

HOME COMPUTER IN MOLECULAR ORBITAL CALCULATIONS Part I. The Huckel Method

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Computer Programs in BASIC language for molecular orbital calculations have been developed for home computer (10 K memory). The M.O. Program can be used for research as well as teaching purposes. The programs are simple and tractable and can be used by nonprofessionals with ease. The program has been tested and found working with less than 15 seconds' time taken for allyl system.

Key words: Home computer; M.O. program Huckel Method; Basic program.

INTRODUCTION

The importance of M.O. calculations and utilization of various parameters (orbital energies, electron densities etc.) in teaching and research is well established. With the advent of computers, such calculations have become a lot easier. However, even with the terminal facilities available, the big computers are out of reach for many. Besides, because of time sharing, running M.O. programs for teaching purposes could be quite expensive. Also some of the programs written by professional programmers, though available in the library, cannot be easily modified to suit our (and the computer's) requirements. If these M.O. calculations can be carried out on small inexpensive and easily accessible computers, many of the above problems can be solved.

With the advent of Home Computers which are now easily accessible even to high schools (and to individuals), it is lot easier and more convenient to handle M.O. calculations by these computers. Besides, because of BASIC Language, the user can understand more easily about the techniques of M.O. calculations. It is more easily traceable to the user.

A computer program in BASIC language has been developed to carry out Huckel M.O. calculation. The program has been tested on a Home Computer with 10K memory.

Molecular orbital theory. Here only a summary of the theory is given. For details one is referred to the literature [1].

Each molecular orbital can be expressed as a linear combination of n atomic orbitals (where n is the number of basis orbitals):

$$\Psi_j = \sum_i^n C_{ji} \phi_i \quad (1)$$

C_{jr} = coefficient of the r^{th} atomic orbital in j^{th} M.O.
 ϕ_i = A.O. for the i^{th} atom

The Huckel Molecular Orbital method is [2] the simplest method for calculating the energies and coefficients of the molecular orbitals.

Using the variational method, a set of linear equations is obtained:

$$\sum C_j (H_{ij} - S_{ij} E) = 0; i = 1, 2, \dots, n \quad (2)$$

Where the quantities

$$H_{ij} = H_{ji} = \int \phi_i^* H \phi_j d\tau \quad (3)$$

$$S_{ij} = \int \phi_i^* \phi_j d\tau \quad (4)$$

are numbers which can be computed from the starting ϕ_i and known H . In the matrix form this set of n equations can be represented as [3].

$$HC = SCE. \quad (5)$$

C = matrix of coefficients (or matrix of eigenvectors). Each column of the matrix C refers to different M.O. elements; S_{ij} of the matrix S can be represented as

$$S_{ij} = \int \phi_i^* \phi_j d\tau$$

Under the assumption that the basis function is orthonormal and matrix S becomes equal to the identity matrix and we are left with the equations $C^+ HC = CE$. Also

Matrix elements of H are known then C and E can be calculated. E in this case is a diagonal matrix.

The diagonal elements of E correspond to the eigenvalues or energies of the M.O.'s.

The problem is now that given a matrix H , to find unitary matrix C such that $C^+ HC$ is diagonal. Details of matrix diagonalization can be obtained from ref. 3. and ref. 4.

The next problem is the evaluation of the matrix elements H_{ij} . H_{ii} represents the energy of an electron in the i^{th} atomic orbital. This integral known as coulomb integral is denoted by the symbol α ($= \int \phi_i H \phi_i d\nu$) where ϕ is the $2p_z$ A.O. of a carbon atom [2]. H_{ij} represents the energy of interaction of orbitals and as a simplification if atoms i and j are bonded then $H_{ij} = \beta$, otherwise (if i and j are not bonded) $H_{ij} = 0$. This is known as the resonance integral. This is the case when we are considering simple conjugated or aromatic hydrocarbons. However in a more general form the matrix elements of the Hamiltonian can be represented as $H_{ii} = \alpha + h_x \beta$ and for neighbouring atoms $H_{ij} = \beta = k_c \beta_0$ where β_0 is taken to be a unit of energy.

All roots are computed relative to α , which is usually taken for convenience to be zero. According to convention $h_x = 0$ if the i^{th} A.O. is the $2p_z$ A.O. However if instead of carbon we have some other heteroatom X as part of the system, then h_x may have a positive or negative value depending upon the electronegativity of the heteroatom relative to the carbon atom.

