Monocopy and Associative Algorithms in an Extended Lisp

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Abstract: An extension of Lisp called HLISP (for Hash-LISP) is described. Two features called monocopy and assoccomp (for Associative Computing) and two data types H-molecules and associators are added to Lisp. The monocopy feature creates H-molecules, which are rewrite protected and are free of duplicating copies among H-molecules. H-molecules are like nonatomic Lisp data in other respects. An associator is a Lisp cell which associates an H-molecular key with a value of any data type. Associators are like atom headers in other respects. Efficient algorithms for copying ordinary lisp data into H-molecules and for performing basic set operations such as union with the number of steps required being proportional to the number of pertinent Lisp cells are given. In the assoccomp feature, the value of prespecified functions is associatively retrieved whenever the value has been evaluated before for the same function for the same argument/s and if the value is remaining in the primary storage. Otherwise it is evaluated as usual. Assoccomp provides a systematic method for increasing the efficiency of some effective algorithms which are inefficient when evaluated by conventional methods. A non-paging virtual memory scheme, enabling a collection of Lisp functions and H-molecular data amounting to several times larger than the primary storage capacity to be used in a single Lisp program, is presented. A hash coding scheme with a dynamic garbage collection capability and some other algorithms crucial for the implementation of HLISP are described in detail.

Key words and phrases: Lisp, Hash Coding, Garbage Collection, Associative Retrieval, Virtual Memory, Effective Algorithm, Efficient Algorithm.

§1. Introduction

At the 1973 Programing Symposium,[1] Sato, Nozaki, Noshita and the author proposed a hash coding scheme for lisp, which will be referred to as monocopy lisp for convenience. In monocopy lisp, the entire free storage area was also to be used as a hashing area so as to eliminate the creation of duplicating copies of S-expressions at a reasonable operating speed without using extra storage space for hash tables. The objectives of monocopy lisp were the saving of storage space and acceleration of checking for equalities.

For example, consider the internal data structures created by the following two lisp functions:

bt[n;x;y]=[n≤1->cons[x;y];T->cons[bt[n-1;x;y];bt[n-1; x; y]]]
ct[n;x;y]=[n≤1->cons[x;y];T->λ[[z];cons[z;z]][ct[n-1;x;y]]].

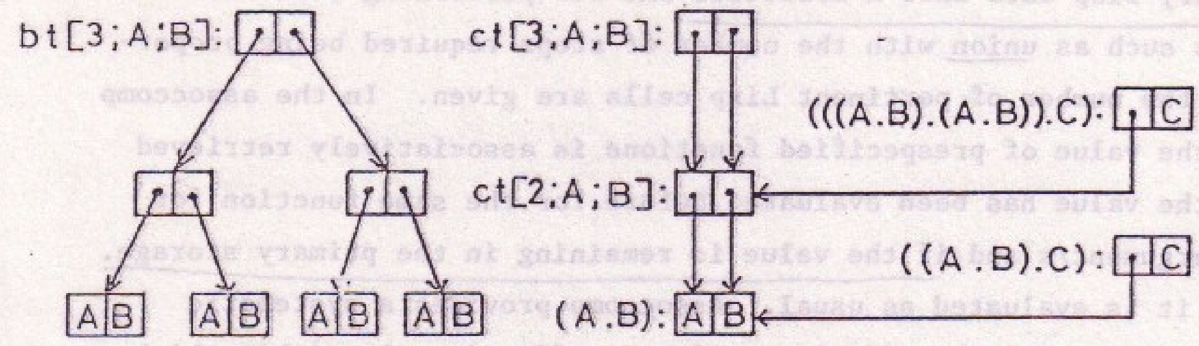


Fig.1 A Binary Tree and Monocopy Structures

Fig.1 shows bt[3;A;b] and ct[3;A;B]. Although the two internal structures are quite different, the two are regarded equal in lisp. Namely equal[bt[n;A;B];ct[n;A;B]]=T for all intevers n. Note that the recursive definition of equal[2] are referenced 2^{n+1}-1 times during the evaluation of the above equal. While bt[n;A;B] consists of 2^{n}-1 cells, ct[n;A;B] consists of n cells (n=3 in Fig.1). While there are 4 duplicating copites of the S-expression (A.B) and 2 copies of ((A.B).(A.B)) in bt[3;A;B], there is no duplication in ct[3;A;B].

In monocopy lisp, the creation of duplicating copies was to be eliminated by modifying the system subroutine for cons, so that bt[n;A;B] would have created the same identical structure as ct[n;A;B] would have. Thus, saving in storage from 2^n-1 cells down to n cells would have resulted in this specific case. The resultant internal data structure of the execution of monocopy lisp functions, bt[3;A;B], cons[bt[2;A;B];C]] and cons[(A.B);C]] would have been as shown in Fig. 1 to the right.

The recursively defined equal was to be replaced by the non-recursive basic function eq so that eq[bt[n;A;B]; ct[n;A;B]]=T for all integers n. Speeding up of at least a factor of 2^{n+1}-1 would have resulted in the evaluation of equal in this specific case.

In this paper, ideas incubated by monocopy lisp are further extended and results of an actual implementation are given. Although the schemes to be described would be applicable to other programming languages as well, lisp is used as the base language for clarity and simplicity.

For convenience, the language to be described is called HLISP (for Hash-Lisp). HLISP is an extension of LISP, which is a specific dialect of lisp and is compatible with other lisps[(2, (3] in its most essential features. Unless stated otherwise, functions and terms are to be understood as the same as in the Lisp 1.5 manual[(2].

Names of functions specific to HLISP shall start from the letter “h”. This turns out to be a consistent convention, since no function in Lisp 1.5 starts from “h”.

Definitions of the basic HLISP functions are given in § 2 with simple examples. An alphabetically ordered list of HLISP functions is also given in the Appendix, which would serve as a short form manual.

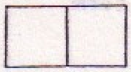
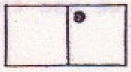
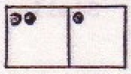
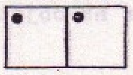
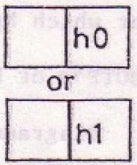
In §3, a copy algorithm to be used frequently in HLISP and fast algorithms for basic set operations are described.

