y \Subset X$ in turn implies a local factorization for all $x \in \mathsf{int}(Y)$ (subject to the technical condition that factors must not be sets consisting of a single point).

It is important to note that we cannot expect to obtain useful information about the local factors of a boundary point $y \in \partial Y = \mathsf{cl}(Y) \setminus \mathsf{int}(Y)$ from a factorization of a subspace $(Y, c_Y) \Subset (X, \mathsf{cl})$.

4.6. Prime Factors and Common Refinement. All the above results can be generalized by induction to a finite number of factors. We write

$$(X, \mathsf{cl}) \simeq \prod_{k=1}^{n} (X_k, c^k) \tag{16}$$

Now consider a set $Q \subseteq X$ and the canonical projections $\chi_{\mathbb{P}_k} : X \to X_k$, $x \to x_k = [x]_{\mathbb{P}_k}$. Clearly we have

$$(Q, c_Q) \Subset \left(\prod_{k=1}^{n} \chi_{\mathbb{P}_k}(Q), \prod_{k=1}^{n} c^k_{\chi_{\mathbb{P}_k}(Q)} \right) \Subset \left(\prod_{k=1}^{n} X_k, \prod_{k=1}^{n} c^k \right) \simeq (X, \mathsf{cl}) \tag{17}$$

where $\Subset$ here means subspace. By abuse of notation we write $x = (x_1, x_2, \ldots, x_n)$ and call this a coordinate representation of x (w.r.t. a given factorization).

In the following we will use the abbreviation

$$Q \Downarrow X_k = \chi_{\mathbb{P}_k}(Q) \tag{18}$$

for the projection of a subset (subspace) $Q \Subset X$ onto the factor space X_k. The most important properties of the projection operator can be summarized as follows. Suppose $A = \prod_k A_k$ with $A_k \subseteq X_k$ and $Q \subseteq A$. Then $A_k = A \Downarrow X_k$ and $Q \Downarrow A_k = Q \Downarrow X_k$. If $Q' \subseteq Q$ then $Q' \Downarrow A_k \subseteq Q \Downarrow A_k$. Finally, $Q \Downarrow A_k = \left[\prod_j (Q \Downarrow A_j)\right] \Downarrow A_k$.

Definition 10. *A factorization* $(X, \mathsf{cl}) \simeq \prod_k (X_k, c^k)$ *is a* prime factor decomposition *if none of the factors* (X_k, c^k) *is factorizable.*

In general, the prime factor decomposition is not unique as the following example by Imrich and Klavžar (2000) shows. We will see below that the so-called strong product of graphs corresponds to the product of finite pretopological spaces. We denote by K_n the complete graph with n vertices (and edges connecting each vertex pair). The symbol $\dot\cup$ stands for the disjoint union of graphs. Using the well known formula $K_p \boxtimes K_q = K_{pq}$ and the validity of the distributive law $A \boxtimes (B \dot\cup C) = (A \boxtimes B) \dot\cup (A \boxtimes C)$ we may write

$$\begin{aligned} K_1 \dot\cup K_2 \dot\cup K_4 \dot\cup K_8 \dot\cup K_{32} = \\ (K_1 \dot\cup K_2 \dot\cup K_2^2) \dot\cup (K_2^3 \dot\cup K_2^4 \dot\cup K_2^5) = \left(K_1 \dot\cup K_2 \dot\cup K_2^2\right) \boxtimes \left(K_1 \dot\cup K_2^3\right) = \\ (K_1 \dot\cup K_2^2 \dot\cup K_2^4) \dot\cup (K_2 \dot\cup K_2^3 \dot\cup K_2^5) = \left(K_1 \dot\cup K_2^2 \dot\cup K_2^4\right) \boxtimes (K_1 \dot\cup K_2) \end{aligned}$$

None of the graphs $G_1 = K_1 \dot\cup K_2^2 \dot\cup K_2^4$, $G_2 = K_1 \dot\cup K_2^3$, $G_3 = K_1 \dot\cup K_2^2 \dot\cup K_2^4$, and $G_4 = K_1 \dot\cup K_2$ is factorizable. Thus non-connected graphs in general do not have a unique prime factor decomposition.

We say that the factorizations of X have the *common refinement property* if the following holds. If $X = X_1 \times X_2 = Y_1 \times Y_2$ then there are spaces Z_{11}, Z_{12}, Z_{21}, and Z_{22} such that $X_1 = Z_{11} \times Z_{12}$, $X_2 = Z_{21} \times Z_{22}$, $Y_1 = Z_{11} \times Z_{21}$ and $Y_2 = Z_{12} \times Z_{22}$.

Of course, if a space has a unique prime factor decomposition then it also has the common refinement property. The converse is not true in general. In the finite case, which we will consider next, however, the existence of unique prime factor decomposition and the common refinement property are equivalent.

5. Finite Sets

5.1. Vicinities. In the applications parts of this contribution we will be interested mostly in the case of finite sets. In this case the neighborhood systems $\mathcal{N}(x)$ have a finite basis, i.e., there is a collection $\mathcal{B}(x) \subset \mathcal{N}(X)$ such that:

(1) If $N \in \mathcal{N}(x)$ then there is $B \in \mathcal{B}(x)$ such that $B \subseteq N$.
(2) If $B', B'' \in \mathcal{B}(x)$ and $B' \subseteq B''$ then $B' = B''$.

Clearly, $\mathcal{B}(x)$ is uniquely defined. Condition (2) guarantees that $\mathcal{B}(x)$ is minimal. Note that existence of $\mathcal{B}(x)$ is guaranteed only in the case.

In particular, if $\mathcal{B}(x)$ contains only a single set, $N(x)$, then $\mathcal{N}(x) = \{N | N(x) \subseteq N\}$ is the "discrete filter" of $N(x)$. We call $N(x)$ the *vicinity* (smallest neighborhood) of x. It follows immediately that a finite neighborhood space is a pretopology if and only if $\mathcal{B}(x) = \{N(x)\}$ for all $x \in X$. In particular, the product of two finite pretopological spaces (X_1, c_1) and (X_2, c_2) with vicinities $N_1(x_1)$ and $N_2(x_2)$, resp., is again a finite pretopological space $(X_1 \times X_2, c_{12})$ with vicinities

$$N_{12}(x_1, x_2) = N_1(x_1) \times N_2(x_2) \tag{19}$$

Furthermore, we have

$$\mathsf{cl}(\{(x_1, x_2)\}) = c_1(\{x_1\}) \times c_2(\{x_2\}) \tag{20}$$

as an immediate consequence of equ.(11).