For a C-X bond the value of the parameter k_{C-X} is not equal to unity [5]. Once the energies and co-efficients of the molecular orbitals are calculated then the electrons are assigned to the M.O.'s according to Pauli's exclusion principle.

According to Coulson the partial mobile bond order of the r - s bond in the j^{th} M.O. is defined as [2].

$$p_{rs}^j = C_{jr} C_{js} \quad (6)$$

$$P_{rs} = \sum p_{rs}^j = \sum n_j C_{jr} C_{js} \quad (7)$$

Bond orders may be associated with the binding power of a bond. The electron density at an atom, q_r , is the sum of electron density contributed by each electron in each M.O.

$$q_r = \sum C_{jr}^2 \quad (8)$$

C_{jr} is the coefficient of atom r in the j^{th} M.O., which is occupied by n_j electrons. The sum is taken over all the M.O.'s.

Huckel calculations are semiempirical in nature and a number of approximations have been introduced. Some of the approximations can be reduced by further techniques within the framework of H.M.O. method; w-technique [2,6] is one of these techniques.

Computational techniques. Molecular Orbital Calculations have been carried out on a 10K Home Computer Sharp (PC-1500) using the simple Huckel Molecular Orbital method. The method is based upon matrix diagonalization in BASIC language and is designed to provide processing for one molecule with one electronic configuration at a time.

A BASIC program for solving Huckel-electron problem is written in the form of subprograms, each of which performs a specific part of the complete calculation.

It consists of a *Main Control Program* which controls the sequence of operation, and several subroutines. These subroutines being INPUT, DIAGONALIZATION, ORDER, BOND ORDER, OUTPUT, PRINTOUT INPUT DATA, PRINTOUT RESULTS, OUTPUT.

The functions of the above mentioned SUBROUTINES are generally known and these do not have to be elaborated briefly:

INPUT Subroutine reads the number of conjugated atoms, the Huckel matrix and the number of electrons. It reads only the upper semi matrix (of the Huckel matrix) and brings down the upper semi matrix to the lower semi-matrix.

The DIAGONALIZATION subroutine diagonalizes the matrix by the Jacobi method.

The subroutine ORDER puts the eigen-values and eigenvectors in a sequence from the lowest to the highest. Negative eigen-values correspond to *bonding* energy levels. The bond order subroutine calculate the charge densities and bond order (eqns 7 and 8). The function of other subroutines are obvious.

There are two points worth mentioning, viz. (i) Form of the Input matrix and (ii) Timing.

(i) Form of the input matrix. The input matrix $H(I, J)$ contains 0'S and 1'S for straight/conjugated aromatic hydrocarbon. For hydrocarbon, the diagonal elements $H(I, I)$ are set equal to zero, off diagonal elements are 1'S for neighboring atoms and 0's for non-neighbouring.

In heteroatomic system not all diagonal elements are 0. If the heteroatom is at the I^{th} position, the $H(I, I)$ is equal to h_x . Also $H(I, J)$ is equal to k_{C-X} when J is the neighbour of the heteroatom.

A point to remember is that as the energy levels are arranged in ascending order (from -ve to +ve values) electron should be filled accordingly.

As an example consider the case of pyridine. Questions will appear on the screen for the number of atoms, $H(I, J)$ matrix and the number of electrons. These are to be "Entered".

| | | |
|------------------|----------------|----------------|
| H (1, 1) = ? 0.5 | H (2, 2) = ? 0 | H (4, 4) = ? 0 |
| H (1, 2) = ? 0.8 | H (2, 3) = ? 1 | H (4, 5) = ? 1 |
| H (1, 3) = ? 0 | H (2, 4) = ? 0 | H (4, 6) = ? 0 |
| H (1, 4) = ? 0 | H (2, 5) = ? 0 | |
| H (1, 5) = ? 0 | | |
| H (1, 6) = ? 0.8 | | |
| | H (3, 3) = ? 0 | H (5, 5) = ? 0 |
| NE (1) = ? 2 | H (3, 4) = ? 1 | H (4, 6) = ? 1 |
| NE (2) = ? 2 | H (3, 5) = ? 0 | H (4, 6) = ? 0 |
| NE (3) = ? 2 | H (3, 6) = ? 0 | |
| NE (4) = ? 0 | | |
| NE (5) = ? 0 | | |
| NE (6) = ? 0 | | |

(ii) Timing.

