HIERARCHICAL ORGANIZATION AND ADAPTIVE DYNAMICS IN RELATIONAL SYSTEMS

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ABSTRACT

HIERARCHICAL ORGANIZATION AND ADAPTIVE DYNAMICS
IN RELATIONAL SYSTEMS

By

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The aim of the thesis is to investigate certain biological concepts related to adaptation of hierarchical systems coupled to general environments. A system model is constructed to account for some mathematically tractable aspects of adaptive behavior.

The organizing principles underlying hierarchical systems are applied to define levels of dynamical invariance of the system structure, and a close relationship between structure and function is demonstrated. Certain dynamical characteristics of general systems are related to structural perturbations due to the environment. The concepts of system complexity, vulnerability and relational stability are discussed within the framework of relational systems.

A class of relational dynamical systems are submitted as natural candidates for realization of a given set of input-output specifications.

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By

Tom Michel Koplyay

A THESIS

Submitted to
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TO

MY ELUSIVE BUTTERFLY

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"...usually, there is a well-marked negative correlation between the scope and the soundness of the writings...The sound work is confined either to engineering or rather trivial applications; ambitious formulations remain vague."

Anatol Rapoport

In light of the above we intend to be relatively ambitious, and hopefully not so vague.

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0. INTRODUCTION

"The time has come," said the Walrus," to speak of many things..."

L. Carrol

The present dissertation explores some of the problems related to structure and behavior in dynamical systems and their influence on adaptation.

The model proposed (we are much too humble and wise to call it a theory) is intended to shed some light on the systems foundation of biological adaptation. Indeed, to be more precise, we focus our attention on certain salient aspects of biological organization that are sufficiently well understood and defined to lend themselves to mathematical analysis.

The methodology of the investigation consists of a judicious blend of ideas and techniques from the diverse but related fields of systems science and relational biology. Both of these fields presuppose a certain amount of mathematical maturity and a reasonable level of competence. In particular, basic knowledge of graph theory, dynamical systems and abstract algebra is assumed.

To a first approximation the model includes the following concepts:

a) Emergent and adaptive behavior in dynamical systems; with biological interpretations.

b) The general properties of system deep and surface structures and their respective role in storage of biological information.

c) The principle of biological function change and adaptive capacity in (M, R)-systems.

d) The functional and structural aspects of hierarchical organization in relational dynamical systems.

e) Identification procedures in systems modeling and the levels of isomorphism between hierarchical structures.

f) Concepts related to self-organization, adaptation and regulation along with the dynamical properties of biosystems coupled to specific environments.

Obviously, as in any other speculative model, there exist definite limitations. Within the present scope and format, we cannot hope to answer all the questions pertaining to adaptive features of real biological systems. What we can do is to offer possible interpretations and solutions to some adaptive phenomena encompassed by the model.

A concrete modeling methodology is developed to describe essential characteristics of adaptation, and beyond the fundamental hypotheses the procedure is fairly algorithmic; however possible flaws in the hypotheses can invalidate some results. For the above reason every attempt was made to incorporate biological principles in a manner that they fit the model framework, yet the biological meaning is not lost in the process of abstraction.

Another inherent and almost inescapable limitation is the personal bias of the investigator.

The formulation of the basic axioms automatically defines the modeling horizons. Hence, the selection of organizing and basic assumptions is to be made with the model content and scope in mind. Content does not necessarily preclude scope, but they do lie at almost opposite ends of the modeling requirements. If the model is to have a fairly large (specific) content then generally the scope is narrowed and conversely. Therefore it is a futile attempt to eliminate all subjectivism on the part of the investigator, only an attempt can be made to find a proper balance.

Assuming that the above problem is under control, there still remains some obstacles related to the particular tools used in the analysis.

The potential complexity of a problem such as adaptation is infinite, yet we must be content to approximate reality by finite means.

Techniques related to identification of structure, function and dynamics of biological systems rely on idealizations that are by physical necessity finite.

Consequently, in view of the above constraints we venture forth the qualified statement that the present model is sufficiently objective, wide in scope and specific in content to satisfy a variety of aesthetic and scientific criteria.

The novelty of the approach lies in the fusion of different fields to yield a unified, if modest picture of adaptive behavior in relational biological systems.

The main contribution of the present thesis is the construction of a graph theoretic systems framework for class of abstract biological systems known as (M,R)-systems. Some results are derived on the realizability of (M,R)-systems within a graph representation context and certain concepts associated with adaptive structural changes are investigated. To relate (M,R)-systems to the basic ideas in systems science and to formulate a concept of hierarchy a methodology is developed whereby fundamental structural components in an arbitrary system can be isolated with respect to an observed set of activities. The literature survey is integrated with the thesis and each topic is reviewed in the appropriate section.

To provide a loose framework for the modeling techniques introduced in Chapter I, we shall examine some problems related to analysis of structure and function in a specific biological discipline; cytology. The discussion is intended to serve as motivation for the ideas exposed in the next chapter on system modeling and the nature of perceived hierarchies.

One important aspect of cellular metabolism is enzyme activity. Depending on the skill and ingenuity of the investigator several structural components can be distinguished for a specific enzyme. These may consist of;

a) individual atoms,

b) NH_2 amino group, COOH-acid group,

c) amino acids,

d) proteins,

The structural decomposition above constitutes a biological hierarchy, in the sense that units at one level aggregate via reactions to form the next level. The amino and acid groups combine to form amino acids, which in turn serve as building blocks for proteins. Within certain biotic and abiotic bounds, units at each level may constitute invariant aggregates for a class of chemical reactions and metabolic activities. For some chemical reactions catalyzed by specific enzymes, for small variations of temperature, pH and substrate concentration the enzymes may be invariant units. If the temperature is increased the enzymes may decompose into proteins and subsequently into the amino and acid groups.

If the original aim of the investigation was to isolate factors responsible for the catalysis of some chemical reactions in the cell and the activity of catalysis is assigned observable (measurable) features such as:

a) pH,

b) temperature of solution,

c) concentration of an identifiable compound (substrate),

then the enzymes should be isolated as responsible chemical units.

The initial point of view concerning the system (cell) is to regard it as an "imperfect" black box. An activity known as catalysis exists and certain outstanding features are recognized as characteristic of the activity. At this stage the cell is a black box, with a class of chemicals as input, catalysis as internal process and a new class of chemicals as output.

However, the investigator is still free to intervene in the system and to perform sets of measurements appropriate to the characteristic features of the catalysis activity. Thus the system identification corresponds to an imperfect black box approach. Once the measurements are made (temperature, pH, substrate concentration, etc.) and some structural entities (enzymes) are isolated as possible significant components generating the catalysis, the components have to be reassembled in a manner to account for features of catalytic activity.

If an abiotic factor such as temperature is strongly varying in the cellular system, then, instead of enzymes the amino acids may be picked as natural candidates for reconstructing the activity.

The function-structure analysis in Chapter I is to be interpreted in this light. A structure underlying and generating a function (activity) in our framework is not absolute but rather perceived. It depends on the original choice of behavioral features associated with the activity, the measurement process, refinement of techniques and other experimental limitations.

The hierarchical organization considered in this thesis roughly corresponds to the meaningful aggregations of structural units with respect to an observed activity.

Consequently enzymes are natural units for catalysis, whereas amino acids may be fundamental for protein synthesis. When enzyme synthesis is considered in the cell, a class of proteins may be associated with that specific metabolic activity.

In many respects biological systems (cells) differ from physical systems. An activity in a biological system can persist in time in spite of the fact that the underlying structure is changing.

As an example again we may refer to enzyme catalysis. The individual enzymes have a relatively fast turnover rate, yet the catalytic activity characteristic of their presence in a chemical reaction persists. On the other hand, structural features may be relatively constant yet the associated activity varies. If amino acids are considered basic then structural protein, enzyme synthesis can be both interpreted as generated by the same structural invariants.

Consequently the structure-function relationship in a biological context is a very delicate matter and no more should be attributed to Chapter I than a possible explanation for aspects of the relationship which may be based on the concept of levels of structural invariance exemplified by the amino acid→protein→enzyme structural succession.

CHAPTER I

SYSTEMS FOUNDATIONS

1.1 Identificaton and Decomposition of Arbitrary Systems

Standard procedure in the analysis of both physical and biological systems is to first isolate the system under consideration from its environment and then to decompose the system into a collection of subunits. The underlying motivation, which is a fundamental postulate of systems science, is that structure and behavior of the total system are reconstructable from the constituent components. The decomposition singles out the subunits that can be relatively well modeled in a free-body form by referencing its dynamics to previously documented analogous forms. Having identified the structure or behavior of the isolated (free-body) components the total system is reassembled by means of the system graph topology and the induced constraint equations.

Usually structure of the fundamental subunits is elusive and general methods exist only to derive the behavioral equations of the system by modeling the components as black-boxes and subjecting each unit to preselected set of test signals, which represents a sampling of the actual environment. [Z-1, Z-2, Z-3]. Immediately several problems surface at the decomposition stage of the system. First, the investigator singles out components that are meaningful in the system structure; by the above we mean that each component is relatively stable within the system over a period of time and that each participates in the system activity as an

identifiable subunit. The identification process consists of observing the system activity, and with respect to the observed behavior performing a set of measurements on the system. The components that are subsequently singled out as meaningful should behave as coherent units, at least over the time interval of the observation and measurement. In addition, each component is assumed to have some effect on the system behavior. It is well known that the possible perturbations caused by the measurement process might alter the system behavior, hence care must be taken to choose a set of measurements to which the system is relatively insensitive.

In the present chapter we shall outline an identification methodology from an arbitrary observer's point of view, which will lead to a general model of hierarchical systems. The procedure incorporates the classical techniques of "tearing and reconstruction" as well as some fairly rigorous methods based on set theoretic foundations.

Each major mathematical tool will be defined as it is introduced. It is assumed the experimental problem of defining system boundaries and separating the system from its environment has been resolved.

Characterization of Fundamental Subunits

Given a system S delineated from its environment E_s structurally, but still coupled to E_s functionally, we undertake the analytical task of specifying its structure and behavior. From the observer's point of view, considering the system as a black box, it may perform a set of simultaneous activities and the problem becomes one of identifying structural characteristics responsible for this activity class.

Let the set of activities be denoted as $[A_1,\ldots A_n]$ (where [ ] denotes an ordered set); any A_i corresponds to measurably differentiated activity from any other A_j in the set. In other words, the set of activities can be pairwise distinguished by at least one physical measurement. Each A_i may differ from any other A_j in several measurable features if $A_i = [f_{i1},\ldots f_{in_i}]$ and $A_j = [f_{j1},\ldots f_{jn_j}]$, but there must exist at least one distinct characteristic feature f_{ij} not shared by any other activity.

Example 1.1-1

a) Physical system - digital computer

$A_i \triangleq$ compiling of a specific program p_i

$A_i = [f_{i1},\ldots f_{in_i}]$

f_{i1} = state of scanning the program p_i

f_{i2} = identification of subroutines

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.
.

f_{in_i} = state of translation to machine language.

b) Biological System - cell metabolism

$A_j \triangleq$ cell mitosis

$A_j = [f_{j2},\ldots f_{in_j}]$

f_{j1} = state of condensation of chromosomes

f_{j2} = concentration of ions in the cell

.
.
.

f_{jn_j} = acidity of chemical medium.

c) Social system - social groups

$A_k \triangleq$ Antagonistic behavior

$A_k = [f_{k1},\ldots,f_{kn_k}]$

f_{k1} = degree of facial contortion

f_{k2} = physical posture

.
.
.

f_{kn_k} = emotional state

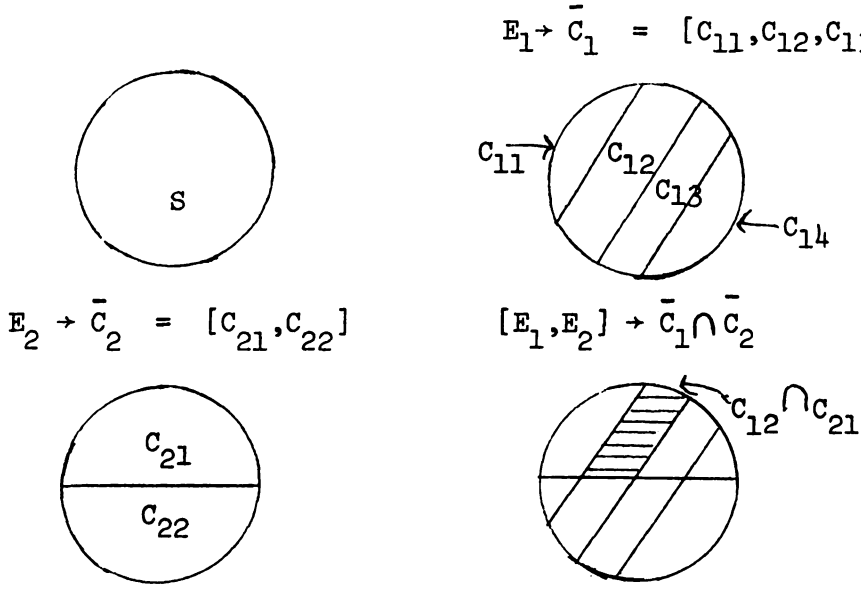
To every A_i, let us associate a specific decomposition of the system S, induced by E_i. The decomposition will be assumed to have the following properties if E_i induces $[C_{i1},\ldots,C_{ik_i}] = \bar{C}_i$, where $\bar{C}_i$ is the set decomposition of S

a) the union of C_{ij}, i = 1,...,n is the total system S

b) the intersection of any two C_{ij} is the null set, i.e.

$C_{ij_1} \cap C_{ij_2} = \emptyset$

Example 1.1-2



E_1, E_2 are the abstract relations inducing the point set equivalence partitioning $\bar{C}_1$ and $\bar{C}_2$ of S. Hence $\bar{C}_1$ can be considered as the realization of E_i.

We recognize the above decomposition as an equivalence partitioning of the system S regarded as a point set. We are assuming there exist nonoverlapping subunits in the system generating the specific activity. By our previous discussion this is a very reasonable assumption. If there exists a decomposition of the system then each subunit should be separable form the rest of the system and be in the same relation to S as the original system was to its environment. At this stage we are presupposing no underlying structure for S, and consider it only as a point set in Euclidean space R^n. The goal is to exhibit a dependent structure derived from the A_i and the induced equivalence partitionings E_i, in order to specify structure from function. The observer-system interaction and subsequent structure identification is at a particular time (or time interval) of the system's existence. Having specified a structure corresponding to $[A_1,\ldots,A_n]$ we shall proceed to extrapolate the structural features to account for activities not in the original experimental class. The A_i can be looked upon as being equivalent to a set of test functions in the modeling of physical systems, except in our case the system activities are measurable and structure is to be specified, whereas in physical systems usually the converse is true.

Since each A_i induces a corresponding E_i the decomposition can be repeated n times and n sets of subunits identified. The subunits of E_i considered as sets can now overlap with subunits of E_j. The superimposed equivalence partitions $[\bar{C}_1, \bar{C}_2,\ldots,\bar{C}_n]$ generate a natural

point set topology for the original system S, ($\bar{C}_i$ is the set representation of E_i) using the basis set of this topology we shall be able to define some characteristic fundamental subunits of S. First we must present some topological notions. [B-9]

Definition 1.1- Topology -- A collection of subsets T of an arbitrary set S, is said to be a topology of S if

a) S and the null set $\emptyset$ belong to T

b) Arbitrary unions in T belong to T $[U_T S_j \in T \mid S_j \in T]$

c) Arbitrary finite intersections belong to T

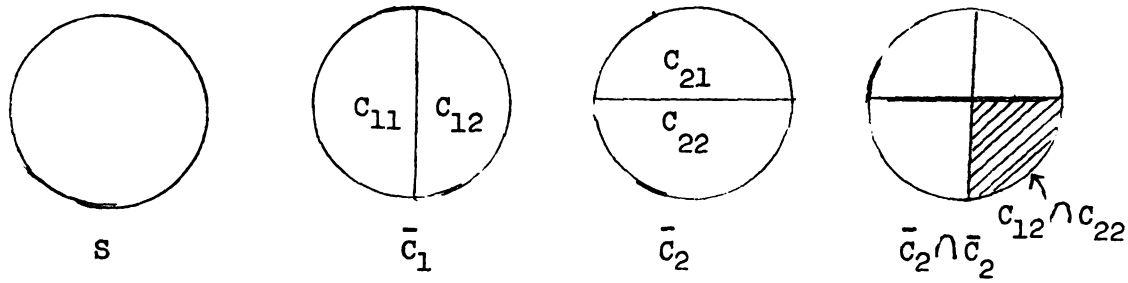
$[\cap_T S_i \in T \mid S_i \in T]$

Definition 1.2 - Basis of a Topology -- A subcollection B of a topology T is a basis for T if every set in T is a union of sets from B.

Hence, the topology T is reconstructible from its associated basis B. (Generally B for a fixed T is not unique.) Let us now demonstrate that $[E_1,\ldots E_n]$ induces a topology on S.

The first equivalence partitioning E_1 subdivides S into a mutually exclusive collection $\bar{C}_1$. Superimposing the next partitioning E_2 on S we obtain $\bar{C}_2$. Let us take the set of all intersections $C_{1k_i} \cap C_{2k_2}$ where k_1, k_2 are indexed over the respective cardinality of the equivalence relations.

Example 1.1-3



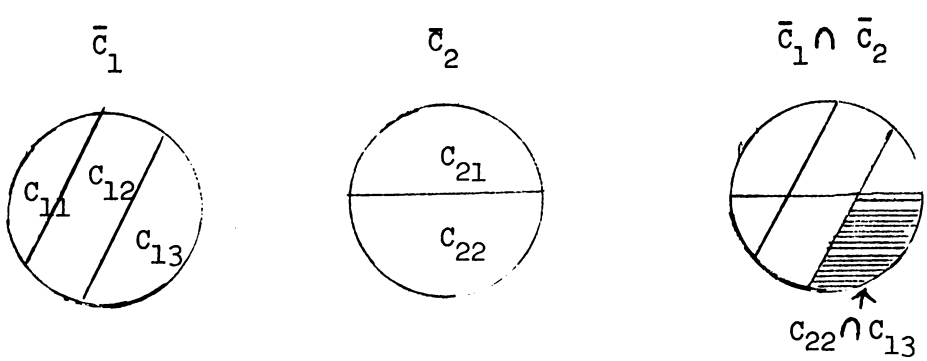
Continuing recursively for each E_j $j = 1,\ldots,n$ we refine at each stage the mesh of the partitioning. At the n-th stage we have the set of all possible intersections $\bigcap^{n} C_{ik_i}$. For every stage of the subdivision we define a topology T in the following manner; let T_j (j-th subdivision) consist of all the subsets of S which are finite unions of particular intersection sets $\bigcap^{p} C_{ik_i}$. $p \leq j$. If $S_T \in T_j$ then $S_T = \bigcup^{N} [\bigcap^{p} C_{ik_i}]$ $p \leq j$. We can give a much more concise definition for T_j by specifying the minimal basis. A basis B is said to be minimal for a topology T generated by B, if B generates T, but no other subcollection of B is a generating set. (Again there may be several minimal bases for a given basis. We are dealing with finite topologies where bases are also finite.) A minimal basis for T_j is the collection $[\bigcap_{i=1}^{j} C_{ik_i}]$. To determine the members of the basis. we must consider only those subsets that lie in all of the equivalence subdivisions $[E_1,\ldots E_j]$. Obviously, since we started with n equivalence classes, the strongest topology we may impose by $[E_1,\ldots,E_n]$ is generated by the minimal subbase $[\bigcap^{n} C_{ik_i}]$. The strongest topology with respect to $[E_1,\ldots E_n]$ represents the depth of the analysis one can perform on S. The classical approach to systems analysis consisted of finding the natural subunits of the system and then establishing the interaction between the subunits.

The first step roughly corresponds to the "tearing" stage; the component identification level whereas the second represents the specification of the dynamics of "reconstruction". Generally once the components are identified, nothing further can be said about their internal structure. The resolving power of the analytical procedure is approximately measured by the relative size of the components compared to the original system. In our frame of reference by interacting with the system simultaneously thru several modes represented by the activities, we can obtain structural information about components in one equivalence class E_j by referring to the maximal topology. Furthermore, using the basis of the maximal topology induced by $[E_1,\ldots,E_n]$, some sets which lie outside any given equivalence subdivision can be analyzed. The superposition of equivalence relations gives rise to possible increase in resolution level in the system.

Example 1.1-4

a) $E_1 \rightarrow \bar{C}_1 = \{C_{11},C_{12},C_{13}\}$

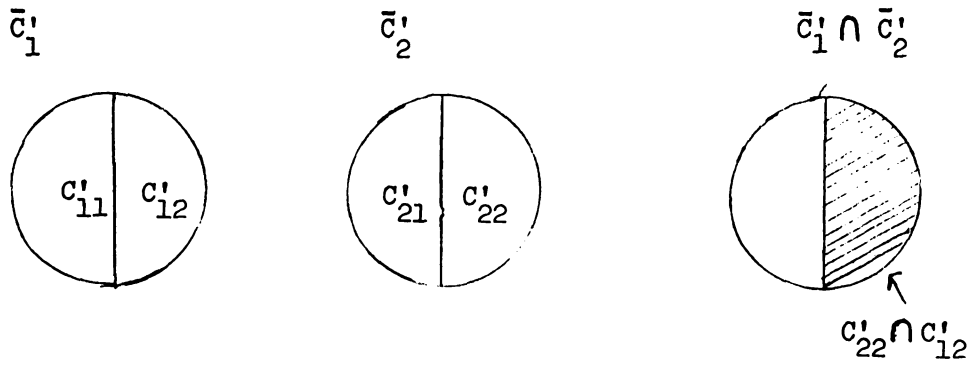
$E_2 \rightarrow \bar{C}_2 = \{C_{21},C_{22}\}$



resolution power increased by superposing $\bar{C}_2$ on $\bar{C}_1$

b) $E'_1 \rightarrow \bar{C}'_1 = \{C'_{11}, C'_{12}\}$

$E'_2 \rightarrow \bar{C}'_2 = \{C'_{21}, C'_{22}\}$



$C'_{11} = C'_{21}$

$C'_{21} = C'_{22}$

resolution power is unaltered by superimposing $\bar{C}'_2$ on $\bar{C}'_1$

An estimate of this increase can be derived by referring to the maximal topology. Let $\bar{K}_i$ by the cardinality of the equivalence partitioning E_i. Then the maximal number of subunits of S that can be isolated by using each E_i in $[E_1,\ldots,E_n]$ separately and successively is $\sum^{n} \bar{K}_i$. The maximal number of subunits analyzable by the simultaneous set $[E_1,\ldots,E_n]$ is the cardinality of the topology T_n. Obviously, since every set of each E_i belongs to T_n, the maximal topology is stronger. Hence, the number of meaningful subunits isolated by T_n is greater. One might wish to establish the upper bound for the number of possible components analyzable by T_n.

Definition 1.3 -- Analyzable sets are elements of the topology T_n.

Theorem 1.1-1 -- Given a set of equivalence classes, $[E_1,\ldots,E_n]$ on S, with cardinalities of partitioning $\{\bar{K}_1,\ldots,\bar{K}_n\}$ the upper bound for the structurally analyzable sets by the strongest

topology $T_n = \{(\bigcap_i^n C^{k_i})\}$ generated by the minimal basis is $\prod_i^n \bar{K}_i$.

Proof -- Let $\bar{K}_i$ be the cardinality of E_1. Assume every set of E_2 intersects every set of E_1. Then the number of intersections is $\bar{K}_1 \cdot \bar{K}_2$. Using the principle of mathematical induction if sets of E_n intersect every set of every E_i, $i \leq n-1$, we have $\prod_1^{n-1} \bar{K}_i \cdot \bar{K}_n = \prod_i^n \bar{K}_i$ as cardinality of maximal analyzable sets.