For finite neighborhood spaces we have the following generalization:

Lemma 11. *Let $\mathcal{B}_i(x_i) = \{B_i^j(x_i) | 1 \leq j \leq \ell_i(x)\}$ be the bases of neighborhood spaces on X_i, $i = 1, 2$. Then*

$$\mathcal{B}_{12}(x_1, x_2) = \{B_1^{j_1}(x_1) \times B_2^{j_2}(x_2) | 1 \leq j_1 \leq \ell_1(x_1),\ 1 \leq j_2 \leq \ell_2(x_2)\} \tag{21}$$

is the (uniquely defined) vicinity-basis of their product. Furthermore, all products of vicinities are distinct vicinities in the product space.

Proof. Eq.(21) follows directly from the definition of the product in eq.(10). To see that $B_1^{j_1}(x_1) \times B_2^{j_2}(x_2) \subseteq B_1^{k_1}(x_1) \times B_2^{k_2}(x_2)$ implies $i_1 = k_1$ and $i_2 = k_2$ we observe that this implies $B_i^{j_i}(x_i) \subseteq B_i^{k_i}(x_i)$, $i = 1, 2$. Equality now follows from item (2) in the definition above. □

5.2. Digraphs. Finite pretopological spaces are equivalent to directed graphs with vertex set X. Before introducing this correspondence we proof the following simple

Lemma 12. *Let (X, cl) be a finite pretopological space. Then $y \in N(x)$ if and only if $x \in \mathsf{cl}(y)$.*

Proof. $x \in \mathsf{cl}(y)$ iff $y \in N$ for all $N \in \mathcal{N}(x)$, i.e., iff $y \in N(y)$. □

At the level of individual points N and cl are therefore "dual" in the same sense as the in-neighbors and the out-neighbors of a directed graph.

Definition 13. *Let (X, cl) be a finite pretopological space. The graph $\Gamma(X, \mathsf{cl})$ is the directed graph with vertex set X and an edge xy if and only if $x \neq y$ and $y \in \mathsf{cl}(x)$, i.e., $x \in N(y)$. We call $\mathsf{cl}(x)$ the out-neighbors of x and $N(y)$ the in-neighbors of y.*

This definition establishes a one-to-one correspondence between finite directed graphs and finite pretopological spaces, see (Stadler et al., 2001). In the following we briefly recall the correspondences between graph-theoretical and topological language.

A graph H is a subgraph of G, $H \subseteq G$, if $V_H \subseteq V_G$ and $E_H \subseteq E_G$. A graph H is an *induced subgraph*, in symbols $H \Subset G$, if $V_H \subseteq V_G$ and for all $x, y \in V_H$, $xy \in E_H$ if and only if $xy \in E_G$. The induced subgraphs are exactly the pretopological subspaces on a given point set. The subgraph of G induced by the vertex set $N(x)$ thus represents the pretopological vicinity in the graph-theoretical context. By abuse of notation we shall use the same symbol for a vertex set and a the corresponding induced subgraph (subspace).

A directed graph is symmetric if the sets of in-neighbors and out-neighbors agree at each vertex, i.e., if $N(x) = \mathsf{cl}(x)$ for all $x \in X$. This is the finite case of the following two symmetry axioms, which are equivalent in neighborhood spaces.

(R0) $x \in \mathsf{cl}(y) = y \in \mathsf{cl}(x)$.
(S) $x \in N'$ for all $N' \in \mathcal{N}(y)$ implies $y \in N''$ for all $N'' \in \mathcal{N}(x)$.

The symmetric digraphs are equivalent to the undirected graphs.

Let $H \Subset G$. Then $x \in V_H$ is an *interior vertex* of $H \Subset G$ if $N(x) \subseteq V_H$, i.e., $N(x) \Subset H$. Again this matches the definition in pretopological spaces: "x is an interior point of H if H contains a neighborhood of x". Consequently, we see that $\mathsf{int}(H)$ is the set of all interior points of H. Conveniently, we will regard $\mathsf{int}(H)$ also as an induced subgraph of H. This allows us to speak e.g. of the connectedness of $\mathsf{int}(H)$. In the following we will regard a vertex set always as an induced subgraph of G unless explicitly stated otherwise.

Remark. We have re-interpreted here the directionality of the arcs of Γ compared to the discussion in (Stadler et al., 2001). In this contribution we regard $\mathsf{cl}(x)$ is the out-neighbors because we interpret the closure $\mathsf{cl}(A)$ instead of the vicinity of A as the set of potential offspring of A. This is the natural interpretation for the recombination case and matches the usage of the recombination closure operator in (Gitchoff and Wagner, 1996; Stadler and Stadler, 2002). The vicinities, which took a central role in the interpretation of the pretopological framework in our previous paper (Stadler et al., 2001) are here represented as the in-neighbors. We argue that representing the "immediate neighbors" of a population A by its closure $\mathsf{cl}(A)$ is more natural than using vicinities because the closure-based formalism extends without modifications to all genetic operators and to the case of infinite spaces while a vicinity-based formalism does not. The reason is that vicinities are in general not neigborhoods in the infinite case.

Fortunately, there is a duality between closures and vicinities of individual points in finite pretopological spaces. This guarantees that the change of the arrow directions does not affect any of the conclusions in our previous paper. Only the graphical represention is modified. To illustrate this fact we briefly outline here one simple example: Let $f : (X, \mathsf{cl}) \to (Y, \mathsf{cl})$ be a function between two pretopological spaces. Then f is *continuous* iff for each x and each neighborhood M of $f(x)$ there is neighborhood N of x such that $f(N) \subseteq M$. Reformulating this argument using vicinities we immediately obtain: "f is continuous at x iff $f(N(x)) \subseteq M(f(x))$." On the other hand, closure preservation yields

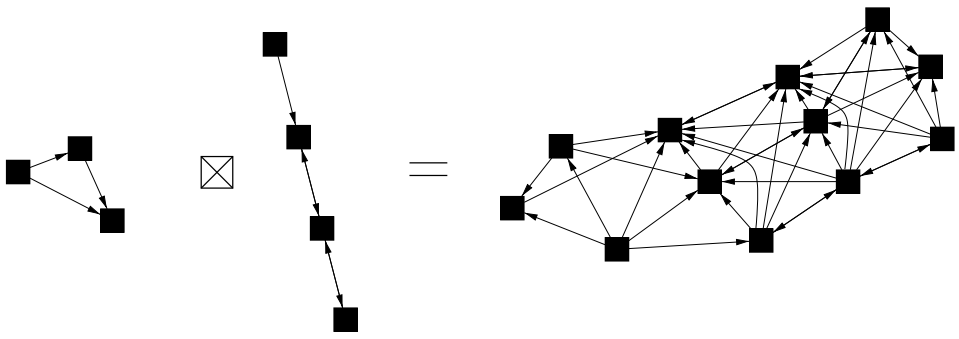

Figure 5. Example of a strong graph product

the analoguous condition: $f(\mathsf{cl}(x)) \subseteq \mathsf{cl}(f(x))$. Hence it does not matter whether we use the in-neighbors or the out-neighbors to determine whether f is continuous. $\triangleleft$

5.3. The Strong Product of Graphs. The product of finite pretopological spaces translates, in the finite case, into the strong product of graphs, see (Stadler et al., 2001).

