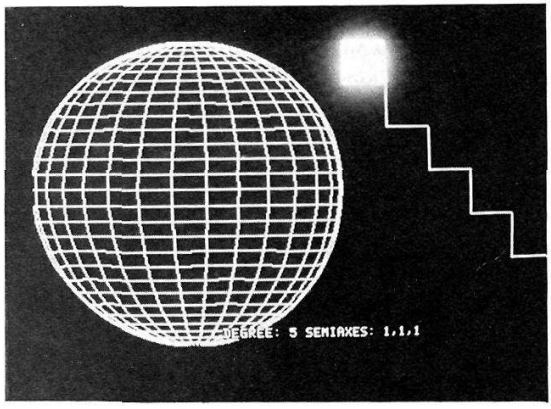
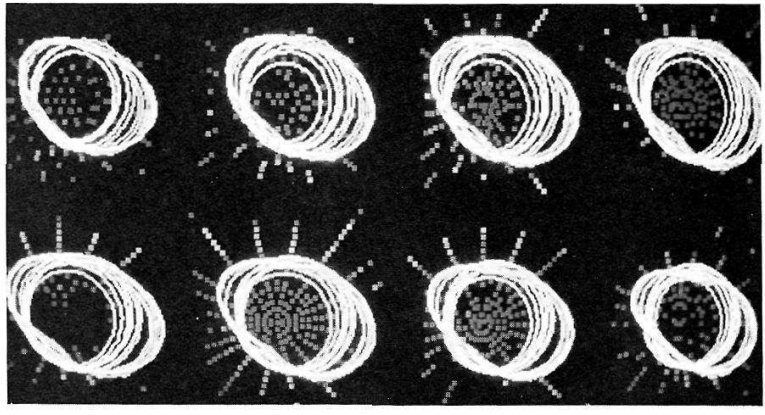
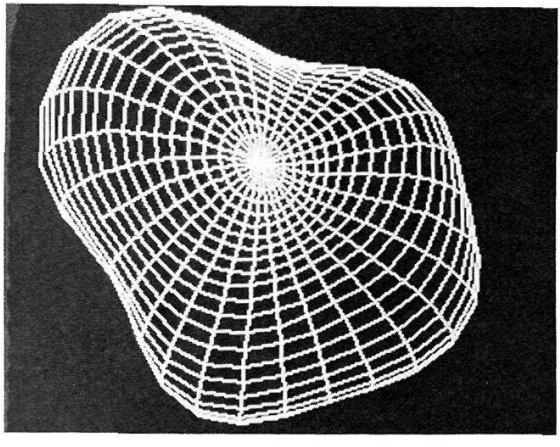



(a)



(b)



(c)

**Fig. 11.3** An example of matching as parameter optimization. (a) Initial parameter set (displayed at left as three-dimensional surface (see Fig. 9.8) (b) Fitting process: iteratively adjust $a$ based on M (see text). (c) Final parameter set yields this three-dimensional surface. (*See color inserts.*)

continuum, and that labeled arcs could be replaced by nodes to yield a directed graph with labeled nodes.

Depending on the attributes of the relational structure and of the correspondence desired, the definition of a match may be more or less elegant. It is always possible to translate powerful representations such as labeled graphs or $n$-ary relations into computational representations which are amenable to formal treatment (such as undirected graphs). However, when graph algorithms are to be implemented with computer data structures, the freedom and power of programming languages often tempts the implementer away from pure graph theory. He can replace elegant (but occasionally restrictive and impractical) graph-theoretic concepts and operations with arbitrarily complex data structures and algorithms.

One example is the "graph isomorphism" problem, a very pure version of relational structure matching. In it, all graph nodes and arcs are unlabeled, and graphs match if there is a 1:1 and onto correspondence between the arcs and nodes of the two graphs. The lack of expressive power in these graphs and the requirement that a match be "perfect" limits the usefulness of this pure model of matching in the context of noisy input and imprecise reference structures. In practice, graph nodes may have properties with continuous ranges of values, and an arbitrarily complex algorithm determines whether nodes or arcs match. The algorithm may even access information outside the graphs themselves, as long as it returns the answer "match" or "no match." Generalizing the graph-theoretic notions in this way can obscure issues of their efficiency, power, and properties; one must steer a course between the "elegant and unusable" and the "general and uncontrollable." This section introduces some "pure" graph-theoretic algorithms that form the basis for techniques in Sections 11.3 and 11.4.

### 11.2.1 The Algorithms

The following are several definitions of matching between graphs [Harary 1969; Berge 1976].

- *Graph isomorphism.* Given two graphs $(V_1, E_1)$ and $(V_2, E_2)$, find a 1:1 and onto mapping (an isomorphism) $f$ between $V_1$ and $V_2$ such that for $v_1, v_2 \in V_1, V_2$, $f(v_1) = v_2$ and for each edge of $E_1$ connecting any pair of nodes $v_1$ and $v'_1 \in V_1$, there is an edge of $E_2$ connecting $f(v_1)$ and $f(v_1')$.
- *Subgraph isomorphism.* Find isomorphisms between a graph $(V_1, E_1)$ and *subgraphs* of another graph $(V_2, E_2)$. This is computationally harder than isomorphism because one does not know in advance which subsets of $V_2$ are involved in isomorphisms.
- *"Double" subgraph isomorphisms.* Find all isomorphisms between *subgraphs* of a graph $(V_1, E_1)$ and *subgraphs* of another graph $(V_2, E_2)$. This sounds harder than the subgraph isomorphism problem, but is equivalent.
- A match may not conform to strict rules of correspondence between arcs and nodes (some nodes and arcs may be "unimportant"). Such a matching criterion may well be implemented as a "computational" (impure) version of one of the pure graph isomorphisms.

Figure 11.4 shows examples of these kinds of matches.

One algorithm for finding graph isomorphism [Corneil and Gotlieb 1970] is based on the idea of separately putting each graph into a canonical form, from which isomorphism may easily be determined. For directed graphs (i.e., nonsymmetric relations) a backtrack search algorithm [Berztiss 1973] works on both graphs at once.

Two solutions to the subgraph isomorphism problem appear in [Ullman 1976]: The first is a simple enumerative search of the tree of possible matches between nodes. The second is more interesting; in it a process of "parallel-iterative" refinement is applied at each stage of the search. This process is a way of rejecting node pairs from the isomorphism and of propagating the effects of such rejections; one rejected match can lead to more matches being rejected. When the iteration converges (i.e., when no more matches can be rejected at the current stage), another step in the tree search is performed (one more matching pair is hypothesized). This mixing of parallel-iterative processes with tree search is useful in a variety of applications (Section 11.4.4, Chapter 12).

"Double" subgraph isomorphism is easily reduced to subgraph isomorphism via another well-known graph problem, the "clique problem." A *clique* of size $N$ is a totally connected subgraph of size $N$ (each node is connected to every other node in the clique by an arc). Finding isomorphisms between subgraphs of a graph A and subgraphs of a graph B is accomplished by forming an *association graph* $G$ from the graphs A and B and finding cliques in G (for details, see Section 11.3.3). Clique

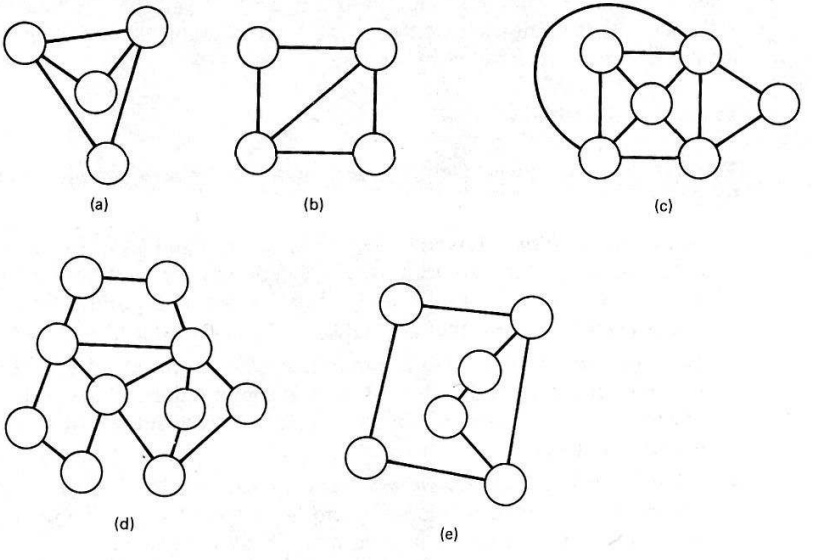



**Fig. 11.4** Isomorphisms and matches. The graph (a) has an isomorphism with (b), various subgraph isomorphisms with (c), and several "double" subgraph isomorphisms with (d). Several partial matches with (e) (and also (b), (c), and (d)), depending on which missing or extra nodes are ignored.

finding may be done with a subgraph isomorphism algorithm; hence the reduction. Several other clique-finding algorithms exist [Ambler et al. 1975; Knodel 1968; Bron and Kerbosch 1973; Osteen and Tou 1973].

### 11.2.2 Complexity

It is of some practical importance to be aware of the computational complexity of the matching algorithms proposed here; they may take surprising amounts of computer time. There are many accessible treatments of computational complexity of graph-theoretic algorithms [Reingold et al. 1977; Aho, Hopcroft and Ullman 1974]. Theoretical results usually describe worst-case or average time complexity. The state of knowledge in graph algorithms is still improving; some interesting worst-case bounds have not been established.

A "hard" combinatorial problem is one that takes time (in a usual model of computation based on a serial computer) proportional to an exponential function of the length of the input. "Polynomial-time" solutions are desirable because they do not grow as fast with the size of the problem. The time to find all the cliques of a graph is in the worst case inherently exponential in the size of the input graphs, because the output is an exponential number of graphs. Both the single subgraph isomorphism problem and the "clique problem" (does there exist a clique of size $k$?) are *NP-complete*; all known deterministic algorithms run (in the worst case) in time exponential in the length of the description of the graphs involved (which must specify the nodes and arcs). Not only this, but if either of these problems (or a host of other NP complete problems) could be solved deterministically in time polynomially related to the length of the input, it could be used to solve all the other NP problems in polynomial time.

Graph isomorphism, both directed and undirected, is at this writing in a netherworld (along with many other combinatorial problems). No polynomial-time deterministic algorithms are known to exist, but the relation of these problems to each other is not as clear-cut as it is between the NP-complete problem. In particular, finding a polynomial-time deterministic solution to one of them would not necessarily indicate anything about how to solve the other problems deterministically in polynomial time. These problems are not mutually reducible. Certain restrictions on the graphs, for instance that they are planar (can be arranged with their nodes in a plane and with no arcs crossing), can make graph isomorphism an "easy" (polynomial-time) problem.

The average-case complexity is often of more practical interest than the worst case. Typically, such a measure is impossible to determine analytically and must be approximated through simulation. For instance, one algorithm to find isomorphisms of randomly generated graphs yields an average time that seems not exponential, but proportional to $N^3$, with $N$ the number of nodes in the graph [Ullman 1976]. Another algorithm seems to run in average time proportional to $N^2$ [Corneil and Gotlieb 1970].

All the graph problems of this section are in NP. That is, a *non*deterministic algorithm can solve them in polynomial time. There are various ways of visualizing

nondeterministic algorithms; one is that the algorithm makes certain significant "good guesses" from a range of possibilities (such as correctly guessing which subset of nodes from graph $B$ are isomorphic with graph $A$ and then only having to worry about the arcs). Another way is to imagine *parallel* computation; in the clique problem, for example, imagine multiple machines running in parallel, each with a different subset of nodes from the input graph. If any machine discovers a totally connected subset, it has, of course, discovered a clique. Checking whether $N$ nodes are all pairwise connected is at most a polynomial-time problem, so all the machines will terminate in polynomial time, either with success or not. Several interesting processes can be implemented with parallel computations. Ullman's algorithm uses a refinement procedure which may run in parallel between stages of his tree search, and which he explains how to implement in parallel hardware [Ullman 1976].

## 11.3 IMPLEMENTING GRAPH-THEORETIC ALGORITHMS

### 11.3.1 Matching Metrics

Matching involves *quantifiable similarities.* A match is not merely a correspondence, but a correspondence that has been quantified according to its "goodness." This measure of goodness is the *matching metric.* Similarity measures for correlation matching are lumped together as one number. In relational matching they must take into account a relational, structured form of data [Shapiro and Haralick 1979].

Most of the structural matching metrics may be explained with the physical analogy of "templates and springs" [Fischler and Elschlager 1973]. Imagine that the reference data comprise a structure on a transparent rubber sheet. The matching process moves this sheet over the input data structure, distorting the sheet so as to get the best match. The final goodness of fit depends on the individual matches between elements of the input and reference data, and on the amount of work it takes to distort the sheet. The continuous deformation process is a pretty abstraction which most matching algorithms do not implement. A computationally more tractable form of the idea is to consider the model as a set of rigid "templates" connected by "springs" (see Fig. 11.5). The templates are connected by "springs" whose "tension" is also a function of the relations between elements. A spring function can be arbitrarily complex and nonlinear; for example the "tension" in the spring can attain very high or infinite values for configurations of templates which cannot be allowed. Nonlinearity is good for such constraints as: in a picture of a face the two eyes must be essentially in a horizontal line and must be within fixed limits of distance. The quality of the match is a function of the goodness of fit of the templates locally and the amount of "energy" needed to stretch the springs to force the input onto the reference data. Costs may be imposed for missing or extra elements.

The template match functions and spring functions are general procedures, thus the templates may be more general than pure iconic templates. Further,

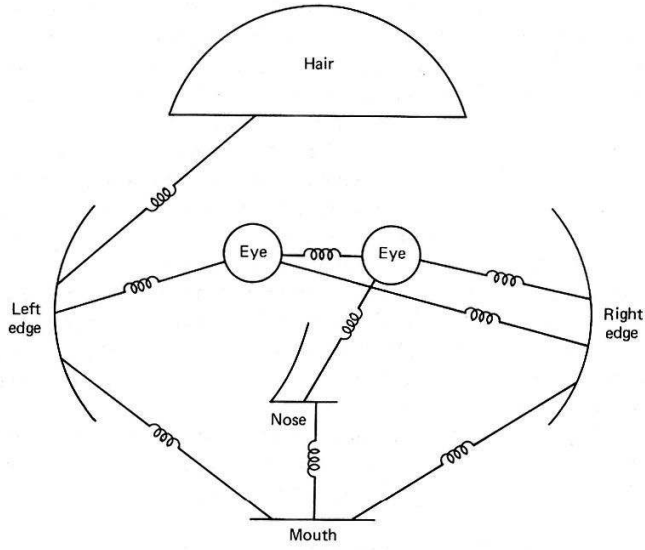



**Fig. 11.5** A templates and springs model of a face.

matches may be defined not only between nodes and other nodes, but between nodes and image data directly. Thus the template and springs formalism is workable for "cross-representational" matching. The mechanism of minimizing the total cost of the match can take several forms; more detailed examples follow in Section 11.4.

Equation 11.3 a general form of the template-and-springs metric. TemplateCost measures dissimilarity between the input and the templates, and SpringCost measures the dissimilarity between the matched input elements' relations and the reference relations between the templates. MissingCost measures the penalties for missing elements. $F(\cdot)$ is the mapping from templates of the reference to elements of the input data. F partitions the reference templates into two classes, those found {FoundinRefer} and those not found {MissinginRefer} in the input data. If the input data are symbolic they may be similarly partitioned. The general metric is

$$\begin{aligned} \text{Cost} = & \sum_{d \in \{\text{FoundinRefer}\}} \text{TemplateCost}(d, F(d)) \\ + & \sum_{(d, e) \in \{\text{FoundinRefer} \times \text{FoundinInput}\}} \text{SpringCost}(F(d), F(e)) \\ + & \sum_{c \in \{\text{MissinginRefer}\} \cup \{\text{MissinginInput}\}} \text{MissingCost}\ (c) \end{aligned} \tag{11.3}$$

Equation 11.3 may be written as one sum of generalized SpringCosts in which the template properties are included (as 1-ary relations), as are "springs" involving missing elements.

As with correlation metrics, there are normalization issues involved with structural matching metrics. The number of elements matched may affect the ultimate magnitude of the metric. For instance, if springs always have a finite cost, then the more elements that are matched, the higher the total spring energy must be; this should probably not be taken to imply that a match of many elements is worse than a match of a few. Conversely, suppose that relations which agree are given positive "goodness" measures, and a match is chosen on the basis of the total "goodness." Then unless one is careful, the sheer number of possibly mediocre relational matches induced by matching many elements may outweigh the "goodness" of an elegant match involving only a few elements. On the other hand, a small, elegant match of a part of the input structure with one particular reference object may leave much of the search structure unexplained. This good "submatch" may be less helpful than a match that explains more of the input. To some extent the general metric (Eq.11.3) copes with this by acknowledging the "missing" category of elements.

If the reference templates actually contain iconic representations of what the input elements should look like in the image, a TemplateCost can be associated with a template and a location in the image by

$$\begin{aligned}&\text{TemplateCost(Template, Location)}\\ &\quad = (1 - \text{normalized correlation metric between}\\ &\qquad \text{template shape and input image at the location}).\end{aligned}$$

If the match is, for instance, to match reference descriptions of a chair with an input data structure, a typical "spring" might be that the chair seat must be supported by its legs. Thus if $F$ is the association function mapping reference elements such as LEG or TABLETOP to input elements,

$$\text{SpringCost}_1(F(\text{LEG}), F(\text{TABLETOP}))$$
$$= \begin{cases} 0 & \text{if } F(\text{LEG}) \text{ appears to support } F(\text{TABLETOP}), \\ 1 & \text{if } F(\text{LEG}) \text{ does not appear to support } F(\text{TABLETOP}). \end{cases}$$

For quantified relations, one might have

$$\begin{aligned}\text{SpringCost}_2 = &\text{ number of standard deviations from the}\\ &\text{canonical mean value for this relation.}\end{aligned}$$

Another version of $\text{SpringCost}_2$ is the following [Barrow and Popplestone 1971].

$$\text{Cost of Match} = \frac{\text{SpringCosts of properties (unary) and binary relations}}{\text{total number of unary and binary springs}} + \frac{\text{Empirical Constant}}{\text{Total number of reference elements matched}} \tag{11.4}$$

The first term measures the average badness of matches between properties (unary relations) and relations between regions. The second term is inversely proportional to the number of regions that are matched, effectively increasing the cost of matches that explain less of the input.

### 11.3.2 Backtrack Search

Backtrack search is a generic name for a type of potentially exhaustive search organized in stages; each processing stage attempts to extend a partial solution derived in the previous stage. Should the attempt fail, the search "backtracks" to the most recent partial solution, from which a new extension is attempted. The technique is basic, amounting to a depth-first search through a tree of partial solutions (Fig. 11.6). Backtracking is a pervasive control structure in artificial intelli-

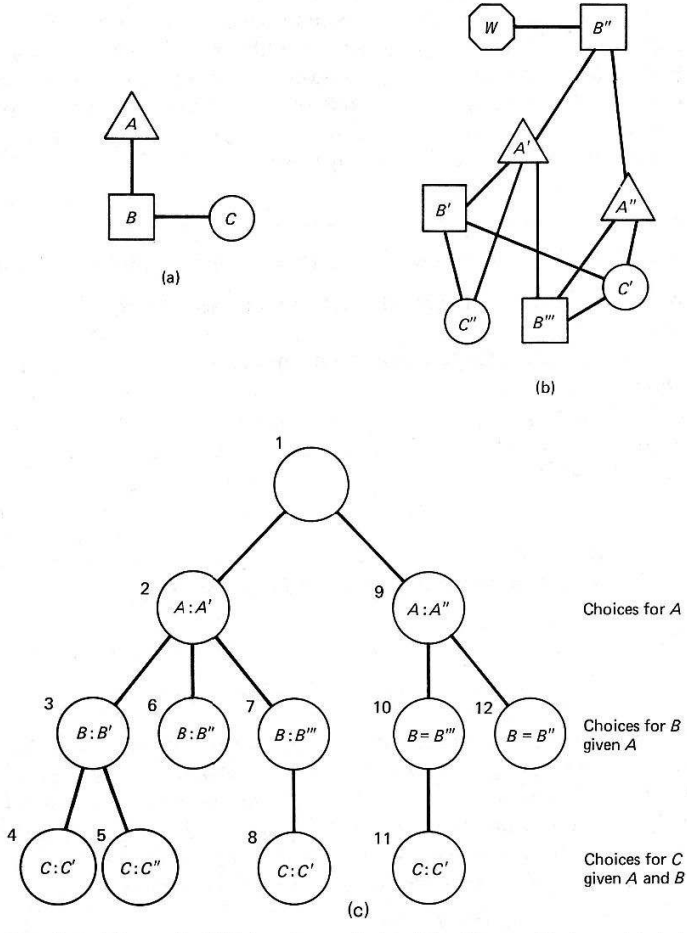



**Fig. 11.6** The graph of (a) is to be matched in (b) with arcs all being unlabeled but nodes having properties indicated by their shapes, (c) is the tree of solutions built by a backtrack algorithm.

gence, and through the years several general classes of techniques have evolved to make the basic, brute-force backtrack search more efficient.

*Example: Graph Isomorphisms*

Given two graphs,

$$X = (V_X, E_X)$$
$$Y = (V_Y, E_Y),$$

without loss of generality, let $V_X = V_Y = \{1, 2, \ldots, n\}$, and let $X$ be the reference graph, $Y$ the input graph. The isomorphism is given by: If $i \in V_X$, the corresponding node under the isomorphism is $F(i) \in V_Y$.

In the algorithm, $S$ is the set of nodes accounted for in $Y$ by a partial solution. $k$ gives the current level of the search in the tree of partial solutions, the number of nodes in the current partial solution, and the node of $X$ whose match in $Y$ is currently being sought. $v$ is a node of $Y$ currently being considered to extend the current partial solution. As written, the algorithm finds all isomorphisms. It is easily modified to quit after finding the first.

---

**Algorithm 11.1** Backtrack Search for Directed Graph Isomorphism

```
Recursive Procedure DirectedGraphIsomorphisms(S,k);
begin
 if S=V_Y then ReportAsIsomorphism(F)
 else
  forall v ∈ (V_Y−S)
    do
    if Match(k,v)
    then
     begin
      F(k) := v;
      DirectedGraphIsomorphisms (S ∈ {v}, k+1);
     end;
end;
```

---

ReportAsIsomorphism could print or save the current value of $F$, the global structure recording the current solution. Match$(k,v)$ is a procedure that tests whether $v \in V_Y$ can correspond to $k \in V_X$ under the isomorphism so far defined by $F$. Let $X_k$ be the subgraph of $X$ with vertices $\{1, 2, \ldots, k\}$. The procedure "Match" must check for $i < k$, whether $(i, k)$ is an edge of $X_k$ iff $(F(i), v)$ is an edge of $Y$ *and* whether $(k, i)$ is an edge of $X_k$ iff $(v, F(i))$ is an edge of $Y$.

*Improving Backtrack Search*

Several techniques are useful in improving the efficiency of backtrack search [Bittner and Reingold 1975]:

1. *Branch pruning.* All techniques of this variety examine the current partial solution and prune away descendents that are not viable continuations of the solution. Should none exist, backtracking can take place immediately.
2. *Branch merging.* Do not search branches of the solution tree isomorphic with those already searched.
3. *Tree rearrangement and reordering.* Given pruning capabilities, more nodes are likely to be eliminated by pruning if there are fewer choices to make early in the search (partial solution nodes of low degree should be high in the search tree). Similarly, search first those extensions to the current solution that have the fewest alternatives.
4. *Branch and bound.* If a cost may be assigned to solutions, standard techniques such as heuristic search and the A* search algorithm [Nilsson 1980] (Section 4.4) may be employed to allow the search to proceed on a "best-first" rather than a "depth-first" basis.

For extensions of these techniques, see [Haralick and Elliott 1979].

### 11.3.3 Association Graph Techniques

*Generalized Structure Matching*

A general relational structure "best match" is less restricted than graph isomorphism, because nodes or arcs may be missing from one or the other graph. Also, it is more general than subgraph isomorphism because one structure may not be exactly isomorphic to a substructure of the other. A more general match consists of a set of nodes from one structure and a set of nodes from the other and a 1:1 mapping between them which preserves the compatibilities of properties and relations. In other words, corresponding nodes (under the node mapping) have sufficiently similar properties, and corresponding sets under the mapping have compatible relations.

The two relational structures may have a complex makeup that falls outside the normal purview of graph theory. For instance, they may have parameterized properties attached to their nodes and edges. The definition of whether a node matches another node and whether two such node matches are mutually compatible can be determined by arbitrary procedures, unlike the much simpler criteria used in pure graph isomorphism or subgraph isomorphism, for example. Recall that the various graph and subgraph isomorphisms rely heavily on a 1:1 match, at least locally, between arcs and nodes of the structures to be matched. However, the idea of a "best match" may make sense even in the absence of such perfect correspondences.

The *association graph* defined in this section is an auxiliary data structure produced from two relational structures to be matched. The beauty of the association graph is that it *is* a simple, pure graph-theoretic structure which is amenable to pure graph-theoretic algorithms such as clique finding. This is useful for several reasons.

