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Testing the Theory of Evolution

An Application of Combinatorial Optimization

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Implications of Charles Darwin's theory of evolution have recently been rigorously tested using combinatorial optimization techniques. It will come as no surprise to many academics that the results of the test in no way invalidate the theory. Dr. David Penny and Dr. Michael Hendy of Massey University, New Zealand, and I have, over the last eight years, been investigating claims that Darwin's theory is not respectable science but mere belief. graph theoretic model of evolution has been constructed and solution techniques for the model have been developed using combinatorial optimization techniques. When the techniques are applied to data gained from modern biochemical methods, they produce solutions which do not support these claims.1

It would require millions of years to verify by observation whether or not the process of evolution actually takes place. Thus all that can be done is to look for evidence which suggests that evolution has or has not taken place in the past. This is in some ways unsatisfactory as it means that the theory cannot be tested by the scientific method in the same way as other scientific theories, such as Einstein's photoelectric effect.

But there is evidence to suggest that each living species possesses a very detailed description of itself in the form of a DNA code, which is apparently used to build genes. There is the possibility that, if the theory of evolution is valid, when species evolve their DNA codes will evolve too. So an analysis of the protein codes from different species may be quite revealing.

What was done was to search for ancestral relationships among five different proteins from 11 vertebrate species. The

proteins can each be characterized by a string of fixed length from an alphabet of four symbols called *nucleotides*. For each protein, the 11 strings (one for each species) can be aligned and analyzed comparatively. It turns out that any 11 species could be related in over 34 million ways. But it was found in this investigation that for each independent protein, the simplest possible pattern of relationship was remarkably similar.

The five different proteins are independent of each other so it seems that the ancestral relationships of the species which can be deduced by these patterns support the idea of some kind of evolutionary process. This is because without such a process it is not clear why the patterns would be so similar. Also it is interesting to note that the pattern tends to conform well with evolutionary trees produced by numerical taxonomists when studying bone structure and fossil records.

Having read thus far, you are probably thinking this is all very well, but what has it to do with mathematical programming? To justify the publication of this article in OPTIMA we shall now briefly outline a graph theoretic model of evolution and some combinatorial optimization techniques which can be used to analyze it.

The theory of evolution predicts that existing biological species have been linked in the past by common ancestors. A diagram showing these links is called a *phylogenetic tree* or *phylogeny*. A typical phylogeny is given in Figure 1. Since the time of Charles Darwin, many scientists have constructed phylogenies which link both existing and extinct species in the fossil record. When the fossil record is inadequate for a set of species, it may be possible to determine its evolutionary history from a knowledge of existing species in the set.

Suppose we wish to construct a phylogeny for a given set of species with little fossil evidence. We must use only

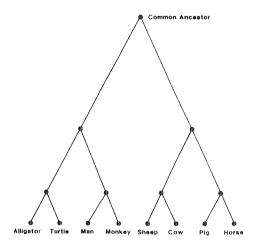


Figure 1: A Phylogenetic Tree

existing species. It is useful to use information about the versions of a protein called cytochrome c. It seems that every living species possesses a version of this protein as it appears to be essential for respiration. Each version can be represented by a string of 312 letters chosen from the following four: A, C, G, and U (nucleotides). It is interesting to compare strings: Man and Rhesus Monkey differ at only one site of the 312. However, the reader will be relieved to know that man and bread mold differ at 129 sites!

Our model is concerned with constructing a phylogeny which can be thought of as a weighted tree in the graph theoretic (Continued next page)

Next MP Symposium at MIT

The MPS Council is pleased to announce that Professor Jeremy Shapiro, Professor of Operations Research and Codirector of the O.R. Center at M.I.T., will be Chairman for organizing the 12th International Symposium on Mathematical Programming. The Symposium will take place on the M.I.T. Campus in August, 1985.

