L. Anolli, S. Duncan Jr., M.S. Magnusson and *G. Riva* (Eds.)
The Hidden Structure of Interaction: From Neurons to Culture Patterns
Amsterdam: IOS Press, 2005 – © All rights reserved - http://www.emergingcommunication.com

1. Understanding Social Interaction: Discovering Hidden Structure with Model and Algorithms

Magnus S. MAGNUSSON

Abstract. The dynamics of interaction between actors making up an organized system is a complex matter where myriads of events are constantly happening within ever changing spatial and temporal contexts that determine the ultimate meaning, effect and function of each event. For the understanding of such systems quantification alone is not enough, matters of pattern and structure must be considered. It is pointed out that most of the behavioural sciences have traditionally accepted repeated patterns among their central concerns. However, tools based on relevant and adequate models and methods have been hard to find in this area and easily available standard statistical methods generally developed for different tasks therefore direct research away from structural approaches. The importance of considering not only order but also real-time when searching for hidden interaction structure is underlined and a real-time model, called the T-system, is advanced together with specifically created detection algorithms and commercially available software (THEME). A particular pattern type, called T-pattern, is the core of the model and its detection is based on the definition of a so called critical interval relation among series of points on a single dimension such as time. It is argued that repeated patterns of the T-pattern type are frequent at highly different levels of organization from information molecules to proteins, neurons, and human verbal and non-verbal interaction. Examples are presented of T-patterns detected in children's interaction as well as interactions among neurons in brain tissue. References are provided to applications of T-pattern analysis within psychology, psychiatry, psychopharmacology, sports science, ethology, and neuroscience. A "bird's eye view" is thus advocated in the search for essential features exemplified by those conserved in genetic materials across all living species where even some genes may be found among practically all life forms. It is suggested that behavioural research is following a logical progression from quantitative to structural analysis somewhat similar to that leading to the discovery of the patterns on DNA molecules, the genetic code and then genetic control programs. It is pointed out that pattern detection is already producing new data for quantitative analysis, classification and diagnostics. It is finally suggested that intelligence may always presuppose interaction and interaction patterns.

Keywords: Context; quantitative; structural; real-time; T-system; detection; neurons; DNA; THEME.

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Price: US$134 / €107 / £72

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ISBN: 1-58603-629-7 NEW
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1.1 Introduction

When two or more individuals interact, whether they are humans, monkeys, mice or fruit flies, many things are happening at the same time. Trunks, heads, limbs and various extremities are moving, sounds and odours are emitted and perceived while whole bodies change postures and locations relative to each other and the environment. All this is occurring at the same time as numerous events of various types occur concurrently and sequentially within and across individuals in countless ways. They are clearly not just ordered as letters or words in lines of text. And the same is actually true for the multitude of events in the sound stream of speech, where linguistic and paralinguistic events are mixed in time and paralinguistic elements sometimes modify or even annul the meaning or effect of verbal ones and vice-versa. Little or none of this is, however, visible in the highly abstract coding in written text. It is after at least tens of thousands of years of talking together that humans have recently become able to transform their speech sounds streams into longer lasting objects, i.e., to produce text. Similarly, the rich and rigorous structure of spoken language, some of which is now expressed in grammars, remained largely unnoticed through thousands and thousands of years. It seems therefore quite possible that much structure in human interactions remains undiscovered, but it also appears that trying to order all that's happening into a simple string may result in misleading oversimplification. But even if this was attempted there would surely be a myriad of ways to do it and only deep understanding of what is essential could guide such an undertaking. That understanding will have to deal with complex real-time streams of behaviour concurrently produced by two or more individuals. The model and methods outlined below were aimed at this task. They are based on an attempted "bird's eye view" as a way to learn from structural analogies across highly different levels of biological organization. Such analogies are assumed to be of special importance and point to something essential just as various stretches of DNA molecules, i.e., some genes, are practically identical across all species and thus point to something essential for life. It seems, moreover, that some structural types, analogous to those in DNA, occur also in the time domain, that is, as patterns in both individual behaviour and interactions and at various time scales.

1.1.1 Actors and Interaction

In this text it is assumed that *interaction* implies more than one party where, minimally, one is influencing one other, while *social* implies some kind of *system* within which each interaction takes place, involving different types of entities, individuals or *actors* (sometimes also called agents, parties, players, etc.). Within a cell the actors may be proteins (see below); in body tissue they are cells; in insect hives or human cities they are individual insects or humans. All have particular shapes and special parts they can move at various characteristic speeds and change postures or shapes thereby changing their attractiveness and relationships with others. And all are sensitive to such aspects in others (for example [1]). The function and place of an individual within the interaction system is affected by its interactions and in turn shapes them and when an individual enters into existence the time and place as well as the system's state at that moment is necessarily beyond the individual's control, but often essential for the individual's fate.

1.1.2 Individual, Whole and the Invisible

"In the existing sciences much of the emphasis over the past century or so has been on breaking systems down to find their underlying parts, then trying to analyze these parts in as much detail as possible. And particularly in physics this approach has been sufficiently successful that the basic components of everyday systems are by now completely known. But just how these components act together to produce even some of the most obvious features of the overall behaviour we see has in the past remained an almost complete mystery" [2, p.3]

Interactions of individuals often become coordinated into a functional whole that at a higher level of organization may be an actor again. This necessitates a flow of control up and down the organizational levels. It may be all the way from proteins to human individuals to large companies or whole cities. However, most of the interaction processes that take place around us and within us are hidden to our naked eyes and ears. The reasons for this differ considerably as interactions take place concurrently within the invisible world of molecules, cells and tissues and deep within hives or cities of insects and humans difficult or forbidden to observe. Others are too complex and/or extended in time and/or space. There seems little doubt that only a tiny fraction of the interaction mechanisms involved in any and all of the biological interaction systems humans are aware of is currently known and that the vast majority is hidden to the eyes, ears, instruments, and methods of modern humans. Figure 1.1 illustrates how difficult it can be to detect patterns directly even under very simple and fairly ideal circumstances, and, surprisingly, for various more complex cases, adequate statistical methods are not readily available to aide in their discovery.

What then if interaction patterns essential for the understanding of our own behaviour and communication go undetected? This also poses problems regarding the most elementary and easily detected behavioural elements since a complex hidden pattern could be the context determining their meaning. Such phenomena clearly raise methodological problems that call for adequate models, methods and tools to allow the detection of such patterns.

1.1.3 From Quantitative to Structural

The discovery of the essence of biological heredity involved a methodological progression from the quantitative to the structural (see, for example [3]). Quantitative measures allowed the detection of particularly high concentrations of a molecular substance in certain places and helped bringing the focus upon it.