- It takes relational structure matching from the ad hoc to the classical domain.
- It broadens the base of people who are producing useful algorithms for structure matching. If the rather specialized relational structure matching enterprise is reducible to a classical graph-theoretical problem, then everyone working on the classical problem is also working indirectly on structure matching.
- Knowledge about the computational complexity of classical graph algorithms illuminates the difficulty of structure matching.

*Clique Finding for Generalized Matching*

Let a relational structure be a set of elements $V$, a set of properties (or more simply unary predicates) $P$ defined over the elements, and a set of binary relations (or binary predicates) $R$ defined over pairs of the elements. An example of a graph representation of such a structure is given in Fig. 11.7.

Given two structures defined by $(V_1, P, R)$ and $(V_2, P, R)$, say that "similar" and "compatible" actually mean "the same." Then we construct an association graph $G$ as follows [Ambler et al. 1975]. For each $v_1$ in $V_1$ and $v_2$ in $V_2$, construct a node of $G$ labeled $(v_1, v_2)$ if $v_1$ and $v_2$ have the same properties [$p(v_1)$ iff $p(v_2)$ for each $p$ in $P$]. Thus the nodes of $G$ denote assignments, or pairs of nodes, one each from $V_1$ and $V_2$, which have similar properties. Now connect two nodes $(v_1, v_2)$ and $(v'_1, v'_2)$ of $G$ if they represent *compatible* assignments according to $R$, that is, if the pairs satisfy the same binary predicates [$r(v_1, v'_1)$ iff $r(v_2, v'_2)$ for each $r$ in $R$].

A match between $(V_1, P, R)$ and $(V_2, P, R)$, the two relational structures, is just a set of assignments that are all mutually compatible. The "best match" could well be taken to be the largest set of assignments (node correspondences) that were all mutually compatible under the relations. But this in the association graph $G$ is just the largest totally connected (completely mutually compatible)—set of nodes. It is a *clique.* A clique to which no new nodes may be added without destroying the clique properties is a *maximal* clique. In this formulation of matching, larger cliques are taken to indicate better matches, since they account for more nodes.

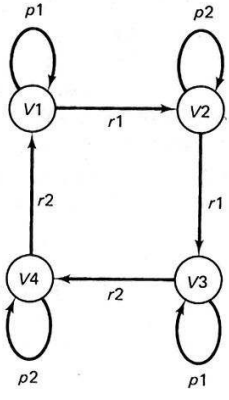



**Fig. 11.7** A graph representation of a relational structure. Elements (nodes) $v_1$ and $v_3$ have property p1, $v_2$ and $v_4$ have property p2, and the arcs between nodes indicate that the relation r1 holds between $v_1$ and $v_2$ and between $v_2$ and $v_3$, and r2 holds between $v_3$ and $v_4$ and between $v_4$ and $v_1$.

Thus the best matches are determined by the largest maximal cliques in the association graph. Figure 11.8 shows an example: Certain subfeatures of the objects have been selected as "primitive elements" of the objects, and appear as nodes (elements) in the relational structures. To these nodes are attached properties, and between them can exist relations. The choice of primitives, properties, and relations is up to the designer of the representation. Here the primitives of the representation correspond to edges and corners of the shape.

The association graph is shown in 11.8e. Its nodes correspond to pairs of nodes, one each from A and B, whose properties are similar. [Notice that there is no node in the association graph for (6,6′)]. The arcs of the association graph indicate that the endpoints of the arc represent compatible associations. Maximal cliques in the association graph (shown as sets of nodes with the same shape) indicate sets of consistent associations. The largest maximal clique provides the node pairings of the "best match."

In the example construction, the association graph is formed by associating nodes with exactly the same properties (actually unary predicates), and by allowing as compatible associations only those with exactly the same relations (actually binary predicates). These conditions are easy to state, but they may not be exactly what is needed. In particular, if the properties and relations may take on ranges of values greater than the binary "exists" and "does not exist," then a measure of similarity must be introduced to define when node properties are similar enough for association, and when relations are similar enough for compatibility. Arbitrarily complex functions can decide whether properties and relations are similar. As long as the function answers "yes" or "no," the complexity of its computations is irrelevant to the matching algorithm.

The following recursive clique-finding algorithm builds up cliques a node at a time [Ambler et al. 1975]. The search tree it generates has states that are ordered pairs (set of nodes chosen for a clique, set of nodes available for inclusion in the clique). The root of the tree is the state ($\varnothing$, all graph nodes), and at each branch a choice is made whether to include or not to include an eligible node in the clique. (If a node is eligible for inclusion in clique $X$, then *each* clique including $X$ must either include the node or exclude it).

---

**Algorithm 11.2:** Clique-Finding Algorithm

Comment *Nodes* is the set of nodes in the input graph.

Comment
  *Cliques* $(X, Y)$ takes as arguments a clique $X$, and $Y$, a set of nodes that includes $X$. It returns all cliques that include $X$ and are included in $Y$.
  *Cliques* ($\varnothing$,Nodes) finds all cliques in the graph.
*Cliques*$(X, Y)$ :=
  *if* no node in $Y-X$ is connected to all elements of $X$
    *then* $\{X\}$
    *else*
      Cliques$(X \cup \{y\}, Y) \cup$ Cliques $(X, Y-\{y\})$
      *where* $y$ is connected to all elements of $X$.

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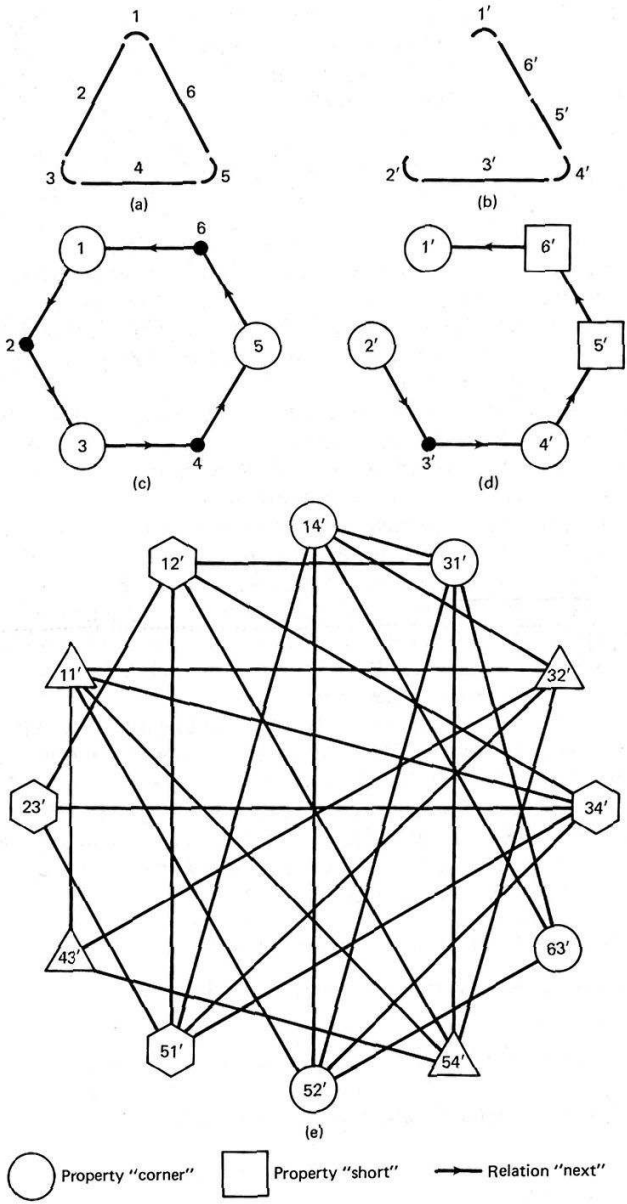



**Fig. 11.8** Clique-finding example. Entities to be matched are given in (a) (reference) and (b) (input). The relational structures corresponding to them are shown in (c) and (d). The resulting association graph is shown in (e) with its largest cliques indicated by node shapes.

*Extensions*

Modifications to the clique-finding algorithm extend it to finding maximal cliques and finding largest cliques. To find largest cliques, perform an additional test to stop the recursion in *Cliques* if the size of $X$ plus the number of nodes in $Y-X$ connected to all of $X$ becomes less than $k$, which is initially set to the size of the largest possible clique. If no cliques of size $k$ are found, decrement $k$ and run *Cliques* with the new $k$.

To find maximal cliques, at each stage of *Cliques*, compute the set

$$Y' = \{z \in \text{Nodes: } z \text{ is connected to each node of Y}\}.$$

Since any maximal clique must include $Y'$, searching a branch may be terminated should $Y'$ not be contained in $Y$, since $Y$ can then contain no maximal cliques.

The association graph may be searched not for cliques, but for $r$-connected components. An *r-connected* component is a set of nodes such that each node is connected to at least $r$ other nodes of the set. A clique of size $n$ is an $n-1$-connected component. Fig. 11.9 shows some examples.

The $r$-connected components generalize the notion of clique. An $r$-connected component of $N$ nodes in the association graph indicates a match of $N$ pairs of nodes from the input and reference structures, as does an $N$-clique. Each matching pair has similar properties, and each pair is compatible with at least $r$ other matches in the component.

Whether or not the $r$-connected component definition of a match between two structures is useful depends on the semantics of "compatibility." For instance, if all relations are either compulsory or prohibited, clearly a clique is called for. If the relations merely give some degree of mutual support, perhaps an $r$-connected component is the better definition of a match.

## 11.4 MATCHING IN PRACTICE

This section illustrates some principles of matching with examples from the computer vision literature.

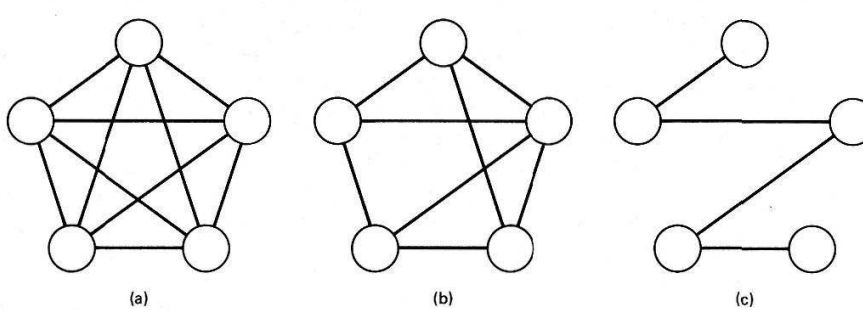



**Fig. 11.9** $r$-connected components. (a) A 5-clique (which is 4-connected). (b) A 3-connected set of 5 nodes. (c) A 1-connected set of 5 nodes.

### 11.4.1 Decision Trees

Hierarchical decision-tree matching with ad hoc metrics is a popular way to identify input data structures as instances of reference models and thus classify the input instances [Nevatia 1974; Ambler et al. 1975; Winston 1975]. Decision trees are indicated when it is predictable that certain features are more reliably extracted than others and that certain relations are either easier to sense or more necessary to the success of a match.

Winston and Nevatia both compare matches with a "weighted sums of difference" metric that reflects cumulative differences between the parameters of corresponding elements and relations in the reference and input data. In addition, Nevatia does parameter fitting; his reference information includes geometrical information.

*Matching Structural Descriptions*

Winston is interested in matching such structures as appear in Fig. 11.10B. The idea is to recognize instances of structural concepts such as "arch" or "house," which are relational structures of primitive blocks (Fig.11.10A) [Winston 1975]. An important part of the program learns the concept in the first place—only the matching aspect of the program is discussed here. His system has the pleasant property of representational uniqueness: reference and input data structures that are identical up to the resolution of the descriptors used by the program have identical representations. Matching is easy in this case. Reflections of block structures can be recognized because the information available about relations (such as LEFT-OF and IN-FRONT-OF) includes their OPPOSITE (i.e., RIGHT-OF and BEHIND). The program thus can recognize various sorts of symmetry by replacing all input data structure relations by their relevant opposite, then comparing with the reference.

The next most complicated matching task after exact or symmetric matches is to match structures in isolation. Here the method is sequentially to match the input data against the whole reference data catalog of structures and determine which match is best (which difference description is most inconsequential). Easily computed scene characteristics can rule out some candidate models immediately.

The models contain arcs such as MUST-BE and MUST-NOT, expressing relations mandatory or forbidden relations. A match is not allowed between a description and a model if one of the strictures is violated. For instance, the program may reject a "house" immediately as not being a "pedestal," "tent," or "arch," since the pedestal top must be a parallelepiped, both tent components must be wedges, and the house is missing a component to support the top piece that is needed in the arch. These outright rejections are in a sense easy cases; it can also happen that more than one model matches some scene description. To determine the best match in this case, a weighted sum of differences is made to express the amount of difference.

The next harder case is to match structures in a complex scene. The issue here is what to do about evidence that is missing through obscuration. Two heuristics help:

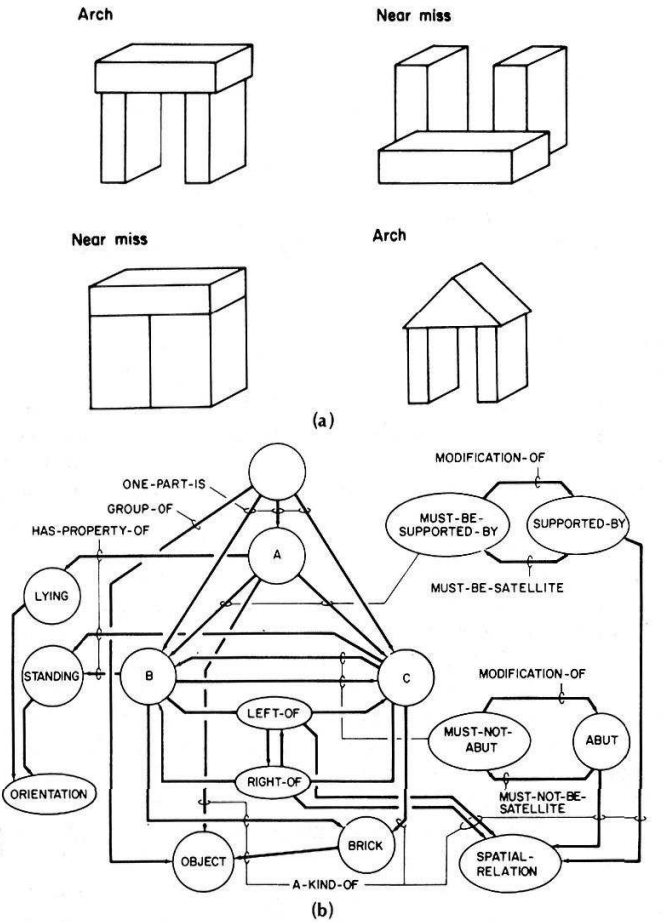



**Fig. 11.10** (a) Several arches and non-arches. (b) The computer-generated arch description to be used for matching.

1. Objects that seem to have been stacked and could be the same type are of the same type.
2. Essential model properties may be hidden in the scene, so the match should not be aborted because of missing essential properties (though the presence of forbidden properties is enough to abort a match).

This latter rule is equivalent to Nevatia's rules about connectivity difference and missing input instance parts (see below). In terms of the general structure metric introduced earlier, neither Winston or Nevatia penalize the match for missing elements or relations in the reference data. One result of this is that the best match is sometimes missed in favor of the first possible match. Winston suggests that com-

plex scenes be analyzed by identifying subscenes and subtracting out the identified parts, as was done by Roberts.

Winston's program can learn shortcuts in matching strategy by itself; it builds for itself a similarity network relating models whose differences are slight. If a reference model does not quite fit an input structure, the program can make an intelligent choice of the next model to try. A good choice is a model that has only minor differences with the first. This self-organization and cataloging of the models according to their mutual differences is a powerful way to use matching work that is already performed to guide further search for a good match.

*Backtrack Search*

Nevatia addresses a domain of complex articulated biological-like forms (hands, horses, dolls, snakes) [Nevatia 1974]. His strategy is to segment the objects into parts with central axes and "cross section" (not unlike generalized cylinders, except that they are largely treated in two dimensions). The derived descriptions of objects contain the connectivity of subparts, and descriptions of the shape and joint types of the parts. Matching is needed to compare descriptions and find differences, which can then be explained or used to abort the match. Partial matches are important (as in most real-world domains) because of occlusions, noise, and so on.

A priori ideas as to the relative importance of different aspects of structures are used to impose a hierarchical order on the matching decision tree. Nevatia finds this heuristic approach more appealing than a uniform, domain-independent one such as clique finding. His system knows that certain parts of a structure are more important than others, and uses them to index into the reference data catalog containing known structures. Thus relevant models for matching may be retrieved efficiently on the basis of easily-computed functions of the input data. The models are generated by the machine by the same process that later extracts descriptions of the image for recognition. Several different models are stored for the same view of the same object, because his program has no idea of model equivalence, and cannot always extract the same description.

The matching process is basically a depth-first tree search, with initial choices being constrained by "distinguished pieces." These are important pieces of image which first dictate the models to be tried in the match, and then constrain the possible other matches of other parts.

There is a topological and a geometrical component to the match. The topological part is based on the connectivity of the "stick figure" that underlies the representation. The geometrical part matches the more local characteristics of individual pieces. Consider Nevatia's example of matching a doll with stored reference descriptions, including those of a doll and a horse.

By a process not concerning us here, the doll image is segmented into pieces as shown in Fig. 11.11. From this, before any matching is done, a connection graph of pieces is formed, as shown in Fig. 11.12.

This connection graph is topologically the same as the reference connection graph for the doll, which looks as one would expect. In both reference and input, "distinguished pieces" are identified by their large size. During reference forma-

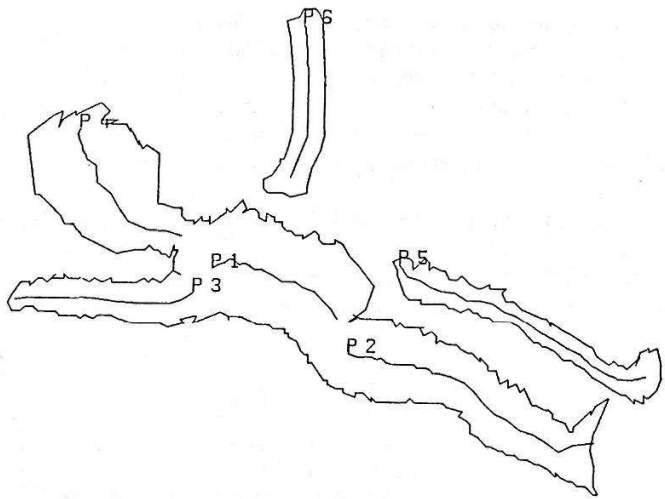



**Fig. 11.11** A view of a doll, with derived structure.

tion time, the two largest pieces were the head and the trunk, and these are the distinguished pieces in the reference. There are the same pieces picked as distinguished in the instance to be matched consistent with the hierarchical decision-tree style, distinguished pieces are matched first.

Because of noise, connections at joints may be missed; because of the nature of the objects, extra joints are hardly ever produced. Thus there is a domain-dependent rule that an input piece with two other pieces connected at a single joint (a "two-ended piece") cannot match a one-ended reference piece, although the reverse is possible.

On the basis of the distinguished pieces in the input instance, the program decides that the instance could be a doll or a horse. Both these possibilities are evaluated carefully; Fig. 11.13 shows a schematic view of the process. Piece-match evaluation must be performed at the nodes of the tree to determine which pieces at a joint should be made to correspond.

The final best match between the doll input and the horse reference model is diagrammed in Fig. 11.14. This match is not as good as the match between the doll input and the doll reference.

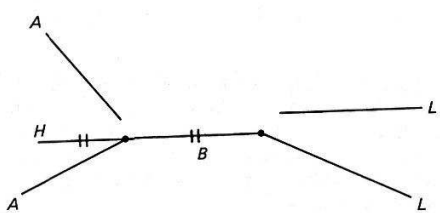



**Fig. 11.12** Connection graph of the doll.

The final choice of matches is made with a version of the general relational structure matching metric (Eq. 11.3). It takes into account the connectivity relations, which are the same in this case, and the quality of the individual piece matches. In the doll-horse match, more reference parts are missing, but this can happen if parts are hidden in a view, and do not count against the match. The doll-doll match is preferred on the basis of piece matching, but both matches are considered possible.

In summary, the selection of best match proceeds roughly as follows: unacceptable differences are first sought (not unlike the Winston system). The number of input pieces not matched by the reference is an important number (not vice versa, because of the possibility of hidden input parts). Only elongated, large parts

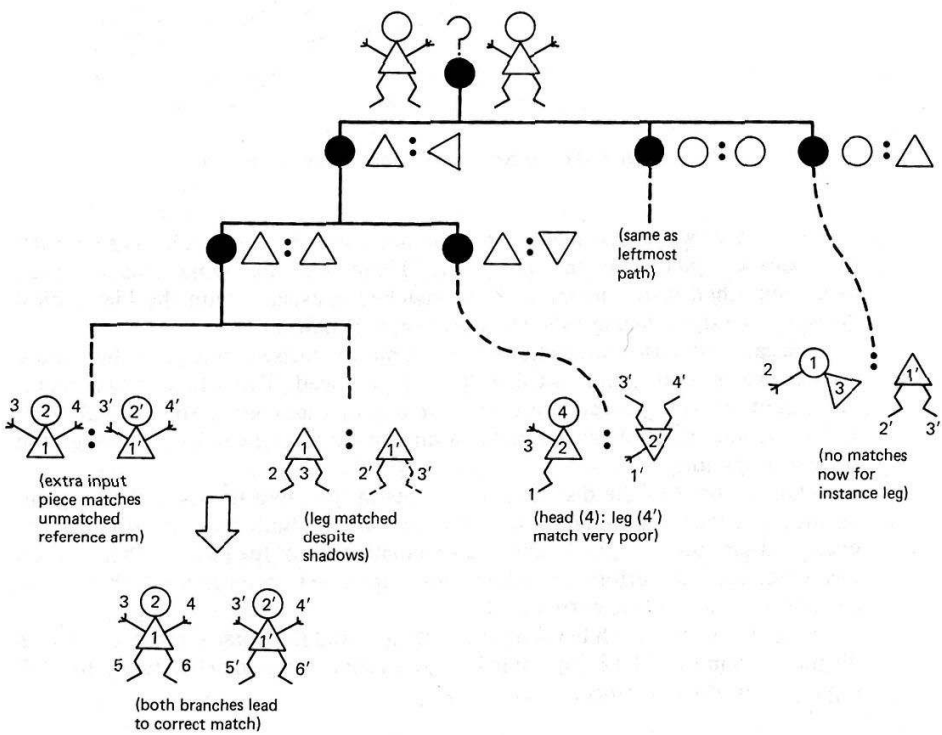



**Fig. 11.13** A pictorial guide to the combinations tried by the matcher establishing the best correspondence of the doll input with the doll reference. The graphic shapes are purely pedagogical: the program deals with symbolic connectivity information and geometric measurements. Inferences and discoveries made by the program while matching are given in the diagram. A:B means that structure A is matched with structure B, with the numbered substructures of A matching their primed counterparts in B.

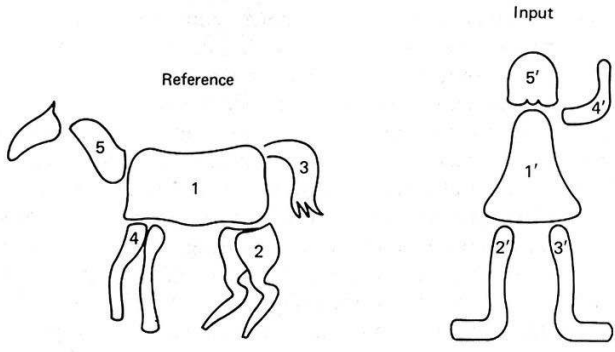



**Fig. 11.14** The best match of the doll input with the horse reference model. One doll arm is unmatched, as is the horse head and two legs.

are considered for this determination, to eliminate small "noise" patches. The match with fewest unmatched input pieces is chosen.

If no deciding structural differences exist, the quality of piece matches determines the quality of the match. These correspond to the template cost term in Eq. (11.3). If a "significant" difference in match error exists, the better match is exclusively selected; if the difference is not so great as that, the better match is merely preferred.

Piece matching is a subprocess of joint matching. The difference in the number of pieces attached at the ends of the piece to be matched is the *connectivity difference.* If the object piece has more pieces connected to it than the model piece, the match is a poor one; since pieces may not be visible in a view, the converse is not true. If one match gives fewer excess input pieces, it is accepted at this point. If not, the goodness of the match is computed as a weighted sum of width difference, length-to-width ratio difference, and difference in acuteness of the generalized cylinders (Chapter 9) forming the pieces. The weighted sum is thresholded to yield a final "yes or no" match result. Shadowing phenomena are accommodated by allowing the input piece to be narrower than the reference model piece with no penalty. The error function weights are derived empirically; one would not expect the viewing angle to affect seriously the width of a piece, for example, but it could affect its length. Piece axis shapes (what sort of space curve they are) are not used for domain-dependent reasons, nor are cross section functions (aside from a measure of "acuteness" for cone-like generalized cylinders).

