The Algebraic Theory of Recombination Spaces

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Abstract

A new mathematical representation is proposed for the configuration space structure induced by recombination which we called "P-structure". It consists of a mapping of pairs of objects to the power set of all objects in the search space. The mapping assigns to each pair of parental "genotypes" the set of all recombinant genotypes obtainable from the parental ones. It is shown that this construction allows a Fourier-decomposition of fitness landscapes into a superposition of "elementary landscapes". This decomposition is analogous to the Fourier decomposition of fitness landscapes on mutation spaces. The elementary landscapes are obtained as eigenfunctions of a Laplacian operator defined for P-structures. For binary string recombination the elementary landscapes are exactly the p-spin functions (Walsh functions), i.e. the same as the elementary landscapes of the string point mutation spaces (i.e. the hypercube). This supports the notion of a strong homomorphisms between string mutation and recombination spaces. However, the effective nearest neighbor correlations on these elementary landscapes differ between mutation and recombination and among different recombination operators. On average, the nearest neighbor correlation is higher for one-point recombination than for uniform recombination. For one-point recombination the correlations are higher for elementary landscapes with fewer interacting sites as well as for sites which have closer linkage, confirming the qualitative predictions of the Schema-Theorem. We conclude that the algebraic approach to fitness landscape analysis can be extended to recombination spaces and provides an effective way to analyze the relative hardness of a landscape for a given recombination operator.

1. Landscapes on Discrete Structures

The notion of a *landscape* plays an important role in the theory of evolution and in optimization theory. Implicit in this idea is a collection of genotypes arranged in an abstract metric space, with each genotype next to those other genotypes which can be reached by a single mutation, as well as a value assigned to each genotype [59]. Such a construction is by no means restricted to the theory of biological evolution. Hamiltonians of disordered systems, such as spin glasses [5, 40], and the cost functions of combinatorial optimization problems [22] have the same mathematical structure. In most applications there is an unambiguous notion of neighborhood, which imposes the structure of a graph on the set of configurations. Unfortunately, this picture is not powerful enough to deal with crossover (recombination) where the relatedness of sequences is determined by pairs of 'parents' rather than individual ancestors.

The intuitive notion of *ruggedness* is closely related to the difficulty of optimizing (or adapting) on a given landscape. It depends obviously on both the fitness

function $f : V \to \mathbb{R}$, and on the geometry of the search space, which is induced by the search process. Two approaches have been considered for the case of landscapes on graphs. Palmer [43] uses the number of local optima, that is of configurations $\hat{x}$ with the property that $f(\hat{x}) \leq f(y)$ holds for all y in the neighborhood of $\hat{x}$, as the measure of ruggedness. Sorkin [48], Eigen *et al.* [17], and Weinberger [56] use correlation measures. This approach is closely related to the algebraic graph theory of the configuration space [50, 51, 53], see section 2.

In order to deal with landscapes as "seen" by crossover (recombination), as in the case of genetic algorithms [32], we need to generalize our notion of a configuration space. Given a *finite* set V of configurations *endowed with some additional geometric structure* $\mathcal{X}$, we define a landscape as a real valued map[1] (*fitness function*) $f : V \to \mathbb{R}$ together with a (geometric) structure $\mathcal{X}$ on V. This structure $\mathcal{X}$ can be a neighborhood-relation implying a graph, it can be a metric, or a more general topology, or another algebraic or combinatorial construction. The question then becomes: given f and $\mathcal{X}$, what do we mean by "ruggedness"? The "geometric" approach based on local optima faces an immediate problem: what exactly do we mean by "local" when the structure $\mathcal{X}$ does not imply a metric distance measure in a natural way? We shall show in this contribution, that the "algebraic" approach based on correlation functions is more general. It can indeed deal with recombination. Two fundamental problems will be addressed:

(1) How can we compare two landscapes f and g given the structure $\mathcal{X}$ arising from a prescribed search procedure?

(2) How can we compare two search procedure inducing the structures $\mathcal{X}$ and $\mathcal{Y}$ for a prescribed landscape f?

These two problems have been adressed in a very interesting way by Wolpert and Macready [38, 58]. Their "no-free-lunch theorem" shows that all algorithms that search for an extremum of a cost function perform exactly the same, when averaged over all possible cost functions. In particular, if algorithm A outperforms algorithm

[1] Alternatively, we might view f simply as an $|V|$ dimensional vector. The function-like notation $f(x)$ will prove to be useful, however.

B on some cost functions, then, loosely speaking, there must exist exactly as many other functions where B outperforms A. Their theory implies that no optimization problems are intrinsically harder than another one as long a no reference is made to an algorithm or a class of algorithms. Classes of problems that are intrinsically harder than others can be defined however by considering the level of hardness of a combinatorial optimization problem for the optimal algorithm that exists for the given problem. Unfortunately, this analysis is non-constructive and does not even in principle provide us with a receipt for the construction of the optimal algorithm for a given landscape.

It is the purpose of this manuscript to explore to what extent an "algebraic graph theory" approach to landscapes on undirected graphs (see section 2 for a brief summary) can be extended to describing "recombination spaces". Such an extension might be useful for devising a constructive approach to the relative hardness of optimization problems and to the relative effectivity of search processes.

The problem of recombination spaces is that recombination acts on pairs of types, e.g., chromosomes or strings, rather than single types as point mutations. The problem was addressed by Culberson [12] for one-point recombination of Boolean strings. Culberson started from the set of unordered pairs of complementary strings and obtained a graph connecting each pair with each other pair that can be reached by one application of the cross-over operator. He showed that the resulting graph is a hypercube and is thus isomorphic to a one-point mutation space. However, the isomorphism only was demonstrated between the mutation space for strings of length n with the recombination space for strings of length $n+1$. Hence, the isomorphism is between mutation and recombination spaces for different sets of objects, in this case strings of different length.

Another limitation of Culberson's approach is that it only considers recombination events among complementary strings and ignores all the other possible recombination events. The latter problem was solved by Jones [34], by constructing recombination landscapes where the vertices are all possible pairs of strings. However, with these structures it is very difficult to see the similarity, or lack of similarity,

to mutation spaces. The vertices of mutation spaces are single strings while the vertices of Culberson and Jones spaces are pairs of strings. This problem was addressed by Gitchoff and Wagner [23] who generalized the notion of a configuration space from simple graphs to hypergraphs. In their approach each vertex is a single type, e.g., a string, and a generalized edge is constructed from the set of all recombinants of a pair of strings. For strings of fixed length it has been shown that the so constructed recombination space is actually homomorphic to the point mutation space of the same set of strings [23].

Although useful for showing the general similarity between mutation and recombination spaces, hypergraphs do not contain enough information to support an algebraic theory of recombination spaces. The main problem is that the elements in the generalized edge of a hypergraph are treated as functionally equivalent [6, 44, 45]. However, it has been shown for one point recombination that only one pair of parental strings can generate exactly this set of recombinants [23]. Hence, we need to attach to each edge of the hypergraph the pair or pairs of parental strings which can generate this set of recombinants.

This is done in this paper by proposing so-called P-structures, which is a mapping of pairs of types to the edges of the recombination hypergraph, see section 3. We shall see that a generalization of the spectral theory of graphs and hypergraphs can be devised for P-structures. In section 4 this construction will be applied to recombination on spaces of strings with constant length. Section 5 contains a comparison of crossover and mutation for a variety of landscapes.

2. The Algebraic Theory of Landscapes on Graphs

2.1. Fourier Series on Graphs

Let $f : V \to \mathbb{R}$ be a landscape. The configuration space is the graph $\Gamma = (V, E)$ which is faithfully described by its *adjacency matrix* $\mathbf{A}$ which has the following entries $\mathbf{A}_{xy} \stackrel{\text{def}}{=\!=} 1$ if $\{x, y\}$ is an edge of Γ and $\mathbf{A}_{xy} \stackrel{\text{def}}{=\!=} 1$ otherwise. We shall write $N \stackrel{\text{def}}{=\!=} |V|$ for the total number of configurations. The number of neighbors of a vertex $x \in V$ is called the *degree* of x; by $\mathbf{D}$ we denote the diagonal matrix of the vertex degrees. It turns out that the *graph Laplacian* $-\Delta \stackrel{\text{def}}{=\!=} \mathbf{D} - \mathbf{A}$ provides a more convenient description of Γ. This matrix is related to the more familiar differential operator Δ in continuous spaces, see [3, 25, 41, 47]. The graph Laplacian $-\Delta$ is non-negative definite, and the smallest eigenvalue $\lambda_0 = 0$ has multiplicity 1 if and only if Γ is a connected graph. A graph is *regular* is all vertices have the same vertex degree, i.e., $\mathbf{D} = D\mathbf{I}$, where $\mathbf{I}$ is the identity matrix and D is the common degree of all vertices. Our prime interest here is sequences spaces which are regular of degree $D = (\alpha - 1)n$, where n is the sequence length and α is the number of different letters in the alphabet. Throughout this section we shall assume that Γ is regular and connected.

A series expansion $f(x) = \sum_{i=1}^{N} a_i \varphi_i(x)$, where the φ_i form a complete and orthonormal system of eigenfunctions of the graph Laplacian $-\Delta$, is termed a *Fourier series* expansion of the landscape f. Note that we write $\varphi_i(x)$ to mean the x-component of the vector φ_i throughout this paper. A landscape is called *elementary* if it is of the form $f(x) = c + \varphi(x)$, where c is an arbitrary constant and φ is an eigenvector of the graph-Laplacian belonging to an eigenvalue $\lambda > 0$, see [26, 53]. Elementary landscapes form an important class because the landscape of the most intensively studied combinatorial optimization problems, such as the travelling salesman problem [37], the graph bipartitioning problem, or the graph coloring problem, are of this type [26].

For boolean hypercubes defined on the alphabet $\{+1, -1\}$, a Fourier basis can easily be determined explicitly. It is easy to verify that "p-spin function"

$$\varepsilon_{i_1 i_2 \ldots i_p}(x) \stackrel{\text{def}}{=\!=} x_{i_1} x_{i_2} \ldots x_{i_p} \qquad \text{with} \quad i_1 < i_2 < \ldots < i_p \tag{1}$$

is an eigenvector of $-\Delta$ belonging to the eigenvalue $\lambda_p = 2p$, see e.g., [57]. In particular, Derrida's p-spin models [16, 15] are superpositions of these basis functions containing only contributions with a single interaction order $p > 0$. This is to say that the p-spin Hamiltonians are eigenfunctions of the Laplacian of the Boolean hypercube irrespective of the particular choice of the interaction coefficients.

2.2. Correlation Functions

If a simple algebraic description of a landscape is not available we need a condensed description of its salient features. This is because the extremely large number of configurations, for instance $N = 4^n$ for RNA sequences or $N = n!$ for n-city travelling salesman problems, renders a complete "listing" infeasible. Correlation measures relating the values of nearby configurations with each other seem to be a natural approach.

Defining mean and variance[2] of a landscape f by

$$\overline{f} \stackrel{\text{def}}{=\!=} \frac{1}{N} \sum_{x \in V} f(x) \qquad \text{and} \qquad \sigma_f^2 \stackrel{\text{def}}{=\!=} \frac{1}{N} \sum_{x \in V} \big(f(x) - \overline{f}\big)^2 = \overline{f^2} - \overline{f}^2$$

we note that $\sigma_f^2 = 0$ if and only if f is constant, i.e., for *flat* landscapes. Two types of *correlation functions* have been investigated. Eigen and co-workers [17] introduced

$$\rho(d) \stackrel{\text{def}}{=\!=} \frac{\langle f(x) f(y) \rangle_{d_H(x,y)=d} - \overline{f}^2}{\sigma_f^2} \,, \tag{2}$$

[2]There is nothing "statistical" about $\overline{f}$ or σ_f^2. Both quantities are functionals of f. They should not be mistaken for the averages over different instances that are commonly used in a statistical mechanics type analysis of what one might call statistical models of landscapes (random fields) [40].

where the notation $\langle\,.\,\rangle_{d(x,y)=d}$ indicates the mean value is calculated from all pairs of sequences x, y with Hamming distance [27] $d_H(x,y) = d$. An alternative approach has been explored by Weinberger [56]. A simple random walk $\{x_0, x_1, \ldots\}$ on the vertex set of Γ generates a "time series" $\{f(x_0), f(x_1), \ldots\}$ with the autocorrelation function

$$r(s) \stackrel{\text{def}}{=\!=} \frac{\langle f(x_t)f(x_{t+s})\rangle_{x_0,t} - \langle f(x_t)\rangle_{x_0,t}\,\langle f(x_{t+s})\rangle_{x_0,t}}{\sqrt{\left(\langle f(x_t)^2\rangle_{x_0,t} - \langle f(x_t)\rangle_{x_0,t}^2\right)\left(\langle f(x_{t+s})^2\rangle_{x_0,t} - \langle f(x_{t+s})\rangle_{x_0,t}^2\right)}} \tag{3}$$

The notation $\langle\,.\,\rangle_{x_0,t}$ emphasizes that the expectation is taken over all "times" t and all initial conditions x_0. We will refer to $r(s)$ as the *"random walk" correlation function* of the landscape f on Γ. A simple random walk [49] on a graph Γ has transition matrix $\mathbf{T} \stackrel{\text{def}}{=\!=} \mathbf{A}\mathbf{D}^{-1}$. It can be shown [53] that

$$r(s) = \frac{1}{\sigma_f^2}\left[\frac{1}{N}\langle f, \mathbf{T}^s f\rangle - \overline{f}^2\right] \tag{4}$$

for a regular graph Γ. The two correlation measures $r(s)$ and $\rho(d)$ are closely related to each other, since $r(s) = \sum_{d=0}^{d_{\max}} \phi_{sd}\rho(d)$, where $d_{\max}$ is diameter of the graph Γ and ϕ_{sd} is the probability that a simple random walks of s steps ends in distance d from its starting point [56]. In particular, the nearest neighbor correlation satisfies $\varrho = r(1) = \rho(1)$.