If $n = 10$ and $\bar{K}_i = 2$ the difference between minimal and maximal analyzable sets is already quite marked.

$$\text{Min} = \sum_i^{10} \bar{K}_i = 20$$

$$\text{Max} = \prod_i^{10} \bar{K}_i = 2^{10} = 1024$$

The observer's interaction with simultaneous activities of the system provides a great deal more information about the decomposition of the system than the individual separate interactions based on one activity at a time. Let us examine a bit closer what is involved here. The ability of the system to engage in simultaneous activities is commensurate with its degree of complexity [M-2,P-1]. The more activities there are the greater need exists for co-ordination, control and organization within the system [B-4,R-16,R-17]. If the observation-measurement interaction is limited to the separate analysis of each existing activity, certain dynamical interactions between the structures generating the activities might be lost. At the outset the investigator has no means at his disposal to functionally differentiate between the activities he selects. The set $[A_1,\ldots,A_n]$ was considered only because each A_i differed from

any other A_j at least in one feature, however, the measurement process provided no test to determine the degree of similarity between activities. Therefore, it is quite conceivable that there exists a (many to one) mapping between the component subdivisions and the system function as displayed by the activities. Experimentally, in view of Theorem 1.H1, this implies the need to choose the A_i so that the class $[E_1,\ldots,E_n]$ induces a topology with maximal analytical power. To pairwise distinguish n different activities we have to perform a minimum of $\binom{n}{2}$ experiments. Assuming every experiment differentiates between a given pair of activities on the first attempt, we can generate under the conditions of the theorem the ideal case. The measurement interaction with the system represents the effort invested in attempting to determine the system substructures corresponding to $[A_1,\ldots,A_n]$. The cardinality of the topology T_n represents the structural information gained thru the measurement. To derive an upper bound for the number of measurements in separating n activitie we proceed as follows.

Let A_i consist of $[f_{i1},\ldots,f_{in_i}]$ measurably distinguishable features. Let us select any pair of (A_i,A_j) and consider the respective feature sets $[f_{i1},\ldots,f_{ip_i}]$, $[f_{j1},\ldots,f_{jp_j}]$ if every feature in the first set differs from every feature in the second set then a single experiment (first attempt) will differentiate A_i from A_j. (This case corresponds to the minimal experimental effort.) At the other extreme one set is properly included in the other. Assume $A_i \subset A_j$, let $p = n_j - n_i$ then the probability of distinguishing between the two sets on the first

attempts $\frac{n_j - n_i}{n_j} = \frac{p}{n_j}$. (If a feature f_{ik} in A_i is tested the effort is unsuccessful.) In general, a maximum of $p_i + 1$ tests must be performed to distinguish each pair (A_i, A_j) (when both feature sets are finite). Let M be the maximum number of elements in a feature set for any $A_i \in [A_1, \ldots, A_n]$. Then the maximal number of experiments to pairwise distinguish two activities is $\binom{n}{2} M$. (Here every activity differs from another in only one respect and all similar features are tested before the identifying one is selected.) Based on the above arguments we can state:

Theorem 1.1-2 -- Given the observed activity set $[A_1, \ldots, A_n]$ for a system S, if the largest feature set has M elements, then the number of separate measurements to pairwise distinguish the activities lies between $\binom{n}{2}$ and $M\binom{n}{2}$.

The implication and meaning of this theorem can be appreciated when we examine system decomposition complexity. We make the assumption that the complexity of the activity (measured by the number of elements in its feature set) is in direct relation with the decomposition complexity of the system substructure generating the activity. This assumption implies the number of sets in E_i induced by A_i is proportional to the number of measurable features of A_i. (If we can percieve A_i to be complex then also the underlying structure should be complex.) Now Theorem 1.1-2 says something about the effort of identification, whereas Theorem 1.1-1 gives bounds for structural analytical power based on the topology T_n. If the assumption about proportional complexity is correct then we see

the upper bound for the measurement effort is much smaller than the potential information gained about the system structure. In fact, letting Max $\bar{K}_i = M$, maximum effort becomes $M\binom{n}{2}$ and maximum structural information yield is M^n. Of course, we have not included several factors which may nullify the above estimate. In particular if the activities of the system are at different hierarchical levels or that the complexity of the substructure underlying an activity arises from interaction with other substructures we cannot use the previous result. A large number of components with simple connectivity may yield the same dynamical complexity as a small number with complex interconnections. Therefore, one may not be able to decide initially whether one is confronted with an activity based on simple substructure strongly converted in the system or complex substructure weakly connected. A great deal depends on how we interact with the system and select the activity set $[A_1,\ldots,A_n]$,[R-16].

In the next section we shall define a hierarchical system based on the topology T_n and further explore the problems of system structuring.

1.2 Structure of Hierarchical Systems

We have discussed how the activity set for a total system S may lead to a component decomposition of S, considered as a set, and exhibited a topology with a finite basis that generates the sets in the equivalence classes induced by the activity set $[A_1,\ldots,A_n]$. In particular, we can answer the question about potentially analyzable sets in S as a consequence of our original interaction with the system in the role of the observer.

Definiton 1.2-1 -- An arbitrary subset Q of S is a potentially meaningful component of S if Q is a set in the topology T_n induced by $[E_1,\ldots,E_n]$ (Q is an analyzable set). Thus, automatically we limit our attention to a well-defined subcollection of S as candidates for further analysis.

Of course, it is not implied that every Q will be a stable and useful component of S. There may be structural and functional limits imposed on the realizability of particular Q as a real component. A physical upper limit may exist for the number of components a given member of the basis of T_n can belong.

Example 1.2-1

a) Social Systems -- If the basis consists of individuals and the components are social organizations then an upper limit exists for membership of any individual in various organizations.

b) Physical Systems -- In a discrete physical system the number of terminals for free-body forms (basis) limits the possible system connectivity.

Since every Q is the union of sets from the basis T_n, the basis becomes a natural fundamental collection in the reconstruction of the original system.

Definition 1.2-2 -- Given a topology T_n induced by $[E_1,\ldots,E_n]$, the generating (finite) basis of T_n is called the fundamental morpheme set of S.

The analogy is borrowed from linguistics where the morpheme is considered as a fundamental unit of meaning. In our model the morphemes

represent the smallest structural units in the system out of which we reconstruct potentially useful components. Once the morpheme set has been specified both the topology T_n and the analyzable components are fixed. Furthermore, the morphemes represent the lower limit of structural resolution of the system.

To specify the structure of the morpheme the original activity class $[A_1,\ldots,A_n]$ is insufficient. The only way to model morphemes (and this is important in the reconstruction of the system) is to abstract it from the system and model it as a free-body. System scientists will recognize the morpheme to be analogous to an object [A-1,Z-2]. We can now proceed to describe the non-trivial problem of modeling the morphemes in the free-body form, defining the stimulus-response orientation and reconstructing the system thru the constraint equations. This is one of the central problems of systems science and although far from complete it is well developed for certain physical systems that may be considered linear [K-5,L-8,Z-2]. The treatment of this aspect of the problem will be somewhat cursory since the methodology is well documented elsewhere [J-1,K-5, Z-1]. There is one very basic difference between the standard approach and ours. It is worthwhile pointing it out at this stage to avoid future misunderstanding. In classical analysis of systems the structural decomposition into morphemes is first accomplished, then the morpheme is modeled as a free-body and the system is subsequently reassembled by means of the system graph. The so-called emergent behavioral features of the system are attributed to the interaction of the morphemes. The methodology is rather straightforward once the morphemes (objects) have been isolated.

In discrete physical systems the identification of the components is relatively easy. There exist discernible physical boundaries to aid in the decomposition. Unfortuntely, this is no longer the case with some biological systems. In addition, the terminals (points of interaction) of components are well defined for discrete physical systems but not readily identifiable in biosystems. Nevertheless, under certain idealized modeling assumptions the biological components may be treated as lumped parameter systems with well-defined discrete terminals. (The problem becomes one of deciding whether the distributed parameter system may be treated as the union of locally lumped systems [C-6,K-5].) One possible approach is to subdivide the system into topologically and dynamically homogeneous regions and to treat each region as a lumped subsystem. The total system is reconstructed with the methods of boundary values by imposing continuity conditions between the homogeneous regions.) Let us outline the basic difference between the two models.

The classical or standard decomposition techniques provide no definite guidelines for the isolation of the fundamental objects. The original formulation of the theories related to systems modeling is motivated by those physical systems where component boundaries are rather obvious. It is subsumed that the objects can be located and abstracted into a free-body form. The free-body modeling stage consists of completely decoupling an object from the ssytem structure and observing a set of input-output data to obtain the stimulus-response relation for each object. At the next stage, invoking the compatibility conditions and the system graph, along with the inherited constraint equations, the total model is reassembled.

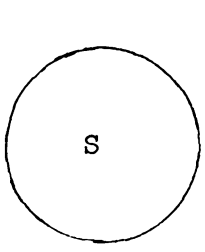
The behavior of the system then can be based on the free-body models of the objects and the blueprint for the assembly is specified by the graph topology. The problem is to decide whether an arbitrary interconnection of components will yield an acceptable system behavior, with respect to the original activity set $[A_1,\ldots,A_n]$. Generally, any compatible and consistent interconnection is acceptable for physical systems. In the present framework this may not be true, because a possible interconnection pattern need not be realizable. Adaptive systems possess a certain selective ability with respect to their component structure, an aspect that is partially incorporated into the adaptive behavior [G-1,A-3,P-1]. This is the main reason why we started out with a real observable activity set $[A_1,\ldots,A_n]$. Relying on the activity set we identify the components of the system with respect to each activity. At the morpheme level we are confronted with the problem of free-body modeling analogous to the standard case. However the methodology of approximation of the morpheme as a discrete multi-terminal component is no longer arbitrary, since we can measure the effectiveness of our methodology by comparing the emergent activity class of the total system, now dependent on our modeling of the free-body morphemes, with the actual observed set $[A_1,\ldots,A_n]$. Consequently, among all the possible modeling alternatives, orientation choices for the morphemes and feasible graph topologies we select the one that provides the best fit for the original activity set $[A_1,\ldots A_n]$. We proceed to outline the methodology for the construction of the model based on the activity set $[A_1,\ldots A_n]$.

Let E_i be the equivalence relation induced by A_i. We define the k-th superposition level as the partitioning of the system S due to the intersection of the k-equivalence classes $[E_1,\ldots,E_k]$.

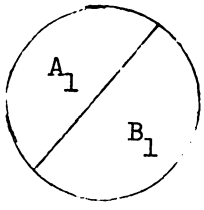
$$L_k(A_1,\ldots,A_k) = \bigcap_{i=1}^{k} E_i = M_k$$

Here M_k is the k-morpheme set (basis for the topology T_k). Among all the possible sets generated by M_k we consider first only those corresponding to complete equivalence classes of any $[E_1,\ldots,E_k]$ considered separately.

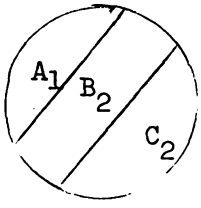
Example 1.2-2



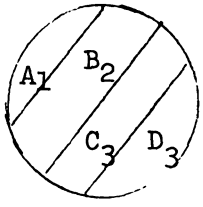
E_1



$E_1 \cap E_2$



$E_1 \cap E_2 \cap E_3$



$k = 3$

Let the vertical lines represent the equivalence partitioning boundaries.

1) Then $[A_1, B_1, A_1 \cap B_2, C_2, A_1 \cap B_2 \cap C_3, D_3]$ constitute the complete equivalence classes for E_1, E_2, E_3.

2) B_2 is an analyzable set, but not a complete equivalence class.

3) $[A_1,B_1] = M_1$

$[A_1,B_2,C_2] = M_2$

$[A_1,B_2,C_3,D_3] = M_3$

The set of complete equivalence classes of the E_i will be called the set of natural components $\bar{C}_i$. These natural components have certain properties of stability in the system; any A_i is an emergent property of the interaction of its $\bar{C}_i$-component structure, and, if the activity A_i persists in time so should the corresponding $\bar{C}_i$.

Example 1.2-3

a) Cell cycle metabolism

A_1 = manufacturing of proteins for growth

A_2 = mitosis and cell division

A_1 may be considered as a continuous activity in the cell cycle, and the supporting structure should also persist in time.

A_2 is a recurrent, discontinuous activity with structure responsible for it also periodic.

b) Individual organism in a species

A_1 = temperature homeostasis

A_2 = antagonistic behavior

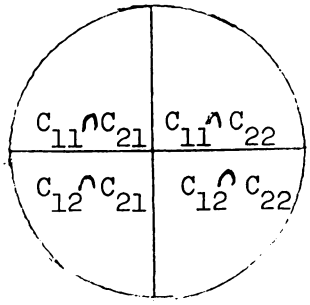
A_1 is a continuous process whereas A_2 is recurrent and discontinuous. Again underlying structure persists as long as corresponding activity does.

Although as we have seen the morphemes constitute the basic structural invariants of the system, the intermediate forms represented by the

$\bar{C}_i$-subassemblies are also important. In fact, we can relate the potential component complexity to the distribution of stable subassemblies which include the $\bar{C}_i$. Obviously, the maximal number depends on the total number of sets in the topology; the set of all analyzable sets. From an evolutionary point of view systems possessing the greatest number of stable subassemblies can exhibit the widest range of emergent behavior[S-6]. An even more important property related to the morpheme topology of the system is the density of stable subassemblies. (The analogous problem with respect to dynamics of systems has been investigated by Peixoto, Smale and others, [P-4,S-7].)

Definition 1.2-2 -- An analyzable set Q is an immediate neighbor of a set Q' for a given topology T_n if Q' differs from Q in only one morpheme.

Example 1.2-4



T_2 generated by M_2 basis.

$$M_2 = [\cup(\overset{2}{\underset{i}{\cap}} C_{ik_i})]$$

$$\bar{C}_1 = [C_{11}, C_{12}]$$

$$\bar{C}_2 = [C_{21}, C_{22}]$$

Let $Q = C_{11} \cap C_{22}$

$Q_1' = C_{11}$

$Q_2' = C_{22}$

$Q_3' = (C_{11} \cap C_{22}) \cup (C_{12} \cap C_{21})$

The set of all neighbors of Q, is the morpheme neighborhood N_Q

of Q. When a particular analyzable set becomes unstable (the activity generating Q ceases) the Q structure may be perturbed by an addition or deletion of a morpheme. If there exists a stable form in the neighborhood N_Q then the analyzable set Q may be transformed to this stable neighbor. (In some systems the structural transition to immediate neighbors may be accomplished by suppression of morpheme dynamics.)

The set of natural components $\bar{C}_i$ are reconstructible from the morphemes, by regular component analysis techniques of systems science.

The levels of superposition are recursively characterized as,

$$L_1(A_1) = E_1 = M_1$$

$$L_2(A_1,A_2) = E_1 \cap E_2 = M_2$$

$$\vdots$$

$$L_n(A_1,A_2,\ldots,A_n) = E_1 \cap E_2,\ldots,\cap E_n = M_n$$

The topologies T_j and respective bases M_j are progressively stronger

$$T_1 \subset T_2,\ldots,\subset T_n$$

Each M_j is a minimal basis for the topology T_j.

Definition 1.2-3 -- The L_j is the structural resolution level for the system and T_j is the resolving power.

The index j of the topology T_j indicates the number of activities required to achieve a resolving power T_j. Given two distinct sets of observed activities $[A_1,\ldots,A_n]$ and $[A_1',\ldots,A_n',]$ we are in a position to compare their decomposition properties.

Definition 1.2-4 -- Two distinct decompositions $[A_1,\ldots,A_n]$ and $[A_1',\ldots,A_n',]$ are analogous if:

a) $n = n'$

b) $\exists$ a homeomorphism $M_j \xrightarrow{h} M_j'$ for each j.

The above definition implies that analogous decompositions have equal maximal resolution level ($n=n'$) and equal resolving power ($M_j \xrightarrow{h} M_j'$). (For the definition of homeomorphism see S. T. Hu, General Topology [H-3].)

A further comparison can be made for different decompositions with respect to the distribution of stable subassemblies, in the collection of analyzable sets. We are dealing with discrete, finite topologies, hence cardinality of the sets in a particular topology is finite and the number of analyzable sets for different decompositions is also finite. A basis of comparison may be the size of the neighborhood N_{D_s} of the set of all stable forms D_s. The most advantageous case is a distribution of stable forms D_s such that N_{D_s} includes all the analyzable sets. We have previously mentioned the relationship between self-organization and decomposition. One of the basic differences between biological and physical systems is the former's capacity to alter its structure and behavior under environmental perturbations [A-3,R-10]. The structural transitions are not arbitrary, certain fundamental units are left invariant depending on the magnitude and complexity of the transition. In the developmental process of organisms the cells may be considered structural invariants. Morphemes become natural candidates of structural invariance in our model.

Definition 1.2-5 -- The states of the self-organization space of an arbitrary system are the stable subassemblies (analyzable sets) generated by the strongest topology induced by $[A_1,\ldots,A_n]$.

Obviously, each $\bar{C}_i$ for every E_i is included in addition to any other subassembly constructed from the morphemes. The magnitude of frequency of the environmental fluctuations may not be strong enough to induce a transition in the self-organization space. The system may react by only partially altering the set of activities $[A_1,\ldots,A_n]$.

Let the equivalence classes E_i be fixed. The specific activity A_i we have observed is generated by a definite interconnection pattern between the equivalence classes of E_i; to alter an activity the graph topology between natural components is varied. Let $\tau_{ij}(\bar{C}_i)$ denote the set of all consistent system graph topologies for a fixed $\bar{C}_i$-equivalence class set of E_i.

Definition 1.2-6 -- The states of the adaptive space for a fixed $\bar{C}_i$-equivalence class are the graph topologies $\tau_{ij}(\bar{C}_i)$. An adaptive space can be defined for each set $\bar{C}_j$ induced by E_j. Consequently, each activity A_i can be altered by a transition in the underlying adaptive space.

The same arguments apply to the distribution of stable states as in the self-organization case. In particular, a distribution of stable graph topologies $\tau'_{ij}(\bar{C}_i)$ allows a greater degree of adaptive freedom to transfer from an unstable form to a stable one. Notice the main difference between self-organization and adaptation is the invariant substructures. In the case of self-organization the morphemes are the fundamental building blocks whereas the natural components $\bar{C}_i$ serve the same purpose for adaptation.

In view of the fact that every activity A_i has its adaptive space, the total adaptive space for the system may be considered as an n-dimensional space (one dimension for each activity). If the class $[E_1,\ldots,E_n]$ is given $[\bar{C}_1,\ldots,\bar{C}_n]$ is defined and the states of the system adaptive space are computable. (Any inconsistent graph topology is rejected.) The interactions between the $\bar{C}_i$ sets for a fixed i may be relatively stable in time as evidenced by the persistence in time of specific activities. To account for the routine minor reactions of the system to small and expected perturbations the concept of system dynamics is required. To deal effectively with systems dynamics we must introduce some ideas of graph theory and re-examine the modeling of morphemes as multi-terminal discrete components. (A good first reference for what follows is D. Johnson and J. Johnson, Graph Theory [J-1].)

We assume the collection of morphemes have been isolated from the system into a free-body form. The free-body concept permits the observer to conduct a set of independent experiments on the morpheme now regarded as a black box. The experiments consist of a sampling of the actual environment the morpheme may be subjected to in the system. Under the environment label we include the original system environment as well as the morpheme set of the system itself. Hence, it is permissible to think of the morpheme as a system except that we have no direct means to deduce its structure. Instead the morpheme is subjected to the above prescribed experiments and the state-space model derived from the observed reaction to the experiments. The morpheme will exhibit a set of characteristic activities (observable and measurable) $[a_1,\ldots,a_k]$ analogous

to the total system activity set. The a_i are not unique or even well defined, they depend to some extent on the investigator's preferences. The total system activity set $[A_1,\ldots,A_n]$ serves as a guideline for the selection of meaningful activity set for the morpheme. The activity set for the morpheme is recorded over time series domain $T = [t_0,t_1,\ldots,t_n]$ and the k-tuple $[a_1,\ldots,a_k]$ (t_i) $0 \leq i \leq n$ is noted. The behavior of the morpheme is defined to be the time sequence of the activity set $[a_1,\ldots,a_k]$ over the domain T. A further assumption is imposed about cause and effect among the activities and the behavioral equation is constructed. Essentially the behavioral equation consists of labeling a certain subset of $[a_1,\ldots,a_k]$ as stimuli, its complement as response and associating the two subsets by an algebraic relation. Let $[a_i,\ldots,a_k]$ be partitioned as $[s_1,\ldots,s_j; r_1,\ldots,r_i) = [\bar{s},\bar{r}]$, $i + j = k$, and let $B[s_1,\ldots,s_j](t) = [r_1,\ldots,r_i](t)$. The relation B expresses the stimulus-response orientation of the morpheme.

Unfortunately B is not always a function and may be a one-to-many mapping.

The concept of state is introduced to reduce the behavioral relation to a function. The state-space description has two basic parts:

1) State-variable $\bar{X}$ varying over a state space ψ.

2) Stimulus-response-state relation $\bar{B}(\bar{x},\bar{s},\bar{r},t)$.

The state-space model satisfies the three conditions [Z-1,Z-2].

Condition 1 -- The oriented activity set $[s_1,\ldots,s_j,r_1,\ldots,r_j]$ belong to the range of the time-series, $\exists$ a state $\bar{X} \in \psi$ such that

($\bar{B}$ agrees with B; $\bar{B}$ includes B).

Condition 2 -- The relation $\bar{B}$ is a function when restricted to domain $\bar{s}$ and range $\bar{r}$. (For any state X_o $\exists$ at most one response for any $\bar{s}$.)

Applying condition 2 we can express the response as a function of the stimuli $\bar{r}(t) = R(\bar{X},\bar{s},t)$. In addition, we need a condition to express the result of two successive stimuli.

Condition 3 -- Given $R(\bar{X}_1(t_1),\bar{s}(t_1) \cdot \bar{s}(t_2)) = \bar{r}(t_2)$ then $\exists$ a state $\bar{X}_2(t_2)$ such that $R(\bar{X}_2(t_2),\bar{s}(t_2)) = \bar{r}(t_2)$

Thus the response function can be updated. The above assures that the result of a sequence of stimuli can be replaced by a state. In other words, if both state and stimulus are known at a specific time, the next state is uniquely determined. Hence, the state variable is the intermediate quantity required to transform the behavioral relation into a state-response function. In particular, if the state at some time t is given, then the next state can be determined. In terms of a differential relation.

$$\frac{d\bar{X}}{dt} = s(\bar{X}(t), \bar{s}(t),t)$$

Consequently, we have the pair of equations

$$\frac{d\bar{X}}{dt} = s(\bar{X}(t), \bar{s}(t), t) \quad \forall t$$

$$\bar{r}(t) = R(\bar{X}(t), \bar{s}(t), t)$$

called the state and response equations respectively.

The first equation continually updates the state of the system, whereas the second expresses the response in terms of state and stimuli.

The state equation represents the total memory of the system required to uniquely determine the response and next state.

It should be observed in retrospect that the behavioral relation and subsequent state-response equations depended on the recorded time series of the activity set for the morpheme. Hence, a different time series or subdivision of the activity set into stimulus-response orientation will yield different state-response equations. The one selected depends finally on the agreement between the reconstructed activity set $[A_1', \ldots, A_n']$ for the total system and the original observed set $[A_1, \ldots, A_n]$ on which the decomposition into constituent morphemes was based.

Once the free-body model of each morpheme is constructed we can proceed to reconstruct the analyzable sets. We examine the restrictions imposed on the behavior of each morpheme in light of the fact they interact to form an analyzable set. (At this stage we may properly call both morphemes and analyzable sets as components since we have imposed a structure thru the state-response equations.)

We assume morphemes are constrained to interact at actual discrete physical terminals. Every interaction is a potential constraint on the behavioral relation. The constraints imposed on the free-body models of the morphemes (the interconnection graph topology) generate the total behavior of an analyzable component. The graph topology for the analyzable component in an adaptive space transition is considered to be fixed but may change in a self-organization situation. At the next level of assembly the interaction of analyzable components is considered again with a set of higher level constraint equations to yield to total

system state-space and response equations. The characterization of analyzable components from morphemes is accomplished as follows.

Given

$$\frac{d}{dt}\bar{x}_i(t) = S_i(\bar{x}_i,\bar{s}_i,t)$$
$$\bar{r}_i = R_i(\bar{x}_i,\bar{s}_i,t)$$

for each morpheme, by the use the interaction constraints and compatibility conditions [Z-3] we may coalesce the free-body forms into

$$\frac{d\bar{X}}{dt} = S(\bar{X},\bar{s},t)$$
$$\bar{r} = R(\bar{X},\bar{s},t)$$

where $\bar{s} = C\bar{r}$ expressed the constraint relations; C is a full rank matrix. Substituting $C\bar{r}$ for $\bar{s}$ in the equations we have

$$\frac{d\bar{X}}{dt} = S(\bar{X},C\bar{r},t)$$
$$\bar{r} = R(\bar{X},C\bar{r},t)$$

if possible the response equation is solved in terms of $\bar{r}$. The technique eliminates the intermediate variables (response and stimuli of the free-body morphemes that are constrained in the system) and only the connected subsystem (analyzable components) remain. The same procedure of grouping components of large-scale system techniques applied to analyzable components yields the system state-space model [K-5].

