



# Canadian Artificial Intelligence

## Intelligence Artificielle au Canada

Autumn 1994

No. 35

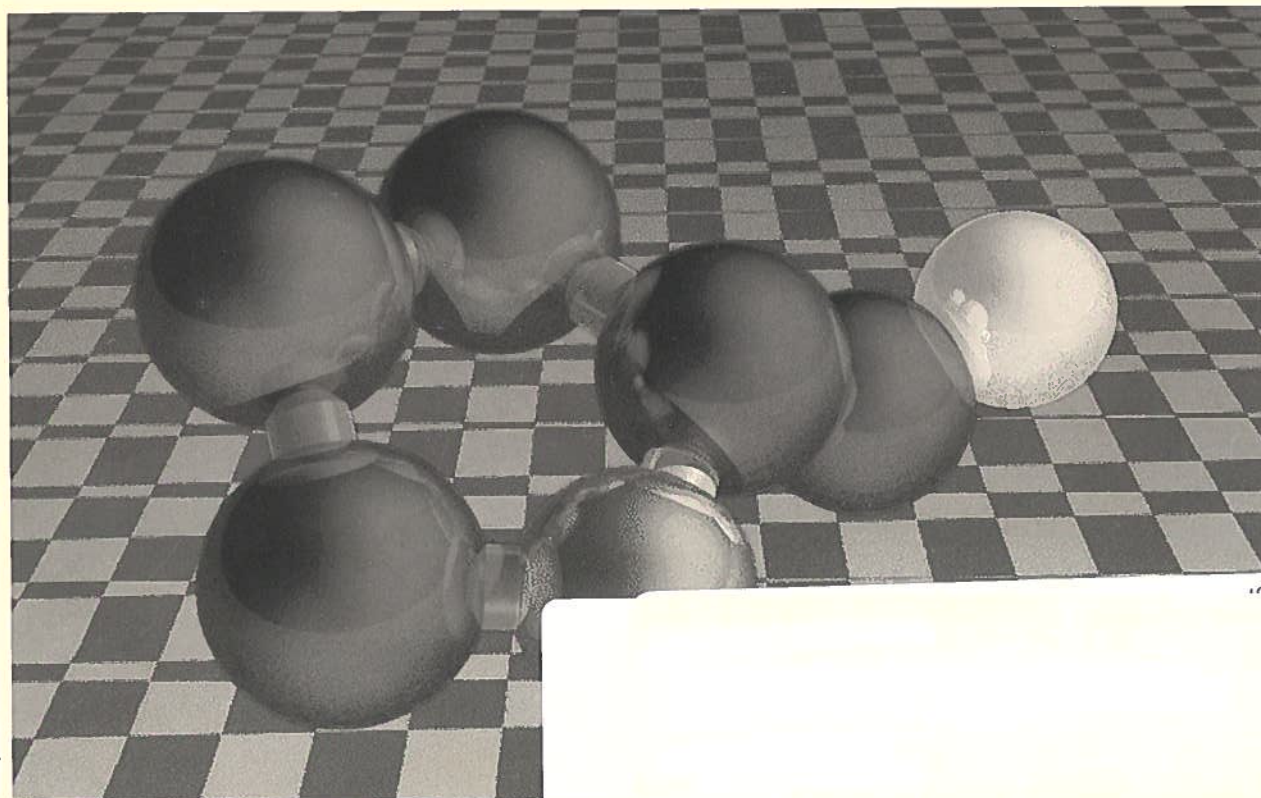
automne 1994

An official publication of CSCSI, the Canadian Society for Computational Studies of Intelligence  
Une publication officielle de la SCEIO, la Société canadienne pour l'étude de l'intelligence par ordinateur

**Special Issue: AI and Molecular Biology in Canada**  
**Edition spéciale: Intelligence artificielle et Biologie moléculaire au Canada**

**NSERC Funding Controversy**  
**NSERC: Controverse sur la politique de financement**

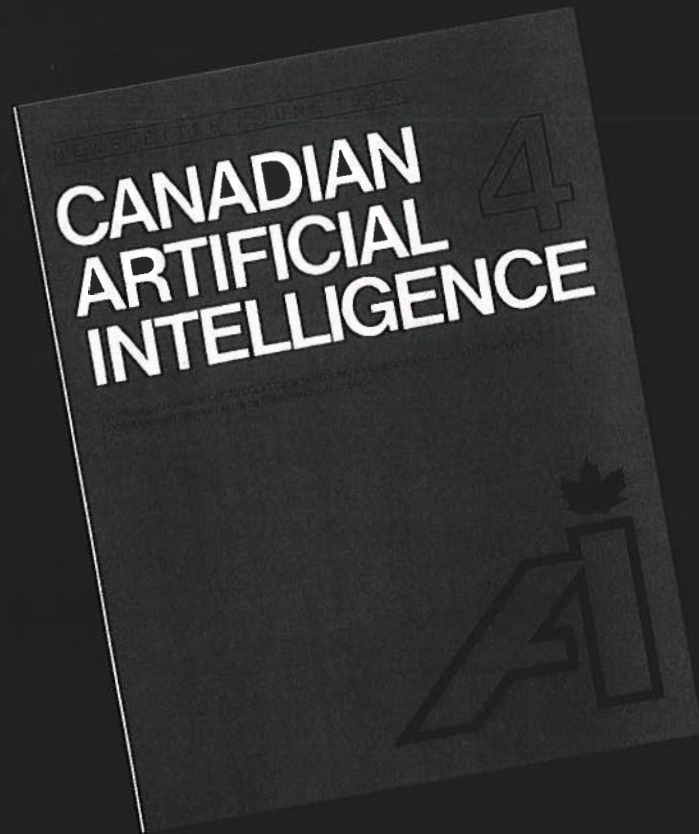
**Tribute to Alan Mackworth, Recipient of 1994 CSCSI Distinguished Service Award**  
**Hommage à Alan Mackworth, récipient du prix de Service Distingué CSCSI 1994**



Computer Generated Model Courtesy Chris Walmsley and Darrell Conklin.

The graphic depicts a Proline amino acid.

# Retrospective



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# Canadian Artificial Intelligence

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## Canada's National AI magazine.

### Editors · Editeurs

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### Production Team · Equipe de production

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Jean-Claude Gavrel

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Graeme Hirst

### Translation · Traduction

Michel Addison, Chantal Désmoreux-Preston

### Advertising · Publicité

Arlene Merling

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## CSCSI Executive

### President · Président:

Stan Matwin, Computer Science Dept., University of Ottawa, Ottawa, ON K1N 6N5; stan@csi.uottawa.ca

### Past-President · Président Précédent:

Janice Glasgow, Dept. of Computing & Information Science, Queen's U., Kingston, ON K7L 3N6; janice@qucis.queensu.ca

### Vice-President · Vice-Président:

Allan Jepson, Department of Computer Science, University of Toronto, Toronto ON M5S 1A4; jepson@vis.utoronto.ca

### Secretary · Secrétaire:

Fred Popowich, School of Computing Science, Simon Fraser University, Burnaby BC V5A 1S6; popowich@cs.sfu.ca

### Treasurer · Trésorier:

Peter van Beek, Dept. of Computing Science, U of A, Edmonton, AB T6G 2H1; vanbeek@cs.ualberta.ca

### Editors · Editeurs:

Peter Turney, Knowledge Systems Laboratory, NRC, Ottawa, ON K1A 0R6; peter@ai.iit.nrc.ca

Sue Abu-Hakima, Knowledge Systems Laboratory, NRC, Ottawa, ON K1A 0R6; sue@ai.iit.nrc.ca

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Alan Mackworth: Travail avec des contraintes  
*Robert J. Woodham*

*Canadian Artificial Intelligence* welcomes submissions on any matter related to artificial intelligence. Please send your contribution, electronic preferred, with an abstract, a photograph and a short bio to:

Dr. Peter Turney  
Co-Editor, Canadian Artificial Intelligence Magazine  
Knowledge Systems Laboratory, Institute for Information Technology  
National Research Council Canada  
M-50 Montreal Road  
Ottawa, Ontario, Canada  
K1A 0R6 or — peter@ai.iit.nrc.ca

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Arlene Merling  
Managing Editor, Canadian Artificial Intelligence Magazine  
Alberta Research Council  
3rd Floor, 6815 - 8 Street N.E.  
Calgary, Alberta, Canada  
T2E 7H7  
Telephone (403) 297-2608 or — merling@arc.ab.ca

Book reviews and candidate books to review should be sent to:

Graeme Hirst  
Canadian Artificial Intelligence  
Department of Computer Science  
University of Toronto  
Toronto, Ontario, Canada  
M5S 1A4 or — gh@ai.toronto.edu



## New Directions for *Canadian Artificial Intelligence Magazine*

*Peter Turney & Suhayya Abu-Hakima*

Hello Readers!

This is our first issue as the new co-editors of *Canadian Artificial Intelligence* magazine. Roy Masrani was the editor from issue # 18 in 1989 to issue # 34 in 1994. During that time, he has set a standard for quality that will be a challenge to maintain. Thanks, Roy, for your contribution both to *Canadian Artificial Intelligence* and to AI work in Canada!

This issue of *Canadian Artificial Intelligence* is a special issue on AI and Molecular Biology in Canada. Molecular Biology is an excellent application for AI technology. For example, the Human Genome Project is expected to cost a total of three billion US dollars. Experts predict that the laboratories involved will need to spend 30% of their total budgets on informatics. This shows the difficulty of managing this volume of data and making it useful to biologists. AI technology certainly has a role to play here. Also in this issue we feature a discussion of the NSERC funding controversy and a tribute to Alan Mackworth, the recipient of the Second CSCSI Distinguished Service Award.