It has been shown [53] that there is an intimate relationship between the Fourier expansion of a landscape and the form of its correlation functions $\rho(d)$ and $r(s)$. For sequence spaces[3] (Hamming graphs) one has

Proposition 1. [53] Let f be a non-flat landscape on the sequence space (Hamming graph) $\mathcal{Q}_\alpha^n$. Then the following statements are equivalent:

(i) f is elementary with $\lambda = p\alpha$.

(ii) The "random walk" correlation function is exponential,

$$r(s) = \varrho^s = (1 - \lambda/D)^s = \left(1 - \frac{\alpha}{\alpha - 1}\frac{p}{n}\right)^s . \tag{5}$$

[3] Analogous results hold for all distance regular graphs.

(iii) The "direct" correlation function is a Krawtchouk polynomial,

$$\rho(d) = \omega_p^{n,\alpha}(d) \stackrel{\text{def}}{=\!=} \frac{1}{\binom{n}{p}(\alpha-1)^p} \sum_{j=0}^{p} (-1)^j (\alpha-1)^{p-j} \binom{d}{j} \binom{n-d}{p-j} . \qquad (6)$$

Since any landscape on Γ is necessarily a superposition of elementary landscapes, their correlation functions are superpositions as well. Let $f = \sum_j a_j \varphi_j$ be a Fourier expansion of f, and denote by λ_p the distinct eigenvalues of $-\Delta$. Furthermore, let I_p be the set of all indices k for which $\Delta\varphi_k + \lambda_p \varphi_k = 0$. The value $p = 0$ corresponds to the flat component of the landscape. Defining the *amplitude* of the p-ary interactions as

$$B_p \stackrel{\text{def}}{=\!=} \frac{\sum_{k \in I_p} |a_k|^2}{\sum_{k \neq 0} |a_k|^2} . \qquad (7)$$

we have $B_p \geq 0$ and $\sum_p B_p = 1$. As a by-product of the proof of Proposition 1 it can be shown [53] that the Fourier expansion of f translates directly into an expansion of the correlation functions:

Proposition 2. $r(s) = \sum_{p \neq 0} B_p (1 - \lambda_p / D)^s$ and $\rho(d) = \sum_{p \neq 0} B_p \omega_p^{n,\alpha}(d)$. (8)

Given a landscape, the crucial information about its correlation structure is therefore contained in the amplitudes B_p which describe the relative importance of the different elementary components and the eigenvalues λ_p which describe the ruggedness of the individual components.

2.3. Ruggedness

The eigenstructure of the graph Laplacian offers a promising formalism for relating the correlation structure of a landscape to the geometry of its local optima. In fact, the geometric structure of an elementary landscape is closely related to the constant the eigenvalue of the graph Laplacian to which f belongs.

- The solutions of the *Laplace equation* $\Delta f = 0$ form the *harmonic functions* on Γ. It is well known that there are no non-trivial harmonic functions on finite

connected graphs; see, e.g., [4, 47]. The harmonic functions are therefore the flat landscapes.

- Define the sets $V_+ = \{x \in V | f(x) \geq 0\}$ and $V_- = \{x \in V | f(x) \leq 0\}$ of all vertices on which f is non-negative or non-positive, respectively, and denote the corresponding induced subgraphs by Γ_+ and Γ_-. The second smallest eigenvalue λ_1 of the graph Laplacian $-\Delta$, which is positive for all connected graphs, is called the *algebraic connectivity* of Γ. A theorem by Fiedler [18, 19], see also [9, Thm.2.5.7], states that both Γ_+ and Γ_- are connected for the corresponding eigenvectors, i.e., there are exactly two nodal domains. Following a suggestion by Kauffman [35] we term this type of landscape *Fujijama" landscapes* because they consist of a single "mountain" Γ_+. For Hamming graphs a much stronger result holds: Fujijama landscapes have no non-global minima or maxima [52].
- The connected components of Γ_+ and Γ_- are called the *nodal domains* of f. The geometry of the nodal domains of a landscape f is of course a very important characteristic of the landscape. Courant's *nodal domain* theorem[4], which has been proved recently for graphs [11], states that, if all eigenvalues of $-\Delta$ are labeled in ascending order, $0 = \lambda_0 \leq \lambda_1 \leq \ldots \leq \lambda_{N-1}$, then the number of nodal domains of an eigenfunction f belonging to λ_k is at most $k + 1$.
- Grover [26] observed that the local optima have a characteristic distribution on elementary landscapes: Let $z_{\min}$ and $z_{\max}$ be a local minimum and a local maximum, respectively. Then $f(z_{\min}) \leq \bar{f} \leq f(z_{\max})$. In other words, all local maxima are in Γ_+ and all local minima are in Γ_- if f is an eigenvector of $-\Delta$.
- A heuristic argument [55] suggests that there should be approximately one local optimum of a landscape in a ball with a radius determined by the *correlation length*

$$\ell \stackrel{\text{def}}{=\!=} \sum_{s=0}^{\infty} r(s)\,. \tag{9}$$

Numerical computations [36, 54, 55] show that this estimate is remarkably accurate for elementary landscapes fulfilling a certain maximum entropy condition.

[4] The original version of this theorem holds for Riemannian manifolds, see [10].

The correlation length ℓ defined in equ.(9) is also closely related to the spectrum: we have

$$\ell = \sum_{p\neq 0} B_p \sum_{s=0}^{\infty} (1-\lambda_p/D)^s = D \sum_{p\neq 0} B_p \lambda_p^{-1} \,, \tag{10}$$

i.e., the correlation length of a landscape is determined by the harmonic mean of the eigenvalues of the Laplacian λ_p of the configuration space weighted by the amplitudes B_p of the landscape. For an elementary landscape we have in particular $\ell = D/\lambda_p$. In addition, there is ample evidence that the correlation length ℓ of a landscape is closely related to the performance of optimization heuristics, see e.g., [39, 20, 21, 46].

3. P-Structures

Search processes using mutations, i.e., rules to modify individual configurations, impose a graph structure on V by assigning edges between configurations that are accessible from each other by a single "move". The search in genetic algorithms works quite differently: two configurations from a population are chosen and a so-called crossover (or recombination) operator creates "offsprings" from the two "parents". In this section we introduce a discrete mathematical structure which allows for a discussion of recombination-like search by methods from algebraic graph theory.

Definition. Let V be a finite set with power set $\mathcal{P}(V)$. A *P-structure*[5] is a pair $(V, \mathcal{R})$ where $\mathcal{R} : V \times V \to \mathcal{P}(V)$. We say that the P-structure is *symmetric* if $\mathcal{R}(x, y) = \mathcal{R}(y, x)$ for all $x, y \in V$.

The (pseudo)digraph $\mathrm{supp}\mathcal{R}$ with vertex set V and edge set

$$E_{\mathcal{R}} \stackrel{\text{def}}{=\!=} \left\{ (x, y) \in V \times V \,\middle|\, \mathcal{R}(x, y) \neq \emptyset \right\} \tag{11}$$

will be called the *support* of the P-structure $(V, \mathcal{R})$. Note that $\mathrm{supp}\mathcal{R}$ has a loop at vertex x whenever $\mathcal{R}(x, x) \neq \emptyset$. We set $M \stackrel{\text{def}}{=\!=} |E_{\mathcal{R}}|$. In the case of symmetric P-structures then we can regard $\mathrm{supp}\mathcal{R}$ as an undirected pseudograph (possible with loops). Throughout this paper we shall assume $\mathcal{R}(x, y) \neq \emptyset$ for all $x, y \in V$, i.e., $\mathrm{supp}\mathcal{R}$ will always be the complete di-graph with loops and thus $M = N^2$.

A *hypergraph* [1] consists of a vertex set V and a collection $\mathcal{E}$ of (not necessarily) distinct subsets of V which are called (hyper)edges. The image of $\mathcal{R}$ is the hypergraph $\mathrm{imag}\mathcal{R}$ with vertex set V and (hyper)edge multiset

$$\mathcal{E} \stackrel{\text{def}}{=\!=} \{ \mathcal{R}(x, y) \in \mathcal{P}(V) \,|\, \mathcal{R}(x, y) \neq \emptyset \text{ and } x, y \in V \} . \tag{12}$$

This construction has been used in [23] in order to represent the structure of recombination on a finite set of genotypes. The hypergraph $\mathrm{imag}\mathcal{R}$ has in general

[5] The term "P-structure" has been chosen because its image set is the **p**ower set of V.

multiple edges. In particular, if $\mathcal{R}$ is symmetric, any set $\mathcal{R}(x,y)$ appears at least twice if $x \neq y$.

Generalizing the notion of the vertex degree for graphs one defines the vertex degree of $x \in V$ as the number of edges $h \in \mathcal{E}$ which contain x. The degree of a (hyper)edge $h \in \mathcal{E}$ equals the number $|h|$ of vertices that it contains. We define the *degree* $\deg(y)$ of a vertex $y \in V$ in the P-structure $(V, \mathcal{R})$ as the number of sets $\mathcal{R}(z, z')$ that contain y. This definition coincides of course with the vertex degree of the hypergraph $\mathrm{imag}\mathcal{R}$.

In appendix B we show that graphs and di-graphs can be represented as particular P-structures. In the following we shall develop an algebraic framework for the investigation of P-structures that can be regarded as generalization of algebraic graph theory and as generalization of the spectral theory of hypergraphs, see appendix A. The details of these connections are collected in appendix B since they are not directly relevant to the main purpose of this paper: the description of recombination spaces.

The set of pairs (x,y), $x \neq y$, with $\mathcal{R}(x,y) = \{x,y\}$ plays a special role in a P-structure. Such a pair could be interpreted as an analogue of a fixed point (under repeated application of $\mathcal{R}$) which implies an intuitive notion of "closeness". The set of all such edges introduces a digraph on V which we call the *backbone graph* $\mathrm{bbg}\mathcal{R}$ of $(V, \mathcal{R})$. P-structures do not necessarily have non-trivial backbone graphs: if $\mathrm{imag}\mathcal{R}$ does not contain (hyper)edges of degree 2 then $\mathrm{bbg}\mathcal{R}$ is the "discrete" graph that does not contain any edges. However, if $\mathrm{bbg}\mathcal{R}$ is a connected graph then it defines **a** natural metric on V. We shall see in the next section that the backbone graph of certain string recombination P-structures are exactly the Hamming graphs.

The *incidence matrix* $\mathbf{H}$, defined component-wise by

$$\mathbf{H}_{x,(y,z)} \stackrel{\text{def}}{=\!=} \begin{cases} 1 & \text{if } x \in \mathcal{R}(y,z) \\ 0 & \text{otherwise}\,, \end{cases} \tag{13}$$

uniquely determines the P-structure $(V, \mathcal{R})$. It has N rows and M columns. The diagonal matrices $\mathbf{V}$ and $\mathbf{W}$ of vertex and (hyper)edge degrees play a prominent

role in the theory of hypergraph spectra, see appendix A. For a P-structure we define

$$\mathbf{V}_{xx} \stackrel{\text{def}}{=\!=} \deg(x) = \sum_{(y,z)} \mathbf{H}_{x,(y,z)} \qquad \text{and} \qquad \mathbf{W}_{(x,x'),(x,x')} = |\mathcal{R}(x,x')| \,. \tag{14}$$

The adjacency matrix of the backbone graph $\mathrm{bbg}\mathcal{R}$ will be denoted by $\mathbf{G}$. The matrices $\mathbf{S}$ and $\mathbf{Q}$, defined component-wise by

$$\begin{aligned} \mathbf{S}_{xy} &\stackrel{\text{def}}{=\!=} 2 \sum_{z \in V} H_{x,(y,z)} \, |\mathcal{R}(y,z)|^{-1} \,, \\ \mathbf{Q}_{xy} &\stackrel{\text{def}}{=\!=} \sum_{z,z' \in V} H_{x,(z,z')} |\mathcal{R}(z,z')|^{-1} H_{y,(z,z')} \,, \end{aligned} \tag{15}$$

will play a dominant role in this contribution. In section 4 we shall argue that $\mathbf{S}$ is directly connected to the properties of search by means of recombination. The symmetric matrix $\mathbf{Q}$ is used to define spectra of hypergraphs, see appendix A. Both $\mathbf{S}$ and $\mathbf{Q}$ can be viewed as generalization of the adjacency matrix of a graph, see appendix B for the details.

Let us now turn to the symmetries of P-structures. An *automorphism* of a P-structure $(V, \mathcal{R})$ is a mapping $\psi : V \to V$ with the property

$$\mathcal{R}(\psi(x), \psi(y)) = \psi(\mathcal{R}(x,y)) \tag{16}$$

for all $x, y, z \in V$. In terms of the incidence matrix this condition becomes

$$\mathbf{H}_{\psi(x),(\psi(y),\psi(z))} = \mathbf{H}_{x,(y,z)} \qquad \text{for all} \quad x,y,z \in V \,. \tag{17}$$

The set of all automorphisms of a P-structure forms of course a group (under composition) which we shall denote by $\mathbf{Aut}[V, \mathcal{R}]$. Any automorphism of a P-structure is a graph automorphism of $\mathrm{supp}\mathcal{R}$ and $\mathrm{bbg}\mathcal{R}$ as well as a hypergraph automorphism of $\mathrm{imag}\mathcal{R}$ and hence $\mathbf{S}$, and $\mathbf{G}$ are invariant under P-structure isomorphisms, see lemma B4 in the appendix. This observation will be of particular importance for our discussion.