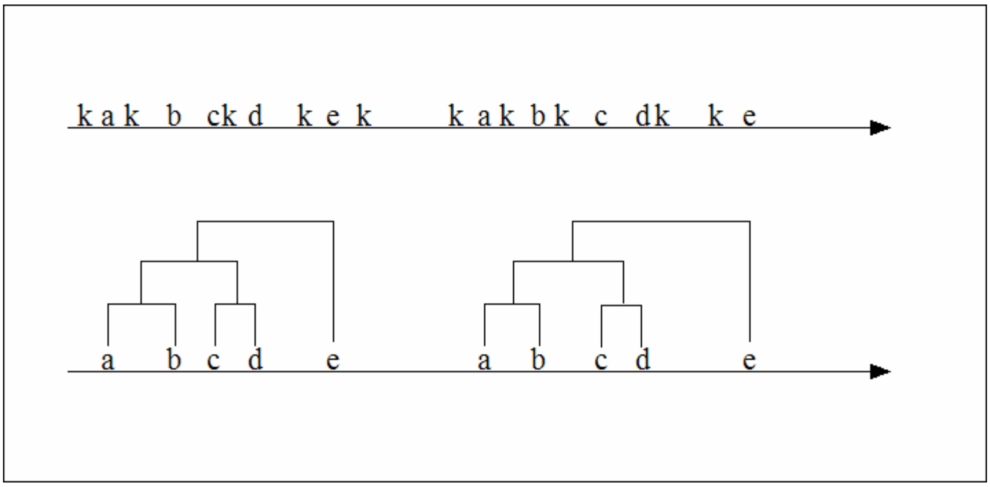

Figure 1.1 This figure illustrates how little it takes for a repeated pattern of the T-pattern type to become invisible to the unaided observer. The upper axis and its letter pattern is a copy of the lower one, but with only a few instances of "k" added.

Then gradually deeper structural analysis, first brought out the cyclical structure of that substance and then the combinatorial system hidden within it as well as some of its “auto-interactive” aspects. Thus was discovered the essential DNA structure [4] (see also [5, 6]) and the genetic code and then feed-back interactions between its parts mediated through their own products, proteins, thus creating control programs [7].

As witnessed amongst other by the chapters of this volume, the analysis of human interactions appears to be following this general methodological path, that is, after focusing on the purely quantitative, i.e., frequencies and durations and then frequency waves, the focus is turning further towards structure and a search for sequences, hierarchical/syntactic patterns, new kinds of “grammars” (see below), and even “programs” (see, chapter 14 in this volume).

This development has been slow to be adopted within Psychology as witnessed by the following rather dramatic quote, but this seems partly true for some related areas such as, for example, ethology:

“Only about 8% of all psychological research is based on any kind of observation. A fraction of that is programmatic research. And, a fraction of that is sequential in its thinking” [8, p. 184].

Early research on “face-to-face” interaction [9, 10] showed how regularities in such behaviour may come to light through the use of adequate methods. Such discoveries depend increasingly on recent technologies to “fix the object (behaviour)”, i.e., film and video, and then to code and to deal with the complex information obtained from their in-depth analysis, i.e., interactive multimedia programs and algorithms implemented in easily accessible software. But for such work to succeed the models (structural ideas or hypotheses), methods and technology applied in the search for hidden structure or regularities must be adequate and powerful. In the opposite case the situation can become a bit like using a hammer to search for square planetary orbits; a hopeless undertaking no matter how hard one works. Theoretical and methodological issues are no doubt particularly important in studies of interaction systems because their complexity is unforgiving. In spite of this, easy access to standard statistical software often seems to decide the choice of approach in behavioural and interaction studies.

The present work, which has evolved over a considerable period [11-18] was initially inspired in very different ways by theoretical and empirical research concerning the structure of behaviour and interactions with special focus on real-time, probabilistic, functional and sequential aspects as well as hierarchical/syntactic structure, creativity, routines and planning (for example, [19-26]).

1.1.4 Interaction and Algorithms

Convergence between views and methodologies at such very different levels of biological organization do not end here but continues into studies of “social” interaction systems:

> “A modern view of molecular biology is concerned with *organization* in time and space. How do the molecules of life arrange themselves amongst the cell’s compartments, how are they shifted around, how do they communicate so as to synchronize their action? We can ask these questions only because we can now inspect the working cell at the molecular level, taking measurements and snapshots of molecules going about their business. And so the cell becomes a community” [27, p. 44].

How interactions organize into a working system thus seems to be a common subject of molecular biology and human interaction research and this is further underlined by the following quote from the same source:

“Molecular biology is not difficult in the way theoretical physics is difficult – *the concepts are not unfamiliar*, *abstract*, *or mathematically abstruse. The difficulty arises because there is so much going on at once*. We react with surprise and shock when things go wrong with our own molecular machinery, but it is far more astonishing that the machinery works at all. Frequently it does so because it is designed to be robust in the face of the world’s vicissitudes. There are checkpoints, safety mechanisms, back-up plans, careful record-keeping” [27, p. 44] (Emphasis added).

The fact that the concepts are not difficult but familiar surely reflects their common use regarding human activity within human communities and cities. The problem of “too much going on at the same time” may also be a fundamental problem associated with the study of the true complexity of interaction systems rather than focusing on their elements and splitting them ever finer and thereby eliminating interaction possibilities.

1.1.5 Algorithms vs. Equations

How to deal with the overwhelming complexity of interaction systems? It seems obvious that without the still ongoing computer revolution any attack on the real complexity of social interaction systems would be futile.

Much hope seems to lie in new and better algorithms and ever more powerful and cheaper computers. Algorithms, considered among mathematics’ greatest inventions, what are they:

”An algorithm is a finite procedure, written in a fixed symbolic vocabulary, governed by precise instructions, moving in discrete steps, 1, 2, 3, …, whose execution requires no insight, cleverness, intuition, intelligence, or perspicuity, and that sooner or later comes to an end” [28, p. xviii].

And the analogy with social interaction processes is immediately noticed:

“After all, what is a bureaucracy but a social organization that has since at least the time of the ancient Chinese patiently undertaken the execution of complicated algorithms?” [28, p. xii].

It is often said that the difference between, for example, social insects and humans in this respect is that humans are conscious about what they are doing. But consider, for example, a simple clerk in a vast (ancient Chinese) bureaucracy. How conscious would he/she be about the ultimate effect of his/her activity? The individual would surely be conscious of each act of “pushing paper”, but not even the director of a whole branch of a bureaucracy might know that its current activity is a part of a strategic move, for example, to deal with a political problem or overtake some neighbouring country. By analogy with proximal and distal causes, one might possibly talk of proximal and distal consciousness, which clearly do not always go together: “Human society contemplated with a tranquil and disinterested eye appears at first to display only the violence of powerful men and the oppression of the weak; the mind is revolted by the harshness of the strong; one is impelled to deplore the blindness of the weak…” [29, p. 17].

From a theoretical and methodological standpoint, it seems that in science the consequences of the computer revolution with its focus on algorithms may go very deep indeed:

> "Tree centuries ago science was transformed by the dramatic new idea that rules based on mathematical equations could be used to describe the natural world. My purpose in this book is to initiate another such transformation, and to introduce a new kind of science that is based on the much more general types of rules that can be embodied in simple computer programs" [2, p. 1].