Example 1.2-2

a) Cytology -- if the collection of organelles in the cell are the morphemes they can be further aggregated into more complex substructures such as the mitochondria, cytoplasm, nucleus (analyzable sets).

b) Physical system (computer) -- The morphemes vary the constituent manufactured components (resistors, capacitors, inductors, switches, etc.). The analyzable sets are aggregates of these morphemes; compiler, sorter, memory bank, printer, etc.

c) Social System -- If morphemes are individuals then analyzable sets may be various social groups which in turn interact to form higher level aggregates. A $\bar{C}_i$-equivalence class may be the family unit.

In all these examples the forces binding the morphemes in an analyzable set are stronger than the interaction between the analyzable sets at the next level.

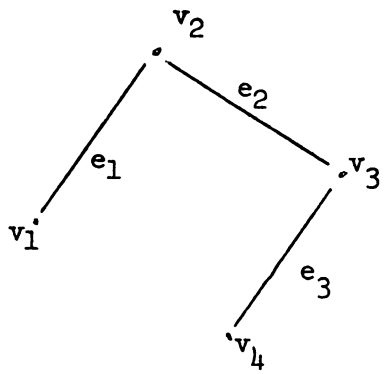
When the number of morphemes is large, the theoretical procedure described to reconstruct the system from the free-body graph can become cumbersome. The constraint equations for such large-scale problems are resolved by means of the system graph which we now describe. First a few preliminary concepts from graph theory.

Definition 1.2-7 -- A graph $G(V,E)$ is a set of objects V called vertices (nodes) with a set of edges E. Each element of E is defined by a pair of vertices (v_j,v_k).

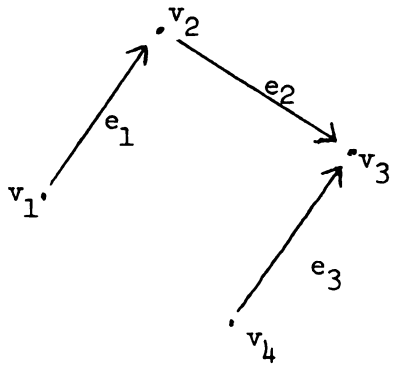
The set of E may be visualized as a collection of lines connecting a set of points (vertices). In the abstract formulation E becomes a binary relation on the set V. Two elements of V, v_1 and v_2 are in relation to E, $v_1 \; E \; v_2$ if v_1 is connected to v_2. When we distinguish between the pair (v_i,v_j) and (v_j,v_i) we assign direction to the edges and

end up with a directed graph (digraph) with the edges denoted by the ordered pair $[v_i,v_j]$.

Example 1.2-3



G_1



G_2

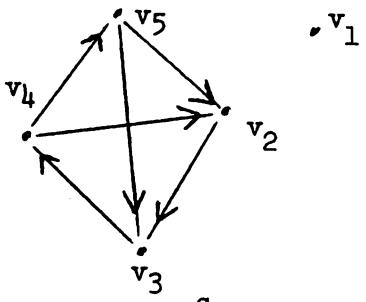
G_1 is undirected and G_2 is directed.

An edge $e_{ij} \overset{\Delta}{=} (v_i,v_j)$ is incident on both v_i and v_j. If $v_i = v_j$ the edge e_{ij} forms a self-loop. A vertex v_k with no incident edges is isolated. The degree of a vertex $d(v)$ is the number of edges incident on v. For digraphs we distinguish two separate degrees; the negative degree of incidence $d^-(v)$ the number of edges directed to v and the positive degree of incidence $d^+(v)$ the number of edges from v.

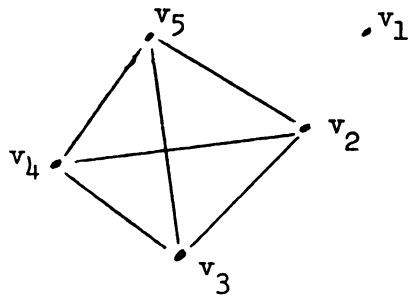
$$d(v) = d^+(v) + d^-(v)$$

Definition 1.2-8 -- Two graphs G and G' are isomorphic if one-to-one correspondence between their edges with all incidences preserved.

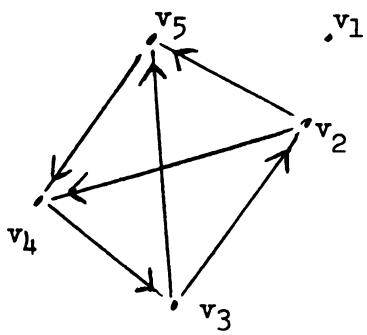
Example 1.2-4



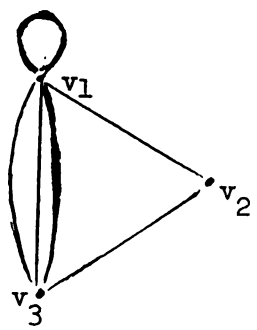
G_1



G_2



G_3



G_4

a) for G_1 $d^+(v_3) = 1$ $d^-(v_3) = 2$ $d(v_3) = 3$

$d^+(v_4) = 2$ $d^-(v_4) = 1$ $d(v_3) = 3$

$d^+(v_1) = d^-(v_1) = 0$

v_1 is isolated.

b) for G_2 $d(v_2) = d(v_3) = d(v_4) = d(v_5) = 3$

c) for G_4 $d(v_1) = 5$ (self-loop counted twice)

d) G_1 is isomorphic to G_3

e) G_1 not isomorphic to G_2 since G_1 is directed and G_2 is not.

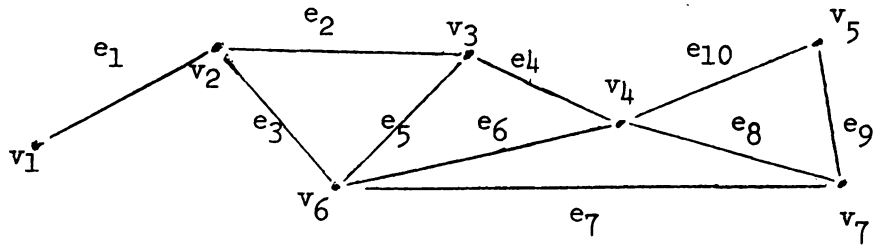
A graph $G_s = (V_s, E_s)$ is a subgraph of $G = (V,E)$ if $V_s \subset V$ and $E_s \subset E$. (If an edge is included so must all its incident vertices.) When $V_s \neq V$ or $E_s \neq E$ then G_s is said to be a proper subgraph. A path is a finite sequence of edges $(e_1, \ldots e_n)$ where $e_i = (v_{i-1}, v_i)$ and the terminal vertex of e_i is the initial vertex of e_{i+1}. A path is simple if all edges are distinct, when $v_o = v_n$ the path is closed. A circuit is a simple closed path.

An undirected graph is connected if there is a path between any two vertices. A digraph is connected if the underlying undirected graph is connected.

Definition 1.2-4 -- A graph G_T which is connected and contains no circuits is a tree. In particular if a tree G_T is a subgraph of G then G_T is a tree of G. If G_T contains all vertices of G it is a spanning tree. Any edge in a tree is called a branch. The complement G_T' of G_T is a cotree with edges known as chords.

Example 1.2-5

G



a) $G_s(V_s,E_s)$

where $V_s = [v_1,v_2,v_3,v_6]$

$E_s = [e_1,e_3,e_5]$ is a subgraph

b) $[e_1,e_2,e_5,e_3,e_2,e_9,e_{10}]$ is a path

c) $[e_1,e_2,e_4,e_{10}]$ is a simple path

$[e_2,e_5,e_3,e_2,e_9,e_6,e_3]$ is a closed path

$[e_2,e_4,e_6,e_3]$ is a circuit

d) $[e_1,e_2,e_4,e_{10},e_9]$ is a tree

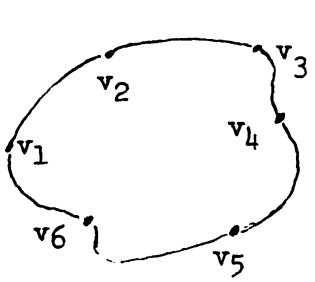
$[e_1,e_2,e_5,e_6,e_8,e_9]$ is a spanning tree

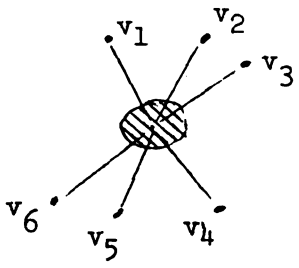
For a connected graph G with v vertices, G_T consists of v-1 edges. A graph G is simple if it has no self-loops and no two edges are incident to the same pair of vertices. For modeling of multi-terminal discrete components simple graphs are not sufficient, after reassembling the free-body models a system graph with multiple edges between vertices may occur. An example is the parallel connection of two terminal components. However, if we agree to reduce a parllel connections to an equivalent single connection we reduce the nonsimple digraph to a simple graph. The reduction consists of modeling the collection of components in parallel, responsible for the multiple edges between two vertices, as a single component. In the process we lose some information on the individual dynamics of some morphemes, but our aim in description of adaptive behavior is the topology of the natural components. The reason we seek a simple graph is to deal more efficiently with the notion of relative complexity, which will be based on the cyclomatic number of a graph. For an arbitrary digraph the cyclomatic number may be infinite and furthermore, the

complexity of the graph may be due to a large number of edges between two vertices only. Hence, the complexity is not distributed throughout the whole graph. In the next chapter we will need only the concept of a simple graph when we introduce the inverse of a graph. (The inverse graph will establish the bridge between input-output block diagrams of relational biology and the terminal graph representation of systems science.) The fundamental postulate of systems science permits us to replace a parallel multi-connection with an equivalent single one. The complementary variables (x_i,y_i), $i = 1,\ldots,n$ for the parallel case are reduced to (x,y) of a single connection. (Of course we lose the instantaneous dynamics of each (x_i,y_i), but the net effect is still reflected in (x,y).) Unless otherwise specified we shall deal only with simple graphs. Where a nonsimple graph is introduced by a construction, the graph is reduced to the simple dynamical equivalent.

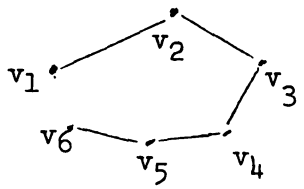
In the original decomposition of the system into morphemes we had to model the morphemes as free-bodies to derive a structure for them. Although no information existed about their internal structure, the structural points of contact (terminal) with other adjacent morphemes could be determined by using the system under investigation is constrained by its system graph. Knowing the terminals we can model the behavior of each morpheme.

Fundamental Postulate of Systems Science -- The behavioral characteristics of an n-terminal component in an identified system structure are completely specified by a set of (n-1) equations in (n-1) pairs of complementary variables $[x_i,y_i]$ identified by an arbitrary terminal graph [K-5].





A six-terminal morpheme with one possible terminal graph.



A terminal graph is a spanning tree for the complete set of terminals (vertices) of the morpheme.

Applying the compatibility conditions the graph of the system is coalesced from the model of the morphemes. By defining an appropriate maximal tree (with respect to the dynamical properties of the morphemes) the constraint equations are derived from two sets of conditions. One is based on the circuits of the system graph defined by the cotree and the other on cut-sets defined for the spanning tree.

The dynamics (behavior) of the total system can now be put into a state-space, response equation format.

$$\frac{d\bar{X}}{dt} = S(\bar{X},\bar{s},t)$$

$$\bar{r}(t) = R(\bar{X},\bar{s},t)$$

and a set of algebraic relations between non-dynamic variables.

Based on the state-space, response equations we can re-examine the emergent activity set $[A_1',\ldots,A_n',]$ as a direct consequence of the dynamics. A qualitative comparison can be made between the model constructed to explain the activity set $[A_1,\ldots,A_n]$ and the actual set obtained represented by $[A_1',A_2',\ldots,A_n']$. Of course, as a first criterion of goodness of fit we expect $n' = n$, implying that if we started with n-

distinguishable activities we should obtain as many. Furthermore, if $n' = n$ then the activity set $[A'_1,\ldots,A'_n]$ can be compared to the set $[A_1,\ldots A_n]$. At the start of the observer-system interaction stage the investigator determined n-different activities in the system by distinguishing certain measurable behavioral features. At the completion of the modeling stage ideally the same differences in the behavioral features should be obtained. Hence, if we map f_p: $[A'_1,\ldots,A'_n] \rightarrow [A_1,\ldots,A_n]$ where f_p is a permutation of $[A'_1,\ldots,A'_n]$ each $f_p(A'_i) \in [A_1,\ldots,A_n]$ can be compared feature by feature to $A'_i \in [A'_1,\ldots,A'_n]$. Initially interacting with the system at a functional level (activity set) we construct an underlying structure generating this function, by means of the morpheme based $\bar{C}_i$-equivalence classes.

Definition 1.2-10 -- A system will be considered functionally hierarchical if it engages in n-distinguishable separate activities. $n \geq 2$.

The observed functional hierarchy leads to a natural structural hierarchy induced by the decomposition into morphemes. The degree n of functional hierarchy is the index of the set $[A_1,\ldots,A_n]$. The corresponding induced structural analysis hierarchy is the level n determined by the morpheme set M_n.

Hence, the degree of difficulty in the modeling is dependent on the power of the resolution required to analyze the components of the system.

We have discussed which subassemblies of the system may be considered as structural invariants depending on whether the change in the system

is adaptive or a self-organization. Both of these involve some perturbation of either structure or system graph topology. Routine maintenance in the system, regulation for example, does not usually require a modification of structure or activities.

Example 1.2-6

Cytology -- active transport across the cell membrane during the cell life cycle may be considered as routine maintenance with no fundamental activity or structural alterations.

The initiation of mitosis produces marked changes in types and levels of activity and corresponding structure changes within the cell.

For the above reason we introduced one further degree of adaptive freedom based on the system dynamics. Given the system topology for the natural components ($\bar{C}_i$-equivalence classes) superimposed is the dynamics derived from the state-space equations. A first reaction of the system to a minor environmental perturbation may be accomplished by modifying the system dynamic parameters. Each parameter varies between specified bounds depending on the physical properties of the corresponding component.

To summarize the results;

1) Given experimental observer-system interaction and measurably distinguishable activity set, based on the feature sets of each A_i, $[A_1,\ldots,A_n] \xrightarrow{\text{induces}} [E_1,\ldots,E_n]$. Superposition hierarchies of analysis are established; $L_1,\ldots,L_n$. Each $\bar{C}_i$ is the set of equivalence classes corresponding to E_i. The $\bar{C}_i$ are the natural components generating the A_i.

2) For self-organization the M_n generated analyzable sets are invariant. For adaptive behavior the $\bar{C}_i$-sets are invariant and connective graph topology changed. For routine regulation problems only the dynamical parameters are modified.

3) The system structure is based on the fundamental invariants M_n (morpheme set). The adaptive structure with respect to M_n and the activity set $[A_1,\ldots,A_n]$ is an ordered 3-tuple $[\bar{C}_i, \tau_{ij}(\bar{C}_i), D_{ijk}(\bar{C}_i,\tau_i)]$ for each $i=1,\ldots,n$ where the $\bar{C}_i$ are functionally determined by E_i and structurally from M_n and the system graph.

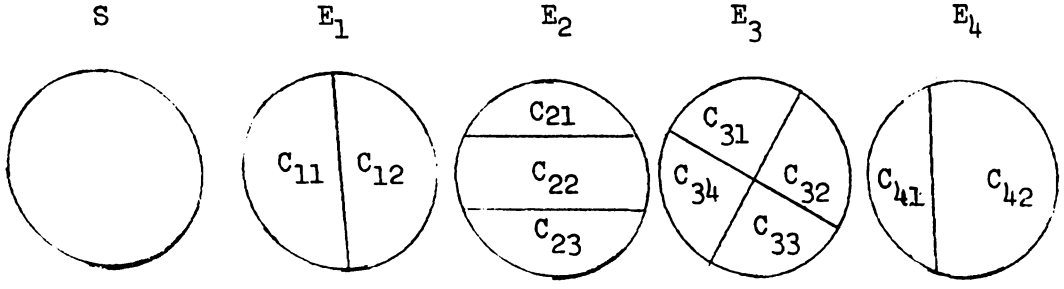
$\tau_{ij}(\bar{C}_i)$ = set of all consistent graph topologies between C_i. ($\bar{C}_i$ considered structurally invariant.)

$D_{ijk}(\bar{C}_i,\tau_i)$ = the set of all possible dynamical realizations for fixed $\bar{C}_i$ and τ_i.

We see that there is progressive natural emergence from the morphemes to natural components, to component topologies and finally system dynamics. The reaction of the system depends on the magnitude and time-duration of the perturbation.

We complete the section with two examples.

Example 1.2-7



a) $L_1(A_1) = E_1 = M_1$

$M_1 = [C_{11}, C_{12}] = \bar{C}_1$

$T_1 = [S, \emptyset, C_{11}, C_{12}]$

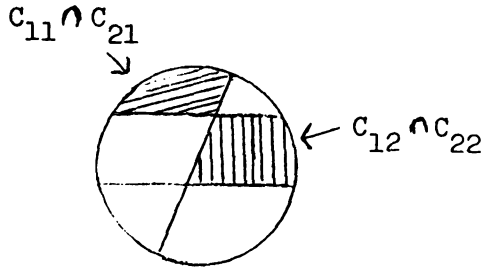
b) $L_2(A_1, A_2) = [E_1 \cap E_2] = M_2$

$M_2 = [C_{11} \cap C_{21},\ C_{11} \cap C_{22}, C_{11} \cap C_{23}, C_{12} \cap C_{21},\ C_{12} \cap C_{22}, C_{12} \cap C_{23}]$

$\bar{C}_2 = [C_{21}, C_{22}, C_{23}]$

$T_2 = [U(X \cap Y):\ X \in T_1, Y \in \bar{C}_2]$

$T_1 \subset T_2$



$Q_1 = [(C_{11} \cap C_{21}) \cup (C_{12} \cap C_{22})]$

Q_1 is an analyzable set.

c) Natural components at level L_2

$[C_{11}, C_{12}, C_{21}, C_{22}, C_{23}]$

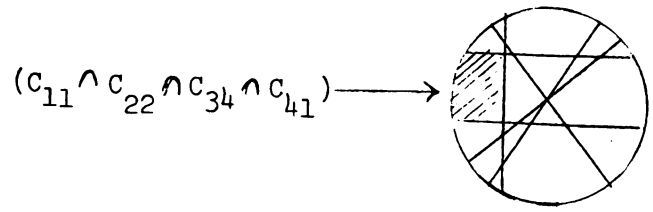
d) Morpheme set at level L_4

$M_4 = [X \cup (Y \cap Z) \mid X \in T_3,\ Y \in T_3,\ Z \in \bar{C}_4]$

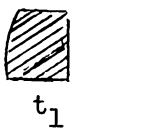
$(C_{11} \cap C_{22} \cap C_{34} \cap C_{41}) \in M_4$

e) Morpheme terminal graph.

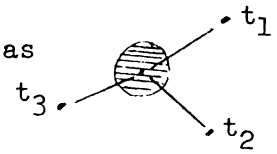
Let morpheme $(C_{11} \cap C_{22} \cap C_{32} \cap C_{42})$ at level L_4 be isolated as a free-body

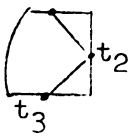


$E_1 \cap E_2 \cap E_3 \cap E_4$

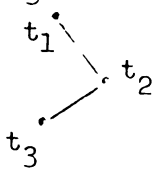


represented as





$[t_1, t_2, t_3]$ terminals



a possible terminal graph for morpheme

Example 1.2-8

Given the observer-system interaction consists of analyzing the metabolic activities of a cell.

$A_1 = (f_{11}, f_{12}, f_{13}]$

f_{11} = reproduction of the chromosomes

f_{12} = level of enzyme activity

f_{13} = ion concentration

$A_2 = [f_{21}, f_{22}]$

f_{21} = production of ATP

f_{22} = ion concentration

$A_3 = [f_{31}, f_{32}]$

f_{31} = state of cell division

f_{32} = protein synthesis

With respect to this activity set $[A_1, A_2, A_3]$, the following equivalence classes may be distinguished.

E_1 = [nucleus, cytoplasm, chromosomes, DNA]

E_2 = [mitochondria, cell membrane, rest of the cell]

E_3 = [ribosomes, nucleus, endoplasmic reticulum, rest of cytoplasm]

The morpheme set consists of all functionally independent subunits (organelles, DNA, cell membrane, etc.) that lie in the intersection of the identified $\bar{C}_i$ for each E_i. Note that the system (cell) at the original observer interaction stage is considered as a black-box when the A_i are identified.

The choice of f_{ij} are arbitrary as long as they can be distinguished by the observer. Although the activity set is derived from the black-box point of view the investigator still has the freedom to make measurements to identify the $\bar{C}_i$-classes. Furthermore once the $\bar{C}_i$ are identified measurements can be performed to determine the terminals (points of interaction) between aggregates (cytoplasm, nucleus) or morphemes (DNA, RNA, rihosomes). Some of these interactions are purely physical (energy, ion, protein exchange) others are behavioral (inhibition, excitation).

1.3 Analogous Systems and Degrees of Isomorphism

Given two dynamical systems a comparison can be made between them at various levels we have introduced. Equipped with the analytical component decomposition of the morpheme set based topology we define the system deep structure.

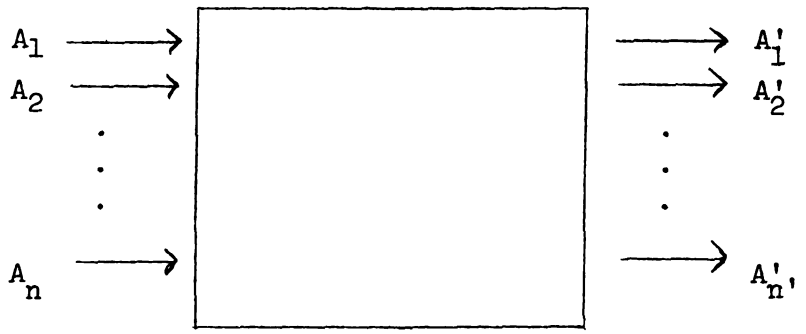
Definition 1.3-1 -- Based on the morpheme set M_n the system deep

structure is defined for each observed activity A_i as the ordered 3-tuple $[\bar{C}_i, \tau_{ij}, (\bar{C}_i), D_{ijk}(\bar{C}_i, \tau_{ij})]$.

Obviously, the $\bar{C}_i$ depend on M_n. The topology τ_{ij} is derived from the permissible interconnection of the natural components $\bar{C}_i$ as components of a system. (The label "natural component" is used to emphasize the relation between A_i and its characteristic decomposition based on E_i.) The definition yields a deep structure only to the depth of adaptive capacity in the sense that only τ_{ij} graph topology may change and system rearrangement due to self-organization is not included. To account for self-organization we should include the set of analyzable sets, thereby allowing a greater degree of permissible reorganization in the system.

In that case the deep-structure becomes an ordered 4-tuple $[T_n(M_n), \bar{C}_i(M_n), \tau_{ij}, D_{ijk}(\bar{C}_i, \tau_{ij})]$. Given a finite number of natural components it is obvious that $\tau_{ij}(\bar{C}_i)$ is finite. We have only assumed boundedness for the dynamic parameters. A continuous variation within the permissible bounds may yield an infinite range of dynamical possibilities. Hence, D_{ijk} should be indexed $D_{ij[k]}$, where [k] is the range for the parameters. In regulation problems it makes quite a difference whether the system dynamics may vary continuously or discretely both for the analytical methods used and the final result. The continuous case may nevertheless be approximated by discrete analogues in most problems and no real generatlity is sacrificed in assuming k to be discrete in the formulation of the deep structure.

An observation is in order about the modeling technique to derive structure from function. Let the activity set be given as $[A_1,\ldots,A_n]$ the results of the model $[A_1',\ldots,A_{n'}']$ are compared and certain conclusions made about the goodness of fit. The whole procedure may be considered as a multi-dimensional feedback problem. The system S is the black-box, the $[A_1,\ldots,A_n]$ serve as input and the $[A_1',\ldots,A_{n'}']$ as output.



The object of the modeling is to minimize the difference between input and output. Thus, the problem can be formulated as multi-dimensional feedback problem [C-6,C-7]. The resolving power induced by the topology indicates at what structural subsets M_n the system is analyzed, and the two sets $[A_1,\ldots,A_n]$ and $[A_1',\ldots,A_{n'}']$ are compared. Unfortunately, the free-body model requirements may impose practical limits on the resolution power. What we can say about the free-body model depends on the actual state of the art. Namely what information is available about entities represented by the morphemes in the particular discipline the model is applied to. It is an exercise in futility to model ecosystem behavior of species based on the cellular decomposition of the individual members of the species. This is not so preposterous an idea from the modeling point of view, but rather, from the biological considerations. The difficulty

of reassembling the species from cellular components stems mainly from the biological information gap between the level of species behavior and cellular structure. (Of course the complexity of the resulting graph topology would make any computer wince.)