### 11.4.2 Decision Tree and Subgraph Isomorphism

A robotics program for versatile assembly [Ambler et al. 1975] uses matching to identify individual objects on the basis of their boundaries, and to match several individual blobs on a screen with a reference model containing the known location of multiple objects in the field of view. In both cases the best subgraph isomorphism between input and reference data structures is found when necessary by the clique-finding technique (Algorithm 11.2).

The input data to the part recognizer consist of silhouettes of parts with outlines of piecewise linear and circular segments. A typical set of shapes to be recognized might be stored in terms of boundary primitives as shown in Fig. 11.15a, with matchable and unmatchable scenes shown in Fig. 11.15b.

Generally, the matching process works on hierarchical structures which capture increasing levels of detail about the objects of interest. The matching works its way down the hierarchy, from high-level, easily computable properties such as size down to difficult properties such as the arrangements of linear segments in a part outline. After this decision tree pre-processing, all possible matches are computed by the clique-finding approach to subgraph isomorphism. A scene can be assigned a number of interpretations, including those of different views of the same part. The hierarchical organization means that complicated properties of the scene are not computed unless they are needed by the matcher. Once computed they are never recomputed, since they are stored in accessible places for later retrieval if needed. Each matching level produces multiple interpretations; ambiguity is treated with backtracking. The system recognizes rotational and translational invariance, but must be taught different views of the same object in its different gravitationally stable states. It treats these different states basically as different objects.

### 11.4.3 Informal Feature Classification

The domain of this work is one of small, curved tabletop objects, such as a teacup (Fig. 11.16) [Barrow and Popplestone 1971]. The primitives in models and image descriptions are regions which are found by a process irrelevant here. The regions have certain properties (such as shape or brightness), and they have certain parameterized relations with other regions (such as distance, adjacency, "aboveness"). The input and reference data are both relational structures. The properties and relations are the following:

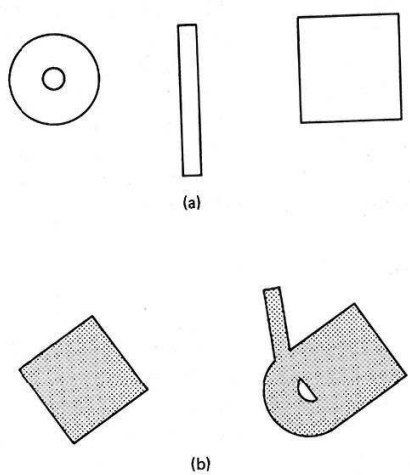



**Fig. 11.15** A small catalog of part boundaries (a) and some sample silhouettes (b). The "heap" will not match any part very well, while the square can match the square model in four different ways, through rotations. Gross properties such as area may be used cheaply to reject matches such as the square with the axle.

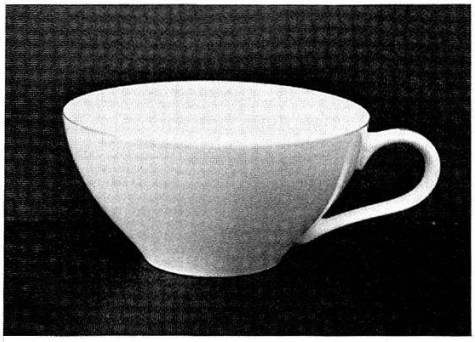


**Fig. 11.16** An object for recognition by relational matching.

1. *Region Properties*

   Shape 1–Shape 6: the first six root mean square amplitudes of the Fourier components of the $\phi$(s) curve [Chapter 8].

2. *Relations between Regions A and B*

   Bigger: Area(A)/Area(B)

   Adjacency: Fraction of A's boundary which also is a boundary of B.

   Distance: Distance between centroids divided by the geometric mean of average radii. The average radius is twice the area over the perimeter. Distance is scale, rotation, translation, reflection invariant.

   Compactness: $4*\pi*area/perimeter^2$

   Above, Beside: Vertical and horizontal distance between centroids, normalized by average radius. Not rotation invariant.

The model that might be derived for the cup of Fig. 11.16 is shown in Fig. 11.17.

The program works on objects such as spectacles, pen, cup, or ball. During training, views and their identifications are given to the program, and the program forms a relational structure with information about the mean and variance of the values of the relations and properties. After training, the program is presented with a scene containing one of the learned objects. A relational structure is built describing the scene; the problem is then to match this input description with a reference description from the set of models.

One approximation to the goodness of a match is the number of successes provided by a region correspondence. A one-region object description has 7 relations to check, a two-region object has 28, a three-region one has 63. Therefore, the "successes" criterion could imply the choice of a terrible three-region interpretation over a perfect one-region match. The solution adapted in the matching evaluation is first to grade failures. A failure weight is assigned to a trial match according to how many standard deviations $\sigma$ from the model mean the relevant

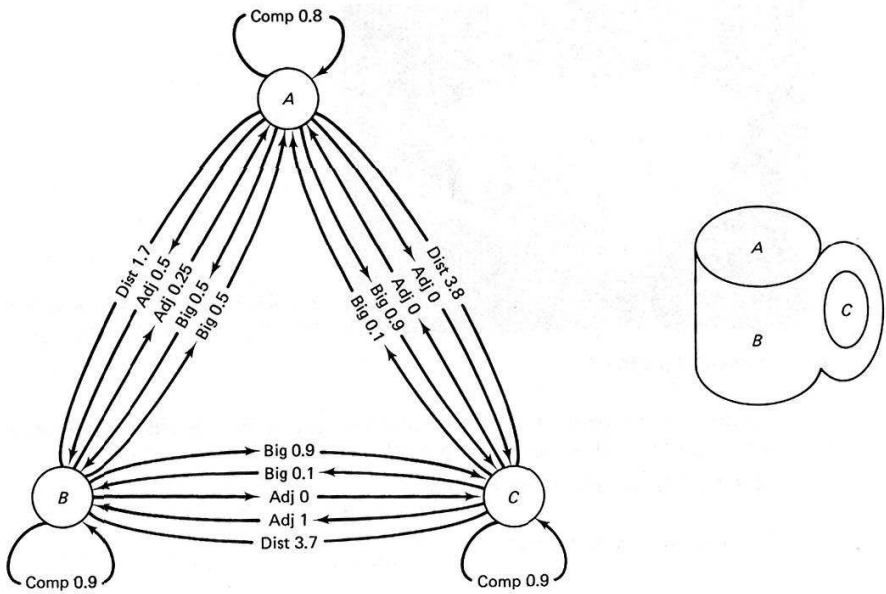



**Fig. 11.17** Relational model for cups such as that of Fig. 11.16.

parameter is. From zero to three $\sigma$ imply a success, or a failure weight of 0; from three to six $\sigma$, a failure weight of 1; from six to nine $\sigma$, failure weight of 2, and so on. Then the measure "trials–cumulative failure weight" is an improvement on just "successes." On the other hand, simple objects are often found as subparts of complex ones, and one does not want to reject a good interpretation as a complex object in favor of a less explanatory one as a simple object. The final evaluation function adapted is

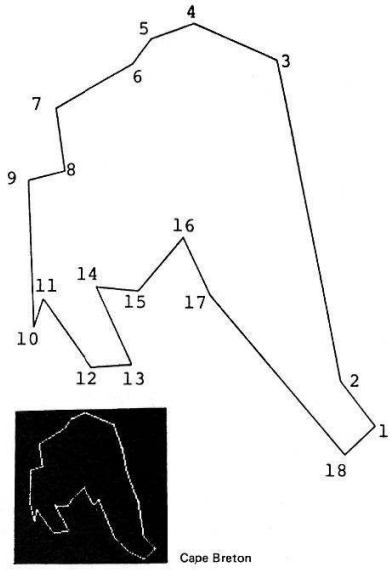
$$\text{Cost of Match} = \frac{1 - (\text{tries-failure weight})}{\text{number of relations}} + \frac{K}{\text{number of regions in view description}} \tag{11.5}$$

As in Eq. (11.4), the first term measures the average badness of matches between properties (unary relations) and relations between regions. The second term is inversely proportional to the number of regions that are matched, effectively increasing the cost of matches that explain less of the input.

### 11.4.4 A Complex Matcher

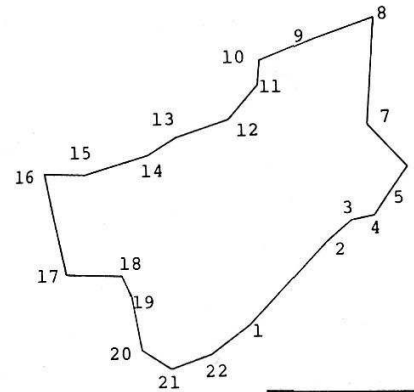
A program to match linear structures like those of Fig. 11.18 is described in [Davis 1976]. This matcher presents quite a diversity of matching techniques incorporated into one domain-dependent program.

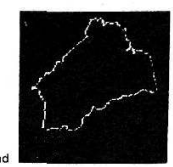
The matching metric is very close to the general metric of Eg. (11.3). The match is characterized by a structural match of reference and input elements and a geometrical transformation (found by parameter fitting) which accounts for the spatial relations between reference and input. Davis forms an association graph between reference and input data. This graph is reduced by parallel-iterative relaxation (see Section 12.4) using the "spring functions" to determine which node associations are too costly. Eliminating one node–node match may render others



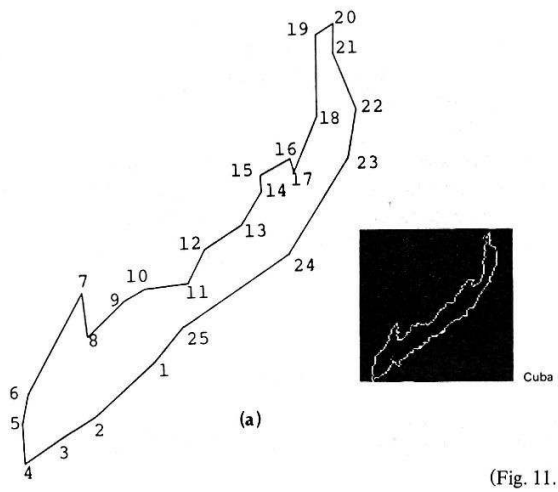



Cape Breton



Baffin Island




(a)



Cuba

(Fig. 11.18 continues on p. 380.)

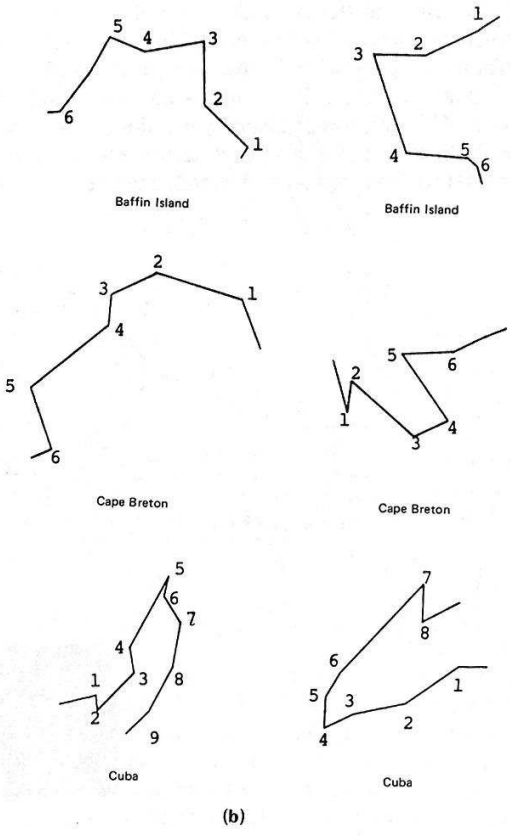



**Fig. 11.18** (a) Reference and (b) input data for a complex shape matching program.

more unlikely, so the node-pruning process iterates until no more nodes are eliminated. What remains is something like an $r$-connected component of the graph, which specifies an approximate match supported by some amount of consistent relations between nodes.

After the process of constraint relaxation, there are still in general several locally consistent interpretations for each component of the input structure. Next, therefore, a tree search is used to establish global consistency and therefore the best match. The tree search is the familiar "best first" heuristic search through the partial match space, with pruning taking place between each stage of search again by using the parallel-iterative relaxation technique.

## EXERCISES

**11.1** Relational structures $A$ and $B$ are to be matched by the association-graph, clique-finding method.

Relational structure $A$: entities $u, v, w, x, y, z$.
relations $P(u), P(w), P(y), R(v), R(x), R(z)$,
$F(u, v), F(v, w), F(w, x), F(x, y), F(y, z), F(z, u)$

Relational structure B: entities $a, b, c, d, e, f$.
relations $P(a), P(b), P(d), Q(e), Q(f), R(c)$
$F(b, c), F(c, d), F(d, e), F(e, f), F(f, a)$.

(a) Construct graph structures corresponding to the structures $A$ and $B$. Label the nodes and arcs.

(b) Construct the association graph of structures $A$ and $B$.

(c) Visually find the largest maximal cliques in the association graph and thus the best matches between $A$ and $B$. (There are three.)

**11.2** Suppose in a geometric match that two input points on the $xy$ plane are identified with two others taken to correspond with two reference points. It is known that the input data comes about only through rotation and translation of the reference data. Given the two input points $(x_1, y_1)$ and $(x_2, y_2)$ and the two reference points $(x'_1, y'_1)$ and $(x'_2, y'_2)$, one way to find the transformation from reference to input is to solve the equation

$$\sum_{i=1}^{2} [x_i - (ax'_i + by'_i + c)]^2 + [y_i - (bx'_i + ay'_i + d)]^2 = 0$$

The resulting values of $a$, $b$, $c$, and $d$ represent the desired transformation. Solve the equation analytically to get expressions for $a$, $b$, $c$, and $d$ in terms of the reference and input coordinates. What happens if the reference and input data are not related by simple rotation and translation?

**11.3** What are the advantages and disadvantages of a uniform method (such as subgraph isomorphism algorithm approach) to matching as compared to an ad hoc (such as a decision-tree approach with various empirically derived metrics) one?

**11.4** In the worst case, for graphs of $n$ nodes, how many partial solutions total will Algorithm 11.1 have to proceed through? Construct "worst case" graphs $X$ and $Y$ (label their nodes $1, \ldots, n$, of course), assuming that nodes of $Y$ are selected in ascending order at any stage.

**11.5** Find out something about the state of associative memories in computers. How do they work? How are they used? Would anything like this technology be useful for computer vision? Introspect about familiar phenomena of visual recall, recognition, and memory. Do you have a theory about how human visual memory could possibly work?

**11.6** What graph of $N$ nodes has the maximum number of maximal cliques? How many does it have?

**11.7** Think about reasoning by analogy and find out something about programs that do analogical reasoning. In what sense can analogical process be used for computer vision, and technically do the matching techniques necessary provide any insight?

**11.8** Compare Nevatia's structure matching with Hinton's relaxation-based puppet recognition (Chapter 12).

**11.9** Verify the observation made in Section 11.4.3 about the number of relations that must be checked between regions (one region, 7; two regions, 28; three regions, 63; etc.).

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# Inference 12

## Classical and Extended Inference

This chapter explores *inference,* the process of deducing facts from other known facts. Inference is useful for belief maintenance and is a cornerstone of rational thought. We start with *predicate logic*, and then explore *extended inference* systems—production systems, relaxation labeling, and active knowledge (procedures).

*Predicate logic* (Section 12.1) is a system for expressing propositions and for deriving consequences of facts. It has evolved over centuries, and many clear accounts describe predicate logic in its various forms [Mendelson 1964; Robinson 1965]. It has good formal properties, a nontrivial but automatable inference procedure, and a history of study in artificial intelligence. There are several "classical" extensions (modal logics, higher-order logics) which are studied in well-settled academic disciplines of metamathematics and philosophy. *Extended inference* (Section 12.2) is possible in automated systems, and is interesting technically and from an implementational standpoint.

A *production system* (Section 12.3) is a general rewriting system consisting of a set of *rewriting rules* ($A \rightarrow BC$ could mean "rewrite $A$ as $BC$") and an executive program to apply rewrites. More generally, the rules can be considered "situation–action" pairs ("in situation $A$, do $B$ and $C$"). Thus production systems can be used to control computational activities. Production systems, like semantic nets, embody powerful notions that can be used for extended inference.

*Labeling schemes* (Section 12.4) are unlike most inference mechanisms in that they often involve mathematical optimization in continuous spaces and can be implemented with parallel computation. Labeling is like inference because it establishes consistent "probability-like" values for "hypotheses" about the interpretation of entities.

*Active knowledge* (Section 12.5) is an implementation of inference in which each chunk of knowledge is a program. This technique goes far in the direction of "proceduralizing" the implementation of propositions. The design issues for such a system include the vocabulary of system primitives and their actions, mechanisms for implementing the flow of control, and overall control of the action of the system.

## 12.1 FIRST ORDER PREDICATE CALCULUS

Predicate logic is in many ways an attractive knowledge representation and inference system. However, despite its historical stature, important technical results in automated inference, and much research on inference techniques, logic has not dominated all aspects of mechanized inference. Some reasons for this are presented in Sections 12.1.6 and 12.2. The logical system that has received the most study is *first order predicate logic.* General theorem provers in this calculus are cumbersome for reasons which we shall explore. Furthermore, there is some controversy as to whether this logical system is adequate to express the reasoning processes used by human beings [Hayes 1977; Collins 1978; Winograd 1978; McCarthy and Hayes 1969]. We briefly describe some aspects of this controversy in Section 12.1.6. Our main purpose is to give the flavor of predicate calculus-based methods by describing briefly how automated inference can proceed with the formulae of predicate calculus expressed in the convenient *clause form.* Clause form is appealing for two reasons. First, it can be represented usefully in relational $n$-tuple or semantic network notation (Section 12.1.5). Second, the predicate calculus clause and inference system may be easily compared to production systems (Section 12.3).

### 12.1.1 Clause-Form Syntax (Informal)

In this section we describe the syntax of clause-form predicate calculus sentences. In the next, a more standard nonclausal syntax is described, together with a method for assigning meaning to grammatical logical expressions. Next, we show briefly how to convert from nonclausal to clausal syntax.

A *sentence* is a set of *clauses.* A clause is an ordered pair of sets of *atomic formulae,* or *atoms.* Clauses are written as two (possibly null) sets separated by an arrow, pointing from the *hypotheses* or *conditions* of the clause to its *conclusion.* The *null clause,* whose hypotheses and conclusion are both null, is written □. For example, a clause could appear as

$$A_1, \ldots, A_n \rightarrow B_1, \ldots, B_m$$

where the $A$'s and $B$'s are atoms. An atom is an expression

$$P(t_1, \ldots, t_j),$$

where $P$ is a predicate symbol which "expects $j$ arguments," each of which must be a *variable, constant symbol,* or a *term.* A term is an expression

$$f(t_1, \ldots, t_k)$$

where $f$ is a *function symbol* which "expects $k$ arguments," each of which may be a term. It is convenient to treat constant symbols alone as terms.

A careful (formal) treatment of the syntax of logic must deal with technical issues such as keeping constant and term symbols straight, associating the number of expected arguments with a predicate or function symbol, and assuring an infinite supply of symbols.

For example, the following are sentences of logic.

→ Obscured(Backface(Block1))
Visible(Kidney) →
Road(x), Unpaved(x) → Narrow(x)

### 12.1.2 Nonclausal Syntax and Logic Semantics (Informal)

*Nonclausal Syntax*

Clause form is a simplified but logically equivalent form of logic expressions which are perhaps more familiar. A brief review of non-clausal syntax follows.

The concepts of constant symbols, variables, terms, and atoms are still basic. A set of *logical connectives* provides unary and binary operators to combine atoms to form *well-formed formulae* (wffs). If $A$ and $B$ are atoms, then $A$ is a wff, as is $\tilde{}A$ ("not $A$") $A \Longrightarrow B$ ("$A$ implies $B$," or "if $A$ then $B$"), $A \vee B$ ("$A$ or $B$"), $A \wedge B$ ("$A$ and $B$"), $A \Longleftrightarrow B$ ("$A$ is equivalent to $B$," or "$A$ if and only if $B$"). Thus an example of a wff is

$$\text{Back(Face)} \vee (\text{Obscured(Face)}) \Longrightarrow \tilde{} (\text{Visible(Face)})$$

The last concept is that of *universal* and *existential quantifiers*, the use of which is illustrated as follows.

$(\forall x)$ (wff using "$x$" as a variable).
$(\exists$ thing) (wff using "thing" as a variable).

A universal quantifier $\forall$ is interpreted as a conjunction over all domain elements, and an existential quantifier $\exists$ as a disjunction over all domain elements. Hence their usual interpretation as "for each element . . ." and "there exists an element . . . ."

Since a quantified wff is also a wff, quantifiers may be iterated and nested. A quantifier quantifies the "dummy" variable associated with it ($x$ and thing in the examples above). The wff within the *scope* of a quantifier is said to have this quantified variable *bound* by the quantifier. Typically only wffs or clauses all of whose variables are bound are allowed.

*Semantics*

How does one assign meaning to grammatical clauses and formulae? The semantics of logic formulae (clauses and wffs alike) depends on an *interpretation* and

on the meaning of connectives and quantifiers. An interpretation specifies the following.

1. A *domain* of individuals
2. A particular domain element is associated with each constant symbol
3. A function over the domain (mapping $k$ individuals to individuals) is associated with each function symbol.
4. A relation over the domain (a set of ordered k-tuples of individuals) is associated with each predicate symbol.

The interpretation establishes a connection between the symbols in the representation and a domain of discourse (such as the entities one might see in an office or chest x-ray). To establish the truth or falsity of a clause or wff, a value of TRUE or FALSE must be assigned to each atom. This is done by checking in the world of the domain to see if the terms in the atom satisfy the relation specified by the predicate of the atom. If so, the atom is TRUE; if not, it is FALSE. (Of course, the terms, after evaluating their associated functions, ultimately specify individuals). For example, the atom

GreaterThan(5,$\pi$)

is true under the obvious interpretation and false with domain assignments such that

GreaterThan means "Is the author of"
5 means the book *Gone With the Wind*
$\pi$ means Rin-Tin-Tin.

After determining the truth values of atoms, wffs with connectives are given truth values by using the *truth tables* of Table 12.1, which specify the semantics of the logical connectives. The relation of this formal semantics of connectives with the usual connectives used in language (especially "*implies*") is interesting, and one must be careful when translating natural language statements into predicate calculus.

The semantics of clause form expressions is now easy to explain. A sentence is the *conjunction* of its clauses. A clause

$$A_1, \ldots, A_n \rightarrow B_1, \ldots, B_m$$

with variables $x_1, \ldots, x_k$ is to be understood

**Table 12.1**

| $A$ | $B$ | $\neg A$ | $A \wedge B$ | $A \vee B$ | $A \Longrightarrow B$ | $A \Longleftrightarrow B$ |
|---|---|---|---|---|---|---|
| T | T | F | T | T | T | T |
| T | F | F | F | T | F | F |
| F | T | T | F | T | T | F |
| F | F | T | F | F | T | T |

$$\forall x_1, \ldots, x_k, \ (A_1 \wedge \ldots \wedge A_n) \Longrightarrow (B_1 \vee \ldots \vee B_m).$$

The null clause is to be understood as a contradiction. A clause with no conditions is an assertion that at least one of the conclusions is true. A clause with null conclusion is a denial that the conditions (hypotheses) are true.

### 12.1.3 Converting Nonclausal Form to Clauses

The conversion of nonclausal to clausal form is done by applying straightforward rewriting rules, based on logic identities (ultimately the truth tables). There is one trick necessary, however, to remove existential quantifiers. *Skolem functions* are used to replace existentially quantified variables, according to the following reasoning.

Consider the wff

$$(\forall x)(\exists y)(\text{Behind}(y, x))).$$

With the proper interpretation, this wff might correspond to saying "For any object $x$ we consider, there is another object $y$ which is behind $x$." Since the $\exists$ is within the scope of the $\forall$, the particular $y$ might depend on the choice of $x$. The Skolem function trick is to remove the existential quantifier and use a function to make explicit the dependence on the bound universally quantified variable. The resulting wff could be

$$(\forall x)\ (\text{Behind}(\text{SomethingBehind}(x), x))$$

which might be rendered in English: "Any object $x$ has another object behind it; furthermore, some Skolem function we choose to call SomethingBehind determines which object is behind its argument." This is a notational trick only; the existence of the new function is guaranteed by the existential quantification; both notations are equally vague as to the entity the function actually produces.

In general, one must replace each occurrence of an existentially quantified variable in a wff by a (newly created Skolem) function of all the universally quantified variables whose scope includes the existential quantifier being eliminated. If there is no universal quantifier, the result is a new function of no arguments, or a new constant.

$$(\exists x)(\text{Red}(x)),$$

which may be interpreted "Something is red," is rewritten as something like

Red(RedThing)

or

"Something is red, and furthermore let's call it RedThing."