1.1.6 Model Pattern and a Detection Algorithm

The problem of "too much happening at the same time", even within a few minutes of face-to-face interaction between two toddlers provided more than sufficient inspiration and material for the theoretical, methodological and technical development that has led to the definition of a particular but very general time pattern type called T-pattern, which can be seen as a hypothesis concerning the real-time structure of behaviour and interactions. Corresponding detection algorithms and software (THEME) have been developed. The main definitions and some of the motivations behind them are outlined here, but a more thorough description with a list of references amongst other to applications in a number of areas has appeared elsewhere [16] (www.hbl.hi.is also contains a regularly updated list of references).

The behavioural sciences have long considered repeated patterns as an essential aspect of behaviour. Clearly, in Linguistics and Ethology repeated temporal patterns are amongst central concerns and radical behaviourism deals with real-time contingencies, i.e., patterns also with a focus on repetition. In Anthropology, Social Psychology and Sociology repeated temporal patterns such as, for example, scripts, plans, routines, strategies, rituals and ceremonies are important concerns. Within the arts and music, in particular, repeated real-time patterns are omnipresent and often fascinate humans to the highest degree. Generally, the patterns in question are not only patterns of elements as their various components are also patterns as, for example, any common phrase that is a repeated pattern of words, which again are composed of letters, etc. Note that, as we go from the phrase to the letter the patterns in question become increasingly frequent, that is, in a standard phrase, each of its words are more frequent than the phrase, and any letter more frequent than a word. On the other hand, there are far more different words than letters.

But behaviour is not always as plain to see as words and letters on a page:

> "*Behaviour* consists of *patterns in time*. Investigations of behaviour deal with sequences that, in contrast to bodily characteristics, are *not always visible*" [30, p.1] (Emphasis added).

Perceptual aids like the microscope and the telescope were developed to deal with detection of phenomena beyond direct human perception. Similarly, behavioural patterns that escape direct human detection call for new perceptual aids ("behaviourscopes"?) based on adequate ideas concerning their structure.

A basic assumption here is that hidden patterns in behaviour do share some structural characteristics with well-known everyday behaviour patterns. Some structural aspects of such patterns were therefore abstracted and combined to create a general, scale independent pattern-type. The aim is double, that is, to allow effective search for hidden patterns and possibly to provide elements for a new kind of real-time probabilistic "grammar" concerning the structure of behaviour and interactions. Here, some characteristics of a few everyday patterns can serve to illustrate the main aspects.

"How are you?" An intra-individual verbal pattern.
"How are you? Fine, thank you." An inter-individual verbal pattern.

Bill says: "Pass me the salt Jack" followed by Jack passing him the salt. An an inter-individual mixed verbal/non-verbal pattern.

"If..then..else" is a verbal pattern with slots (here indicated with dots) that may be filled in various ways.

A typical dinner (in the western world) is also such a pattern of components which themselves are patterns, for example, a person "(1) sits down at table…(2) has a starter…(3) a main course…(4) a dessert…(5) coffee…(6) stands up from table". See figure 1.2.

As in "if..then..else", each of the components of the dinner is itself a pattern and there are also the "free" (dotted) time slots where various other behavioural elements may occur in various numbers. It is exactly this last aspect that makes the detection of such patterns so difficult using sequential analysis methods based exclusively on the sequential order of events, but the algorithm described below deals with that problem by considering, simultaneously, the order of events, the time distances between them, their positions on a real-time scale and the average probability of occurrence per time unit of each and every component at all hierarchical levels.

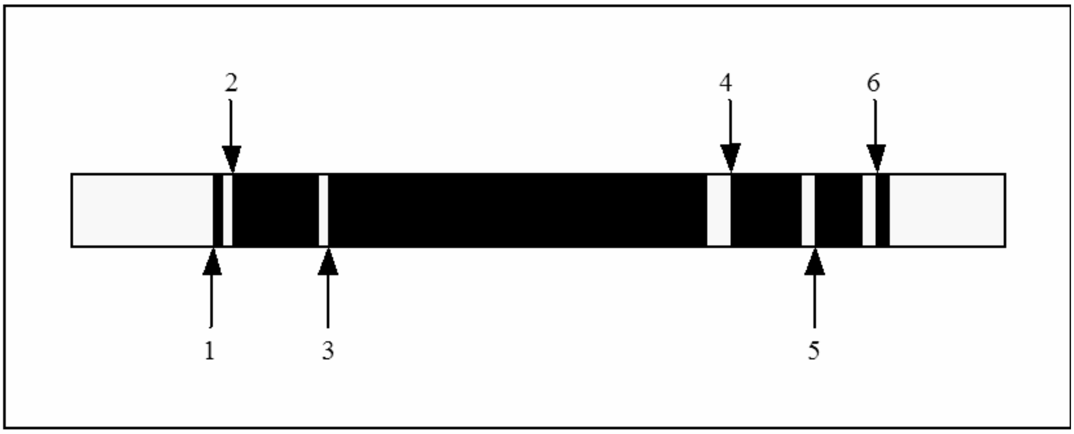

Figure 1.2 This figure, which could be called a "dinner-gene" can be interpreted in different ways, explained in the text. The numbers 1 to 6 show where its six component patterns begin. The figure should be thought of as being flexible or elastic, such that the object and/or any number of its dark and light parts could be stretched and squeezed changing their relative lengths but to a limited extent, i.e., as a rubber band. See text.

In each of these patterns, the components occur in a particular order and the temporal distance from one to the next is of an approximate length that is characteristic for the particular pattern. If these time distances between components become too short or too long the pattern becomes strange or disappears altogether. Squeezed and stretched too much, a spoken sentence or a melody will cease to be. The same is actually true for the great molecules of life, they are quite flexible, but can only be stretched to a limit. The limits of flexibility are typically quite strict making the occurrence of patterns of this kind highly improbable a priori, that is, they would hardly ever recur with such similarity if their components were simply occurring independently and randomly with their observed frequencies.

These constrains are here essential for the detection of patterns often impossible to detect on the basis of component order alone because of the highly varied number of other behaviours that occur between their components. This is especially true if the pattern is complex and rare as often is the case for important phenomena.

When considered in this way, as patterns on a single dimension, which may be either temporal or spatial, the above everyday patterns seem to correspond to a large class of patterns in individual and inter-individual behaviour as well as patterns within information molecules such as DNA.

1.2 The T-pattern

In the following sections the more formal definitions of the T-pattern and the derived "T-system" are outlined (for further details see [16]). The T-pattern definition refers to a particular, but essentially well known data type.