Definition 14. *Let $G = (V_G, E_G)$ and $H = (V_H, E_H)$ be finite simple graphs (directed or undirected). The* strong product $G \boxtimes H$ *has the vertex set $V_{G\boxtimes H} = V_G \times V_H$ and $(x_1, x_2)(y_1, y_2) \in E_{G\boxtimes H}$ if either (i) $x_1 = y_1$ and $x_2y_2 \in E_H$, or (ii) $x_1y_1 \in E_G$ and $x_2 = y_2$, or (iii) $x_1y_1 \in E_G$ and $x_2y_2 \in E_H$. The edges of type (i) and (ii) are called* Cartesian edges*, edges of type (iii) are non-Cartesian.*

A graph G is *prime* or *non-factorizable* if it is not isomorphic to a $\boxtimes$-product of at least two non-trivial (i.e., empty or one-vertex) graphs.

We denote the degree, in-degree and out-degree of a vertex x in a graph G by $d_G(x)$, $d^i_G(x)$, and $d^o_G(x)$, respectively. For later reference we note the following simple fact:

$$d^\zeta_{G\times H}(x_1, x_2) = d^\zeta_G(x_1) + d^\zeta_H(x_2) + d^\zeta_G(x_1)d^\zeta_H(x_2) \tag{22}$$

for ζ denoting the superscript for in-degree, out-degree, or undirected degree, respectively. For the case of multiple factors equ.(22) generalizes to

$$\begin{aligned} d^\zeta_{\prod_i H_i}(x_1, x_2, \ldots x_n) = &\sum_{i=1}^{n} d^\zeta_{H_i}(x_i) + \sum_{i<j}^{n} d^\zeta_{H_i}(x_i)d^\zeta_{H_j}(x_j) \\ &+ \sum_{i<j<k}^{n} d^\zeta_{H_i}(x_i)d^\zeta_{H_j}(x_j)d^\zeta_{H_k}(x_k) + \ldots + \prod_{l=1}^{n} d^\zeta_{H_l}(x_l) \end{aligned} \tag{23}$$

Probably the most important property of the strong product is

Proposition 15. (Imrich and Klavžar, 2000, chap.5) *Every connected graph G has a unique prime factor decomposition*

$$G = {}^{\boxtimes}\prod_{k=1}^{n} G_k \tag{24}$$

up to the ordering of the factors.

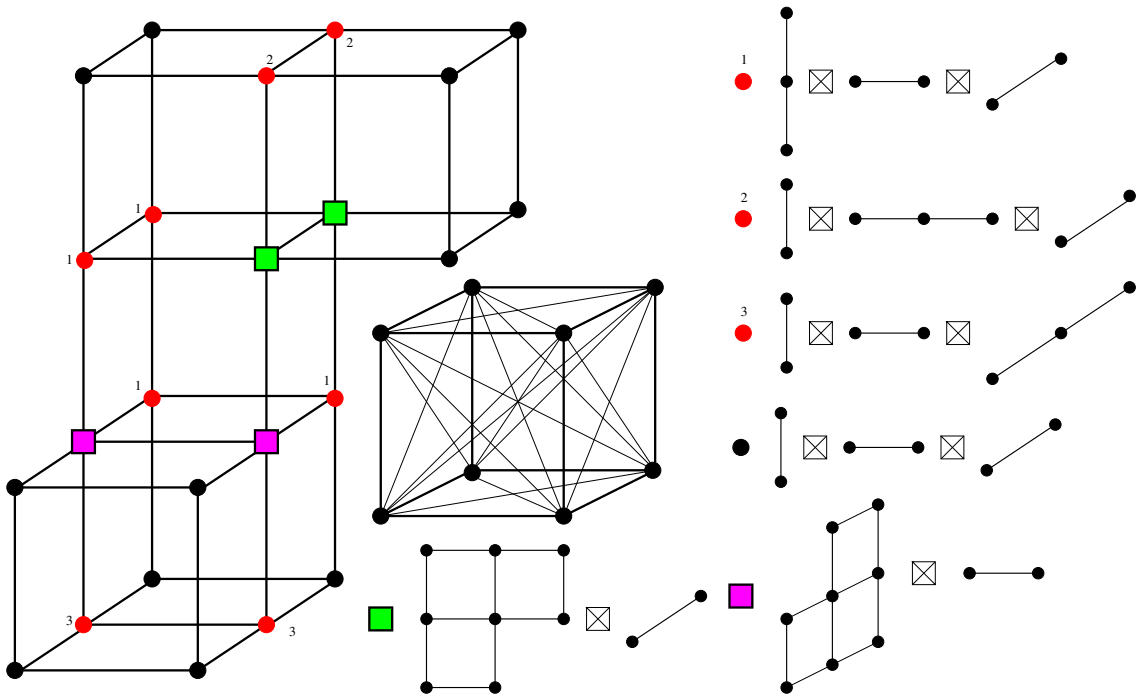

Figure 6. This graph (the non-Cartesian edges in each cube are omitted for clarity) is locally factorizable at each vertex but not globally factorizable.

Hence the *dimension of a graph* G, defined as the number of $\dim G = n$ of prime factors is well-defined. By definition $\dim G = 1$ if and only if G is prime.

It is well known that the strong product of two graphs is connected if and only if each factor is connected. A related result for directed graphs is the following simple

Lemma 16. *A directed graph* $G = {}^{\boxtimes}\prod_{k=1}^{n} G_k$ *is strongly connected if and only if each factor is strongly connected.*

Proof. It is clear that the product of two strongly connected graphs is strongly connected. Conversely, suppose G is strongly connected. Consider $x_k, y_k \in V_{G_k}$ and let x, y be two arbitrary vertices that have coordinates x_k and y_k in the k-th factor. By assumption there is a directed path from x to y. The projection of this path onto G_k is necessarily a connected directed path from x_k to y_k. Thus G_k is strongly connected. □

Not surprisingly, factorization at a global level is not necessary for local factorizability. Figure 6 gives an example of a graph that is prime but allows for local factorizations at every vertex.