In §4, a system feature called assoccomp (for associative computing) is presented. This feature is believed to give a reasonable compromise between the choice whether a function is to be computed or the value is to be retrieved from a table. This feature would provide a systematic method for speeding up some recursive algorithms which are effective but inefficient when evaluated by conventional methods.

An implementation of HLISP is described in §5 and a non-paging virtual memory scheme is described in §6.

§2. HLISP Objects and Basic Functions

In HLISP, the objects visible from the user are classified into the following five types: L(for Lisp)-molecules, H(for Hash)-molecules, associators, headers and basic integers as shown in Fig.2.

HLISP Term	L-(Lisp-) Molecule	H-(Hash-) Molecule	Associator	Header	Basic Integer	H0-Cell	H1-Cell
Prime Predicates	consp[x]	hconsp[x]	hassocp[x]	headerp[x]	intp [x]	h0p[x]	h1p[x]
LISP object?	Yes	No	No	Yes	Yes	Only for	
atom[x]	NIL	NIL	T	T	T	System Use.	
molecule [x]	T	T	NIL	NIL	NIL	Invisible	
hp [x]	NIL	T	T	T	T	from HLISP	
hdotp[x]	NIL	NIL	T	T	NIL	User.	
car/cdr value/ key	car cdr --- ---	·car cdr --- ---	car cdr value key	car cdr value key	---- ----	car cdr --- ---	
DIAGRAMS				 or A,B,X1A,...	. . .,-2,-1 0,1,2,. . .		

Examples of Diagrams

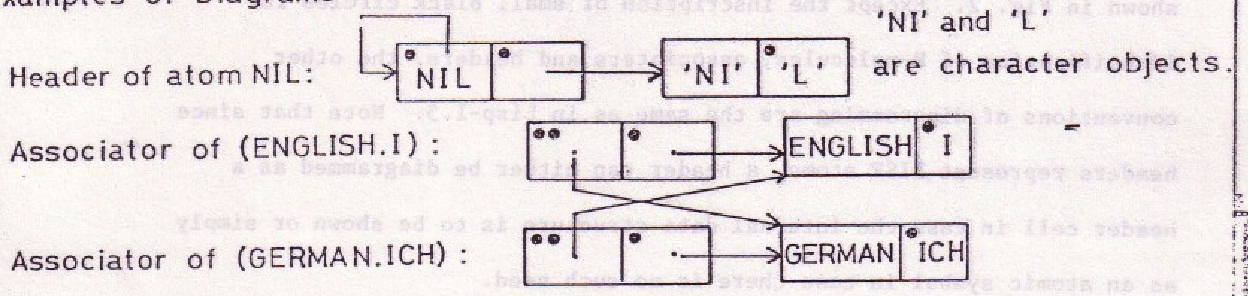

Header of atom NIL:
NIL
'NI'
'L'
'NI' and 'L' are character objects.
Associator of (ENGLISH.I) :
ENGLISH
I
Associator of (GERMAN.ICH) :
GERMAN
ICH

Fig.2 Classification of HLISP Objects, Predicates and Diagrams.

As indicated in the top two lines in Fig. 2, each type is respectively identified by prime predicates consp, hconsp, hassocp, headerp, or intp. For example, for L-molecular x, consp[x]=T and the values of the remaining four predicates are NIL. The other two types, H0-cells and H1-cells, are invisible from the user. They represent inactive free storage cells and are treated in §5.

LISP makes use of L-molecules, headers, and basic integers only. L-molecules are the same as non-atomic (molecular) data in other lisps. Headers are functionally equivalent to atom headers of Lisp-1.5.

Truth values of some other type predicates, atom[x], molecule[x]=not[atom[x]], hp[x] and hdotp[x], are given in Fig. 2. Just like calling HLISP objects x, for which atom[x]=T, simply atoms, we call objects x, for which hp[x] = T, HP's or HP-objects. Similarly, we use the term HDOTP's or HDOTP-objects.

Diagraming of data structures has been very helpful for understanding the principles of lisp. We shall, therefore, diagram HLISP objects as shown in Fig. 2. Except the inscription of small black circles for identification of H-molecules, associators and headers, the other conventions of diagraming are the same as in Lisp-1.5. Note that since headers represent LISP atoms, a header can either be diagranmed as a header cell in case the internal data structure is to be shown or simply as an atomic symbol in case there is no such need.

In the present version of HLISP, like in other lisps, the internal representative of any HLISP object x is an integer, say i and we write i=m[x] in terms of a function m (for machine). Except for basic integers, i specifies an HLISP cell which actually consists of two array elements, mcar[i] and mcdr[i]. Basic integers are represented by non-existing array addresses. Actually in terms of system constants maxh, module, minint=maxh+1, izero=maxh+module and maxint=izero+module-1, i represents a basic integer i-izero, if minint≤i≤maxint. Hence, izero=m[0], i.e., izero is the internal representative of the basic integer 0. The system constant, module sets the maximum absolute magnitude of basic integers which can be handled directly by the system. Integers of greater magnitudes, rational fractions, floating point numbers and so on are represented differently from basic integers and they are to be handled by suitable HLISP functions or subroutines. Only basic integers will be treated in this paper. The system constant maxh specifies the maximum address of the arrays mcar and mcdr. Hence, if i≤maxh, i represents an HLISP object accompanying an HLISP cell. For identifying the types of an HLISP cell, flag bits (actually the sign bits) in the car and cdr parts of the cell are used as one would imagine from the diagrams in Fig.2. Another method is given in §5.

H-molecules are similar to ordinary lisp cells (L-molecules) except in the following points.

1. <u>cons</u> and functions containing <u>cons</u> (<u>list</u> <u>append</u>} etc.) create L-molecules but never H-molecules;
2. hcons, defined as the following, is the only basic function which can create an H-molecule:

   hcons[x;y] = [hp[x] ∧ hp[y] -> mhcons[x;y];T->cons[x;y]].

   A non-HP-object, i.e., an L-molecule, may or may not have a duplicating L-molecular or H-molecular copy. On the other hand, an HP-object shall never have a duplicating HP-object. If either x or y represents a non-HP-object, the value of hcons[x;y] is an L-molecule as a result of <u>cons</u> to ensure no duplicating HP-object. Only if both x and y represent HP-objects, the system function mhcons[x;y] gives an H-molecular value to hcons[x;y]. The following gives an effective procedure for mhcons[x;y]:

Search through all HLISP cells for an H-molecule with address i, such that m[x]=mcar[i] and m[y]=mcdr[i]. If found i is the result, otherwise take an inactive free storage cell, the jth say, make a new H-molecule by the substitutions mcar[j]:=m[x], mcdr[j]:=m[y] and return j as the result. Actually, the speed of the search through operation in this procedure is improved by using a hash coding scheme, which is described in §5.