-Alex Orden

sense. Each of the given species is represented by a node in the phylogeny. The other nodes represent other existing or extinct species. The weight of each arc in the phylogeny is defined to be the number of sites at which the strings it connects differ. The objective is to find a phylogeny which spans the given set of species and which is of minimum total weight as a sum of the weights of its arcs. The objective is known to biologists by the somewhat contradictory title of maximum parsimony. parsimony for the species in a realistic study

small artificial example which has been phylogenies has been enumerated assuming constructed for expository purposes. Sup-various restrictions.²,³ pose we have five species: S₁, S₂, ..., S₅, possibilities grows astronomically, complete with strings that are only eight characters enumeration is out of the question. The long rather than the usual 312 characters. model appears on the surface to be a mini-The strings are given in Table 1, where each mal spanning tree problem which is, of row is the string for a species:

	1	2	3	4	5	6	7	8
$\overline{S_1}$	A	G	U	G	U	U	A	A
S_2	C	A	A	G	U	U	A	\mathbf{A}
S_3	C	G	\mathbf{U}	C	C	G	A	A
S ₄	A	A	U	G	U	U	C	A
S_{5}	C	G	U	G	U	U	C	U

Table 1

As the sequences have been aligned, each column corresponds to a site.

What we want to do is to connect the five species by a spanning tree where each species is represented by a node of the tree. Suppose we join S_1 and S_4 directly by an arc in the tree as shown in Figure 2. If we compare S_1 and S_4 we see that the two strings differ at sites 2 and 7 only. At site 2 S_1 has a G and S_4 has an A. We label the S_1 - S_A arc with the symbols 2GA to denote one difference between the strings. These three symbols are together called a substitution. We also add the substitution 7AC to the arc to denote the difference at site 7. As there are no other differences there are no other substitutions associated with the S_1 - S_A arc. Given one of the two strings and the substitutions, we can deduce the other of their solutions provide valid lower bounds string. What we wish to do is to construct a spanning tree for (S₁, S₂, S₃, S₄, S₅) and label the arcs of the tree with the appropriate substitutions. A possible spanning tree the total number of substitutions.



Figure 2: The $S_1 - S_4$ arc

Finding the phylogeny of maximum To make this clearer, we now furnish a is no easy task. The number of possible As the number of course, straightforward to solve. However, the introduction of additional sequences representing extra species (either existing or - extinct) often leads to a phylogeny with greater parsimony (a tree of less weight). Therefore, the model can be seen to be a variation of the Steiner tree problem on the n-cube. This problem is notorious for its intractability and indeed the phylogeny model has been shown to be NP-complete.4 Given this gloomy state of affairs, it seems unlikely that a polynomial time algorithm exists for the general problem. Yet all is not lost. It has been possible to modify existing minimal spanning tree algorithms by using a clustering algorithm to produce a phylogeny of relatively low weight. What are clustered are collections of columns of the matrix of data. This phylogeny of low weight is then analyzed with view to either proving that it is of maximum parsimony or modifying it so that it becomes one of maximum parsimony. The approach is to use the clustering algorithm to partition the matrix of data vertically. This breaks up each original string into a number of smaller substrings. Each set of substrings represents a separate, smaller problem. These smaller problems are of substitutions. In applying it to our tree then analyzed and if necessary a further decomposition is made. Eventually the subdecomposition is made. Eventually the sub- in both 2GA (on arcs S_1 - S_4 and S_4 - S_5) problem can be solved directly. The weights and 1CA (on arcs S_3 - S_1 and S_1 - S_2) which are used to prove the minimality of in Figure 5, which has 10 substitutions. We either the original phylogeny or a modifica- have introduced two new strings: S6 and tion thereof.

We now illustrate the ideas just is given in Figure 3. The total number of presented by returning to the example minimal Steiner tree we analyze Table 1. substitutions in this tree is 12. The objective problem. A natural first attempt at solution is to find a spanning tree which minimizes is to use either the Prim or Kruskal method for the minimal spanning tree problem

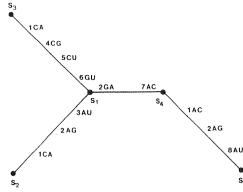


Figure 3: A Spanning tree for the five species

(MSTP). Let's see how this approach turns out for our example. The number of substitutions necessary for each pair of strings is given in Table 2.