In the next issue of *Canadian Artificial Intelligence* there will be an article on the World Wide Web. The Web is a hypermedia document that spans the Internet. Among other things, the Web is a valuable resource for AI researchers. For those of you who are familiar with the Web, *Canadian Artificial Intelligence* magazine can be reached at "[http://ai.iit.nrc.ca/cscsi\\_point.html](http://ai.iit.nrc.ca/cscsi_point.html)". We plan to make much of the content of *Canadian Artificial Intelligence* magazine available through the Web. Our model is *Wired Magazine*, "<http://wired.com/>," an award-winning magazine that is available both on the newsstands and through the Web. In the next issue, we will also have another Canadian AI Success Story to report.

In future issues, we plan to have a "Student Corner" for regular reports from AI students. This is an opportunity for students to tell the world about their Ph.D. or Masters research. If you are a student and you want to contribute, please let us know. If you are a professor and you are supervising students, please ask them to contribute. A report




*Peter Turney*



*Suhayya Abu-Hakima*

might take the form of a summary of the work or a statement of a controversial claim with some discussion. Submissions by e-mail (to [suhayya@ai.iit.nrc.ca](mailto:suhayya@ai.iit.nrc.ca)) are most welcome.

We hope to maintain an even balance of academic and industrial articles. We will continue the series of Canadian AI Success Stories. For objectivity, we would like these success stories to be written by a person who was not directly involved in the successful project. If you would like to write a success story, let us know; we have a list of candidate stories for future articles. If you have a success story, let us know, so we can add it to the list. Closet reporters, take note: this is a great opportunity to discover first-hand what it takes to be successful in Canadian AI.

Most of our subscribers are Canadian. We hope to expand our audience (and our subscription base) by taking an international perspective on AI. We will invite international authors to contribute reports on AI research in their countries. However, our emphasis will still be on Canadian AI. Our mandate remains as it has been since issue #1, to report on all aspects of AI in Canada, or of special interest in Canada, and to provide a forum for reporting Canadian AI to the world. 

# A Message from the President

Hi!

As many of you may already know, I have been elected the President of our Society at its last meeting in Banff this May. I've agreed to serve because I think that the Society is a worthwhile organization for those of us who do AI, in all its forms and venues, in Canada and elsewhere. My decision was motivated by the feeling of debt to all those that have generously given their time to the Society for the last 18 years. I felt that we all, including me, have to repay this debt to Alan Mackworth, Nick Cercone, Gord McCalla, Dick Peacocke, Ian Witten, and Janice Glasgow.

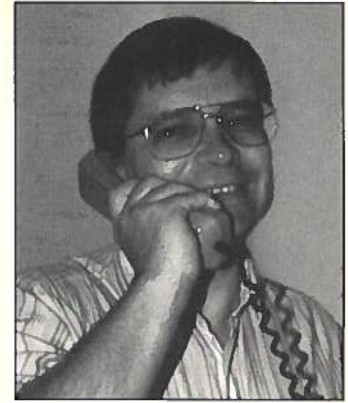
I would like to take a few minutes of your time to let you know about the plans I have as the incoming President. I would also like to view this letter as an invitation to discuss the mission, the goals, and the strategies of the Society. I hope you will not mind me repeating the media cliché that for once, I believe, correctly describes our times as an era of change that permeates all aspects of our lives, from the technological advances to national and global economics and politics. We have to work together to confront all these changes, to understand them, and to learn how to adapt the Society to this changing world. Neither I, nor the executive, pretend to have all the answers, and we hope that all of you will join us in a discussion proposing specific tasks and their solutions that CSCSI can undertake.

Hopefully, at the end of my two-year term we will be able together to verify how much of this plan has actually been achieved, and analyze where and why we may have erred. Here are some of the areas which are in my mind important for the Society and on which I would like to focus initially:

1. The membership. We have to maintain and strengthen our membership. I think that one mechanism that would help us achieve this is to rely on a network of volunteers who would actively solicit new and renewed membership from their colleagues. Who would like to become a member of such a network?

2. Student members. Perhaps we should intensify our efforts to attract student members. What would make the Society more attractive for them? Should we investigate student fees even lower than the ones that are in place?


*Stan Matwin*



3. A related issue of dues. As many of you know, this is associated with our relationship with CIPS, which has not always been the easiest. I hope to put in place a system that will enable the Executive to monitor CIPS's timeliness in approaching members for renewal of dues. If all dues were collected on time, the Society would be in a much better financial shape than it finds itself in.

4. I would like to work with the Executive towards moving the Society into the electronic age. As the first, modest step, thanks to Peter Turney and Sue Abu-Hakima, CSCSI has now its own page on the World Wide Web (you can find us at [http://ai.iit.nrc.ca/cscsi\\_point.html](http://ai.iit.nrc.ca/cscsi_point.html)). The page includes the statement of mission of the Society, as well as the membership form. More on this in the letter from the magazine editors in this issue.

5. CSCSI participates in IJCAI '95. We are being consulted on all aspects of the Canadian presence in IJCAI '95 in Montreal, including invited speakers, tutorials, funding, etc. We stand to share the financial effects of the conference; we hope it will be a net gain for the Society, but whether it will indeed happen depends on how attractive the conference is in order to draw attendees in large numbers. What other ways could we suggest to give IJCAI '95 a distinct and attractive Canadian flavour?

These are some of the thoughts and tasks on which I will work hand in hand with the Executive: Allan Jepson (Vice-President), Fred Popowich (Secretary), Peter van Beek (Treasurer), Peter Turney and Sue Abu-Hakima (Editors of the magazine). Let me take this opportunity to thank them for agreeing to work together for the next two years. Let me also thank my colleagues who have served on the previous Executive: Janice Glasgow, Roy Masrani, Peter Patel-Schneider, and Eric Neufeld. Let us hope that we will be able to meet the high standards and expectations that they have set during their term. 



## NSERC Controversy

### Introduction

*Tout récemment, il y a eu une controverse sur la politique de financement au Conseil de Recherche en Sciences naturelles et Ingénierie (NSERC). La publication Canadian Artificial Intelligence ne désire pas participer dans cette controverse, mais pense que nos lecteurs aimeraient être informés à ce sujet. Pour minimiser le parti pris de notre reportage, nous indiquons ci-dessous les citations directes des personnes impliquées politiquement à NSERC, des chercheurs affectés par cette politique, et de quelques observateurs intéressés. Les commentaires de l'Éditeur sont en italiques. Tous autres commentaires sont de citations directes.*

### Petition

*The following petition has been circulating through the academic community in Canada. At each university, it was sponsored by a different group of professors. The version below came from the University of Alberta, where it was sponsored by Vince Di Lollo (Department of Psychology), Ole Hindsgaul (Department of Chemistry), and Ernie Kanasewich (Department of Physics).*

In the week of February 14-18, Dr. Morand, president of NSERC, met with several grant selection committees in Ottawa. In his meeting with GSC 33 (Molecular and Developmental Genetics), Dr. Morand described his vision for the future of NSERC. This vision involved an end to the individual Research Grants Program and its replacement with a program of highly-funded — but few — group grants. Upon the Committee's request to repeat that statement, Dr. Morand did so, and provided a time-frame of about 10 years. When GSC 33 made this widely known to other committees, Dr. Morand issued a denial, claiming to have been quoted out of context. However, several other committees received much the same message. For example, in his meeting with GSC 12 (Psychology) Dr. Morand noted that the days of support for "personalized, curiosity-driven" research are drawing to a close.

Dr. Morand's remarks may be regarded as impetuous and injudicious, but cannot be dismissed lightly; in fact, the phasing out of the Research Grants Program is already under way. In 1986, the Research Grants Program received 49.1% of total NSERC expenditures; in 1993, it received only 39.7%. Had funding been maintained at the 1986 levels, an additional \$47 million would have been available last year. A further decline occurred this year in order to fund the Collaborative Project Grants Program and other expenses. The trend is clear — there is a consistent decline in the

### Introduction

*Recently there has been some controversy about the funding policy of the Natural Sciences and Engineering Research Council. Canadian Artificial Intelligence magazine does not wish to take sides in this controversy, but we believe that our readers would like to be informed about the issues involved. To minimize the bias of our reporting, we print below direct quotations from some of the people involved in determining NSERC policy, from some of the researchers affected by this policy, and from some interested observers. Editorial comments are in italics. Anything not in italics is a direct quotation.*

proportion of NSERC's budget that is allocated to the Research Grants Program. Dr. Morand claims that this proportional decline must be attributed to the influx of funds to support new programs such as the University-Industry program. The validity of this assertion is based on the premise that there is only one way to increase the overall budget of NSERC, by introducing new, preferably industry-related programs and initiatives. We disagree: that decline might well have been reversed had an enlightened leadership made a case for the importance of basic research for the Nation's industrial, economic and social health.

We, the constituency of Canadian researchers, have made countless representations to Dr. Morand and, through him, to Council to little or no avail. Our warnings have gone unheeded and the replies to our arguments have been little more than blandishments and homilies. It is time to let our politicians know of the damage being done to the National research base. To this end, we must convey to members of Parliament our lack of confidence in the policies enacted by Dr. Morand and by Council, a governing body appointed largely by the previous government during Dr. Morand's period of tenure.

Here are other areas of concern that are being ignored by the present Council to the severe detriment of Canadian science and engineering:

1. The individual Research Grants Program must be regarded as the world's most enlightened scheme for funding university-based research. It is admired around the world both for its flexibility and, more importantly, for its productivity. It is also a distinctively Canadian scheme that, with its explicit support of the individual researcher, has permitted Canadian scientists and engineers to match and

even surpass the productivity of more highly-funded foreign colleagues. We voice our extreme concern at the progressive erosion of this model in favour of the more rigid and restrictive project-oriented model.