Generally, one does not aim for an exact fit between $[A_1,\ldots,A_n]$ and $[A_1',\ldots,A_n',]$. The practical requirements will provide adequate error tolerances between input $[A_1,\ldots,A_n]$ and output $[A_1',\ldots,A_n',]$ to leave the morpheme decomposition at a reasonable level. (The present dissertation is not concerned with system simulation, and consequently the accuracy of the model will not be discussed further. The problem will be considered in a future paper.)

In passing we note that n' can be expected to be less than or equal to n, since in the modeling process certain information about the system may be lost and the resultant system complexity is less than the original.

Two arbitrary systems modeled by the 4-tuple $[T_n,\bar{C}_i,\tau_{ij},D_{ijk}]$ can exhibit four different degrees of analogy with respect to an activity A_i.

Definition 1.3-2 -- Given $[A_1,\ldots,A_n]$ and T_n for two arbitrary hierarchical systems

$$S_1 = [T_n^1,\bar{C}_i^1,\tau_{ij}^1,D_{ijk}^1]$$

$$S_2 = [T_n^2,\bar{C}_i^2,\tau_{ij}^2,D_{ijk}^2]$$

with respect to each pair $\{A_i^1,A_i^2\}$ the two systems will be isomorphic if.

a) $\exists$ a homeomorphism between T_n^1 and T_n^2,

b) the cardinality of the sets $\bar{C}_i^1$ and $\bar{C}_i^2$ is the same,

c) The sets of all permissible graph topologies τ^1_{ij} and τ^2_{ij} are equal,

d) For a fixed τ^1_{ij} and its graph isomorph (Definition 1.2-7) τ^2_{ij}, the corresponding system dynamics D^1_{ijk} and D^2_{ijk} have the same canonical form [R-20].

If only adaptive behavior is compared then condition (a) can be neglected, since analyzable sets are invariant for adaptive transitions. (The analyzable sets for this case are the $\bar{C}_i$-equivalence classes.) The definition clearly demonstrates why in hierarchical systems comparison of dynamics and graph topology is not sufficient. The system activity set and supporting structure varies in time. Every transition at some deep structure level implies changes at every level dependent on it. For example, if a self-organization transition is induced both graph topology and dynamics are altered. The frequency of change decreases with the depth of the level affected. In increasing order of transition frequency

$\bar{C}_i,(M_n)$ - self-organization

$\tau_{ij}(\bar{C}_i)$ - adaptation

$D_{ij}(\bar{C}_i,\tau_{ij})$ - regulation.

An adaptive change for an activity A_i that consists of a deletion of some edges in the graph topology between elements of $\bar{C}_i$ may be considered as a step towards specialization. A loss of the degree of freedom represented by cessation of graph edges <u>may</u> guarantee a greater stability for the total system structure. This problem will be qualitatively examined in the next chapter and analytically in Chapter III. It is

also very plausible that any transition is the minimal possible; the degree of reorganization is minimal with respect to a given purpose, assuming the system has an optimization capacity.

1.4 Nature of Complexity and Organizational States

The functional complexity of the system at initial observer interaction is measured by the activity set $[A_1,\ldots,A_n]$. Obviously, the more complex the system the greater the activity set. We have indicated that functional complexity should be reflected in structural complexity. Hence, if we begin with a large number of distinguishable activities we expect the underlying morpheme set to be proportional and the graph topology associated with the natural components relatively complex. The idea of absolute complexity, measured by the number of vertices and edges in the system graph is of no real importance, at least for most systems, in determining stability properties or adaptive capacity. In the following chapters we shall examine the relationship between system complexity and various stability properties. This will give us some interesting insights into the nature of physical growth and increase of relative complexity in biosystems. For the moment we shall be content to describe the nature of complexity for the deep structure of hierarchical systems.

Definition 1.4-1 -- The degree of functional complexity of the system is the number of distinguishable activities of the observer level.

This implies that the observed functional complexity depends on the observer-system interaction. A system considered simple by one set of measurements may be promoted to complex echelons by a different observer interaction.

Definition 1.4-2 -- The induced self-organization complexity of the system is the cardinality of the basis of the topology T_n.

The induced complexity then becomes the set of all potentially meaningful components. Complexity is dependent strongly on the equivalence classes $[E_1,\ldots,E_n]$ derived from $[A_1,\ldots A_n]$. Hence, high functional complexity implies similar complexity at the level of the deep structure. To examine the complexity of the graph topology we need some results from graph theory.

Given the vertices $[v_1,\ldots,v_n]$ a graph, G(V,E) can be constructed by inserting edges between the vertices. The maximal number of edges that can be placed to construct a simple graph of n-vertices is $\binom{n}{2} = \frac{n(n-1)}{2}$. The total number of subgraphs for such a maximally connected simple graph is $2^{n(n-1)/2}$. (Any edge may or may not be included in the subgraph.) A tree is the minimal number of edges required to connect n-vertices (Definition 1.2-10).

The fundamental cyclomatic number of a graph with respect to a tree T is the number of edges in the cotree. The fundamental cyclomatic number represents the excess connectivity (system constraints) above the minimal required for a connected system. Given a graph G with n vertices and p edges the fundamental cyclomatic number is $C_F = (p - n + 1)$. The maximal value of the cyclomatic number for n-vertices in a simple graph;

$$\text{Max}_C = \frac{n(n-1)}{2} - (n - 1) = \frac{n(n-1) - 2(n-1)}{2} = \frac{n^2-3n+2}{2}$$

$\frac{n(n-1)}{2}$ = maximal possible connectivity

$(n-1)$ = edges for a tree

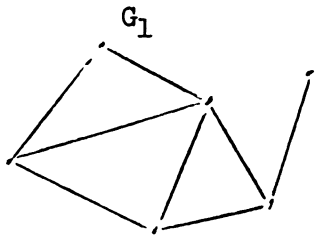
The relative complexity in a connected simple graph is the actual C_F divided by Max_C. Let G consist of p edges and n vertices, and let G be simply connected ($p \geq n-1$) then

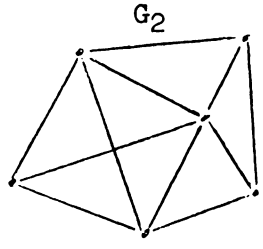
Definiton 1.4-3 -- The relative complexity of the system S at the adaptive level is measured by

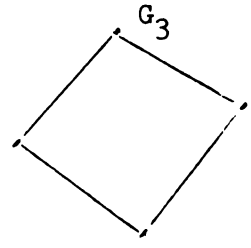
$$R_C(n) = \frac{C_F}{Max_C}(n) = \frac{p - n + 1}{(n^2 - 3n + 2)/2} = \frac{2(p - n + 1)}{n^2 - 3n + 2}$$

$$Max_C(2) \overset{\Delta}{=} 1 \quad \text{where} \quad p \leq n(n-1)/2, \quad n \geq 2$$

Example 1.4-1

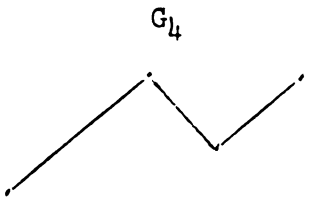


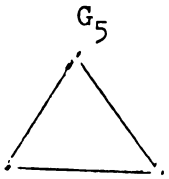


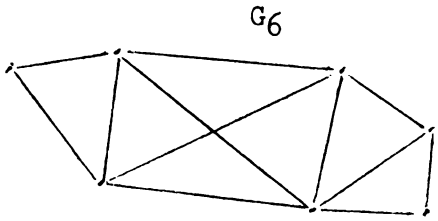


$V_1 = 6$	$V_2 = 6$	$V_3 = 4$
$p_1 = 8$	$p_2 = 11$	$p_4 = 4$
$C_F = 3$	$C_F = 6$	$C_F = 1$
$R_C = 3/10$	$R_C = 3/5$	$R_C = 1/3$

C_F does not depend on the specific tree chosen for the graph.







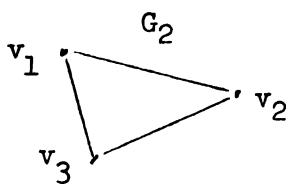
$V_4 = 4$	$V_5 = 3$	$V_6 = 7$
$p_4 = 3$	$p_5 = 3$	$p_7 = 12$
$C_F = 0$	$C_F = 1$	$C_F = 6$
$R_C = 0$	$R_C = 1$	$R_C = 2/5$

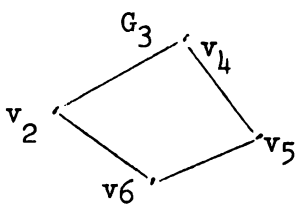
We see, for example, that G_2 and G_6 have the same C_F but $R_C^2 > R_C^6$.

It is easy to show $0 \leq R_C \leq 1$ for any graph. For graphs that are not connected R_C is computed for each connected subgraph and the total graph R_C is the sum of the subgraph R_C divided by the number of subgraphs.

Example 1.4-2

G is the minimal union of $[G_1, G_2, G_3]$ such that the subgraphs are joined at corresponding vertices only.





$V_1 = 1$	$V_2 = 3$	$V_3 = 4$
$p_1 = 0$	$p_2 = 3$	$p_3 = 4$
$C_F = 0$	$C_F = 1$	$C_F = 1$
$R_C^1 = 0$	$R_C^2 = 1$	$R_C^3 = 1/3$

$$R_C(G) = \frac{0 + 1 + 1/3}{3} = 4/9$$

We see in this example the complexity of the total graph G is greater than the minimal and less than the maximal for its component subgraphs. This is true generally, if the union of two disjoint graphs initially consists of one vertex union. Given a graph G as the union of disjoint subgraphs $G_1,\ldots,G_n$, let

$\min R_C$ be the minimum of the relative complexities

$\text{Max } R_C$ be the maximum of the relative complexities

then

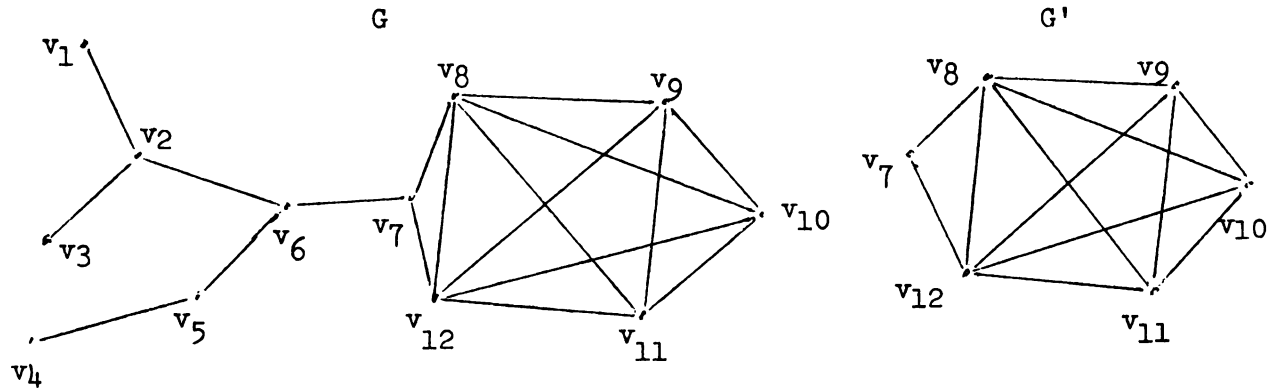
$$\min R_C(G_i) \leq R_C(G) \leq \text{Max } R_C(G_j)$$

where G is minimal union of subgraphs $[G_1,\ldots G_n]$. A minimal union consists of joining only two vertices of disjoint graphs as in Example 1.4-2. To see this fact consider the following

$$\min R_C = \frac{n \min R_C}{n} \leq \frac{\sum^{n} R_C}{n} = R_C(G) \leq \frac{n \text{ Max } R_C}{n} = \text{Max } R_C$$

The result is not particularly exciting unless we associate it with specialization of the system. If specialization can be considered as suppression of certain functions (with corresponding components) then it may be advantageous for the system to decouple some components with low relative complexity by an adaptive transition. We will later associate relative complexity with a stability property.

Example 1.4-3



G' is an adaptive transition of G with a subgraph of G becoming inactive in G'.

$R_C(G) = 7/55$ $\quad V_G = 12$ $\quad E_G = 18$

$R_C(G') = 7/10$ $\quad V_{G'} = 6$ $\quad E_{G'} = 12$

If the reverse process is considered and the original system graph is G' and the graph transition yields G then $R_C(G)$ is greatly decreased from $R_C(G')$. The union of the two systems can be interpreted as a growth process, if number of vertices are proportional to physical size of the system. If growth is quite sudden as in the above example the relative complexity of the resultant system may be greatly reduced. If, on the other hand, a system decomposes into separate graphs under an adaptive change we expect the decomposition to yield relatively stable subsystems. In fact, the decomposition should stop at the maximal stable components. The process of assembling a complex structure consists of several substages where each substage results in the completion of a stable component, these components are then linked at the next stage. There is a definite advantage to such a hierarchical construction. If the process is interrupted at some point in time and the actual completed stage

decomposes into stable substages the loss of effort is minimized if the distribution of stable forms D_S is dense in D [A-3,S-6]. The potential number of stable subgraphs of a given graph G(V,E) with n-vertices and k edges is 2^k. The effort of construction is minimized if for any perturbation the graph is decomposed into only two subgraphs. It is somewhat more difficult to find a useful criterion for the complexity of the system dynamics. For reasons that will become more meaningful later we choose the measure of dynamic complexity as

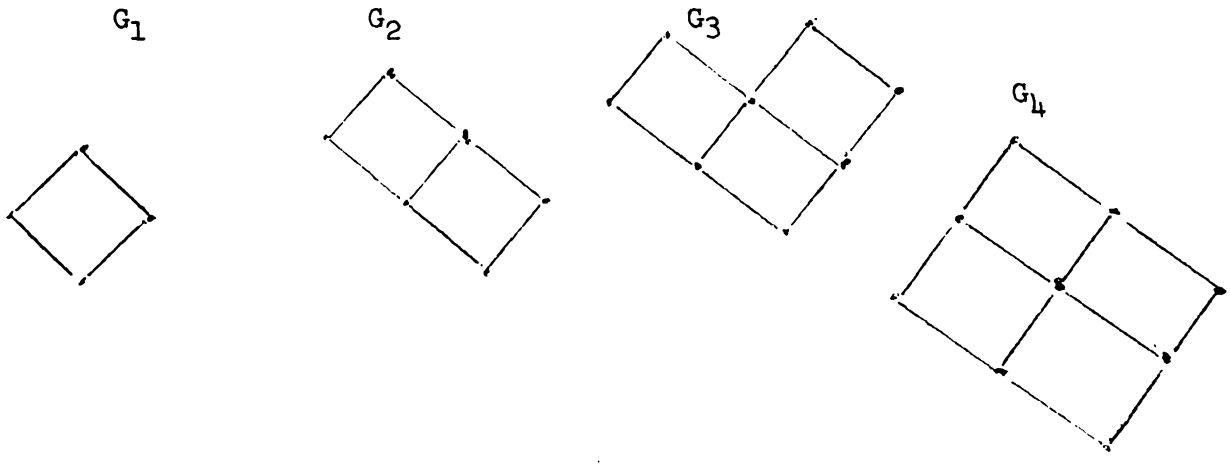
Definition 1.4-4 -- The degree of complexity of the system dynamics is the dimension of the state vector $\bar{X}$ of the state-space equation [L-4] (state variables are continuous). The state-space equation $\dot{\bar{X}} = S(\bar{X},\bar{Cs},t)$ is often referred to as the memory or updating equation of the system. The dimension of the state vector is the number of observables required to specify the dynamics and the response. Therefore, a system with higher dimensional state-vector implies intuitively a greater memory capacity and a more complex internal dynamical process. To "state" it more precisely, from the observer's point of view the more complex the dynamics the more involved its description via the state-equation.

In a series of articles Rashevsky introduced the idea of organismic sets [R-7]. The motivation relied on the analogy between certain functions in biology and corresponding ones in sociology. It demonstrated that some activities of hierarchically organized systems may be considered similar from a relational viewpoint. One of the fundamental results postulated dealt with the spontaneous aggregation of organismic sets to form new

entities. If we consider our structurally stable subgraphs as potential realizations of organismic subsets we see that (spontaneous) aggregation may be formulated in terms of total graph complexity. The fundamental cyclomatic number for each subgraph indicates the degree of interaction between the system components. A cyclomatic number of four expresses the fact that four subunits of the organismic set are in a state of interaction. The length of the cycle corresponds to the number of elements involved.

Now two organismic subsets will aggregate into a new organismic set if the cyclomatic complexity of the new graph is increased, indicating a greater degree of co-operation between subunits. Furthermore, the distribution of length of cycles measures the relative sizes of interacting sets. A high frequency of low cyclomatic numbers indicates the organismic set has a high number of interacting units with low membership per unit. The structural repetition of a cycle with low cyclomatic number may lead to progressively higher numbers in the new cycle superimposed, hence increases the structural complexity of the system, but not the index of relative complexity.

Example 1.4-4



By repeating the fundamental cycle [1,2,3,4] in Example 1.4-4 we obtain G_2 from G_1 and G_i from G_{i-1} by joining G_{i-1} to G_i along one edge. Let $N(G_i)$ denote (fundamental) cyclomatic number.

a) $N(G_1) = 1$ $\quad R_C(G_1) = 1/3$

b) $N(G_2) = 2$ $\quad R_C(G_2) = 1/10$

c) $N(G_3) = 3$ $\quad R_C(G_3) = 1/15$

d) $N(G_4) = 4$ $\quad R_C(G_4) = 1/21$

In general, a space filling repetition of a simple cycle of length n yields a sequence of increasing structural complexity but decreasing relative (graph) complexity. Consequently, if we look at the repetition of a cycle as the aggregation of two organismic sets (natural growth for example) then it is obvious that each growth stage is a period of instability which should be followed by a period of stabilization. The stabilization process consists of developing new relations in the system. In the model this is accomplished by increasing the cyclomatic number.

If this is not done then the aggregated system becomes progressively less stable reaching a point where it may decompose into its comparatively more stable subcomponents [S-6,R-6,R-7]. Any growth process decreases relative complexity and hence system stability, in the sense of Rashevsky. The mechanism regulating growth processes will have minimal simplicity of description if accomplished by the repetition of a basic structural pattern exemplified by a simple cycle. Thus, we see from the above arguments that in our framework there is no spontaneous (natural) aggregation of subunits only feasible or consistent ones. After a consistent union

of the subsystem graphs is accomplished, the unity and certain stability features of the resulting system are improved by increasing the system interaction thru the increase in the cyclomatic numbers.

It was shown in the first two sections how function represented by the activity set $[A_1,\ldots,A_n]$ induced a structure on the system based on the morpheme set M_n. The natural components $\bar{C}_i$ reconstructed from the morphemes free-body model served as a natural invariant class with respect to adaptation. The system graph imposed on the $\bar{C}_i$ gave rise to a set $[A_1',\ldots,A_n',]$ comparable to $[A_1,\ldots,A_n]$. Therefore, we can consider both structure and function of the system (since one generates the other) as manifestations of a common feature; system organization. Both functional and structural descriptions attempt to summarize the state of organization in the system. The common currency used to evaluate both is information gathered initially from the observer-system interaction.

In addition to the information contained in the system (function, structure) description the dynamics of the system gives further insight into the capacity of the system to accumulate and process information from the environment. The reason for selection of the order of the state vector was motivated by the above. Hence, taking the cybernetic point of view [G-1,G-4,L-6], we can distinguish two separate levels of information capacity in a system.

Definiton 1.4-5

a) Information on the permanent organization of the system is contained in the deep-structure description.

b) Transient organization of the system is measured by the order of the state vector.

c) The total organizational state of a system consists of the permanent and transient components.

Example 1.4-5 -- In linear systems (consisting of resistive, inductive and capacitive components) and open to the environment for information exchange and closed otherwise;

a) R-components represent information loss,

b) L-components represent information delay,

c) C-components represent information storage.

Hence, L and C type elements contribute to the total information content in the system and among all the possible dynamical realizations of graph topologically stable states, the one with maximal state vector might be selected. The system dynamics then serves as an intermediate stage between imparting of information from the environment and its incorporation into the permanent system deep structure. Systems processing and incorporating information into the permanent structure may be considered to possess learning ability [G-4].

Definition 1.4-6 -- If the transient information in the system is incorporated into the permanent structure by a transition of the natural component topology a learning capacity at the adaptive level exists.

Definition 1.4-7 -- If a sequence of adaptive changes induce a corresponding change at the self-organization level the system will be called evolutionary.

Adaptive changes are characteristic of a biological system with a fixed lifetime (individual organism). In a given lifetime of an individual organism the self-organization level cannot change. If a large number of these are subjected to the same sequence of adaptive changes, say from activity A_i to A_i', then the next generation of individuals might surface in the environment with A_i replaced by A_i'. The process of replacement is a genetic (self-organization) change and is accomplished by rearranging the $\bar{C}_i$ class by modifying the morpheme sets in the next generation.

Within the lifetime of the individual system the morpheme class is invariant. New activities may be introduced by adaptive changes ($\bar{C}_i$ invariance). In our framework then evolution is analogous to self-organizing ability and adaptation to transitions of a prescribed set τ_{ij} of $\bar{C}_i$ graph topologies. System specialization at the adaptive stage is either partial cessation of an activity A_i (decoupling of the $\bar{C}_i$-graph) or total deletion of an activity. (Introduction of new activities would be the opposite of specialization.)

In general, the mechanisms underlying learning (transient to permanent structure) are difficult to isolate, however, for a class of systems with strong biological significance, adaptation can be represented within the framework of structural perturbation of large-scale systems. These systems are called relational. The next chapter will deal with general properties of relational systems and their place in the theory of general systems.

CHAPTER II

RELATIONAL SYSTEMS

2.1 Relational Biology and Representation of (M,R)-Systems

The concepts exposed in the present section were originally formulated for the study of abstract biological systems, but with suitable generalizations can be applied to any dynamical system exhibiting structural or functional organization. The first successful attempt to introduce set theory and topology into the investigation of biosystems is due to Rashevsky. The publications on the topic span a couple of decades and the main results are summarized in a sequence of four papers published in the late sixties [R-8,R-9,R-10,R-11]. The essence of the theory is that biological phenomena may be classified into two categories; metric and relational. The former is concerned with chemical and physical structure of biological systems (in the strict sense of the word) whereas the latter contains the organizational features of the system as subject matter. Rashevsky's investigations focused on relational problems of biology and culminated in a rather general theory under the topic of "Organismic Sets". Certain formal analogies can be deduced about biological systems that exhibit the same relational properties, and based on relational comparisons, systems far removed in the biological natural hierarchy such as multicellular organisms and societies may be comparable. In the systems framework what matters ultimately is not the actual physical make up

of the components but rather the interrelationship between them. Thus, in our framework the specific content of the morphemes is immaterial as long as the free-body models and system graph are available. There are several useful concepts of organismic sets that we shall presently expose and incorporate into the model.

First we state three of the basic postulates of organismic sets [R-7,R-8]:

1) The degree of complexity of the system is directly proportional to its adaptability and chances of survival in a given environment.

2) The sequence of organizational structures during the development of a multicellular organism is determined by the requirement of maximal probability of survival during the whole lifetime of the organism including the period of development.

3) The course of development of any organismic system is such that during this course the total number of relations as well as the variety of different relations is maximized.

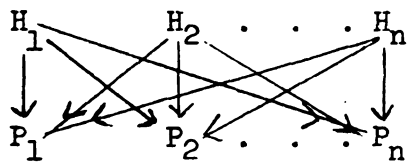
The above postulates are not exhaustive but constitute aspects of the theory which lend themselves readily to application in our framework. The three postulates together appear to indicate that complexity of a system is a measure of stability in the following sense: The total number of relationships developed within the system serve as pathways of communication between components to assure survival in the environment. The information capacity of the system is increased if the order of the

state vector increases. In general, for a fixed number of interacting components, the transient complexity is reflected by the state vector which represents dynamical capacity to react to the environment, and by the index of relative complexity R_C indicating the relative information content of the underlying structure. If the system is now represented by a graph the number of basic relationships developed between the nodes (components) is derived from the total number of connections between nodes. To provide a canonical characterization of the relationships the postulates of systems science are invoked. With respect to a tree in a (connected) system the fundamental circuit and cut set equations serve as a generative basis for all other dynamical interactions. The circuits define potential type interactions whereas cut sets specify flow type constraints. If the internal dynamics process a quantity such as information or energy, all internal changes can be defined in terms of potential and flow between terminals. Thus, Rashevksy's n-ary interactions are summarized by the above relations between components, and the relational aspect accounted for in a dynamical framework. The organism optimizes its chances of survival by developing interactions between components and hence buffering itself against unexpected environmental perturbations. With respect to a given number of components, represented by the nodes of a graph and the relationships given by the edges, we can now define the measure of adaptive capacity in the sense of Rashevsky, based on the concept of relative complexity introduced in Chapter I.