	$\mathbf{s_2}$	$^{\mathrm{S}}3$	S_4	S ₅	
$\overline{S_1}$	3	4	2	3	
S_2		5	3	4	
$\overline{S_3}$			5	5	
S_4				3	

Table 2

Applying a MSTP algorithm we can obtain (among other minimal trees) the tree given in Figure 3. There is the possibility of the introduction of new strings in order to reduce the total number of This is brought about by substitutions. using a process called coalescement. This process can be explained as follows. Suppose we have a substitution at site n between nucleotides X and Y which appears on two adjacent arcs in a spanning tree, as shown in Figure 4(a). The tree can be modified to produce a spanning tree with one less substitution by the introduction of a new string \overline{S}_m , (called a Steiner point) which differs from the S_i string only at site n. It has a Y rather than an X there. This process can be used repeatedly to reduce the number we can remove one instance of duplication substitution. This produces the tree shown

To discover whether this tree is a Consider the three sites: 1,2, and 7. If substitutions corresponding to the other

sites are removed, the tree collapses to the one in Figure 6. It has one Steiner point. The introduction of more than one Steiner point would lead to a tree with more substitutions. Can we create a tree with fewer substitutions by having no Steiner points? This is a normal MSTP. The substrings based on sites 1, 2, and 7 are given in Table 3. Any minimal solution to the MSTP for this data has five substitutions. Therefore, we know that sites 1, 2, and 7 jointly require at least five substitutions in any phylogeny. The other sites: 3, 4, 5, 6 and 8 require at least one substitution each as their columns in Table I each have two nucleotides. Thus, any phylogeny must have at least 5 + 1 + 1 + 1 + 1 + 1 = 10 substitutions. As the phylogeny constructed in Figure 6 has exactly 10 substitutions, it must be minimal. It is not uniquely minimal.

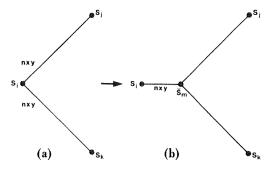
We now return to the general, large problems. Sometimes the site decomposition process produces subproblems which are small enough to be solved by a branch and bound algorithm. This branch and bound algorithm guarantees to produce all phylogenies of maximum parsimony on any data set with no more than 12 species in reasonable computing time. So it was used to calculate directly the phylogenies for the 11 species problems mentioned earlier.

	1	2	7	
$\overline{s_1}$	A	G	A	
S_2	C	A	A	
S_3^-	C	G	A	
S_4	\mathbf{A}	A	C	
S_{5}	C	G	C	

Table 3

There is no guarantee that the decomposition technique just described will converge to a phylogeny of maximum parsimony when applied to a large data set. However, it has been used interactively with a computer and has uncovered minimal solutions to all data sets to which it has been applied (up to 23 species).

The theory of evolution predicts that similar phylogenies should be obtained from different protein sequences. We have tested this specific prediction from the theory, rather than the general theory itself. Our results are consistent with the theory of evolution.



Firgure 4: The Coalescement Process

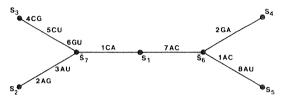


Figure 5: The Minimal Phylogeny

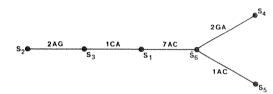


Figure 6: A Phylogeny for Sites: 1, 2 and 7

This idea of testing specific predictions from an hypothesis, rather than the hypothesis itself, is inherent in the writing of one of the leading scientific philosophers of the day, Karl Popper. It is more clearly expressed by Lakatos. 6

There may be exceptions when different protein sequences will lead to different trees as, for example, in the serial symbiosis theory. Also in the pre-cellular evolution a network with circuits may be a far better model than a tree. An interesting philosophical question would arise if the results of this work had falsified the prediction that the phylogenies would be similar. This would not necessarily disprove the theory of evolution as it may be that the strings simply changed so rapidly that they lost all information about their early history. It could be argued that because protein strings from different species can be aligned so readily that this, in itself, is independent evidence that the proteins retain evolutionary information.