We favour change when it is warranted. We favour the evolution of existing programs and the introduction of new ones in response to — and in anticipation of — a rapidly changing world. But these programs and initiatives should not be implemented to the detriment of one of the world's most successful research-funding schemes. We reject the changes made recently at NSERC as retrogressive and harmful.

2. The Research Grants Program ensures a broad base for scientific and engineering research in Canada. This fosters a diversity of creative thought that will be drastically diminished if support continues to be shifted to a small number of collaborative projects run by a handful of senior researchers. We strongly favour a highly selective and competitive funding scheme that fosters excellence and eliminates mediocrity. We believe that the Research Grants Program does this while still providing a broad base of funding to permit the development of future scientists. For these reasons, we oppose the initiative to channel most of the funds into a few, select research programs. Such a policy is resulting in the elimination of very capable researchers. More importantly, it is removing the broad base of support that is necessary for producing scientists and engineers of international stature.

3. Perhaps the most damaging consequences of the erosion of individual research grants is being felt in the national supply of highly-skilled personnel. Graduate and advanced undergraduate student training is one of the major accomplishments of the laboratories supported by individual NSERC grants. Shifting patterns of support have necessitated the closing of some productive laboratories. Many more will close as Dr. Morand's and Council's policies are implemented. The inevitable result is a drastic reduction in the number of students that can be trained in a diminishing number of laboratories — no matter how richly funded. The devastating repercussions in the national supply of highly-trained personnel need hardly be stressed.

4. We strongly believe that successful research is often collaborative. Further, we believe that students are best trained in a collaborative environment. And we practice what we believe: research-grant applications and the vast majority of publications by NSERC research-grant holders indicate extensive collaboration. What is important about this collaboration is that it is spontaneous and driven by specific — and often unpredictable — needs as they arise in the course of research. By contrast, the Collaborative Project program (introduced despite the overwhelming and explicit opposition voiced by the research community) makes

collaboration a prerequisite for access to funds. As a consequence, collaboration is contrived, and it becomes a bureaucratic rather than a scientific goal. The best way to promote truly collaborative efforts is to support individual scientists.

In this respect, it must be noted that another major federal agency, the Medical Research Council of Canada, has recognized the drawbacks and limitations of just the type of project-oriented funding that NSERC is introducing. In its place, MRC is considering shifting support to individual researchers. Wisely, MRC is making provision — in the form of infrastructure funds — to aid the spontaneous coalescence of individually-funded researchers as collaborative needs arise.

5. A strong NSERC tradition has been its open interaction with the research community in the development of granting policies. But there is strong evidence that consultation with the constituency of researchers — as represented in the membership of the grant-selection committees — has played a diminishing role in the past several years. We are frustrated by our diminishing role in the decision-making process and believe that key decisions reached by Dr. Morand and Council have potentially devastating consequence for Canadian science and engineering.

We must express our frustration and grave concerns to our elected representatives and to the cabinet ministers responsible for the health of the Canadian research enterprise. Many amongst us — and the students in our diminishing laboratories — have already felt the impact of such decisions. We must act before more damage is done to the national research base. Write to your member of parliament, quoting from this message and adding your own concerns. Send a copy to the Minister of Industry and to the Secretary of State for Science, Research and Development.

### **NSERC's Reply**

*On March 21, 1994, Peter Morand, President of NSERC, sent the following memorandum to university presidents across Canada.*

The purpose of this note is to correct some misinformation that has been circulating about NSERC programs.

Contrary to rumour, Council has not decided to terminate its Research Grants program, nor has Council ever discussed this possibility. Individual Research Grants are one of the most important means by which NSERC supports the broad spectrum of university research from basic science to engineering design. Council also fully recognizes that basic research is a key component of university research.

The budget for the Research Grants program stands at \$200M this year compared to \$129M ten years ago, and the number of grantees served by the program has grown almost every year over this period. Until the most recent competition, the growth in the community was accommodated by adding funds to the program's budget.

While Council's overall funding level has not changed for the last two years, the university research community has continued to increase in size. This makes the allocation process a challenging one, both within and among programs. Council must adjust program allocations, taking into account the diversity of approaches within the research community and the need to maintain an appropriate balance.

Council recognizes and values the co-operative and interdependent relationship that exists between NSERC and the scientific and engineering community. The challenge of change is best faced in a spirit of consensus and trust. Our common objective must be to strengthen university research and to secure a greater appreciation of its contribution to the quality of life and prosperity of all Canadians.

Please feel free to distribute this letter within your institution as you see appropriate.

### **Impact on Canadian AI Research**

Canadian Artificial Intelligence magazine approached several well-known Canadian AI Researchers, asking for an opinion on how the changes to NSERC will affect AI research in Canada. John Mylopoulos of the University of Toronto was one of the researchers who replied. John won the CSCSI/SCEIO's 1992 Outstanding Service Award for service to the Canadian AI community.

I'm all for change within NSERC for two reasons. Firstly, because computer science (and AI) are not getting their fair share of the NSERC budget compared to other, more established disciplines such as the physical sciences. Secondly, because until recently, there was little opportunity to conduct, in Canada, research projects that involved several researchers and were run on the basis of several full-time research associates and programmers.

NSERC's operating grants programme is indeed excellent and should continue to exist. But it needs to be complemented with other programmes that are directed towards areas that are technologically strategic and focus on applied research and technology transfer to industry.

AI (and computer science) is already benefitting from such programmes, with the renewal of the IRIS network (funded in part by the Federal Networks of Excellence programme), with several recent industrial chairs, funded in part by NSERC, with industrial R&D projects managed by PRECARN and funded in part by federal R&D programmes and other provincial research programmes that would not have been there if we kept a one-programme (i.e., operating grants), one-source (i.e., federal government) mentality.

*Stan Matwin of the University of Ottawa is the current President of CSCSI/SCEIO. His opinion of the changes to NSERC follows.*

This is a difficult issue: on the one hand, the research grant programme serves well the broad-based community, and, as they say, "If it ain't broken, don't fix it." On the other hand, I agree with the opinions about the need to fund

collaborative efforts of strategic importance to Canada. Some degree of change of NSERC funding is inevitable. I think that our community should unite and focus on a single objective of convincing NSERC about further re-allocation of funds, from traditional, extremely well-funded areas such as physics and chemistry, to more modern disciplines and strategically important fields, such as computer science. This was also mentioned in the opinion of Professor John Mylopoulos above. Within our own field, I would defend the research grant programme, with one important modification. Quite clearly, one of the main mandates and benefits of NSERC research funding to Canadian society is its support of training of research personnel. I would suggest a very thorough review of grants in which the bulk of funds is NOT directed towards support of graduate students. Research grant applications from departments which do not have a graduate programme should be approved only if the research they produce is of exceptional quality.

*Randy Goebel of the University of Regina is well known in the Canadian AI community.*

Recent meetings between NSERC and University representatives make it clear that the funding profile of NSERC is changing: individual research grants will be reduced over the next few years, and collaborative and industrially-relevant funding will increase. It is also clear, from recent review and renewal of technology projects like Ontario's ITRC and the federal NCE, that there is increasing political and economic pressure to meet the development and market demands of the Canadian industrial community.

Is that all that can be said without slipping into an advocacy position for one side or another? Let's consider a few ways in which we can disentangle some of the more common advocacy positions:

Position A (Irate academic): The caricature is of an academic researcher who perceives the changing NSERC funding profile as a direct attack on individual curiosity-driven basic research.

This is a familiar lament, from which many issues can be unraveled. For example, this position rarely acknowledges that neither "basic" nor "curiosity-driven" entails "individual." Perhaps one message in the funding changes is that not every academic is worth investing in as an individual curiosity-driven basic researcher? By itself, it is naive to imagine that the planned changes would destroy our basic research capabilities; the history of scientific achievement is rife with successful collaborative efforts for which "basic" and "curiosity-driven" are aptly attributed.

Position A can often be perceived as a shallow suggestion to pour more dollars into individual programs, with no analysis of why. This is not typically the case, for Position A is often articulate regarding the direction suggested by funding changes, and vocal about "fixing" something that, by external evidence, is not broken. It is, after all, popular opinion that our foreign (especially American) colleagues



view our NSERC individual research grants program with admiration.

However, the recent discussions haven't produced much in the way of alternatives which could withstand the perceived deterioration and still respond to a changing world. While a collection of players does not a team make, perhaps we should be reminded of the often blind subscription to the sanctity of the individual.

Position B (Irate industrialist): This caricature is of an industrial technology manager driven by the quarter-to-quarter bottom line of a company, who perceives a market but not the products to fill it. An increased political will to encourage the development portion of "R&D" is gleefully received, for who wouldn't be pleased that more of those "curiosity-driven" academics will be publicly funded for a "reality check," with the prospect of perhaps accidentally accelerating products to market?

It is common to ignore this position by appealing to the "lack of foresight" argument, and point out that only with long range research and development plans can one create sustainability. However, it seems that Canadian industry is not a leader in this regard, and so it is natural for a politically aware government to take measures to address the problem.

So we find ourselves embroiled in a controversy over NSERC funding policies, which support academics, but are driven by economically-motivated political factors. The real and ultimate problem is whether NSERC's approach is appropriate for the world we find ourselves in. In this regard, what seems to be required is more discussion about what the real impact will be, without trotting out the old clichés. Is it possible to sustain an adequate foundation of basic research without insisting that it be dominated by individuals? Can we steer NSERC programs toward filling the gap between laboratory "proof of concept," and product prototype? Are there valuable lessons from ITRC and NCE which can help promote real collaboration that is more than a sum of its parts? Is there a Canadian industrial identity that can sustain a serious program of co-operative research and development? I don't know the answer, but I'm learning Japanese just in case.