The time taken by the computer to run the above mentioned programs for allyl radical (or cation) and benzene molecule (or ion) is given below

| | |
|---------------|----------|
| Alkyl radical | 18 secs |
| Benzene | 100 secs |

on larger computer, e.g. APPLE IIC, considerable less time is required for computation.

In case of the Jacobi diagonalization time taken is proportional to N_3 (Where N = No. of atoms in a molecule)

$$\frac{T_1}{T_2} = \frac{N_1^3}{N_2^3}$$

The above mentioned data are found to be in rough agreement with this rule.

Printouts: Input Data and Results (H.M.O.)

H.M.O CALCULATIONS

| | |
|---------------|------------------------|
| ALLYL RADICAL | H (2, 3) = -1 |
| | H (3, 3) = 0 |
| INPUT DATA | NE (1) = NO. OF ELECTO |
| H (1, 1) = 0 | NS IN THE ITH M.O |
| H (1, 2) = 1 | NE (1) = 2 |
| H (1, 3) = 0 | NE (2) = 1 |
| H (2, 2) = 0 | NE (3) = 0 |

RESULTS

| | |
|----------------------|---------------------|
| EIGENVALUES | CHARGE DENSITIES |
| E (1) = -1.414213563 | Q (1) = 1 |
| E (2) = -2.850934661 | Q (2) = 1 |
| E - 12 | Q (3) = 9.999999998 |
| E (3) = 1.414213563 | E - 01 |

| | |
|----------------------|----------------------|
| EIGENVECTORS | 812E - 01 |
| U (1, 1) = 5.000000 | U (3, 3) = -0.5 |
| 001E - 01 | |
| U (1, 2) = -7.071067 | BONDORDERS |
| 811E - 01 | P (1, 1) = 1 |
| U (1, 3) = -5.000000 | P (1, 2) = 7.071067 |
| 001E - 01 | 812E - 01 |
| U (2, 1) = 7.071067 | P (1, 3) = 5.2E - 11 |
| 812E - -01 | P (2, 1) = 0 |
| U (2, 2) = 2.099388 | P (2, 2) = 1 |
| 572E - 10 | P (2, 3) = 7.071067 |
| U (2, 3) = 7.071067 | 812E - 01 |
| 812E - 01 | P (3, 1) = 0 |
| U (3, 1) = 4.999999 | P (3, 2) = 0 |
| 999E - 01 | P (3, 3) = 9.999999 |
| U (3, 2) = 7.071067 | 998E - 01 |

1. H.M.O. Programme For Sharp PC - 1500 Home Computer (10 K)

```

H.M.O.
10: Print "H.M.O. Calculations"
15: RC = 1
20: GOSUB 80
25: GOSUB 230
30: GOSUB 600
35: GOSUB 700
40: GOSUB 800
45: END

```

```

Bondorders Subroutine
700: Rem Subroutine Bondorders
705: FOR R = 1 TO N
710: FOR S = R TO N
715: SM = 0
720: FOR J = 1 TO N
725: SM = SM ÷ NE (J) * U (R, J) * U (S, J)
730: NEXT J
740: P (R, S) = SM
745: NEXT S
750: NEXT R
755: RETURN

```

```

Input Subroutine
80: REM "INPUT SUB ROUTINE"
85: INPUT "NAME?"; N$
90: INPUT "NO OF ATOMS = ?"; N
95: DIM H (N, N): DIM HD (N): DIM NE (N): DIM U
(N, N): DIM UT (N): DIM P (N, N)
100: WAIT 0
105: FOR I = 1 TO N

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110: FOR J = I TO N
115: CLS: PRINT "H (; I, ; , ; J;) = ";
120: INPUT H (I, J)
125: H (J, I) = H (I, J)
130: NEXT J
135: NEXT I
140: FOR I = I TO N
145: CLS: PRINT "NE (; I;) = ";
150: INPUT NE (I)
155: NEXT I
160: WAIT 100: CLS: PRINT "CHECK T HE INPUT H
(I, J)"
165: FOR I = I TO N
170: FOR J = I TO N
175: CLS: WAIT 0: PRINT "H (; I, ; , ; J;) = "; H (I, J)
180: CURSOR 20: INPUT H (I, J)
185: H (I, J) = - H (I, J)
190: H (J, I) = H (I, J)
195: HD (I) = H (I, I)
200: NEXT J
205: NEXT I
210: WAIT
215: CLS: INPUT "PR INTOUT INPUT D ATA REOD?";
U$
220: IF U$ = "YES" THEN GOSUB 400 0
225: RETURN