Conjecture 17. *Any connected finite neighborhood space has a unique prime factor decomposition.*

Remark. This is suggested by the discussion of combinatorial structures in (Lovász, 1967, 1971) that are very similar in to the finite neighborhood spaces considered here. The unique prime factor decomposition of finite neighborhood spaces will be considered elsewhere in more detail. ◁

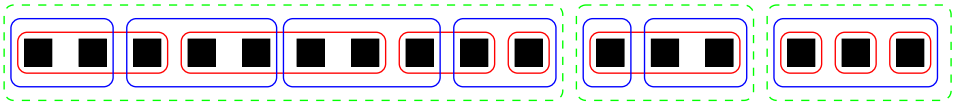

Figure 7. Proof of Theorem 19. The black boxes represent the prime factors of $N(x)$. The factorizations of A and B each introduce a partition of the prime factors of $N(x)$, shown here by red and blue boxes. The common factors correspond to the finest partition that is refined by both the A and the B partition, which is indicated by the dashed green boxes.

5.4. Overlapping Local Factorizations. *For the sake of clarity we will restrict our discussion in this subsection to the case of finite graphs although the results remain valid whenever we work in a situation in which the unique prime factor theorem holds.*

The most important observation here concerns the intersection of two factorizable induced subgraphs $A, B \Subset G$. The following lemma simply rephrases the Unique Prime factor Theorem for the special case of neighborhoods of a single point.

Lemma 18. *Suppose $A, B \Subset G$ are factorizable such that $A = {}^{\boxtimes}\prod_{k=1}^{m} A_k$ and $B = {}^{\boxtimes}\prod_{l=1}^{n} B_l$ and let $x \in \mathsf{int}(A) \cap \mathsf{int}(B)$, i.e., $N(x) \Subset A$ and $N(x) \Subset B$. Then for each of the factors A_k and B_l there is a collection of prime factors of $N(x) = {}^{\boxtimes}\prod_{j=1}^{q} N_j(x_j)$ such that*

$$N(x) \Downarrow A_k = {}^{\boxtimes}\prod_{j \in I_k} N_j(x_j) \qquad \text{and} \qquad N(x) \Downarrow B_l = {}^{\boxtimes}\prod_{j \in J_l} N_j(x_j) \tag{25}$$

Furthermore, the index sets $\{I_k | 1 \leq k \leq m\}$ and $\{J_l | 1 \leq l \leq n\}$ each form a partition of $\{1 \dots q\}$.

In simpler words, the q prime factors of $N(x)$ are combined in different "packages" to yield the restrictions of the given factorizations on A and B to $N(x)$. (In the general case, corresponding expressions hold for all vicinities $N_i(x) \in \mathcal{B}(x)$.)

We say that A and B *have the factor $A_k \sim B_l$ in common* if there is $x \in \mathsf{int}(A) \cap \mathsf{int}(B)$ such that $N(x) \Downarrow A_k = N(x) \Downarrow B_l$. Since the factorizations of A and B, respectively, each define a partition on the set of prime factors of $N(x)$ we see that the number of common factors is the number of classes in the join of these two partitions, see Figure 7. We define $\phi(A, B)$ as the number of factors that the prime factor decompositions of A and B have in common. The number $\phi(A, B)$ is well-defined as a consequence of the uniqueness of the the prime factor decomposition. Of course, we have

$$1 \leq \phi(A, B) \leq \min\{\dim A, \dim B\} \tag{26}$$

Recall that $\mathsf{int}(A \cap B) = \mathsf{int}(B) \cap \mathsf{int}(B)$ holds in pretopological spaces but not in general neighborhood spaces.

We can use this observation to derive a lower bound on the number of factors into which $N(x)$ must decompose:

Theorem 19. *Let $A, B \Subset G$ be factorizable and let $x \in \mathsf{int}(A) \cap \mathsf{int}(B)$. Then*

$$\dim N(x) \geq \dim A + \dim B - \phi(A, B) \tag{27}$$

where $\phi(A, B)$ is the number of factors that A and B have in common at x.

Proof. As a consequence of the discussion above we have to solve the following combinatorial problems, Figure 7. Let $\mathbf{A}$ and $\mathbf{B}$ be two partitions of a finite set X. *What is the minimum cardinality of X given the number of classes of $\mathbf{A}$, $\mathbf{B}$, and $\mathbf{A} \vee \mathbf{B}$?* (Recall that $\mathbf{A} \vee \mathbf{B}$ is the partition of X defined as the transitive closure of the relation "x and y belong to the same class of $\mathbf{A}$ or $\mathbf{B}$". Similarly, the classes of $\mathbf{A} \wedge \mathbf{B}$ are defined by "x and y belong to the same class of both $\mathbf{A}$ and $\mathbf{B}$", i.e., they are the non-empty intersections of the form $A \cap B$ with $A \in \mathbf{A}$ and $B \in \mathbf{B}$.)
Of course, $\dim N(x) \geq |\mathbf{A} \wedge \mathbf{B}|$, because each class must contain at least one factor of $N(x)$. The result follows directly from the inequality

$$|\mathbf{A} \wedge \mathbf{B}| \geq |\mathbf{A}| + |\mathbf{B}| - |\mathbf{A} \vee \mathbf{B}| \tag{28}$$

which is easily proved by induction in the number of classes of B. □

5.5. Continuation of a Local Factorization.

Definition 20. *Let (X, cl) be a neighborhood space. Two points $x, y \in X$ have* consistent local factorizations *if there is a subset $Y \subseteq X$ such that $x, y \in \mathsf{int}(Y)$ and the subspace $Y \Subset X$ has a factorization $Y \simeq \prod_j Y_k$.*

Under these assumptions we see that $\mathcal{N}(x)$ has a basis consisting of sets of form $\prod_k N'_k$, where $N'_k \subseteq \mathcal{N}(x_k)$ and $N'_k \subseteq Y_k$. Analogously, $\mathcal{N}(y)$ has a basis of the form $\prod_k N''_k$ with $N''_k \subseteq \mathcal{N}(y_k)$ and $N''_k \subseteq Y_k$. This establishes a correspondence between the neighborhoods N'_k and N''_k, even though the sets N'_k and N''_k will in general be disjoint. In fact, the set of points with consistent factorizations is not necessarily connected in G. A simple counterexample is given on the l.h.s. of Figure 8.

Definition 21. *Two points x and y are* directly prime-factorization consistent, *$x \hat{\sim} y$, if there is subspace $Y = \prod_k Y_k$ of X such that $x, y \in \mathsf{int}(Y)$ and the factors Y_k are not locally factorizable at x and y.*

In this case Y_k is also prime provided x_k and y_k do not both have a neighborhood consisting of a single point.

Definition 20 can be recast in graph-theoretical language:

Lemma 22. *Let G be a graph $x, y \in V_G$ with local (not necessarily prime) factorizations $N(x) = {}^{\boxtimes}\prod N_k^x$ and $N(y) = {}^{\boxtimes}\prod N_k^y$, respectively. Then these local factorizations are* consistent *if there is an induced subgraph $H \Subset G$ that has a (not necessarily prime) factorization $H = {}^{\boxtimes}\prod H_k$ such that*

1. *x and y are interior points of H;*
2. *for all k holds $N_k^x = N(x) \Downarrow H_k$ and $N_k^y = N(y) \Downarrow H_k$ (with a suitable numbering of the local factors at x and y).*

We write $N_k^x \hat{\asymp} N_k^y \hat{\asymp} H_k$ for the corresponding factors.