*Nick Cercone of the University of Regina was profiled in issue #32 of Canadian Artificial Intelligence magazine.*

[The relationship between products, production, consumption, materials, energy, organizations, infrastructure, etc. is in delicate balance today; small changes in any one entity in isolation may dictate major changes in the rest. Our present period of socio-economic change is now firmly meshed in the social and economic fabric of our society and such change embodies conflict. Inventions such as the wheel, the internal combustion engine, and the transistor transformed economic and social relations of their times. In our time, it would appear that the old hierarchical organization by which industry was well-known is gone and North American companies are evolving as a loosely knit set of smaller

organizations which each focus on its core competency.] A liberal paraphrase of an email message of R. Lipsey, CIAR Fellow and Professor, SFU.

In contradistinction, the university, it appears, and government agencies as well, may be the last organizations to react to such global changes. Organization charts are still hierarchical and despite the more recent avocation toward interdisciplinary and multidisciplinary efforts, these efforts do not find themselves reflected well in the hierarchies. Rather than resisting change, and in addition to seeking to understand such inevitable change, we should promote policies which make the transition to the New worlds as humane as possible. Simultaneously, we must also be realistic.

Much of the private sector in developed countries has undergone major change; companies simply had no choice. New technologies, global competition, and new production methods have launched the virtual company and dissolved the status-quo. For universities, this task still lies largely ahead and recent government deficit-induced budget cuts may serve as catalyst for change. Just as corporations today bear little semblance to corporations of two decades ago, the university of tomorrow will bear little relation to today's university — in part because technology will force it and government has started the process with budget constraints.

NSERC has evolved a system of funding research to which we researchers have grown accustomed and we welcome. NSERC has been creative to find ways to fund research and has tried to be innovative when responding to political pressure for nearly 20 years. Peer review has always been the cornerstone of each and every funding program. Perhaps, then, our choices are not as obvious, certainly not so easily articulated as merely labeling this section the NSERC controversy; the choice between individual curiosity-driven research and applications oriented (applied, sponsored, industrial) research. Perhaps the choice is quite a different one: what research can we afford, what is the appropriate balance between curiosity-driven and applications-oriented — is there really a difference and, if so, is there a difference between individual and collaborative, etc. The distinction between basic and applied research has always seemed to me a vacuous distinction. Good research is good research, whether individual, collaborative, applications-intensive, or "pure."

We now have an opportunity to evaluate NSERC's first 20 years in a wider context and must decide whether our investment has had a maximum benefit to Canada. As a taxpayer, it seems to me that all of our public support programs are undergoing scrutiny and they should; NSERC is no different. NSERC of today and tomorrow should be different than NSERC of the past, if only to reflect the changing research demographics and capabilities. The question of funding is really one of finding the appropriate balance to respond to challenges in today's rapidly changing world. We can defend the old way arguing against change,

or we can seek to understand the nature and potential of change and work to create the new vision which accounts for technological and socio-economic change as it applies to our research environment. I believe that vision will be vastly different than the status-quo and I, for one, would like to be involved in the discussion/transition rather than have someone else do it for us.

### **A Committee Member's Perspective**

*Tamer Ozsu of the University of Alberta is past chair (his term ended on June 30, 1994) of the NSERC Computer Science Grant Selection Committee.*

There seems to be an undercurrent in the country that the scientists should be working on more "economically relevant" issues to get the highest "bang for the buck." Translated, this means that we are being asked to work on technologies that can quickly be commercialized by Canadian industry. This is reflected in the comments of NSERC officials even though they deny any such move by indicating that there is no Council decision to move away from curiosity-based research. This denial, of course, is far from answering the criticism that the actions of the NSERC officials will inevitably cause an erosion of curiosity-driven research. There is great danger in this since without this type of research the really important inventions that give the biggest bang for the buck when commercialized would not happen. If this approach continues, I am afraid that in ten years time, we may not have a sufficient number of basic science inventions coming out of the Canadian science community that can then be commercialized. If no water is coming out of the spring, you cannot build a dam downstream.

I think this is only part of the issue, however. The problem is not whether the NSERC officials intentionally want to readjust the balance of research toward what they consider more economically relevant, but whether their actions (perhaps unintentionally) will lead to that result. There is very limited research funding in Canada and the scientists are being asked to spend more and more of their time going after smaller pieces of the pie. Every new program that is introduced comes at the detriment of another one since there are no new funds. The Collaborative Research Projects Program is a good example, having taken away \$2M from the research grants program this year (in addition to the funds it drains from other NSERC programs). CRPP will take \$6M from the research grants by the time it reaches its steady state level. This is significant. A rough calculation shows that NSERC now has over 60 programs. I submit this is unrealistically many for such a small budget. It has to be realized that scientists have to spend significant amount of their time writing grants for each of these. There has to be some rationalization of NSERC programs.

### **Industry Perspective**

*Dick Peacocke has worked in industry for 20 years. He is a past President of CSCSI and a former member of the*

*NSERC Grant Selection Committee for Computing and Information Science.*

Both individual research grants and project funding have to coexist. Evaluating the relative merits of NSERC funding pure or applied (targeted) research is like deciding whether fitness of the heart or lungs is more important. However, in today's climate, applied research needs little justification but pure research needs all the support it can get — even from those of us in industry. Curiosity driven research may sound dilettante, but it isn't.

The following is from a speech Sir J.J. Thomson made in 1916 to Lord Crewe, then Lord President of the Council. [From "J.J. Thomson and the Cavendish Laboratory in His Day," by G.P. Thomson, New York: Doubleday, 1965, pp.167-8].

"By research in pure science I mean research made without any idea of application to industrial matters but solely with the view of extending our knowledge of the laws of nature. I will give just one example of the 'utility' of this kind of research, one that has been brought into great prominence by the war — I mean the use of X-rays in surgery. Now, how was this method discovered? It was not the result of a research in applied science starting to find an improved method of locating bullet wounds. This might have led to improved probes, but we cannot imagine it leading to the discovery of X-rays. No, this method is due to an investigation in pure science, made with the object of discovering what is the nature of electricity. The experiments which led to this discovery seemed to be as remote from 'humanistic interest' — to use a much misappropriated word — as anything that could well be imagined. The apparatus consisted of glass vessels from which the last drops of air had been sucked, and which emitted a weird greenish light when stimulated by formidable looking instruments called induction coils. Near by, perhaps, were great coils of wire and iron built up into electromagnets. I know well the impression it made on the average spectator, for I have been occupied in experiments of this kind nearly all my life, notwithstanding the advice, given in perfect good faith, by non-scientific visitors to the laboratory, to put that aside and spend my time on something useful."

### **An Outside View**

*Mark Goresky of Northeastern University in Boston is a former member of the Mathematics Grant Selection Committee. He is very familiar with the granting process in both Canada and the US.*

During the last decade I have heard many of my American colleagues express the wish that the NSF were modeled on the "Canadian system." They often point out that although they have often visited Canadian universities and collaborated with Canadian researchers, they were only able to do so because the Canadians paid for all travel expenses from their research grants. NSERC has built an individual grants program which is the envy of the world and it would be a

shame to see it dismantled.


The introduction of large collaborative grants represents the start of a shift in federal funding away from the individual researcher. Whether or not NSERC plans to completely phase out (individual) research grants is probably irrelevant: the trend towards support of large projects and directed research is perceived as a political necessity, and it follows similar changes in funding patterns which have already occurred in England, USA, and Europe.

Certainly there are important projects which may succeed only in a co-operative environment, and others which stand to gain enormously from this sort of funding. But in many areas of scientific research (and especially in the highly theoretical areas with which I am most familiar), research activity simply does not fit into the "collaborative" mould. The best individual researchers have thought deeply and for many years about which new directions are likely to hold the most promise for the future. It is from these individuals (and small teams) that the most spectacular achievements have come. To refer to this work as "curiosity driven" research is to belittle the efforts of Canada's very best researchers.

Nevertheless, I believe these changes are inevitable.

Government funding agencies expect the loudest complaints to come from those who stand to lose the most, and they are therefore prepared to ignore these complaints. Our most decisive course of action may be to contact our European and American colleagues and to ask them how they are attempting to keep individual research initiatives alive in the current funding climate.

### Conclusion

*We have presented here a set of quotes, with minimal editorial intervention. Of course, the very act of soliciting quotes must introduce a bias. What is the conclusion? What is the best funding policy for Canadian AI research? The answer is left as an exercise for the reader.* 



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Intelligence  
Artificielle  
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## IJCAI '95

A mailing with detailed information regarding IJCAI'95 was recently sent out.

### Pointers to where to get information via the Internet:

International Joint Conference on AI  
(IJCAI '95) Call For Papers  
World Wide Web URL: [gopher://sigart.acm.org/00/Announcements/Conferences/ijcai-95.cfp](http://gopher://sigart.acm.org/00/Announcements/Conferences/ijcai-95.cfp)  
IJCAI '95 Panel, Tutorial, Workshop & Video Calls

Watch for detailed articles on IJCAI '95 in the next issue of



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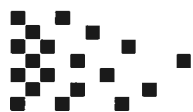
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## ***Special Feature: AI and Molecular Biology in Canada***

### **Artificial Intelligence and Molecular Biology 1994**

*Lawrence Hunter*

#### **Introduction**

L'application de techniques en intelligence artificielle aux problèmes de biologie moléculaire a contribué à l'avancement de l'intelligence artificielle ainsi que la biologie. Plusieurs des calculs difficiles affectés par la biologie moléculaire moderne ont été adressés avec succès par la technologie d'intelligence artificielle, et ces problèmes, en retour, ont conduit à de nouvelles idées qui se généralisent au delà du domaine. Cet article démontre un exemple du travail en cours, comprenant la recherche en raisonnement qualitatif, représentation de connaissances, apprentissage automatique, linguistique informatique, modèle de Markov, réseaux neurologiques et autres approches en intelligence artificielle. Le matériel de ce rapport a été tiré des conférences ISMB, dont leur source d'information dans la matière est excellente.