```

Diagonalization Subroutine

```

230: REM DIAGONALIZATION
235: REM SUBROUTINE
240: FOR J = I TO N
245: FOR I = I TO N
250: U (I, J) = 0
255: U (I, I) = 1
260: NEXT I
265: NEXT J
270: EP = IE - 16
275: MX = 0
280: FOR I = 2 TO N
285: FOR J = I TO (I - 1)
298: H (I, I) @ HD (I)
295: H (J, J) = HD (J)
300: SQ = H (I, J) 2
310: IF SQ > MX THEN LET MX = SQ
315: IF SQ <= EP THEN GOTO 515
320: D = HD (I) - HD (J)
325: IF D >= 0 THEN GOTO 340
330: SN = - 2: D = - D
335: GOTO 345
340: SN = 2

```

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345: TD = (D + √ (( D * D) + (4 * SQ)))
350: TN = (SN * H (I, J) )/TD
355: C = I/(√ (I ÷ (TN * T N)))
380: S = C * TN
370: FOR K = I TO N
380: XJ = C * U (K, J) - S * U (K, I)
385: U (K, I) = S * U (K, J) ÷ C * U (K, I)
390: U (K, J) = XJ
395: IF K = J THEN GOTO 485
400: IF K > J THEN GOTO 435
410: XT = C * H (J, K) - S * H (I, K)
420: H (I, K) = S * H (J, K) + C * H (J, K)
425: H (J, K) = XJ
430: GOTO 485
435: IF K = I THEN GOTO 485
440: IF K > I THEN GOTO 470
450: XJ = C * H (K, J) - S * H (I, K)
455: H (I, K) = S * H (K, J) + C * H (I, K)
460: H (K, J) = XJ
465: GOTO 485
470: XJ = C * H (K, J) - S * H (K, J)
475: H (K, I) = S * H (K, J) + C * K (K, I)
480: H (K, J) = XJ
495: NEXT K
490: HD (J) = (S * S * H (J, I) ) + (S * S * H (J, J) ) +
(2 * S * S * H (I, J) )
500: HD (J) = (S * S * H (J, J) ) + (S * S * H (J, I) ) -
(2 * S * S * H (J, J) )
510: H (J, J) = 0
515: NEXT J
520: NEXT I
525: IF MX > EP THEN GOTO 275
530: RETURN
540: END

```

Output Sueroutines

```

800: REM SUBROUTINE OUTPUT
805: BEEF 5, 10, 100
810: PRINT "EIGENUA LUES"
815: FOR I = I TO N
820: WAIT
825: PRINT "E (; I; ) HD (I)
830: NEXT I
840: INPUT "EIGENUE GTORS REQD. ?"; U$
845: IF U$ = "NO" THEN GOTO 875
850: FOR J = I TO N
860: PRINT "U (; I, ; , ; J;) = "; U (I, J)
865: NEXT I
870: NEXT J
875: INPUT "CHARGE DENSITIES REQD ?"; C$

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880: IF C$ = "NG" THEN GOTO 900
885: FOR I = I TO N
890: PRINT "Q (;I,") = "; P (I, I)
895: NEXT I
900: INPUT "BOUNDORD ERS REQD? "; P$
905: IF P$ = "NO" THEN GOTO 935
910: FOR I = I TO (N - I)
915: FOR J = (I + I) TO N
920: PRINT "P (;I,") = "; P (I, J)
925: NEXT J
930: NEXT I
935: INPUT "PRINTOUT RESULTS REQD?"; U$
940: IF U$ = "YES" THEN GOSUB 800 0
950: RETURN

```

Order Subroutine

```

600: REM SUBROUTINE ORDER
605: FOR K = I TO N
610: HT = HD (K)
615: JT = K
620: FOR J = K TO N
625: IF HD (J) >= HT THEN GOTO 640
630: HT = HD (J)
635: JT = J
640: NEXT J
645: HD (JT) = HD (K)
650: HD (K) = HT
655: FOR I = I TO N
660: UT (I) = U (I, JT)
665: U (I, JT) = U (I, K)
678: U (I, K) = UT (I)
675: NEXT I
680: NEXT K
685: RETURN
690: END

```

Printout Subroutines