The conversion from nonclausal to clausal form proceeds as follows (for more details, see [Nilsson 1971]). Remove all implication signs with the identity $(A \Longrightarrow B) \Longleftrightarrow ((\neg A) \vee B)$. Use DeMorgan's laws (such as $\neg(A \vee B) \Longleftrightarrow ((\neg A) \wedge (\neg B))$, and the extension to quantifiers, together with cancellation of double negations, to force negations to refer only to single predicate letters. Rewrite vari-

ables to give each quantifier its own unique dummy variable. Use Skolem functions to remove existential quantifiers. Variables are all now universally quantified, so eliminate the quantifier symbols (which remain implicitly), and rearrange the expression into conjunctive normal form (a conjunction of disjunctions.) The $\wedge$'s now connect disjunctive *clauses* (at last!). Eliminate the $\wedge$'s, obtaining from the original expression possibly several clauses.

At this point, the original expression has yielded multiple disjunctive clauses. Clauses in this form may be used directly in automatic theorem provers [Nilsson 1971]. The disjunctive clauses are not quite in the clause form as defined earlier, however; to get clauses into the final form, convert them into implications. Group negated atoms, reexpanding the scope of negation to include them all and converting the $\vee$ of ~'s into a ~ of $\wedge$'s. Reintroduce one implication to go from

$$B_1 \vee B_2 \ldots \vee B_m \vee (\sim(A_1 \wedge A_2 \ldots \wedge A_n))$$

to

$$A_1 \wedge \ldots \wedge A_n \rightarrow B_1 \vee B_2 \ldots \vee B_m$$

To obtain the final form, replace the connectives (which remain implicitly) with commas.

### 12.1.4 Theorem Proving

Good accounts of the basic issues of automated theorem proving are given in [Nilsson 1971; Kowalski 1979; Loveland 1978]. The basic ideas are as follows. A sentence is *inconsistent*, or *unsatisfiable*, if it is false in every interpretation. Some trivially inconsistent sentences are those containing the null clause, or simple contradictions such as the same clause being both unconditionally asserted and denied. A sentence that is true in all interpretations is *valid.* Validity of individual clauses may be checked by applying the truth tables unless quantifiers are present, in which case an infinite number of formulae are being specified, and the truth status of such a clause is not algorithmically decidable. Thus it is said that first order predicate calculus is *undecidable.* More accurately, it is *semidecidable*, because any valid wff can be established as such in some (generally unpredictable) finite time. The validation procedure will run forever on invalid formulae; the rub is that one can never be sure whether it is running uselessly, or about to terminate in the next instant.

The notion of a *proof* is bound up with the notion of logical entailment. A clause *C logically follows* from a set of clauses *S* (we take *S* to *prove C*) if every interpretation that makes *S* true also makes *C* true. A formal proof is a sequence of inferences which establishes that *C* logically follows from *S*. In nonclausal predicate logic, inferences are rewritings of axioms and previously established formulae in accordance with *rules of inference* such as

Modus Ponens: From $(A)$ and $(A \Longrightarrow B)$ infer $(B)$
Modus Tollens: From $(\sim B)$ and $(A \Longrightarrow B)$ infer $(A)$
Substitution: e.g. From $(\forall x)(\text{Convex}(x))$ infer $(\text{Convex}(\text{Region31}))$
Syllogisms,

and so forth.

Automatic clausal theorem provers usually try to establish that a clause $C$ logically follows from the set of clauses $S$. This is accomplished by showing the *unsatisfiability* of $S$ and $(C)$ taken together. This rather backward approach is a technical effect of the way that theorem provers usually work, which is to derive a contradiction.

The fundamental and surprising result that all true theorems are provable in finite time, and an algorithmic (but inefficient) way to find the proof, is due to Herbrand [Herbrand 1930]. The crux of the result is that although the domain of individuals who might participate in an interpretation may be infinite, only a finite number of interpretations need be investigated to establish unsatisfiability of a set of clauses, and in each only a finite number of individuals must be considered. A computationally efficient way to perform automatic inference was discovered by Robinson [Robinson 1965]. In it, a single rule of inference called *resolution* is used. This single rule preserves the *completeness* of the system (all true theorems are provable) and its *correctness* (no false theorems are provable).

The rule of resolution is very simple. Resolution involves matching a condition of one clause $A$ with a conclusion of another clause $B$. The derived clause, called the *resolvent*, consists of the unmatched conditions and conclusions of $A$ and $B$ instantiated by the matching substitution. *Matching* two atoms amounts to finding a substitution of terms for variables which if applied to the atoms would make them identical.

Theorem proving now means resolving clauses with the hope of producing the empty clause, a contradiction.

As an example, a simple resolution proof goes as follows. Say it is desired to prove that a particular wastebasket is invisible. We know that the wastebasket is behind Brian's desk and that anything behind something else is invisible (we have a simpleminded view of the world in this little example). The givens are the wastebasket location and our naive belief about visibility:

$$\rightarrow \text{Behind}(\text{WasteBasket}, \text{DeskOf}(\text{Brian})) \tag{12.1}$$

$$\text{Behind}(\text{object}, \text{obscurer}) \rightarrow \text{Invisible}(\text{object}) \tag{12.2}$$

Here Behind and Invisible are predicates, DeskOf is a function, Brian and WasteBasket are constants (denote particular specific objects), and object and obscurer are (universally quantified) variables. The negation of the conclusion we wish to prove is

$$\text{Invisible}(\text{WasteBasket}) \rightarrow \tag{12.3}$$

or, "Asserting the wastebasket is invisible is contradictory." Our task is to show this set of clauses is inconsistent, so that the invisibility of the wastebasket is proved. The resolution rule consists of matching clauses on opposite sides of the arrow which can be unified by a substitution of terms for variables. A substitution that works is:

Substitute WasteBasket for object and DeskOf(Brian) for obscurer in (12.2).

Then a cancellation can occur between the right side of (12.1) and the left side of (12.2). Another cancellation can then occur between the right side of (12.2) and

the left side of (12.3), deriving the empty clause (a contradiction), Quod Erat Demonstrandum.

Anyone who has ever tried to do a nontrivial logic proof knows that there is searching involved in finding which inference to apply to make the proof terminate. Usually human beings have an idea of "what they are trying to prove," and can occasionally call upon some domain semantics to guide which inferences make sense. Notice that at no time in a resolution proof or other formal proof of logic is a specific interpretation singled out; the proof is about all possible interpretations. If deductions are made by appealing to intuitive, domain-dependent, semantic considerations (instead of purely syntactic rewritings), the deduction system is *informal.* Almost all of mathematics is informal by this definition, since normal proofs are not pure rewritings.

Many nonsemantic heuristics are also possible to guide search, such as trying to reduce the differences between the current formulae and the goal formula to be proved. People use such heuristics, as does the Logic Theorist, an early nonclausal, nonresolution theorem prover [Newell et al. 1963].

A basic resolution theorem prover *is* guaranteed to terminate with a proof if one exists, but usually resource limitations such as time or memory place an upper limit on the amount of effort one can afford to let the prover spend. As all the resolvents are added to the set of clauses from which further conclusions may be derived, the question of selecting which clauses to resolve becomes quite a vital one. Much research in automatic theorem proving has been devoted to reducing the search space of derivations for proofs [Nilsson 1980; Loveland 1970]. This has usually been done through heuristics based on formal aspects of the deductions (such as: make deductions that will not increase drastically the number of active clauses). Guidance from domain-dependent knowledge is not only hard to implement, it is directly against the spirit of resolution theorem proving, which attempts to do all the work with a uniform inference mechanism working on uninterpreted symbol strings. A moderation of this view allows the "intent" of a clause to guide its application in the proof. This can result in substantial savings of effort; an example is the treatment of "frame axioms" recommended by Kowalski (Section 13.1.4). Ad hoc, nonformalizable, domain-dependent methods are not usually welcome in automatic theorem-proving circles; however, such heuristics only guide the activity of a formal system; they do not render it informal.

### 12.1.5 Predicate Calculus and Semantic Networks

Predicate calculus theorem proving may be assisted by the addition of more relational structure to the set of clauses. The structure in a semantic net comes from *links* which connect *nodes*; nodes are accessed by following links, so the availability of information in nodes is determined by the link structure. Links can thus help by providing quick access to relevant information, given that one is "at" a particular node.

Although there are several ways of representing predicate calculus formulae in networks, we adopt here that of [Kowalski 1979; Deliyanni and Kowalski 1979]. The steps are simple:

1. Use a partition to represent the clause.
2. Convert all atoms to binary predicate atoms.
3. Distinguish between conditions and conclusions.

Recall that in Chapter 10, a partition is defined as a set of nodes and arcs in a graph. The internal structure of the partition cannot be determined from outside it. Partitioning extends the structure of a semantic net enough to allow unambiguous representations of all of first order predicate calculus.

The first step in developing the network representation for clauses is to convert each relation to a binary one. We distinguish between conditions and conclusions by using an additional bit of information for each arc. Diagrammatically, an arc is drawn with a double line if it is a condition and a single line if it is a conclusion. Thus the earlier example $S = \{(12.1), (12.2), (12.3)\}$ can be transformed into the network shown in Fig. 12.1.

This figure hints at the advantages of the network embedding for clauses: It is an indexing scheme. This scheme does not indicate which clauses to resolve next but can help reduce the possibilities enormously. If the most recent resolution involved a given clause with a given set of terms, other clauses which also have those terms will be represented by explicit arcs nearby in the network (this would *not* be true if the clauses were represented as a set). Similarly, other clauses involving the same predicate symbols are also nearby being indexed by those symbols. Again, this would not be true in the set representation. Thus the embedded network

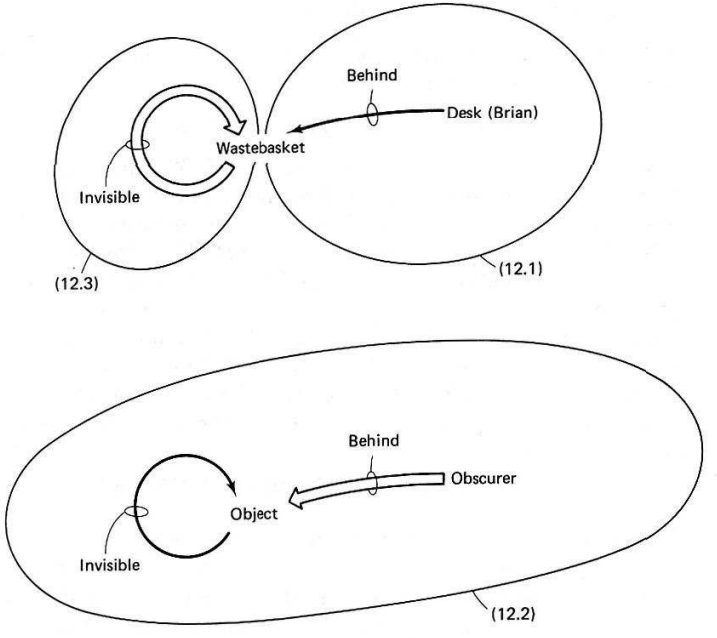



**Fig. 12.1** Converting clauses to networks.

representation contains argument indices and predicate indices which can be extremely helpful in the inference process.

A very simple example illustrates the foregoing points. Suppose that $S$ consists of the set of clauses

$$\text{SouthOf(river2,}x\text{), NorthOf(river1,}x\text{)} \rightarrow \text{Between(river1, river2,}\ x\text{)} \quad (12.4)$$
$$\rightarrow \text{SouthOf (}u\text{, silo30)} \quad (12.5)$$
$$\rightarrow \text{NorthOf (river1, silo30)} \quad (12.6)$$

Clause (12.5) might arise when it is determined that "silo30" is south of some feature in the image whose identity is not known. *Bottom up inference* derives new assertions from old ones. Thus in the example above the variable substitutions

$$u = \text{river2} \qquad x = \text{silo30}$$

match assertion (12.5) with the general clause (12.4) and allow the inference

$$\text{NorthOf(river1, silo30)}$$
$$\rightarrow \text{Between(river1, river2, silo30)} \quad (12.7)$$

Consequently, use (12.6) and (12.7) to assert

$$\rightarrow \text{Between(river1, river2, silo 30)} \quad (12.8)$$

Suppose that this was not the case: that is, that

$$\text{Between(river1, river2, silo30)} \rightarrow \quad (12.9)$$

and that $S = \{(12.4), (12.9)\}$. One could then use *top-down inference*, which infers new denials from old ones. In this case

$$\text{NorthOf(river1,silo30), SouthOf(river2,silo30)} \rightarrow \quad (12.10)$$

follows with the variable substitution $x = \text{silo30}$. This can be interpreted as follows: "If $x$ is really silo30, then it is neither north of river1 or south of river2." Figure 12.2 shows two examples using the network notation.

Now suppose the goal is to prove that (12.8) logically follows from (12.4) through (12.6) and the substitutions. The strategy would be to negate (12.8), add it to the data base, and show that the empty clause can be derived. Negating an assertion produces a denial, in this case (12.9), and now the set of axioms (including the denial) consists of $\{(12.4), (12.5), (12.6), (12.9)\}$. It is easy to repeat the earlier steps to the point where the set of clauses includes (12.8) and (12.9), which resolve to produce the empty clause. Hence the theorem is proved.

### 12.1.6 Predicate Calculus And Knowledge Representation

Pure predicate calculus has strengths and weaknesses as a knowledge representation system. Some of the seeming weaknesses can be overcome by technical "tricks." Some are not inherent in the representation but are a property of the common interpreters used on it (i.e., on state-of-the-art theorem provers). Some problems are relatively basic, and the majority opinion seems to be that first order

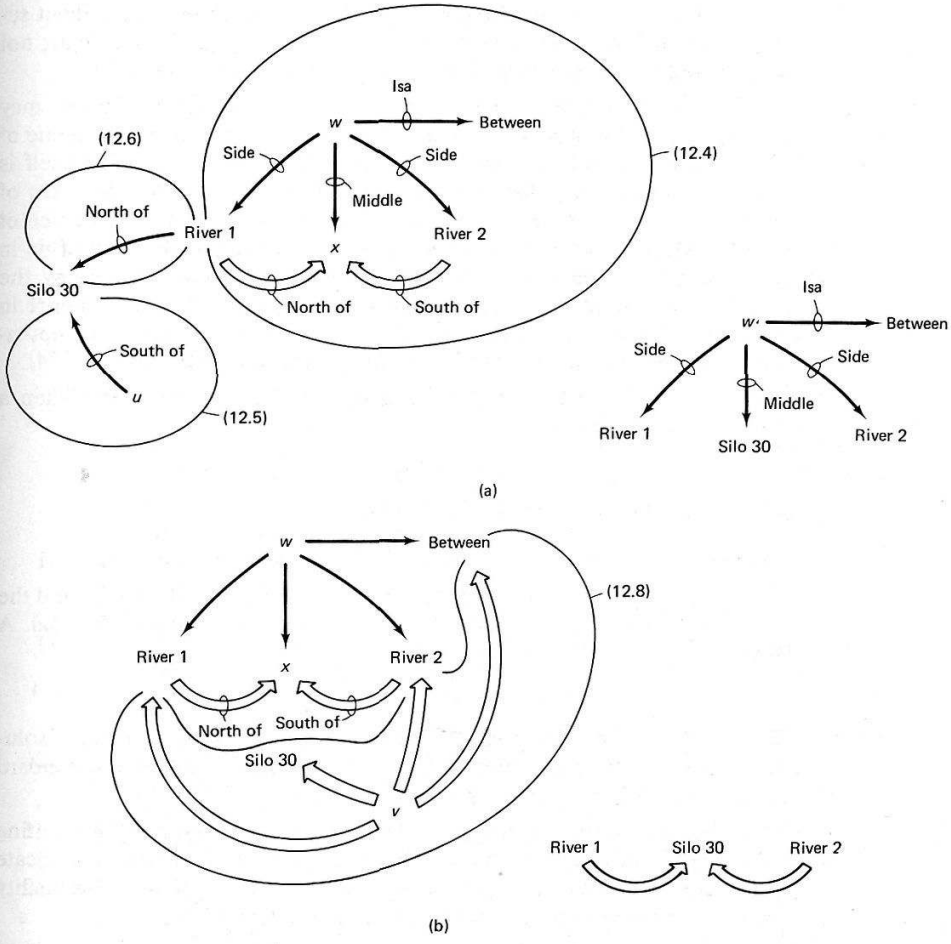



**Fig. 12.2** Resolution using networks. (a) Bottom-up inference as a result of substitutions $u$ = river2, $x$ = silo30. (b) Top-down inference as a result of substitutions $w = v$, $x$ = silo30.

predicate logic must be extended in order to become a representation scheme that is satisfactorily matched to the power of the deductive methods applied by human beings. Opinion is divided on the technical aspects of such enhancements. Predicate calculus has several strengths, some of which we list below.

1. Predicate logic is a well-polished gem, having been refined and studied for several generations. It was designed to represent knowledge and inference. One knows what it means. Its model theory and proof theory are explicit and lucid [Hayes 1977; 1980].

2. Predicate logic can be considered a language with a machine-independent semantics; the meaning of the language is determined by the laws of logic, not the actual programming system upon which the logic is "executed."
3. Predicate calculus clauses with only one conclusion atom (Horn clauses) may be considered as "procedures," with the single conclusion being the name of the procedure and the conditions being the procedure body, which itself is made up of procedure calls. This view of logic leads to the development of predicate logic-based programming languages (such as PROLOG [Warren et al. 1977; McDermott 1980]). These programs exhibit nondeterminism in several interesting ways; the order of computations is not specified by the proof procedure (and is not restricted by it, either). Several resolutions are in general possible for any clause; the combinations determine many computations and several distinguishable forms of nondeterminism [Kowalski 1974].
4. Predicate logic may be interpreted as a problem-reduction system. Then a (Horn) clause of the form

$$\rightarrow B$$

represents a solved problem. One of the form

$$A_1, \ldots, A_n \rightarrow$$

with variables $x_1, \ldots, x_k$ is a goal statement, or command, which is to find the $x$'s that solve the problems $A_1, \ldots, A_n$. Finding the $x$'s solves the goal. A clause

$$A_1, \ldots, A_n \rightarrow B$$

is a solution method, which reduces the solution of $B$ to a combination of solutions of $A$'s. This interpretation of Horn clauses maps cleanly into a standard and–or goal tree formulation of problem solving.
5. Resolutions may be performed on the left or right of clauses, and the resulting derivation trees correspond, in the problem-solving interpretation of predicate calculus, to top-down and bottom-up versions of problem solving. This duality is very important in conceptualizing aspects of problem solving.
6. There is a uniform proof procedure for logic which is guaranteed to prove in finite time any true theorem (logic is semidecidable and complete). No false theorems are provable (logic is correct). These and other good formal properties are important when establishing formally the properties of a knowledge representation system.

Predicate calculus is not a favorite of everyone, however; some of the (perceived) disadvantages are given below, together with ways they might be countered.

1. Sometimes the axioms necessary to implement relatively common concepts are not immediately obvious. A standard example is "equality." These largely technical problems are annoying but not basic.

2. The "first order" in first order predicate calculus means that the system

does not allow clauses with variables ranging over an infinite number of predicates, functions, assertions and sentences (e.g., "All unary functions are boring" cannot be stated directly). This problem may be ameliorated by a notational trick; the situations under which predicates are true are indicated with a Holds predicate. Thus instead of writing On(block1, surface, situation1), write Holds (On(block1,surface), situation1). This notation allows inferences about many situations with only one added axiom. The "situational calculus" reappears in Section 12.3.1. Another useful notational trick is a Diff relation, which holds between two terms if they are syntactically different. There are infinitely many axioms asserting that terms are different; the actual system can be made to incorporate them implicitly in a well-defined way. The Diff relation is also used in Section 12.3.1.

3. The *frame problem* (so called for historical reasons and not related to the frames described in Section 10.3.1) is a classic bugbear of problem-solving methods including predicate logic. One aspect of this problem is that for technical reasons, it must be explicitly stated in axioms that describe actions (in a general sense a visual test is an action) that almost all assertions were true in a world state *remain* true in the new world state after the action is performed. The addition of these new axioms causes a huge increase in the "bureaucratic overhead" necessary to maintain the state of the world. Currently, no really satisfactory way of handling this problem has been devised. The most common way to attack this aspect of the frame problem is to use explicit "add lists" and "delete lists" ([Fikes 1977], Chapter 13) which attempt to specify exactly what changes when an action occurs. New true assertions are added and those that are false after an action must be deleted. This device is useful, but examples demonstrating its inadequacy are readily constructed. More aspects of the frame problem are given in Chapter 13.

4. There are several sorts of reasoning performed by human beings that predicate logic does not pretend to address. It does not include the ability to describe its own formulae (a form of "quotation"), the notion of defaults, or a mechanism for plausible reasoning. Extensions to predicate logic, such as modal logic, are classically motivated. More recently, work on extensions addressing the topics above have begun to receive attention [McCarthy 1978; Reiter 1978; Hayes 1977]. There is still active debate as to whether such extensions can capture many important aspects of human reasoning and knowledge within the model-theoretic system. The contrary view is that in some reasoning, the very *process* of reasoning itself is an important part of the semantics of the representation. Examples of such extended inference systems appear in the remainder of this chapter, and the issues are addressed in more detail in the next section.

## 12.2 COMPUTER REASONING

Artificial intelligence in general and computer vision in particular must be concerned with *efficiency* and *plausibility* in inference [Winograd 1978]. Computer-based knowledge representations and their accompanying inference processes often sacrifice classical formal properties for gains in control of the inference process and for flexibility in the sorts of "truth" which may be inferred.

does not allow clauses with variables ranging over an infinite number of predicates, functions, assertions and sentences (e.g., "All unary functions are boring" cannot be stated directly). This problem may be ameliorated by a notational trick; the situations under which predicates are true are indicated with a Holds predicate. Thus instead of writing On(block1, surface, situation1), write Holds (On(block1,surface), situation1). This notation allows inferences about many situations with only one added axiom. The "situational calculus" reappears in Section 12.3.1. Another useful notational trick is a Diff relation, which holds between two terms if they are syntactically different. There are infinitely many axioms asserting that terms are different; the actual system can be made to incorporate them implicitly in a well-defined way. The Diff relation is also used in Section 12.3.1.

3. The *frame problem* (so called for historical reasons and not related to the frames described in Section 10.3.1) is a classic bugbear of problem-solving methods including predicate logic. One aspect of this problem is that for technical reasons, it must be explicitly stated in axioms that describe actions (in a general sense a visual test is an action) that almost all assertions were true in a world state *remain* true in the new world state after the action is performed. The addition of these new axioms causes a huge increase in the "bureaucratic overhead" necessary to maintain the state of the world. Currently, no really satisfactory way of handling this problem has been devised. The most common way to attack this aspect of the frame problem is to use explicit "add lists" and "delete lists" ([Fikes 1977], Chapter 13) which attempt to specify exactly what changes when an action occurs. New true assertions are added and those that are false after an action must be deleted. This device is useful, but examples demonstrating its inadequacy are readily constructed. More aspects of the frame problem are given in Chapter 13.

4. There are several sorts of reasoning performed by human beings that predicate logic does not pretend to address. It does not include the ability to describe its own formulae (a form of "quotation"), the notion of defaults, or a mechanism for plausible reasoning. Extensions to predicate logic, such as modal logic, are classically motivated. More recently, work on extensions addressing the topics above have begun to receive attention [McCarthy 1978; Reiter 1978; Hayes 1977]. There is still active debate as to whether such extensions can capture many important aspects of human reasoning and knowledge within the model-theoretic system. The contrary view is that in some reasoning, the very *process* of reasoning itself is an important part of the semantics of the representation. Examples of such extended inference systems appear in the remainder of this chapter, and the issues are addressed in more detail in the next section.

## 12.2 COMPUTER REASONING

Artificial intelligence in general and computer vision in particular must be concerned with *efficiency* and *plausibility* in inference [Winograd 1978]. Computer-based knowledge representations and their accompanying inference processes often sacrifice classical formal properties for gains in control of the inference process and for flexibility in the sorts of "truth" which may be inferred.

Automated inference systems usually have inference methods that achieve efficiency through implementational, computation-based, inference criteria. For example, truth may be defined as a successful lookup in a data base, falsity as the failure to find a proof with a given allocation of computational resources, and the establishment of truth may depend on the order in which deductions are made.

The semantics of computer knowledge representations is intimately related to the inference process that acts on them. Therefore, it is possible to define knowledge representations and interpreters in computers whose properties differ fairly radically from those of classical representations and proof procedures, such as the first-order predicate calculus. For instance, although the systems are deterministic, they may not be formally consistent (loosely, they may contain contradictory information). They may not be complete (they cannot derive all true theorems from the givens); it may be possible to prove P from $Q$ but $\neg P$ from $Q$ and $R$. The set of provable theorems may not be recursively enumerable [Reiter 1978]. Efforts are being made to account for the "extended inference" needed by artificial intelligence using more or less classical logic [McCarthy 1978; Reiter 1978; Hayes 1977; 1978a; 1978b; Kowalski 1974, 1979]. In each case, the classical view of logic demands that the deductive process and the deducible truths be independent. On the other hand, it is reasonable to devote attention to developing a nonclassical semantics of these inference processes; this topic is in the research stage at this writing.