#### **Introduction**

The application of artificial intelligence techniques to problems in molecular biology has created significant advances in both AI and biology. Many of the difficult computational problems posed by modern molecular biology have been successfully addressed by AI technology, and those problems have in turn led to new ideas and approaches that generalize far beyond the domain.

There are several aspects of molecular biology that make it particularly well-suited to the current state of the art in artificial intelligence. Unlike many other areas in science, molecular biology has a significant qualitative element. Systems of biochemical reactions are often described in symbolic or semi-quantitative terms, rather than by differential equations. Objects in biological systems can often be represented in compact inheritance hierarchies. (Biological evolution is, of course, the source of the inheritance hierarchy metaphor.) A core aspect of research in structural biology is the ability to reason abstractly about shape, space, and time. Other kinds of biological inference seem to map well onto neural network topologies. Many of the problems molecular biologists are facing seem to require programs that can manage shifts in representation, cleverly search through huge conceptual spaces, or organize and use large, complex systems of knowledge. These requirements

can be met in part by existing AI approaches, and at the same time suggest promising new research directions for AI scientists.

The beginning of the field can be marked by the 1990 AAAI Spring Symposium which was the first gathering of AI researchers dedicated to the molecular biology domain. The pace of research has been brisk over the last four years, and both the problems and the approaches have expanded from just a few papers in 1989 and 1990 to encompass hundreds of papers in various conferences and journals just four years later.

There are now many venues for the presentation of work in the area. The first meeting of the international conference on Intelligent Systems for Molecular Biology (ISMB) was held in Bethesda, Maryland, USA in 1993, and the second was held in Stanford, California, USA in 1994. The third conference will probably be held in London, England in 1995. This is the only meeting dedicated specifically to AI and molecular biology, although there are also meetings on biological computing generally, such as the Hawaiian Conference on System Sciences Biotechnology Computing Track and the tri-annual Genes and Machines meetings, which have a significant AI presence. This year also marked the founding of the Journal of Computational Biology which explicitly calls for AI articles, and the publication of a special issue of the Machine Learning journal on molecular biology applications. The MIT Press published an edited volume entitled Artificial Intelligence and Molecular Biology in 1993 which provides in-depth material in a wide variety of topics.

A comprehensive survey of the area would require far more space than is available in this forum, so this article presents a small sampling of the current work, intended to be at least partially representative. It covers research in qualitative reasoning, knowledge representation, machine learning, computational linguistics, hidden Markov modeling, neural networks, and a range of other AI approaches. Much of the material for this review is taken from the ISMB conferences, which are an excellent source of information about the field.

## **A survey of significant domain problems**

Molecular biology presents a wide variety of computational problems, ranging from managing laboratory information in genome sequence laboratories to the modeling of entire ecosystems. AI approaches have been successfully applied to many of these problems.

The core of modern computational biology is the genetic sequence. All organisms inherit structural and functional information from their progenitors in the form of genes. Deoxyribonucleic acid (DNA) is the molecule that carries genetic information, encoded in a linear sequence of nucleotide bases. There are four such bases, generally abbreviated A, C, T, and G, so that DNA is generally represented as a long string drawn on a four letter alphabet. Acting in concert with the environment, these DNA molecules (called the genome or genotype) determine the structure, function, and behaviour (called the phenotype) of all living things.

Biotechnology has made it possible for scientists to read off the genetic sequence of any organism relatively inexpensively. The goal of the international Human Genome project is to collect the sequences of human DNA, as well as that of model research organisms such as the bacteria *E. coli*, the nematode worm *C. elegans*, and the ubiquitous laboratory mouse. Related genome sequencing efforts are underway on other economically significant organisms, such as corn, rice, and tobacco. However, the gene sequences of these organisms are extremely large, and it takes significant time and effort to both create the data, and, most importantly, to interpret it.

A string of As, Cs, Ts, and Gs in DNA follows a long, complex and indirect path to effecting the phenotype (that is, the ultimate characteristics) of an organism. The main function of DNA is to code for proteins, which are the workhorse molecules of living systems. Proteins are made of linear sequences of 20 amino acids, which, in the right environment, fold up on themselves to form complex three-dimensional structures exhibiting a breathtaking array of biochemical properties. Although the mapping from DNA sequence to the linear sequence of amino acids that make up a protein (its primary structure) is well understood, the problem of understanding how a particular amino acid sequence will fold up into a specific shape (its tertiary structure) and exhibit a specific function is a key open problem, called protein structure prediction.

Specifying the sequence of proteins is the main function of DNA. However, only a small proportion of human DNA actually codes for proteins. The rest contains control patterns and various other regions whose function is less well understood. The task of picking out the protein coding regions is a fundamental informational task called gene finding and an AI system is the reigning champion for accomplishing this task. The system, described in more detail below, is used via internet by thousands of researchers around the planet, and is rapidly becoming one of the most frequently cited AI systems ever published. The control

regions in DNA are used by the cellular machinery to turn genes on and off. Each cell in a multicellular organism (like a human) has precisely the same DNA. What makes one cell a neuron and another a blood cell involves controlling which genes are turned on and off in the cell. Also, the regulatory mechanism can turn genes on or off in response to environmental cues such as temperature change, introduction of a new type of food, or a memory trace to be stored in the brain. The task of identifying the control regions and modeling how they interact with each other is another significant AI problem which will bear on open biological questions in development, cancer, and neurobiology at least. The very first steps in understanding these regions have been in using machine learning systems to create pattern discriminators that can identify promoters (a specific kind of regulatory signal) in bacterial genome sequences.

Proteins work together to carry out biological functions in complex networks of chemical reactions. These networks make up an organism's metabolism, and metabolic modeling is an important new application area for AI systems. Since quantitative information is lacking for most metabolic reactions, qualitative modeling is a promising method. Even the representation of these complex, non-linear networks of substances and reactions is difficult to fit into traditional computer science tools such as relational databases, and object-oriented, knowledge-based systems seem to provide a significant step in the necessary direction. Several researchers are exploring the application and extension of AI tools to this task. AI and data-/knowledge-base techniques are also being applied to other areas in molecular biology, including managing the large, loosely coupled collection of semi-independent datasets that have sprung up around the world by the use of software agents and federated database models.

In addition to the problems involved in understanding the structure and function of a single organism at a molecular level, biologists are interested in examining the relationship among many organisms. Examining the similarities and differences in the protein and gene sequences of dozens or hundreds of organisms is a commonly pursued approach to understanding the function of a gene, and of its constituent parts, and also to build the evolutionary trees that capture the relationships among organisms. The computational power required to find the relationships between hundreds of different but similar strings is overwhelming, and AI methods from fields as diverse as speech recognition and unsupervised machine learning have been successfully applied to addressing this particular problem. Even more ambitious systems have been proposed to model entire ecosystems in order to address the complex issues of climate modeling and the population dynamics supporting biodiversity.

## **A sampling of AI applications**

The limited scope of this survey precludes covering the approaches to even one of the problems described above in adequate breadth. However, by describing a few

representative recent AI applications in some detail, it may be possible to get a feel for how the computer science and biology interact.

### **Gene Finding with GRAIL**

One of the most important early problems in the human genome effort is the task of finding genes in anonymous sequences. The technical method for reading the DNA sequences does so by reading small random chunks of this very large molecule. Human DNA contains more than three billion nucleotides, which is about as many letters as there are in every word of three years of the New York Times. Although it is possible to direct the sequencing process, say to an area of the genome that is suspected of harbouring a disease gene, often there is no information about the structure or function of the sequenced region other than the DNA sequence itself, hence the sobriquet anonymous. In order to understand what that chunk of DNA sequence does, a researcher has to solve a variety of problems. First, the sequence may include the code for one or more proteins. If so, the part of the sequence that actually codes for the protein must be identified, and then translated into a protein sequence. This is called the gene finding problem.

There are actually several subproblems to be solved in gene finding. The DNA sequences that code for proteins in higher organisms are interrupted at arbitrary points by non-coding sequences called introns. These introns are spliced out of the DNA sequence by the cell before the protein is produced. The mechanism by which the four letter DNA alphabet codes for the 20 different amino acids that constitute proteins is a mapping from three letter words of DNA, called codons, to each amino acid. For any given DNA sequence, there are therefore three different translations, called reading frames. Finally, the DNA is on a double helix where complementary nucleotides bind to each other (A with T and G with C). Each strand of the helix is the complement of the other, but they run in opposite directions. A gene can be found in any of the three reading frames going in either direction, for a total of six possible orientations.