```

4000: REM SUBROUTINE
4001: REM PRINTOUT INPUT DATA
4005: C SIZE 3: LF 3
4010: ON RC GOTO 4020, 34030, 4040
4020: L PRINT "H. M. O CALCULATIONS"
4025: GOTO 4050
4030: L PRINT "H.M.O WITH W-TECHNIQUE"
4035: GOTO 4050
4040: L PRINT "H.M.O WITH MCLAC HLAN METHOD"
4050: LF I: C SIZE 2
4860: L PRINT N$
4070: LF 1
4080: L PRINT "INPUT DATA"
5000: FOR I = I TO N

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```

5010: FOR J = I TO N
5020: L PRINT "H (;I,") = "; H (I, J)
5030: NEXT J
5040: NEXT I
5060: LF 2
5070: L PRINT "NE (I) = NO. OF ELECTONS IN THE
ITH M.O"
5080: FOR I I TO N
5090: L PRINT "NE (;I,") = "; NE (I)
6000: NEXT I
6010: RETURN
6050: REM PRINTOUT INPUT
6055: REM DATA S.T.C.F.
6060: LT I: C SIZE 3
6070: L PRINT "S.C.C CALCULATIONS"
6080: C SIZE 2: LT I
6090: L PRINT N$
7000: LF 1
7010: FOR I = I TO N
7020: L PRINT "X (;I,") = "; X (I,")"; "Y (;I,") =
"; Y (I)
7040: NEXT I
7045: LF I
7050: L PRINT "NE (I) = NO. OF ELECTRONS IN THE
ITH M.O.
7060: FOR I = I TO N
7070: L PRINT "NE (;I,") = "; NE (I)
7080: NEXT I
7090: RETURN
8000: REM SUBROUTINE PRINTOUT RESULTS
8005: LF 2: C SIZE 3
8010: L PRINT "RESULTS"
8022: IF RC = I THEN GOTO 8040

```

Printout Results Subroutine

```

8000: REM SUBROUTINE PRINTOUT RESULTS
8005: LF 2: C SIZE 3
8010: L PRINT "RESULTS"
8020: IF RC = I THEN GOTO 8040
8030: C SIZE 2: L PRINT "ITERATION NO. "; K, K
8040: C SIZE 2: LF 1
8050: L PRINT "EIGEN VALUES"
8060: L PRINT "E (;I,") = "; HD (I)
8080: NEXT I
8090: LF 2: L PRINT "CHARGE DENSITIES"
9000: FOR I = I TO N
9010: L PRINT "Q (;I,") = "; P (I, I)
9020: NEXT I
9025: LF 2
9030: L PRINT "EIGENVECTORS"

```

```

9040: FOR I = I TO N
9050: FOR J = I TO N
9060: L PRINT "U ("; I; ", "; J; ") = "; U (I, J)
9070: NEXT J
9080: LF 2
9090: L PRINT "BOND ORDERS"
10000: FOR I = I TO N
10010: FOR J = I TO N
10020: L PRINT "P ("; I; ", "; J; ") = "; P (I, J)
10030: NEXT J
10040: NEXT I
10050: RETURN

```

2. H.M.O. Programme for Sharp PC - 7000; Apple II.