Definition 2.1-1 -- (Relative Complexity) -- The degree of relative complexity R_C, of a system is proportional to the probability of survival

in a specific environment.

The concept of relational stability is not dependent on the dynamical properties. An interesting example is furnished by a simple mathematical model of an ecosystem [M-5]. It is assumed that a class of predators and prey exist and the trophic interactions are governed by Volterra-Lotka type dynamics. May demonstrates in the paper that if the system is modified by the addition of an equal number of predators and prey and the new interactions are only of the predator-prey type, then the total dynamical stability of the system must decrease. Let us represent the system graphically, with P_i as the prey nodes and H_i the predator nodes.



In the original system every H_i is connected to every P_i. There are no direct competitive links at either prey or predator level. The relative complexity for the n-member system is

$$R_C(n) = C_F/Max_C = \frac{2(n^2 - n + 1)}{(4n^2 - 6n + 2)}$$

$$\lim_{n\to\infty} R_C(n) = 1/2 \quad \text{whereas} \quad R_C(2) = 1$$

The relative complexity of the system decreases from a maximal volume as new predator-prey pairs are added. Furthermore the new relations developed in the system are of a single predation type, and

ther the H_i or P_i levels are viable subsystems. Two of Rashevsky's otheses are violated; relative complexity and the variety of relations the system. The above system can be considered in a state of growth mplified by the addition of predator-prey nodes.

In view of the discussion in Chapter I on growth and stability, we the system in this case becomes less stable both from dynamical and vival points of view. Consequently a growth stage should be followed a period of stabilization. The mechanism of relational stabilization sists of developing new relations in the system by increasing the ree of relative complexity.

Biological systems are characterized by finite lifetimes in any ironment. Genetic modifications are induced from one generation to next. In our model an individual biosystem has reactive capacity only the depth of the adaptation level. (Adaptation for an individual tem is to be understood as a change in behavior characterized by a graph topological transition. To rearrange the $\bar{C}_i$-equivalence classes morpheme transition a new generation must emerge.) To account for sation of activities due to the environment interaction we introduce relational organization of an arbitrary system. The concepts related relational theory within a graph context are due to Rosen [R-13,R-14]. subsequent development of the theory followed the path of algebraic egories and general automata theory. These mathematical tools were uired to introduce a precise definition of system components in terms input-output relations, to account for internal dynamics and external

nvironmental forces. The theory now is quite well developed with the ajor modeling problems isolated [R-13,R-14,R-15,R-17,A-2,B-1,B-2,D-1, -4,M-4].

We propose to outline a different approach based mainly on graph heory and the ideas of Chapter I. The advantage in such a formulation ies with the incorporation of systems science methodology into relational ystems. In particular we can exhibit a class of relational systems that re functionally hierarchical. Later we shall examine the problem of ealization for relational systems in terms of input-output specification f constituent components. We now proceed to outline the basic ideas f relational theory.

As a first approximation the theory was formulated to account for the ulnerability of biological systems coupled to their environment. The eep structure we have developed so far fails to account for this aspect. he main concern of Rosen's theory is the behavior of an arbitrary system nce a component has been inhibited. What class of components can be ppressed (for the system to still survive) and how are components in the ystem replaced? The first problem relates to the degree of vulnerability f the system, whereas the second deals with problems of self-repair.

eneral Properties of (M,R)-Systems

It is assumed that an arbitrary system S is decomposed into a ollection of $\bar{C}_i$-components (Chapter I). The components are furnished with dynamical structure via the free-body modeling techniques. The ndamental units with respect to the original activity class $[A_1,\ldots,A_n]$

the $\bar{C}_i$-equivalence classes equipped with an appropriate dynamical
cription. Let us denote these dynamical $\bar{C}_i$-components as the funda-
tal system modules M_i. (We are now concerned with a realization of a
structure in a specific environment of a single generation of
anisms, hence self-organization transitions do not occur. For adaptive
sitions the M_i are fundamental invariant units.)

The cause-effect relations between the modules can be represented by
raph where the M_i are vertices and the input-output relations are the
es. A particular input which is not an output of a module is an environ-
tal input, an edge which is not an input to M_i is an environmental
ut [R-13].

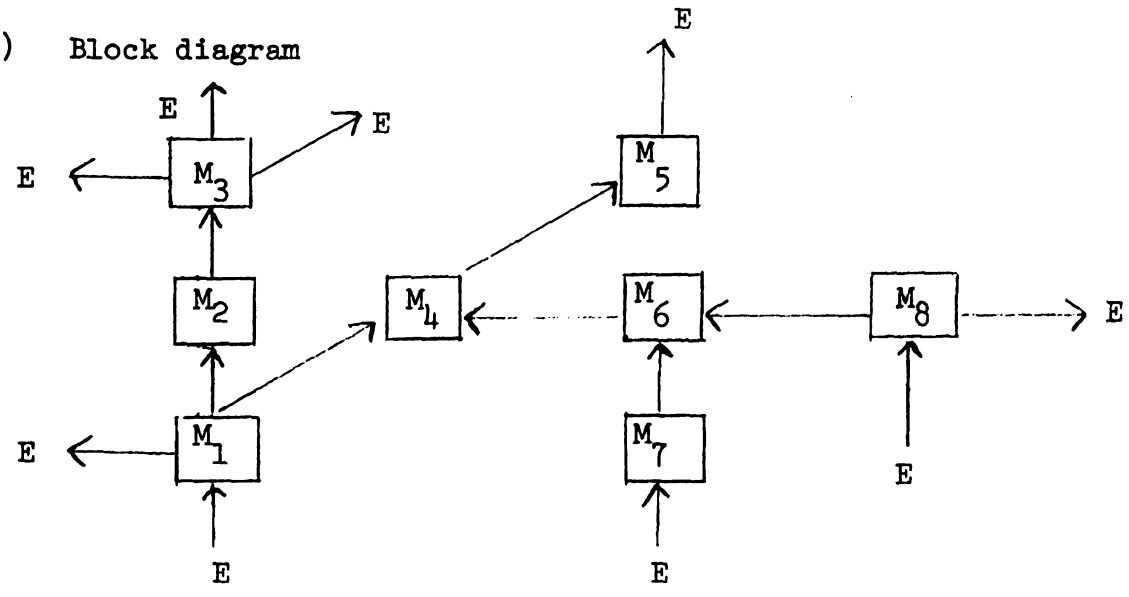
Definition 2.1-2 -- A subsystem S' of S is a subset of modules
ected analogously to S', such that

1) S' receives no input from any module of S not in S'.

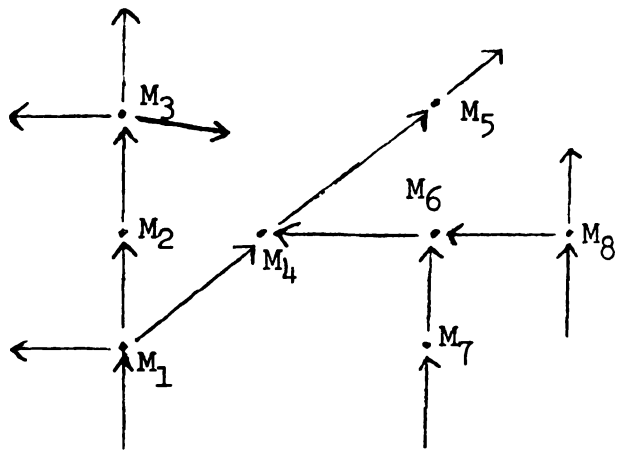
2) The set of environmental outputs of S' contain a subset of the environmental outputs of S.

Example 2.1-1

a) Block diagram

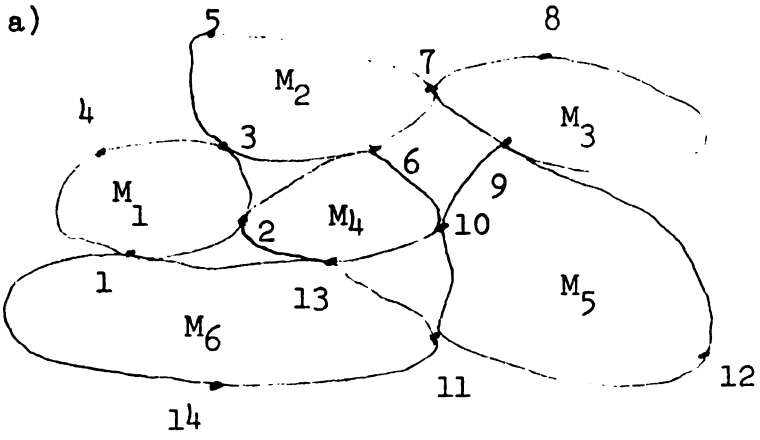


b) Input-output graph

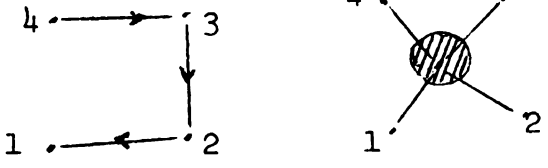


In example 2.1-1 $[M_1, M_2, M_3]$ constitutes a subsystem but $[M_1, M_2, M_3, M_4]$ es not. (If the environment E is considered as an additional vertex e graph can be simplified with all environmental inputs and outputs nnected to this vertex.) The system graph is directed and the underlying directed graph connected. The methodology we have introduced in apter I does not lead to a similar graph for the system S, instead of dules we have terminals of modules as graph nodes. It is possible to oceed directly from the system representation to the module graph by entifying the module M_j with its corresponding set of terminals, and troducing between adjacent terminals of two modules an edge. The rminals corresponding to an M_j emerge in the new representation as one rtex. The procedure is analogous to reducing a set of multi-terminal mponents in a large-scale system [K-5]. The addition of edges between jacent terminal can be viewed as a two-terminal approximation of time gs in real physical systems.

Example 2.1-2

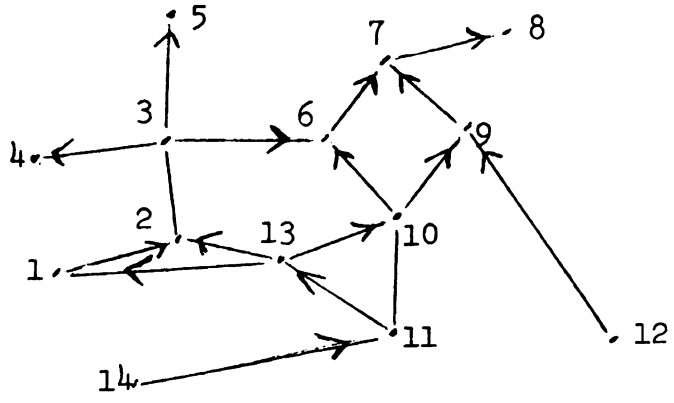
a) 

system S.

b) 

free-body model of M_1

and a terminal graph

c) 

a system graph

d) M_1 = [1,2,3,4] component terminal sets

M_2 = [3,5,6,7]

M_3 = [7,8,9]

M_4 = [2,6,10,13]

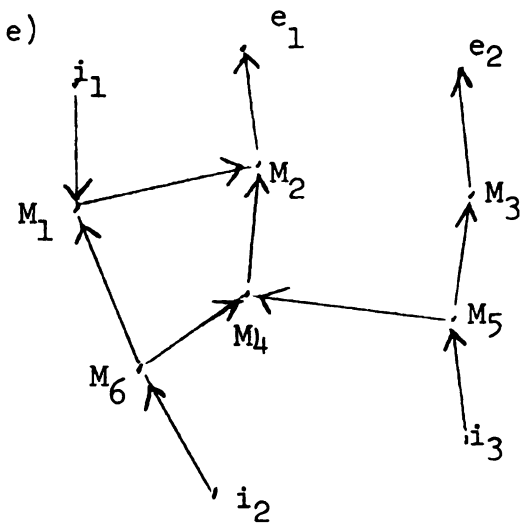
M_5 = [9,10,11,12]

M_6 = [1,11,13,14]

set [4,5,8,12,14] represent the potential environmental input-output

olings.

e)



A module graph.

Input set $I_s = [i_1, i_2, i_3]$

Output set $T_s = [e_1, e_2]$

e the module graph is obtained by merging the complete terminal set Mi into one vertex and introducing a new edge between the new adjacent terls. The edges are directed with orientations dependent on system mics.

Definition 2.1-2 -- Given the system graph of S_1 the inverse graph onstructed by

1) Identifying the terminal set of each M_i and representing the set as a vertex,

2) Introducing a directed edge between adjacent terminals.

The concept of the inverse graph allows us to proceed from the systems resentation to the relational module graph. The orientations of the es are dependent on the dynamical properties of the system and are ved from the constraint equations. The graph represents the basic se-effect relations in the system and these relations are subject to ge under the influence of the dynamics. At a specific time instance orientation of each edge is fixed.

Let θ represent the set of all environmental outputs of S, and to module M_i we assign a set $S_i \subset \theta$, which is the subset of outputs

inated when M_i is inhibited. Following Rosen's terminology S_i alled the dependent set of the module M_i. Two fundamental assumptions needed to bring the model closer to biological reality.

1) The module graph represents the metabolic activity of the system and each M_i is dependent on M_j from which it receives inputs. It is assumed no M_i functions unless all of its inputs are active. This property is known as non-contractibility. This permits the identification of each S_i (for a fixed time instance) from the module digraph.

2) Every M_i has a finite life-time. The ordered pair $[M_i, t(M_i)]$ defines the module and its life span. If $t(M_i)$ is exceeded the M_i ceases to function. To compensate for the finite life-time restriction every M_i is provided with a dual component R_i the activity of which consists of replacing the M_i [R-13].

Therefore, associated with the metabolic graph based on the module we have a related graph consisting of the repair set. The inputs to the R_i are constructed from the environmental output set θ of system. If M_i has environmental outputs in the system at least one he outputs serves as an input to a R_j. Let T_{M_i} be the set of ronmental outputs of a module M_i, then

$$T_{M_i} \cap (\cup \theta_j) \neq \emptyset \quad \text{if} \quad T_{M_i} \neq \emptyset$$

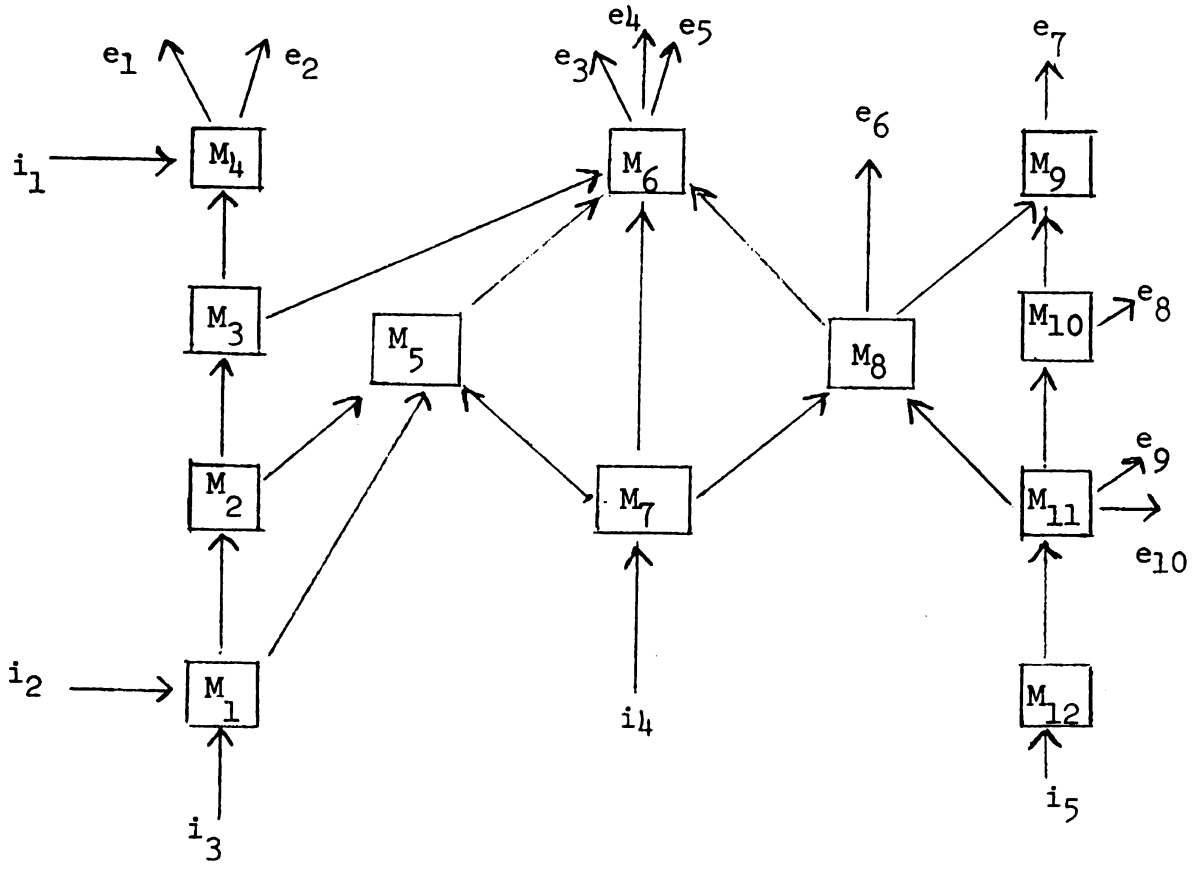
The above will be referred to as the feedback relation, or the covering thesis.

The structure outlined is called a (M,R)-system with metabolic vities (systems dynamics) represented by the module graph (M-graph)

the self-repair functions by the repair graph (R-graph). Let us show to construct the R-graph from the M-graph.

Example 2.1-3

a) Module block diagram.



Input set $I_s = [i_1, i_2, i_3, i_4, i_5]$

Output set $T_s = [e_1, \ldots, e_{10}]$

$T_{M1} = T_{M_2} = T_{M_3} = T_{M_5} = T_{M_7} = T_{M_{12}} = \emptyset$

$T_{M_4} = [e_1, e_2]$

$T_{M_6} = [e_3, e_4, e_5]$

$T_{M_8} = [e_6]$

$T_{M_9} = [e_7]$

$T_{M_{10}} = [e_8]$

$T_{M_{11}} = [e_9, e_{10}]$

$\theta_1 = [e_1, e_8]$

$\theta_2 = [e_2]$

$\theta_3 = [e_4, e_7]$

$\theta_4 = [e_4]$

$\theta_5 = [e_7, e_8]$

$\theta_6 = [e_1, e_2, e_6, e_8]$

$\theta_7 = [e_7]$

$\theta_8 = [e_6]$

$\theta_9 = [e_7]$

$\theta_{10} = [e_2, e_3]$

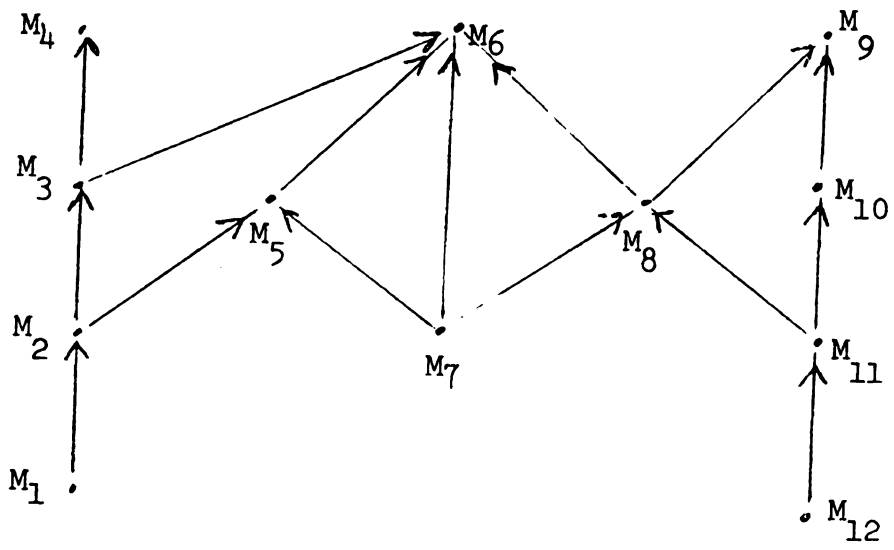
$\theta_{11} = [e_3]$

$\theta_{12} = [e_6, e_9]$

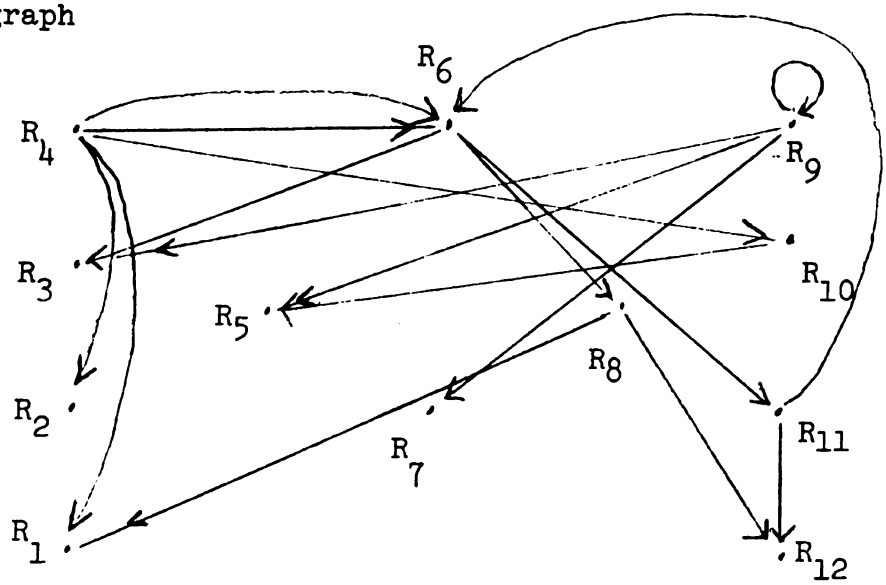
The feedback relation is satisfied, but θ is a proper subset of

since e_5, e_{10} are not in θ.

b) M-graph (with environmental couplings suppressed)

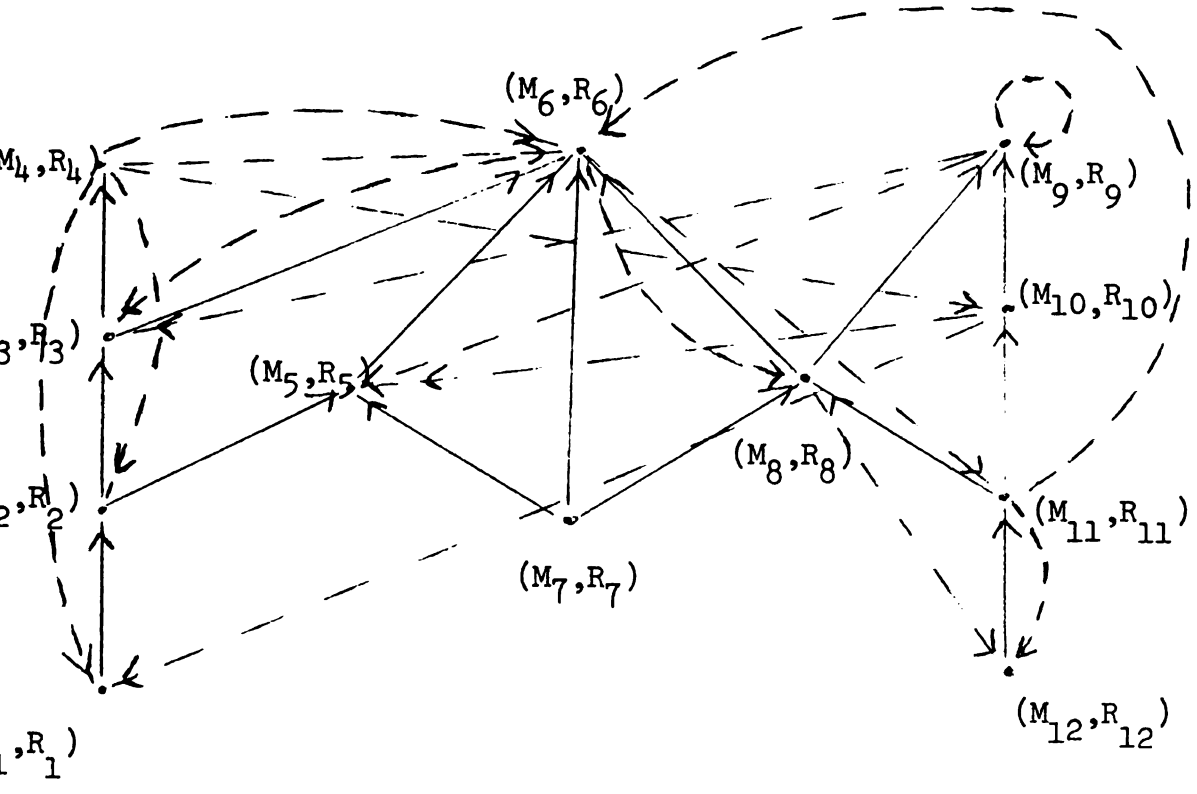


c) R-graph



The R-graph has edges originating only at terminal modules $[M_4, M_6, M_8, M_{10}, M_{11}]$ of M-graph.

d) (M,R)-graph is constructed by superimposing on the M-graph the R-graph. An R_i vertex is the same as its corresponding M_i. Thus, each vertex now is considered as representing the pair $(M_i R_i)$. The input set and environmental outputs not in θ are deleted



an output in T_{M_i} is fed back to an R_j then an edge is superimposed the M-graph between vertices M_k (terminal modules) and R_j.