This article has indicated a new application for various techniques of combinatorial optimization. Minimal spanning tree methods, matching, and branch and bound enumeration are useful in the construction of phylogenies. The next challenge is to sharpen the decomposition technique so as to be able to guarantee success with larger data sets.

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STUDIES ON GRAPHS AND DISCRETE PROGRAMMING edited by Pierre Hansen Annals of Discrete Mathematics, Vol. 11 North-Holland, Amsterdam, 1981

This volume contains 26 papers, which were presented partly at the Workshop on Applications of Graph Theory to Management, Brussels March 1979; partly at the Xth Mathematical Programming Symposium, Montréal, August 1979.

These X-rays of discrete optimization reveal a particularly healthy field. There is still room for innovation and for fresh approaches to traditional applications.

The book shows a good balance between theory and applications: 14 papers are theoretical (even though many of them are algorithmically oriented); 8 deal with specific applications, including network design, cutting-stock, location, school timetabling, fault detection, maintenance, traffic assignment and even sports scheduling, while the four remaining ones are computational.

Another distinctive feature of the book is its breadth: 8 papers deal with graphs, while the other ones cover many important areas of discrete optimization, ranging from submodular functions to totally dual integral systems, from the geometry of numbers to ordered semigroups (matroids are the only noticeable absence). As for current research trends, 8 papers deal with complexity aspects, 5 with polyhedral combinatorics, 2 with heuristics, 2 with threshold functions.

The basic ingredient of a proceedings volume is the quality of its individual papers. Here the quality is indeed excellent. This, perhaps, ultimately explains the large success the volume is having on the market.

- Bruno Simeone, University of Rome

The Theory of Games and Markets, VIII, 554 p Joachim Rosenmüller North-Holland, Amsterdam, 1981

Rosenmüller's book contains a careful and rigorous treatment of many parts of modern game theory. Omitted are multiple-stage games, the analysis of the role of information in games, and a treatment of games modelled as atomless measure spaces of players. All other parts of game theory are represented. As the title promises some room is given to the presentation of relations between games and markets.

Although cooperative game theory and characteristic function forms of games dominate the book, non-cooperative games and the normal and extensive forms are not neglected. On the contrary, a detailed analysis of dynamic game models is given, leading from game trees via dynamic games to differential games. Though differential games are not represented in the most general possible framework the use of differential manifolds, Hamilton-Jacobi-Systems, partial differential equations and measurable mappings requires a good mathematical background of the reader. The chapter on two-person-zero-sum and -non-zero-sum games reveals the connection between game theory and optimization theory. In this context I consider it useful that a presentation of the Lemke-Howson algorithm, which cannot be found in most treatments of game theory, is included. Also it is nice that a thorough treatment of those structures needed in the modelling of individual decision making precedes the proper game theoretical part of the book.

For some economists a more extensive economic motivation and interpretation would have perhaps been helpful. Yet, I recommend this book as a very good and useful one for students of mathematics as well as of economics. It provides enough material for several courses in game theory. I found it useful to partially base my lectures on games and decision theory at Bonn University on this book.

- W. Trockel, Bonn University

Algebraic Methods in Graph Theory Vol. I and Vol. II edited by L. Lovasz and Vera T. Sós North-Holland Amsterdam-Oxford-New York, 1981

The two volumes "Algebraic Methods in Graph Theory" are the proceedings of a conference of the same title organized by the Attila Jozsef University and the Janos Bolyai Mathematical Society in Szeged, Hungary, August 24-31, 1978. The conference intended to give an account of the state-of-the-art in the field. This is reflected in the 850 pages of these proceedings.