Furthermore, x and y are factorization consistent if N_k^x and N_k^y are prime for all k.

The relations $\hat{\asymp}$ and $\hat{\sim}$ are obviously reflexive ($x \hat{\sim} x$ for all x) and symmetric. They are not transitive however, as the r.h.s. example in Figure 8 shows. Their transitive closures $\sim$ and $\asymp$ are therefore equivalence relations.

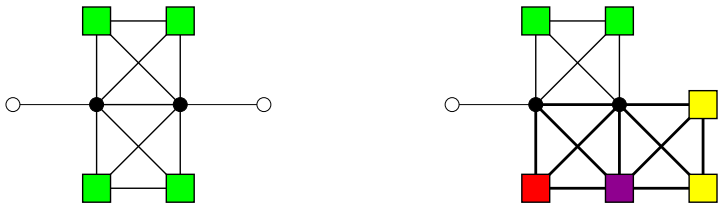

Figure 8. L.h.s.: The induced subgraph highlighted by thick edges is factorizeable ($H = P_1 \boxtimes P_2$). Its interior vertices are indicated by green squares. In these four points the local factors ($P_1 \boxtimes P_1$) are induced subgraphs of the factors of H. Hence their local factorizations are mutually consistent. However, G is not locally factorizable in the two points shown as black circles (because of the spikes attached to them).
R.h.s.: The vertex in red has consistent factorizations in common with both the green vertices (mediated by the vertical rectangle) and the yellow and violet vertices (mediated by the horizontal rectangle). The green and the yellow vertices are factorization-consistent (via the the red vertex as an intermediate) even though they are not directly related by the factorization of any subgraph.

We will say that two vertices are *prime factorization-consistent* if $x \sim y$, i.e., if there is a sequence of vertices $x = x_0, x_1, \ldots, x_{k-1}, x_k = y$ such that x_{j-1} and x_j have consistent factorizations for all $1 \leq j \leq k$. By definition, the factorization-consistent points form an equivalence relation. If there are locally non-factorizable points in G, these will form a separate class of this equivalence relation (only a single factor, trivially mediated through the graph G itself). A necessary condition for a class of factorization-consistent vertices with non-trivial factorization to be connected is that the induced subgraphs H in definition of the relation $\hat{\sim}$ has a connected set of interior points.

Similarly, local factors N_k^x and N_l^z are equivalent, $N_k^x \asymp N_l^z$ if there is a sequence of points $x = y_0, y_1, \ldots, y_m = z$ with local factors $N_{j_i}^{y_i}$ such that $N_{j_{i-1}}^{y_{i-1}} \hat{\asymp} N_{j_i}^{y_i}$. Note that if $N_k^x \asymp N_k^z$ for $k = 1, \ldots, m$ then ${}^{\boxtimes}\prod_{j\in J} N_j^x \asymp {}^{\boxtimes}\prod_{j\in J} N_j^z$ for all index sets $J \subseteq \{1, \ldots, m\}$. In other words, if x and z have some consistent factors, than any product of a number of these factors is also consistent.

Now consider a factor F of a local factorization of the space at some point $x \in X$. Let $\mathcal{H}[F]$ be the collection of induced subgraphs of X that have a factor $F' \asymp F$ consistent with F. Clearly, $\mathcal{H}[F]$ is a partial covering of G. The set $G_F = \bigcup \mathcal{H}[F]$ of points covered can be interpreted as the maximal subset of G on which we can speak of the identity of the factor F. Clearly, there is a local factor $N_z \asymp F$ consistent with F at a point z if and only if $z \in \mathsf{int}(G_F)$. Hence $\mathsf{int}(G_F)$ is the set of all phenotypes for which the character F is defined.

6. Interpretations

The starting point of the current study is Lewontin's idea of quasi-independence (Lewontin, 1978) as a bases for the development of a character concept. A mathematical interpretation of this idea was given before (Stadler et al., 2001) with the notion of structural decomposability of the phenotype space. Characters are identified with factors or dimensions of a region of the phenotype space. We will call the so identified

characters "variational characters." Then we asked what one can say about the identity of characters in two species or organisms, also known as homology, making no other assumption than the existence of quasi-independence. An intuitive summary of the main results has been given in section 3. Here we discuss the biological interpretation and some of the conceptual implications of these results. In particular we will focus on homology, evolutionary novelties and the stability of body plans.

6.1. Identity of Quasi-Independent Characters and Homology. The original definition of homology by Owen identified two characters as homologous if they are *"the same"* in some unspecified way. The meaning of "sameness" was implicitly defined through the morphological criteria used to separate between superficial and essential similarity, i.e. between analogy and homology. This notion was re-interpreted by Darwin with reference to a common ancestor. In the Darwinian tradition homologues are two characters in different species that correspond to the same character in a common ancestor of these species. Homology is thus identified with continuity of descent of an entity, which does not tend to change its identity during the process of descent with modifications. This homology concept can be called "historical" since it is defined solely on the basis of historical, genealogical relationships, but it does not clarify what character identity means (Wagner, 1989b,a).

In fact, the historical homology concept also presupposes a notion of sameness, just as Owen's does, otherwise the phrase "the same character in a common ancestor" would not be defined. An attempt to clarify the notion of sameness that underlies, both Owen's as well as Darwin's notions of homology, is the so-called biological homology concept (Wagner, 1994). It is based on the idea that homologues are clusters of observable attributes that remain stable during adaptive evolution by natural selection. They are thus thought of as causally homeostatic parts of the body which thus retain their identity during (most) evolutionary transformations (Wagner, 1999). This notion is, in its definition, independent of continuity of descent and thus has an unclear relationship to the historical homology concept. Here we argue that both homology concepts and their relationship can be accommodated in a theory of character identity based on quasi-independence. In section 5.5 it is shown that identity of variational characters is well defined and determines a class of (in most cases) variationally connected phenotypes sharing this factor. This means that phenotypes which share a certain factor/character can evolve into each other without going through states where the character is not defined. The notion of character identity based on quasi-independence is thus fully consistent with the historical homology concept.