Several knowledge representations and inference methods using them are "classical" in the artificial intelligence world; that is, they provide paradigmatic methods of dealing with the issues of computational inference. They include STRIPS [Fikes and Nilsson 1971], the situational calculus [McCarthy and Hayes 1969], PLANNER and CONNIVER [Hewitt 1972; Sussman and McDermott 1972], and semantic net representations [Hendrix 1979; Brachman 1979].

To illustrate the issue of consistency, and to illustrate how various sorts of propositions can be represented in semantic nets, we address the question of how the order of inference can affect the set of provable theorems in a system.

Consider the semantic net of Fig. 12.3. The idea is that in the absence of specific information to the contrary, one should assume that railroad bridges are narrow. There are exceptions, however, such as Bridge02 (which has a highway bridge above the rail bridge, say). The network is clearly inconsistent, but trouble is avoided if inferences are made "from specific to general." Such ordering implies that the system is incomplete, but in this case incompleteness is an advantage.

Simple ordering constraints are possible only with simple inferential powers in the system [Winograd 1978]. Further, there is as yet little formal theory on the effects of ordering rules on computational inference, although this has been an active topic [Reiter 1978].

## 12.3 PRODUCTION SYSTEMS

The last section explored why the process of inference itself could be an important part of the semantics of a knowledge representation system. This idea is an impor-

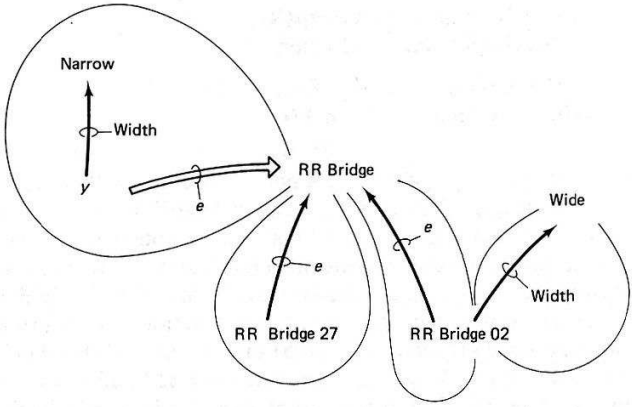



**Fig. 12.3** An inconsistent network.

tant part of production systems. Perceived limitations in logic inference mechanisms and the seductive power of arbitrary algorithmic processes for inference has spawned the development of *rule-based* systems which differ from first-order logic in the following respects:

- Arbitrary additions and deletions to the clausal data base are allowed.
- An interpreter that controls the inference process in special ways is usually an integral part of the system.

Early examples of systems with the first addition are STRIPS [Fikes and Nilsson 1971] and PLANNER [Hewitt 1972]. Later examples of systems with both additions are given in [Waterman and Hayes-Roth 1978]. The virtues of trying to control inferences may be appreciated after our brief introduction to clausal automatic theorem proving, where there are no very good semantic heuristics to guide inferences. However, the price paid for restricting the inference process is the loss of formal properties of consistency and correctness of the system, which are not guaranteed in rule-based systems. We shall look in some detail at a particular form of rule-based inference system called production systems.

A *production system* supports a general sort of "inference." It has in common with resolution that matching is needed to identify which inference to make. It is different in that the action upon finding a matching data item is less constrained. Actions of arbitrary complexity are allowed. A production system consists of an explicit set of situation–action nodes, which can be applied against a data base of situations. For example, in a very constrained visual domain the rule

$$(\text{Green } (\text{Region } X)) \rightarrow (\text{Grass } (\text{Region } X)) \tag{12.11}$$

could infer directly the interpretation of a given region. Segmentation rules can also be developed; the following example merges two adjacent green regions into a single region.

(Green(Region $X$))$\wedge$(Green(Region $Y$))$\wedge$
(Adjacent(Region $X$), (Region $Y$))

$\rightarrow$ (Green(Region $Z$))$\wedge$((Region $Z$) :=
(Union(Region $X$, Region $Y$)))

These examples highlight several points. The first is that basic idea of production systems is simple. The rules are easy to "read" by both the programmer and his program and new rules are easily added. Although it is imaginable that "situations" could extend down to the pixel level, and production systems could be used (for instance) to find lines, the system overhead would render such an approach impractical. In the visual domain, the production system usually operates on the segmented image (Chapters 4 and 5) or with the high-level internal model. In the rules above, X and Y are variables that must be bound to specific instances of regions in a data base. This process of binding variables or matching can become very complex, and is one of the two central issues of this kind of inference. The other is how to choose rules from a set all of whose situations match the current situation to some degree.

### 12.3.1 *Production System Details*

In its simplest form a production system has three basic components:

1. A data base
2. A set of rules
3. An interpreter for the rules

The vision data base is usually a set of facts that are known about the visual environment. Often the rules are considered to be themselves a manipulable part of the data base. Examples of some visual facts may be

(ABOVE (Region 5) (Region 10))
(SIZE (Region 5) 300)
(SKY (Region 5)) (12.12)
(TOP (Region 5) 255)

The data base is the sole storage medium for all state variables of the system. In particular, unlike procedurally oriented languages, there is no provision for separate storage of control state information—no separate program counter, push-down stack, and so on [Davis and King 1975].

A rule is an ordered pair of *patterns* with a left-hand side and a right-hand side. A pattern may involve only data base primitives but usually will have variables and special forms as subpatterns which are matched against the data base by the interpreter. For example, applying the following rule to a data base which includes (12.12),

(TOP (Region X) (GreaterThan 200))

→ (12.13)

(SKY (Region X))

region 5 can be inferred to be sky. The left-hand side matches a set of data-base facts and this causes (SKY (Region 5)) to be added to the data base. This example shows the kinds of matching that the interpreter must do: (1) the primitive TOP in the data base fact matches the same symbol in the rule, (2) (Region X) matched (Region 5) and $X$ is bound to 5 as a side effect, and (3) (GreaterThan 200) matches 255. Naturally, the user must design his own interpreter to recognize the meaning of such operational subpatterns.

However, even the form of the rules outlined so far is relatively restrictive. There is no reason why the right-hand side cannot do almost arbitrary things. For instance, the application of a rule may result in various productions being deleted or added from the set of productions; the data base of productions and assertions thus can be adaptive [Waterman and Hayes-Roth 1978]. Also, the right-hand side may specify programs to be run which can result in facts being asserted into the data base or actions performed.

Control in a basic production system is relatively simple: Rules are applied until some condition in the data base is reached. Rules may be applied in two distinct ways: (1) a match on the left-hand side of a rule may result in the addition of the consequences on the right-hand side to the data base, or (2) a match on the right-hand side may result in the addition of the antecedents in the left-hand side to the data base. The order of application of rules in the first case is termed *forward chaining* reasoning, where the objective is to see if a set of consequences can be derived from a given set of initial facts. The second case is known as *backward chaining*; the objective is to determine a set of facts that could have produced a particular consequence.

### 12.3.2 Pattern Matching

In the process of matching rules against the data base, several problems occur:

- Many rule situations may match data base facts
- Rules designed for a specific context may not be appropriate for larger context
- The pattern matching process may become very expensive
- The data base or set of rules may become unmanageably large.

The problem of multiple matches is important. Early systems simply resolved it by scanning the data base in a linear fashion and choosing the first match, but this is an ineffective strategy for large data bases, and has conceptual problems as well. Accordingly, strategies have evolved for dealing with these conflicts. Like most inference-controlling heuristics, their effectiveness can be domain-dependent, they can introduce incompleteness into the system, and so on.

On the principle of *least commitment*, when there are many chances of errors, one strategy is to apply the most general rule, defined by some metric on the com-

ponents of the pattern. One simple such metric is the number of elements in a pattern. Antithetical to this strategy is the heuristic of applying the *most specific pattern.* This may be appropriate where the likelihood of making a false inference is small, and where specific actions may be indicated (match (MAD DOG) with (MAD DOG), not with (DOG)). Another popular but inelegant technique is to exercise control over the *order of production application* by using state markers which are inserted into the data base by right-hand sides and looked for by left-hand sides.

1. $A \rightarrow B \wedge <\text{marker } 1>$.
2. $A \rightarrow B \wedge <\text{marker } 2>$.
3. $B \wedge <\text{marker } 1> \rightarrow C$.
4. $B \wedge <\text{marker } 2> \rightarrow D$.

Here if rule 1 is executed, "control goes to rule 3," i.e., rule 3 is now executable, whereas if rule 2 is applied, "control goes to rule 4." Similarly, such control paradigms as subroutining, iteration and co-routining may be implemented with production sytems [Rychner 1978].

The use of connectives and special symbols can make matching become arbitrarily complex. Rules might be interpreted as allowing all partial matches in their antecedent clauses [Bajcsy and Joshi 1978]. Thus

$$(A\ B\ C) \rightarrow (D)$$

is interpreted as

$$(ABC) \vee (BC) \vee (AB) \vee (AC) \vee (A) \vee (B) \vee (C) \rightarrow (D)$$

where the leftmost actual match is used to compare the rule to others in the case of conflicts.

The problem of large data bases is usually overcome by structuring them in some way so that the interpreter applies the rules only to a subset of the data base or uses a subset of the rules. This structuring undermines a basic principle of pure rule-based systems: Control should be dependent on the contents of the data base alone. Nevertheless, many systems divide the data base into two parts: an active smaller part which functions like the original data base but is restricted in size, and a larger data base which is inaccessible to the rule set in the active smaller part. "Meta-rules" have actions that move situation-action rules and facts from the smaller data base to the larger one and vice versa. The incoming set of rules and facts is presumably that which is applicable in the context indicated by the situation triggering the meta-rule. This two-level organization of rules is used in "blackboard" systems, such as Hearsay for speech-understanding [Erman and Lesser 1975]. The meta-rules seem to capture our idea of "mental set," or "context," or "frame" (Section 10.3.1, [Minsky 1975]). The two data bases are sometimes referred to as short-term memory and long term memory, in analogy with certain models of human memory.

### 12.3.3 An Example

We shall follow the actions of a production system for vision [Sloan 1977; Sloan and Bajcsy 1979]. The intent here is to avoid a description of all the details (which may be found in the References) and concentrate on the performance of the system as reflected by a sample of its output. The program uses a production system architecture in the domain of outdoor scenes. The goal is to determine basic features of the scene, particularly the separation between sky and ground. The interpreter is termed the "observer" and the memory has a two-tiered structure: (1) short term memory (STM) and (2) long term memory (LTM), a data base of all facts ever known or established, structured to prefer access to the most recently used facts. The image to be analyzed is shown in Fig. 12.4, and the action may be followed in Fig. 12.5. The analysis starts with the initialization command

*(look 100000 100 nil)

This command directs the Observer to investigate all regions that fall in the size range 100 to 100000, in decreasing order of size. The LTM is initialized to NIL.

our first look at (region 11)

| *x* | *y* | *r-g* | *y-b* | *w-b* | size | top | bottom | left | right |
|---|---|---|---|---|---|---|---|---|---|
| 35 | 2 | 24 | 29 | 6 | 2132 | 35 | 97 | 2 | 127 |

This report is produced by an image-processing procedure that produces assertions about (region 11). This region is shown highlighted in Fig. 12.5c.

_____ Progress Report _____

regions on this branch:
(11)
context stack:

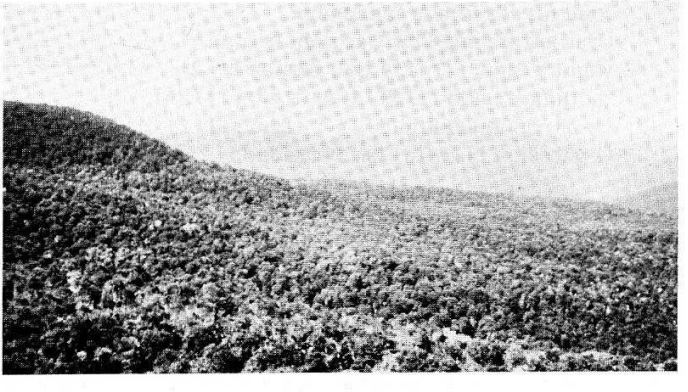


**Fig. 12.4** Outdoor scene to be analyzed with production system.

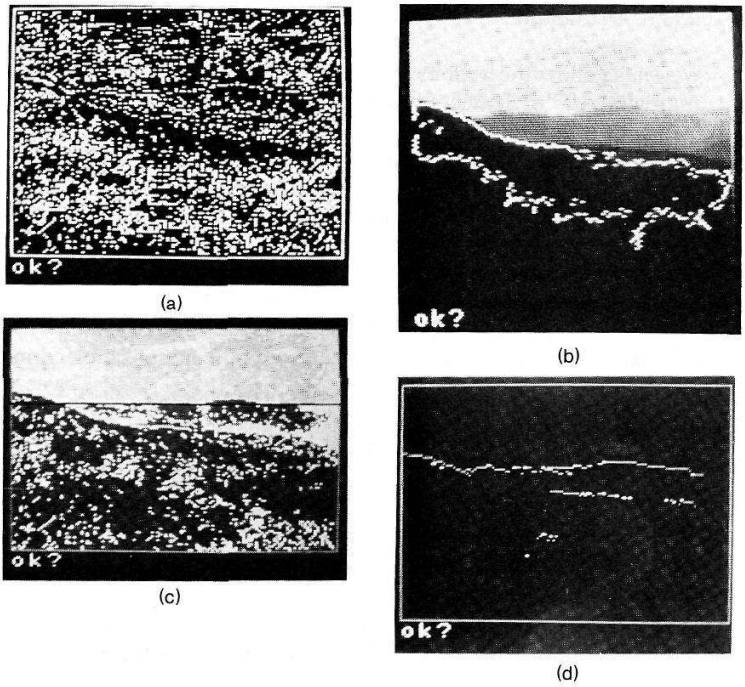



**Fig. 12.5** Images corresponding to steps in production system analysis. (a) Texture in the scene. (b) Region 11 outlined. (c) Sky-Ground separation. (d) Skyline.

nil
contents of short term memory:
((far-left (region 11)) (far-right (region 11))
(right (region 11) 127) (left (region 11) 2)
(bottom (region 11) 97) (top (region 11) 35)
(*w-b* (region 11) minus) (*y-b* (region 11) zero)
(*r-g* (region 11) zero) (size (region 11) 2132))

———— end of progress report ————

Note that gray-level information is represented as a vector in opponent color space (Chapter 2), where the components axes are WHITE-BLACK (*w-b*), RED-GREEN (*r-g*), and YELLOW-BLUE (*y-b*). Three values (plus, zero, minus) are used for each component. The display above is generated once after every iteration of the Observer. The report shows that (REGION 11) is being investigated; there is no known context for this investigation; the information about (REGION 11) created by the image-processing apparatus has been placed in STM. The context stack is for information only, and shows a trace of activated sets of rules.

i think that (far-left (region 11))
i think that (far-right (region 11))
i think that (right (region 11) 127)
i think that (left (region 11) 2)
i think that (bottom (region 11) 97)
i think that (top (region 11) 35)
i think that (size (region 11) 2132)

This portion of the trace shows assertions moving from STM to LTM. They are reported because this is the first time they have been REMEMBERed (a special procedure in the Observer).

_____ Progress Report _____

regions on this branch:
(11)
context stack:
nil
contents of short term memory:
((color (region 11) black))

_____ end of progress report _____

The assertions created from the region data structure have been digested, and lead only to the conclusion that (REGION 11) is BLACK, based on a production that looks like:

($w$-$b$ (region $x$) minus) $\wedge$ ($r$-$w$ (region $x$) zero)
$\wedge$ ($b$-$w$ (region $x$) zero) $\rightarrow$ (color (region $x$) black)

_____ Progress Report _____

regions on this branch:
(11)
context stack:
nil
contents of short term memory:
((ground (region 11)) (shadow (region 11)))

_____ end of progress report _____

The observer knows that things that are black are GROUND and SHADOW. The facts it deduces about region 11 are again stored in the LTM.

Having discovered a piece of ground, the Observer has activated the GROUND-RULES, and changed context. It now investigates the neighbors of (REGION 11).

our first look at (region 16)

| $x$ | $y$ | $r$-$g$ | $y$-$b$ | $w$-$b$ | size | top | bottom | left | right |
|---|---|---|---|---|---|---|---|---|---|
| 58 | 2 | 23 | 30 | 3 | 1833 | 57 | 119 | 2 | 127 |

(REGION 16) is a neighbor of (REGION 11), and the observer is trying to determine whether or not they are sufficiently similar, in both color and texture, to justify merging them.

_____ Progress Report _____

regions on this branch:
(16 11)
context stack:
(ground)
contents of short term memory:
((texture-difference (region 16) (region 11)))
(color-similar (region 16) (region 11))
(distance (region 16) near) (ground (region 16))
(color (region 16 black))

_____ end of progress report _____

The Observer decides that (REGION 16) is ground because it is at the bottom of the picture.

The ground-growing process continues, until finally one of the neighbors of a ground region is a piece of sky. The Observer will not immediately recognize this region as sky, but will see that a depth discontinuity exists and that the border between these two regions represents a section of three dimensional skyline.

our first look at (region 8)

| *x* | *y* | *r-g* | *y-b* | *w-b* | size | top | bottom | left | right |
|---|---|---|---|---|---|---|---|---|---|
| 27 | 2 | 13 | 13 | 33 | 394 | 15 | 38 | 2 | 57 |

_____ Progress Report _____

regions on this branch:
(8 13 16 11)
context stack:
(ground ground ground)
contents of short term memory:
((new-neighbor (region 800) (far-left (region 8))
(right (region 8) 57) (left (region 8) 2) (bottom (region 8) 38)
(top (region 8) 15) (*w-b* (region 8) zero) (*y-b* (region 8) minus)
(*r-g* (region 8) minus) (size (region 8) 394))

_____ end of progress report _____

texture descriptors for (region 8) are (54 50)
texture descriptors for (region 13) are (44 51)

Texture measurement is appropriate in the context of ground areas.

_____ Progress Report _____

regions on this branch:
(8 13 16 11)
context stack:
(ground ground ground)
contents of short term memory:
((texture-similar (region 8) (region 13)) (color-difference
(region 8) (region 13)) (color (region 8) blue-green))

_____ end of progress report _____

(REGION 8) passes the texture similarity test, but fails the color match.

_____ Progress Report _____

regions on this branch:
(8 13 16 11)
context stack:
(ground ground ground)
contents of short term memory:
((darker (region 13) (region 8)) (brighter (region 8) (region
13))
(yellower (region 13) (region 8)) (bluer (region 8) (region 13))
(redder (region 13) 13)
(below (region 13) (region 8)) (above (region 8) (region 13)))

_____ end of progress report _____

checking the border between (region 13) and (region 8)

_____ Progress Report _____

regions on this branch:
(8 13 16 11)
context stack:
(skyline ground ground ground)
contents of short term memory:
((segments built) (skyline-segment ((117 42)) (region 13)
(region 8)) (skyline-segment ((14 40) (13 40)) (region 13)
(region 8)))

_____ end of progress report _____

_____ Progress Report _____

regions on this branch:
(8 13 16 11)
context stack:
(skyline ground ground ground)

contents of short term memory:
((peak (14 40)) (peak (17 42)))

_____ end of progress report _____

Two local maxima have been discovered in the skyline. On the basis of a depth judgment, these peaks are correctly identified as treetops.

The analysis continues until all the major regions have been analyzed. The sky-ground separation is shown in Fig. 12.5a and skyline in Fig. 12.5e.

In most cases, complete analysis of the image follows from the context established by the first (largest) region. This implies that initial scanning of such scenes can be quite coarse, and very simple ideas about gross context are enough to get started. Once started, inferences about local surroundings lead the Observer's attention over the entire scene, often returning many times to the same part of the image, each time with a bit more knowledge.

### 12.3.4 Production System Pros and Cons

In their pure form, the productions of production systems are completely "modular," and are themselves independent of the control process. The data base of facts, or situations, is unordered set accessed in undetermined order to find one matching some rule. The rule is applied, and the system reports the search for a matching situation and situation-action pair (rule). This completely unstructured organization of knowledge could be a model for the human learning of "facts" which become available for use by some associative mechanism that finds relevant facts in our memories. The hope for pure production systems is that performance will degrade noncatastrophically from the deletion of rules or facts, and that the rules can interact in synergistic and surprising ways. A learning curve may be simulated by the addition of productions. Thus one is encouraged to experiment with how knowledge may best be broken up into disjoint fragments that interact to produce intelligent behavior.

Together with the modularity of productions in a simple system, there is a corresponding simplicity in the overall control program. The pure controller simply looks at the data base and somehow finds a matching situation (left-hand side) among the productions, applies the rule, and cycles. This simple structure remains constant no matter how the rules change, so any nondeterminism in the performance arises from the matcher, which may find different left hand side matches for sets of assertions in the data base.

The productions usually have a syntax that is machine-readable. Their semantics is similarly constrained, and so it begins to seem hopeful that a program (perhaps fired up by a production) could reason about the rules themselves, add them, modify them, or delete them. This is in contrast to the situation with *procedurally embedded knowledge* (Section 10.1.3), because it is difficult or impossible for programs to answer general questions about other programs. Thus the claim is that a production system can more easily reason about itself than can many other knowledge representation systems.

Productions often interact in ways that are not foreseen. This can be an advantage or a drawback, depending on the behavior desired. The pattern-matching control structure allows knowledge to be used whenever it is relevant, not only when the original designer thought that it might be. Symbiotic interaction of knowledge may also produce unforeseen insights. Production systems are a primary tool of *knowledge engineering*, an enterprise that attempts to encode and use expert knowledge at such tasks as medical diagnosis and interpretation of mass spectrograms [Lindsay et al. 1980; Buchanan and Mitchell 1978; Buchanan and Feigenbaum 1978; Shortliffe 1976; Aikins 1980].

There are many who are not convinced that production systems really offer the advantages they initially seem to. They use the following sorts of arguments.

The pure form of production system is almost never seen doing anything useful. In particular, the production system is most naturally a forward-chaining inference system, and one must exercise restraints and guidelines on it to keep it from running away and deducing lots of irrelevant facts instead of doing useful work. Of course, production systems may be written to do backward chaining by hypothesizing a RHS and seeing which LHS must be true for the desired RHS to occur (the process may be iterated to any depth). In practical systems based on production systems, there is implicit or explicit ordering of production rules so the matcher tries them in some order. Often the ordering is determined in a rather complex and dynamic manner, with groups of related rules being more likely to be applied together, the most recently used rule not allowed to be reapplied immediately, and so on. In fact, many production systems's controllers have all the control structure tricks mentioned above (and more) built into them; the simple and elegant "bag of rules" ideal is inadequate for realistic examples. When the rules are explicitly written with an idiosyncratic control structure in mind, the system can become unprincipled and inexplicable.

On the same lines, notice how difficult it is to specify a time-ordered sequence of actions by a completely modular set of rewriting rules. It is unnatural to force knowledge about processes that may contain iteration, tests, and recursion into the form of independent situation–action rules. A view that is more easily defensible is that knowledge about procedures for perception should be encoded as (embedded in) computer procedures, not assertions or rules. The causal chain that dictates that some actions are best performed before others is implicit in the sequential execution of procedures, and the language constraints, such as iterate and test, test and branch, or subroutine invocation, are all fairly natural ways to think about solving certain problems. Production systems can in fact be made to perform all these procedural-like functions, but only through an abrogation of the ideal of modular, unordered, matching-oriented rule invocation which is the production system ideal. The question turns into one of aesthetics; how to use productions in a good style, and to work with their philosophy instead of against it.

To summarize the previous two objections: Production-based knowledge systems may in practice be no more robust, easily modified, modular, extensible, understandable, or self-understanding than any other (say, procedural) system unless great care is taken. After a certain level of complexity is reached, they are

likely to be as opaque as any other scheme because of the control-structuring methods that must be imposed on the pure production system form.

## 12.4 SCENE LABELING AND CONSTRAINT RELAXATION

The general computational problem of assigning labels consistently to objects is sometimes called the "labeling problem," and arises in many contexts, such as graph and automata homomorphism, graph coloring, Latin square generation, and of course, image understanding [Davis and Rosenfeld 1976; Zucker 1976; Haralick and Shapiro 1979]. "Relaxation labeling," "constraint satisfaction," and "cooperative algorithms" are natural implementations for labeling, and their potential parallelism has been a very influential development in computer vision. As should any important development, the relaxation paradigm has had an impact on the conceptualization as well as on the implementation of processes.

Cooperating algorithms to solve the labeling problem are useful in low level vision (e.g., line finding, stereopsis) and in intermediate-level vision (e.g., line-labeling, semantics-based region growing). They may also be useful for the highest-level vision programs, those that maintain a consistent set of beliefs about the world to guide the vision process.

Section 12.4.1 presents the main concepts in the labeling problem. Section 12.4.2 outlines some basic forms that "discrete labeling" algorithms can take. Section 12.4.3 introduces a continuing example, that of labeling lines in a line drawing, and gives a mathematically well-behaved probabilistic "linear operator" labeling method. Section 12.4.4 modifies the linear operator to be more in accord with our intuitions, and Section 12.4.5 describes relaxation as linear programming and optimization, thereby gaining additional mathematical rigor.