1.2.1 The data type

An *event-type* here refers to some behaviour that occurs or not at a particular point on a discrete time scale, but has no duration otherwise: For example, "Bill begins walking" (or short: bill,b,walk) and Sue ends talking (sue,e,talk) are event types. They may also be further qualified, for example, bill,b,walk,fast; sue,e,talk,loud,bill (Sue ends talking loudly to Bill). The behaviour is coded in terms of the occurrence times of such beginnings and endings (points) on a discrete time scale. Each beginning and/or ending thus occurs or not at a discrete time point. Any number of event-types may occur at the same point (i.e., basic time unit). The time unit can be of any size, for example, milliseconds or days (see, for example, chapters 4 and 5 in this volume), but can also be years, decades, etc., depending on the system being studied. The occurrences of all event-types within a given continuous observation period thus constitute the type of multivariate time point process (see, for example, [31]), here called T-data or T-dataset, that is referred to by the T-pattern definition. Event types can also be other than behavioural in the strict sense such as, for example, it begins to rain, heart-rate increases, car breaks down, earthquake begins, alarm clock rings, shares fall, storm ends, temperature decreases, the sun comes out, etc.

Figure 1.3 shows an example of a T-dataset with 82 event type occurrence series. This particular data is the result of coding approximately 13.5 min of interaction between two children using interactive multimedia software and 1/15 s as the time unit (i.e., one video frame in this case) and a pre-existing list of behavioural categories [32].

1.2.2 The T-pattern structure

A T-pattern with m components $X_{i..m}$ (each an event type or a T-pattern) can be noted as:

$$X_1\ [d_1, d_2]_1\ X_2\ [d_1, d_2]_2 \ldots X_i\ [d_1, d_2]_i\ X_{i+1} \ldots X_{m-1}\ [d_1, d_2]_{m-1}\ X_m$$

$[d_1, d_2]_i$ stands for the interval within which the characteristic distances vary. $X_i\ [d_1, d_2]_i\ X_{i+1}$ thus means: if X_i ends at t, it is followed within $[t+d_1, t+d_2]_i$ by the beginning of component X_{i+1}. Furthermore, any T-pattern can be described as a binary tree by splitting it recursively (top-down) into left and right halves until the event-type level is reached.

Thus, for detection purposes, the T-pattern definition is narrowed to a binary tree of *critical intervals* between left and right branches:

X_{left} $[d_1, d_2]$ X_{right}

Where X_{left} stands for the first part, ending at t, followed within $[t+d_1, t+d_2]$ by the beginning of X_{right}; where $0 \leq d_1 \leq d_2$. In $[d_1, d_2]$, t is omitted to simplify notation. Note that, when the two branches are concurrent, 0 = d1 = d2.

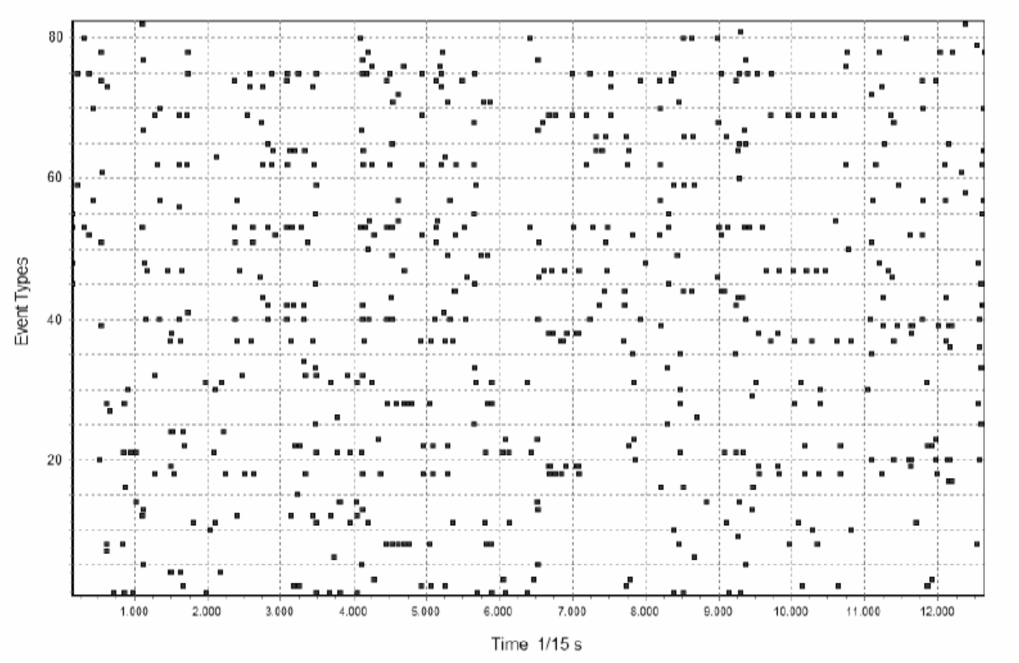

Figure 1.3 This figure shows a typical data set of the kind that is referred to by the T-pattern definition and is the input to the T-pattern detection algorithm. It shows the occurrence times (point) series of the 82 event types coded from a video recording of two five-year-olds 13.5 min dyadic object play.

1.2.3 The detection algorithm

In behaviour records with a hundred event-types each occurring at least twice, the number of possible patterns involving, for example, ten event-types is colossal, that is, far greater than 100^{10}. Trying out all possible sequences of all lengths is thus not an option. Instead, the algorithm reveres the above top-down recursive splitting and performs bottom-up construction. Beginning with T-data it uses a critical interval detection algorithm to build binary T-pattern trees.

The *critical interval algorithm* measures the time from each occurrence (end) of X_{left} to the first following or concurrent occurrence (beginning) of X_{right}. Using this distribution and some preset significance level, it searches for the longest possible interval $[d_1, d_2]$ such that (X_{left}) (ending at t) is, significantly more often than expected by h0, followed within $[t+d_1, t+d_2]$ by the beginning of another component (X_{right}); where h0 is that (X_{right}) is independently randomly distributed over the observation period $[t_1, t_2]$ with a constant probability per time unit = $N(X_{right}) / (t_2-t_1+1)$; where $N(X_{right})$ is the number of occurrences of X_{right}. If found, the critically related instances of each of the two components are connected and added to the data as the occurrences of a new T-pattern, which later in the process may become the (left or right) part of a more complex pattern. Increasingly complex patterns may thus be detected as patterns of patterns of patterns, etc.

However, a T-pattern of length > 2 may be represented as a binary tree in various ways, for example, ABCD as ((A (B C)) D), ((A B)(C D)), (((A B) C) D), etc. Complex T-patterns existing in the data may thus be detected (constructed) in many different ways. This can easily lead to numerous partial and/or redundant detections. To deal with this, patterns are automatically compared and those occurring only as parts of other more *complete* patterns are dropped. The search ends when no more critical intervals can be found.

At very low preset significance levels no patterns are found. At some higher level (often near 0.005) all the most complex patterns have been detected, while at still higher levels the same patterns are redundantly discovered as more and more binary trees become significant for each underlying pattern. Pattern *growth* (construction) and completeness *competition* thus often lead to the *evolution* of both simple and complex patterns that are the result of the search process.