<u>hconspp</u>[x;y]=[hp[x] ∧ hp[y] ∧ (hcons[x;y] is present) →
    prog2[setq[*aside;hcons[x;y]];T];T→NIL]

This is the presence predicate for hcons[x;y]. In case hcons[x;y] is present as an H-molecule, the value of <u>*aside</u> is set aside to the already existing hcons[x;y]. <u>hconspp</u> neither creates a new H-molecule nor a new L-molecule.

The car and cdr parts of an associator will be called respectively the value and key parts hereinafter so as to stress their meaning rather than a specific implementation (cf. Fig.2). Any HP-object, say x, can have at most one associator. If x has an associator, the content of the key part of the associator is m[x]. Non HP-objects, i.e. L-molecules, shall never have associators. Hence, the content of the key part of an associator is necessarily an HP-object.

For an HP-object x, the value of a function hassoc[x] is the associator of x. Similarly to hcons, the following gives an effective procedure for hassoc[x]: Search through all HLISP cells for an associator with address I such that m[x]=mcdr[i]. If found i is the result, otherwise take an inactive free storage cell, the jth say, make a new associator by the substitutions mcar[j]:=d0, mcdr[j]:=m[x] and return j as the result. Speeding up by hash coding is described in §5 and d0 is a system constant which stands for undefined values. The content of the value part of an associator can be any HLISP object or d0.

dzerop[x] = [hdotp[x] ∧ (The value of x is d0, i.e., undefined)->T;T->NIL]

is the predicate to check for d0 valued HDOTP's. The pseudo function dzero[x]=x, in value, sets the value of x to d0 if x is an HDOTP,

otherwise it has no effect.

```
hassopp[x]=[not[hdotp[x]] ∨ (associator of x absent)->NIL;
     setq[*aside; hassoc[x]] -> [dzerop[*aside] -> 0;T->1]]
```

This is the presence predicate for associator of x.

For an associator a, evaluation of set[a;v] sets v into the value part of a. Conversely, hvalue[a] gives the value part of a as its value; in case a is d0 valued, it is regarded as an error.

Headers are similar to associators. The above explanations of associators all hold for headers as well by changing the word “associator” into “header” and the function names hassoc/hassopp/hassocpp into header/headerp/headerpp. HLISP utilizes headers for associating the print names of literal atoms with its value (cf. header of NIL in Fig.2) and for assoccomp to be described in §4. In this respect headers may be termed system associators. In the present implementation of HLISP, header is a pure system function and is not explicitly exposed to the user in order to avoid possible confusions and conflicts between the system and the user programs.

As an example of the use of associators, the data structure with two associators in Fig. 2 can be created by executing the following

LISP program (= stands for “define” and ===, for “the value is”):

```
makedic[x;y;u;w] = set[hassoc[hcons[x;y]]; hcons[u;w]] === (MAKEDIC)
makedic[ENGLISH;I;GERMAN;ICH] === (GERMAN.ICH)
makedic[GERMAN;ICH;ENGLISH;I] === (ENGLISH.I)
```

The content of this miniature dictionary can be retrieved associatively in the following way:

```
readdic[x;y]=[
     hconsp[x; y]→[onep[hassocpp[*aside]]→hvalue[*aside];T→NIL];T→NIL]
     === (READDIC)
readdic[ENGLISH;I]===(GERMAN.ICH), readdic[GERMAN;ICH] === (ENGLISH.I)
readdic[ENGLISH;ICH] === NIL, readdic[ENGLISH;HE] === NIL.
```

Suppose the item introduced by

```
makedic[ENGLISH;YOU;GERMAN;DU] === (GERMAN.DU)
```

is to be cancelled for some reason. This is done in the following way:

```
deletedic[x;y] = dzero[hassoc[hcons[x; y]]]=== (DELETEDIC)
deletedic[ENGLISH;YOU] === (ENGLISH.YOU), readdic[ENGLISH;YOU] === NIL.
```

It would be worth noting that the effect of list structure altering pseudo functions, rplaca, rplacd etc. must be prohibited from rewriting HP-objects to ensure the duplicate copy free (or the monocopy) feature of the HP-objects. In other words, H-molecular cells and the key part of HDOTP's must be regarded as rewrite protected read only storage. The garbage collector only are allowed to reclaim them into the inactive free storage state. This rewrite protection feature has the following fringe benefit. rplaca and rplacd and their derivatives (nconc etc.) are very useful for writing efficient algorithms. On the other hand, unexpected alteration of data structures including S-expression programs often causes program bugs which are difficult to locate. In HLISP, data not to be rewritten can be represented as HP-objects. Unexpected data alteration would result in the printing of error messages and/or errorset treatments.

F. Motoyoshi pointed out that type predicates hconsp, hassocp and headerp can be defined in terms of the corresponding presence predicates in the following way:

hassocp[x]=[hdotp[x]->[hassocpp[hkey[x]]->eq[*aside; x];T→NIL];T→NIL].

It is impossible, however, to express presence predicates in terms of other functions except hnext[].

§3. Monocopy Algorithms

An important HLISP function hcopy can be defined as:

```
hcopy[x]=[hp[x]->x;T->hcons[hcopy[car[x]];hcopy[cdr[x]]]].
```

hcopy gives an HP-object equal to x. One may use LISP to create some data structures by using L-molecules for speed or for some other reason and then switch to hcopied data so as to utilize the speed in checking equalities among the data.

If this hcopy were applied to the data structure ct[n;A;B], consisting of n L-molecules, it would result in 2^{n+1}-1 recursive calls of hcopy. Thus, the execution of hcopy would become impracticable even for rather small value of n.