### 12.4.1 Consistent and Optimal Labelings

All labeling problems have the following notions.

1. A set of *objects*. In vision, the objects usually correspond to entities to be labeled, or assigned a "meaning."
2. A finite set of *relations* between objects. These are the sorts of relations we saw in Chapter 10; in vision, they are often geometric or topological relations between segments in a segmented image. Properties of objects are simply unary relations. An input scene is thus a relational structure.
3. A finite set of *labels*, or symbols associated with the "meanings" mentioned above. In the simplest case, each object is to be assigned a single label. A *labeling* assigns one or more labels to (a subset of) the objects in a relational structure. Labels may be weighted with "probabilities"; a (label, weight) pair can indicate something like the "probability of an object having that label."
4. *Constraints*, which determine what labels may be assigned to an object and what sets of labels may be assigned to objects in a relational structure.

A basic labeling problem is then: Given a finite input scene (relational structure of objects), a set of labels, and a set of constraints, find a "consistent labeling." That is, assign labels to objects without violating the constraints. We saw this problem in Chapter 11, where it appeared as a matching problem. Here we shall start with the discrete labeling of Chapter 11 and proceed to more general labeling schemes.

As a simple example, consider the indoor scene of Fig. 12.6. The segmented office scene is to have its regions labeled as Door, Wall, Ceiling, Floor, and Bin, with the obvious interpretation of the labels. Here are some possible constraints, informally stated. Note that these particular constraints are in terms of the input relational structure, not the world from which the structure arose. A more complex (but reasonable) situation arises if scene constraints must be derived from rules about the three dimensional domain of the scene and the imaging process. Unary constraints use object properties to constrain labels; n-ary constraints force sets of label assignments to be compatible.

*Unary constraints*

1. The Ceiling is the single highest region in the image.
2. The Floor must be checkered.

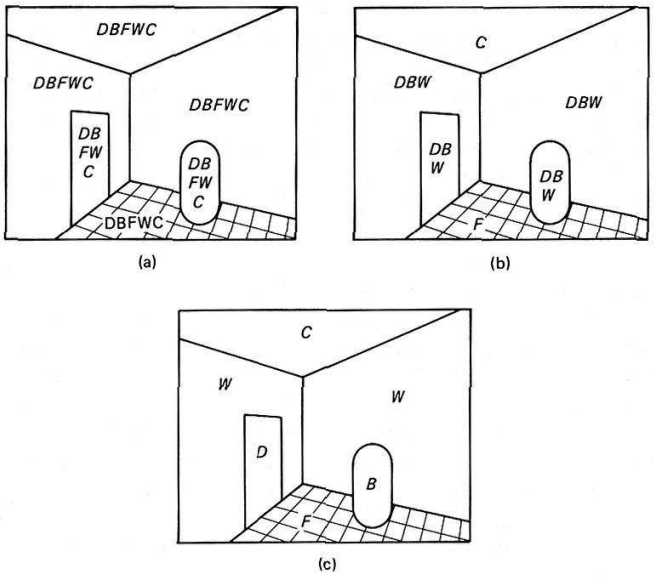



**Fig. 12.6** A stylized "segmented office scene." The regions are the objects to be assigned labels D, B, F, W, C (Door, Bin, Floor, Wall, Ceiling). In (a), each object is assigned all labels. In (b) unary constraints have been applied (see text). In (c), relational constraints have been applied, and a unique label for each region results.

*N-ary constraints*

3. A Wall is adjacent to the Floor and Ceiling.
4. A Door is adjacent to the Floor and a Wall.
5. A Bin is adjacent to a Floor.
6. A Bin is smaller than a Door.

Obviously, there are many constraints on the appearance of segments in such a scene; which ones to use depends on the available sensors, the ease of computation of the relations and their power in constraining the labeling. Here the application of the constraints (Fig. 12.6) results in a unique labeling. Although the constraints of this example are purely for illustration, a system that actually performs such labeling on real office scenes is described in [Barrow and Tenenbaum 1976].

Labelings may be characterized as *inconsistent* or *consistent.* A weaker notion is that of an *optimal* labeling. Each of these adjectives reflects a formalizable property of the labeling of a relational structure and the set of constraints. If the constraints admit of only completely compatible or absolutely incompatible labels, then a labeling is consistent if and only if all its labels are mutually compatible, and inconsistent otherwise. One example is the line labels of Section 9.5; line drawings that could not be consistently labeled were declared "impossible." Such a black-and-white view of the scene interpretation problem is convenient and neat, but it is sometimes unrealistic. Recall that one of the problems with the line-labeling approach of Chapter 9 is that it does not cope gracefully with missing lines; strictly, missing lines often mean "impossible" line drawings. Such an uncompromising stance can be modified by introducing constraints that allow more degrees of compatibility than two (wholly compatible or strictly incompatible). Once this is done, both consistent and inconsistent labelings may be ranked on compatibility and likelihood. It is possible that a formally inconsistent labeling may rank better than a consistent but unlikely labeling.

Some examples are shown in Fig. 12.7. In 12.7b, the "inconsistent" labels are not nonsensical, but can only arise from (a very unlikely) accidental alignment of convex edges with three of the six vertices of a hexagonal hole in an occluding surface. The vertices that arise are not all included in the traditional catalog of legal vertices, hence the "inconsistent" labeling. The "floating cube" interpretation is consistent, but the "sitting cube" interpretation may be more likely if support and gravity are important concepts in the system. In Fig.12.7c, the scene with a missing line cannot be consistent according to the traditional vertex catalog, but the "inconsistent" labels shown are still the most likely ones. Labelings are only "consistent," "inconsistent," or "optimal" with respect to a given relational structure of objects (an input scene) and a set of constraints. These examples are meant to be illustrative only.

### 12.4.2 Discrete Labeling Algorithms

Let us consider the problem of finding a consistent set of labels, taken from a discrete finite set. This problem may be placed in an abstract algebraic context [Haralick and Kartus 1978; Haralick 1978; Haralick et al. 1978]. Perhaps the sim-

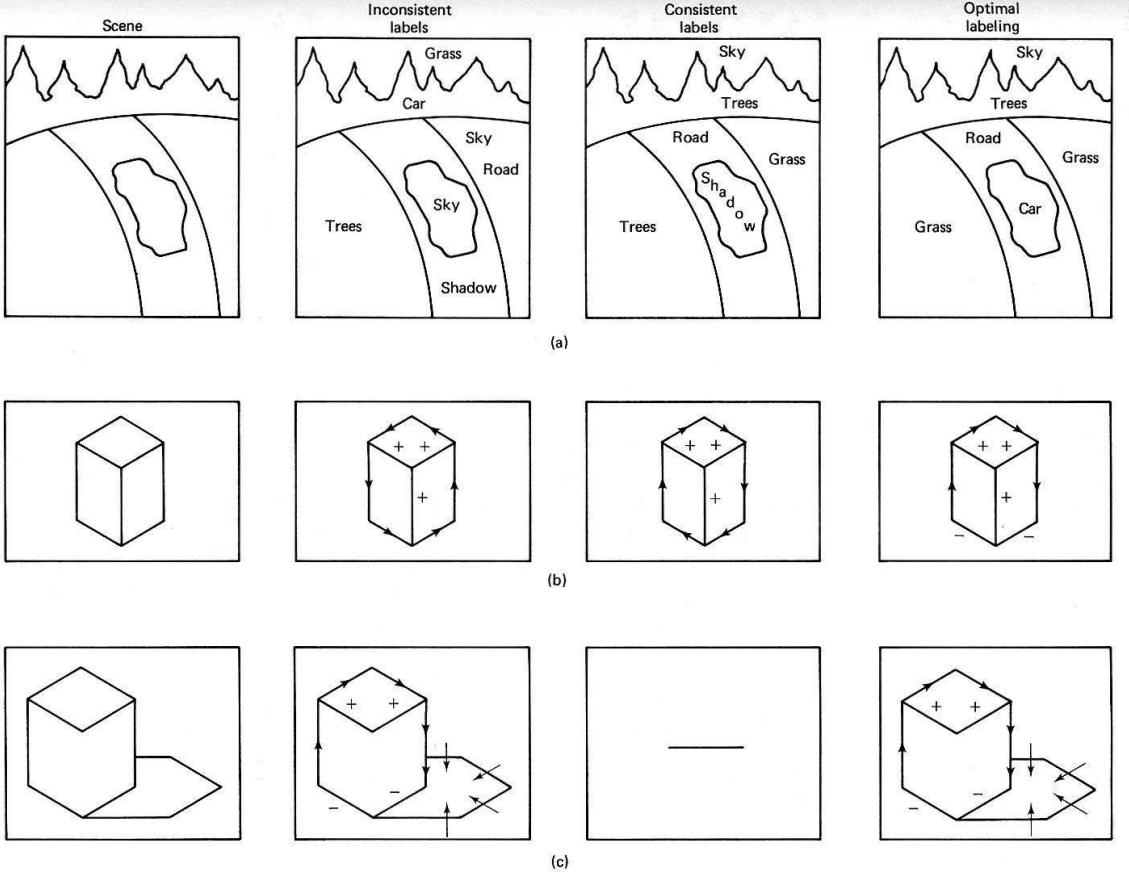



**Fig. 12.7** Three scenes (A, B, C) and their labelings. Labelings are only "consistent," "inconsistent," or "optimal" with respect to a given relational structure of objects (an input scene) and a set of constraints. These examples are meant to be illustrative only.

plest way to find a consistent labeling of a relational structure (we shall often say "labeling of a scene") is to apply a depth-first *tree search* of the labeling possibilities, as in the backtracking algorithm (11.1).

Label an object in accordance with unary constraints.

Iterate until a globally consistent labeling is found:

> Given the current labeling, label another object consistently—in accordance with all constraints.
>
> If the object cannot be labeled consistently, backtrack and pick a new label for a previously labeled object.

This labeling algorithm can be computationally inefficient. First, it does not prune the search tree very effectively. Second, if it is used to generate all consistent labelings, it does not recognize important independences in the labels. That is, it does not notice that conclusions reached (labels assigned) in part of the tree search are usable in other parts without recomputation.

In a *serial relaxation*, the labels are changed one object at a time. After each such change, the new labeling is used to determine which object to process next. This technique has proved useful in some applications [Feldman and Yakimovsky 1974].

Assign all possible labels to each object in accordance with unary constraints.

Iterate until a globally consistent labeling is found:

> Somehow pick an object to be processed.
>
> Modify its labels to be consistent with the current labeling.

A *parallel iterative* algorithm adjusts all object labels at once; we have seen this approach in several places, notably in the "Waltz filtering algorithm" of Section 9.5.

Assign all possible labels to each object in accordance with unary constraints.

Iterate until a globally consistent labeling is found:

> In parallel, eliminate from each object's label set those labels that are inconsistent with the current labels of the rest of the relational structure.

A less structured version of relaxation occurs when the iteration is replaced with an *asynchronous interaction* of labeled objects. Such interaction may be implemented with multiple cooperating processes or in a data base with "demons" (Ap-

pendix 2). This method of relaxation was used in MSYS [Barrow and Tenenbaum 1976]. Here imagine that each object is an active process that knows its own label set and also knows about the constraints, so that it knows about its relations with other objects. The program of each object might look like this.

> If I have just been activated, and my label set is not consistent with the labels of other objects in the relational structure, then I change my label set to be consistent, else I suspend myself.
>
> Whenever I change my label set, I activate other objects whose label set may be affected, then I suspend myself.

To use such a set of active objects, one can give each one all possible labels consistent with the unary constraints, establish the constraints so that the objects know where and when to pass on activity, and activate all objects.

Constraints involving arbitrarily many objects (i.e., constraints of arbitrarily high *order*) can efficiently be relaxed by recording acceptable labelings in a graph structure [Freuder 1978]. Each object to be labeled initially corresponds to a node in the graph, which contains all legal labels according to unary constraints. Higher order constraints involving more and more nodes are incorporated successively as new nodes in the graph. At each step the new node constraint is *propagated*; that is, the graph is checked to see if it is consistent with the new constraint. With the introduction of more constraints, node pairings that were previously consistent may be found to be inconsistent. As an example consider the following graph coloring problem: color the graph in Fig. 12.8 so that neighboring nodes have different colors. It is solved by building constraints of increasingly higher order and propagating them. The node constraints are given explicitly as shown in Fig. 12.8a, but the higher-order constraints are given in functional implicit form; prospective colorings must be tested to see if they satisfy the constraints. After the node constraints are given, order two constraints are synthesized as follows: (1) make a node for each node pairing; (2) add all labelings that satisfy the constraint. The result is shown in Fig. 12.8b. The single constraint of order three is synthesized in the same way, but now the graph is inconsistent: the match "$Y,Z$: Red,Green" is ruled out by the third order legal label set (RGY,GRY). To restore consistency the constraint is propagated through node $(Y,Z)$ by deleting the inconsistent labelings. This means that the node constraint for node Z is now inconsistent. To remedy this, the constraint is propagated again by deleting the inconsistency, in this case the labeling $(Z{:}G)$. The change is propagated to node $(X,Z)$ by deleting $(X,Z$: Red,Green) and finally the network is consistent.

In this example constraint propagation did not occur until constraints of order three were considered. Normally, some constraint propagation occurs after every order greater than one. Of course it may be impossible to find a consistent graph. This is the case when the labels for node Z in our example are changed from $(G,Y)$ to $(G,R)$. Inconsistency is then discovered at order three.

It is quite possible that a discrete labeling algorithm will not yield a unique label for each object. In this case, a consistent labeling exists using each label for the

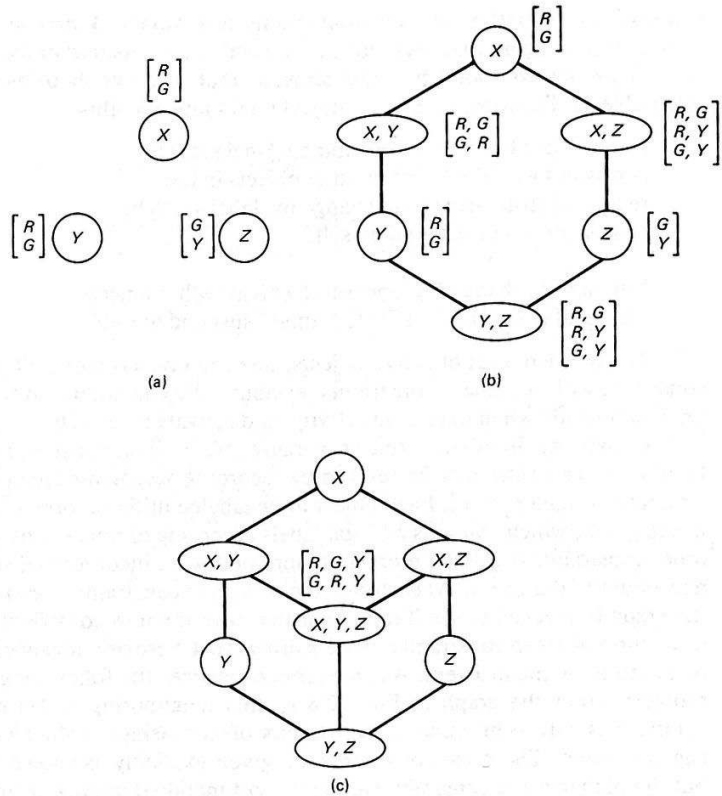



**Fig. 12.8** Coloring a graph by building constraints of increasingly higher order.

object. However, which of an object's multiple labels goes with which of another object's multiple labels is not determined. The final enumeration of consistent labelings usually proceeds by tree search over the reduced set of possibilities remaining after the relaxation.

*Convergence properties* of relaxation algorithms are important; convergence means that in some finite time the labeling will "settle down" to a final value. In discrete labeling, constraints may often be written so that the label adjustment phase always reduces the number of labels for an object (inconsistent ones are eliminated). In this case the algorithm clearly must converge in finite time to a consistent labeling, since for each object the label set must either shrink or stay stable. In schemes where labels are added, or where labels have complex structure (such as real number "weights" or "probabilities"), convergence is often not guaranteed mathematically, though such schemes may still be quite useful. Some probabilistic labeling schemes (Section 12.4.3) have provably good convergence properties.

It is possible to use relaxation schemes without really considering their mathematical convergence properties, their semantics (What is the semantics of weights attached to labels—are they probabilities?), or a clear definition of what exactly the relaxation is to achieve (What is a good set of labels?). The fact that some schemes can be shown to have unpleasant properties (such as assigning nonzero weights to each of two inconsistent hypotheses, or not always converging to a solution), does not mean that they cannot be used. It only means that their behavior is not formally characterizable or possibly even predictable. As relaxation computations become more common, the less formalizable, less predictable, and less conceptually elegant forms of relaxation computations will be replaced by better behaved, more thoroughly understood schemes.

### 12.4.3 A Linear Relaxation Operator and a Line Labeling Example

*The Formulation*

We now move away from discrete labeling and into the realm of continuous *weights* or *supposition values* on labels. In Sections 12.4.3 and 12.4.4 we follow closely the development of [Rosenfeld et al. 1976]. Let us require that the sum of label weights for each object be constrained to sum to unity. Then the weights are reminiscent of probabilities, reflecting the "probability that the label is correct." When the labeling algorithm converges, a label emerges with a high weight if it occurs in a probable labeling of the scene. Weights, or supposition values, are in fact hard to interpret consistently as probabilities, but they are suggestive of likelihoods and often can be manipulated like them.

In what follows $p$ refers to probability-like weights (supposition values) rather than to the value of a probability density function. Let a relational structure with n objects be given by $a_i$, $i = 1, \ldots, n$, each with $m$ discrete labels $\lambda_1, \ldots, \lambda_m$. The shorthand $p_i(\lambda)$ denotes the weight, or (with the above caveats) the "probability" that the label $\lambda$ (actually $\lambda_k$ for some $k$) is correct for the object $a_i$. Then the probability axioms lead to the following constraints,

$$0 \leqslant p_i(\lambda) \leqslant 1 \tag{12.14}$$

$$\sum_{\lambda} p_i(\lambda) = 1 \tag{12.15}$$

The labeling process starts with an initial assignment of weights to all labels for all objects [consistent with Eqs. (12.14) and (12.15)]. The algorithm is parallel iterative: It transforms all weights at once into a new set conforming to Eqs. (12.14) and (12.15), and repeats this transformation until the weights converge to stable values.

Consider the transformation as the application of an operator to a vector of label weights. This operator is based on the *compatibilities* of labels, which serve as constraints in this labeling algorithm. A compatibility $p_{ij}$ looks like a conditional probability.

$$\sum_{\lambda} p_{ij}(\lambda | \lambda') = 1 \qquad \text{for all } i, j, \lambda' \tag{12.16}$$

$$p_{ii}(\lambda|\lambda') = 1 \qquad iff\ \lambda = \lambda', \quad \text{else } 0. \tag{12.17}$$

The $p_{ij}(\lambda|\lambda')$ may be interpreted as the conditional probability that object $a_i$ has label $\lambda$ given that another object $a_j$ has label $\lambda'$. These compatibilities may be gathered from statistics over a domain, or may reflect a priori belief or information.

The operator iteratively adjusts label weights in accordance with other weights and the compatibilities. A new weight $p_i(\lambda)$ is computed from old weights and compatibilities as follows.

$$p_i(\lambda) := \sum_j c_{ij} \{ \sum_{\lambda'} p_{ij}(\lambda|\lambda') p_j(\lambda') \} \tag{12.18}$$

The $c_{ij}$ are coefficients such that

$$\sum_j c_{ij} = 1 \tag{12.19}$$

In Eq. (12.18), the inner sum is the expectation that object $a_i$ has label $\lambda$, given the evidence provided by object $a_j$. $p_i(\lambda)$ is thus a weighted sum of these expectations, and the $c_{ij}$ are the weights for the sum.

To run the algorithm, simply pick the $p_{ij}$ and $c_{ij}$, and apply Eq. (12.18) repeatedly to the $p_i$ until they stop changing. Equation (12.18) is in the form of a matrix multiplication on the vector of weights, as shown below; the matrix elements are weighted compatibilities, the $c_{ij}p_{ij}$. The relaxation operator is thus a matrix; if it is partitioned into several *component* matrices, one for each set of non-interacting weights, linear algebra yields proofs of convergence properties [Rosenfeld et al. 1976]. The iteration for the reduced matrix for each component does converge, and converges to the weight vector that is the eigenvector of the matrix with eigenvalue unity. This final weight vector is independent of the initial assignments of label weights; we shall say more about this later.

*An Example*

Let us consider the input line drawing scene of Fig. 12.9a used in [Rosenfeld et.al. 1976]. The line labels given in Section 9.5 allow several consistent labels as shown in Fig. 12.9b-e, each with a different physical interpretation.

In the discrete labelling "filtering" algorithm presented in Section 9.5 and outlined in the preceding section, the relational structure is imposed by the neighbor relation between vertices induced by their sharing a line. Unary constraints are imposed through a catalog of legal combinations of line labels at vertices, and the binary constraint is that a line must not change its label between vertices. The algorithm eliminates inconsistent labels.

Let us try to label the sides of the triangle $a_1$, $a_2$, and $a_3$ in Fig. 12.9 with the solid object edge labels $\{>, <, +, -\}$. To do this requires some "conditional probabilities" for compatibilities $p_{ij}(\lambda|\lambda')$, so let us use those that arise if all eight interpretations of Fig. 12.9 are equally likely. Remembering that

$$p(X|Y) = \frac{p(X,Y)}{p(Y)} \tag{12.20}$$

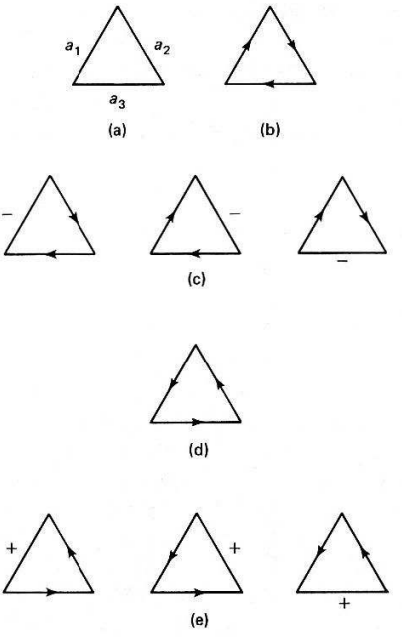



**Fig. 12.9** A triangle and its possible labels. (a) Edge names. (b) Floating. (c) Flap folded up. (d) Triangular hole. (e) Flap folded down.

and taking $p(X, Y)$ to mean the probability that labels $X$ and $Y$ occur consecutively in clockwise order around the triangle, one can derive Table 12.2. Of course, we could choose other compatibilities based on any considerations whatever as long as Eqs. (12.16) and (12.17) are preserved.

Table 12.2 shows that there are two noninteracting components, $\{-,>\}$ and $\{+,<\}$. Consider the first component that consists of the weight vector

$$[p_1(>),\ p_1(-),\ p_2(>),\ p_2(-),\ p_3(>),\ p_3(-)] \tag{12.21}$$

The second is treated similarly. This vector describes weights for the subpopulation of labelings given by Fig. 12.9b and c. The matrix $M$ of compatibilities has columns of weighted $p_{ij}$.

$$M = \begin{bmatrix} c_{11}p_{11}(>|>) & c_{21}p_{21}(>|>) & \cdots \\ c_{11}p_{11}(>|-) & c_{21}p_{21}(>|-) & \cdots \\ c_{12}p_{12}(>|>) & c_{22}p_{22}(>|>) & \cdots \\ c_{12}p_{12}(>|-) & c_{22}p_{22}(>|-) & \cdots \\ c_{13}p_{13}(>|>) & c_{23}p_{23}(>|>) & \cdots \\ c_{13}p_{13}(>|-) & c_{23}p_{23}(>|-) & \cdots \end{bmatrix} \tag{12.22}$$

**Table 12.2**

| $\lambda_1$ | $\lambda_2$ | $p(\lambda_1, \lambda_2)$ | $p(\lambda_1 \mid \lambda_2)$ |
|---|---|---|---|
| > | > | 1/4 | 2/3 |
| > | − | 1/8 | 1 |
| − | > | 1/8 | 1/3 |
| − | − | 0 | 0 |
| > | < | 0 | 0 |
| > | + | 0 | 0 |
| − | < | 0 | 0 |
| − | + | 0 | 0 |
| < | > | 0 | 0 |
| + | > | 0 | 0 |
| < | − | 0 | 0 |
| + | − | 0 | 0 |
| < | < | 1/4 | 2/3 |
| < | + | 1/8 | 1 |
| + | < | 1/8 | 1/3 |
| + | + | 0 | 0 |

If we let $c_{ij} = 1/3$ for all $i$, $j$, then

$$M = \frac{1}{3}\begin{bmatrix} 1 & 0 & 2/3 & 1/3 & 2/3 & 1/3 \\ 0 & 1 & 1 & 0 & 1 & 0 \\ 2/3 & 1/3 & 1 & 0 & 2/3 & 1/3 \\ 1 & 0 & 0 & 1 & 1 & 0 \\ 2/3 & 1/3 & 2/3 & 1/3 & 1 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 \end{bmatrix} \tag{12.23}$$

An analytic eigenvector calculation (Appendix 1) shows that the M of Eq. (12.23) yields (for any initial weight vector) the final weight vector of

$$[3/4,\ 1/4,\ 3/4,\ 1/4,\ 3/4,\ 1/4] \tag{12.24}$$

Thus each line of the population in the component we chose (Fig. 12.9b and c) has label > with "probability" 3/4, —with "probability" 1/4. In other words, from an initial assumption that all labelings in Fig. 12.9b and c were equally likely, the system of constraints has "relaxed" to the state where the "most likely" labeling is that of Fig. 12.9b, the floating triangle.