Obviously the construction tends to be unwieldy and is much simpler resented by the adjacency matrix of the graph[J-1].

Example 2.1-4 (Refer to Example 2.1-3)

a) Let $a_{ij} \in V(M)$ the adjacency matrix for the M-graph.

$$a_{ij} = \begin{cases} n & \text{if there are n strictly parallel edges from } M_i \text{ to } M_j. \\ 0 & \text{otherwise.} \end{cases}$$

For example, some entries are:

$a_{89} = 1 \qquad a_{13} = 0 \qquad a_{12} = 1$

b) Let $b_{ij} \in V(R)$ the adjacency matrix for the R-graph.

$$b_{ij} = \begin{cases} m & \text{if there are m strictly parallel edges from } R_i \text{ to } R_j. \\ 0 & \text{otherwise.} \end{cases}$$

$b_{13} = 0 \qquad b_{42} = 1 \qquad b_{46} = 2$

$b_{63} = 1 \qquad b_{62} = 0 \qquad b_{86} = 1$

c) Let $c_{ij} \in V(M,R)$ the adjacency matrix for the (M,R)-graph

$$c_{ij} \overset{\Delta}{=} a_{ij} + b_{ij}$$

$c_{12} = 1 \qquad c_{13} = 0 \qquad c_{99} = 1$

$c_{86} = 2 \qquad c_{41} = 1$

Therefore all structural features of the (M,R)-graph can be summarized the matrix form. The feedback matrix may be simplified by reducing rictly parallel edges between any (M_k,R_j), consequently all entries of e feedback matrix are zero or one. We have already permitted the duction of parallel edges between modules in the M-graph (if the con- ction in the M-graph represents signal flow then one potential variable and one flow variable y_i suffice). The matrix resulting from the perposition has entries {0,1,2}, since there exist at most two strictly rallel edges between vertices.

2 Re-establishable and Central Modules

A module in the relational system is said to be central if its nibition implies the cessation of all environmental outputs. (From e observer's point of view the activity class $[A_1,\ldots,A_n]$ ceases to ist.)

For an arbitrary module the augmented dependent set consists of all vironmental outputs that eventually cease to function when the module is nibited. In other words, all outputs from the system that are either

ffected by the inhibition of the module in the M-graph or those depending the feedback relation from the terminals M_k inhibited by the module (a rminal module M_k is a module producing an environmental output). A dule M_i is <u>re-establishable</u> if it does not inhibit any terminal M_k oducing a feedback signal to its own repair set R_i. Both concepts of ntrality and re-establishability can be conveniently defined on the ,R) graph, using the property of non-contractibility of the $[M_i,R_i]$ rtices.

<u>Definition 2.2-1</u> -- An (M,R)-circuit originating at M_i and including feedback edge from a terminal M_k to R_i is a proper feedback circuit.

<u>Theorem 2.2-1</u> -- Assume the M-graph and R-graph are free of directed rcuits. Given the (M,R)-graph representation of relational systems a dule M_i is

1) Central iff every terminal M_k is connected to M_i by a directed M-path from M_i to M_k.
2) Re-establishable iff there does not exist an (M,R)-directed proper feedback circuit originating at M_i.

<u>Proof</u>:

1) $\Rightarrow$ if the M_i is central every terminal M_k is inhibited, implying the eventual inhibition of every M_i by an (M_k,R_i) feedback cycle.

   $\Leftarrow$ if there exists a directed M-path to any M_k from an M_i, every R_j will eventually cease to function, since every terminal is inhibited, and corresponding M_j eventually fails.

2) Let us show the contrapositive

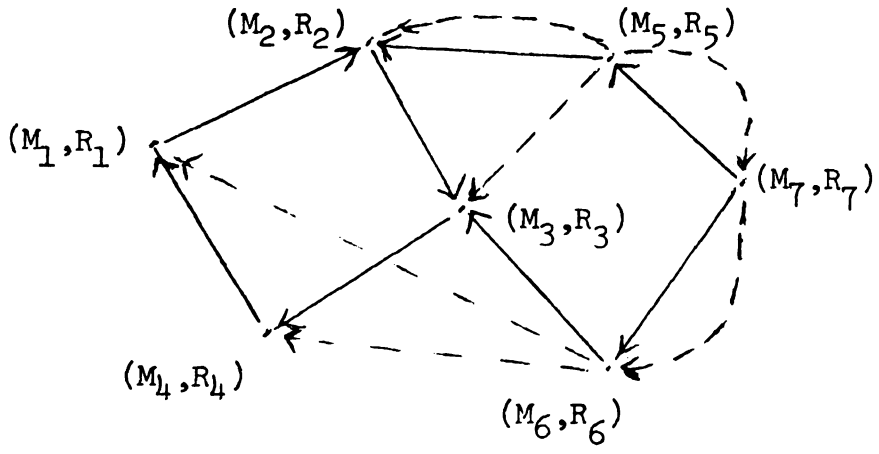
$\Rightarrow$ if M_i is non re-establishable then there exists a terminal M_k inhibited by M_i such that an (M_k,R_i) edge exists. By the property of non-contractibility there is a directed path from M_i to M_k. But (M_k,R_i) is a directed edge completing the circuit.

$\Leftarrow$ Assume there exists a directed circuit based on M_i. Then the circuit must pass thru a terminal M_k since the M-graph is circuit free. The directed edge (M_k,R_i) represents a feedback edge. If M_k is now inhibited by M_i so is R_i by the feedback edge (M_k,R_i).

The assumption that the M-graph and R-graph are free of directed circuits can be relaxed. It is sufficient to require that there be no directed proper feedback circuits in the (M,R)-graph based on M_i. To show that the exclusion of M-circuits is not necessary we consider the following example.

Example 2.2-1

a) $T_s = [M_5,M_7,M_6]$



$\theta_1 \subset T_{M_6}$

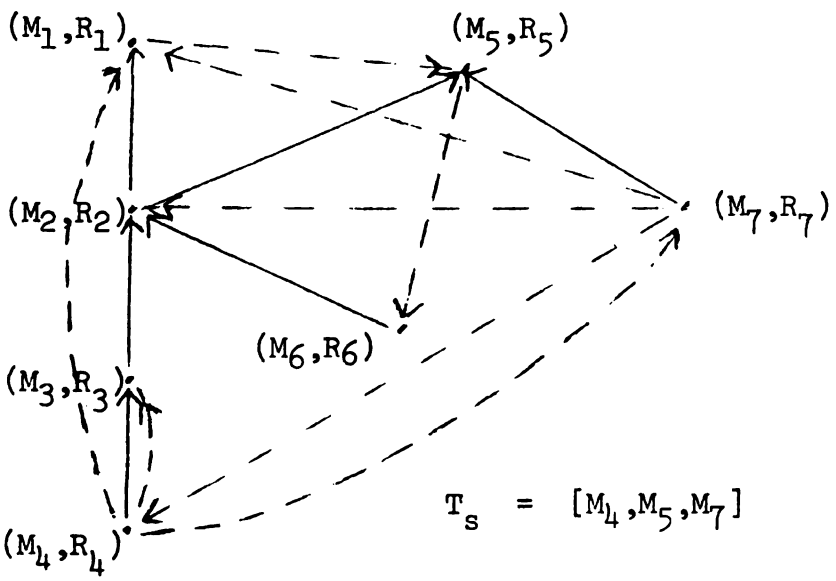
$\theta_2 \subset T_{M_5}$

$\theta_3 \subset T_{M_5} \quad T_{M_7}$

$\theta_4 \subset T_{M_6}$

$[M_1, M_2, M_3, M_4]$ is a directed circuit in the M-graph, yet all $[M_1, M_2, M_3, M_4]$ are re-establishable.

b) To show an arbitrary circuit in the (M,R) graph is not sufficient to produce a non re-establishable module.



$T_s = [M_4, M_5, M_7]$

$\theta_1 \subset T_{M_4} \cup T_{M_7}$

$\theta_2 \subset T_{M_7}$

$\theta_3 \subset T_{M_4}$

$\theta_4 \subset T_{M_7}$

$\theta_5 \subset T_{M_1}$

$\theta_6 \subset T_{M_5}$

$\theta_7 \subset T_{M_4}$

(It is assumed every terminal producing a feedback relation has at least as many environmental outputs.)

1) M_6 is non re-establishable $[M_6, M_2, M_5, R_6]$ is a proper feedback circuit including an input to R_6.

2) M_1 is re-establishable even though $[M_1, R_5, R_6, M_2, M_1]$ is an (M,R)-circuit. The circuit does not include an input to R_1. $(\theta_1 \in T_{M_7})$

3) $[M_4, M_7]$ are potentially non re-establishable, if the R_i time lags are considered.

The respective R-circuits include edges of θ_4 and θ_7.

If M_7 in the example is inhibited at the moment the life-time of M_4 is exceeded then both M_4, and M_7 will fail since there exists an R-circuit between them. In particular if M_7 fails and the remaining time of operation for M_4 is less than the time required by R_7 to replace M_7 then both M_6 and M_7 will fail. Therefore R-graph circuits may create conditions of non re-establishability if the operational life-times are considered. When a non re-establishable module M_i is connected to a central component by an R-graph circuit, in light of the above discussion M_i may also have the same effect on the system as a central component. One of Rosen's original hypotheses eliminates this troublesome condition by requiring the replacement of a module to be produced instantaneously. In our model Rosen's hypothesis eliminates the need to consider R-circuits at the present stage. Systems with time delays in the R_i-components appear to closer approximate biological phenomena by incorporating the operational time lags inherent in the real components of biological systems. We shall outline briefly the methodology to include operational time lags, in section 2.5 under optimization. Unless otherwise stated we assume none of the R_i have operational time lags.

The set of central components is obviously a subset of the non re-establishable components. We can give an algebraic criterion for the existence of re-establishable modules in terms of the adjacency matrices of the M-graph and (M,R)-graph.

Lemma 2.2-1 -- Given the adjacency matrix V of a directed graph, the matrix V^n gives the number of directed paths of length n between any two vertices.

Proof: if $a_{ik} \in V$ is the number of edges joining v_i to v_k and $a_{kj} \in V$ the number of edges between v_k and v_j, then $a_{ik} \cdot a_{kj} \in V^2$ is the number of different paths between v_i and v_j. Summed over all k, all paths of length 2 are computed. V^2 has entries $a_{ik} \cdot a_{kj}$. Assume result is true for V^{n-1}, then $V^n = V^{n-1} \cdot V$ yielding the number of paths of length n between corresponding vertices.

Corollary 2.2-1 -- If $V^n = 0$ for $n \geq N$ then there exist no directed circuits in the graph.

Proof: if there exists a circuit, then a path of infinite length can be constructed by repeating the circuit.

Applying the corollary we can reformulate Theorem 2.2-1 in terms of adjacency matrices.of the respective graph

Theorem 2.2-1' -- Let $V(M)$, $V(R)$, be the adjacency matrices of the respective graphs. $([a_{ij}] = V(M), [b_{ij}] = V(R))$.

Assume (M,R)-graph consists of m vertices and

$$V^n(M) = 0 \quad \text{for} \quad n \geq N_1$$

$$V^n(R) = 0 \quad \text{for} \quad n \geq N_2$$

then

a) The module M_i is re-establishable iff given the terminal module set $[M_{k_i}]$ producing a feedback input to R_i

$[a_{ik}]_i = 0$ V_k such that $M_k \in [M_{k_i}]$ $([a_{ik}]_j = V^j(M)$ and $1 \leq j \leq N_1$

b) The module M_j is <u>central</u> iff the set of terminals $[M_{k_j}]$ inhibited by M_j thru an M-path satisfy the following conditions

1) For the terminal set $[M_k - M_{k_j}]$ not directly inhibited by M_j there exists for each $M_{k'} \in [M_k - M_{k_j}]$ a feedback edge $(M_{k_j}, R_{k'})$ i.e. $[b_{k_j k'}] \neq 0$.

2) For every $M_{k'} \in [M_k - M_{k_j}]$ and $M_{k'} \notin [M_{k_j}]$ if a feedback edge $(M_{k'}, R_{k'_j})$ exists then also $(M_{k''_j}, R_{k'_j})$ exists, with $M_{k''_j} \in [M_{L_j}]$ i.e., if $[b_{k'k'_j}] \neq 0$ then $[b_{k'_j k''_j}] \neq 0$.

<u>Proof</u>:

a) $\Rightarrow$ if M_i is re-establishable then M_i may not inhibit a terminal M_k producing a feedback input to R_i, which implies there is no directed M-path to M_k.

This implies $[a_{ik_i}]_j = 0 \ \forall k$ such that $M_k \in [M_{k_i}]$. Since $V^n(M) = 0$ for $n \geq N_1$ the maximal path that may exist is of length $j \leq N_1$.

$\Leftarrow$ if $[a_{ikj}]_j = 0$ for $1 \leq j \leq N_1$

then there exists no directed M-path from M_i to a terminal M_{k_i} producing a feedback edge, hence no proper feedback circuit can be completed. Threfore M_i must be re-establishable.

b) $\Rightarrow$ Assume M_j is central and $[M_{kj}]$ is the terminal set directly inhibited by M_j, if $M_{k'} \in [M_k - M_{k_j}]$ then $M_{k'}$ survives unless it is inhibited by an $M_{k'_j} \in [M_{k_j}]$, therefore $[b_{k_j k'}] \neq 0$ for at least one terminal in $[M_{k_j}]$.

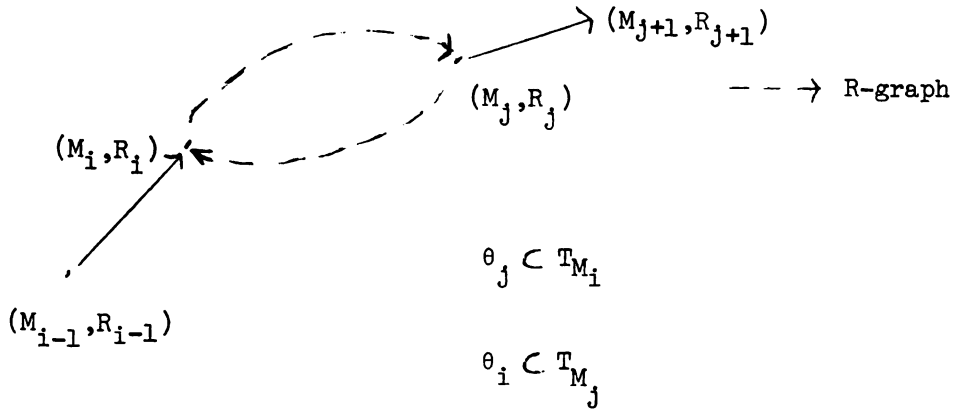
On the other hand, for a terminal $M_{k'_j} \in [M_{k_j}]$ if the corresponding $R_{k'_j}$ received feedback input from only $[M_k - M_{k_j}]$ then M_{k_j} is re-establishable which implies M_j is not central. Therefore, if $[b_{k'k'_j}] \neq 0$ then also $[b_{k'_j k''_j}] \neq 0$.

$\Leftarrow$ Let $[M_{k_j}]$ be the directly inhibited terminal set of M_j. If for $M_{k'} \in [M_k - M_{k_j}]$ a feedback edge exists from the set $[M_{k_j}]$ i.e., $[b_{k_j k'}] \neq 0$ and if the set $[M_{k_j}]$ is non re-establishable ($[b_{k'k'_j}] \neq 0 \Rightarrow [b_{k_j k''_j}] \neq 0$ for some $M_{k_j}, M_{k''_j} \in [M_{k_j}]$) then eventually all terminals will fail. Hence in the system every M_i will also fail. This implies M_j is central.

The conditions $V^n(R) = 0$, $V^n(M) = 0$ for $n \geq \text{Max}[N_1, N_2]$ are not necessary, but are included to provide more realistic constraints for relational systems that represent biological systems. The existence of directed circuits in the R-graph imply strong vulnerability and mutual dependence for modules connected in the circuit. The assumption that $V^n(M) = 0$ implies the conditions for re-establishability, however with some modifications in the proof, the condition can be relaxed.

Note that the theorem relies heavily on two properties of relational systems, non-contractability and the replacement of an M_i without time delay. If the second condition is relaxed and the operational time lag is required to produce an arbitrary M_i the situation becomes quite complicated. In that case not only proper feedback circuits but any circuit in both (M,R)-graph and R-graph have to be considered.

Example 2.2-2'



Both M_i and M_j serve as feedback inputs to each other. If M_i is inhibited at $t=t_o$ and the life expectency at $t=t_o$ of M_j is $t(M_j)$ with the replacement time for M_i greater than $t(M_j)$ both M_i and M_j will fail and become non re-establishable.

This is true generally. Let a set of modules $[M_1,\ldots,M_n]$ and $[M_1',\ldots,M_n']$ be given in a relational system. If $\theta_i \subset T_{M_j}$ for $M_j \in [M_1,\ldots,M_n']$ and $\theta_j \subset T_{M_i}$ for M_i $[M_1,\ldots,M_n]$, when either set is inhibited if modules in the other cease to function before the first set is replaced both sets will cease to function eventually. The idea can be applied to define generalized non re-establishable modules.

Let two modules M_i and M_j be given such that there exists a directed circuit of length two between (R_i,R_j) i.e., $[b_{ij}]_2 \neq 0$ in $V^2(R)$. Let $t(R_i)$ be the replacement time for M_i and $t_o(M_j)$ be the operational time remaining for M_j at $t=t_o$. Let M_i be inhibited at $t=t_o$.

If $t_o(M_j) < t(R_i)$ then both M_i and M_j become non re-establishable at $t_o + t_o(M_j)$.

With respect to remaining operational times and replacement times a system can be classified into generalized non re-establishable sets of modules following the inhibition of any module M_i.

If the (M,R)-graph is strongly connected then obviously every module is central and non re-establishable. On the other hand an acyclic (M,R)-graph has every module as re-establishable. Similarly a subsystem of an (M,R)-system survives when an M_j is inhibited only if M_j is not in the subsystem and there exist no directed paths from M_i and is an R_j in the subsystem. In particular, if a directed (M,R)-path exists to a subset of the system, as long as the terminals producing the feedback signals to the R_i-set corresponding to the subset are not inhibited, the set will be re-established. Inhibition in this sense is only temporary. Therefore circuits existing in the metabolic M-graph are of no real importance from the survival point of view for the components. Only (M,R) circuits producing proper feedback, and R-circuits establishing

generalized central modules are of interest. An important observation on relational systems satisfying the covering hypothesis is derived from the following theorem due to Rosen.

Theorem 2.2-2 [R-13] -- Given an (M,R)-system satisfying the covering hypothesis, if the system is connected then there exists at least one non re-establishable component (module).

Proof: Assume every module is re-establishable. Then a terminal M_k^1 is re-establishable. By the covering hypothesis there exists a feedback edge from M_k^1 to an R_i. The edge (M_k^1, R_i) cannot serve as an input to

an M_i that is connected to M_k by a directed M-path. (Otherwise an (M,R)-circuit is constructed.)

Let M_k^2 be a terminal reachable from M_i by a directed (M,R)-path, since M_k^2 is re-establishable the feedback edge from M_k^2 cannot serve as an input to any R_i directly connected to $[M_k^1, M_k^2]$. Hence a further terminal is inhibited which is also re-establishable. By repeating the above argument the set of finite terminals is exhausted and the last M_k^n must produce a feedback edge to an R_i directly connected to at least one M_k^j thus completing an (M,R)-circuit.

Hence there exists at least one non re-establishable module.

The theorem implies the impossibility of realizing an (M,R)-system by an <u>acyclic</u> (M,R)-graph; it must contain at least one proper (M,R)-feedback circuit. A question comes to mind immediately as to how the covering hypothesis can be relaxed to permit the realization of a relational system with no non re-establishable modules. This problem is of importance in the synthesis of relational systems, and will be examined under the section of optimization on (M,R)-graphs. Certain properties however are obvious and can be pointed out at this stage. Any module associated with an R-self-loop is automatically non re-establishable. If a component produces a feedback signal to its own repair mechanism it cannot be re-established. Any strongly connected (M,R)-system is maximally vulnerable in the sense that all of its components are central and hence non re-establishable. An acyclic (M,R)-system is minimally vulnerable from the inhibition point of view. The solution

to the optimization problem must then lie between these two extremes. In the sense of Rashevsky survival stability requires the increase of system interaction between components as measured by the degree of relative complexity. This definition of stability considers the alternative modes of interaction available to the components to compensate for lack of information about the environment. On the other hand a high R_C implies a greater probability of existence of proper feedback (M,R)-circuits and the system becomes more vulnerable in the sense of Rosen. In addition the restrictions imposed by the type of dynamics superimposed on the graph topology act as a potential constraint on the optimization process. Therefore dynamical stability, survival stability (degree of complexity) and vulnerability enter simultaneously as constraints on the realization of possible (M,R)-systems. Subsystems of a relational system (Definition 2.1-2) are characterized in the (M,R)-graph by the following.

Definition 2.1-2' -- A set of vertices $[M_i]$ constitute a subsystem iff there do not exist directed (M,R)-paths to the set $[M_i]$ from any M_j not in $[M_i]$.

A module M_j in the subsystem may not inhibit a terminal M_k producing a feedback edge to an R_i of a module in the subsystem consequently we can reformulate a theorem of Rosen's on the survival set of a system.

Theorem 2.2-3 (Rosen) -- If a module M_j is inhibited either

a) the entire system fails,

b) there exists a subsystem which survives.

Proof: Assume there exists an M_i which is not terminated (otherwise case (a) holds) then there is at least one terminal M_k not inhibited, otherwise R_i has no non-inhibited inputs. Now the totality of terminals $[M_k]$ serving as inputs to R_i are also not affected. In addition any module connected to the surviving terminal set $[M_k]$ must also survive. The collection of all these surviving $[M_k]$ and associated $[M_k]$ directly connected to $[M_k]$ form a subsystem.

If this were not the case then some $M_j, \in [M_j]$ is inhibited and by the non-contractability so is at least one terminal M_k serving as an input to R_i implying the inhibition of M_i, which is a contradiction.

Therefore, the failure of a relational system is either total or some viable subsystem survives. Again we are led to a paradoxical situation as far as realization of (M,R)-systems are concerned. We have seen that a module M_i responsible for self-repair is automatically non re-establishable. Analogously for subsystems if all self-repair (feedback signals) originates from terminals contained in the subsystem, the vulnerability is increased. Hence feedback signals should be produced by terminals in the complementary set of the subsystem, but these terminals cannot be too strongly connected to other modules in the system. Otherwise probability of inhibition is increased. Furthermore, in view of non-contractibility, the feedback set to each R_i should be minimal for survival of the M_i.

The Rashevsky hypotheses favor strong metabolic interactions but Rosen's conditions discourage strong connectivity. A possible solution is

to relax the non-contractability property and to assume an R_i can be activated and inhibited by several on-off feedback relations. In that case one needs threshold conditions in terms of the total feedback state to determine whether an R_i is inhibited.

2.3 Realization of (M,R)-Systems

It is assumed the system graph is free of self-loops. In the M-graph self-loops are unnecessary for dynamical description and in the R-graph a self-loop implies automatic non re-establishability. Within Rashevsky's framework the existence of a self-loop corresponds to a relation developed by a module with itself, clearly superfluous. Furthermore we rule out the possibility of a strongly connected (M,R)-graph since a system represented by such a graph is terminated if any module is inhibited. (This eliminates the possibility of achieving an optimal solution for survival stability since the degree of complexity R_C is only maximal if the (M,R)-graph is strongly connected.) We assume strictly paralled edges in both the M-graph and R-graph are reduced, and R_C is computed for digraphs with two possible edges between vertices.