This consistence, however, takes an interesting form. It shows that continuity of descent is sufficient to establish character identity. Hence descent from a common ancestor is sufficient to establish character identity, as implied in the historical homology concept. But continuity of descent is not necessary for character identity. There is no intrinsic reason, although may be unlikely, why two lineages could not independently evolve phenotypes which have the same variational character. Nothing in the theory of phenotype spaces would forbid that. One can thus say that the historical homology concept is an appropriate criterion of homology but may be deficient as a definition of homology. This

potential deficiency is the same that causes the ambiguity with respect to the meaning of parallel evolution. Parallel evolution is the independent derivation of the same character from an ancestral phenotype (Futuyma, 1998). Can a character which is physically and genetically the same but arose independently be something different? This is a matter of definition, but a strict adherence to the definition of the historical homology concept may lead to biologically meaningless distinctions among different instances of the same biological character.

The relationship between variational characters and the biological homology concept is less obvious. The biological homology concept directly refers to the physical realization of the character and its variational properties, i.e. common developmental constraints. In contrast, the variational character concept is entirely abstract from what phenotypes and characters physically are. It is only based on the topological relationships of phenotypes defined by the variational mechanisms that transform phenotypes (say the underlying genotypes) by mutation and recombination. Variational characters are thus defined as statements about the symmetries of phenotype space and make no explicit reference to a description of the phenotypes themselves. The connection between variational characters and biological homologues, however, is provided through the fact that every set of orthogonal factors implies a set of orthogonal partitions, as shown in Stadler et al. (2001).

A partition $\mathbb{P}$ of a set A is a set of equivalence classes $P \in \mathbb{P}$, $P \subseteq A$, which collectively contain all the elements in this set. This means that each character state of a variational character can be understood as an equivalence class consisting of all the phenotypes which have the same state of the variational character but which may be different in other respects. In that way an abstract factor can be translated into a cluster of phenotypic and genotypic attributes, which is what we usually think of when we speak of an organismal character, for instance a bone with a certain shape and location in the body. Regardless of whether a character is defined as an attribute cluster in the sense of the biological homology concept, or as a variational character based on quasi-independence, these two notions are translatable into each other, due to the connection between factors and partitions. In either way a character can be understood as a hypothesis about the existence of homeostatic mechanisms that maintain the identity of a part of the phenotype and which makes them thus combinable with different contexts of other characters. We conclude that quasi-independence is a strong enough concept to explain and accommodate both the historical as well as the biological homology concept. Nothing else is needed but quasi-independence to clarify these concepts.

6.2. Evolutionary Novelties. The novelty concept is about as elusive as the homology concept, and closely connected to the notion of character identity (Nitecky, 1990). A novelty can be defined as any character that arises in evolution which is neither homologous to a character in an ancestor or serially homologous to any other part of the organism (Müller and Wagner, 1991). In the language of phenotype space topology as developed in (Stadler et al., 2001) and this paper, the evolution of a novelty is equivalent to evolution from one part of the phenotype space into another part that has a different

regional factorization. In other words, the origin of a novelty is the appearance of a variational character that is not defined in the ancestral lineage. Formal phenotype spaces and their factorizations provides a mathematical language in which the process of the evolutionary innovation can be described. This is a major advantage over other, established mathematical theories of phenotypic evolution, like quantitative genetics, where the set of characters is assumed to be fixed. In these models the origin of novelties is structurally impossible to model. In fact the search for a language that can accommodate evolutionary novelties was a major motivation for developing the present theory. The result most relevant to the evolution of novelties is theorem 19, which determines the minimal dimensionality of phenotypes that belong to the overlap between two areas of regional factorization, say A and B.

Any maximal part of the phenotype space, which has its own regional factorization, can be thought of as a particular type or body plan. They consist of all the mutationally connected phenotypes that can be decomposed onto the same set of variational characters. One implicit results of Theorem 19 is that types can overlap and that overlap among body plans is in fact natural in the way factorization works. Types or body plans defined on the basis of variational characters are thus not mutually exclusive classes but can to various degrees be connected to each other. In this context there can be transitional forms that connect two different body plans. Hence a variational body plan concept is, in contrast to a typological body plan concept, fully compatible with evolutionary theory. No hopeful monsters are necessary (although logically possible, see below) to evolve a new body plan and no logical contradictions exist between evolution and body plans as those suggested by Medawar and Medawar (1983, p.281-282). There are however some topological restrictions that arise in the transition between different body plans. We will explore those below.

Theorem 19 tells us that if there is a phenotype x which belongs to the overlap of types A and B its dimensionality has to be larger than the sum of the dimensionalities of A and B, minus the number of factors that A and B share, $\phi(A, B)$

$$\dim N(x) \geq \dim A + \dim B - \phi(A, B)$$

The reason simply is that any phenotype that belongs both to A as well as B has to be compatible with both regional factorizations. Any factor of A and any factor of B has to correspond to one or a combination of local factors of $N(x)$. Now let us consider a few scenarios to see whether this result makes intuitive sense.

Let us consider cases where evolution proceeds from A to B and B is the same as A except that it has one factor more that is not present in A, i.e. a single novelty. Then $\phi(A, B) = \dim A$ and the local dimensionality of x only has to be at least as high as B: $\dim N(x) \geq \dim B$. This is a simple accretion of a novelty. An analogous argument can be made for the loss of a character, $\dim B = \dim A - 1$ and $\dim B = \phi(A, B)$.

More interesting is the case where the two types differ by more than one variational character and do not simply differ by accretion of characters on top of those of A, $\phi(A, B) < \min\{\dim A, \dim B\}$. Two situations need to be distinguished: 1) the two types do not directly overlap, and 2) the two types overlap and thus share transitional phenotypes that belong to either. In the first case the theory makes not predictions

except that there have to be other types D, E, F, etc. that form a chain of overlapping types, or some arbitrary non-decomposable forms. In the second case, however, topological constraints mandate that the transitional form is strictly more complex (has more variational characters) than either of the two types. This is easily seen by rewriting $\dim A = \phi(A, B) + n_A$, where n_A is the number of unique variational characters of A not shared with B, and $\dim B = \phi(A, B) + n_B$, analogously. From this it immediately follows that

$$\dim N(x) \geq \dim B + n_A \tag{29}$$

or $\dim N(x) > \max\{\dim A, \dim B\}$ by assumption. If there are transitional forms between A and B (phenotypes which belong to both A and B) have to represent a *complexity hump* since they need to have all the variational characters of either type. Of course these new characters do not need to appear all at once, since any phenotype that has acquired some of the characters of B but not all of them does not strictly belong to B and thus is not in the overlap of A and B (both of them open sets).

Although not strictly necessary, from a mathematical point of view, transitional forms which possess a combination of plesiomorphic and apomorphic characters is a natural consequence of topological constraints on local factor decompositions. The only constraint is that there has to be at least one form that has all the characters of the ancestor and the derived body plan. Otherwise the evolution has to go through forms that belong neither to type A nor to type B.