```

1 TGOTO 2600
10 PRINT "H.M.O. Calculations"
15 RC = 1
20 GOSUB 80
25 GOSUB 230
30 GOSUB 600
35 GOSUB 700
40 RETURN
45 END
79 REM
80 REM "input subroutine"
81 REM
85 INPUT "name"; N$
90 INPUT "no. of atoms"; N
95 DIM H (N, N): DIM HD (N): DIM NE (N): DIM U
(N, N): DIM UT (N): DIM P (N, N)
105 FOR I = I TO N
110 FOR J = I TO N
115 FOR J = I TO N
115 PRINT "H ("; I; ", "; J; ") = ";
120 INPUT H (I, J)
125 H (J, I) = H (I, J)
130 NEXT J
135 NEXT I
140 FOR I = I TO N
145 PRINT "NE ("; I; ") = ";
150 INPUT NE (I)
155 NEXT I
159 PRINT
160 COLOR 3: PRINT "VERIFICATION of H (I, J)":
PRINT "To confirm, press the SPACE bar"
161 PRINT "To alter, press the = key, then key-in the
correct value, then press CR": COLOR 7
165 FOR I = I TO N
170 FOR J = I TO N
175 PRINT "H ("; I; ", "; J; ") = ", H (I, J),
177 U$ = IN KEY $: IF U$ = " " THEN 177
178 IF U$ = "=" THEN PRINT "O.K.": GOTO 185
179 IF U$ = " " THEN PRINT " = "; : INPUT H (I, J):
GOTO 185
185 H (I, J) = - H (I, J): H (J, I) = H (I, J): HD (I) = H
(I, I)
200 NEXT J
205 NEXT I
215 PRINT "print-out of input data required? (y/n)",
220 U$ = IN KEY$: IF U$ = " " THEN 220
221 PRINT U$
222 PRINT "BUSY"
225 RETURN
229 REM
230 REM diagonalisation subroutine
231 REM
240 FOR J = I TO N
245 FOR I = I TO N
250 U (I, J) = 0: U (I, I) = I
260 NEXT I
265 NEXT J
270 EP = IE - 16
275 MX = 0
280 FOR I = 2 TO N
285 FOR J = I TO (I - 1)
290 H (I, I) = HD (I): H (J, J) = HD (J): SQ = (H (J, J)
2
310 IF SQ > MX THEN LET MX = SQ
315 IF SQ <= EP THEN 510
320 D = HD (I) - HD (J)
325 IF D >= 0 THEN 340
330 SN = - 2: D = - D
335 GTO 345
340 SN = 2
345 TD = D + SQR ((D * D) + (4 * SQ)): TN = (SN * H
(I, J))/TD
355 C = I/(SQR (1 + (TN * TN))): S = C * TN
370 FOR K = I TO N
380 IF K = J THEN 485
400 IF K > J THEN 435
450 XJ = C * H (K, J) - S * H (I, K): H (I, K) = S * H
(K, J) + C * H (I, K): H (K, J) = XJ
465 GOTO 485
470 XJ = C * H (K, J) - S * H (K, I): H (K, I) = S * H
(K, J) + C * H (K, I): H (K, J) = XJ
485 NEXT
490 HD (I) = (C * C * H (I, I)) + (S * S * H (J, J)) +
(2 * S * C * H (I, J))
500 HD (J) = (C * C * H (J, J)) + (S * S * H (I, I)) -

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```

      (2 * S * C * H (I, J))
505 H (I, J) = O
510 IF MX > EP THEN 275
530 RETURN
540 END
599 REM
600 REM order subroutine
601 REM
605 FOR K = I TO N
615 HT = HD (K): JT = K
620 FOR J = K TO N
625 IF HD (J) >= HT THEN 640
630 HT = HD (J): JT = J
640 NEXT J
645 HD (JT) = HD (K): HD (K) = HT
655 FOR I = I TO N
660 UT (I) = U (I, JT): U (I, JT) = U (I, K) = UT (I)
670 NEXT: NEXT
685 RETURN
690 END
699 REM
700 REM subroutine bond-orders
701 REM
705 FOR R = I TO N
710 FOR S = R TO N
715 SM = O
720 FOR J = I TO N
725 SM = SM + NE (J) * U (R, J) * U (S, J)
730 NEXT J
740 P (R, S) = SM
745 NEXT S
750 NEXT R
755 RETURN
799 REM
800 REM
801 REM output subroutine
2600 REM bondorders and forceconstants
2605 GOSUB 10
2610 FOR R = I TO (N - I)
2615 FOR S = (R + I) TO N
2620 IF H (R, S) = O THEN LET P (R, S) = O
2625 P (S, R) = P (R, S)
2645 NEXT: NEXT
2655 IF ( (N/2) - INT (N/2) ) = O THEN GO TO 2685
2660 X = (N + 1)/2
2675 NE (X) = 2
2680 GOTO 2700
2685 X = (N/2) + 1
2695 NE (X) = NE (X) + 1
2700 GOSUB 700

```