A permutation group is said to act *transitively* of a set V if for any two elements $x, y \in V$ there is a group element $\psi \in \mathbf{Aut}[V, \mathcal{R}]$ such that $y = \psi(x)$. A permutation group on V is *generously transitive* [8, 24] if for any two elements $x, y \in V$ there is a group element ψ such that $\psi(x) = y$ and $\psi(y) = x$. We say that $(V, \mathcal{R})$ is *vertex transitive* (*generously transitive*) if $\mathbf{Aut}[V, \mathcal{R}]$ acts (generously) transitive on V. This is analogous to the corresponding definition for graphs.

Consider now the *orbits* of $\mathbf{Aut}(V, \mathcal{R})$ on the set $V \times V$ of vertex pairs, that is, the sets of the form

$$\mathcal{X} = \left\{ (x, y) \,\middle|\, \exists \psi \in \mathbf{Aut}[V, \mathcal{R}] \,:\quad x = \psi(x_0),\, y = \psi(y_0) \right\}$$

that are generated by applying all P-structure automorphism to a pair (x_0, y_0) of reference vertices. To each orbit $\mathcal{X}$ we can associate a characteristic matrix $\mathbf{X}$, with entries $\mathbf{X}_{xy} = 1$ if $(x, y) \in \mathcal{X}$ and $\mathbf{X}_{xy} = 0$ otherwise. These matrices are by construction invariant under all P-structure automorphisms and they form a basis of a matrix algebra $\mathcal{A}[V, \mathcal{R}]$ which is coherent in the sense of Higman [28, 29, 30], see e.g., [8, chap.2] for detailed discussion. We note that $\mathbf{I}, \mathbf{J}, \mathbf{V}, \mathbf{S}, \mathbf{G} \in \mathcal{A}[V, \mathcal{R}]$.

If the group $\mathbf{Aut}[V, \mathcal{R}]$ is generously transitive then $\mathcal{A}[V, \mathcal{R}]$ is a commutative algebra consisting of symmetric matrices. It is the so-called Bose-Mesner algebra [7] of a (symmetric) association scheme, see [8, 24] for details. For our purposes only the following proposition, which is a trivial rewriting of well known properties of symmetric association schemes, will be of importance.

Proposition 3. Suppose the P-structure $(V, \mathcal{R})$ is generously transitive. Then there is a common basis $\{\varphi_k\}$, $1 \le k \le N$, of eigenvectors for all matrices $\mathbf{Y} \in \mathcal{A}[V, \mathcal{R}]$, which we shall call the *Fourier basis* of the (generously transitive) P-structure.

Definition. Suppose bbg$\mathcal{R}$ is a connected graph and let $d : V \times V \to \mathbb{R}$ be the associated metric distance on V. We say that the P-structure is distance transitive with respect to its backbone (*b.d.transitive*) if for any two pairs (x, y) and (u, v) with $d(x, y) = d(u, v)$ there is an automorphism $\psi \in \mathbf{Aut}[V, \mathcal{R}]$ such that $x = \psi(u)$ and $y = \psi(v)$.

Theorem 1. If $(V, \mathcal{R})$ is a b.d.transitive P-structure then its Bose-Mesner algebra $\mathcal{A}[V, \mathcal{R}]$ coincides with the adjacency algebra of the backbone graph bbg$\mathcal{R}$, i.e., $\mathcal{A}[V, \mathcal{R}]$ is generated by $\mathbf{G}$.

The algebraic properties of a b.d.transitive P-structure are therefore determined already by its backbone graph. The adjacency algebra of a graph is discussed in some detail in [3]. Connectedness of bbg$\mathcal{R}$ is a crucial condition in the above definition; it cannot be relaxed. We note finally, the backbone graph of a b.d.transitive P-structure is distance transitive. We shall see in the next sections that some forms of recombination P-structures have this property.

4. Recombination of Strings

Gitchoff and Wagner [23] used the following axioms to describe the action of a recombination in terms of what we call here P-structures.

Definition. A P-structure $(V, \mathcal{R})$ is a *recombination structure* if for all $x, y, z \in V$ holds:

(i) $\mathcal{R}(x, x) = \{x\}$.

(ii) $\mathcal{R}(x, y) = \mathcal{R}(y, x)$.

(iii) $\{x, y\} \subseteq \mathcal{R}(x, y)$.

(iv) For all $z \in \mathcal{R}(x, y)$ holds $|\mathcal{R}(x, z)| \leq |\mathcal{R}(x, y)|$.

In order to characterize a fitness landscape f, as it is perceived by a recombination-driven search process, we consider a random population of strings. The probability of constructing sequence x in a recombination event using string y as the "mother" is $\mathbf{T}_{xy} = \sum_{z \in V} t^x_{yz} p_z$ where p_z is the frequency of the potential "father" z in the population. The coefficients t^x_{yz} form the transmission tensor, which is defined as the probability of constructing x from the parents y and z. For a uniform population we have of course $p_z = 1/N$. In order to evaluate the transition rates we *define* that all possible recombination products should occur with equal probability[6]. In this case we have the transmission tensor $t^x_{yz} = \mathbf{H}_{x,(z,y)} \cdot |\mathcal{R}(y, z)|^{-1}$, which leads to the transition matrix

$$\mathbf{T}_{xy} \stackrel{\text{def}}{=\!=} \sum_{z \in V} \mathbf{H}_{x,(y,z)} |\mathcal{R}(y, z)|^{-1} \frac{1}{N} = \frac{1}{2N} \mathbf{S}_{xy} \,. \tag{18}$$

It is easy to check that $\mathbf{T}$ is in fact a stochastic matrix, because $\sum_x \mathbf{S}_{xy} = 2N$. A similar "walk" on V was used in [33] in order to generate the "times-series" for a numerical correlation analysis of Nk landscapes under recombination.

[6] This assumption is not necessarily strictly satisfied in a GA simulation. For instance, then 1-point crossover is simulated by chosing a recombination point from a uniform distribution, then the frequency distribution of the recombinants depends on the position of the non-conserved letters in the strings. We shall not persue this complication in this contribution.

In order to determine the structure of the landscape f we consider now samples obtained from individual "family lines", that is sequences of vertices $x_0, x_1, x_2, \ldots$ such that $x_k \in \mathcal{R}(x_{k-1}, z_{k-1})$ where the "mates" z_j are random choices from the population. The transition matrix of the associated Markov process is exactly the matrix $\mathbf{T}$ defined above. The samples of the landscape, $\{f(x_0), f(x_1), \ldots\}$ forms a "time-series" that generalizes Weinberger's [56] procedure for mutation spaces. The autocorrelation function of this time series is defined as in equ.(3). Following the discussion in [53] we can show that equ.(4) holds without changes for the transition matrix defined in equ.(18).

Obviously, $\mathbf{S}$ and $\mathbf{T}$ have the same eigenvectors. We need more information about $\mathbf{S}$, however, in order to obtain results corresponding to the two propositions in sect. 2. In this contribution we shall restrict our discussion to recombinaton operators on strings of equal length n.

The only type of crossover operators that we consider in some depth in this contribution is defined on the set $V = \mathcal{Q}_\alpha^n$ of strings of length n over an alphabet consisting of α letters. We introduce the mapping $\times_k : V \times V \to V \times V$ defined as

$$\times_k(x, y) \stackrel{\text{def}}{=\!=} \Big((y_1, y_2, \ldots, y_{k-1}, x_k, \ldots, x_n)\,,\, (x_1, x_2, \ldots, x_{k-1}, y_k, \ldots, y_n) \Big)$$

for $1 \le k \le n$, to describe the action of crossover at position k. Let us call $\times_k$ an *elementary* crossover operator. Note that the notation here is different from [23]. In particular, $\times_1$ is the identity mapping. We follow here the spirit of [34] when we regard a crossover operator as producing pairs of sequences rather than a single sequence from a pair of "ancestors". Another useful basis of crossover operators consists of the mappings

$$\diamondsuit_k(x, y) \stackrel{\text{def}}{=\!=} \Big((x_1, \ldots, x_{k-1}, y_k, x_{k+1}, \ldots, x_n)\,,\, (y_1, \ldots, y_{k-1}, x_k, y_{k+1}, \ldots, y_n) \Big)$$

$1 \le k < n$, which swap position k between the two x and y. Obviously we have

$$\times_k = \diamondsuit_1 \circ \diamondsuit_2 \circ \ldots \circ \diamondsuit_{k-1} \qquad \text{and} \qquad \diamondsuit_k = \times_k \circ \times_{k+1}\,. \tag{19}$$

The basic algebraic properties of the single position operators $\diamondsuit_k$ follow directly from the definition: They are all involutions, i.e., $\diamondsuit_k \circ \diamondsuit_k = \times_1$, and since different positions do not interfer with each other they commute, $\diamondsuit_k \circ \diamondsuit_l = \diamondsuit_l \circ \diamondsuit_k$. A general crossover operator χ is a finite, but otherwise arbitrary, composition of elementary recombination operators. Details on the algebraic properties of crossover operators can be found in appendix C.

Definition. Let F be a family of (general) crossover operators on $\mathcal{Q}_\alpha^n$. Then we define the P-structure $(\mathcal{Q}_\alpha^n, \mathcal{R})$ associated with F by setting

$$\mathcal{R}(x,y) = \bigcup_{\chi \in F} \chi(x,y)\,, \tag{20}$$

where we interpret $\chi(x,y)$ as a set rather than an ordered pair here. If $\chi \in F$ we shall say that χ *contributes* to $\mathcal{R}$, and write $\chi \in F(\mathcal{R})$.

The first three of the following four examples are discussed in more detail in [23], where it is also shown that they fulfil the axioms of a recombination structure.

$\mathcal{R}_1$ *One-Point Crossover* is defined by the collection of all elementary operators, $F = \{\times_1, \times_2, \ldots, \times_n\}$.

$\mathcal{R}_2$ *Two-Point Crossover* consists of all compositions $\times_k \circ \times_l$, $k,l \neq 1$. For technical reasons we include the identity as well.

$\mathcal{R}_\Omega$ *Uniform Crossover* allows for all possible recombinations to take place, i.e., $F(\mathcal{R}_\Omega) = \left\{ \xi = \prod_{j \in J} \diamondsuit_j \;\middle|\; J \subseteq \{1,2,\ldots,n-1\} \right\}$.

$\mathcal{R}_\diamondsuit$ *Single-Position-Exchange* is given by
$F(\mathcal{R}_\diamondsuit) = \{\diamondsuit_1, \diamondsuit_2, \ldots, \diamondsuit_{n-1}, \bar{\diamondsuit}_n, \times_1\}$,
where $\bar{\diamondsuit}_n \stackrel{\text{def}}{=\!=} \diamondsuit_1 \circ \diamondsuit_2 \circ \ldots \circ \diamondsuit_{n-1}$ amounts to the exchange of the last string position.

Let F be an arbitrary family of string crossover operators. Then the associated P-structure is a recombination structure if and only if the identity $\times_1$ is contained in F, see appendix C for the proof. The fact that $\times_1 \in F$ is required can be regarded as a mere technicality. We conclude hence that the Gitchoff-Wagner definition of

a recombination structure indeed captures the most salient features of crossover. String recombination P-structures have considerable symmetry. In appendix C we prove the following result which forms the basis for most of the subsequent analysis:

Theorem 2. The automorphism group $\mathbf{Aut}(\mathcal{Q}_\alpha^n, \mathcal{R})$ of a string recombination structure is generously transitive.

Corollary. The matrix $\mathbf{S}$ is symmetric for all string recombination P-structures.

Definition. A string recombination structure is *separable* if for any two positions k, l there is a crossover operator $\chi \in F(\mathcal{R})$ such that either $\diamondsuit_k$ or $\diamondsuit_l$ is contained in the product representation of χ, but not both. In other words, there is a crossover operator that separates the sequence positions k and l.

The four string recombination P-structures defined above are separable. An example of a recombination P-structure that is not separable is a subset F' of 1-point X-over operators that allow for crossover only at certain "cross-over spots" but not at all sequence positions. As a consequence certain adjacent positions can never be separated by recombination.

Theorem 3. The backbone graph of a string recombination P-structure $(\mathcal{Q}_\alpha^n, \mathcal{R})$ is the Hamming graph $\mathcal{Q}_\alpha^n$ if and only if it is separable.

This result justifies Culberson's approach to used the Hamming distance as the canonical distance in the context of recombination operators [12]. The results of Manderick and co-workers [39] and Jones' "fitness distance correlation" [34] are also based on correlation lengths with respect to Hamming distance.

If a separable recombination P-structure is b.d.transitive then its Fourier basis coincides with the Fourier basis of corresponding point-mutation space (Hamming space) and we can immediately compare mutation with recombination.

5. Comparison of Operators

A generalized Laplace operator on V can be associated with any symmetric non-negative matrix $N \times N$ matrix by defining

$$-\Delta_{\mathbf{C}} f(x) \stackrel{\text{def}}{=\!=} \sum_{y \in V} \mathbf{C}_{xy} \Big[f(x) - f(y) \Big] . \tag{21}$$

The operator $-\Delta_{\mathbf{C}}$ has therefore the off-diagonal entries $-\mathbf{C}_{xy}$, while the diagonal is determined by $(-\Delta_{\mathbf{C}})_{xx} = \sum_{y \neq x} \mathbf{C}_{xy}$. Laplacians are special cases of Schrödinger operators, see e.g. [11].

Since the search by recombination is associated with $\mathbf{S}$ we suggest to characterize the ruggedness of a landscape f on a string recombination structure in terms of the spectrum of the Laplacian

$$-\Delta_{\mathbf{S}} = 2N\mathbf{I} - \mathbf{S} . \tag{22}$$

This has to be compared with the Laplacian

$$-\Delta_{\text{mut}} = D\mathbf{I} - \mathbf{A} \tag{23}$$

which is associated with the adjacency matrix $\mathbf{A}$ of the graph which is induced by mutation.