In order to remedy such a hazard the following function, rplach ("replace H") could be used instead of hcopy.

```
rplach[x] = [hp[x]→x;T→hcons[rplaca[x;rplach[car[x]]];
                          rplacd[x; rplach[cdr[x]]]]].
```

This pseudo function would replace the contents of L-molecules in (the sub-structures of) x by their "hcopies", so that the execution time for any data structure x would be proportional to the number of L-molecules in x. This replacement would be useful if such side effects were the intention of the user. But if not, another hazard! This can be remedied by keeping records of the replacements made during the execution of rplach and by restoring the original data before completion. For machine language implementations the system push down stack can be used for such recording. In the following definition of hcopyl, a list, pds (for Push Down Stack) is used instead.

```
hcopy1[x]=prog[[pds,result];setq[result;rplach1[x]];
     A [null[pds]→return[result]];
     rplaca[car[pds];cadr[pds]];rplacd[car[pds];caddr[pds]];
     setq[pds;cdddr[pds]];go[A]]
rplachl[x]=prog[[];[hp[x]->return[x]];
     setq[pds;cons[x;cons[car[x];cons[cdr[x];pds]]]];return[
     hcons[rplaca[x;rplachl[car[x]]];rplacd[x;rplachl[cdr[x]]]]]]
```

The execution time of hcopyl is proportional to the number of L-molecules in x and there is no hazardous side effects any more. The function eq[hcopyl[x]; hcopyl[y]] checks the equality of x and y, with the execution time being proportional to the number of L-molecules in x and y.

We shall also make use of the following function which gives the list of hcopied list elements as its result:

```
mapcarhcopy[x]=mapcar[x;function[hcopyl]]
            =[null[x]->x;T->cons[hcopyl[car[x]];mapcarhcopy[cdr[x]]]].
```

We now discuss the application of the monocopy feature to the basic set operation union which is defined in Lisp-1.5 (2 as:

```
union[a;b]=(a U b)=[null[a]→b;member[car[a];b]→union[cdr[a];b];
                  T->cons[car[a];union[cdr[a];b]]]
member[x;y]=[null[y]->y;equal[x;car[y]]->T;T->member[x;cdr[y]]]
```

Given two lists a and b with N_a and N_b elements, the execution time of union is proportional to $N_a \cdot N_b$, since $N_a \cdot N_b$ references are made of equal to check for the equality among the elements. In case many of the elements are non-atomic (molecular), use of hcopied elements would greatly speed up the equality checking operations.

Further improvements can be attained in case the elements are presorted. Note that the internal representatives of HP-objects establish a perfect linear order, to be called H-order, among HP-objects. Now, let align be a function which aligns the HP-objects in a given list in the ascending H-order. For example, align[((A_{15}, B_3, $(A.B)_9$); function[hltp]] = (B_3, $(A.B)_9$, A_{15})} with suffices indicating the internal representatives at the moment of evaluation of align. For align, the well-known sortmerge algorithm is to be used, which aligns n elements with the execution time being proportioned to $n.\log_2 n$ in the worst case. If both elements in lists a and b are aligned in the ascending H-order, union can be realized as a merge algorithm, of which the execution time is proportional to N_a+N_b. Thus, we obtain the following algorithm with the predicate hltp being given as a functional argument:

```
union[a;b]=merge[align[mapcarhcopy[a];function[hltp]];
                align[mapcarhcopy[b];function[hltp]];function[hltp]]
merge[a;b;p]=[null[a]→b;null[b]→a;
     p[car[a];car[b]]->cons[car[a];merge[cdr[a];b;p]];
     p[car[b];car[a]]→cons[car[b];merge[a;cdr[b];p]];
     T->cons[car[a];merge[cdr[a];cdr[b];p]]]
align[a;p]=[null[a]->a;T->car[sort[sort2[a;a;p];p]]]
sort[x;p]=[null[x]→x;null[cdr[x]]→x;
           T->sort[cons[merge[car[x];cdr[x];p]];sort[cddr[x];p]];p]]
sort2[x;y;p]=[null[cdr[y]]→list[x];p[car[x];cdr[y]]→sort2[x;cdr[y];p];
             T->consign[sort1[x];sort2[cdr[y];cdr[y];p]]]
sortl[x]=eq[x; y]->list[car[x]];T->cons[car[x];sortl[cdr[x]]]]
```

In case the given lists a and b are already aligned in the ascending H-order, align is designed to give the result with the execution time being proportional to N_a+N_b. Note that the resultant list of merge is aligned in the ascending H-order.

Thus, the execution times of this algorithm is proportional to

N_a+N_b in case one can consistently use H-ordered lists throughout the program and is proportional to $N_a \cdot \log_2 N_a + N_b \cdot \log_2 N_b$ in case prealignment is necessary.

The H-order may also be termed subjective or relative order, since no objective or absolute order is specified by the user of union. The H-order is also relative in that the specific H-order to be established among HP-objects depends upon the entire state of the free storage. Nevertheless, the monocopy feature with the rewrite protection mechanism establishes a consistent H-order during the execution of an HLISP program, and this is just what is needed for the present scheme.

When prealignments are needed, the following algorithm, of which the execution time is always proportional to N_a+N_b, is more recommendable:

```
union[a;b]=λ[[u];bindq[[u;remdup[u];NIL]][mapcar[append[a;b];
                           function[A[[v]; hassoc[hcopy[v]]]]]]]
remdup[w]=[null[w]→NIL;hvalue[car[w]]→remdup[cdr[w]];
           set[car[w];T]->cons[hkey[car[w]];remdup[cdr[w]]]].
```

An example: ((..A) is the associator of A. cf. print in Appendix)

```
union[(A,(A.B));(B,(A.B))]
=remdup[((..A), (..(A.B)),(..B),(..(A.B)))]=(A,(A.B),B)
```

The initial argument to remdup is the list, u of associators of hcopied elements of append[a;b]. The values of the associators are initially all NIL and are set to T when the pertinent elements are enlisted in the result so as to remove duplicating enlistments.

Other basic set operations such as intersection[x;y]=x ∩ y, setdifference[x;y]=x ∩ ¬y, subsetp[x;y]=[x ⊆ y->T;T->NIL], etc. can be implemented similarly.