```

2750 L = O
2710 FOR R = I TO (N - I)
2715 FOR S = (R + I) TO N
2720 IF H (R, S) = O THEN LET P (R, S) = O
2730 K = 5.47 * (1 + P (S, R)) - 2.06
2737 KA = 5.47 * (1 + P (R, S)) - 2.06
2740 L = L + ( ( (K * KA) * ( (.18 * (P (R, S) - S, R) ) ) ) ) / (K + KA) )
2745 NEXT: NEXT
2750 PRINT "L = "; L * 6.25
2755 INPUT "LO = "; LO
2760 G = (L + LO)/4
2765 PRINT "FREE ENERGY ="; G
2770 END

```

Pyridene input data

```

H (1, 1) = .5
H (1, 2) = 1
H (1, 3) = 0
H (1, 4) = 0
H (1, 5) = 0
H (1, 6) = 1
H (2, 2) = 0
H (2, 3) = 1
H (2, 4) = 0
H (2, 5) = 0
H (2, 6) = 0
H (3, 3) = 0
H (3, 4) = 1
H (3, 5) = 0
H (3, 6) = 0
H (4, 4) = 0
H (4, 5) = 1
H (4, 6) = 0
H (5, 5) = 0
H (5, 6) = 1
H (6, 6) = 0

```

NE (I) No. of electrons in the Ith M.O.

```

NE (1) = 2
NE (2) = 2
NE (3) = 2
NE (4) = 0
NE (5) = 0
NE (6) = 0

```

RESULTS

| | |
|-------------------|-----------------|
| Pyridene | E (3) = - 1 |
| Eigenvalues | E (4) = .840961 |
| E (1) = - 2.10745 | E (5) = .999999 |
| E (2) = - 1.16719 | E (6) = 1.93368 |

Charge Densities

Q (1) = 1.19521
 Q (2) = .922953
 Q (3) = 1.00449
 Q (4) = .949912
 Q (5) = 1.00449
 Q (6) = .922953

Eigenvectors

u (1, 1) = .520706
 u (1, 2) = .571374
 u (1, 3) = 1.47859E - 07
 u (1, 4) = .545913
 u (1, 5) = 2.75323E - 07
 u (1, 6) = -.323073
 u (2, 1) = .418504
 u (2, 2) = .190608
 u (2, 3) = -.5
 u (2, 4) = -.366024
 u (2, 5) = -.5
 u (2, 6) = .393128
 u (3, 1) = .361268
 u (3, 2) = .348896
 u (3, 3) = -.5
 u (3, 4) = -.238101
 u (3, 5) = .499999
 u (3, 6) = -.43711
 u (4, 1) = .342849
 u (4, 2) = .597838
 u (4, 3) = -1.42913E - 07
 u (4, 3) = .566257
 u (4, 5) = 2.96085E - 07
 u (4, 6) = .452101
 u (5, 1) = .361268
 u (5, 2) = .348897
 u (5, 3) = .5
 u (5, 4) = -.2381

u (5, 5) = -.5
 u (5, 6) = -.437109
 u (6, 1) = .418504
 u (6, 1) = .418504
 u (6, 2) = -.190608
 u (6, 3) = .5
 u (6, 4) = -.366024
 u (6, 5) = .5
 u (6, 6) = .393127

Bondorders

P (1, 1) = 1.19521
 P (1, 2) = .653652
 P (1, 3) = -2.24717E - 02
 P (1, 4) = -.326131
 P (1, 5) = -2.24719E - 02
 P (1, 6) = .653652
 P (2, 1) = 0
 P (2, 2) = .922953
 P (2, 3) = .669378
 P (2, 4) = 5.90611E - 02
 P (2, 5) = -.330621
 P (2, 6) = -.077046
 P (3, 1) = 0
 P (3, 2) = 0
 P (3, 3) = 1.00449
 P (3, 4) = .664888
 P (3, 5) = 4.48656E - 03
 P (3, 6) = -.330621
 P (4, 1) = 0
 P (4, 2) = 0
 P (4, 3) = 0
 P (4, 4) = .949912
 P (4, 5) = .664888
 P (4, 6) = .059061
 P (5, 1) = 0

P (5, 2) = 0
 P (5, 3) = 0
 P (5, 4) = 0
 P (5, 5) = 1.00449
 P (5, 6) = .669378
 P (6, 1) = 0

P (6, 2) = 0
 P (6, 3) = 0
 P (6, 4) = 0
 P (6, 5) = 0
 P (6, 6) = .922953

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