Many methods have been proposed to identify regions of DNA that code for proteins, most of them based on the statistics of short subsequences. However, each of these many methods makes somewhat different predictions than the others, and none is much better than 70% accurate. Edward Uberbacher and his colleagues at the Oak Ridge National Laboratory developed a sensor fusion system that assembles these many modestly accurate predictions into a single prediction that is now over 99% correct. The system, called GRAIL, was built by examining the interactions of hundreds of different sensors, ranging from the subsequence frequency counts to a neural network that uses a sliding window to predict coding regions. All of these sensors were combined by another neural network that learned weightings and interactions for each of the sensors. The network predicts

for each nucleotide in the sequence whether it will be in a coding region or not. Since there are also global coherence constraints, a separate expert system examines the output of the prediction network and modifies it to meet the global criteria. For example, introns have a certain minimum length; a single intron prediction in the middle of a coding sequence is almost certainly a mistake. In recent work, the prediction network has been changed to make it recurrent so that it is better able to take into account the global coherence properties within the network itself.

GRAIL is an interesting system in many ways. Not only is it one of the first complex sensor fusion neural network systems to be published in the open literature, it is also a model for rapid incremental development. Uberbacher's group has a large user community of biologists who rely on the predictions of the system on a day-to-day basis, either connecting to it directly via an X-windows interface or via email. They generate significant feedback about the accuracy and usefulness of the system, and make specific suggestions for its improvement. Taking advantage of that large community, the group has made an order of magnitude increase in the accuracy of GRAIL's predictions in just three years. In addition there is an effort to expand the GRAIL system to other organisms; for now it is specialized in finding only human genes.

### **Hidden Markov Models for multiple sequence alignment**

Now that the genome database contains hundreds of thousands of genetic sequences from tens of thousands of organisms, the task of comparing similar sequences from many different organisms has gained increasing importance. Gene sequence for a protein that performs a given function can differ in many ways, reflecting the history of mutations that caused the organisms to diverge from each other. Some of the mutations in a genetic (or protein) sequence have very little effect, while others may change the function of the coded-for protein tremendously. In order to compare a set of differing sequences, they must be assembled into a multiple sequence alignment, showing which positions are the same and which have changed. These multiple sequence alignments are also useful in inferring the evolutionary relationship among organisms.

Because mutations can include the insertion or deletion of nucleotides or amino acids, and because some substitutions are more costly than others, this problem is a computationally complex one. A correct solution to this alignment problem can be found using dynamic programming (along with a substitution and deletion cost matrix). However, dynamic programming is exponential in the number of sequences aligned, and not practical for problems involving more than two, or at most three, long strings, even on parallel computers.

Several AI labs have applied the idea of hidden Markov models, which are an important component in speech recognition research, to this problem, most notably David

Haussler and collaborators and UC Santa Cruz. The idea is that a multiple sequence alignment defines a statistical model of the sequences in it. At each position of the alignment, the probability of a particular constituent (usually an amino acid) can be identified, as can the probability that the position is deleted from the sequence. This relationship can be reversed as well, so that a set sequence can be aligned to the model, rather than trying to align them to each other. If such models were available, then the multiple alignment problem would reduce to a much simpler problem. Haussler and colleagues devised a method to take an unaligned collection of related sequences and build just this kind of model.

The type of statistical model they build is a hidden Markov model, which identifies a set of positions in the sequence that have significantly non-random statistics. For each position in the model the relative probabilities of each constituent are given, as is the probability that the constituent at that position is deleted, or that, some other constituent has been inserted into the sequence. In addition, there are probabilities that, once a deletion or insertion has begun, it will be extended. Once such a model has been developed, then it is a matter of taking the inverse log of the probability to produce a scoring penalty for mismatches, and rapidly determining the probability that a sequence is a member of the family, and its most probable alignment to the model.

The difficult part of this task is creating the model from unaligned sequence data. These models can have hundreds or even thousands of parameters, and there is limited data to use for fitting. The fitting of the model from a collection of unaligned sequences is accomplished by an application of a variation of the well-known Expectation Maximization method called the Viterbi Algorithm. Roughly speaking, a model with a priori probabilities and a small amount of added noise is fitted to the data. The model parameters are then updated to reflect the frequency of the occurrence of particular amino acids at particular points in the model. This process, which is a process similar to bootstrapping and Gibbs sampling, is guaranteed to improve the fit of the model at each iteration. The approach has been tested by comparing the generated multiple alignments with gold standard alignments generated by using protein three-dimensional structures (which are known only for a very small proportion of proteins) and demonstrated remarkable acuity on groups of proteins of sufficient size. This work has spawned quite a few related efforts, for example, using stochastic context free grammars instead of HMMs, or using Dirichlet priors for updating the model at each step. [Papers and data from this group are available via anonymous ftp from <ftp.cse.ucsc.edu>]

### **Protein Structure Prediction**

Discovering the mapping from a protein amino acid sequence to its final folded shape is a key open problem in molecular biology. Although there are various exceptions,

most proteins will spontaneously refold themselves into their native structures in a test tube if they have been stretched out. This fact implies that all of the information necessary to determine that folded shape is somehow inherent in the protein sequence. Since determining the sequence of a protein can be done directly from a genetic sequence, but the determination of a protein structure directly (either by X-ray crystallography or nuclear magnetic resonance) is time-consuming and difficult, many computational biologists have addressed this problem.

There are two main approaches to predicting the structure of a novel protein: physicochemical modeling and machine learning. Physicochemical modeling is limited by the extraordinary computational demands of simulating the interactions of tens of thousands of atoms in a protein (and the surrounding aqueous environment) for the trillions of time steps it takes to do an adequate simulation. Nevertheless, this method is particularly important in understanding protein chemistry.

Machine learning methods rely on the existing database of several hundred known protein structures to induce patterns in the data that can be used for generalization to unseen structures. These methods all slide a relatively short window down the amino acid sequence, and predict the secondary structure class of the central amino acid in the window. The secondary structure class is a coarse indication of the local three dimensional structure, indicating whether it is in a tightly packed helix, an extended sheet, or something else (called random coil). Although quite useful information if predicted correctly, it is much lower resolution than the output of physicochemical modeling, which predicts the positions of each atom in the molecule. The most successful methods so far have all involved the use of neural networks. The most accurate method to date, described by Rost and Sander of the European Molecular Biology Laboratory in the proceedings of the HICSS '94 meeting, uses a multiple sequence alignment to weight the importance of each kind of amino acid at each point in the input window. This method exceeds 70% correct classification of secondary structure class, measured at each position.

In addition to de novo structure prediction, AI methods have been applied to related tasks. One such task is to determine the general topology of the protein, rather than predicting local structure amino acid by amino acid. Recognizing larger scale structures, such as four helix bundles, or helix-turn-helix motifs is often more biologically significant than making secondary structure predictions. For example, the helix-turn-helix motif is an indication that a protein is likely to bind to DNA as part of gene regulation. Rawlings, Clark, and coworkers at the Imperial Cancer Research Fund have been using constraint logic programming to predict overall protein topologies from imperfect secondary structure predictions and functional classifications of the protein. Other groups have devised neural network based systems for similar tasks. Both approaches are relatively successful at this task.

In recent years, the reverse structure prediction task has received increasing attention. In this problem, the backbone of a protein structure is provided as a given, and the task is to find a sequence that is compatible with the structure. The most successful method for predicting the structure of a new protein is to find a protein of known structure that has a similar sequence, and assume the structures are also similar. The idea behind the reverse folding problem is to define the space of protein sequences that are compatible with a particular known structure, giving specific meaning to similar proteins. A subclass of this problem is the task of threading a protein. That is, given a structure backbone and a sequence, find which atoms in the structure correspond to which amino acids in the sequence. When done for appropriate substructures of proteins, these methods provide a powerful mechanism for identifying structural motifs in sequences.

Exponentially many possible alignments of a sequence to a known structure are possible if naturally occurring genetic mutations, insertions, and deletions of the sequence are allowed, and a knowledge-based or learned objective function must be created to discriminate good from bad alignments. Because the different amino acid types have different physical and chemical properties, they exhibit statistical preferences for being in certain types of environments and in contact with certain other types of amino acids. The objective function reflects the extent to which amino acids from the sequence are located in preferred environments and adjacent to preferred neighbours. In this approach, protein folding consists of searching for a structure, sequence, and alignment that optimize the objective function, and hence maximizes the degree to which environment and adjacency preferences are satisfied.

The process is difficult because the objective function reflects weak trends and preferences, and must be inferred from data using machine learning or statistical techniques; because the search for the optimal alignment is NP-hard in the general case; and because the accessible data does not readily reveal the appropriate abstractions. Recently, a heuristic branch-and-bound search was developed by Richard Lathrop of the MIT AI Lab and Temple Smith of the Dana Farber Cancer Institute that can find the globally optimal threading in most cases of interest, and provides a two - order of magnitude speedup over the previously proposed search method. These methods are very useful when the protein whose structure is to be predicted, or at least a significant part of it, is similar to a known protein. The methods have also proven useful in threading proteins whose structures were determined crystallographically, even identifying a few genuine errors in the existing structure databases. As research progresses, the knowledge-based and machine learning approaches show increasing promise on this difficult problem.

### **Metabolic Modeling**

Metabolism is the densely connected, intricate, and

precisely regulated dance of chemical reactions that underlies all living systems. Metabolism is the process that transforms food, water, oxygen, sunlight, and other basic materials into proteins, DNA, usable energy, and all the other components that make up living systems. The process is quite reliable under an enormous variety of circumstances, including extremes of temperature, acidity, and moisture as well as functioning on a tremendous variety of different inputs. Even the simplest bacterial metabolism involves thousands of reactions. Interestingly enough, there is a core set of substances and reactions that are shared by nearly every organism, from bacteria to humans. Although many of the interconnected systems of reactions (called metabolic pathways) have been known for some time, knowledge of the integrated functioning of metabolic systems remains elusive.