This relaxation method is a crisp mathematical technique, but it has some drawbacks. It has good convergence properties, but it converges to a solution entirely determined by the compatibilities, leaving no room for preferences or local scene evidence to be incorporated and affect the final weights. Further, the algorithm perhaps does not exactly mirror the following intuitions about how relaxation should work.

1. Increase $p_i(\lambda)$ if high probability labels for other objects are compatible with assignment of $\lambda$ to $a_i$.
2. Decrease $p_i(\lambda)$ if high probability labels are incompatible with the assignment of $\lambda$ to $a_i$.
3. Labels with low probability, compatible or incompatible, should have little influence on $p_i(\lambda)$.

However, the operator of this section decreases $p_i(\lambda)$ the most when other labels have both low compatibility and low probability. Thus it accords with (1) above, but not with (2) or (3). Some of these difficulties are addressed in the next section.

### 12.4.4 A Nonlinear Operator

*The Formulation*

If compatibilities are allowed to take on both positive and negative values, then we can express strong incompatibility better and obtain behavior more like (1), (2), and (3) just above. Denote the compatibility of the event "label $\lambda$ on $a_i$" with the event "label $\lambda$ on $a_j$" by $r_{ij}(\lambda, \lambda')$. If the two events occur together often, $r_{ij}$ should be positive. If they occur together rarely, $r_{ij}$ should be negative. If they are independent, $r_{ij}$ should be 0. The *correlation coefficient* behaves like this, and the compatibilities of this section are based on correlations (hence the the notation $r_{ij}$ for compatibilities). The correlation is defined using the covariance.

$$\text{cov}(X, Y) = p(X, Y) - p(X)p(Y)$$

Now define a quantity $\sigma$ which is like the standard deviation

$$\sigma(X) = [p(X) - (p(X))^2]^{1/2} \tag{12.25}$$

then the correlation is the normalized covariance

$$\text{cor}(X, Y) = \frac{\text{cov}(X, Y)}{\sigma(X)\sigma(Y)} \tag{12.26}$$

This allows the formulation of an expression precisely analogous to Eq. (12.18), only that $r_{ij}$ instead of $p_{ij}$ is used to obtain a means of calculating the positive or negative change in weights.

$$q_i^{(k)}(\lambda) = \sum_j c_{ij} \left[\sum_{\lambda'} r_{ij}(\lambda, \lambda') p_j^{(k)}(\lambda')\right] \tag{12.27}$$

In Eqs. (12.27)–(12.29) the superscripts indicate iteration numbers. The weight change (Eq. 12.27) could be applied as follows,

$$p_i^{(k+1)}(\lambda) = p_i^{(k)}(\lambda) + q_i^{(k)}(\lambda) \tag{12.28}$$

but then the resultant label weights might not remain nonnegative. Fixing this in a straightforward way yields the iteration equation

$$p_i^{(k+1)}(\lambda) = \frac{p_i^{(k)}(\lambda)[1 + q_i^{(k)}(\lambda)]}{\sum_{\lambda} p_i^{(k)}(\lambda)[1 + q_i^{(k)}(\lambda)]} \tag{12.29}$$

The convergence properties of this operator seem to be unknown, and like the linear operator it can assign nonzero weights to maximally incompatible labelings. However, its behavior can accord with intuition, as the following example shows.

*An Example*

Computing the covariances and correlations for the set of labels of Fig. 12.9b-e yields Table 12.3.

Figure 12.10 shows the nonlinear operator of Eq. (12.29) operating on the example of Fig. 12.9. Figure 12.10 shows several cases.

1. Equal initial weights: convergence to apriori probabilities ($\frac{3}{8}, \frac{3}{8}, \frac{1}{8}, \frac{1}{8}$).
2. Equal weights in the component $\{>, -\}$: convergence to "most probable" floating triangle labeling.
3. Slight bias toward a flap labeling is not enough to overcome convergence to the "most probable" labeling, as in (2).
4. Like (3), but greater bias elicits the "improbable" labeling.
5. Contradicatory biases toward "improbable" labelings: convergence to "most probable" labeling instead.
6. Like (5), but stronger bias toward one "improbable" labeling elicits it.
7. Bias toward one of the components $\{>, -\}$, $\{<, +\}$ converges to most probable labeling in that component.
8. Like (7), only biased to less probable labelling in a component.

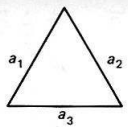
### 12.4.5 Relaxation as Linear Programming

*The Idea*

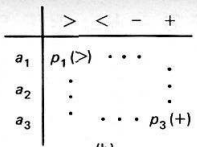
Linear programming (LP) provides some useful metaphors for thinking about relaxation computations, as well as actual algorithms and a rigorous basis [Hummel and Zucker 1980]. In this section we follow the development of [Hinton 1979].

**Table 12.3**

| $\lambda_1$ | $\lambda_2$ | $\text{cov}(\lambda_1, \lambda_2)$ | $\text{cor}(\lambda_1, \lambda_2)$ |
|---|---|---|---|
| $>$ | $>$ | $\frac{7}{64}$ | $\frac{7}{15}$ |
| $>$ | $-$ | $\frac{5}{64}$ | $5/\sqrt{105}$ |
| $-$ | $>$ | $\frac{5}{64}$ | $5/\sqrt{105}$ |
| $-$ | $-$ | $-\frac{1}{64}$ | $-\frac{1}{7}$ |
| $>$ | $<$ | $-\frac{9}{64}$ | $-\frac{3}{5}$ |
| . | . | . | . |
| . | . | . | . |
| . | . | . | . |




(a)




(b)

| Case | Initial weights | | | | After 2 to 3 iterations | | | | After 20 to 30 iterations | | | | Limit | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 0.25 | 0.25 | 0.25 | 0.25 | 0.3 | 0.3 | 0.2 | 0.2 | 0.33 | 0.33 | 0.17 | 0.17 | 0.37 | 0.37 | 0.13 | 0.13 |
| (1) | 0.25 | 0.25 | 0.25 | 0.25 | 0.3 | 0.3 | 0.2 | 0.2 | 0.33 | 0.33 | 0.17 | 0.17 | 0.37 | 0.37 | 0.13 | 0.13 |
| | 0.25 | 0.25 | 0.25 | 0.25 | 0.3 | 0.3 | 0.2 | 0.2 | 0.33 | 0.33 | 0.17 | 0.17 | 0.37 | 0.37 | 0.13 | 0.13 |
| | 0.5 | 0 | 0.5 | 0 | 0.8 | 0 | 0.2 | 0 | 0.98 | 0 | 0.2 | 0 | 1 | 0 | 0 | 0 |
| (2) | 0.5 | 0 | 0.5 | 0 | 0.8 | 0 | 0.2 | 0 | 0.98 | 0 | 0.2 | 0 | 1 | 0 | 0 | 0 |
| | 0.5 | 0 | 0.5 | 0 | 0.8 | 0 | 0.2 | 0 | 0.98 | 0 | 0.2 | 0 | 1 | 0 | 0 | 0 |
| | 0.5 | 0 | 0.5 | 0 | 0.62 | 0 | 0.37 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| (3) | 0.4 | 0 | 0.6 | 0 | 0.49 | 0 | 0.51 | 0 | 0.97 | 0 | 0.03 | 0 | 1 | 0 | 0 | 0 |
| | 0.5 | 0 | 0.5 | 0 | 0.62 | 0 | 0.37 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| | 0.5 | 0 | 0.5 | 0 | 0.64 | 0 | 0.36 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| (4) | 0.3 | 0 | 0.7 | 0 | 0.36 | 0 | 0.64 | 0 | 0.07 | 0 | 0.93 | 0 | 0 | 0 | 1 | 0 |
| | 0.5 | 0 | 0.5 | 0 | 0.64 | 0 | 0.36 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| | 0.3 | 0 | 0.7 | 0 | 0.5 | 0 | 0.5 | 0 | 0.95 | 0 | 0.05 | 0 | 1 | 0 | 0 | 0 |
| (5) | 0.3 | 0 | 0.7 | 0 | 0.5 | 0 | 0.5 | 0 | 0.95 | 0 | 0.05 | 0 | 1 | 0 | 0 | 0 |
| | 0.5 | 0 | 0.5 | 0 | 0.84 | 0 | 0.16 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| | 0.2 | 0 | 0.8 | 0 | 0.3 | 0 | 0.7 | 0 | 0.06 | 0 | 0.94 | 0 | 0 | 0 | 1 | 0 |
| (6) | 0.3 | 0 | 0.7 | 0 | 0.51 | 0 | 0.49 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| | 0.5 | 0 | 0.5 | 0 | 0.83 | 0 | 0.17 | 0 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| | 0.3 | 0.2 | 0.3 | 0.2 | 0.41 | 0.13 | 0.32 | 0.14 | 0.98 | 0 | 0.02 | 0 | 1 | 0 | 0 | 0 |
| (7) | 0.3 | 0.2 | 0.3 | 0.2 | 0.41 | 0.13 | 0.32 | 0.14 | 0.98 | 0 | 0.02 | 0 | 1 | 0 | 0 | 0 |
| | 0.3 | 0.2 | 0.3 | 0.2 | 0.41 | 0.13 | 0.32 | 0.14 | 0.98 | 0 | 0.02 | 0 | 1 | 0 | 0 | 0 |
| | 0.3 | 0.2 | 0.3 | 0.2 | 0.38 | 0.17 | 0.29 | 0.16 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| (8) | 0.25 | 0.25 | 0.25 | 0.25 | 0.35 | 0.20 | 0.25 | 0.20 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| | 0.2 | 0.2 | 0.4 | 0.2 | 0.23 | 0.16 | 0.45 | 0.16 | 0.2 | 0 | 0.8 | 0 | 0 | 0 | 1 | 0 |

(c)

**Fig. 12.10** The nonlinear operator produces labelings for the triangle in (a). (b) shows how the label weights are displayed, and (c) shows a number of cases (see text).

To put relaxation in terms of linear programming, we use the following translations.

- LABEL WEIGHT VECTORS $\Longrightarrow$ POINTS IN EUCLIDEAN N-SPACE. Each possible assignment of a label to an object is a *hypothesis*, to which a weight (supposition value) is to be attached. With N hypotheses, an N-vector of weights describes a labeling. We shall call this vector a (hypothesis or label) *weight vector.* For $m$ labels and $n$ objects, we need at most Euclidean $nm$-space.
- CONSTRAINTS $\Longrightarrow$ INEQUALITIES. *Constraints are mapped into linear inequalities* in hypothesis weights, by way of various identities like those of "fuzzy logic" [Zadeh 1965]. Each inequality determines an infinite half-space. The weight vectors within this half-space satisfy the constraint. Those outside do not. The convex solid that is the set intersection of all the half-spaces includes those weight vectors that satisfy all the constraints: each represents a "consistent" labeling. In linear programming terms, each such weight vector is a *feasible solution.* We thus have the usual geometric interpretation of the linear programming problem, which is to find the best (optimal) consistent (feasible) labeling (solution, or weight vector). Solutions should have *integer*-valued (1- or 0-valued) weights indicating convergence to actual labelings, not probabilistic ones such as those of Section 12.4.3, or the one shown in Fig. 12.10c, case 1.
- HYPOTHESIS PREFERENCES $\Longrightarrow$ PREFERENCE VECTOR. Often some hypotheses (label assignments) are preferred to others, on the basis of a priori knowledge, image evidence, and so on. To express this preference, make an $N$-dimensional *preference vector*, which expresses the relative importance (preference) of the hypotheses. Then
  - The *preference of a labeling* is the dot product of the preference vector and the weight vector (it is the sum for all hypotheses of the weight of each hypothesis times its preference).
  - The preference vector defines a *preference direction* in $N$-space. The optimal feasible solution is that one "farthest" in the preference direction. Let $\mathbf{x}$ and $\mathbf{y}$ be feasible solutions; they are $N$-dimensional weight vectors satisfying all constraints. If $\mathbf{z} = \mathbf{x} - \mathbf{y}$ has a component in the positive preference direction, then $\mathbf{x}$ is a better solution than $\mathbf{y}$, by the definition of the preference of a labeling.

  It is helpful for our intuition to let the preference direction define a "downward" direction in N-space as gravity does in our three-space. Then we wish to pick the lowest (most preferred) feasible solution vector.
- LABELING $\Longrightarrow$ OPTIMAL SOLUTION. The relaxation algorithm must solve the linear programming problem—find the best consistent labeling. Under the conditions we have outlined, the best solution vector occurs generally at a vertex of the $N$-space solid. This is so because usually a vertex will be the "lowest" part of the convex solid in the preference direction. It is a rare coincidence that the solid "rests on a face or edge," but when it does a whole edge or face of the solid contains equally preferred solutions (the preference direction is normal to

the edge or face). For integer solutions, the solid should be the convex hull of integer solutions and not have any vertices at noninteger supposition values.

The "simplex algorithm" is the best known solution method in linear programming. It proceeds from vertex to vertex, seeking the one that gives the optimal solution. The simplex algorithm is not suited to parallel computation, however, so here we describe another approach with the flavor of hill-climbing optimization. Basically, any such algorithm moves the weight vector around in $N$-space, iteratively adjusting weights. If they are adjusted one at a time, serial relaxation is taking place; if they are all adjusted at once, the relaxation is parallel iterative. The feasible solution solid and the preference vector define a "cost function" over all $N$-space, which acts like a potential function in physics. The algorithm tries to reach an optimum (minimum) value for this cost function. As with many optimization algorithms, we can think of the algorithm as trying to simulate (in $N$-space) a ball bearing (the weight vector) rolling along some path down to a point of minimum gravitational (cost) potential. Physics helps the ball bearing find the minimum; computer optimization techniques are sometimes less reliable.

*Translating Constraints to Inequalities*

The supposition values, or hypothesis weights, may be encoded into the interval [0, 1], with 0 meaning "false," 1 meaning "true." The extension of weights to the whole interval is reminiscent of "fuzzy logic," in which truth values may be continuous over some range [Zadeh 1965]. As in Section 12.4.3, we denote supposition values by $p(\cdot)$; $H$, $A$, $B$, and $C$ are label assignment events, which may be considered as hypotheses that the labels are correctly assigned. $\tilde{}$, $\vee$, $\wedge$, $\Longrightarrow$ and $\Longleftrightarrow$ are the usual logical connectives relating hypotheses. The connectives allow the expression of complex constraints. For instance, a constraint might be "Label $x$ as '$y$' if and only if $z$ is labeled '$w$' or $q$ is labelled '$v$'." This constraint relates three hypotheses: $h_1$: ($x$ is "$y$"), $h_2$: ($z$ is "$w$"), $h_3$: ($q$ is "$v$"). The constraint is then $h_1 \Longleftrightarrow (h_2 \vee h_3)$.

Inequalities may be derived from constraints this way.

1. *Negation.* $p(H) = 1 - p(\tilde{}(H))$.
2. *Disjunction.* The sums of weights of the disjunct are greater than or equal to one. $p(A \vee B \vee \ldots \vee C)$ gives the inequality $p(A) + p(B) + \ldots + p(C) \geqslant 1$.
3. *Conjunction.* These are simply separate inequalities, one per conjunct. In particular, a conjunction of disjunctions may be dealt with conjunct by conjunct, producing one disjunctive inequality per conjunct.
4. *Arbitrary expressions.* These must be put into conjunctive normal form (Chapter 10) by rewriting all connectives as $\wedge$'s and $\vee$'s. Then (3) applies.

As an example, consider the simple case of two hypotheses $A$ and $B$, with the single constraint that $A \Longrightarrow B$. Applying rules 1 through 4 results in the following five inequalities in $p(A)$ and $p(B)$; the first four assure weights in [0, 1]. The fifth arises from the logical constraint, since $A \Longrightarrow B$ is the same as $B \vee \tilde{}(A)$.

$$0 \leqslant p(A)$$
$$p(A) \leqslant 1$$
$$0 \leqslant p(B)$$
$$p(B) \leqslant 1$$
$$p(B) + (1 - p(A)) \geqslant 1 \qquad \text{or} \qquad p(B) \geqslant p(A)$$

These inequalities are shown in Fig. 12.11. As expected from the $\Longrightarrow$ constraint, optimal feasible solutions exist at: (1,1) or $(A,B)$; (0,1) or $(\tilde{}(A),B)$; (0,0) or $(\tilde{}(A), \tilde{}(B))$. Which of these is preferred depends on the preference vector. If both its components are positive, $(A,B)$ is preferred. If both are negative, $(\tilde{}(A), \tilde{}(B))$ is preferred, and so on.

*A Solution Method*

Here we describe (in prose) a search algorithm that can find the optimal feasible solution to the linear programming problem as described above. The description makes use of the mechanical analogy of an $N$-dimensional solid of feasible solutions, oriented in $N$-space so that the preference vector induces a "downward" direction in space. The algorithm attempts to move the vector of hypothesis weights to the point in space representing the feasible solution of maximum preference. It should be clear that this is a point on the surface of the solid, and unless the preference vector is normal to a face or edge of the solid, the point is a unique "lowest" vertex.

To establish a potential that leads to feasible solutions, one needs a measure of the infeasibility of a weight vector for each constraint. Define the amount a vector violates a constraint to be zero if it is on the feasible side of the constraint hyperplane. Otherwise the violation is the normal distance of the vector to the hyperplane. If $\mathbf{h}_i$ is the coefficient vector of the $i^{th}$ hyperplane (Appendix 1) and $\mathbf{w}$ the weight vector, this distance is

$$d_i = \mathbf{w} \cdot \mathbf{h}_i \tag{12.30}$$

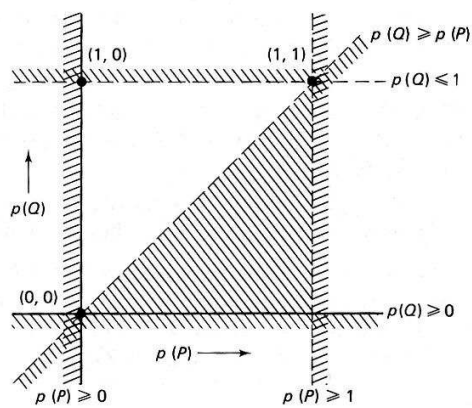



**Fig. 12.11** The feasible region for two hypotheses A and B and the constraint A B. Optimal solutions may occur at the three vertices. The preferred vertex will be that one farthest in the direction of the preference vector, or lowest if the preference vector defines "down."

If we then define the infeasibility as

$$I = \sum_i \frac{d_i^2}{2} \tag{12.31}$$

then $\partial I/\partial d_i = d_i$ is the rate the infeasibility changes for changes in the violation. The force exerted by each constraint is proportional to the normal distance from the weight vector to the feasible region defined by that constraint, and tends to pull the weight vector onto the surface of the solid.

Now add a weak "gravity-like" force in the preference direction to make the weight vector drift to the optimal vertex. At this point an optimization program might perform as shown in Fig. 12.12.

Figure 12.12 illustrates a problem: The forces of preference and constraints will usually dictate a minimum potential outside the solid (in the preference direction). Fixes must be applied to force the weight vector back to the closest (presumably the optimum) vertex. One might round high weights to 1 and low ones to 0, or add another local force to draw vectors toward vertices.

*Examples*

An algorithm based on the principles outlined in the preceeding section was successfully used to label scenes of "puppets" such as Fig. 12.13 with body parts [Hinton 1979].

The discrete, consistency-oriented version of line labeling may be extended to incorporate the notion of optimal labelings. Such a system can cope with the explosive increase in consistent labelings that occurs if vertex labels are included for cases of missing lines, accidental alignment, or "two-dimensional" objects such as folded paper. It allows modeling of the fact that human beings do not "see" all possible interpretations of scenes with accidental alignments. If labelings are given

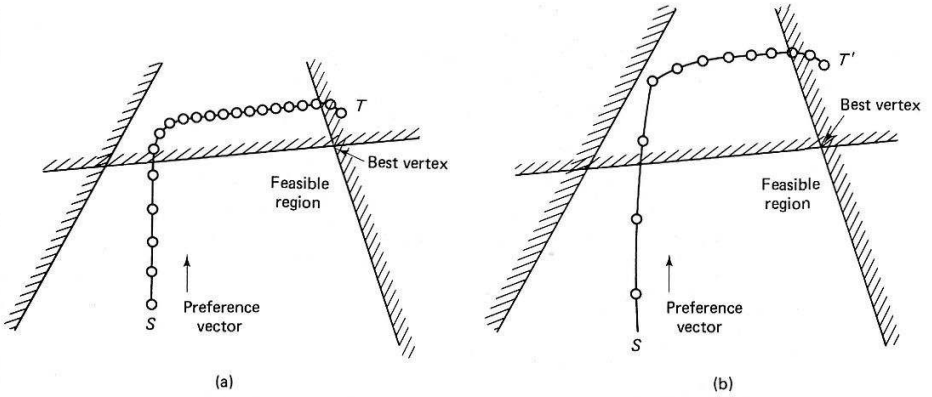
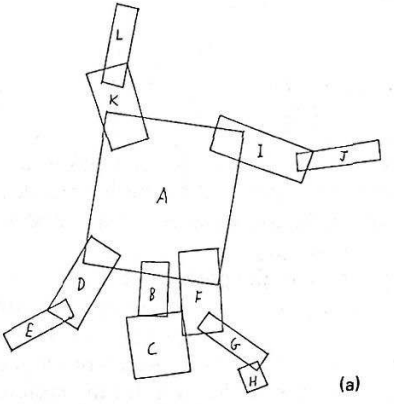



**Fig. 12.12** In (a), the weight vector moves from S to rest at T, under the combined influence of the preferences and the violated constraints. In (b), convergence is speeded by making stronger preferences, but the equilibrium is farther away from the optimal vertex.

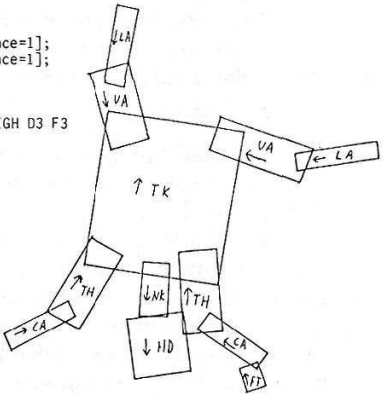



```
!.bestset;
A1  BOT TRUNK  NECK B1  UPPERARM D2 F2  THIGH 13 K2
B1  BOT NECK  HEAD C1  TRUNK A1
C1  BOT HEAD  NECK B1
D2  TOP UPPERARM  TRUNK A1  LOWERARM E4
E4  TOP LOWERARM  UPPERARM D2  HAND -
F2  TOP UPPERARM  TRUNK A1  LOWERARM G2
G2  TOP LOWERARM  UPPERARM F2  HAND H2
H2  TOP HAND  LOWERARM G2
I3  TOP THIGH  TRUNK A1  CALF J4
J4  BOT CALF  THIGH I3  FOOT -
K2  BOT THIGH  TRUNK A1  CALF L4
L4  BOT CALF  THIGH K2  FOOT -
```

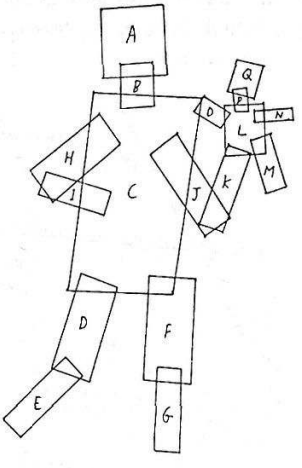
(a)

```
!trytointerpret [trunk as upright importance=1];
!trytointerpret [thigh as upright importance=1];

!.bestset;
A2  TOP TRUNK  NECK -  UPPERARM I2 K1  THIGH D3 F3
B1  BOT NECK  HEAD C1  TRUNK -
C1  BOT HEAD  NECK B1
D3  TOP THIGH  TRUNK A2  CALF E3
E3  TOP CALF  THIGH D3  FOOT -
F3  TOP THIGH  TRUNK A2  CALF E3
G3  TOP CALF  THIGH F3  FOOT H1
H1  TOP FOOT  CALF G3
I2  TOP UPPERARM  TRUNK A2  LOWERARM J3
J3  BOT LOWERARM  UPPERARM I2  HAND -
K1  BOT UPPERARM  TRUNK A2  LOWERARM L3
L3  BOT LOWERARM  UPPERARM K1  HAND -
```




(b)




```
!.bestset;
A1  TOP HEAD  NECK B1
B1  TOP NECK  HEAD A1  TRUNK C2
C2  TOP TRUNK  NECK B1  UPPERARM H1 J1  THIGH D3 F3
D3  TOP THIGH  TRUNK C2  CALF E3
E3  TOP CALF  THIGH D3  FOOT -
F3  TOP THIGH  TRUNK C2  CALF G3
G3  TOP CALF  THIGH F3  FOOT-
H1  TOP UPPERARM  TRUNK C2  LOWERARM I1
I1  TOP LOWERARM  UPPERARM H1  HAND -
J1  TOP LOWERARM  TRUNK C2  LOWERARM K4
K4  BOT LOWERARM  UPPERARM J1  HAND L6
L6  BOT HAND  LOWERARM K4
```

(c)

**Fig. 12.13** Puppet scenes interpreted by linear programming relaxation. (a) shows an upside down puppet. (b) is the same input along with preferences to interpret the trunk and thighs as upright; these result in an interpretation with trunk and neck not connected. In (c), the program finds only the "best" puppet, since it was only expecting one.

costs, then one can include labels for missing lines and accidental alignment as high-cost labels, rendering them usable but undesirable. Also, in a scene-analysis system using real data, local evidence for edge appearance can enhance the a priori likelihood that a line should bear a particular label. If such preferences can be extracted along with the lines in a scene, the evidence can be used by the line labeling algorithm.