The title chosen for the conference only loosely ties together the many combinatorial disciplines that are the topics of the various papers. Since it is impossible here to treat the papers individually (there are 47 of them!), I will just attempt a general outline of the main themes.

There are two classical approaches to study graphs algebraically. One may try to study graphs through their automorphism groups and thus draw from the powerful methods of group theory. On the other hand, the representation of a graph by its adjacency matrix yields a spectral theory for graphs. Furthermore, the vertex-edge incidence matrix leads to the investigation of the matroidal properties of a graph. Stopping short before matroids, chain-groups provide a means to attack, for example factorization problems of graphs.

Thus the topics include more general combinatorial structures ranging from relational structures, hypergraphs and matroids over partial geometries and association schemes (of interest for the Shannon capacity of a graph) to two-graphs. In particular, the interplay between graphs and matroids receives much attention (arboresences, matchings, matroid union, decomposition, etc.) and a study of matroid constructions from the point of view of exterior algebra is presented.

Other investigations go in the opposite direction and ask for the realizability of given structures by certain graphs (this problem is completely solved for graphical regular representations of finite groups). Moreover, the methods of the theory of graphs and related combinatorial structures are applied to other fields, e.g., number theory and geometry.

In recent years, the algorithmic aspect of combinatorics has become increasingly important. Several papers deal with the problem to efficiently construct a combinatorial object and/or to efficiently verify a certain property (graphicness of matroids, listing the circuits of planar graphs, the general matroid matching problem).

Of course, in the more than four years since the conference, much progress has been achieved and many of the results in the papers of the proceedings have been complemented and extended (to give just one example: Seymour's decomposition of regular matroids). Some of the papers mention pertinent recent developments "added in proof." Nevertheless, the two volumes will be of interest to every researcher in the field of graph theory and related areas since they provide survey articles as well as special research results covering a wide range of theory and applications and still open problems. If this review whets the appetite of the reader to take a close look at these proceedings, it has fulfilled its purpose.

Last but not least, the reader should not be too disappointed if he cannot learn about "the minimization of truth" as promised in the table of contents. The volumes offer other rewards.

- Ulrich Faigle, University of Bonn

The ILLIAC IV by R. Michael Hord Springer Verlag Berlin-Heidelberg-New York, 1982

Dr. Slotnik's conception of the first "supercomputer" was originated in the mid-sixties. The ILLIAC IV was put into operation 1975. In the shortlived world of computers this belongs to history today. However, the present trend to more parallelism in hardware and software structures creates new interest in this unique computer. The book is a

comprehensive report of the investigation and implementation activities presenting a lot of detailed information, analysing hardware and software problems and explaining success and failures. Computer experts of many special fields may derive great benefit from it for design and development of hardware, operation systems, programming environment, user's software, etc., for unconventional multiprocessor structures. More than half of the book is dedicated to application problems which have a demand for high processing power, as for example, in the field of hydrodynamics, picture processing, seismology, and astronomy. This selection of application fields, however, is hardly representative for potential users of large future parallel computers.

- G. Fritsch, Erlangen-Nürnberg

Modern Applied Mathematics - Optimization and Operations Research edited by Bernhard Korte North-Holland, Amsterdam - New York, 1982

"Optimization and Operations Research" was the title of a summer school organized by the Institute of Operations Research of the University of Bonn, and the 17 State-of-the-Art articles of this volume are basically the written versions of the lectures. The volume is divided into seven parts dealing with the following topics: Foundations, Convex Analysis, Polyhedral Theory, Complexity, Nonlinear Programming, Control and Approximation Theory and Numerical Analysis, Combinatorial Optimization, Game Theory, Statistics, and Economics.