An arbitrary module in the system block diagram form can be considered as specified by a set of input-output relations. Within the (M,R)-graph framework a vertex corresponding to a module is specified by its incidence set $(d^+,d^-)(v)$. ($d^+(v)$ is the set of outgoing degrees and $d^-(v)$ is the set of incoming degrees.) The ordered pair $(d^+,d^-)(v)$ is the degree pair of the node v. Hence a finite collection of modules can be represented by a set of non-negative ordered integer pairs. For purposes of synthesis

the representation problem becomes one of constructing an (M,R)-graph given the degree pair (input-output) description of the modules.

Definition 2.3-1 -- A (p,s)-digraph is a directed graph in which the number of strictly parallel edges is less than or equal to p and the number of self-loops bounded by s.

We are concerned with connected graphs where $p \leq 2$ and $s = 0$. An (M,R)-graph may have two strictly parallel edges as long as one belongs to the M-graph and the other to the R-graph.

Let us now state a rather general theorem on the realizability of an arbitrary collection of degree pairs $[(d_i^+,d_i^-)]$.

Theorem 2.3-1 [C-2] -- The necessary and sufficient conditions for a set of n degree pairs $[(d_i^+,d_i^-)]$ to be realizable as a (p,s)-digraph are

1) $\sum_{i}^{n} d_i^+ = \sum_{i}^{n} d_i^-$

2) $\sum_{d_i^+ \in \bar{S}_A} \min[d_i^+,\alpha(S_A)p] + \sum_{d_j^+ \in S_A} \min[d_j^+,[\alpha(S_A)-1]p + s] \geq \sum_{d_k^- \in S_B} d_k^-$

where

$A = [d_1^+,\ldots,d_n^+]$

$B = [d_1^-,\ldots,d_n^-]$

$S_A \subset A \qquad \bar{S}_A = A - S_A$

$S_B \subset B$

$\alpha(S_A)$ = cardinality of the set S_A

and

$d_x^- \in S_B \Leftrightarrow d_x^+ \in S_A \qquad x = 1,\ldots,n$

Proof: [C-2, Chapter 6]

Corollary 2.3-1 -- A necessary and sufficient condition for the set $[(d_i^+,d_i^-)]$ to be realizable as the degree pairs of an n-mode (∞,∞)-digraph is

$$\Sigma\, d_i^+ = \Sigma\, d_i^-$$

Proof: Let $p = \infty$, $s = \infty$ in the theorem.

The corollary is the representation condition for a digraph (not necessarily connected) without constraints on p or s.

Corollary 2.3-2 -- The set $[(d_i^+,d_i^-)]$ is realizable as the degree pair set of an n-node digraph without self-loops if and only if

1) $\sum_{i=1}^{n} d_i^+ = \sum_{i=1}^{n} d_i^-$

2) $\sum_{\substack{i=1 \\ i\neq j}}^{n} d_i^+ \geq d_j^- \qquad j = 1,2,\ldots,n$

Proof: Let $s = 0$ $p = \infty$ in the theorem.

A realization of an arbitrary set $[(d_i^+,d_i^-)]$ need not be unique. Let $[G_i(R)]$ represent the set of all realizations, the problem of generating $G_j(R)$ from a given realization is now examined.

Definition 2.3-2 -- (d-invariant transformations) -- Two (p,s)-digraphs $G_i(R)$ and $G_j(R)$ are d-invariant if there exists a one-to-one correspondence between nodes preserving the degree pairs for every node. (Note that d-invariant graphs need not be isomorphic.)

One can define a sequence of elementary (p,s) d-invariant transformations between digraphs such that the result of each step is a d-invariant digraph [C-2]. Any two (p,s)-digraph realizations $G_i(R)$ and $G_j(R)$ can be transformed as $G_i \rightarrow G_j$ by a finite sequence of (p,s) d-invariant

graph transformations. Hence the set of all realizations $[G_i(R)]$ is (p,s) d-invariant and can be considered equivalent from this point of view [C-2]. The invariant transformations can be applied to study the notion of biotopological mappings introduced by Rashevsky in his theory on organismic sets [R-4,R-5,R-7]. The set $[G_i(R)]$ can be viewed as different physical (biological) realization of an identical input-output specified relational system. From the standpoint of (p,s) d-invariant transformations some problems of sociology and biology can be studied in a unified relational framework.

Definition 2.3-3 -- Two (p,s)-digraphs $G_a(R)$ and $G_b(R)$ realize the same biological relational system if there exists a finite sequence of (p,s) d-invariant graphs $[G_i(R)]$ i=1,...,n such that $G_1(R) = G_a(R)$ and $G_n(R) = G_b(R)$.

The problem of constructing an (M,R)-graph from the degree pair set $[(d_i^+,d_i^-)]$ is important in its own right. The procedures however require more graph theory than is possible to include within the confines of the present thesis. A forthcoming paper will examine this same problem in detail. To state the results on the realizability of connected digraphs we need the following.

Lemma 2.3-1 [C-2] -- Let G be a (p,s)-digraph containing k graph components (disconnected subgraphs) with $p \neq 0$ and $k \geq 2$. If G has no isolated vertices and if one of the graph components contains a circuit (need not be directed) then there exists a (p,s) d-invariant digraph transform of G with k-1 graph component.

Proof: The proof depends on properties of bipartite graphs and d-invariant substitutions [C-2,Chapter 6].

Theorem 2.3-2 -- The necessary and sufficient conditions for a set $[(d_i^+,d_i^-)]$ to be realizable as the degree pair set of a connected (p,s)-digraph with n vertices ($n \geq 2$) are

1) Conditions of theorem 2.3-1 be satisfied

2) $d_i^+ + d_i^- \neq 0 \quad i = 1,2,\ldots,n$

3) $p \neq 0$ and $\sum_{i=1}^{n} d_i^+ \geq (n-1)$

Proof: $\Leftarrow$ Let G be a connected (p,s)-digraph realization of $[(d_i^+,d_i^-)]$, condition (1) is true by theorem 2.3-1. $d_i^+ + d_i^- \neq 0$ since G is connected, similarly for $p \neq 0$. The number of edges in a connected (p,s)-digraph is at least (n-1), which is the number of edges in a spanning tree. Hence $\sum_{i}^{n} d_i^+ \geq (n-1)$.

$\Rightarrow$ by theorem 2.3-1 there exists a (p,s)-digraph realization. We have to show it is connected. Assume there are at least two graph components ($k \geq 2$). We may assume there are no circuits, otherwise using Lemma 2.3-1 G can be shown connected. If all components of G are circuitless then the number of edges in G is (n-k) so $\sum_{i}^{n} d_i^+ = n - k \geq (n-1)$ which implies $k \leq 1$, but $k \geq 2$ by assumption and is clearly impossible.

We now state the conditions for a strongly connected, directed and self-loopless graph. By the previous discussions on non re-establishable modules the hypotheses guarantee the existence of a relational system that is maximally vulnerable.

Theorem 2.2-3 -- The necessary and sufficient conditions for $[(d_i^+,d_i^-)]$ to be realizable as degree pair set of a strongly-connected digraph without self-loops are:

1) conditions of corollary 2.3-2 are satisfied,

2) $\min[(d_i^+,d_i^-)] \neq 0 \quad i = 1,\ldots,n.$

Proof:

$\Leftarrow$ 1) obvious from corollary 2.3-2,

2) $\min[(d_i^+,d_i^-)] \neq 0 \quad i = 1,\ldots,n$ implies the graph is connected.

$\Rightarrow$ Proof sufficiency [C-2, Chapter 6].

Corollary 2.3-3 -- If the set $[(d_i^+,d_i^-)]$ is realizable as the degree pairs of a self-loopless digraph then, the necessary and sufficient condition for all such realizations to be acyclic is that $\min[(d_i^+,d_i^-)] \neq 0$ for at most one i, $i = 1,\ldots,n$.

Proof: $\Rightarrow$Let G be self-loopless realization of the set with the property, $\min[(d_{io}^+,d_{io}^-)] \neq 0 \quad i = i_o$ for at most one i_o, Now a directed circuit of length greater than one contains at least two vertices with $\min[(d_i^+,d_i^-)] \neq 0$ hence G is acyclic.

$\Leftarrow$ Assume an acyclic realization G exists, such that $\min[(d_i^+,d_i^-)] \neq 0$ for at least two vertices. Let i,j be the vertices. Then there exist edges (u,i), (i,v), (y,j), (j,z) in G. Now G is acyclic and so $u \neq i \neq v$ and $y \neq j \neq z$. Replace edges [(u,i), (i,v), (y,j), (j,z)] by [(u,v), (i,i), (j,j), (y,z)]. The substitution (d-invariant) yields a d-invariant graph G' of G with two self-loops. If in G' now replace the two self-loops by edges (i,j) and (j,i) a directed graph G_2

(d-invariant of G) results. G_2 contains at least one directed circuit which is a contradiction.

The corollary unfortunately does not guarantee the existence of an acyclic self-loopless representation, only the properties of an acyclic characterization are defined.

In certain cases the set of realizations $[G_i(R)]$ reduces to a single element. These unique realizations may be of significant biological interest serving as prototypes of maximally constrained realization conditions. A set of conditions is said to maximally constrain a relational graph if the set of realizations $[G_i(R)]$ reduces to a unique graph. The study of this problem requires the same graph topological background as the algorithms for constructing digraphs, and will be included in a separate paper.

The (M,R)-digraph can be interpreted to represent the metabolic activity of an organism, where the internal dynamics are described via the inverse graph in the format of state-space equations. A connected graph represents a single organism. If conditions of theorem 2.3-2 are not satisfied then within the confines of relational systems there is no single organism realizing the constraints.

Furthermore, even when conditions of the theorem are satisfied the resulting graph need not be equivalent to an (M,R)-graph unless all edges in the R-graph originate at terminals of the M-graph, and $p \leq 2$, one has to isolate the R-graph and with respect to the R-graph define the set of potential terminal modules of the M-graph. This is a problem one is

confronted with in the synthesis of relational systems. We have presented certain conditions (constraints) in the theorems of this section, under which relational systems may be representable as (M,R)-graphs. The results shed some light on the nature and number of the module interactions possible in a relational system given the input-output specification of each module in the system. The set of environmental outputs are prescribed by the covering hypothesis, but the environmental inputs are independent of the realization and consequently have to be derived from the fine structure of the individual modules.

The fine structure problem was examined in Chapter I under the topic of assembling the system from the $\bar{C}_i$-equivalence classes.

2.4 (M,R)-Systems and Surface Structures

The deep structure developed in Chapter I defined the various levels of dynamical invariance with respect to the activity class $[A_1,\ldots,A_n]$ of a given system. It was assumed each of these activities A_i had a measurably distinguishable feature class $[f_{i1},\ldots,f_{in_i}]$ used in defining the activities in the observer-system interaction. The derived hierarchical structure denoted by the ordered 4-tuple $[T_n(M_n),\bar{C}_i(M_n),\tau_{ij}(\bar{C}_i),D_{ijk}(\bar{C}_i,\tau_{ij})]$ defined the levels of invariance with respect to each A_i, although the generative topology with the morpheme basis required knowledge of the complete activity set $[A_1,\ldots,A_n]$.

With respect to a given generation of biological organism the $\bar{C}_i$-equivalence classes (modules) are fixed. (From this point of view the level of self-organization may be considered to be part of the genetic

structure.) Hence, for an individual organism only the 3-tuple $[\bar{C}_i(M_n),\tau_{ij}(\bar{C}_i),D_{ijk}(\bar{C}_i,\tau_{ij})]$ is required to define the deep structure (Definition 1.3-1). To bring the deep structure closer to biological reality the notions of finite life-times, possibility of component inhibition and environmental couplings are needed. These concepts are readily available in the framework of (M,R)-systems.

The graph topology developed for the deep structure corresponds to the M-graph of relational systems. With the aid of the feedback relation we can superimpose on the metabolic structure represented by the M-graph a new graph with identical vertex set representing the repair functions in the system. This repair capacity is embodied in the R-graph. The resulting (M,R)-system, now based on the analysis of the deep structure will be called the surface structure corresponding to the activity set $[A_1,\ldots,A_n]$. By means of the surface structure and the use of the inverse graph we can observe the environment-system interaction from different vantage points. Problems related to system activity, structural complexity, dynamical stability, relational stability and vulnerability may be simultaneously studied in the same framework.

Definition 2.4-1 -- Given a system deep structure with an activity class $[A_1,\ldots,A_n]$, with respect to the deep structure $[T_n(M_n),\bar{C}_i(M_n),\tau_{ij}(\bar{C}_i),D_{ijk}(\bar{C}_i,\tau_{ij})]$ an (M,R)-system is a surface structure if the M-graph corresponds to an admissible topology τ_{ij}.

In section 2.3-1 we have seen that if the graph topology is defined via a vertex set and the incidence sets (degree pairs) several possible

realizations of an (M,R)-system may exist, which are equivalent from the point of view of (p,s) d-invariant transformations.

Hence, for any deep structure there may be a class of surface structures realizing that particular deep structure.

The environment may limit the number of possible realizations and is considered to be the context within which the deep structure surfaces via the (M,R)-system realization. If the realization is dependent on the environment it will be called context-sensitive, otherwise it is context free. In a context-free situation all possible realizations of the (M,R)-graph may serve as a surface structure whereas the set of context-sensitive realizations are constrained by environmentally produced selective criteria. Context-free realizations are essentially environmental constraint independent and are subject only to the Principle of Adequate Design, whereas context-sensitive surface structures are selected on the basis of the Principles of Optimal Design [R-5,R-7,M-4,R-17,R-23].

2.5 Optimization on (M,R)-Graphs

At each level of the hierarchical system deep structure certain dynamical and structural features are selected for, based on some measure of system performance and subject to operational and environmental constraints. The selection of an appropriate realization of an (M,R)-system from the class of all possible surface structures $[G_i(M,R)]$ is accomplished at the level of self-organization. The biological system surfaces in the environment with a fixed module structure and a specified set of interconnections in the model. The adaptive transitions are equivalent to the

perturbations of the graph topology. If the dynamical responses can be handled as a routine regulation problem or by variation of system dynamical parameters the M-graph is invariant. There is a definite ordering of the degree of system response depending on the magnitude and frequency of environmental perturbations. Within this context if a system performs graph topology transitions based only on the history of environmental forcings, it can be viewed as a learning system. Thus (M,R)-graph transitions fall into two categories;

a) Environmentally forced. (The system either adjusts or faces extinction.)

b) Internally initiated. (The system samples the dynamical history and searches for an optimal graph topology.)

The factors influencing the (M,R)-graph topology fall into the following classes:

1) Dynamical stability,

2) Relational stability,

3) Vulnerability,

4) Capacity to process information.

Quantitative measures can be developed to define the above system characteristics. Given an (M,R)-system the (M,R)-graph representation decomposes into the M-graph and R-graph. Since metabolic (dynamical) activities take place in the domain of the M-graph and if, for example, energy is a quantity processed then potentials and flows (x,y) continually reorient the M-graph. Centrality and non re-establishability of modules

is to be understood in this perspective. For a fixed instance of time $t=t_o$ the graph orientation is fixed and results derived on non re-establishability can be applied. The source for the reorientation process is the system dynamics superposed on the M-graph topology.

Therefore, dynamical activities have a dual function in the system. On the one hand dynamics serve as mechanisms of homeostasis and regulation, on the other the M-graph is oriented in a manner to reduce system vulnerability. The R-graph cannot be influenced in the orientation sense by the internal dynamics, but the R-graph structure (feedback relations) can change under an adaptive transition. If the dynamics are linear the qualitative measure for each of the four classes influencing the optimization process can be given,

1') Dynamical stability -- if $\dot{\bar{X}} = A\bar{X} + Bu$ is the state equation and $(\lambda_1,\ldots,\lambda_n)$ are the eigenvalues of A. Then sufficient condition for dynamical stability is $\text{Max}\,[\text{Re}\,\lambda_i] \leq 0$ where $\text{Re}\lambda_i$ = real component of the complex eigenvalue.

2') Relational stability -- the index of relative complexity R_C is maximized (Definition 1.4-3). If the (M,R)-graph consists of n nodes.

$$R_C(n) = \frac{C_F}{\text{Max } C} = \frac{2(p - n + 1)}{n^2 - 3n + 2} \qquad n \geq 2$$

$\text{Max}(2) \overset{\Delta}{=} 2$ for directed graphs where the actual cyclomatic number $p - n + 1$ is to be maximized. Obviously $R_C(n) \leq 1$

3') Vulnerability -- The number of (M,R)-graph proper directed feedback circuits (Theorem 2.2-1) is minimized.

4') Information capacity -- The order of the state vector X is maximized (Definition 1.45b).

For a fixed (M,R)-graph (adaptive state) the only variable is the dynamical property. Within the bounds of stability ($Max[R_e\lambda_i] \leq 0$) the orientation of the M-graph is controlled by feedback dynamics to minimize system vulnerability. The order of the state vector, the index of relative complexity and the R-graph are invariant for a fixed adaptive state.

If the re-orientation of the M-graph is of high frequency then non re-establishable components may survive inhibition. For example, if a non re-establishable module M_i has the capacity to survive inhibition for a time interval $t_i(M_i)$, then a reorientation of the M-graph in time less than $t_i(M_i)$ guarantees the survival of M_i.

Given the characteristic survival times $t_j(M_i)$ $j = 1,\ldots,m$, following inhibition of each non re-establishable module, the dynamical re-orientations of the M-graph can be increased in frequency to exceed $Min[t_j(m_j)]$.

Unfortunately by increasing the reorientation frequency the likelihoodof inhibiting a central component is also increased. To determine the optimal reorientation frequency a suboptimal problem has to be solved, constrained now by the distribution of central components, the real part of the eigenvalues of the matrix A_i and the characteristic survival times. The whole process of optimization can be decomposed into levels of suboptimal processes such that the results of one level are used

as inputs to the next higher level. In case the dynamics are nonlinear an appropriate linearization may be derived or some other measure of stability defined is used.

The solution effort in decomposing an optimization problem into suboptimal stages for hierarchical systems was examined by J. Pearson in a cybernetic context [P-3]. It is interesting to note that every constraint on the system introduces additional complexities into the optimization process. Every new constraint contributes a new system measure to be incorporated into a performance index. If the constraints are sufficiently strong then the set of solutions may reduce to a single element and hence the system is specified uniquely thru its constraints. The main problem is to locate a system measure that is characteristic of all the constraints and only of these. In biological systems specialization of constraint system measures is not well developed, but in cybernetics the duality between specifying the system directly or thru its constraints is well recognized [C-1]. We shall not develop such an approach here but note that the selection of a context-sensitive realization of an (M,R)-graph is a problem of optimization based on environmentally induced constraints.

We now propose a solution of the generalized feedback relations required to realize a relational (M,R)-graph. Although an acyclic realization eliminates the need for a vulnerability constraint the question remains whether the (M,R)-graphs are representations of real biological systems.

Theorem 2.5-1 -- Assume the degree pair set $[(d_i^+,d_i^-)]$ is realizable as a directed self-loopless graph. If $\text{Min}[(d_i^+,d_i^-)] \neq 0$ for at least two i then among all the realizations there exists at least one with a directed circuit.

Proof: Corollary 2.3-3.

The theorem implies that among all possible realizations of an input-output set $[(d_i^+,d_i^-)]$ there must be at least one with a directed circuit, if $\text{Min}[(d_i^+,d_i^-)] \neq 0$ for two modules.

For relational systems if every module receives an R-feedback from some terminal and if the M-graph is connected then $\text{Min}[(d_i^+,d_i^-)] \neq 0$ for every terminal and every module connected to a terminal. Hence in the set $[G_i(M,R)]$ there exists at least one with a non re-establishable module. Under the generalized feedback relation of every R_i receiving an input from some terminal M_k we can guarantee at least one (M,R)-graph with a directed proper feedback circuit. Therefore when Rosen's covering hypothesis is relaxed and the generalized feedback relation holds, the non re-establishability property is still valid for at least one representation the class $[G_i(M,R)]$.

If operational time lags are introduced in the system for the repair components Ri then a module may become non re-establishable even though the proper feedback circuit does not exist (Examples 2.2-1b and 2.2-2). Generally, if any terminal M_k fails that produces a feedback signal to an R_i while the module M_i is being replaced then M_i is non re-establishable. Furthermore, directed circuits in the R-graph may have the

same effect as proper feedback circuits in the (M,R)-graph. Given a R-graph directed circuit with vertices $[(M_1,R_1),(M_2,R_2),\ldots,(M_p,R_p)]$ if an R_i $i \leq i \leq p$ requires a time $t_i(R_i)$ to replace its dual M_i and if $t_i(R_i) \geq t_j(M_j)$ then eventually all M_j will fail when as M_j is inhibited, since all life-times $t_j(M_j)$ will be exceeded before M_i is replaced. Consequently a necessary condition for modules connected by a directed path in the R-graph to be re-establishable are:

a) If M_i is inhibited at time $t = t_o$, then all terminals producing input to R_i are functioning and have life expectancy longer than $t_i(R_i)$.

b) The time required to replace M_i is no greater than the expected life-times of all R_j to which M_i serves as an input if M_i is a terminal.

These are just partial results, to completely determine the effect on the system the inhibition of an M_i at $t = t_o$ all the life expectancies at $t = t_o$ of each module have to be known in addition to the individual survival times under state of inhibition. The fact that the M-graph is continuously reoriented greatly complicates the problem. It is of interest to determine in advance if an (M,R)-graph yields strong-connectedness for an arbitrary orientation.

Definition 2.4-1 -- (Orientability) -- A non-directed connected graph is orientable if under an arbitrary orientation of the edges the resulting graph is strongly connected.

Hence, given the basic interactions between the vertex pairs (M_i,R_i) both in the M and R domain the question is posed whether the (M,R)-graph

is orientable. (The problem may be considered at two separate levels.)

a) With R-graph orientation fixed, determine an appropriate M-graph orientation to yield a strongly connected (M,R)-graph.

b) Find an (M,R)-graph with strong connectivity, specify the R-graph (feedback relations) along with a corresponding terminal module set such that there are a minimal number of central components.

Theorem 2.4-2 -- A connected (M,R)-graph is orientable if every edge of $G(M,R)$ is contained in at least one circuit.

Proof: If there exists an edge not contained in a circuit then $\text{Min}[(d_i^+,d_i^-)] = 0$ for at least two nodes and conditions of theorem 2.3-3 are violated.

if (M,R)-graph is strongly connected let M_i be an arbitrary node for any M_j there is a directed path from M_i to M_j and conversely. The union of the two paths forms a circuit with M_i as origin.

The theorem indicates that strong-connectivity can be deduced form the circuit matrix of the system. If every column is non-empty in the circuit matrix the (M,R)-graph is orientable as a strongly-connected graph. In an optimization process for realizing an (M,R)-graph, if the circuit matrix is specified with an empty column the resulting (M,R)-graph cannot be strongly connected for any orientation.

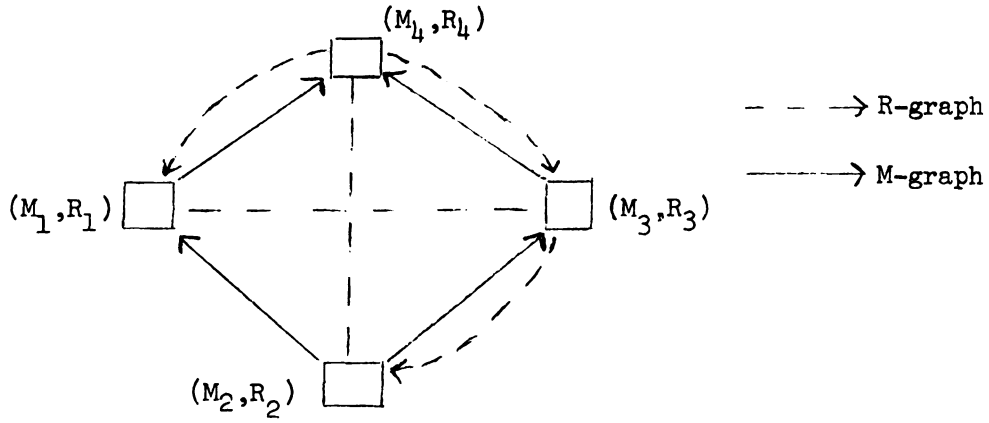
Given a surface structure realization $G_i(M,R)$ of a particular deep structure $[T_n(M_n),\bar{C}_i(M_n),\tau_{ij}(\bar{C}_i),D_{ijk}(\tau_{ij},\bar{C}_i)]$ for every activity A_i of the system (S), the dynamical reorientations of the (M,R)-graph yield

a different incidence set $[(d_i^+, d_i^-)]$ for every possible orientation of the M-graph. The initial specified input-output set $[(d_i^+, d_i^-)]$ generates a sequence of possible dynamical alternatives.