1.2.4 Regular vs. similar

Repetition is essential in the current definition of the T-pattern type. A single instance of a T-pattern is typically not regular in any way and such regularity is not a defining characteristic. For a given T-pattern, even if none of its instances are regular, they are all similar in the particular way specified by the above definition that relates to the overall frequency of the components and their hierarchical/syntactic relations. From other points of view, the instances of a T-pattern may be seen as not similar at all.

1.2.5 Statistical methods and T-patterns

The essential T-pattern algorithms were initially developed [11, 12] after careful consideration of standard statistical methods and especially those commonly used in behaviour analysis (see, for example, [33-35]) and implemented in various statistical packages and in behaviour analysis software (for example, [36, 37]). Such methods were not, however, developed for and do not allow the detection of complex T-patterns. They neither provide a T-pattern definition, automatic critical interval detection, multi-ordinal bottom-up pattern construction nor pattern evolution through completeness competition.

1.2.6 The T-system

Other terms have consequently been derived from the T-pattern to gradually form the so called, *T-system*, which is proposed as the possible beginning of a kind of probabilistic "grammar" for the description and analysis of the real-time structure of behaviour and interaction. Definitions of the main terms derived from the T-pattern follow.

T-set: all the patterns detected within the same T-dataset.

T-marker: a T-pattern component that rarely occurs independently of that pattern and thus strongly indicates its occurrence (presence) [38].

T-associate, positive or negative (+/-): some behaviour (event-type or pattern) that is *not* a component of a T-pattern Q, but with significant positive vs. negative tendency to occur within or near Q. It may thus serve as an indicator of the occurrences of Q; a *T-satellite* of Q is a positive T-associate occurring exclusively with Q, while a *T-taboo* of Q is a negative T-associate that never accompanies Q.

T-attraction zones of a pattern Q (positive and negative). A positive zone stretches from zp1 time units before to zp2 time units after each occurrences of Q and is the smallest zone where positive associates of Q are found. Thus if $[a_i, b_i]$; $i=1..NQ$ is the series of durations intervals of Q, then $[a_i - zp1, b_i + zp2]$; $i=1..NQ$ is its series of positive attraction intervals. Similarly, $[a_i - zn1, b_i + zn2]$ is its series of negative attraction intervals.

T-packet: a T-pattern with its positive and negative associates and +/- attraction zones.

T-drifters are behaviours belonging to none of the other categories of the system.

T-coverage of a pattern is the total amount of time when the pattern is in progress (its total duration) that can be expressed as a percentage of the observation period.

T-composition: for a given initial set X of patterns (such as the T-set) it refers to the sub-set of alternating non-overlapping patterns that has the highest combined coverage of all possible sub-sets of X.

T-path: when the event types of a T-pattern correspond to points in space, a T-pattern defines a path in that space called a T-path (see figure 1.7).

T-path network: two or more paths belonging to the same T-set (see figure 1.8).

1.3 Research application and the THEME software

Special software, called THEME, has been developed for the detection and analysis of T-patterns and an increasing number of other T-system elements. Its development continues at PatternVision Ltd (see www.patternvision.com) in collaboration with the Human Behavior Laboratory, University of Iceland (see www.hbl.hi.is).

T-pattern analysis with THEME has been applied in a number in different research areas such as psychology, psychiatry, ethology, psychophysiology and sports science (for example [39-56]).

International marketing and support for THEME is in the hands of Noldus Information Technology (see www.noldus.com, which also maintains a data-base of THEME application references).

1.3.1 T-pattern Examples and Diagrams

In this section T-patterns detected in human interaction (figures 1.4 and 1.5) and in interactions between neurons in brain tissue (figures 1.6 and 1.7) are presented using diagrams specially developed to make even complex T-patterns as accessible as possible. A diagram of this kind shows the binary tree structure, i.e., how a T-pattern has been gradually detected as pairs of already detected patterns or event types. It also shows the occurrences time series of the original event types (as in figure 1.3) involved in the pattern and which occurrences of each were connected to form the pattern.

The first example concerns a pattern detected in an interaction between two five-year-old girls playing with a toy, a handheld viewer for viewing picture cards. The T-dataset is that shown in figure 1.3, but figures 1.4 and 1.5 present in different ways the longest (highest value of m) T-pattern detected in this data.

In figure 1.4, the left box shows the full sequence (string) of event-types (i.e., $X_1..X_{m;}$ here $m = 27$) and the binary tree relations between them. Level-by-level, from level 0 (initial event types) to level 9, the event types of the pattern are connected into patterns of growing complexity (length). Note that some of the event types are repeated within the terminal string (sequence) of 27 event types, but different instances are involved. Moreover, in all but the last occurrence of this particular pattern, its last event is the first event of its next occurrence. The right box shows the occurrence times of each of the 27 event types in the pattern immediately to its right (some of these series are thus repeated).

Connection lines, corresponding to the tree on the left, show how the critically related instances of event-types and/or sub-patterns are connected on the basis of detected critical interval relationships. Sub-patterns occurring sometimes outside the full pattern are also visible.

The upper box in figure 1.5 is the same as the right box of figure 1.4 except that its height has been reduced and it has been aligned with a different presentation shown in the lower-box, which only shows occurrences of the complete T-pattern tree and in a manner similar to the trees in the lower part of figure 1.1, but without the labels. (Note that when event-types occur concurrently within a pattern, lines overlap and branching disappears.)

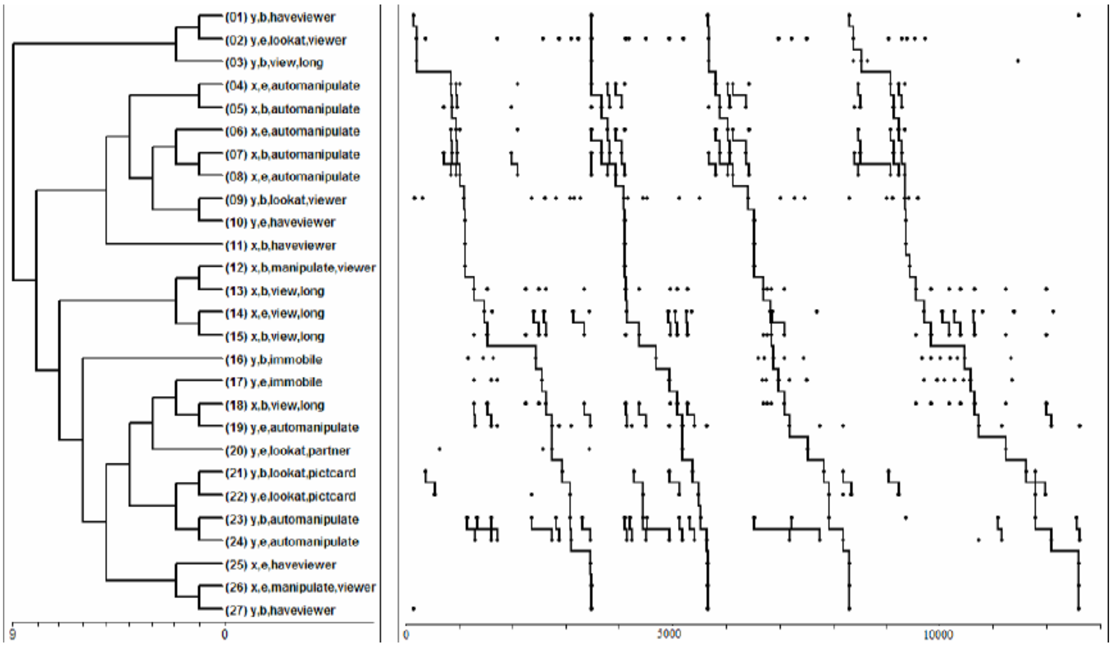

Figure 1.4 This figure shows a pattern detected by the T-pattern detection algorithm in the data shown in figure 1.3. See text on how to read this kind of pattern and explanations of label meanings.