All articles are of high quality - some are excellent from the didactical point of view. However most of the monographic articles address readers who have at least a basic knowledge of the area. This book is definitely a welcome contribution to the literature on "applicable" mathematics and should be of utmost interest and use to everybody who is working in fields like mathematical economics or operations research, and who is willing to discuss and apply modern mathematical methods. Moreover the book is ideally suited to serve as background text for teaching or the basic reference for a seminar on modern applied mathematics.

- U.Derigs, University of Bonn

JOURNALS & STUDIES

Volume 27, No.1

- D. Goldfarb and A. Idnani, "A Numerically Stable Dual Method for Solving Strictly Convex Quadratic Programs."
- M. L. Overton, "A Quadratically Convergent Method for Minimizing a Sum of Euclidean Norms,"
- R.D. Armstrong and P.O. Beck, "The Best Parameter Subset Using the Chebychev Curve Fitting Criterion."
- D. F. Karney, "A Duality Theorem for Semi-Infinite Convex Programs and Their Subprograms."
- J. G. Ecker and M. Kupferschmid, "An Ellipsoid Algorithm for Nonlinear Programming,"
- D. P. Bertsekas, "Distributed Asynchronous Computation of Fixed Points."

Volume 27, No. 2

- Ge Ren-pu and M. J. D. Powell, "The Convergence of Variable Metric Matrices in Unconstrained Optimization."
- R. G. Jeroslow, "Uniform Duality in Semi-Infinite Convex Optimization."
- A. Buckley and A. LeNir, "QN-Like Variable Storage Conjugate Gradients."
- T. Steihaug, "Local and Superlinear Convergence for Truncated Iterated Projection Methods."
- R. W. Cottle and R. E. Stone, "On the Uniqueness of Solutions to Linear Complementarity Problems."
 - J. B. Orlin, "Maximum-Throughput Dynamic Network Flows."

(Journal contents are subject to change by publisher)

CONFERENCE NOTES

NATO Advanced Study Institute on Computational Mathematical Programming July 23 to August 2, 1984 Bad Windsheim, Germany F.R.

The Committee on Algorithms (COAL) of the Mathematical Programming Society announces a summer school on Computational Mathematical Programming to be held in Bad Windsheim, West Germany, from July 23 to August 2, 1984, under the sponsorship of NATO (Advanced Study Institute). The ASI consists of tutorials with the emphasis on new mathematical programming algorithms, software products, computational experiments, numerical test results, and practical optimization models. The following topics will be treated: large linear systems; integer programming; model building in linear and integer programming; networks; nonlinear programming; model building and computational aspects in nonlinear programming: large scale nonlinear programming; geometric programming; nondifferentiable optimization; global optimization; generation of test problems, experimental design and comparative performance evaluation; optimal control; stochastic optimization; parallel computing. Some time will be reserved for participants of the ASI to lecture about their own research activities. A limited fund is available for participants from NATO-countries to cover a part of the travelling and accommodation costs. Participation is possible only by invitation. For more information and an application form, write to Klaus Schittkowski, Institut für Informatik, Universität Stuttgart, Azenbergstr. 12, D-7000 Stuttgart I, Germany F,R,

The Fourth Mathematical Programming Symposium, Japan

This annual symposium will be held on November 14-15, 1983 at the International Conference Center Kobe, Kobe, Japan. The symposium will consist of the following three sessions:

1. Mathematical programming, general. Chairman: M. Kojima. 2. Markov Decision Process. Chairman: K. Sawaki. 3. Applications. Chairman: T. Morikiyo.

The first two sessions will consist of three or four talks of expository nature and those presenting original development. No contributed paper will be called for, and only invited papers will be presented.

Participation from abroad will be welcomed. The conference language is Japanese but non-Japanese participants may use English.

For further information contact Organizing Chairman, Professor Masao Iri, Faculty of Engineering, University of Tokyo, Bunkyo-ku, Tokyo 113, Japan, or Program Chairman, Professor R. Manabe, Kobe University of Commerce, Tarumi, Kobe 655, Japan.