The inconsistency constraints for line labels may be formalized as follows. Each line and vertex has one label in a consistent labeling; thus for each line $L$ and vertex $J$,

$$\sum_{\text{all line labels}} p(L \text{ has label LLABEL}) = 1 \tag{12.32}$$

$$\sum_{\text{all vertex labels}} p(J \text{ has label VLABEL}) = 1 \tag{12.33}$$

Of course, the VLABELS and LLABELS in the above constraints must be forced to be compatible (if $L$ has LLABEL, JLABEL must agree with it). For a line $L$ and a vertex $J$ at its end,

$$p(L \text{ has LLABEL}) = \sum_{\substack{\text{all VLABELS} \\ \text{giving LLABEL to } L}} p(J \text{ has label VLABEL}) \tag{12.34}$$

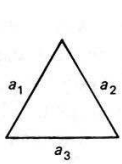
This constraint also enforces the coherence rule (a line may not change its label betwen vertices).

Using these constraints, linear programming relaxation labeled the triangle example of Fig. 12.7 as shown in Fig. 12.14, which shows three cases.

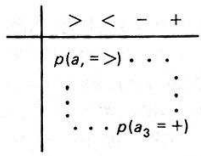
1. Preference 0.5 for each of the three junction label assignments (hypotheses) corresponding to the floating triangle, 0 preference for all other junction and line label hypotheses: converges to floating triangle.
2. Like (1), but with equal preferences given to the junction labels for the triangular hole interpretation, 0 to all other preferences.
3. Preference 3 to the convex edge label for a 2 overrides the three preferences of 1/2 for the floating triangle of case (1). All preferences but these four were 0.

*Some Extensions*

The translation of constraints to inequalities described above does not guarantee that they produce a set of half-spaces whose intersection is the convex hull of the feasible integer solutions. They can produce "noninteger optima," for which supposition values are not forced to 1 or 0. This is reminiscent of the behavior of the linear relaxation operator of Section 12.4.3, and may not be objectionable. If it is, some effort must be expended to cope with it. Here is an example




(a)




(b)

| Case | After 10 iterations | | | | After 20 iterations | | | | After 30 to 40 iterations | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| (1) | 0.65 | 0.22 | 0.01 | 0.14 | 0.90 | 0.07 | 0 | 0.04 | 0.99 | 0 | 0 | 0 |  |
| | 0.65 | 0.22 | 0.01 | 0.14 | 0.90 | 0.07 | 0 | 0.04 | 0.99 | 0 | 0 | 0 | |
| | 0.65 | 0.22 | 0.01 | 0.14 | 0.90 | 0.07 | 0 | 0.04 | 0.99 | 0 | 0 | 0 | |
| (2) | 0.39 | 0.89 | 0 | 0 | 0.14 | 0.95 | 0 | 0 | 0 | 0.99 | 0 | 0 |  |
| | 0.39 | 0.89 | 0 | 0 | 0.14 | 0.95 | 0 | 0 | 0 | 0.99 | 0 | 0 | |
| | 0.39 | 0.89 | 0 | 0 | 0.14 | 0.95 | 0 | 0 | 0 | 0.99 | 0 | 0 | |
| (3) | 0.56 | 0.48 | 0 | 0.05 | 0.81 | 0.23 | 0 | 0 | 0.99 | 0 | 0 | 0 |  |
| | 0 | 0.34 | 0 | 0.99 | 0 | 0.15 | 0 | 0.99 | 0 | 0 | 0 | 0.99 | |
| | 0.56 | 0.48 | 0 | 0.05 | 0.81 | 0.23 | 0 | 0 | 0.99 | 0 | 0 | 0 | |

(c)

**Fig. 12.14** As in Fig. 12.10, the triangle of (a) is to be assigned labels, and the changing label weights are shown for three cases in (c) using the format of (b). Supposition values for junction labels were used as well, but are not shown. All initial supposition values were 0.

of the problem. Assume three logical constraints, $\tilde{}(A \wedge B)$, $\tilde{}(B \wedge C)$, and $\tilde{}(C \wedge A)$. Suppose $A$, $B$, and $C$ have equal preferences of unity (the preference vector is $(1, 1, 1)$). Translating the constraints yields

$$\begin{aligned} p(A) + p(B) &\leqslant 1 \\ p(B) + p(C) &\leqslant 1 \\ p(C) + p(A) &\leqslant 1 \end{aligned} \tag{12.35}$$

The best feasible solution has a total preference of 1½, and is

$$p(A) = p(B) = p(C) = \tfrac{1}{2} \tag{12.36}$$

Here the "best" solution is outside the convex hull of the integer solutions (Fig. 12.15).

The basic way to ensure integer solutions is to use stronger constraints than those arising from the simple rules given above. These may be introduced at first, or when some noninteger optimum has been reached. These stronger constraints are called *cutting planes*, since they cut off the noninteger optima vertices. In the example above, the obvious stronger constraint is

$$p(A) + p(B) + p(C) \leqslant 1 \tag{12.37}$$

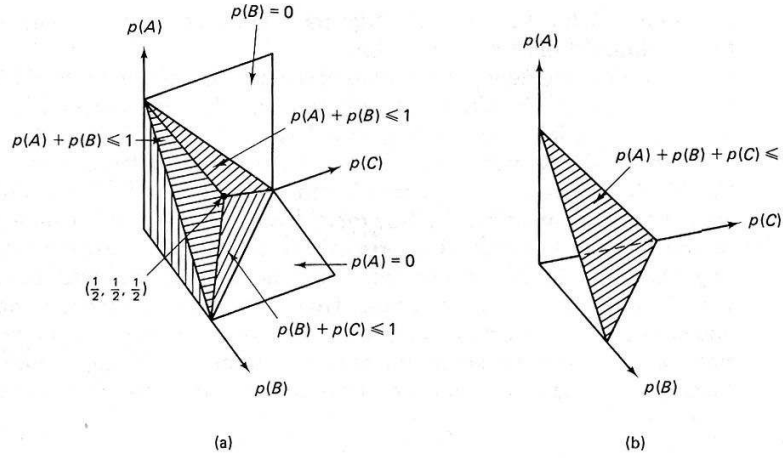



**Fig. 12.15** (a) shows part of the surface of the feasible solid with constraints $\neg (A \ \& \ B)$, $\neg (B \ \& \ C)$, $\neg (C \ \& \ A)$, and the non-integer vertex where the three halfspaces intersect. (b) shows a cutting plane corresponding to the constraint "at most one of $A$, $B$, or $C$" that removes the non-integer vertex.

which says that at most one of $A$, $B$, and $C$ is true (this is a logical consequence of the logical constraints). Such cutting planes can be derived as needed, and can be guaranteed to eliminate all noninteger optimal vertices in a finite number of cuts [Gomory 1968; Garfinkel and Nemhauser 1972]. Equality constraints may be introduced as two inequality constraints in the obvious way: This will constrain the feasible region to a plane.

Suppose that one desires "weak rules," which are usually true but which can be broken if evidence demands it? For each constraint arising from such a rule, add a hypothesis to represent the situation where the rule is broken. This hypothesis is given a negative preference depending on the strength of the rule, and the constraint enhanced to include the possibility of the broken rule. For example, if a weak rule gives the constraint $P \vee Q$, create a hypothesis $H$ equivalent to $\tilde{}(P \vee Q) = (\tilde{}(P) \wedge \tilde{}(Q))$, and replace the constraint with $P \vee Q \vee H$. Then by "paying the cost" of the negative preference for $H$, we can have neither $P$ nor $Q$ true.

Hypotheses can be created as the algorithm proceeds by having demon-like "generator hypotheses." The demon watches the supposition value of the generator, and when it becomes high enough, runs a program that generates explicit hypotheses. This is clearly useful; it means that all possible hypotheses do not need to be generated in advance of any scene investigation. The generator can be given a preference equal to that of the best hypotheses that it can generate.

Relaxation sometimes should determine a real number (such as the slope of a line) instead of a truth value. A generator-like technique can allow the method to refine the value of real-valued hypotheses. Basically, the idea is to assign a (Boolean-valued) generator hypothesis to a range of values for the real value to be

determined. When this generator triggers, more hypotheses are generated to get a finer partition of the range, and so on.

The enhancements to the linear programming paradigm of relaxation give some idea of the flexibility of the basic idea, but also reveal that the method is not at all cut-and-dried, and is still open to basic investigation. One of the questions about the method is exactly how to take advantage of parallel computation capabilities. Each constraint and hypothesis can be given its own processor, but how should they communicate? Also, there seems little reason to suppose that the optimization problems for this form of relaxation are any easier than they are for any other multidimensional search, so the method will encounter the usual problems inherent in such optimization. However, despite all these technical details and problems of implementation, the linear programming paradigm for the relaxation computation is a coherent formalization of the process. It provides a relatively "classical" context of results and taxonomy of problems [Hummel and Zucker 1980].

## 12.5 ACTIVE KNOWLEDGE

*Active knowledge* systems [Freuder 1975] are characterized by the use of procedures as the elementary units of knowledge (as opposed to propositions or data base items, for instance). We describe how active knowledge might work, because it is a logical extreme of the procedural implementation of propositions. In fact, this style of control has not proven influential; some reasons are given below.

Active knowledge is notionally parallel and heterarchical. Many different procedures can be active at the same time depending on the input. For this reason active knowledge is more easily applied to belief maintenance than to planning; it is very difficult to organize sequential activity within this discipline. Basically, each procedure is responsible for a "chunk" of knowledge, and knows how to manage it with respect to different visual inputs. Control in an active knowledge system is completely distributed. Active knowledge can also be viewed as an extension of the constraint relaxation problem; powerful procedures can make arbitrary detailed tests of the consistency between constraints.

Each piece of active knowledge (program module) knows which other modules it depends on, which depend on it, which it can complain to, and so forth. Thus the choice of "what to do next" is contained in the modules and is not made by an exterior executive.

We describe HYPER, a particular active knowledge system design which illustrates typical properties of active knowledge [Brown 1975]. HYPER provides a less structured mechanism for construction and exploration of hypotheses than does LP-relaxation. Using primitive control functions of the system, the user may write programs for establishing hypotheses and for using the conclusions so reached. The programs are "procedurally embedded" knowledge about a problem domain (e.g. how events relate one to another, what may be conjectured or inferred from a clue, or how one might verify a hypothesis).

When HYPER is in use on a particular task in a domain, hypotheses are created, or instantiated, on the basis of low-level input, high-level beliefs, or any

reason in between. The process of establishing the initial hypotheses leads to a propagation of activity (creation, verification, and disconfirmation of hypotheses). Activation patterns will generally vary with the particular task, in heterarchical fashion. A priority mechanism can rank hypotheses in importance depending on the data that contribute to them. Generally, the actions that occur are conditioned by previous assumptions, the data, the success of methods, and other factors. HYPER can be used for planning applications and for multistep vision processing as well as inference (procedures then should generate parallel activity only under tight control). We shall thus allow HYPER to make use of a context-oriented data base (Section 13.1.1). It will use the context mechanism to implement "alternative worlds" in which to reason.

### 12.5.1 Hypotheses

A HYPER hypothesis is the attribution of a predicate to some arguments; its name is always of the form (PREDICATE ARGUMENTS). Sample hypothesis names could be (HEAD-SHAPED REGION1), (ABOVE A B), (TRIANGLE (X1,Y1) (X2,Y2) (X3,Y3)). A hypothesis is represented as a data structure with four components; the *status*, *contents*, *context*, and *links* of the hypothesis.

The *status* represents the state of the HYPER's knowledge of the truth of the hypothesis; it may be T(rue), F(alse), (in either case the hypothesis has been *established*) or P(ending). The *contents* are arbitrary; hypotheses are not just truth-valued assertions. The hypothesis was asserted in the data-base context given in *context*. The *links* of a hypothesis H are pointers to other hypotheses that have asked that H be established because they need H's contents to complete their own computations.

### 12.5.2 HOW-TO and SO-WHAT Processes

Two processes are associated with every predicate P which appears as the predicate of a hypothesis. Their names are (HOW-TO P) and (SO-WHAT P). In them is embedded the procedural knowledge of the system which remains compiled in from one particular task to another in a problem domain. (HOW-TO P) expresses how to establish the hypothesis (P arguments). It knows what other hypotheses must be established first, the computations needed to establish (P arguments), and so forth. It has a backward-chaining flavor. Similarly, (SO-WHAT P) expresses the consequences of knowing P: what hypotheses could possibly now be established using the contents of (P arguments), what alternative hypotheses should be explored if the status of (P arguments) is *F*, and so on. The feeling here is of forward chaining.

### 12.5.3 Control Primitives

HYPER hypotheses interact through *primitive control statements*, which affect the investigation of hypotheses and the ramification of their consequences. The primi-

tives are used in HOW-TO and SO-WHAT programs together with other general computations. Most primitives have an argument called priority, which expresses the reliability, urgency, or importance of the action they produce, and is used to schedule processes in a nonparallel computing environment (implemented as a priority job queue [Appendix 2]). The primitives are GET, AFFIRM, DENY, RETRACT, FAIL, WONDERIF, and NUDGE.

GET is to ascertain or establish the status and contents of a hypothesis. It takes a hypothesis H and priority PRI as arguments and returns the status and contents of the hypothesis. If H's status is T or F at the time of execution of the statement, the status and contents are returned immediately. If the status is P (pending), or if H has not been created yet, the current HOW-TO or SO-WHAT program calling GET (call it CURPROG) is exited, the proper HOW-TO job (i.e., the one that deals with H's predicate) is run at priority PRI with argument H, and a link is planted in H back to CURPROG. When H is established, CURPROG will be reactivated through the link mechanism.

AFFIRM is to assert a hypothesis as true with some contents. AFFIRM(H,CONT,PRI) sets H's status to T, its contents to CONT, activates its linked programs and then executes the proper SO-WHAT program on it. The newly activated SO-WHAT programs are performed with priority PRI.

DENY is to assert that a hypothesis with some contents is false. DENY(H,CONT,PRI) is like AFFIRM except that no activation though links occurs, and the status of H is of course set to F.

ASSUME is to assert a hypothesis as true hypothetically. ASSUME(H,CONT,PRI) uses the data base context mechanism to create a new context in which H is AFFIRMED; the original context in which the ASSUME command is given is preserved in the context field of H. H itself is stored into a context-dependent item named LASTASSUMED; this corresponds to remembering a decision point in PLANNER. By using the information in LASTASSUMED and the primitive FAIL (see below), simple backtracking can take place in a tree of contexts.

RETRACT(H) establishes as false a hypothesis that was previously ASSUMEd. RETRACT is always carried out at highest priority, on the principle that it is good to leave the context of a mistaken assumption as quickly as possible. Information (including the name of the context being exited) is transmitted back to the original context in which H was ASSUMEd by passing it back in the fields of H.

FAIL just RETRACTs the hypothesis that is the value of the item LASTASSUMED in the present context.

WONDERIF is to pass suggested contents to HOW-TO processes for verification. It can be useful if verifying a value is easier than computing it from scratch, and is the primitive that passes substantive suggestions. WONDERIF(H1, CONT, H2, PRI) approximates the notion "H2 wonders if H1 has contents CONT."

NUDGE is to wake up HOW-TO programs. NUDGE(H,PRI) runs the HOW-TO program on H with priority PRI. It is used to awaken hypotheses that might be able to use information just computed. Typically it is a SO-WHAT pro-

gram that NUDGEs others, since the SO-WHAT program is responsible for using the fact that a hypothesis is known.

### 12.5.4 Aspects of Active Knowledge

The active knowledge style of computation raises a number of questions or problems for its users.

A hypothesis whose contents may attain a large range can be established for some contents and thus express a perfectly good fact (e.g., that a given location of an x-ray does not contain evidence for a tumor) but such a fact is usually of little help when we want to reason about the predicate (about the location of tumors). The SO-WHAT program for a predicate should be written so as to draw conclusions from such negative facts if possible, and from the conclusions endeavor to establish the hypothesis as true for some contents. Usually, therefore, it would set the status of the hypothesis back to P and initiate a new line of attack, or at its discretion abandon the effort and start an entirely new line of reasoning.

*Priorities*

A major worry with the scheme as described is that priorities are used to schedule running of HOW-TO and SO-WHAT processes, not to express the importance (or supposition value) of the hypotheses. The hypothesis being investigated has no way to communicate how important it is to the program that operates on it, so it is impossible to accumulate importance through time. A very significant fact may lie ignored because it was given to a self-effacing process that had no way of knowing it had been handed something out of the ordinary.

The obvious answer is to make a supposition value a field of the hypothesis, like its status or contents—a hypothesis should be given a measure of its importance. This value may be used to compute execution priorities for jobs involving it. This solution is used in some successful systems [Turner 1974].

*Structuring Knowledge*

One has a wide choice in how to structure the "theory" of a complex problem in terms of HYPER primitives, predicates, arguments, and HOW-TO and SO-WHAT processes. The set of HOW-TO and SO-WHAT processes specify the complete theory of the tasks to be performed; HYPER encourages one to consider the interrelations between widely separated and distinct-sounding facts and conjectures about a problem, and the structure it imposes on a problem is minimal.

Since HOW-TO and SO-WHAT processes make explicit references to one another via the primitives, they are not "modular" in the sense that they can easily be plugged in and unplugged. If HOW-TO and SO-WHAT processes are invoked by patterns, instead of by names, some of the edge is taken off this criticism. Removing a primitive from a program could modify drastically the avenues of activation, and the consequences of such a modification are sometimes hard to foresee in a program that logically could be running in parallel.

Writing a large and effective program for one domain may not help to write a program for another domain. New problems of segmenting the theory into predicates, and quantifying their interactions via the primitives, setting up a priority

structure, and so forth will occur in the new domain, and it seems quite likely that little more than basic utility programs will carry over between domains.

## EXERCISES

**12.1** In the production system example, write a production that specifies that blue regions are sky using the opponents color notation. How would you now deal with blue regions that are lakes (a) in the existing color-only system; (b) in a system which has surface orientation information?

**12.2** This theorem was posed as a challenge for a clausal automatic theorem prover [Henschen et al. 1980]. It is obviously true: what problems does it present?

$$\{[(\exists x)(\forall y)(P(x) \iff P(y))]$$
$$\iff [[(\exists x)Q(x)] \iff [(\forall y)(P(y))]]\} \iff$$
$$\{[(\exists x)(\forall y)(Q(x) \iff Q(y))]$$
$$\iff [[(\exists x)P(x)] \iff [(\forall y)(Q(y))]]\}$$

**12.3** Prove that the operator of Eq. (12.18) takes probability vectors into probability vectors, thus deriving the reason for Eq. (12.19).

**12.4** Verify (12.23).

**12.5** How do the $c_{ij}$ of (12.18) affect the labeling? What is their semantics?

**12.6** If events $X$ and $Y$ always co-occur, then $p(X, Y) = p(X) = p(Y)$. What is the correlation in this case? If $X$ and $Y$ never co-occur, what values of $p(X)$ and $p(Y)$ produce a minimum correlation? If $X$ and $Y$ are independent, how is $p(X, Y)$ related to $p(X)$ and $p(Y)$? What is the value of the correlation of independent $X$ and $Y$?

**12.7** Complete Table 12.3.

**12.8** Use only the labels of Fig. 12.9b and c to compute covariances in the manner of Table 12.3. What do you conclude?

**12.9** Show that Eq. (12.29) preserves the important properties of the weight vectors.

**12.10** Think of some rival normalization schemes to Eq. (12.29) and describe their properties.

**12.11** Implement the linear and nonlinear operators of Section 12.4.3 and 12.4.4 and investigate their properties. Include your ideas from Exercise 12.10.

**12.12** Show a case that the nonlinear operator of Eq. (12.29) assigns nonzero weights to maximally incompatible labels (those with $r_{ij} = -1$).

**12.13** How can a linear programming relaxation such as the one outlined in sec. 12.4.5 cope with faces or edges of the feasible solution solid that are normal to the preference direction, yielding several solutions of equal preference?

**12.14** In Fig. 12.11, what $(P, Q)$ solution is optimal if the preference vector is $(1, 4)$? $(4, 1)$? $(-1, 1)$? $(1, -1)$?

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# Goal Achievement 13

## Goal Achievement and Vision

Goals and plans are important for visual processing.

- Some skilled vision actually is like problem solving.
- Vision for information gathering can be part of a planned sequence of actions.
- Planning can be a useful and efficient way to guide many visual computations, even those that are not meant to imply "conscious" cognitive activity.

The artificial intelligence activity often called *planning* traditionally has dealt with "robots" (real or modeled) performing actions in the real world. Planning has several aspects.

- Avoid nasty "subgoal interactions" such as getting painted into a corner.
- Find the plan with optimal properties (least risk, least cost, maximized "goodness" of some variety).
- Derive a sequence of steps that will achieve the goal from the starting situation.
- Remember effective action sequences so that they may be applied in new situations.
- Apply planning techniques to giving advice, presumably by simulating the advisee's actions and making the next step from the point they left off.
- Recover from errors or changes in conditions that occur in the middle of a plan.

Traditional planning research has not concentrated on plans with information gathering steps, such as vision. The main interest in planning research has been the expensive and sometimes irrevocable nature of actions in the world. Our goal is to give a flavor of the issues that are pursued in much more detail in the planning

literature [Nilsson 1980; Tate 1977; Fahlman 1974; Fikes and Nilsson 1971; Fikes et al. 1972a; 1972b; Warren 1974; Sacerdoti 1974; 1977; Sussman 1975].

Planning concerns an active agent and its interaction with the world. This conception does not fit with the idea of vision as a passive activity. However, one claim of this book is that much of vision is a constructive, active, goal-oriented process, replete with uncertainty. Then a model of vision as a sequence of decisions punctuated by more or less costly information gathering steps becomes more compelling. Vision often is a sequential (recursive, cyclical) process of alternating information gathering and decision making. This paradigm is quite common in computer vision [Shirai 1975; Ballard 1978; Mackworth 1978; Ambler et al. 1975]. However, the formalization of the process in terms of minimizing cost or maximizing utility is not so common [Feldman and Sproull 1977; Ballard 1978; Garvey 1976]. This section examines the paradigms of planning, evaluating plans with costs and utilities, and how plans may be applied to vision processing.

## 13.1 SYMBOLIC PLANNING

In artificial intelligence, planning is usually a form of problem-solving activity involving a formal "simulation" of a physical world. (Planning, theorem proving, and state-space problem solving are all closely related.) There is an agent (the "robot") who can perform actions that transform the state of the simulated world. The robot planner is confronted with an initial world state and a set of goals to be achieved. Planning explores world states resulting from actions, and tries to find a sequence of actions that achieves the goals. The states can be arranged in a tree with initial state as the root, and branches resulting from applying different actions in a state. Planning is a search through this tree, resulting in a path or sequence of actions, from the root to a state in which the goals are achieved. Usually there is a metric over action sequences; the simplest is that there be as few actions as possible. More generally (Section 13.2), actions may be assigned some cost which the planner should minimize.

### 13.1.1 Representing the World

This section illustrates planning briefly with a classical example—block stacking. In one simple form there are three blocks initially stacked as shown on the left in Fig. 13.1, to be stacked as shown.

This task may be "formalized" [Bundy 1978] using only the symbolic objects Floor, $A$, $B$, and $C$. (A formalization suitable for a real automated planner must be much more careful about details than we shall be). Assume that only a single block can be picked up at a time. Necessary predicates are CLEAR($X$) which is true if a block may be put directly on $X$ and which must be true before $X$ may be picked up, and ON($X, Y$), which is true if $X$ is resting directly on $Y$. Let us stipulate that the Floor is always CLEAR, but otherwise if ON($X, Y$) is true, $Y$ is not CLEAR. Then the initial situation in Fig. 13.1 is characterized by the following assertions.