The event type labels of figure 1.4 are composed in the following way:

x and y represent the two five-year-olds actors.

b and e mean, respectively, begins and ends.

The list from 1 to 27 means: 1) y begins having the viewer; 2) y ends looking at the viewer; 3) y begins looking for a long time, i.e., per definition, > 3s; 4) x ends touching herself (i.e., her hand touches any part of her body); 5) x begins touching herself; 6) x ends touching herself; 7) x begins touching herself; 8) x begins touching herself; 9) y begins looking at viewer; 10) y ends having viewer; 11) x begins having the viewer; 12) x begins manipulating the viewer; 13) x begins viewing for a long time, >3s; 14) x ends viewing for a long time; 15) x begins viewing for a long time; 16) y begins being immobile, no visible movement, i.e., she “freezes”; 17) y ends being immobile; 18) x begins viewing for a long time; 19) y ends touching herself; 20) y ends looking at the other (her partner); 21) y begins looking at a picture card (not in the viewer); 22) y ends looking at a picture card; 23) y begins touching herself; 24) y ends touching herself; 25) x ends having the viewer; 26) x ends manipulating the viewer; 27) y begins having the viewer.

At the first level the following pairs are connected: (1-2), (4-5), (7-8), (9-10), (12-13), (14-15), (18-19), (21-22), (23-24), (26-27); at the second level, for example, ((1-2)-3), ((12-13)-(14-15)), (17-(18-19)), (25-(26-27)); at third level, for example, ((17-(18-19))-20), etc.

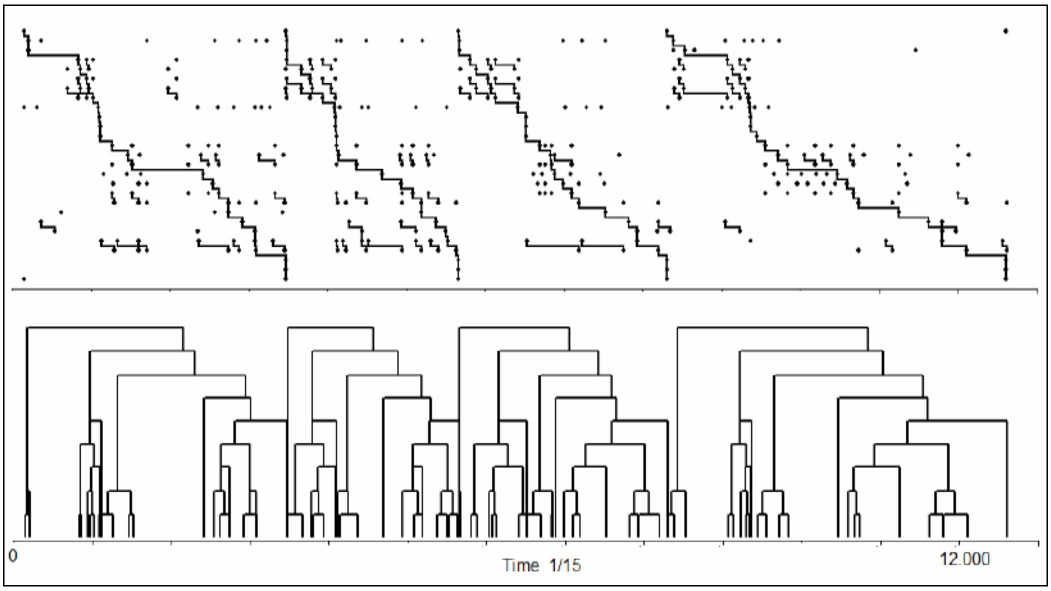

Figure 1.5 This figure's upper part is the same as figure 1.4 except that the box on the left has been removed and the height of right box has been reduced. The lower part gives a corresponding binary tree view of the occurrences of the pattern. The tree is the same as that in figure 1.4 but is here turned, the labels removed, and the shape of the tree follows the real-time shape of the pattern instances much as the binary trees in the lower part of figure 1.1.

1.3.2 T-patterns and T-paths in Neuronal Interactions

Results described notably in other chapters in this book suggest that T-patterns are examples of such structural types that can be found across different levels of organization involving different actors, i.e., not only humans but also, for example, neurons or drosophila. The most recent test of the relevance of the T-pattern structure across areas and levels of biological interaction systems is a search for T-patterns in interactions between individual neurons, i.e., brain cells, within a living brain (see chapter 4 in this volume). Figures 1.6, 1.7 and 1.8 give an idea of the kind of patterns found and illustrate relations between T-patterns, T-paths and T-path networks. Figures 1.6 and 1.7 both represent the same T-pattern, respectively, as a time pattern and as a spatial (here 2D) path on a 2D grid of electrodes. Each electrode registers the spikes from a few individual neurons. The numerical event type names therefore represent the locations of individual neurons. The neurons are the actors and they have only one behaviour: firing; and this event has a particular location in both time and space. (That is, the behaviour is always of the same kind, but the actors and positions change.)

Figure 1.6 This figure shows a T-pattern detected in the interactions between individual neurons within the brain of a rat while presented with odour for 10 seconds and breaths in and out during this time. The event types 50,5003 stands for "breaths in" while other event types refer to various individual neurons. See chapter 4 in this volume.

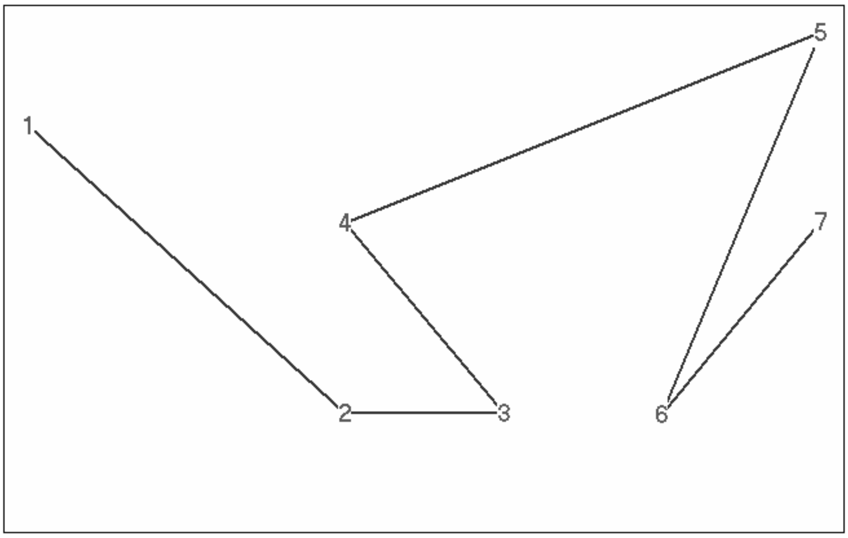

Figure 1.7 This figure shows the T-path of the pattern in figure 1.6 on the electrode grid used to register the activity of individual neurons. See chapter 4 in this volume.