Let us now consider the special case of binary strings, and suppose that the string recombination P-structure $(\mathcal{Q}_2^n, \mathcal{R})$ is separable. We have seen in the previous section that in this case the adjacency matrix of the Boolean hypercube $\mathbf{A}$ is contained in the Bose-Mesner algebra $\mathcal{A}[\mathcal{Q}_2^n, \mathcal{R}]$, and hence a Fourier basis for this algebra consists of eigenvectors of $\mathbf{A}$. We have even more information on the eigenvectors: If φ is in the Fourier basis, then it is a superposition of p-spin functions with a common value of p. In particular, if $(\mathcal{Q}_2^n, \mathcal{R})$ is b.d.transitive then the p-spin functions are a Fourier basis and the eigenvalues depend only p. In appendix C we prove the following result:

Theorem 4. The recombination P-structures $(\mathcal{Q}_2^n, \mathcal{R}_\diamondsuit)$ and $(\mathcal{Q}_2^n, \mathcal{R}_\Omega)$ are distance transitive with respect to their backbone graphs.

Corollary. The matrix elements $\mathbf{S}_{xy}$ of the recombination P-structures $(\mathcal{Q}_2^n, \mathcal{R}_\diamondsuit)$ and $(\mathcal{Q}_2^n, \mathcal{R}_\Omega)$ depend only on the Hamming distance $d_H(x, y)$.

In general, not all eigenfunctions of $\mathbf{A}$, i.e., not all linear combinations of the form

$$\sum_{i_1<i_2<\ldots<i_p} a_{i_1 i_2 \ldots i_p} \varepsilon_{i_1 i_2 \ldots i_p} \tag{24}$$

will be eigenfunctions of all members of the matrix algebra $\mathcal{A}[\mathcal{Q}_2^n, \mathcal{R}]$. Thus we observe a "splitting" of the eigenspaces of $\mathbf{A}$, as in the case of 1-point and 2-point crossover discussed below. We do not have a proof for the following conjecture at the moment, although we have not encountered a counterexample at this point:

Conjecture. The p-spin functions $\varepsilon_{i_1,i_2,\ldots,i_p}$ defined in equ.(1) form a Fourier basis of the Bose-Mesner algebras of all separable string recombination structures on the boolean hypercube.

The ruggedness of a landscape can be measured by its (relative) location in the spectrum of the Laplacian that is associated with the search strategy. For instance, landscapes on the boolean hypercube become more rugged as the interaction order p increases. Conversely, we propose to measure the suitability of a particular search procedure by comparing the values of B_k and λ_k that are obtained for the same landscape f with *different* Laplacians. The absolute location of λ_k in the Laplacian spectrum is depends to a certain extent on the normalization of the Laplacian — for instance, there is a factor of 2 between the usual definition of the graph Laplacian and the definition of the Laplacian on hypergraphs, see [42]. The crucial information is thus contained in the relative location. Using the correlation function $r(s)$ or the correlation lenght ℓ directly suffers from a similar problem. The diagonal entries in the transition matrix that is used to define $r(s)$ are to a certain extent arbitrary; again, the ordering of the corresponding eigenvalues is not affected by this ambiguity.

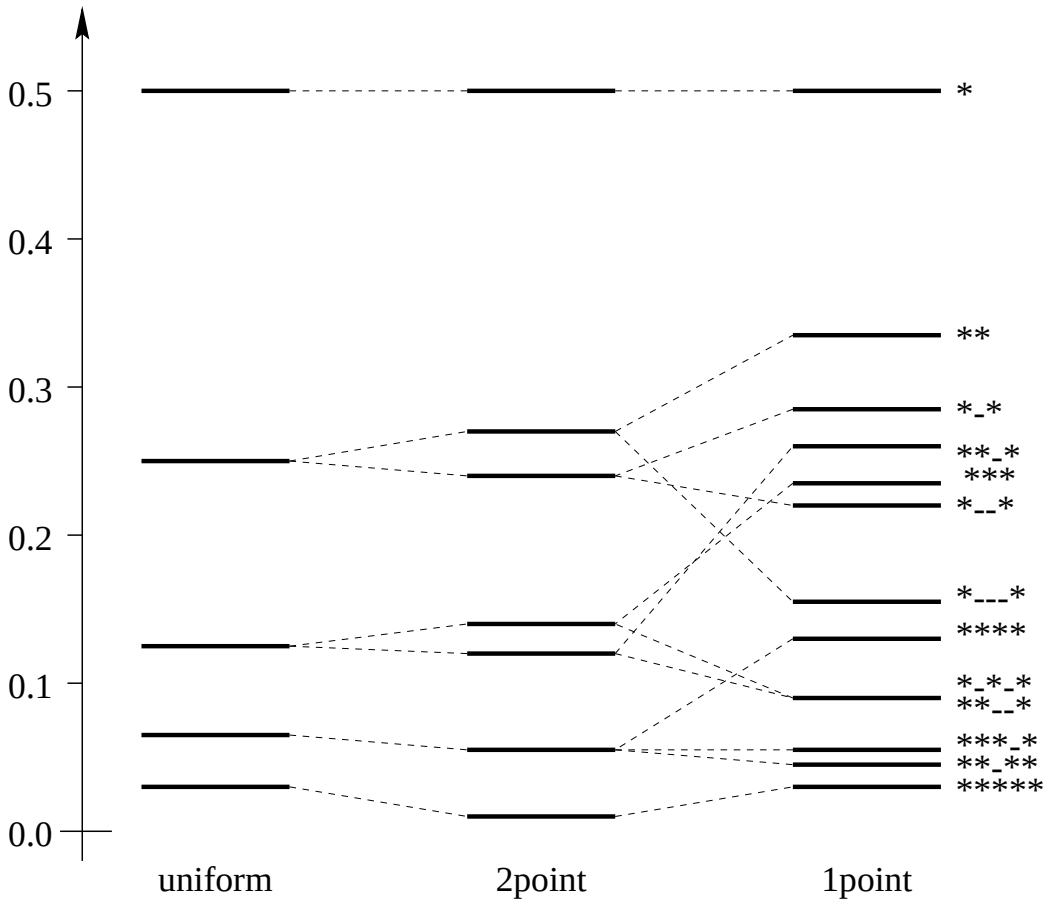

Figure 1: Nearest neighbor correlations $r(1)$ for the landscapes that are eigenfunctions of $\mathbf{S}$ for $n = 5$.
L.h.s: uniform recombination; middle: 2-point crossover; r.h.s: 1-point crossover. Eigevalues belonging to the same eigenfunction are connected by dashes lines. The symbols on the right indicate the interaction pattern of the spins which defines the classes of eigenfunctions with a common eigenvalue.

Let us now consider uniform recombination of binary strings in some details. Lemmas C6 through C8 in the appendix allow us to explicitly evaluate $\mathbf{S}_{xy}$.

Theorem 5. For the uniform string recombination structure $(\mathcal{Q}_2^n, \mathcal{R}_\Omega)$ we have

$$\mathbf{S}_{xy} = 2(3/2)^n 3^{-d_H(x,y)} \,. \tag{25}$$

Lemma C9 in the appendix implies the following explicit formula for the eigenvalues of $\mathbf{S}$:

Theorem 6. The spectrum of $\mathbf{S}$ of the uniform string recombination structure $(\{+1,-1\}^n, \mathcal{R}_\Omega)$ is given by

$$\lambda_p^{\mathbf{S}} = 2^{n+1}\,(1/2)^p\,. \tag{26}$$

The eigenvalues of both matrices are $\binom{n}{p}$-fold degenerate. The p-spin functions $\varepsilon_{i_1,i_2,\ldots,i_p}(\sigma)$ with $i_1 < i_2 < \ldots < i_p$ form an orthogonal basis of the corresponding eigenspaces.

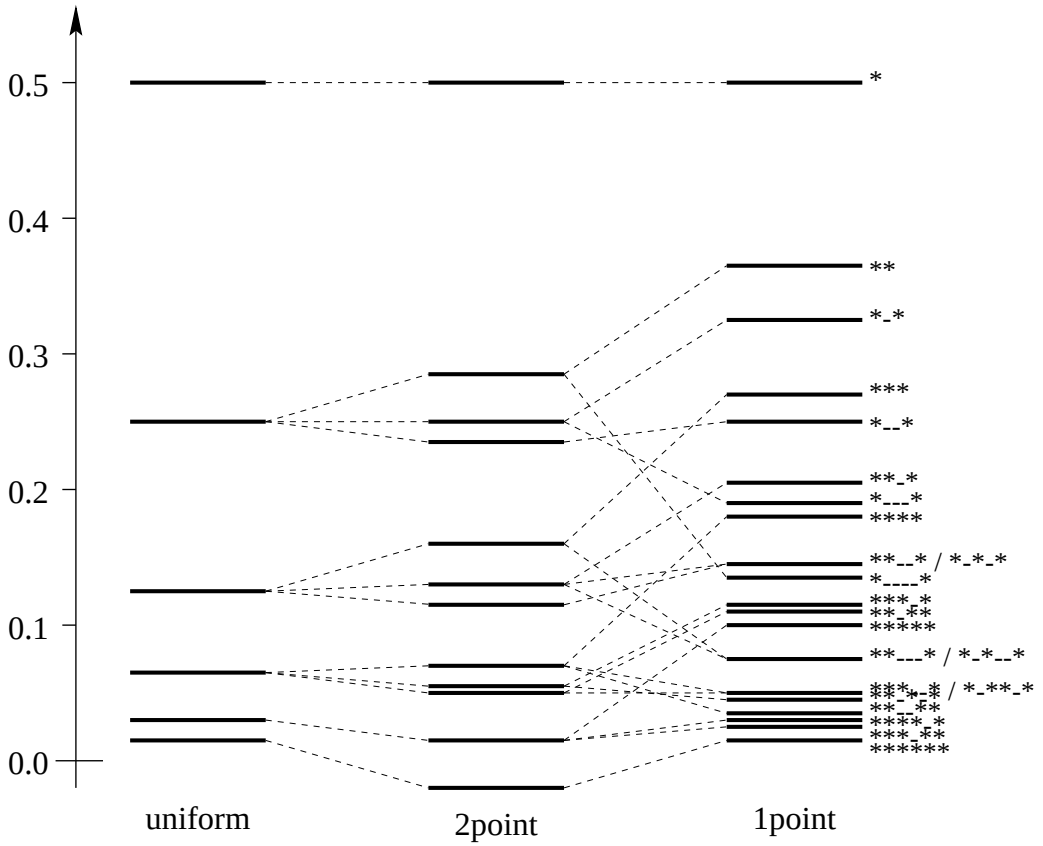

Figure 2: Nearest neighbor correlations $r(1)$ for the landscapes that are eigen functions of $\mathbf{S}$ for $n = 6$.
L.h.s: uniform recombination; middle: 2-point crossover; r.h.s: 1-point crossover.
Eigevalues belonging to the same eigenfunction are connected by dashes lines. The symbols on the right indicate the interaction pattern of the spins which defines the classes of eigenfunctions with a common eigenvalue.

The situation is different for one-point-crossover. Figure 1, for instance, shows for the case $n = 5$ that not all p-spin functions belong to the same eigenvalue (and

hence to the same value of $r(1)$). Nevertheless, for the few cases that we computed explicitly, we always found that $\varepsilon_{i_1,i_2,\ldots,i_p}$ is an eigenfunction of $\mathbf{S}$.

A close inspection of the "splitting" of the spectrum of a given interaction order p shows that the relative arrangement of the interacting spins (i.e., of the indices i_1 through i_p) infuences $r(1)$ is a systematic way. The eigenfunctions are characterized by the pattern of spin-interactions along the sequence. The length of the interaction is $L = i_p - i_1 + 1$. For instance, the class of functions $\sigma_k\sigma_{k+1}\sigma_{k+4}$ has interaction order $p = 3$ and interaction length $L = 5$ for all k. We shall write `[**--*]` for this type of eigenfunctions.

We observe the following rules for the nearest neighbor correlations under 1-point crossover.

(1) For a given interaction order, the landscape is smoother for the more local spin interaction. For example, `[***]` is smoother than `[*-**]` which is smoother than `[*-*-*]`.

(2) For a given interaction length, the landscape with the fewer interactions is smoother, i.e., `[*-*]` is smoother than `[***]`.

These rules do not hold for 2-point crossover. The "spectra" of nearest neighbor correlations are shown in Figures 1 and 2 for $n = 5$ and $n = 6$, respectively.

6. Discussion

Adaptation by natural selection is based on spontaneously arising genetic variation. There are two basic classes of mechanisms generating genetic variation: mutation, which acts on individual chromosomes and recombination, which acts on pairs of chromosomes simultaneously. The relative importance of these two classes of processes is still an open question, both in evolutionary genetics as well as in evolutionary algorithms. For instance, an extensive empirical literature on the performance of GA's is inconclusive as of whether the success of GA's is predicated on recombination or mutation or both. Recently, the emphasis has shifted from empirical approaches to investigations of the structure of the search spaces induced by mutation and recombination operators [12, 23, 34, 39, 52, 53, 56]. The question about the relative role of mutation and recombination became a special case of the question posed in the introduction: How can one compare two search procedures inducing two different structures $\mathcal{X}$ and $\mathcal{Y}$ for a prescribed fitness function f?

In this contribution, we propose a way to make recombination induced search structures directly comparable to mutation induced search structures. The approach is based on the algebraic method for the analysis of search space structures [52, 53, 56]. In previsions work it has been shown that there is an intimate relationship between auto-correlations on fitness landscapes and its Fourier-decomposition (see [52, 53, 56] and sections 1 and 2). The problem addressed in this contribution is that methods for Fourier decomposition of landscapes on graphs are not applicable to recombination spaces. In [23] it is argued that recombination induced structures can not be represented by simple graphs with the same vertex set as mutation spaces. We propose to use so-called P-structures, which essentially are mappings from the pairs of "parental" configurations (e.g. chromosomes or strings) to the set of "recombinant" configurations. It is argued that an algebraic analysis of the symmetries of this structures provides insight into the expected performance of search procedures on a given fitness function.