§4. The Assoccomp (<u>Asso</u>ciative <u>Comp</u>uting) Feature

This system feature of HLISP may best be explained by examples. Many mathematical functions are characterized, defined or evaluated in terms of recurrence formulas. These formulas can be directly translated into lisp functions such as

(4.1) fb*[n]=[n=0→fb0;n=1→fb1;T→u[fb*[n-1];fb*[n-2];n]] and

(4.2) c*[n;m]=[m=0->c0;m=n->c1;T->v[c*[n-1;m];c*[n-1;m-1];n;m]].

These algorithms are effective, i.e., the results are obtained eventually for all integers n≥m≥0, provided that u and v always yield some values (symbolic or numerical) for given arguments. In the special cases fb0=fb1=c0=c1=1, u[x;y;z]=v[x;y;z;w]=x+y, (4.1) and (4.2) give Fibonacci numbers fb[n] and binomial coefficients c[n;m] respectively. These algorithms, however, are known to be notoriously inefficient. The reason for this can be explained simply by the diagrams shown in Fig.3.

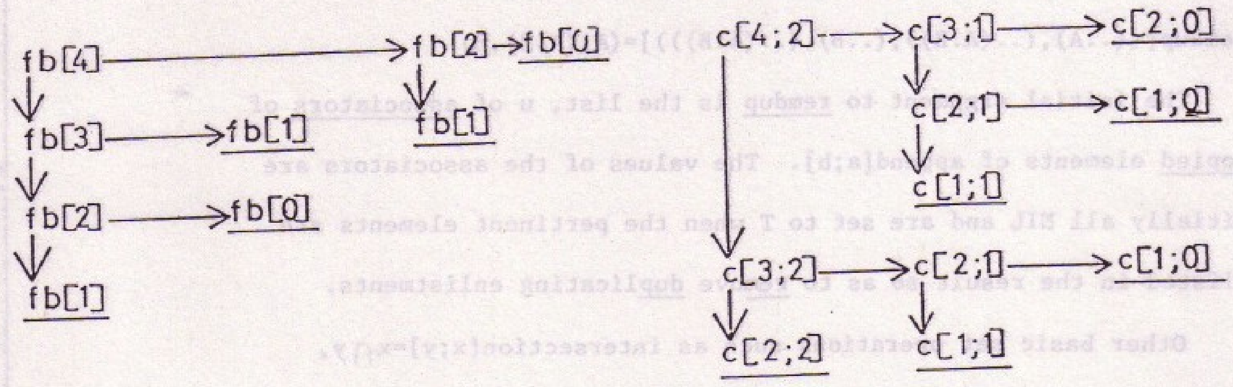


Fig.3 Recursive References in the Evaluation of a Fibonacci Number and a BINOMIAL Coefficient.

These diagrams show the recursive reference made by the functions for the given argument/s. For example, fb[4] refers fb[3] and fb[2], fb[3] refers fb[2] and fb[1] and so on. For both fb and c the reference diagrams are binary trees, ending at leaves where the values of the function evaluate to 1. Since, fb and c are defined so as to sum up the 1's on the leaves, there must be fb[n] and c[n;m] leaves respectively. Since there are one less branches than leaves in any binary tree, the total number of recursive references and their asymptotic forms for large n and m=n/2 (which maximizes c for given n) are given respectively by
$rfb[n]=2\cdot fb[n]-1\cong 0.894.(1.62)^{n+1}$, $rc[n]=2\cdot c[n;m]-1\cong 2^{n+2}/\sqrt{2\pi n}$.
These results are independent of the choice of functions u and v and of the values fb0, fb1, c0 and c1. Because of such exponential explosions in the execution time, the recursive algorithms (4.1) and (4.2) are regarded impractical and faster (recursive or non-recursive) algorithms, such as
fb[n]=fb3[1;1;1],fb3[i;j;k]=[n≤i->j;T->fb3[i+1;j+k;j]],
are usually used instead.

Such explosions are actually caused by the repeated evaluation of the same function for the same argument/s, as in the cases of fb[2] and c[2;1] in Fig.3. In hand calculations, the human computer would avoid such repetitions by memorizing the previous results. The assoccomp feature may be regarded as a mechanized version of such a computational procedure.

The pseudo function assoccomp is syntactically the same as trace and takes arbitrary number of function names as its arguments. It may be regarded as an instruction for the system to tabulate functions and make use of the tabulated values whenever possible. Actually, execution of assoccomp[fb;c] === (FB C) sets an assoccomp flag on the definitions of fb and c, similarly to the case of trace[fb;c] === (FB C).

In case of a traced function, the system would print “THE ARGUMENT OF FB IS 2” upon entering the evaluation of fb[2], and would print “THE VALUE OF FB IS 2” upon completion. The assoccomp works similarly. Upon entering the evaluation of fb[2] the system makes an associative search for whether fb[2] has been evaluated before. If this is the case the previous result is retrieved. Otherwise the system evaluates fb[2] by making use of the effective procedure (4.1) and stores the information necessary for possible future retrieval upon completion. For assoccomped n argument function g, the system upon entering the evaluation of g with actual (evaled) arguments a_1, ..., a_n, first makes k=hcopy[(g,a_1, ..., a_n)]. Headers are used in assoccomp for associative retrieval. Namely, the system next does the following:

```
    [onep[headerpp[k]]→hvalue[*aside];zerop[headerpp[k]]→error[
$$$CYCLIC DEFINITION ASSOCCOMP$];T->set[header[k];apply[g;($a_1$, ..., $a_n$)]]
```

Note that programing errors caused by cyclic definitions, such as

fb[n]=[n≤1->1;T->fb[n]+f[n-1]](fb[n] in the definition of fb[n]), are detected by making use of d0 valued headers.

Thus, the assoccomp feature would remedy the exponential time explosion hazards often encountered in recursive algorithms such as (4.1) and (4.2). Actually in the Fibonacci case, fb[n] on the present HLISP system, the first evaluation of fb[20], which has to compute fb[19], fb[18] ... fb[1] and fb[0], was made 200 times faster and reevaluations of fb[20], 4000 times faster by using assoccomp. These figures will be further improved by level ups to be made in the system, especially by those in the hash coding subroutine.

In the binomial case (4.2), the assoccomp feature would also have the following merits in comparison to other methods. Firstly, the use of the close form formula c[n;m]=n·(n-1)...(n-m+1)/m for m≤n/2 could yield very large intermediate results and a sophisticated multiprecision arithmetic functions or subroutines would be needed, while there is no such need in *assoccomp*ed (4.2). Secondly, in many application of the binomial coefficients many different coefficients would be used repeatedly. The *assoccomp* would soon provide a complete table for all such coefficients.