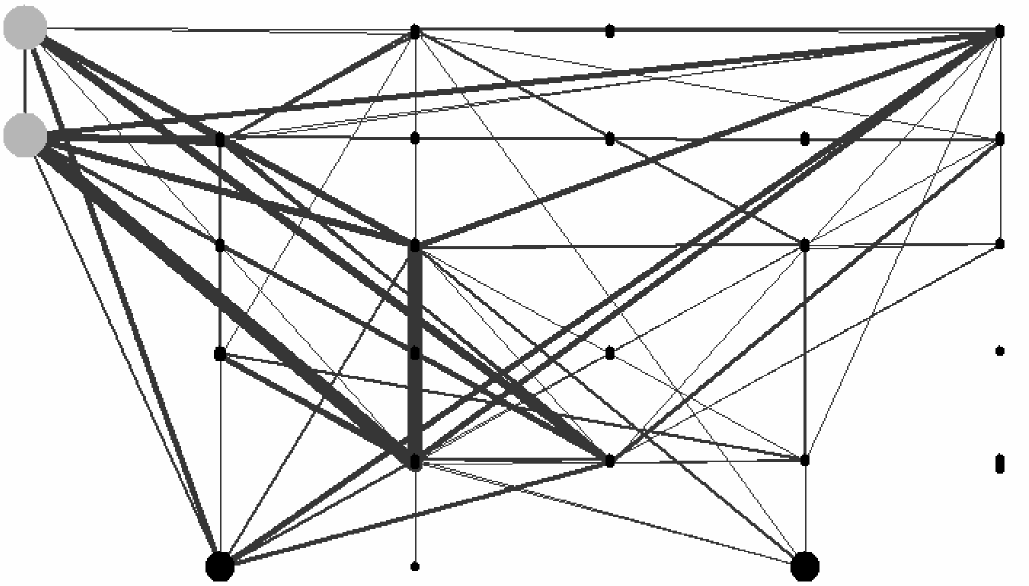

Figure 1.8 This figure combines all the 49 different T-paths (T-patterns) involving inhalation detected within 10 seconds of interactions between neurons. The paths are drawn one over the other and the more often a line is drawn (in the more frequent direction) the thicker the line. See chapter 4 in this volume.

1.3.3 T-patterns in DNA & proteins

The elements used to code information along the DNA molecules contained in chromosomes are themselves molecules called *bases*. These are of only four kinds commonly referred to as G, T, C, and A. The so-called backbone of the DNA molecule is a cyclical structure of alternating molecules, somewhat like the ticks on a scale (or a ticking clock), with a base occurring at each tick. Much as a byte in a computer has 8 bits that can be arranged in 256 different ways to represent letters and various other symbols, the series of bases are translated three at the time, i.e., in triplets called *codons*. Each codon is translated into one of 20 different *amino acid* molecules (thus conveniently referred to by letters of the alphabet, a coincidence?) and a protein is a particular chain of such molecules. A (structural) *gene* is a stretch of DNA containing a particular series of codons, which at various moments is translated into varying numbers of copies of a particular protein. Different chains thus make up the great number of proteins in a cell that is called its *proteome*, i.e., its population of proteins at each moment.

Actually, in complex organisms such as Drosophila and humans, the series of codons in a stretch of DNA corresponding to a gene is often interrupted by nonsense segments as if a paragraph of text were repeatedly interrupted by various nonsense series of letters, or a serious discussion or a speech by periods of small talk or chat. The alternating meaningful and nonsense segments of a gene are, respectively, called exons and introns. When a gene is transcribed into a protein only the exons are used, but the non-coding introns define distances and possibly some effective content between the exons characteristic for the gene. But this is also one of the essential aspects of a T-pattern, where time distances of characteristic lengths but with more or less free content separate the components, which frequently are T-patterns themselves. Moreover, within the exons in terms of codons or equivalently amino acids there are so called *motives*. These can again show this same kind of structure where some particularly important stretch is fixed (occurs across species) while stretches separating them can vary freely. Moreover, since the genes are also separated by introns, the whole genome can be seen as a massively repeated T-pattern within the cells of the organism, influencing from within the internal functioning and thereby the behaviour of each cell as a whole.

DNA and proteins are typically depicted as strings of equally spaced letters like in a line of text, but in reality the molecules are *flexible*. The real distances between and within exons and introns, i.e., within a gene, can thus vary even if the number of elements separating them remains the same (see, for example [57]) and this is in particular true for proteins [1, p. 46]. This further strengthens the analogy with temporal behaviour patterns as described by the T-pattern model. Moreover, only 2% of human DNA contains genes and:

"Genes appear to be concentrated in random areas along the genome, with vast expanses of noncoding DNA between. Stretches of up to 30,000 C and G bases repeating over and over often occur adjacent to gene-rich areas, forming a barrier between the genes and the *junk DNA*. These CpG islands are believed to help regulate gene activity." Copied 14/10/04 from www.ornl.gov/sci/techresources/Human_Genome/project/info.shtml

This appears to mean that from chromosomes, to gene rich areas to genes to exons and motives, the whole structure is analogous to the T-pattern time structure of common every-day behaviour patterns as described by the T-pattern model. It remains to be established whether T-pattern detection can therefore be of important use in the search for unknown structure in information molecules. Initial analysis has identified T-patterns in proteins and in DNA often showing good correlation with well-known patterns while other highly statistically significant cases are being evaluated (Magnusson & Oskarsson, in preparation, Icelandic Research Center, grants: 013220001 and 013220002).

Figure 1.2 illustrates the kind of structural analogy discussed here between genes and behavioural T-patterns as it can be read in two entirely different ways: as a description of a dinner composed of six shorter patterns numbered 1 to 6 and separated by flexible time-slots with unspecified or "free" content, or as a common graphical representation of a gene (see, for example, [58, p. 33]) here composed of six exons numbered 1 to 6 and separated by introns, which can be seen as flexible space-slots with mostly non-essential freely varying content.

Moreover, regulatory mechanisms exist such that special proteins get attached to DNA and modify a gene's effect (how it is expressed) within the internal community of the cell. It is therefore tempting to note that particular events may also occur during or around a dinner (disputes, flirting, etc) that may influence the unfolding of that dinner and its effect on future interactions and relations within a community.