Example 2.4-1 -- Given input-output degree pair set

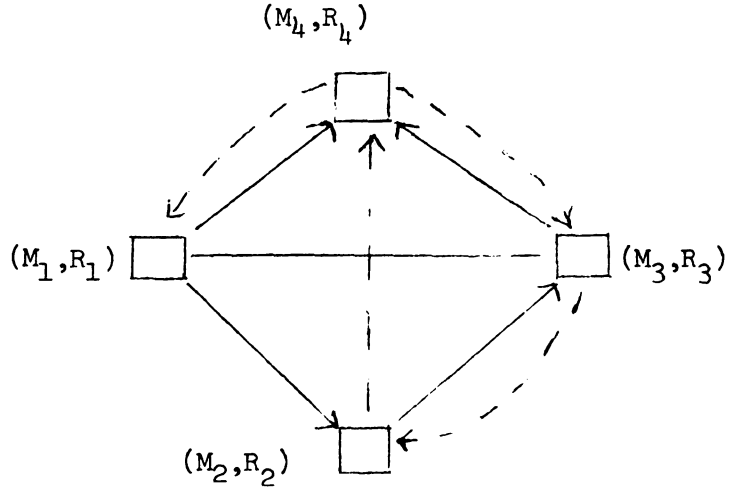
$[(1,3),(3,1),(3,2),(2,2)]$

a) Realization as a (1,0)-directed (M,R)-graph with terminal module set $T_s = [M_2, M_3, M_4]$



b) One possible dynamical reorientation as (1,0)-directed (M,R)-graph.

$[(2,3),(1,2),(3,2),(2,2)]$



It can be shown that in the above example there are no other dynamical reorientations (with R-graph invariant) that satisfy the (1,0)-directed graph conditions.

Any other M-graph orientation yields a graph with at least two strictly parallel edges in the (M,R)-graph. In general given the adjacency matrices V(M) and V(R) the set of all possible dynamical reorientations of a (1,0)-directed graph are obtained by perturbing the entries of the V(M) matrix subject to the condition that,

a) V(R) is invariant,

b) V(M,R) has no entries equal to two.

(In each matrix V(R), V(M) the entries are zero or one.)

The set of all possible dynamical reorientations as a (p,s)-directed graph depends on the

a) M-graph,

b) Specified terminal module set $[M_{k_1},\ldots,M_{k_1}]$,

c) R-graph (invariant).

For every dynamical reorientation the results of theorem 2.2-1' can be applied to determine the central and non re-establishable components.

A perturbation consisting of reorienting a single edge in the M-graph may be represented by a relatively simple perturbation of the degree pair set $[(d_i^+,d_i^-)]$. If an edge in the M-graph is reoriented (Example 2.4-1) the degree pair set is perturbed for two entries. Let the edge exist between M_i and M_j. Then the original incidence pairs (d_i^+,d_i^-), (d_j^+,d_j^-) change to $(d_i^+ + 1,\ d_i^- - 1)$ and $(d_j^+ - 1,\ d_j^- + 1)$ if the edge

existed as an (M_j, M_i) orientation. The new incidence set is determined by substituting $[(d_i^+ + 1, d_i^- - 1), (d_j^+ - 1, d_j^- + 1)]$ for $[(d_i^+, d_i^-), (d_j^+, d_j^-)]$. Any reorientation is computable by the above scheme. If the M-graph consists of p edges then the theoretical maximal of dynamical reorientations is p^2. Of course not all of these need satisfy the (p,s)-directed graph conditions. However, the computation to determine whether the perturbed incidence set satisfied the (p,s)-conditions is straightforward. For every M-graph edge two entries of the matrix $V(M)$ are changed. The composite graph $V(M,R)$ is altered analogously. The (p,s)-condition is satisfied if the new $V(M,R)$-graph has no diagonal entries greater than s_1 and no off-diagonal entries greater than p. Hence all perturbations of the incidence set $[(d_i^+, d_i^-)]$ are allowed as long as $[v_{ij}] \in V(M,R)$ is such that $[v_{ij}] \leq s$ and $[v_{ij}] \leq p$.

CHAPTER III

STABILITY OF ADAPTIVE DYNAMICS

3.1 State Space of Adaptive Transitions

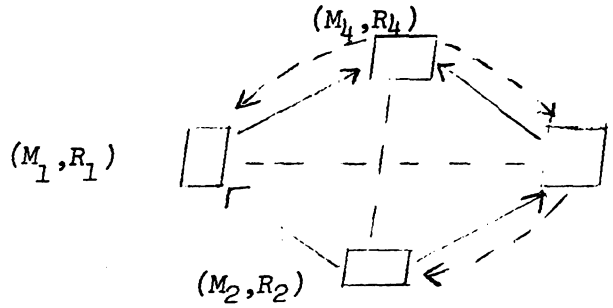
In this chapter a framework for adaptive transitions is developed based on the structural properties of the (M,R) graph. Certain questions related to the dynamical stability properties of interacting large-scale systems will be investigated via the techniques developed by Siljak [S-1,S-2,S-3,S-5]. As pointed out in the section on optimization the first constraint imposed on the (M,R)-system is dynamical stability with respect to the system dynamics $D_{ijk}(\tau_{ij},\bar{C}_i)$ imposed on the (M,R)-topology.

If the modules of the (M,R)-system are constrained to participate in the total system activity by an (on,off)-criterion, then a convenient condition of the permissible topology τ_{ij} is based on the (M,R)-graph. Given a module M_i in the realization of an (M,R)-system, the module is

a) Off: if M_i ceases to function as a separate node in the M-graph.

b) On: if M_i exists as a separate node in the M-graph.

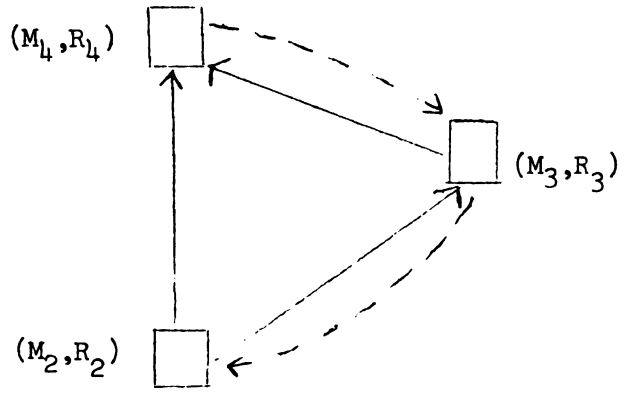
Example 3.1-1 -- (2,0)-directed (M,R)-graph.



$T_s = [M_2,M_3,M_4]$

a) (M,R) on

b) (M_1,R_1) off.



The R-graph edges corresponding to (M_1,R_1) are deleted and all M-paths passing through (M_1,R_1) are replaced by one edge.

Given a realization $G_i(M,R)$ of an input-output at $[(d_i^+,d_i^-)]$ a subset of the adaptive states is defined to be the set of all (M,R)-topologies resulting from the(on,off)-state of any module M_i.

Definition 3.1-1 -- With respect to a fixed realization $G_i(M,R)$ of the incidence set $[(d_i^+,d_i^-)]$ as a (p,s)-graph the adaptive states are the set of all permissible topologies τ_{ij} resulting from the (on,off)-state of any M_i $i = 1,\ldots,n$.

The above definition is a special case of definition 1.2-6, with the (on,off)-state of each M_i providing the perturbations of τ_{ij}. Obviously if the (p,s)-condition is satisfied for $G_i(M,R)$ then deletion of edges (some M_i in an off-state) also satisfy the condition. For a specific adaptive state, corresponding to $[M_1,\ldots,M_k]$, $[M_{k+1},\ldots,M_n]$ where modules in first set are on, and the second set off, the (M,R)-graph topology can be reoriented via the system dynamics.

If the dynamical stability properties of the free-body forms for each M_i are known under certain assumptions the stability of the total (M,R)-system can be determined (Section 3.3). If a terminal M_k is off in the system then the covering hypothesis for the (M,R)-system may be violated. In Example 3.1-1 the cessation of (M_3,R_3) node implies the termination of the feedback relation (M_3,R_1). To eliminate problems arising from the existence of modules without R-graph feedback, we restrict the (on,off)-condition to non-terminal modules. Therefore, given an initial realization $G_i(M,R)$ with a terminal module set $[M_{k_1},\ldots,M_{k_j}]$, for any adaptive graph transitions τ_{ij} all elements of the terminal set are active.

Definition 3.1-2 -- (Adaptive (M,R)-states) -- A permissible adaptive state (Definition 3.1-1) is an (M,R)-state if every terminal in the original $G_i(M,R)$ realization is active.

A particular realization of the deep structure as an (M,R)-system constrains the set of possible topologies τ_{ij} by means of the covering hypothesis.

The (M,R)-system may perform an adaptive transition whenever

a) The system dynamics are unstable in the present state and cannot be stabilized by parameter feedback,

b) The degree of relative complexity R_C is increased in the next adaptive state,

c) The number of non re-establishable components is reduced in the next state,

d) The order of state vector is increased in the next state.

Any combination of the above factors may also result in an adaptive transition. It is difficult to establish an order of importance for transitions, but dynamical stability and low vulnerability appear to dominate [R-11,A-3,R-10]. However, stability and vulnerability may impose different constraints in the system graph and a dynamically unstable system may possess low vulnerability with respect to the environment. The reason for the above conflict arises from the fact that vulnerability is defined for the (M,R)-graph, whereas system dynamics are superposed on the graph, and as demonstrated by May's example, relational and dynamical stability are not necessarily dependent. This result is not very surprising when one considers that vulnerability, relational stability and information processing capacity are defined on structural features of the system which usually persist in time whereas dynamical stability is a more transient feature. It is possible to introduce Markov processes to account for the dynamics of adaptive transitions in a stochastic framework [K-2,K-4].

For such an approach to be useful a relatively complete list of the factors influencing adaptive changes must exist. We have isolated only four of these factors and presumably many others exist that are just as important. There is no common denominator for the definition of adaptive changes in dynamical system, but generally structural modifications due to external or internal influences are recognized as examples of adaptation [R-5,S-6,C-3,L-8,M-7]. In the following sections we shall be concerned

with the dynamical stability properties of (M,R)-systems specified through the free-body models of the constituent modules.

3.2 Dynamical Description of Large-Scale (M,R)-Systems

Let the state space representation for a relational (M,R)-system be given as

$$\dot{\bar{X}} = F(t,\bar{X}) \qquad \bar{X}(t) \in R^n \tag{3.3}$$

Let $F: TxR^n \to R^n$ be globally Lipschitz continuous, so that unique solutions to (3.3) exist and are continuous for all initial conditions $(t_o,\bar{X}_o) \in T \times R^n$ [H-1]. The (M,R)-system is composed of the n $\bar{C}_i$-equivalence class generated modules M_i. Assume the free-body model for each M_i is

$$\dot{\bar{X}}_i = F_i(t,\bar{X}_i) \qquad \bar{X}_i \in R^{n_i} \qquad R^{n_i} \subset R^n \tag{3.4}$$

Let the constrained interconnected M_i be modeled by

$$\dot{\bar{X}}_i = F_i(t,\bar{X}_i) + \sum_{i=1}^{n} c_{ij}\, G_j(\bar{Y}_j)$$

$$\bar{Y}_i = H_i(\bar{X}_i) \tag{3.5}$$

Here $\bar{X}_i$ is the state vector for the i-th module M_i, $\bar{Y}_i$ is the output of the M_i and G_{ij} are the interconnection constraints.

$$F_i : T \times R^{n_i} \to R^{n_i}$$

$$H_i : R^{n_i} \to R^{m_i}$$

$$G_{ij} : R^{m_j} \to R^{n_i}$$

such that G_{ij} are Lipschitz continuous

$$||G_{ij}[\bar{Y}_j]|| = ||G_{ij}[H_j(\bar{X}_j)]|| \leq e_{ij}||\bar{X}_i|| \quad i,j = 1,2,\ldots,n \tag{3.6}$$

and $||\cdot||$ is the Euclidean norm of a vector.

$$e_{ij} = \begin{cases} 1 & \text{if } M_j \text{ acts on } M_i \\ 0 & \text{if } M_j \text{ does not act on } M_i \end{cases}$$

In terms of the τ_{ij} topology, if M_j is a node in an adaptive state and if the M-graph directed edge (M_j, M_i) exists then $e_{ji} = 1$. The total state vector is $\bar{X} = (\bar{X}_1, \ldots, \bar{X}_n)$ and the dimension of $\bar{X}$ is the sum of the dimensions of the $\bar{X}_i$.

An interconnection matrix E_i (nxn) can be represented by the adjacency matrix $V(M)$ of the M-graph for any τ_{ij}.

The structural perturbations of the (M,R)-system corresponding to the (on,off)-condition of each M_i yield a class of adaptive states (subset of τ_{ij} topologies). If a module M_i is in the off-state all $e_{ik} = 0$, (the interconnection matrix E has a zero k-th column). A module either participates in the system metabolic activity or it is totally in the off-state and no constituent morpheme interacts with the system. This implies the M_i-nodes of the M-graph are not subdividable for adaptive transitions. If the M_i is off in the metabolic process so is all its R-graph feedback edges. To express the structural perturbations we consider a real (nxn) matrix $A = [a_{ij}]$ and define the q x q principal submatrix A_q as

$$A_q = A\begin{pmatrix} i_1 i_2 \cdots i_q \\ i_1 i_2 \cdots i_q \end{pmatrix} = \begin{bmatrix} a_{i_1 i_1} & \cdots & a_{i_1 i_q} \\ a_{i_q i_1} & \cdots & a_{i_q i_q} \end{bmatrix}$$

where

$$1 \leq i_1 < i_2, \ldots, < i_q \leq n \qquad 1 \leq q \leq n.$$

The determinant $D(A_q)$ will be called the principal minor [F-1]. The fundamental interconnection matrix $E_f(M,R)$ is a matrix with zero, one entries corresponding to (on,off)-condition for each M_i for any τ_{ij} topology. All entries corresponding to the terminal modules $[M_{k_i}]$ are invariant ones. (a terminal module is always in an active state) and non-existing interconnections are invariant zeros. A structural perturbation is obtained by manipulating the entries of $E_f(M,R)$ subject to the above stated invariance.

In our framework the $E_f(M,R)$ matrix is constructed from the adjacency matrix $V(M)$ of the original realization $G_i(M,R)$ for the input-output set $[(d_i^+,d_i^-)]$. Hence $E_f(M,R)$ contains the maximal number of entries. An entry $[e_{ij}]_f \in E_f(M,R)$ is one if there exists a corresponding edge in the M-graph of the realization $G_i(M,R)$.

The interconnection matrices E_i are derived from $E_f(M,R)$ by setting an M_i-module in the off state (Example 3.1-1). Each E_j represents a τ_{ij} topology (state of the adaptive space).

The structural changes can be represented by canonical form matrices E_p, which are row-column transformations of E_i into a quasidiagonal form [S-2].

$$E_p = \begin{bmatrix} E_{q_1} & & & \\ & E_{q_2} & & \\ & & \ddots & \\ & & & E_{q_i} \end{bmatrix}$$

From a dynamical viewpoint the E_p matrix sorts the M_i-modules into dynamically independent groups. (The groups need not correspond to the subsystems we have defined in Chapter II Definition 2.1-2.)

Under the assumption that the origin of the state space is a unique equilibrium point for the (M,R)-system and the M_i-module free-body models, i.e.,

$$F(t,\bar{0}) = \bar{0}$$

$$F_i(t,\bar{0}) = \bar{0}$$

Certain conclusions can be derived about the (M,R)-system stability from the stability behavior of the M_i-module free-body dynamics

3.3 Connective Stability of (M,R)-Systems

We now provide a definition of the dynamical stability of an (M,R)-system, which is invariant under the structural perturbations.

Definition 3.3-1 -- (Connective Stability) -- The equilibrium state $\bar{X} = \bar{0}$ of a free dynamic (M,R)-system is connectively stable if and only if it is stable in the sense of Lyapunov for all canonical interconnection matrices E_p. (For definition of Lyapunov stability see Koenig, et al. [K-5].)

A necessary condition for connective stability of the (M,R)-system is the stability of each M_i-module. This can be seen by setting E_p equal to the zero matrix; with no interconnections each M_i must be stable separately. However, the perturbation of the $E_f(M,R)$ matrix corresponds to the inhibition of a module, hence the necessary condition is trivially satisfied for each disconnected (inhibited) module.

Definition 3.3-2 -- (Exponential connective stability) -- The equilibrium state $\bar{X} = \bar{0}$ of a free dynamic system S is exponentially connectively stable if and only if there exists $\alpha > 0$, $\beta > 0$ independent of initial conditions (t_o, X_o) such that

$$||\bar{X}(t,t_o X_o)|| \leq \alpha \, || \bar{X}_o || e^{-\beta(t-t_o)} \quad \forall t \in T$$

for all $(t_o, \bar{X}_o) \in T \times R^n$ and all canonical interconnection matrices E_p.

Lemma 3.3-1 -- The equilibrium state $\bar{X}_i = \bar{0}$ of a free-body dynamic M_i-module is exponentially stable if and only if there exists a positive definite function $v_i(t, \bar{X}_i)$ on $T \times R^{n_i}$ such that

$$\mu_{i_1}||\bar{X}_i|| \leq v_i \leq \mu_{i_2}||\bar{X}_i|| \tag{3.7}$$

$$\dot{v}_i \leq -\mu_{i_3}||\bar{X}_i||$$

$$||\text{grad } v_i|| \leq n_{i_4}$$

where

$\mu_{i_1}, \mu_{i_2}, \mu_{i_3}, \mu_{i_4}$ are positive numbers

and

$$\dot{v}_i = \frac{\partial}{\partial t} v_i + (\text{grad } v_i)^T F_i$$

Proof: [S-2]

Theorem 3.3-1 -- (Siljak) -- The equilibrium state $\bar{X} = \bar{0}$ of the free dynamic (M,R)-system is exponentially connectively stable if the elements

$$a_{ij} = \delta_{ij} \mu_{i2}^{-1} \mu_{i3} + e_{ij} \xi_{ij} \mu_{jl}^{-1} \mu_{i4} \tag{3.8}$$

of the real (nxn) matrix $A = [a_{ij}]$ satisfy the inequalities.

$$(-1)^q D(A_q) > 0 \quad \forall q = 1,2,\ldots,n \tag{3.8'}$$

corresponding to the fundamental interconnection matrix $E_f(M,R)$.

(δ_{ij} is the Kroenecker delta.)

Proof: To prove the theorem we need the following results from stability of dynamical systems and matrix theory.

(R1) Let $\bar{v}(t,t_o,v_o)$ be a solution of the differential inequality $\dot{\bar{v}} \leq A\bar{v}$ for $\bar{v}_o = \bar{v}(t_o;t_o,v_o)$ and let $\bar{r}(t,t_o,v_o)$ be a solution of the comparison equation $\dot{\bar{r}} = A\bar{r}$ for

$\bar{r}_o = r(t_o,t_o,r_o)$. If $\bar{v}_o = \bar{r}_o$ and all $[a_{ij}] \geq 0$ and real, then $\bar{v}(t,t_o,r_o) \leq \bar{r}(t,t_o,r_o)$ $\forall t \in T$ [B-3,W-1].

(R2) A real (nxn) matrix $A = [a_{ij}]$ with $a_{ij} \geq 0$ for $i,j = 1,2,\ldots,n$ $j \neq i$ has all eigenvalues λ_k with negative real parts if and only if $(-1)^q D(A_q) > 0$ is satisfied [L-1].

Now the proof of the theorem:

The total time derivative along system trajectories is given by

$$\dot{v}_i = \frac{\partial}{\partial t}\dot{v}_i + (\text{grad } v_i)^T \left(\sum^n e_{ij}\, G_{ij}[H_j(\bar{X}_j)]\right) \tag{3.9}$$

Apply inequalities (3.6) and (3.7) and rewrite (3.9) as

$$\dot{v}_i \leq -\mu_{i2}^{-1}\,\mu_{i3}\,v_i + \mu_{i4}\left(\sum_{j=1}^{n} e_{ij}\,\xi_{ij}\,\mu_{j1}^{-1}\,v_j\right)$$

for every interaction G_{ij}. Define an n-vector $\bar{v} = (v_1,v_2,\ldots,v_n)^T$ and form the differential inequality

$$\dot{\bar{V}} \leq A\bar{v}$$

$[a_{ij}]$ are given by (3.8). Apply (R1) and (R2) to satisfy conditions for asymptotic stability. (The system $\dot{\bar{X}} = F_i(t,\bar{X})$ is assymtotically stable if $\underset{k}{\text{Max}}\, R_e(\lambda_k) < 0$, $k = 1,2,\ldots,n$.) Now let $\sigma = \underset{k}{\text{Max}}\, R_e(\lambda_k)$ then there exist two positive numbers $\epsilon < |\sigma|$ and $\rho = \rho(\epsilon)$ such that

$$||e^{A(t-t_o)}|| \leq \rho\, e^{(\sigma+\epsilon)(t-t_o)} \qquad \forall t \in T \tag{3.10}$$

(C-6]. Use inequalities (3.7) and (3.10) along with some properties of Euclidean norms to obtain

$$||\bar{X}(t,t_o,x_o)|| \leq \alpha||\bar{X}_o||e^{-\beta(t-t_o)}$$

for all $(t_o,X_o) \in T \times R^n$ where

$$\alpha = n_1^{-1} n_2 \qquad n_1 = \operatorname{Min}_i \mu_{i2} \qquad n_2 = \operatorname{Max}_i \mu_{i2}$$

$\beta = -\sigma - \epsilon$, $\sigma = \operatorname{Max} R_e \lambda_k < 0$ if system is asymptotically stable. Since $\epsilon < |\sigma| \Rightarrow -\beta < 0$. By definition 3.3-2 the system $\dot{\bar{X}} = F(t,\bar{X})$ is exponentially stable.

The theorem gives us an algebraic criterion (3.8') under which the (M,R)-system stability can be inferred from the stability properties of the M_i-modules. Since the stability of each M_i is a necessary condition for (M,R)-system stability, if an M_i becomes unstable an adaptive transition occurs in the (M,R)-graph. The transition decouples the unstable M_i from the system graph. The question related to the distribution of stable forms (Chapter I) can now be rephrased in light of connective stability.

Definition 3.3-3 -- An interconnection matrix E_{fi} is an immediate neighbor of the matrix E_{fj} if E_{fi} differs from E_{fj} at only one entry.

If a structural perturbation of the (M,R)-system is representable as the modification of the fundamental interconnection matrix $E_f(M,R)$, then the distribution of stable (dynamical) forms depends on the stable configurations of $E_f(M,R)$. Every possible perturbation can be tested by theorem 3.3-1. Let the possible stable interconnections correspond to the fundamental matrices $[E_{f1}, E_{f2}, \ldots, E_{fm}]$. The above distribution of stable forms will be called dense in the set of all structural perturbations if any perturbation E_{fi} is an immediate neighbor of a stable form.

If an adaptive transition consists of perturbing a simple entry of $E_f(M,R)$, then for a particular unstable form it is important to know whether a stable form exists in the immediate neighborhood. A dense distribution of stable forms guarantees such a neighbor. Therefore an (M,R)-system satisfying the density criterion for its adaptive state space has some degree of adaptive flexibility. The results we have stated for connective assymtotic stability relies on the asymptotic stability of the constituent components. Further research is needed to determine under what conditions can the stability criterion for components be relaxed.

CHAPTER IV

CONCLUSIONS

The dissertation is intended to serve as a framework for introducing dynamical principles into relational systems. The first chapter outlined a general systems methodology for identification of components of an arbitrary system underlying a specific observed activity class $[A_1,\ldots,A_n]$. The identification process depends strongly on the observer-system interaction and possesses a generative capacity in reconstructing structure from function. A system deep structure is isolated and invariant structural features identified with respect to environmental perturbations.

In Chapter II a specific surface structure is appended to the deep structure incorporating biological limitations of a system under the finite-lifetime and non re-establishable hypotheses of (M,R)-systems.

A set of stability criteria are proposed for (M,R)-systems and certain optimization problems explored based on these measures. The main applications of the model will be in subsequent investigations of the organizational properties of biological systems within the scope of (M,R)-representations. Questions related to realization of arbitrary input-output specified (M,R)-systems can now be answered by the results of Section 2.3.

Furthermore, if biological function change can be shown to be generated by structural changes in a system, then the state space of

adaptive dynamics can be applied to investigate some problems of biological significance such as degree of specialization and irreversibility of behavioral changes in an (M,R)-system.

The nature of hierarchical organization is somewhat elusive, and whether a correlation exists between the functional levels, as displayed in the system activity, and the inputed structure is debatable. We have offered a plausible connection between the two modes of system description.

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