A. Nozaki suggested that for many numbers in combinatorics, Stirling's number and the partition number for example, no closed form formulas are known and they are to be computed by recurrence formulas. The assoccomp scheme would be useful in such cases.

The assoccomp scheme should not be regarded as a universal remedy for speeding up any arbitrary computations. First of all for many basic operations, it would be faster to compute rather than trying to retrieve the previous results. In the present HLISP, therefore, *assoccomp* on basic built-in functions are all neglected. For user defined functions, it is the programmer's prerogative to select the functions to be *assoccomp*ed for the best result.

There can be a storage explosion hazard in the assoccomp scheme, since headers used in the scheme consume free storage. In the present HLISP, in case the ordinary garbage collector (GBC) fails to reclaim enough free storage space, a subroutine called the grand garbage collector (GGBC) is called for. GGBC cancels all headers used in assoccomp and return them to the free storage. When this takes place, the *assoccomp*ed functions are computed according to the effective but not necessarily efficient original algorithm. If there is a reasonable space in the storage, the headers of the frequently used assoccomped functions would be reconstructed and the system would soon regain the speed. If there is not enough space for assoccomp headers, the computation would proceed mainly by using the effective (but inefficient) original algorithm.

Methods used for reducing the volume of mathematical tables would also apply to assoccomp. For example, the following definition for c[n;m] would halve the storage requirements, in most cases, by subjecting d only to assoccomp.

c[n;m]=[m≤n-m->d[n;m];T->d[n;n-m]],d[n;m]=[m=0->1;T->c[n-1;m]+d[n-1;m-1]].

Reading of files (drums or disks) would provide another interesting example. Let file[x] be a pure function of which the value is the S-expression read from the file from the entry specified by x. The assoccomp feature applied to file would bring the most frequently and recently used data into the high speed storage enabling them to be accessed faster upon reuse.

Among numerous other possibilities, application to association lists would be worth noting. Association list schemes, provided by functions (2 assoc[x;a] and pairlis[x;y;a] or the similar, are frequently used in lisp programs, including the Lisp-1.5 system itself. The assoccomp applied to assoc or the similar would provide a logically consistent scheme for speeding up the retrieval of data from association lists. This would be particularly efficient when the association list is deep. It would be interesting to apply this scheme to the A-list of Lisp-1.5 and to compare and evaluate the performances.

§5. An Implementation of HLISP

The most crucial feature of HLISP consists in the hash coding scheme for accelerating the storage search procedures. Besides the flag bit method (cf. Fig.2), L-molecules can be identified by separating the storage areas. Namely, in terms of a system constant minh, x is an L-cell (L-molecule), if m[x]=i<minh, otherwise x is an HP-object. Inflexibility in the number of L- and H-cells available to the user is the drawback of this method. It seems impossible to shift the value of minh dynamically during the execution of HLISP programs, especially if the H-order feature (cf. §3) is to be used. Nevertheless, this method was employed in the first version of HLISP and will also be explained here because of its simplicity.

The scheme employed is essentially a rehashing method. It makes use of two types of inactive cells H0 and H1 (cf. Fig.2) to allow for dynamical cancellations invoked by the GBC (garbage collector).

H0-cells are inactive cells without conflict and H1-cells are those with conflict, i.e., cells which have been reclaimed by GBC which had been active cells in conflict. The following gives an algorithm for mhcons (cf. §2).

```
mhcons[x;y]=prog[[i;j;k];i:=hashcons[x;y;k];
  A  [h0p[i]->go[D];h1p[i]->go[B];eqhconsp[x;y;i]->return[i]];
     i:=rehash[i;k];go[A];
  B  j:=i
  C  j:=rehash[j;k];[h0p[j]->go[D];eqhconsp[x; y; j]->return[j]];go[C];
  D  mcar[i]:=m[x];mcdr[i]:=m[y];nh0:=nh0-1;[nh0≤mnh0->gbc[]];return[i]]
eqhconsp[x;y;i]=hconsp[i] ∧ (mcar[i]=m[x]) ∧ (mcdr[i]=m[y])
```

, where *hashcons* maps the two HP's, x and y, onto the H-area (i.e., i such that minh≤i≤maxh);

rehash maps i in H-area onto H-area with the maximum periodicity, i.e., the period is equal to the size of the H-area, nhash=maxh-minh+1 and k is a variable of which the value is initialized by hashcons and advanced by *rehash* in order to improve the clustering characteristics.

The followings are the simplest hashing and rehashing functions with rather poor clustering characteristic because of negligence of k:

```
hashcons[x;y;k]=remainder[m[x]+m[y];nhash]+minh
rehash[i;k]=[i=maxh->minh;T->i+1]
```

The speed and other performances critically depend upon the choice of these functions. The best choice, however, largely depends on the repertoire and the relative speeds of the machine instructions.

hassoc and *header* can be implemented similarly to *mhcons*. For *hassoc*, *hashcons* in *mhcons* is to be replaced by hashassoc[x;k] which maps x onto the H-area; *eqhconsp*, by

eqhassocp[x;i]=hassocp[i] ∧ (hkey[i]=m[x]) and the line starting from D, by substitutions described in §2. As seen from *mhcons*, H1-cells can be reused but they cannot serve as terminals of the rehashing cycle. Only H0-cells serve as terminals. Hence, the average length of hash-rehash cycle is 1/p0=nhash/nh0, where nh0 is the number of H0-cells and p0 is their fraction among H-cells. When nh0 becomes less than a system constant, nh0=minp0·nh0, with minp0=0.2 in the present HLISP, GBC is called so as to preserve the speed of the hashing process by keeping 1/p0≤5.0.

The GBC proceeds in the following steps. The effect of GBC on L-molecules are the same as in other lisps.

G1. Mark (as in other lisps) all cells referred from active system registers, from the system pushdown stack and from non-d0-valued HDOTP's.

G2. Change all unmarked H-cells (including H0 and H1-cells) into H0-cells.

G3. Unmark all H-cells.