Next we want to ask whether it is mathematically possible to have a direct evolutionary transition between two types but avoids the complexity hump, i.e. are there cases not covered by theorem 19. We will proceed by asking what follows from a violation of the dimensionality equation for $N(x)$. It is easy to show that $\dim N(x) < \dim A + \dim B - \phi(A, B)$ implies that x will not an element of $\mathsf{int}(A)$ or not an element of $\mathsf{int}(B)$, or both. This condition can be satisfied if x is neither internal to A nor to B, but then there would be no direct transition between them either. The other possibility to satisfy this condition amounts to the definition of a *hopeful monster*. We translate the notion of a hopeful monster as a phenotypes that can be reached from the ancestor A by a single step but is not part of A, $x \notin \mathsf{int}(A)$, but belongs to B, $x \in \mathsf{int}(B)$. Whether this is possible depends on the kind of space the phenotype space represents. If A and B are open sets in a topological space, this is not possible, because it is true that if $\mathsf{int}(A) \cap \mathsf{int}(B) = \emptyset$, then also $\mathsf{int}(A) \cap \mathsf{cl}(B) = \emptyset$. In pretopological spaces and neighborhood spaces, however, a hopeful monster is possible in principle, though may be biologically not likely. If one wants to avoid the complexity hump in a direct transition between two types then 1) the transition has to occur in a pretopological space and 2) has to involve a hopeful monster, i.e. a descendant of A but not a representative of the type A and already a fully fledged member of type B. Hopeful monsters are (pre-) topologically possible but this theory can not speak to the biological likelihood of such a transition.

6.3. The Stability of Body Plans. In the previous section a body plan or type was conceptualized as a part of the phenotype space with its own regional factorization, or set of variational characters. Types, however, are not only characterized by their

own set of characters but often, if not always, display remarkable evolutionary stability. This stability can have multiple causes, from developmental constraints to functional integration. Here we propose two additional factors that may contribute to the stability of body plans. The first has to do with the topological properties of factorizable spaces, the second with the evolvability of modular body plans.

In section 5.3, eqns. (22) and (23) give an equation about the vertex degree of factorizable graphs. Note that graphs are a model of finite pretopological spaces, where each vertex represents a phenotype and each edge a possible genetic transformation of the phenotype. The vertex degree is the number of edges that end or originate at a particular vertex. A graph is called vertex regular, if each vertex has the same number of edges, and irregular if they do not.

The vertex degree is an interesting property of graphs for the following reason. If one considers a graph as a "map" of possible paths to go, as we do with phenotype spaces, then the vertex degree tells us how often a vertex is visited during a random walk on the graph. In other words the vertex degree is proportional (in undirected graphs) to the probability that a random walk will be at the given vertex. Of course the probability will also depend on the degree of the other vertices in the graph, but the vertices with the higher degree will be visited more often than those with lower vertex degrees.

If a graph, that represents a configuration space for a genetic operator, has vertices with a much higher degree than others there will be an "intrinsic (entropic) pull" towards the states represented with higher vertex degree. This pull is independent and can be opposed to any evolutionary force caused by natural selection. In contrast, in configuration spaces that are vertex regular, no such preferred directions exist. Examples are the Hamming graph representing nucleotide sequences with constant length and base substitutions as variational operator. On a vertex regular configuration space any directionality has to come from natural selection rather than from intrinsic tendencies. With this in mind let us now consider product spaces.

Equation 22 tells us that if each factor is vertex regular, so will be the product space obtained from these factors. If, however, the factors are vertex irregular, this irregularity will be transmitted to the product space and even amplified. If each factor has mildly preferred states, i.e. vertices with somewhat higher vertex degree, these preferences translate into a cluster of highly preferred states in the product space. This is because the vertex degree of the vertex in the product space is a multilinear function of the vertex degrees of all of the vertices in the factors. In other words, a product space generically will contain one or more clusters of highly preferred states. Furthermore, in particular in undirected graphs, these island of preferred states will be in the interior of the factorizable region. This means that the preferred states in a product space will be the ones that are not poised to leave the factorizable region. In other words, the preferred states make it less likely to realize a mutation that leaves the type. Hence there is a generic tendency for types to evolve states within the same type and thus preserves the type. This factor is entirely statistical and adds to the other mechanistic reasons for the stability of types, like functional and developmental integration.

Note that this suggestion implies that irregular product spaces are predicted to be both, highly evolvable among states within the type as well as stable against transformations that affect the type itself. Factorizability can also been seen as a condition of modularity, i.e., the existence of independently changeable parts of the organism. It is widely thought that if modularity matches the different functions the organism has to perform, it can increase evolvability. Hence evolution within a type is likely to be facilitated, while phenotypes outside factorizable regions are likely to be less evolvable. Hence there are two reasons why adapative evolution is predicted to occur preferntially within the confines of a given type than leading to another type or any other state outside the focal type. There is an entropic pull to the interior of the part of the phenotype space representing the type. In addition there is a higher chance to increase fitness by evolution within a type (due to modularity) than with mutational steps leaving regions of high modularity. Both of these factors make it more likely that adaptive challenges will be met by phenotypic states within a given type than leading to the evolution of a new type.

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References

L. Ancel and W. Fontana. Plasticity, evolvability and modularity in RNA. *J. of Exp. Zoology (Molecular and Developmental Evolution)*, 288:242–283, 2000.

R. Bürger. *The Mathematical Theory of Selection, Recombination, and Mutation*. Wiley, Chichester, UK, 2000.

E. Čech. *Topological Spaces*. Wiley, London, 1966.

M. Changat, S. Klavžar, and H. M. Mulder. The all-path transit function of a graph. *Czech. Math. J.*, 51:439–448, 2001.

J. Cupal, S. Kopp, and P. F. Stadler. RNA shape space topology. *Artificial Life*, 6:3–23, 2000.

M. M. Day. Convergence, closure, and neighborhoods. *Duke Math. J.*, 11:181–199, 1944.

N. Eldredge and S. J. Gould. no title. In T. J. M. Schopf, editor, *Models in Paleobiology*, pages 82–115. Freeman, San Francisco, 1972.

H. R. Fischer. Limesräume. *Math. Annalen*, 137:269–303, 1959.

W. Fontana and L. W. Buss. "the arrival of the fittest":towards a theory of biological organisation. *Bull. Math. Biol.*, 56(1):1–64, 1994.

W. Fontana, W. Schnabl, and P. Schuster. Physical aspects of evolutionary optimization and adaption. *Phys. Rev. A*, 40:3301–3321, 1989.

W. Fontana and P. Schuster. Continuity in Evolution: On the Nature of Transitions. *Science*, 280:1451–1455, 1998a.

W. Fontana and P. Schuster. Shaping Space: The Possible and the Attainable in RNA Genotype-Phenotype Mapping. *J. Theor. Biol.*, 194:491–515, 1998b.