The power of the algebraic approach is based on the fact that arbitrary fitness landscapes can be decomposed into a superposition of "elementary" landscapes,

which are given by the eigenfunctions of the Laplacian operator on the search space structure (see section 2 for details on graph Laplacians). Once these eigenfunctions are known, these elementary landscapes can be studied individually. The information about the effective hardness of an elementary landscape is contained in the relative ordering of the associated eigenvalues. In addition the eigenvalues can be used to predict the expected nearest neighbor correlation.

One of the main results of this paper is implicitly contained in the Theorems 1, 2, 3 and 4 as well as Proposition 3. In this paragraph we provide a somewhat simplified intuitive interpretation of these results (see below for a discussion of details). It turns out that the algebraic properties of a P-structure and by inclusion also those induced by recombination depend on the so-called backbone graph. A backbone graph connects all the vertices which reproduce only themselves under application of the recombination operator. In the case of string recombination, the backbone graph connects all pairs of strings which have a Hamming distance of one, i.e. those which differ at exactly one position. The theorems mentioned above tell that if the backbone graph fulfills certain symmetry conditions (e.g. being generously transitive etc.), the eigenfunctions of the Laplacian of the P-structure are the same as the eigenvectors of the backbone graph. In other words, all recombination operators which share the same backbone graph (and fulfill certain symmetry condition) have the same elementary landscapes. In the case of string recombination, the backbone graph turns out to be just the hypercube or the Hamming graph, depending on the size of the alphabet. The backbone graph is isomorphic to the point mutation space. Consequently, the recombination spaces and the mutation space on the same set of strings have the same Fourier basis; a landscape that is elementary for string recombination is also elementary for point mutation on strings. This extends the results of Culberson [12] and Gitchoff and Wagner [23] about the homomorphism of mutation and recombination spaces. However, this does not imply that the effective ruggedness of these elementary landscapes is the same for mutation and recombination or for different recombination operators (see below).

In fact the above characterization of the results is a cartoon of what the theorems actually say. In this paragraph we want to summarize the implications of these results for the recombination landscapes in three simple Corollaries.

Corollary 1. If (V, R) is both b.d.transitive and generously transitive, then the P-structure Laplacian has the same eigenvectors as the backbone graph Laplacian.

This corollary summarizes Proposition 3 and Theorem 1 and gives the conditions under which the structure of the backbone graph is sufficient to determine the eigenfunctions of the P-structure Laplacians and thus the elementary landscapes of the recombination space. The next Corollary goes a step further and applies this result to string recombination.

Corollary 2. If (V, R) is separable (i.e. each pair of positions can be separated by recombination) and if it is also b.d.transitive then the eigenfunctions of the Hamming graph Laplacian are also the eigenfunctions of the P-structure Laplacian.

With this result we come closer to the relationship between mutation and recombination spaces, since the Hamming graph is the configuration space of the point mutation space. The next corollary gives a definite answer as to the eigenfunctions of the configuration space induced by uniform recombination.

Corollary 3. The eigenfunctions of the Laplacian of the uniform recombination P-structure of binary strings are the p-spin functions, i.e. the eigenfunctions of the corresponding hypercube Laplacian.

This last result is mainly due to Theorem 4 which asserts that the free recombination P-structure is distance transitive. Hence, there is an analytical proof that the eigenfunctions of the free recombination P-structure are identical to the eigenfunctions of the point mutation space, the hypercube graph. The one-point and two-point recombination operators, in contrast, are not distance transitive with respect to their backbone graphs. Consequently we do not know for sure what the Fourier bases of these P-structures are. All we know is that there is always an orthonormal base of vectors that are eigenvectors of the Lapacians of the Hamming graph and that of a separable string recombination structure. However, we

calculated the spectrum for one and two point recombination operators on binary strings of $n \leq 6$ and found that they have the p-spin functions as eigenfunctions. We suspect that this is the case in general, as expressed in the Conjecture in section 5.

As mentioned above, even if the elementary landscapes for mutation and recommendation are identical, the effective ruggedness of the landscapes need not be the same. Let us compare the nearest neighbor correlation on the elementary landscapes for mutation and uniform recombination. In both cases the nearest neighbor correlations only depend on p, the number of interacting sites. The nearest neighbor correlation for mutation is predicted to be

$$r_{\mathrm{mut}}(1) = \left(1 - \frac{2p}{n}\right) \qquad \text{and} \qquad r_{\mathrm{free}}(1) = \frac{1}{2^p} \tag{27}$$

for uniform recombination (Theorem 5), respectively. SOne immediately observes that the correlations for point mutations become negative as soon as $2p > n$, i.e. with more rugged landscapes due to multiple interactions among the sites, mutation is predicted to have more difficulty optimizing. The correlations for free recombination are always positive, but approach zero as p approaches n. In other words, recombination is doing increasingly better than mutation as the "complexity" of the landscapes increases. While we think that this is in fact the case the absolute magnitude of the correlations for uniform recombination is an overestimate. The reason is that the Laplacian used here assumes that all configurations are available for recombination with equal frequency. On the other hand the point mutation Laplacian only considers the local topology found around each configuration. The relatively high nearest neighbor correlations predicted for the uniform recombination reflects the fact that there are many pathways to produce a particular string from many pairs of strings. However, neither in natural populations nor in GA-runs are all configurations simultaneously available with equal frequency. We interpret the present result as predicting that for recombination the effective ruggedness of an landscape is decreasing as the genetic variation in the population increases. On the other hand, if the genetic variation is low the effective ruggedness of the landscape might approach that of the mutation space.

Now let us turn to the comparison of various recombination operators, in particular uniform recombination and one-point and two-point recombination. As noted above, we do not have an analytical proof that one- and two-point recombination have the same elementary landscapes as uniform recombination and mutation, but in all cases where we checked they in fact do. However, what is different is the spectrum. The eigenvalues of the one- and two-point recombination Laplacians do not only depend on p, the number of interacting sites on the string, but also on the distribution of interacting sites along the string. Consequently also the predicted nearest neighbor correlations can be different for elementary landscapes with identical p. This reflects the fact that one-point recombination sets are smaller than for uniform recombination and that they are unique for each pair of parental strings if they have a Hamming distance larger than 2 (for details see [23]). It is interesting to compare the nearest neighbor correlations predicted for uniform and one-point recombination (tables 1 to 4 and Figures 1 and 2). In general the correlations for a given p value can be higher or lower in the case of one-point recombination as compared to uniform recombination. However, the mean correlation averaged over all elementary landscapes with a given p is always higher for one-point recombination. Hence the one-point recombination landscape tends to be smoother than the uniform recombination landscape, even if there are some elementary landscapes which are much more rugged for one point recombination than for uniform recombination. An example is the landscape `[*----*]` in the $n = 6$ case, i.e. the landscape caused by the interaction of sites at the end of the string. Clearly every non-trivial one-point recombination event will separate the two interacting sites (and may destroy a building block). However, in the case of two-point and uniform recombination, every recombination event with two crossover sites leaves the two interacting positions together. Therefore uniform recombination has a much higher nearest neighbor correlation on this landscape than one-point recombination. On the other hand any elementary landscape which results from the interaction of neighboring sites on the string has a higher correlation under one-point recombination than under uniform or two-point recombination. The reason is also quite obvious: only one in $n-1$ recombination events will separate the two

interacting sites. However, there are many events under uniform recombination which separate the interacting sites. The total interaction length, i.e. the number of positions that separate the interacting sites, influences the nearest neighbor correlations. There is an intriguing relationship between elementary landscapes for string recombination and schemata *sensu* Holland [2, 31, 32]. Each elementary landscape corresponds to a partitioning of the set of strings. Each equivalence class in this partitioning is a schema in the sense of Holland and all the schema which make up this partitioning have the same positions fixed. An elementary landscape is a landscape which assumes that only the fixed positions in the schema actually influence fitness. This was first noted by Weinberger in his seminal paper on Fourier and Taylor series of fitness landscapes [57]. Our results, however, show for the first time that this is a legitimate way of decomposing the configuration space of string recombination. In addition, the predicted nearest neighbor correlations quantify the qualitative result of the schema theorem. The smaller the "defining length" of a schema, the better it fares in a GA. Note, however, that there is a fundamental difference between the schema theorem and the present results. The schema theorem is a statement about whether a particular schema will or will not be selected in competition against all other strings, i.e. whether it could act as a "building block". The present result about the nearest neighbor correlations on elementary landscapes is a statement about how easily a recombination operator is able to find the best schema among the set of all schemata with the same fixed positions.

The results presented here support the view that the algebraic approach to search space analysis can help resolving complex questions like the relative performance of different recombination operators. However, the present results leave several questions open, which have to be addressed in the future. First among them is the question whether the Laplacians of all separable recombination operators on binary strings have the same eigenvectors as the point mutation Laplacian. As mentioned above numerical calculations support the Conjecture but an analytical proof would definitely be desirable. Then there are a few symmetry assumptions which have been incorporated for the sake of mathematical tractability. The most important

ones are the assumption that all recombinants are produced with equal frequency, which is not the case, and the second is the assumption that all possible configurations are equally available for recombination. Relaxing these assumptions does not require a fundamentally different formalism. Rather it would only be necessary to weight the terms in calculating the Laplacian **S** from the incidence matrix **H** with the appropriate probabilities. It is easily conceivable to move from the Laplacians discussed in this paper to "population-Laplacians" which take into account the relative frequency of the strings available for recombination in the population. Finally it is desirable to compare the present predictions about the ruggedness of elementary landscapes with computer simulations of GA performance.

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Appendix A: Spectra of Hypergraphs

Definition. [1] Let V by a finite set, and let E be a family of (not necessarily distinct) subsets of V such that $\bigcup_{h\in E} h = V$. Then we call $\Upsilon = (V, E)$ a *hypergraph* with *vertex set* V and edge-set in E. A hypergraph is *simple* if $h' \subseteq h$ implies $h' = h$ for all $h, h' \in E$.

The number of vertices is denoted by $N \stackrel{\text{def}}{=} |V|$, the number of edges is $M \stackrel{\text{def}}{=} |E|$. A hypergraph Υ can be represented by a $N \times M$ matrix $\mathbf{H}$ with entries

$$\mathbf{H}_{xh} = \begin{cases} 1 & \text{if } x \in h \\ 0 & \text{otherwise} \end{cases} \tag{A.1}$$

The matrix $\mathbf{H}$ is called the *incidence matrix* of the hypergraph Υ. The hypergraph Υ^+ with the $M \times N$ incidence matrix $\mathbf{H}^+$ is called the *dual* hypergraph of Υ. The diagonal matrices $\mathbf{V}$ and $\mathbf{W}$ contain the vertex and (hyper)edge degrees

$$\mathbf{V}_{xx} = \sum_{h\in E} \mathbf{H}_{xh} \qquad \mathbf{W}_{hh} = \sum_{x\in E} \mathbf{H}_{xh}, \tag{A.2}$$

respectively.

A hypergraph Υ is *regular* if $\mathbf{V}$ is a multiple of the identity matrix $\mathbf{I}$; it is called *uniform* if $\mathbf{W}$ is a multiple of the identity matrix. We write $\mathbf{V} = V\mathbf{I}$ for regular hypergraphs and $\mathbf{W} = W\mathbf{I}$ for uniform hypergraphs, respectively. For example, a 2-uniform hypergraph is a loop-free multigraph, and a simple 2-uniform hypergraph is a simple graph.

Definition. [6] Let $\mathbf{H}$ be the incidence matrix of a hypergraph Υ with vertex and edge degree matrices $\mathbf{V}$ of and $\mathbf{W}$, respectively. Then we call

$$-\Delta \stackrel{\text{def}}{=} \mathbf{V} - \mathbf{H}\mathbf{W}^{-1}\mathbf{H}^+ \tag{A.3}$$

the *Laplacian (matrix)* of the hypergraph Γ.

The analogy of this definition with the more common graph Laplacians, see e.g., [41, 42, 3], is discussed in [6]. If Υ is a simple graph We have $\mathbf{W} = 2\mathbf{I}$ and

$\mathbf{HH}^+ = \mathbf{V} + \mathbf{A}$, where $\mathbf{A}$ is the *adjacency matrix* of the graph, see e.g., [3, p.18]. Thus $\Delta = \mathbf{V} - (1/2)(\mathbf{A} + \mathbf{V}) = (1/2)(\mathbf{V} - \mathbf{A}) = (1/2)\Delta_{\text{graph}}$ coincides with the usual definition of the graph Laplacian up to a factor of 2.

A similar approach to hypergraph spectra was persued by Runge in the seventies. In the PhD thesis [44] the matrix $\mathbf{K} \stackrel{\text{def}}{=\!=} \mathbf{V}^{-1}\mathbf{H}\mathbf{W}^{-1}\mathbf{H}^+$ was studied intensively. The corresponding matrix for the dual hypergraphs is $\overline{\mathbf{K}} \stackrel{\text{def}}{=\!=} \mathbf{W}^{-1}\mathbf{H}^+\mathbf{V}^{-1}\mathbf{H}$. It can be shown [45] that $\xi^M \det(\xi\mathbf{I} - \mathbf{K}) = \xi^N \det(\xi\mathbf{I} - \overline{\mathbf{K}})$. As a consequence the non-zero part of the $\mathbf{K}$-spectrum of a hypergraph and its dual coincide.

The transpose $\mathbf{K}^+$ of $\mathbf{K}$ has a more intuitive interpretation than $\mathbf{K}$ itself, since it is the transition matrix of a certain type of random walk on the vertex set V. Of course, both matrices have the same spectrum.

Definition. A *fair random walk* on a hypergraph has the following transition rule: Given a vertex $x_k \in V$ one first chooses a (hyper)edge $h \in E$ incident with x_k with uniform probability and then a vertex $y \in h$ is selected, again with uniform probability.