G4. Execute the following, which changes H0-cells in conflict into H1-cells.

```
h0toh1[]=prog[[*hnext;i];
  A   [null[hnext[]]->return[NIL]];i:=hashall[*hnext; k];
  B   [i=*hnext→go[A];h0p[i]→seth1[i]];i:=rehash[i;k];go[B]]
```

, where hashall[j;k] gives the hash number of HP-object j and seth1[i] changes the H0-cell i into an H1-cell.

G5. A step to be added in §6 to improve performance.

G6. Call GGBC if the number of H0-cells reclaimed is insufficient.

An important feature of this dynamic hash coding scheme consists in the fact that the fraction of H1-cells p1 does not grow beyond a certain limit which is about 0.16 in the present system. This was first verified by simulation and a more detailed analysis will be given in a separate report[4]. Thus, about 64% of H-cells are available as active cells and about 36% are reserved for the hashing process. The actual saving in storage space effected by the monocopy feature is about 30 to 40% depending upon the nature of the program. Thus, this saving is approximately offset by the hashing overheads.

A few comments would be sufficient for the rest of implementation. As indicated in the appendix, similarly to Lisp-1.6[3], the present HLISP does not use the A-list of Lisp-1.5[2]. The BCP (Binding context pointer) mechanism in Lisp-1.6 is not used either for the sake of speed and simplicity, which is rather essential for virtualizing the pushdown stack to be described in §6. The two features in which the use of the A-list is essential in Lisp-1.5 are treated as in the following. Optional freezing is used for quoting functional arguments and a single variable *fexpr is reserved for FEXPR's (cf. Appendix). The library functions *syntax* or *scompile* would give warnings to appearance of unfrozen free variables in functional arguments and to the use of the variable *fexpr in places other than in the definition of FEXPR's. The header of an atom does not have a P-(Property-) list (cf. Fig.2). P-list functions (*attrib*, *prop*, *get*, *remprop*) are implemented similarly to *makedic*, *readdic* and *deletedic* of §2, but the system does not make use of them for the sake of speed. Each SUBR or FSUBR is given a unique code number, which is used as an index of a computed goto jump (in FORTRAN terminology) for deciphering it in a single step. EXPR's are identified by LAMBDA or LABEL and FEXPR's, by FEXPR. In case of pure interpretation, SUBR- and FSUBR-name atoms are supposed to have the corresponding code numbers in their value parts. *syntax* would give warnings to the use of these names as λ- or prog-variables. *scompile* would translate these names into the code numbers and would make various short cuts. The form (EQ (CAR X) (QUOTE PLUS)) would be *scompile*d into (-9503(-9499 X) (-9466 PLUS)), which short cuts three references to the array mcar (cf. Fig.2). In case idiomatic combinations of basic functions, such as *eqq*, *atomcar*, *eqqcar* (*eq* with the 1st argument *quote*d and the 2nd argument *car*ed), etc., are built in, the form above would be *scompile*d into (-9570 PLUS X).

HLISP is fully coded in FORTRAN for the sake of machine independence. Hand recompiling of the object codes was very rewarding for a small machine with a poorly optimized compiler (in FACOM 270/20 with 16KW of 16 bit words, the speed was doubled and code length, halved). For a larger machine with an optimized compiler, (FACOM-230/75 with 192KW of 36 bit words), hand recompiling was hardly meaningful.

§6. A Non Paging Virtual Memory Scheme in HLISP

By virtual memory in this section, it is meant schemes, logically invisible from the user, which utilize the secondary storage (drum or disc to be called “file” hereinafter) as an extension of the primary storage (core or IC, to be called “core” hereinafter). Core paging schemes, occasionally regarded synonymous to virtual memories, will not be considered here.

Virtualization of the system pushdown stack is simple and almost trivial. When the stack in the core overflows, the stack is “pushed down” halfway in the core and the bottom half is saved in the file. When the stack in the core underflows (or is over-popuped), the bottom half of the stack in core is restored from file. The only parameter the system designer has to select is the size of the stack to be placed in core so as to keep the file read/write overhead times below a reasonable level. 1KW would be sufficient in most cases.

Storage for H-molecules is virtualized in the following way: An HDOTP is called a FILEP if the value part contains a special number called the file address. Actually in terms of system constants maxf and minf=maxint+1, a system predicate filep is defined as:

filep[x]=hdotp[x] ∧ (minf≤mcar[x]≤maxf).

A file address represents the (direct or indirect) address in the file, where an H-molecule has been filed, in a S-expression format, by the GGBC. Whenever a FILEP is evaled (by the eval part of the system or by hvalue), the H-molecule corresponding to the file address is reconstructed in core and the value part of the FILEP is replaced by a pointer to the H-molecule reconstructed. This file address and the pointer are registered in a table called the “file record”, which is used to prevent the GGBC from spending unnecessary file space and time in repetitively refiling the same H-molecule. (Note that the contents of H-molecules are never altered.)

The GGBC, called from the last step G6. of GBC, proceeds in the following steps:

GG1. Cancel all headers used in assoccomp (cf. §4).

GG2. For each item in the file record, exchange the file address and the content of the car part of the H-molecule.

GG3. Replace the value parts of HDOTP's and values in the pushdown stack by the file addresses, if the values represent H-molecules with file addresses in the car parts. This step efficiently refiles H-molecules which have been filed before.

GG4. Restore the car parts of H-molecules from the file record.

GG5. Cancel all file records.

GG6. File H-molecules in the value parts of HDOTP's and in the pushdown stack and replace them by the corresponding file addresses. This step creates new files of H-molecules which have not been filed before.

GG7. Call GBC. If still not enough H0-cells are reclaimed the execution of the HLISP program is terminated.

G5. In the fifth step G5. in GBC, items in the file record with pointers to H0- or H1-cells are (and must be) cancelled.

Since sequential addressing is sufficient for the functioning of file records, they are stored in the file with a small buffer in core.

In order to fully utilize the virtual memory scheme, the standard definitions of functions or library functions are loaded in the file together with the HLISP system. When a d0-valued atom is *eval*ed or *hvalue*d, the system searches for a standard definition in the file. If found, the definition is written in the core as an HP. (If unfound, an error.) The standard definition of *define* or *scompile* gives *hcopi*ed results.

The virtual memory has enabled the use of collection of functions amounting to several times larger than the free storage capacity in a single HLISP program without any difficulty or complexity at a reasonable operating speed[5)]. This would be meaningful for application areas of lisp, wherein programs become very large to obtain results of any significance whatsoever.