D. J. Futuyma. *Evolutionary Biology*. Sinauer Associates, Sunderalnd, Massachusetts, 1998.

G. C. Gastl and P. C. Hammer. Extended topology. Neighborhoods and convergents. In N.N., editor, *Proceedings of the Colloquium on Convexity 1965*, pages 104–116, Copenhagen, DK, 1967. Københavns Univ. Matematiske Inst.

S. F. Gilbert. Genes classical and genes developmental: the difference uses of genes in evolutionary theory. In P. Beurton, R. Falk, and Rheinberger H.-J., editors, *The concept of the gene in development and evolution*, pages 178–192, New York, 2000. Cambridge University Press.

P. Gitchoff and G. P. Wagner. Recombination induced hypergraphs: a new approach to mutation-recombination isomorphism. *Complexity*, 2:37–43, 1996.

S. Gniłka. On extended topologies. I: Closure operators. *Ann. Soc. Math. Pol., Ser. I, Commentat. Math.*, 34:81–94, 1994.

D. Graur and W.-H. Li. *Fundamentals of Molecular Evolution*. Sinauer Associates, Sunderland, Massachusetts, 2000.

P. C. Hammer. Extended topology: Set-valued set functions. *Nieuw Arch. Wisk. III*, 10:55–77, 1962.

M. A. Huynen, P. F. Stadler, and W. Fontana. Smoothness within ruggedness: The role of neutrality in adaptation. *Proc. Natl. Acad. Sci. USA*, 93:397–401, 1996.

W. Imrich and S. Klavžar. *Product Graphs: Structure and Recognition*. Wiley, New York, 2000.

R. E. Lenski and M. Travisano. Dynamics of adaptation and diversification: A 10,000-generation experiment with bacterial populations. *Proc. Natl. Acad. Sci. USA*, 91: 6808–6814, 1994.

R. C. Lewontin. *The Genetic Basis of Evolutionary Change*. Columbia University Press, New York, New York, 1974.

R. C. Lewontin. Adaptation. *Sci. Am.*, 239:156–169, 1978.

L. Lovász. Operations with structures. *Acta Math. Acad. Sci. Hung.*, 18:321–328, 1967.

L. Lovász. Unique factorization in certain classes of structures. In *Mini-Conf. Univers. Algebra, Szeged 1971*, pages 24–25. Bolyai Janos Math. Soc., 1971.

P. B. Medawar and J. S. Medawar. *Aristotle to Zoos. A philosophical Dictionary of Biology*, volume Cambridge, MA. Harvard University Press, 1983.

G. B. Müller and G. P. Wagner. Novelty in evolution: Restructuring the concept. *Annu. Rev. Ecol. Syst.*, 22:229–256, 1991.

J. May nard Smith, R. Burian, S. A. Kauffman, P. Alberch, J. Campbell, B. Goodwin, R. Lande, D. Raup, and L. Wolpert. Developmental constraints and evolution. *Quart. Rev. Biol.*, 60:265–287, 1985.

M. H. Nitecky. *Evolutionary Innovations*. University of Chicago Press, Chicago, 1990.

C. M. Reidys and P. F. Stadler. Combinatorial landscapes. *SIAM Review*, 44:3–54, 2002.

C. D. Schlichting and M. Pigliucci. *Phenotypic Evolution: A Reaction Norm Perspective*. Sinauer Associates, Inc., Sunderland, Massachusetts, 1998.

P. Schuster, W. Fontana, P. F. Stadler, and I. L. Hofacker. From sequences to shapes and back: A case study in RNA secondary structures. *Proc. Roy. Soc. Lond. B*, 255: 279–284, 1994.

K. Schwenk. A utilitarian approach to evolutionary constraint. *Zoology*, 98:251–262, 1995.

M. Shpak and G. P. Wagner. Asymmetry of configuration space induced by unequal crossover: implications for a mathematical theory of evolutionary innovation. *Artificial Life*, 6:25–43, 2000.

S. Spiegelman. An approach to experimental analysis of precellular evolution. *Quart. Rev. Biophys.*, 4:213–253, 1971.

B. M. R. Stadler and P. F. Stadler. Higher separation axioms in generalized closure spaces. Technical report, Institute for Theoretical Chemistry and Structural Biology, University of Vienna, Vienna, Austria, 2001. `www.tbi.univie.ac.at/papers/`.

B. M. R. Stadler, P. F. Stadler, M. Shpak, and G. P. Wagner. Recombination spaces, metrics, and pretopologies. *Z. Phys. Chem.*, 216:217–234, 2002.

B. M. R. Stadler, P. F. Stadler, G. P. Wagner, and W. Fontana. The topology of the possible: Formal spaces underlying patterns of evolutionary change. *J. Theor. Biol.*, 213:241–274, 2001.

B. M. R. Stadler and Peter F. Stadler. Generalized topological spaces in evolutionary theory and combinatorial chemistry. *J. Chem. Inf. Comput. Sci.*, 2002. In press; Proceedings MCC 2001, Dubrovnik;.

P. F. Stadler, R. Seitz, and G. P. Wagner. Evolvability of complex characters: Population dependent Fourier decomposition of fitness landscapes over recombination spaces. *Bull. Math. Biol.*, 62:399–428, 2000.

P. F. Stadler and G. P. Wagner. The algebraic theory of recombination spaces. *Evol. Comp.*, 5:241–275, 1998.

J. W. Szostak and A. D. Ellington. *In Vitro* selection of functional RNA sequences. In R. F. Gesteland and J. F. Atkins, editors, *The RNA World*, pages 511–533. Cold Spring Harbor Laboratory Press, Plainview, NY, 1993.

G. P. Wagner. The origin of morphological characters and the biological basis of homology. *Evolution*, 43:1157–1171, 1989a.

G. P. Wagner. The variance allocation hypothesis of stasis and punctuation. In P. Hoyningen-Huene and F. M. Wuketits, editors, *Molecular Biology and Organisms*, pages 161–185. Reidel, Boston, 1989b.

G. P. Wagner. Homology and the mechanisms of development. In B. K. Hall, editor, *Homology: The Hierarchical Basis of Comparative Biology*, pages 273–299. Academic Press, San Diego, California, 1994.

G. P. Wagner. A research programme for testing the biological homology concept. In G. R. Bock and G. Cardew, editors, *Homology*, pages 125–134. John Wiley, New York, New York, 1999.

G. P. Wagner and L. Altenberg. Complex adaptations and the evolution of evolvability. *Evolution*, 50:967–976, 1996.

G. P. Wagner, C.-H. Chiu, and M. D. Laubichler. Developmental evolution as a mechanistic science: the inference from developmental mechanisms to evolutionary processes. *Am. Zool.*, 40:108–120, 2000.

G. P. Wagner and M. D. Laubichler. Character indentification in evolutionary biology: The role of the organism. *Theory Biosci.*, 119:20–40, 2000.