The probability of choosing edge $h \in E$ is thus $\mathbf{H}_{x,h} \cdot \mathbf{V}^{-1}_{xx}$, while the probability of chosing $y \in h$ given h has been selected is $\mathbf{H}_{y,h} \cdot \mathbf{W}^{-1}_{hh}$. Consequently we have the transition probabilities

$$\begin{aligned} p_{x\to y} &= \sum_{h\in E} \mathbf{H}_{x,h} \cdot \mathbf{V}^{-1}_{xx} \mathbf{H}_{y,h} \cdot \mathbf{W}^{-1}_{hh} = \sum_{j\in E} \mathbf{H}_{y,h} \cdot \mathbf{W}^{-1}_{hh} \mathbf{H}^{+}_{h,x} \cdot \mathbf{V}^{-1}_{xx} \\ &= (\mathbf{H}\mathbf{W}^{-1}\mathbf{H}^+\mathbf{V}^{-1})_{yx} = (\mathbf{V}^{-1}\mathbf{H}\mathbf{W}^{-1}\mathbf{H}^+)_{xy} == \mathbf{K}_{xy}\,. \end{aligned} \tag{A.4}$$

Therefore $\mathbf{K}^+$ is the transition matrix of the fair random walk on the hypergraph[7].

[7] This definition does not reduce to the usual notion of the *simple* random walk on a graph, although it is closely related. If Υ is a graph we have

$$\mathbf{K}^+ = \frac{1}{2}(\mathbf{H}\mathbf{H}^+)\mathbf{V}^{-1}\frac{1}{2}(\mathbf{A} + \mathbf{V})\mathbf{V}^{-1} = \frac{1}{2}\mathbf{I} + \frac{1}{2}\mathbf{A}\mathbf{V}^{-1}\,,$$

while Spitzer's definition [49] of a simple random walk on a graph leads to the transition matrix $\mathbf{A}\mathbf{V}^{-1}$. A corresponding definition for hypergraphs is obtained by replacing $\mathbf{W}$ by $\mathbf{W} - \mathbf{I}$.

The matrix $\mathbf{K}^+$ is closely related to the hypergraph Laplacian. The matrix $\mathbf{Q}$ defined as $\mathbf{Q} \stackrel{\text{def}}{=\!=} \mathbf{H}\mathbf{W}^{-1}\mathbf{H}^+$ is related to the hypergraph Laplacian and the transition matrix of the fair random walk by $-\Delta = \mathbf{Q} - \mathbf{V}$ and $\mathbf{K}^+ = \mathbf{Q}\mathbf{V}^{-1}$, respectively. If Υ is a regular hypergraphs then the matrices $\mathbf{K} = \mathbf{K}^+$, $\mathbf{Q}$, and $-\Delta$ have the same eigenvectors. A number of different applications of hypergraphs spectra can be found in [45, 44] and [6].

Appendix B: P-Structures and Spectral Graph Theory

In this appendix we explore the relation between P-structures and graphs. In addition we prove a few technical results that are used in the main text. Our starting point is the observation that any any pseudo-digraph Γ with vertex set V and edge set H can be interpreted as a P-structure by means of the following construction: We set $\mathcal{R}(x,y) = \{x,y\}$ if $(x,y) \in H$ and $\mathcal{R}(x,y) = \emptyset$ for all other pairs of vertices. By construction $(V,\mathcal{R})$ is a P-structure on V. Conversely, a P-structure with the property that $\mathcal{R}(x,y)$ equals either $\{x,y\}$ or the empty set defines a pseudo-digraph with vertex set V and edge set $H = \{(x,y)|\mathcal{R}(x,y) \neq \emptyset\}$. Provided $\mathcal{R}(x,x) = \emptyset$ for all $x \in V$ we have a digraph, which can be considered as an undirected graph if and only if $\mathcal{R}$ is symmetric. An obvious consequence is

Lemma B1. Suppose the P-structure $(V,\mathcal{R})$ represents a pseudo-digraph Γ. Then $\Gamma = \mathrm{supp}\mathcal{R}$.

It will be convenient to define $\mathbf{H}$ for all values of y and z by setting $\mathbf{H}_{x,(y,z)} \stackrel{\text{def}}{=\!=} 0$ whenever $(y,z) \notin E_{\mathcal{R}}$. It is customary to define the *weight* of a pair (y,z) by

$$w_{x,y} \stackrel{\text{def}}{=\!=} \begin{cases} 1/|\mathcal{R}(x,y)| & \text{if } (x,y) \in E_{\mathcal{R}} \\ 1 & \text{otherwise} \end{cases}$$

For a P-structure $(V,\mathcal{R})$ we define the matrices $\mathbf{S}$ and $\mathbf{Q}$ component-wise by

$$\begin{aligned} \mathbf{S}_{xy} &\stackrel{\text{def}}{=\!=} 2 \sum_{z \in \vec{\partial}(y)} H_{x,(y,z)} \, |\mathcal{R}(y,z)|^{-1} = 2 \sum_{z \in V} H_{x,(y,z)} w_{yz} \qquad \text{and} \\ \mathbf{Q}_{xy} &\stackrel{\text{def}}{=\!=} \sum_{(z,z') \in E_{\mathcal{R}}} H_{x,(z,z')} w_{z,z'} H_{y,(z,z')} \, . \end{aligned} \tag{B.1}$$

This definition generalizes the discussion the main text to P-structures with non-complete support. The adjacency matrix of $\mathrm{supp}\mathcal{R}$ has the entries

$$\mathbf{B}_{xy} \stackrel{\text{def}}{=\!=} \begin{cases} 1 & \text{if} \quad (y,x) \in E_{\mathcal{R}} \\ 0 & \text{otherwise} \end{cases} \tag{B.2}$$

Note that $\mathbf{B}$ is the transpose of the more conventional definition in [9]. As an immediate consequence of the definition we have $\mathbf{H}_{x,(y,z)} = \mathbf{H}_{x,(y,z)}\mathbf{B}_{zy}$.

Lemma B2. Suppose the P-structure $(V, \mathcal{R})$ represents a pseudo-digraph Γ. Then

$$\mathbf{H}_{x,(y,z)} = (\delta_{xy} + \delta_{yz})\mathbf{B}_{zy} - \delta_{xy}\delta_{yz}\mathbf{B}_{yy}\,. \qquad (B.3)$$

Proof. Let us consider the case $y \neq z$ first. All entries with $(y,z) \notin E_{\mathcal{R}}$ vanish of course; this is taken care of by the factor $\mathbf{B}_{zy}$. For an edge (y,z) we have $\mathbf{H}_{x,(y,z)} = 1$ if and only if x coincides with either y or z, which accounts for the first term. If $y = z$ and (y,y) is a loop, the only non-zero entry is obtained for $x = y = z$, i.e., $\mathbf{H}_{x,(y,y)} = \delta_{xy}\mathbf{B}_{yy}$. Substituting $z = y$ in the expression for the off-diagonal terms we find twice this entry. Subtracting this term yields the closed formula for all entries of $\mathbf{H}$. ∎

We write $\vec{\partial}(y) \stackrel{\text{def}}{=\!=} \{x \in V \,|\, (x,y) \in E_{\mathcal{R}}\}$ and $\overleftarrow{\partial}(y) \stackrel{\text{def}}{=\!=} \{x \in V \,|\, (y,x) \in E_{\mathcal{R}}\}$ for the sets of terminal vertices of edges initiating in y and the set of initial vertices of edges terminating in y, respectively. In $(V, \mathcal{R})$ is symmetric we have $\vec{\partial}(y) = \overleftarrow{\partial}(y)$. In this case we simply drop the direction symbols $\leftarrow$ and $\rightarrow$. It will be useful to define the diagonal matrices $\overleftarrow{\mathbf{D}}$ and $\vec{\mathbf{D}}$ of the in-degrees and out-degrees of $\mathrm{supp}\mathcal{R}$ with entries $\overleftarrow{\mathbf{D}}_{yy} = |\overleftarrow{\partial}(y)|$ and $\vec{\mathbf{D}}_{yy} = |\vec{\partial}(y)|$, respectively. A number of quantities can be easily obtained from the incidence matrix $\mathbf{H}$ and $\mathbf{B}$. In particular, we have

$$|\mathcal{R}(x,y)| = \sum_{x \in V} \mathbf{H}_{x,(y,z)}\,, \qquad |\vec{\partial}(y)| = \sum_{x \in V} \mathbf{B}_{xy}\,, \qquad |\overleftarrow{\partial}(y)| = \sum_{x \in V} \mathbf{B}_{yx}\,. \qquad (B.4)$$

Furthermore we shall make use of the diagonal matrix $\mathbf{V}$ of vertex degrees of the hypergraph $\mathrm{imag}\mathcal{R}$.

The following result shows that both $\mathbf{Q}$ and $\mathbf{S}$ are generalizations of conventional graph spectra, see e.g. [13, 42]. This suggests that they contain crucial information about $(V, \mathcal{R})$ in algebraic form.

Lemma B3. Let $(V, \mathcal{R})$ be a P-structure representing a pseudo-digraph. Then

$$\mathbf{S} = \mathbf{B} + \vec{\mathbf{D}} \qquad \text{and} \qquad \mathbf{Q}_{xy} = \frac{1}{2}(\mathbf{B}_{xy} + \mathbf{B}_{yx}) + \frac{1}{2}\delta_{xy}(\vec{\mathbf{D}}_{xx} + \overleftarrow{\mathbf{D}}_{xx} - 2\mathbf{B}_{xx})\,. \qquad (B.5)$$

In particular, if $(V, \mathcal{R})$ represents a simple undirected graph (without loops) we have $\mathbf{S} = \mathbf{Q} = \mathbf{B} + \mathbf{D}$.

Proof. It is convenient to recast the explicit formular for $\mathbf{H}$ of a digraph as

$$\mathbf{H}_{x,(y,z)} = (1-\delta_{yz})(\delta_{xz}+\delta_{xy})\mathbf{B}_{zy} + \delta_{yz}\delta_{xz}\mathbf{B}_{zy}\,.$$

From this we obtain directly

$$\begin{aligned}\mathbf{S}_{xy} &= 2\sum_z (1-\delta_{yz})(\delta_{xz}+\delta_{xy})\mathbf{B}_{zy}\cdot\frac{1}{2} + 2\sum_z \delta_{yz}\delta_{xz}\mathbf{B}_{zy}\cdot 1 \\ &= \sum_z (\delta_{xz}+\delta_{xy})\mathbf{B}_{zy} + \sum_z \delta_{zy}[-(\delta_{xz}+\delta_{xy}) + 2\delta_{xz}]\mathbf{B}_{zy}\,.\end{aligned}$$

It is now easy to check that the terms in the second sum cancel, and we are left with $\mathbf{S}_{xy} = \mathbf{B}_{xy} + \delta_{xy}|\vec{\partial}(y)|$.
In order to evaluate $\mathbf{Q}_{xx'}$ we start with the same expression. Using $\mathbf{B}^2_{zy} = \mathbf{B}_{zy}$ and the analogous property of the Kronecker symbols we obtain

$$\mathbf{Q}_{xx'} = \frac{1}{2}\sum_{y,z}\mathbf{B}_{yz}\big[\,(1-\delta_{yz})(\delta_{xz}+\delta_{xy})(\delta_{x'z}+\delta_{x'y}) + 2\delta_{yz}\delta_{xz}\delta_{x'z}\,\big]\,.$$

Expanding this expression, collecting all terms containing δ_{yz} and carrying out the sums over y and z yields

$$\mathbf{Q}_{xx'} = \frac{1}{2}(\mathbf{B}_{xx'}+\mathbf{B}_{x'x}) + \frac{1}{2}\delta_{xx'}(|\vec{\partial}(y)| + |\overleftarrow{\partial}(y)|) - \delta_{xx'}\mathbf{B}_{xx}\,.$$

For loop-free graphs we have $\mathbf{B}_{xx} = 0$, and the lemma follows. ∎

Finally, we compute the row sums of $\mathbf{S}$ and $\mathbf{Q}$ and find

$$\begin{aligned}\sum_{x\in V}\mathbf{S}_{xy} &= 2|\vec{\partial}(y)| = 2\vec{\mathbf{D}}_{yy} \\ \sum_{x\in V}\mathbf{Q}_{xy} &= \deg(y) = \mathbf{V}_{yy}\end{aligned} \qquad (B.6)$$

The following two lemmata are simple consequences of the definition of P-structure automorphisms.

Lemma B4. Any automorphism of a P-structure is a graph automorphism of $\mathrm{supp}\mathcal{R}$ and $\mathrm{bbg}\mathcal{R}$, and a hypergraph automorphism of $\mathrm{imag}\mathcal{R}$.

Proof. For any automorphism ψ we have $\mathbf{B}_{\psi(z)\psi(y)} = \mathbf{B}_{zy}$ since automorphisms maps pairs (y,z) with $\mathcal{R}(y,z) = \emptyset$ to pairs with empty image and pairs with non-empty image to pairs with non-empty image.
Set $\tilde{\mathbf{G}}_{yx} \stackrel{\text{def}}{=\!=} 2\mathbf{H}_{x,(x,y)}\mathbf{H}_{y,(x,y)}w_{xy}(1-\delta_{xy})$. For $x = y$ the entry $\tilde{\mathbf{G}}_{yx}$ vanishes by definition. Thus only vertex pairs with $w_{xy} \leq 1/2$ can give non-zero entries, i.e., $\tilde{\mathbf{G}}_{xy} \leq 1$. An entry is 1 if and only if $\mathcal{R}(x,y)$ has exactly two entries, and both x and y are among them. Since $\tilde{\mathbf{G}}$ is invariant under automorphisms of $(V,\mathcal{R})$ by construction, the same is true for $\mathbf{G}$.
The hypergraph part follows from the fact that $\mathbf{H}$ is the incidence matrix of $\mathrm{imag}\mathcal{R}$.