The monocopy and the rewrite protected features of H-molecules are essential for the present virtual memory scheme. Design of a logically consistent and reasonably efficient virtual memory scheme for lisp data subjected to arbitrary use of rplaca and rplacd (L-molecules in HLISP term) seems to be an open problem within the author's knowledge.

In the present HLISP, if the L-molecular data explodes during the execution of a program, the program has to be revised. Making hcopies of some L-molecular data not subjected to _rplaca_ or _rplacd_ would work in some cases.

The present GGBC takes all conceivable measures to reclaim the greatest number of free storage cells in a single stage. It may be a better strategy to break it down into three stages as follows and proceed to the next stage only if it fails to reclaim enough H0-cells: The 1st the refiling (GG2-4.), the 2nd the new filing (GG6.) and the 3rd the cancellation of _assoccomp_ headers (GG1.) stages.

§7. Concluding Remarks

Hash Coding is practiced in many language processors, including lisp[6], for matching strings of symbols in identifiers. HLISP may be regarded as a straightforward extension of such practices.

Use of the simplest possible data structure--the binary trees-- and the ability to define or bootstrap the system in terms of a very few basic functions are the characteristic features of lisp. In order to comply with this philosophy of lisp, the binary association of keys with values has been employed in HLISP because it seems to be the simplest. It should be possible to efficiently represent more complex associative structures, such as those used in LEAP[7 for example, in terms of binary trees and binary associators.

The present HLISP functions do not allow for circular list (loop or ring) arguments. Endless recursion would result in most cases as in many lisp functions. Generalization of the present HLISP scheme to treat more general types of internal data structures in a logically consistent manner would be an interesting theme.

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APPENDIX

The following is the list of basic HLISP functions and LISP functions subjected to extension or modification in HLISP.

apply[fn; x] The third argument (A-list) of Lisp-1.5 is deleted, since the present HLISP does not use an A-list, similarly to Lisp-1.6.

assoccomp[f_1; ...; f_n] f_1, ..., f_n are function names. cf. §4.

atom[x] associators are regarded as atoms. cf. Fig. 2

bind[x;y;z]=apply[list[LAMBDA;x;y];z]. x must represent a list of HDOTP's, y a form and z a list of HLISP objects. If list z is shorter than list x, z is regarded as if there were extra list elements NIL. Associators and headers are treated equally.

bindq[x;y;z] Same as bind except in that y is quoted.

bindq[(A,B,C);plus[a;b;c];(1,2,3)] is the same as

λ[[a;b;c];plus[a;b;c]][1;2;3]=6

These functions are used to λ-bind the values of HDOTP's resulting from the evaluation of x with elements of z, during the evaluation of form y. The former values of the HDOTP's are restored (from the pushdown stack) upon completion.

car[x], cdr[x] x must be a molecule, otherwise an error. Unlike in Lisp 1.5 car and cdr can not go beyond (atom) headers and associators. To go beyond, use hkey, hvalue or dzerop instead.

cons[x;y] x and y can be any HLISP-object. The result is always an L-molecule.

consp[x] Type predicate for L-molecules. cf. Fig.2.

dzero[x], dzerop[x] Undefine and predicate for undefined. cf. §2

eval[e] The second argument is deleted for the same reason as in apply.

eq[x;y]=[m[x]=m[y]->T;T->NIL] Checks equality of internal representatives.

equal[x;y]=[hp[x] ∧ *hp[y]→eq[x;y];atom[x]* \/ atom[y]->NIL;
equal[car[x];car[y]]→equal[cdr[x];cdr[y]];T→NIL]

In case both x and y are HP's, equal reduces to non-recursive eq by virtue of the first conditional.

fexpr FEXPR's are defined as in the following example for or.

```
define[[[or;fexpr[[null[*fexpr]→NIL;eval[car[*fexpr]]→T;
                   T->apply[or;cdr[*fexpr]]]]]]]
```

Namely, fexpr[<form>] is syntactically regarded as a <function> and the value of *fexpr is λ-bound to the unevaled list of arguments. cf. §5.

function[fn;x_1; ...; x_n] x_1, ..., x_n (optional) are the names of free variables in the functional argument fn to be frozen. cf. §5.

hassoc[x]/hassocp[x]/hassocpp[x]   creater/type predicate/presence predicate
hcons[x;y]/hconsp[x]/hconspp[x;y] for associators, H-molecules
header[x]/headerp[x]/headerpp[x]   and headers. cf. §2 and Fig.2.

hcopy[x], hcopyl[x] cf. §3.

hdotp[x]=hassoc[x] ∨ header[x] cf. Fig. 2.

hkey[x]=[hdotp[x]->(key part of x);T->error[HKEY]]

Extracts the key part of HDOTP's. cf. Fig.2.

hltp[x;y]=[m[x]<m[y]→T;T→NIL]

Similar to lessp. It works on internal representatives. For basic integers, the result is the same as lessp.

hnext[]=*hnext in value. Advances the value of *hnext to the next H-molecule, associator or header in storage. All existing headers except NIL, for example, are printed out by executing:

```
prog[[*hnext];
A [null[hnext[]]→return[NIL];headerp[*hnext]-
>print[*hnext]];go[A]].
```

hp[x] cf. Fig. 2.

hvalue[x] Extracts the value of HDOTP's. cf. §2 and Fig.2.

m[x] = (Internal representative of x). Is used to express system functions in M-expressions. cf. §2.

mapcarhcopy[x] cf. §3.

print[x], printl[x] Print with or without line termination.

The key part of headers are printed as the p-name of literal atoms as in other lisps. Associators, L-molecules and H-molecules are printed as in the following examples:

print[hassoc[hcons[ENGLISH;I]] prints (..ENGLISH.I)} with dots;
print[cons[ENGLISH;I]] prints (ENGLISH . I) with extra blanks;
print[hcons[ENGLISH;I]] prints (ENGLISH.I) without extra blanks.

rplaca[x;y], rplacd[x;y]   x must be an L-molecule, otherwise an error.
y can be any HLISP object. cf. §2.

set[x;y]=y in value. x must be an HDOTP. y can be any HLISP object.

In HLISP set and cset; setq and csetq are synonyms. cf. § 2.