It is often difficult for non-biologists to envision the immense complexity and interdependency of metabolic networks. One useful metaphor is a complex chemical plant, such as a petroleum refinery, with all its measuring devices, control signals, pipes, reaction chambers, and valves. Components of metabolic systems convey material and electrical charge from place to place, act as long or short term storage elements, or exert selective control over other reactions or whole systems of reactions based on measurements of demand, stocks, and competing needs. Most of the work in metabolic systems is done by proteins, acting as highly specific enzymes, catalyzing particular reactions.

Artificial intelligence methods are important in many aspects of understanding metabolism, ranging from the design of knowledge bases to containing the diverse forms of information about compounds and reactions and heuristic graph layout systems for visualizing them to qualitative modeling of metabolic reactions and scientific hypothesis formation. A recent survey article on these applications was published in *IEEE Expert* (Aug. 1994).

AI knowledge representation methods appear to be necessary for storing and manipulating the complex data that has been accumulated about metabolic systems. Hierarchical descriptions of classes of enzymes are necessary, as each particular enzyme is usually a member of one or more general classes of closely related enzymes (e.g., catalyzing similar reactions in different organisms), which in turn are members of broader and broader classes. Within this class structure, some features can be thought of as inheritable, and others not; instances of multiple inheritance can be found.

Peter Karp at SRI International and his collaborators are endeavouring to build a knowledge base of the metabolism of the bacterium *E. coli*. The effort involves systematically searching the scientific literature (as well as textbooks and other sources of knowledge) for information about metabolic compounds, reactions, and pathways. Their group has built a set of knowledge acquisition tools that speeds the process



of finding and extracting relevant information from both traditional and electronic sources, and placing it in the appropriate portion of the knowledge base. In addition, the group has also had to extend available frame representation systems to handle the requirements of very large knowledge bases accessed by many users at a time.

Even more ambitious than knowledge-base development efforts are the attempts to build computational systems for the simulation of metabolism. Effective simulation requires a vast array of biochemical data as well as automated knowledge of biological principles and regularities. The difficulty of the problem is exacerbated by the sparse, uncertain, and qualitative nature of the available data. AI methods such as order of magnitude reasoning and qualitative analysis have proven useful in several systems attempting to simulate small portions of metabolism (e.g., the work of Mavrovouniotis at Northwestern University or Daniel Weld at the University of Washington, Seattle). Many challenges remain in building metabolic models. One of the most interesting is taking advantage of very fine-grained, detailed information (e.g., the three-dimensional structure of an enzyme) when it exists only for a small portion of a much more coarsely modeled system. Information about biological

molecules will continue to become available incrementally, and our metabolic models should ideally be able to use such information as it becomes available.

### Modeling of Genetic Regulation and Development

Every cell in the body has precisely the same DNA, yet cells specialize (e.g., as neurons or toenails). It is the process of genetic regulation, turning genes on and off, or controlling how much of a particular gene product is produced, that determines a cell's fate. The process of development from fertilized egg to adulthood likewise involves many changes in genetic expression. Like metabolism, the process of genetic control and regulation is a complex, intricate dance involving many interacting factors. Models of this process are difficult to build using traditional mathematical means such as systems of partial differential equations. Artificial intelligence techniques appear to have made a significant contribution to this task as well. Like other biological application areas, the task of modeling genetic regulation has led to innovations in AI methods as well.

The most successful models of genetic regulation and development are the result of a collaboration between John Reinetz at Mount Sinai Medical College, Eric Mjolsness at

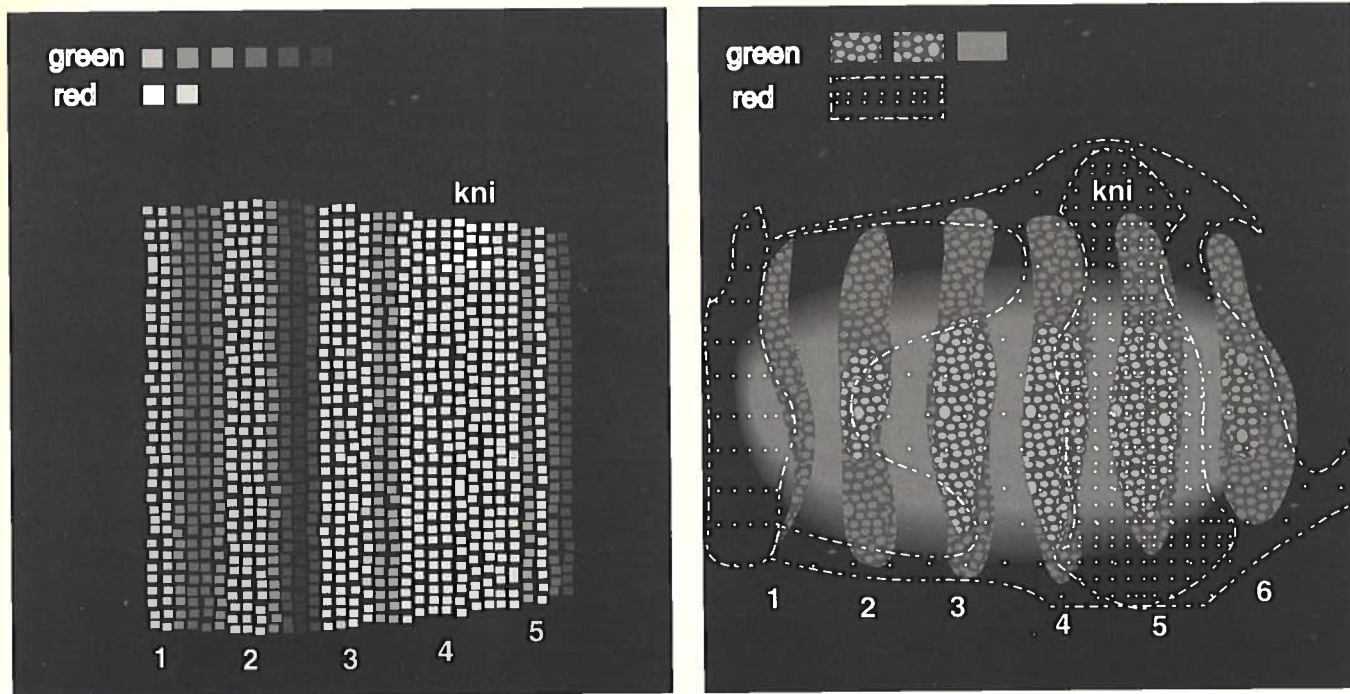


Figure 1. A comparison of the predictions of Reinetz, et al's computer model of gene expression with actual expression levels, using a modified representation of the original images. The image on the left is generated by the model. The green (light to medium grey) indicates expression of the gene *eve*, and the red (dark grey) *knirps*. The amount of the predicted gene product concentrations is indicated by the shading of the corresponding greys. The image on the right is a representation of a *Drosophila* embryo, stained and photographed by Mike Levine. Using the same grey assignments mentioned previously, it shows the actual expression of *eve* in green and *knirps* in red. Original image courtesy John Reinetz.

Editor's note: the original color images where converted to greyscale and all distinction between red and green was lost. To maintain the integrity and message of the images, the red color was inverted, turning it to black, and then the images were converted to greyscale achieving the tonal distinction between the colors.

Yale, and David Sharp at Los Alamos National Laboratory. They have developed a series of modeling techniques aimed at capturing developmental change in biological systems. The developmental modeling system uses a weight matrix similar to a recurrent neural network for specifying the relationships between the level of any gene product at a given time, and the amount of any other gene product at the next moment. The model does a non-linear transformation to the weighted sum of these influences to determine the level of expression predicted for each gene. By iterating the application of this model, predictions about the time course of the expression of genes within a cell can be made. Using these levels of gene expression as a state vector describing a cell, a multicellular model of cell division, can be layered over the genetic expression model, using a grammar to identify the states that lead to cell division and the results of a division on the daughter cells initial state vectors.

This general modeling framework, which uses both the dynamics of neural network systems and grammars for specifying transformations of the architecture and initial states of a collection of networks, has proven useful in quantitatively describing a wide variety of different biological phenomena. An implementation which theoretically explored the relationship between development and evolution suggested novel mechanisms for the control of the size of multicellular organisms and demonstrated the emergence of cell types not imposed directly by the environment. Another implementation, using only the gene regulation portion of the model, was applied to explaining some phenomena in the early development of the fruit fly *Drosophila* with surprising success, addressing several complicated open questions with data that had already been known, but whose implications were not fully understood. As in this case, AI models often have the ability to squeeze additional information out of available data.

The *Drosophila* development example modeled the levels of six gene products that were known to be important in determining the segmental boundaries in the fly's body plan. By measuring the amount of the products of these genes at several stages of development, and in mutants where one of the genes had been deleted, it was possible to gather enough data to fit the general model described above using simulated annealing. The model could be shown to fit the training data closely, as well as accurately predicting the levels of gene expression in circumstances that it was not trained on, such as earlier and later in developmental stage, and at different spatial locations. It is the spatial predictions that turned out to be biologically most significant, showing, for example, that there were two gene product gradients involved in the initial stages, not one as had been previously assumed. Also, the model identified detailed mechanisms for the creation of the stripes that are the first indication of the adult fly's body plan which made quite specific predictions that were later confirmed by independent empirical work (see figure).

## Conclusion

Molecular biology continues to be a fruitful area for research in artificial intelligence. This application domain has grown enormously over the last five years, and now involves hundreds of researchers from a variety of fields. Advances in the area have been correspondingly rapid.

The work reported on here is quite different in character than many of the earlier AI systems in the area. The projects described here show greater levels of biological sophistication, and almost all of them involve collaborations between biologists and AI researchers. The AI idea of knowledge engineering is rarely applicable in this domain; sustained, active, coequal participation tends to be the rule in molecular biology applications.