-R. Manabe

CALLIMAUFRY

Herbert E. Scarf (Yale) has been awarded the John von Neumann Theory Prize by ORSA/TIMS. The award cited Professor Scarf's contributions in the computation of fixed points, in (s,S) policies in inventory theory, in balanced games, and in general equilibrium theory in economics. . . .Haverly Systems, Inc. of Denville, N.J. has received an award for "excellence in exporting" from U.S. President Reagan. The company's major software products include linear programming systems and other packages designed to solve optimization problems in a variety of applications. . . .Ubaldo Garcia Palomares (Univ. Simon Bolivar) is visiting Argonne National Laboratory from June 15 to December 15, 1983. . . A workshop on "Algorithms and Software for Nonlinear Optimization" will be held Sept. 21-23, 1983 in Cetraro, Italy. Contact Mrs. Chiara Zanini, Via Bernini, n.5, 87036 Quattromiglia di Rende (Cosenza) Italy, Tel. (0984), 839711-839738. . . . New MPS dues for 1984 have been announced: 32 US dollars, 20 UK pounds, 68 Swiss francs, 250 French francs, 84 German marks, or 94 Dutch guilders.

The Discrete Applied Mathematics journal is preparing a special issue on network algorithms and applications. Please submit papers (deadline was August 15, 1983), to Professor Darwin Klingman, David Burton Jr. Centennial Chair in Business Decision Analysis, Department of General Business, GSB 4.138, University of Texas, Austin, Texas 78712. All contributions will be thoroughly referred.

Deadline for the next OPTIMA is December 1, 1983.

This public document was promulgated at a cost of \$426.15 or \$0.61 per copy to inform researchers in mathematical programming of recent research results.

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CALENDAR

Maintained by the Mathematical Programming Society (MPS)

This Calendar lists noncommercial meetings specializing in mathematical programming or one of its subfields in the general area of optimization and applications, whether or not the Society is involved. (The meetings are not necessarily 'open'.) Any one knowing of a meeting that should be listed here is urged to inform Dr. Philip Wolfe, IBM Research 33-221, POB 218, Yorktown Heights, NY 10598, U.S.A; Telephone 914-945-1642, Telex 137456.

Some of these meetings are sponsored by the Society as part of its world-wide support of activity in mathematical programming. Under certain guidelines the Society can offer publicity, mailing lists and labels, and the loan of money to the organizers of a qualified meeting.

Substantial portions of meetings of other societies such as SIAM, TIMS, and the many national OR societies are devoted to mathematical programming, and their schedules should be consulted.

1983

September 21-23: International Workshop on Algorithms and software for nonlinear optimization, Cetraro (Cosenza), Italy. Contact: Mrs. Chiara Zanini, CRAI, Via Bernini No. 5, 87036 Quattromiglia di Rende (Cosenza), Italy. Telephone (0984) 938711.

1984

- June 12-14: SIAM Conference on Numerical Optimization, Boulder, Colorado, U.S.A. Contact: Hugh B. Hair, SIAM Services Manager, 1405 Architects Building, 117 South 17 Street, Philadelphia, Pennsylvania 19103, U.S.A. Telephone 215-564-2929.
- July 23 August 2: NATO Advanced Study Institute on Computational Mathematical Programming, Bad Windsheim, Federal Republic of Germany. Contact: Dr. Klaus Schittkowski, Institut für Informatik, Azenbergerst. 12, 7000 Stuttgart 1, Federal Republic of Germany. Telephone 0711 2078 335. Sponsored by the Society through the Committee on Algorithms.

1985

August 5-9: Twelfth International Symposium on Mathematical Programming in Cambridge, Massachusetts, U.S.A. Contact: Professor Jeremy Shapiro, Sloan School of Management, Massachusetts Institute of Technology, Cambridge, MA 02139, U.S.A. Telephone 617-253-7165. Official triennial meeting of the MPS.