∎

Definition. We say that a P-structure is *regular* if $\vec{\mathbf{D}}$, $\overleftarrow{\mathbf{D}}$ and $\mathbf{V}$ are multiples of the identity matrix $\mathbf{I}$.

Lemma B5. A vertex transitive P-structure is regular.

Proof. For the out-degrees we have for instance

$$\vec{\mathbf{D}}_{yy} = \sum_{x\in V} \mathbf{B}_{xy} = \sum_{x\in V} \mathbf{B}_{\psi(x)\psi(y)} = \sum_{x'\in V} \mathbf{B}_{x'\psi(y)} = \vec{\mathbf{D}}_{\psi(y)\psi(y)} \,.$$

The same procedure shows that $\overleftarrow{\mathbf{D}}_{yy}$ and $\mathbf{V}_{yy}$ are independent of $y \in V$. ∎

Theorem 1. Let $(V,\mathcal{R})$ be a b.d.transitive P-structure. Then its Bose-Mesner algebra $\mathcal{A}[V,\mathcal{R}]$ coincides with the adjacency algebra of the backbone graph $\mathrm{bbg}\mathcal{R}$, i.e., $\mathcal{A}[V,\mathcal{R}]$ is generated by $\mathbf{G}$.

Proof. Consider the orbits of the automorphism groups of the full P-structure and of its backbone graphs, respectively. In the latter case the orbits are exactly the distance classes of $\mathrm{bbg}\mathcal{R}$. Since $\mathbf{Aut}[V,\mathcal{R}] \subseteq \mathbf{Aut}(\mathrm{bbg}\mathcal{R})$ we know that the orbits of $\mathbf{Aut}[V,\mathcal{R}]$ are contained in the orbits of $\mathbf{Aut}(\mathrm{bbg}\mathcal{R})$. On the other hand, the distance classes are contained in the orbits of $\mathbf{Aut}[V,\mathcal{R}]$ because the backbone graph $\mathrm{bbg}\mathcal{R}$ is distance transitive as immediate consequence of the definition. Thus $\mathcal{A}[V,\mathcal{R}]$ coincides with the coherent algebra defined by the distance classes of the backbone graph which is in turn identical with the adjacency algebra of $\mathrm{bbg}\mathcal{R}$, again because of the distance transitivity of the backbone graph, see [3] for more the details. ∎

Appendix C: Algebraic Properties of String-Crossover

A general crossover operator χ is characterized by a subset J of positions which are swapped under its action: $\chi = \prod_{j\in J} \diamondsuit_j$. As compositions of single position operators, all crossover operators are all involutions, i.e., $\chi \circ \chi = \times_1$. From $\diamondsuit_k(x,x) = (x,x)$ we conclude immediately $\chi(x,x) = (x,x)$. If we set $\diamondsuit_k(x,y) = (x',y')$ then $\diamondsuit_k(y,x) = (y',x')$. This symmetry is present in all recombination operators: $\chi(x,y) = (x',y')$ implies $\chi(y,x) = (y',x')$. Finally, since we have not defined a swap operator for the n-th position there is no recombination operator for which $\chi(x,y) = (y,x)$ for all pairs of sequences. This restriction will be useful for some the proofs below.

Lemma C1. Let $u \in \mathcal{R}(x,y)$. Then

(i) $\chi(x,y) = (x,y)$ implies $\chi(x,u) = (x,u)$ for all $\chi \in F(\mathcal{R})$.

(ii) Set $(x',y') = \chi(x,y)$ for an arbitrary $\chi \in F(\mathcal{R})$. The $(x',y') \neq (x,y)$ implies $\{x,y\} \cap \{x',y'\} = \emptyset$.

(iii) $\chi(x,u) \neq \xi(x,u)$ implies $\chi(x,y) \neq \xi(x,y)$ for any two $\chi, \xi \in F(\mathcal{R})$.

Proof. The condition in (i) implies that χ consists only of $\diamondsuit_k$'s operating on positions k where $x_k = y_k = u_k$.

(ii) The sequence x occurs in $\chi(x,y)$ if and only if χ acts only on positions in which x and y agree; this would imply $\chi(x,y) = (x,y)$. Since the same argument holds for y, and the claim follows.

(iii) Since χ acts position-wise we have $[\chi(x,y)]_i = [\chi(x,u)]_i$ for all positions i for which $u_i = y_i$. Since u is a recombinant of x and y this is the case for all positions for which $x_i = y_i$, i.e., $[\chi(x,u)]_i = [(x,x)]_i$. Thus two operators χ and χ' for which $\chi(x,u) \neq \chi'(x,u)$ act differently at least on one position j for which $x_j \neq u_j$, i.e., $u_j = y_j$. Therefore we have $\chi(x,y) \neq \chi'(x,y)$. Setting $(x',y') = \chi(x,y)$ and $(u',v') = \chi'(x,y)$ we have $\{x',y'\} \cap \{u',v'\} = \emptyset$ by the same argument as in item (ii) above. ∎

Lemma C2. Let F be a family of string recombination operators. Then the associated P-structure is a recombination structure if and only if $\times_1 \in F$.

Proof. The symmetries of χ imply that $\mathcal{R}(x,x) = \{x\}$ and $\mathcal{R}(x,y) = \mathcal{R}(y,x)$. From $\times_1(x,y) = (x,y)$ we find immediately $\{x,y\} \in \mathcal{R}(x,y)$. To show the converse, consider two sequences x and y with Hamming distance $d(x,y) = n$. Recall that there is no recombination operator χ fulfilling $\chi(x,y) = (y,x)$, thus $x' \neq y$. The only operator for which $\chi(x,y) = (x,y)$ is therefore identity since x and y differ by construction in all positions.
The properties of the recombinations operators described in lemma C1 above implies that each operator creates at least as many different sequences from (x,y) as from (x,u). Combined with item (iii) in lemma C1 this implies $|\mathcal{R}(x,y)| \geq |\mathcal{R}(x,u)|$. ∎

Let us now turn to the symmetry properties of χ. The following technicality will be used repeatedly below:

Lemma C3. Let ϕ_i, $i = 1$ through n, be a set of one-to-one mappings of the alphabet $\mathcal{Q}_\alpha$ into itself. Then $\phi \stackrel{\text{def}}{=\!=} (\phi_1, \phi_2, \ldots, \phi_n)$ is one-to-one on $\mathcal{Q}_\alpha^n$ and for any recombination operator χ holds $\chi(\phi(x), \phi(y)) = \phi(\chi(x,y))$.

Proof. It is sufficient to note that ϕ_i commutes with $\diamondsuit_i$. A construction similar to this one was used in [23]. ∎

Theorem 2. The automorphism group $\mathbf{Aut}(\mathcal{Q}_\alpha^n, \mathcal{R})$ of a string recombination structure is generously transitive.

Proof. Given two strings $x = (x_i)$ and $y = (y_i)$ we define φ position wise by $\phi_i(x_i) = y_i$, $\phi_i(y_i) = x_i$ and $\phi_i(z) = z$ for all $z \in \mathcal{Q}_\alpha \setminus \{x_i, y_i\}$. This gives rise to the mapping $\phi = (\phi_1, \ldots, \phi_n)$ which fulfils the conditions of the previous lemma. From $\mathcal{R}(\phi(x), \phi(y)) = \{\chi_1(\phi(x), \phi(y)), \chi_2(\phi(x), \phi(y)), \ldots, \chi_n(\phi(x), \phi(y))\} = \{\phi(\chi_1(x,y)), \phi(\chi_2(x,y)), \ldots, \phi(\chi_n(x,y))\} = \phi(\mathcal{R}(x,y))$ we conclude immediately that ϕ is in fact an automorphism of $(V, \mathcal{R})$. Therefore $\mathbf{Aut}(V, \mathcal{R})$ acts generously transitively on V. ∎

Theorem 3. The backbone graph of a string recombination P-structure $(\mathcal{Q}_\alpha^n, \mathcal{R})$ is the Hamming graph $\mathcal{Q}_\alpha^n$ if and only if it is separable.

Proof. By definition we have $\mathcal{R}(x,y) = \{x,y\}$ if $d_H(x,y) = 1$, i.e., the Hamming graph $\mathcal{Q}_\alpha^n$ is always *contained* in the backbone. If $d_H(x,y) > 1$ then there are two sequence positions k and l at which x and y differ. Since $(\mathcal{Q}_\alpha^n, \mathcal{R})$ is separable there is a crossover operator $\chi \in F(\mathcal{R})$ that separated k and l. Thus the offsprings of x and y are different from their parents and hence $|\mathcal{R}(x,y)| > 2$, and thus (x,y) is not an edge of $\mathrm{bbg}(\mathcal{R})$.
Conversely, suppose that $d(x,y) = 2$ with x and y differing at positions k and l. If there is no crossover operator that separates k and l then $\mathcal{R}(x,y) = \{x,y\}$, i.e., (x,y) is an edge of $\mathrm{bbg}\mathcal{R}$ which does not belong to the Hamming graph. ∎

For some recombination structure we can prove even stronger symmetry properties:

Lemma C4. For any two pairs of strings (x,y) and (u,v) with equal Hamming distance $d_H(x,y) = d_H(u,v)$ there is an automorphism π of $(\mathcal{Q}_\alpha^n, \mathcal{R}_\diamondsuit)$ such that $u = \pi(x)$ and $v = \pi(y)$.

Proof. We have already seen that a string recombination structure is invariant under arbitrary renamings of positions. Now consider a permutation π of the positions 1 through n. Since the crossover operators in $F(\mathcal{R}_\diamondsuit)$ are $\diamondsuit_k$'s it follows that we obtain the same result when we (a) recombine using $\diamondsuit_j$ and permute the positions afterwards and when we (b) permute the positions first and recombine using the operator $\diamondsuit_{\pi(j)}$. Thus we have $\pi(\mathcal{R}_\Omega) = \mathcal{R}_\Omega$, i.e., π is an automorphism of $(V, \mathcal{R}_\diamondsuit)$. In particular, we can always find a permutation π that reorders the positions such that the all positions in which to given strings x and y differ have index 1 through $d_H(x,y)$. In a second step we can use a renaming ϕ such that $\hat{x} = (0,\ldots,0)$ and $\hat{y} = (1,\ldots,1,0\ldots0)$ with 1s in the first $d(x,y)$ positions and 0s in the remaining $n - d(x,y)$ positions. Lemma C3 guarantees that ϕ is an automorphism as well. Thus the composition $\phi \circ \pi$ is also an automorphism.
Given two pairs of sequences, (x,y) and (u,v) with the same mutual distance $d_H(x,y) = d_H(u,y) = d$ we can use the above procedure to construct a two automorphisms ψ_1 and ψ_2 such that $\psi_1(x,y) = \psi_2(u,v) = (\hat{x},\hat{y})$, i.e., $\psi_2^{-1}(\psi_1(x,y)) = (u,v)$, which is of course again an automorphism of $(\mathcal{Q}_\alpha^n, \mathcal{R}_\Omega)$. ∎

Lemma C5. For any two pairs of strings (x, y) and (u, v) with equal Hamming distance $d_H(x, y) = d_H(u, v)$ there is an automorphism π of $(\mathcal{Q}_\alpha^n, \mathcal{R}_\Omega)$ such that $u = \pi(x)$ and $v = \pi(y)$.

Proof. We argue as in lemma C4. Consider a permutation π of the positions 1 through $n-1$. Since any recombination operator is a composition of $\diamondsuit_k$'s it follows that $\chi_{\pi(J)}(\pi(x), \pi(y)) = \pi(\chi_J(x, y))$. Since $\chi_{\pi(J)} \in F(\mathcal{R}_\Omega)$ whenever $\chi_J \in F(\mathcal{R}_\Omega)$, we find that π is a bijection in $F(\mathcal{R}_\Omega)$, and hence $\pi(\mathcal{R}_\Omega) = \mathcal{R}_\Omega$. In other words, π is an automorphism of $(V, \mathcal{R}_\Omega)$. Since the order of the first $n-1$ positions can be changed without changing the P-structure we may as well place position n where we please. The reminder of the proof is the same as for the single position exchange operator in lemma C4. ∎

An immediate corollary of lemma C4 and lemma C5 is

Theorem 4. The recombination P-structures $(\mathcal{Q}_2^n, \mathcal{R}_\diamondsuit)$ and $(\mathcal{Q}_2^n, \mathcal{R}_\Omega)$ are distance transitive with respect to their backbone graphs.

Lemma C6. Consider $(\mathcal{Q}_2^n, \mathcal{R}_\Omega)$, and set $d_H(x, y) = d$. Then

$$\sum_{\substack{z \\ d_H(y,z)=d'}} \mathbf{H}_{x,(y,z)} = \binom{n-d}{d'-d}.$$

Proof. Lemma C5 allows us to fix $\hat{x}$ and $\hat{y}$ as in the proof above. The 0 in the first d positions of $\hat{x}$ can be obtained only if $z_i = 0$ for $1 \le i \le d$. In the remaining positions we can get $\hat{x}_i = 0$ from either $\hat{y}$ or z, thus there is no restriction on z for the latter $n-d$ positions. Thus there are exactly 2^{n-d} sequences z for which $\hat{x} \in \mathcal{R}(\hat{y}, z)$. The distance $d' \stackrel{\text{def}}{=\!=} d_H(z, y)$ is of course d plus the number $k = d' - d$ of positions $z_i = 1$ in the latter $n-d$ positions. Given d', there are exactly $\binom{n-d}{d'-d}$ different choices for z. Each one contributes 1 to the sum, and the lemma follows. ∎

Lemma C7. For $(\mathcal{Q}_2^n, \mathcal{R}_\Omega)$ we find $\mathbf{S}_{xy} = 2(3/2)^n 3^{-d_H(x,y)}$.