1.3.4 Strings, Traces and Control in Cells and Cities

The molecular information chains (strings) such as DNA and RNA are produced by cell organs and are more or less durable traces of their behaviour. In that context, it is interesting to note that earlier in evolution cell organs leaving those traces may have been independent organisms and to recall that a common analogy used to describe the patterning of information molecules is text, also a more or less durable trace of behaviour. Here, information molecules and text will therefore be referred to as *information objects*.

The complete set of information objects (DNA) in a cell is referred to as its *genome* and it is typically stored within a central place (core), but only a tiny fraction or approximately 2% contains the essential genes while the rest is considered mostly "junk". The genome is to a large part composed of highly repeated meaningless segments, but these may serve an important function in separating other parts. Moreover, in the community of cells making up a body, practically all the cells carry identical copies of the same genome and various stretches of its string (genes) are turned into different proteins. But, in "cell city", these proteins are a) the specialized "actors" that perform most life functions or b) construction materials. Some of these molecules are enzymes:

> "If the cell is a city, enzymes are the workers. To keep the city running, raw materials are imported and converted into useful items. Enzymes populate the cellular factories in which this is done. One curious aspect of this manufacturing industry is that it includes factories for making the workers themselves: enzymes too are put together on a production line" [27, p. 46].

Replacing the word "worker" here by "specialized individual" then, in human cities, such factories could be, for example, schools, where various kinds of "specialized individuals" (including teachers) are created by other specialized individuals (notably teachers) mostly by exposing them to particular verbal materials, spoken and written, typically within a process of patterned face-to-face verbal and nonverbal interaction.

While the genome of a cell is stable, the composition of its protein population (its proteome) at each moment results from fluctuating rates of translation of different genome fractions under complex environmental influence, which includes interactions with the current proteome (population). A typical modern human city also has its information objects, most notably texts, and essential parts are also carefully stored in central places (libraries). The totality of text within a community could be called a "textome" and again a large part has little or no information value. Its various fractions (knowledge) also make it possible to create (educate) at varying rates the various specialized actors needed by the city as well as to produce a multitude of materials and tools requiring complex prescriptions no single person could remember. Particular parts of the textome, such as a holy script, a constitution, and particular elements of history, law, regulations, etc. are also shared by the majority of the individuals of the city providing them amongst other with the essential religious and political standpoints of the particular society. And human societies seem deeply dependent on such standard information objects:

> “Yet religions have persisted in almost every society in the world – and where they have not they have been replaced by systems of political dogma…” [59, p. 2].

Within a society, information objects may be dispersed at first but later become concentrated in particular locations somewhat like the evolution from primitive cells (prokaryotes) where the genome is spread throughout the cell to the more advanced ones (eukaryotes) where nearly all of it is kept within a central core.

1.4 Discussion and conclusion

The information value of a single newly discovered T-pattern can vary greatly. It may be impossible to make sense of or it may tell about well known phenomena, but it may also provide new insight into some particular type of interaction and together with other T-patterns discovered in the same or different interactions it may be useful or even the missing brick in shaping a global picture. (Regarding the complex matters of meaning see chapter 2 in this volume.)

This search for patterns was begun with the hope of finding rather fixed and universal repeated patterns in human interaction, but even if some such can of course be found, a much more striking aspect is the apparently endless creativity. That is, two interactions never seem to be the same. This is true, even if the participants interactively co-construct new patterns which they then repeat in a similar way within that interaction, while in each new interaction more or less different patterns are formed and repeated.

But why do the T-patterns differ so much between interactions relating the same kind of individuals even in very similar conditions? Does this mean that very different underlying rules or processes are operating? According to findings within other areas this does not have to be the case as many dynamic systems have been found to be highly sensitive to the most minute differences in conditions (see, for example, [60]). Social interaction may simply be highly sensitive to internal (physiological) and external conditions, which well corresponds with common sense.

> “The patterns detected in social interactions are often quite complex, but does this mean that the underlying rules must also be complex? Apparently, this does not have to be the case at all, as it has been shown that even the simplest rules can produce great complexity” [2, p. 28].

As pointed out notably by Duncan and colleagues [61], there has been a tendency to look at the analysis of interactions as a means to other ends such as the detection of effects of external variables rather than as a subject of study in its own right. To this can be added that, for results to be considered acceptable at all, it is sometimes required that the external variables relate to differences between groups and, moreover, have a clinical or diagnostic quality. What consequences could such viewpoints have had for the demanding research leading to the discovery of the structure of DNA and the genetic code, undoubtedly amongst the most important discoveries in the history of humanity? But that discovery, purely about structure and pattern, has opened fascinating new perspectives in a multitude of areas and in particular those related to health.

Structural and quantitative analysis does of course combine naturally, but it is worth underlining that this can work in both directions, that is, through structural analysis new entities may be discovered and provide a new basis for quantification. As witnessed, for example, by a number of chapters in this volume, detected patterns rather than just elements can be counted and measured, thus allowing the detection of otherwise hidden effects of independent variables.

It appears that structures of the T-pattern type exist in behaviour and interactions not only across species, but also across time and space, thus suggesting considerable global conservation of a structural principle. If so, this seems to call for careful attention: Does the real-time organization of overt human behaviour reflect to this extent the spatial structure of the DNA molecules present within each of the trillion cells in a human body?

A long list of questions is waiting to be answered: Is there some kind of "code" analogous to that of biological heredity involved in social interactions and then of what kind, in what sense, how? Are the seemingly omnipresent repeated patterns of social interaction integrated parts of a global system of organic codes (see [62]) ranging from DNA to cultural patterns? Are there possibly fairly few, simple and discoverable rules behind the generation of much of the regularities we know or sense directly and those we begin to detect with the help of special models and algorithms? What about the T-system as a candidate for a new kind of grammar? Do the T-pattern model and algorithms in any way reflect the nature of underlying regular processes or is the relationship arbitrary and entirely superficial? How can hidden interaction programs be discovered and described? How to answer such questions?

In any case, colossal tasks lie ahead:

"Deriving meaningful knowledge from the DNA sequence will define research through the coming decades to inform our understanding of biological systems. This enormous task will require the expertise and creativity of tens of thousands of scientists from varied disciplines in both the public and private sectors worldwide." Copied 10.10.2004 from www.ornl.gov/sci/techresources/Human_Genome/project/info.shtml

Discovering and deciphering the integrated systems of information objects and real-time interaction patterns within human social systems seems an analogous and no lesser task that has also just begun and holds limitless promises such as a better understanding of the mechanisms behind the age old and painful social problems of inequality, injustice, and violence. It will probably also be at least as dependent on structural hypotheses and automation, i.e., on the development and application of specially designed models (patterns) and algorithms, but given the analogies between the tasks at different levels of biological organization there seems to be to much hope for useful cross-fertilization.

Finally, about intelligence and with one eye on the above neuronal interaction patterns: Is there really any use for the term "collective intelligence", i.e., is all intelligence really collective? Is there ever any intelligence without interaction? And is there ever without interaction patterns?

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