Proof. Using the lemma C6 we have

$$\mathbf{S}_{xy} = 2\sum_{d'=0}^{n} \sum_{\substack{z \\ d_H(y,z)=d'}} \mathbf{H}_{x,(y,z)} |\mathcal{R}_\Omega(y,z)|^{-1} = 2\sum_{d'=d}^{n} 2^{d'} \binom{n-d}{d'-d}$$

$$= 2\cdot 2^{-d} \sum_{k=0}^{n-d} \binom{n-d}{k} 2^{-k} = 2\cdot 2^{-d}(1+1/2)^{n-d} = 2(3/2)^n \cdot 3^{-d}$$

where $d = d_H(x,y)$. ∎

Lemma C8. For $(\mathcal{Q}_2^n, \mathcal{R}_\Omega)$ we find $\mathbf{Q}_{xy} = 2^{n-d_H(x,y)}$.

Proof. Using $|\mathcal{R}_\Omega(x,y)| = 2^{d_H(x,y)}$ we can rewrite the definition of the matrix elements as

$$\mathbf{Q}_{xy} = \sum_{d'=0}^{n} 2^{-d'} \sum_{\substack{z,z' \\ d_H(z,z')=d'}} \mathbf{H}_{x,(z,z')} \mathbf{H}_{y,(z,z')} \,.$$

In order to evaluate the second sum we set $x = \hat{x}$, $y = \hat{y}$ and $d = d_H(x,y)$. For the first d positions we have $x_i = 0$ and $y_i = 1$. Thus (z_i, z_i') must be either $(1,0)$ or $(0,1)$. Thus we have 2^d choices there, and the contribution of the first d positions to the distance $d' = d_H(z,z')$ is always d. In the remaining part of the sequence we must be able to obtain a 0 in each sequence position, thus (z_i, z_i') is one of $(0,0)$, $(1,0)$, or $(0,1)$. Exactly $d'-d$ positions must be either $(1,0)$ or $(0,1)$ so that the total distance between z and z' equals d'. There are $\binom{n-d}{d'-d}$ choices for these positions and 2 alternatives at each one of them. Consequently there are $2^d \times \binom{n-d}{d'-d} \times 2^{d'-d}$ pairs of strings (z,z') with given distance d' for which $\mathbf{H}_{\hat{x},(z,z')}\mathbf{H}_{\hat{y},(z,z')} = 1$. Hence we have

$$\mathbf{Q}_{xy} = \sum_{d'=0}^{n} 2^{-d'} 2^{d'} \binom{n-d}{d'-d} = \sum_{k=0}^{n-d} \binom{n-d}{k} = 2^{n-d} \,,$$

and the lemma is proved. ∎

Lemma C9. Let $\mathbf{C}$ be a $2^n \times 2^n$ matrix with rows and colums indexed by binary strings of length n from the alphabet $\{+1,-1\}$ such that $\mathbf{C}_{xy} = q^{d_H(x,y)}$, and let $0 < q < 1$. Then $\mathbf{C}$ is positive definite, has $n+1$ distinct eigenvalues

$$\lambda_p^{\mathbf{C}} = (1+q)^n \left(\frac{1-q}{1+q}\right)^p \qquad 0 \le p \le n$$

with multiplicity $\binom{n}{p}$. The corresponding eigenvectors are the p-spin functions $\varepsilon_{i_1,i_2,\ldots,i_p}(\sigma) \stackrel{\text{def}}{=\!=} \sigma_{i_1}\sigma_{i_2}\ldots\sigma_{i_p}$, equ.(1), with $i_1 < i_2 < \ldots < i_p$ and $\sigma \in \{+1,-1\}^n$.

Proof. (i) Let $\mathbf{A}$ denote the adjacency matrix of the hypercube. Since this graph is distance transitive the matrices $\mathbf{A}^{(d)}$, with entries $\mathbf{A}^{(d)}_{xy} = 1$ if $d_H(x,y) = d$ and $\mathbf{A}^{(d)}_{xy} = 0$ otherwise, can be written as polynomials of order d in terms of $\mathbf{A}$ [14], see also [3]. Since $\mathbf{S}$ and $\mathbf{Q}$ are linear combinations of the $\mathbf{A}^{(d)}$ they are polynomials of order n in $\mathbf{A}$. Hence they have the same eigenvectors as $\mathbf{A}$ and the eigenvalues are polynomials of the eigenvalues of $\mathbf{A}$. The eigenvalues of $\mathbf{A}$ are $\lambda_p^{\mathbf{A}} = n - 2p$ for the $\binom{n}{p}$ eigenvectors $\varepsilon_{i_1,i_2,\ldots,i_p}$. We conclude that the ε's are eigenvectors of $\mathbf{S}$ and $\mathbf{Q}$, and vectors with the same number p of indices correspond to the same eigenvalue.

Distance transitivity implies that the eigenvalue problem can be reduced to the "collapsed adjacency matrix" $\hat{\mathbf{A}}$ with entries

$$\hat{\mathbf{A}}_{d',d} \stackrel{\text{def}}{=\!=} \sum_{x:d_H(x,y)=d'} \mathbf{A}_{xy}$$

for all y with $d(y,\vec{1}) = d$, where the "reference vertex" $\vec{1}$ can be chosen arbitrarily. The left eigenvectors of this matrix are the functions

$$\omega_p(d) = \frac{1}{\binom{n}{p}}\binom{n}{d}\sum_{l=0}^{n}(-1)^l\binom{d}{l}\binom{n-d}{p-l},$$

the eigenvalues are the same as those of $\mathbf{A}$. The sum is a Krawtchouk polynomial. The details of this construction can be found explicitly in [51]. Consequently we have

$$\sum_{d=0}^{n}\omega_p(d)q^d = \lambda_p^{\mathbf{C}}\omega_p(0),$$

we $\omega_p(0) = 1$. Thus we have to evaluate

$$\lambda_p^{\mathbf{C}} = \frac{1}{\binom{n}{p}}\sum_l(-1)^l\sum_d\binom{n}{d}\binom{d}{l}\binom{n-d}{p-l}.$$

It is easy to verify that $\binom{n}{d}\binom{d}{l}\binom{n-d}{p-l} = \binom{n}{p}\binom{p}{l}\binom{n-p}{d-l}$; thus we have

$$\lambda_p^{\mathbf{C}} = \sum_l(-1)^l\binom{p}{l}\sum_d q^d\binom{n-p}{d-l} = \left(\sum_l(-1)^l\binom{p}{l}q^l\right)\left(\sum_{d'}\binom{n-p}{d'}q^{d'}\right)$$

which simplies to $\lambda_p^{\mathbf{C}} = (1-q)^p(1+q)^{n-p}$. ∎

The matrices $\mathbf{S}$ and $\mathbf{Q}$ of the uniform recombination structure are of the above form with $q = 1/3$ and $q = 1/2$, up to a multiplicative constant.

Appendix D: Nearest Neighbor Correlations

Table 1. Nearest neighbor correlations of landscapes over the set $\mathcal{Q}_2^n$ of binary strings of length $n = 3$ for point mutations, free (uniform) recombination, and one-point recombination.

p	vector	r(1)							
		mut.	$\mathcal{R}_\Omega$	$\mathcal{R}_2$			$\mathcal{R}_1$		
0	0	1	1	1	1.000	1.000	1	1.000	1.000
1	1			1/2	0.500		1/2	0.500	
	2	1/3	1/2	1/2	0.500	0.500	1/2	0.500	0.500
	3			1/2	0.500		1/2	0.500	
2	12			1/4	0.250		7/24	0.291	
	23	−1/3	1/4	1/4	0.250	0.250	7/24	0.291	0.263
	13			1/4	0.250		5/24	0.208	
3	123	−1	1/8	1/8	0.125	0.125	1/8	0.125	0.125

Remark. We have the same spectrum for $\mathcal{R}_2$ and $\mathcal{R}_\Omega$ for $n = 3$. This is no coincidence, of course, since $\mathcal{R}_\Omega = \mathcal{R}_2$ in this case.

Table 2. Nearest neighbor correlations of landscapes over the set $\mathcal{Q}_2^n$ of binary strings of length $n = 4$ for point mutations, free (uniform) recombination, and one-point recombination.

p	vector	r(1)							
		mut.	$\mathcal{R}_\Omega$	$\mathcal{R}_2$			$\mathcal{R}_1$		
0	0	1	1	1	1.000	1.000	1	1.000	1.000
1	1			1/2	0.500		1/2	0.500	
	2	1/2	1/2	1/2	0.500	0.500	1/2	0.500	0.500
	3			1/2	0.500		1/2	0.500	
	4			1/2	0.500		1/2	0.500	
2	12			29/112	0.259		31/96	0.323	
	23			29/112	0.259		31/96	0.323	
	34	0	1/4	29/112	0.259	0.253	31/96	0.323	0.274
	13			27/112	0.241		1/4	0.250	
	24			27/112	0.241		1/4	0.250	
	14			29/112	0.259		17/96	0.177	
3	123			1/8	0.125		9/48	0.188	
	234	−1/2	1/8	1/8	0.125	0.125	9/48	0.188	0.146
	124			1/8	0.125		5/48	0.104	
	134			1/8	0.125		5/48	0.104	
4	1234	−1	1/16	3/56	0.053	0.053	1/16	0.063	0.063

Table 3. Nearest neighbor correlations of landscapes over the set $\mathcal{Q}_2^n$ of binary strings of length $n = 5$ for point mutations, free (uniform) recombination, and one-point recombination.

p	vector	r(1)							
		mut.	$\mathcal{R}_\Omega$	$\mathcal{R}_2$			$\mathcal{R}_1$		
0	0	1	1	1	1.000	1.000	1	1.000	1.000
1	1			1/2	0.500		1/2	0.500	
	2			1/2	0.500		1/2	0.500	
	3	3/5	1/2	1/2	0.500	0.500	1/2	0.500	0.500
	4			1/2	0.500		1/2	0.500	
	5			1/2	0.500		1/2	0.500	
2	12			355/1232	0.272		111/320	0.347	
	23			355/1232	0.272		111/320	0.347	
	34			355/1232	0.272		111/320	0.347	
	45			355/1232	0.272		111/320	0.347	
	13	1/5	1/4	299/1232	0.243	0.257	271/960	0.282	0.282
	24			299/1232	0.243		271/960	0.282	
	35			299/1232	0.243		271/960	0.282	
	14			299/1232	0.243		209/960	0.218	
	25			299/1232	0.243		209/960	0.218	
	15			355/1232	0.272		49/320	0.153	
3	124			27/224	0.121		31/192	0.258	
	134			27/224	0.121		31/192	0.258	
	235			27/224	0.121		31/192	0.258	
	245			27/224	0.121		31/192	0.258	
	123	−1/5	1/8	31/224	0.138	0.129	15/64	0.234	0.200
	234			31/224	0.138		15/64	0.234	
	345			31/224	0.138		15/64	0.234	
	125			31/224	0.138		17/192	0.089	
	145			31/224	0.138		17/192	0.089	
	135			27/224	0.121		17/192	0.089	
4	1234			17/308	0.055		42/320	0.131	
	2345			17/308	0.055		42/320	0.131	
	1235	−3/5	1/16	17/308	0.055	0.055	9/160	0.056	0.084
	1345			17/308	0.055		9/160	0.056	
	1245			17/308	0.055		23/480	0.048	
5	12345	−1	1/32	1/112	0.009	0.009	1/32	0.031	0.031

Table 4. Nearest neighbor correlations of landscapes over the set $\mathcal{Q}_2^n$ of binary strings of length $n = 6$ for point mutations, free (uniform) recombination, and one-point recombination.

p	vector	r(1)					
		mut.	$\mathcal{R}_\Omega$	$\mathcal{R}_2$		$\mathcal{R}_1$	
0	0	1.000	1.000	1.000	1.000	1.000	1.000
1	1			0.500		0.500	
	2			0.500		0.500	
	3	0.667	0.500	0.500	0.500	0.500	0.500
	4			0.500		0.500	
	5			0.500		0.500	
	6			0.500		0.500	
2	12			0.286		0.366	
	23			0.286		0.366	
	34			0.286		0.366	
	45			0.286		0.366	
	56			0.286		0.366	
	13			0.250		0.327	
	24			0.250		0.327	
	35	0.333	0.250	0.250	0.262	0.327	0.293
	46			0.250		0.327	
	14			0.238		0.250	
	25			0.238		0.250	
	36			0.238		0.250	
	15			0.250		0.192	
	26			0.250		0.192	
	16			0.286		0.134	
3	123			0.158		0.270	
	234			0.158		0.270	
	345			0.158		0.270	
	456			0.158		0.270	
	124			0.129		0.206	
	134			0.129		0.206	
	235			0.129		0.206	
	245			0.129		0.206	
	346			0.129		0.206	
	356	0.000	0.125	0.129	0.136	0.206	0.173
	125			0.129		0.141	
	145			0.129		0.141	
	236			0.129		0.141	
	256			0.129		0.141	
	135			0.114		0.141	
	246			0.114		0.141	
	126			0.158		0.077	
	156			0.158		0.077	
	146			0.129		0.077	
	136			0.129		0.077	
4	1234			0.071		0.183	
	2345			0.071		0.183	
	3456			0.071		0.183	
	1235			0.055		0.117	
	1345			0.055		0.117	
	2346			0.055		0.117	
	2456			0.055		0.117	
	1245	−0.333	0.063	0.053	0.061	0.110	0.101
	2356			0.053		0.110	
	1236			0.071		0.051	
	1456			0.071		0.051	
	1346			0.053		0.051	
	1246			0.055		0.044	
	1356			0.055		0.044	
	1256			0.071		0.037	
5	12345			0.013		0.099	
	23456			0.013		0.099	
	12346	−0.667	0.031	0.013	0.013	0.032	0.052
	13456			0.013		0.032	
	12356			0.013		0.024	
	12456			0.013		0.024	
6	123456	−1.000	0.016	−0.020	−0.020	0.016	0.016

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