The significance of the results of current AI and molecular biology research can be seen in at least three areas. First, there are programs like Uberbacher's GRAIL which provide crucial tools to the biological community. Nearly all human genome sequencing laboratories use GRAIL to identify genes; it is probably one of the most frequently cited AI results ever. Second, modeling efforts such as those by Reinetz, Mjolsness, and Sharp have answered open questions about fundamental biological processes involved in development. And, perhaps most importantly to the AI community working in other domains, this work has generated broadly useful new AI tools and techniques in response to the unusual demands of the domain. Karp's work on strengthening frame representation systems, Uberbacher's methods of sensor fusion, and the Reinetz, et al's integration of grammars and neural networks are all likely to find useful application outside of biological domains.

AI and molecular biology have demonstrated a clear synergy. Harold Morowitz, one of the founders of the field, suggested that computer science may be for biology what math was for physics; it provides the basic language in which theories about the world can be expressed. If the frenzy of activity in the last five years is any indication, the next five will be even more exciting.

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*Lawrence Hunter is the Director of the Machine Learning Project at the US National Library of Medicine. His research interests range from cognitive modelling of human learning and discovery to evolutionary programming and artificial life, with an emphasis on biomedical applications. His recent MIT Press book, **Artificial Intelligence and Molecular Biology**, was the first to document the field.*

Contact information:  
National Library of Medicine, Bldg. 38A, MS-54  
Bethesda, MD 20894  
(301) 496-9300, fax: (301) 496-0673  
internet: hunter@nlm.nih.gov



# Canadian Genome Analysis and Technology (CGAT) Program

Nick Cercone

*Cet article donne un aperçu des buts et opportunités du Programme canadien de technologie et d'analyse des Genomes, en mettant l'emphase sur les possibilités de projets se rapportant à l'Intelligence artificielle.*

Much of this article has been borrowed shamelessly (and with the blessing of the Canadian Genome Analysis and Technology Program Management Committee) from Genexpress 1(1), October, 1993, the newsletter of the CGAT Program.

Funding for a Canadian human genome project was first announced in June, 1992 by the honourable William Winegard, then Minister for Science. The announcement contained a new allocation of \$12 million for the program, which, when combined with \$5 million from the Medical Research Council (MRC) and \$5 million from the National Cancer Institute of Canada (NCIC), created a new scientific initiative with \$22 million in funding for the first five years. The CGAT Program provides support for research grants, career development grants, and interactions.

The Canadian program is the responsibility of and administered by the MRC. A Management Committee sets the overall program direction and determines resource allocation. Chaired by Dr. Ronald Worton, Professor of Molecular and Medical Genetics at the University of Toronto and Geneticist-in-Chief at the Hospital for Sick Children, it is composed of individuals nominated by the three Granting Councils (MRC, NSERC and SSHRC), NCIC, and Industry Canada. The Management Committee is assisted by both Advisory and Peer Review Committees.

## Objectives

The CGAT program, as a component of the international human genome project, has as its objective the analysis of the human and other selected genomes, including the development of related technologies and informatics and the study of corresponding medical, ethical, legal, and social issues.

Proposals in the following areas are encouraged:

- high resolution mapping of a specific region of a specific human chromosome. This should involve physical mapping with an emphasis on YAC (yeast artificial chromosome) and cosmid contig building, and/or genetic mapping with highly informative markers;
- functional aspects of the human genome, e.g., projects that identify sequence and map large numbers or large blocks of genes (including cDNAs), matrix attachment regions, regulatory sequences, or other functional domains;
- high resolution physical and genetic mapping and/or functional aspects of genomes in complex model organisms, especially the mouse;

- mapping and sequencing of DNA from simple organisms and organelles (e.g., prokaryotes, yeast, mitochondria);
- technology development including new methods, automation, robotics, software, and instruments;
- informatics, including design of genome databases, development of algorithms, imaging and visualization, and data exchange standards and networks;
- development of regional and/or national resources for the CGAT Program (e.g., YAC or cDNA libraries, DNA banking/cell banking for selected population/diseases);
- research to address and anticipate the medical, ethical, legal, and social implications of genome research and related applications for individuals and society.

While sequencing of simple organisms will be supported, sequencing of complex genomes, including human, will not be supported until the cost is significantly reduced by the development of new technology.

Research targeted at specific genes or focused on the search for specific disease gene loci will not be considered. Such research is eligible for support through MRC, NSERC, and NCIC.

It should be noted that, due to the rapid progress in these research areas, funding priorities may change over time.

## Eligibility

Applications will be accepted from individuals or groups from academic or industrial institutions proposing to undertake biological, technological, social, legal, and ethical research projects clearly relevant to the objectives of the CGAT Program. Large-scale collaborative and/or multidisciplinary proposals involving researchers from different centres are particularly encouraged.

## Program Components

### a) Research Grants

Funds are provided for personnel support (technicians, research assistants, programmers/analysts, etc.), trainees (students, post-doctoral fellows, etc.), materials, supplies, and equipment.

Research Grants are awarded for one to three years and are renewable subject to availability of funds and program continuation.

Major equipment may be requested up to \$100,000. For expensive items, particularly those over \$100,000, the CGAT program will expect to share costs with the host institution or other agencies.

Travel and accommodation to attend scientific meetings will be a normal part of research grants. It is recognized that travel may be a substantial part of a research grant in those disciplines where meetings and workshops constitute a major component of the research.

#### b) Career Development Grants

Career Development Grants are available to new investigator(s) or those new to genome-related research. Salary support for the applicant as well as technical personnel, materials, and equipment support will be available for a maximum of three years.

Applications must be accompanied by a letter of support from a Canadian institution. The letter should describe the available supportive infrastructure including a stimulating intellectual environment for the conduct of the proposed research.

#### c) Interactions

Grants will also be provided to organizers of conferences, workshops, symposia, etc., to be held in Canada. Eligible expenses will be travel and accommodation for invited participants, room rentals, printing, meals, and technical support. Maximum opportunity should be given to Canadian participation including students. Every attempt should be made to seek other sponsors and/or sources of revenue. The CGAT Program will accept applications for travel funds to attend scientific meetings related to the human genome. Normally, this will be limited to applicants who have organizational or functional responsibilities related to the meeting.

### Evaluation Criteria

Suitability of the project for CGAT funding is determined first by a letter of intent. Projects deemed suitable will proceed to a full application.

Excellence of the research proposal is the principal criterion on which applications are judged. In addition, applications are evaluated on one or more of the following criteria:

- the extent to which the proposal satisfies the goals and objectives of the CGAT Program,
- represents a unique Canadian contribution or capitalizes on special Canadian strengths,
- has possible commercial and/or medical applications,
- fosters multidisciplinary research activities, fosters interaction with the international genome community.

### Applications

#### a) Research Grants or Career Development Grants

An application for a Research Grant or a Career Development Grant is made in two stages: i) Letter of Intent, and ii) Full Application

##### (i) Letter of Intent

Submitted by the principal investigator, the letter of intent should identify the title of the project and its relevance to the CGAT Program goals, list all co-applicants, and provide a one-page summary of the project.

The deadline dates for receipt of letters of intent are January 2, April 1, July 2, and October 1. The letters of intent should be submitted on CGAT Program Form 103.

##### (ii) Full Application

If the letter of intent is judged suitable for consideration in the context of the CGAT Program, the principal investigator will be invited to submit a full application for peer-review.

If the letter of intent is approved, full application will be accepted by the deadline dates of March 1 and September 15. Apply using CGAT Program Form 100 for Research Grants and CGAT Program Form 100, plus Form 101, for Career Development Grants.

#### a) Interaction Grants

Interaction Grants include: i) Support for Conference, Workshop, or Symposium, and ii) Travel Grants.

##### (i) Conference, Workshop, or Symposium

Applications for support of a Conference, Workshop, or Symposium will be accepted at any time. Apply using CGAT Program Form 102.

##### (ii) Travel Grant

Applications for Travel Grants will be accepted at any time. Only a letter need be submitted. Information about CGAT Programs and application forms can be obtained from:

The Canadian Genome Analysis  
and Technology (CGAT) Program  
Holland Cross, Tower B, 5th Floor  
1600 Scott Street  
Ottawa, Ontario  
K1A 0W9

### Committee Composition

As the lead agency, MRC worked with the Natural Sciences and Engineering Research Council (NSERC), the Social Sciences and Humanities Research Council (SSHRC), and NCIC to develop a Management Committee. The management committee for the CGAT Program consists of:

Dr. Ronald Worton, Chairman, Hospital for Sick Children  
Dr. Alan Bernstein, Mount Sinai Hospital, Toronto (NCIC)  
Dr. Nick Cercone, University of Regina (NSERC)  
Dr. W. Ford Dolittle, Dalhousie University (MRC)  
Dr. Hubert Doucet, Universite Saint Paul, Ottawa (SSHRC)  
Dr. Philippe Gros, McGill University (NCIC)  
Dr. Judith Hall, Children's Hospital, Vancouver (MRC)  
Dr. David Head, Industry Canada (IC)  
Dr. Bartha Knoppers, Universite de Montreal (SSHRC)  
Dr. Alastair Matheson, University of Victoria (NSERC)  
Dr. Henri Rothschild, Industry Canada (IC)

## Observers:

Ms. Barbara Conway (NSERC)  
Ms. Elaine Isabelle (SSHRC)  
Dr. Louis Slotin (MRC)  
Dr. Michael Wosnick (NCIC)

The Management Committee met in July and August 1992, and by September 1 had put in place the overall program direction and a system of peer review to determine resource allocation. The initiative was named the Canadian Genome Analysis and Technology (CGAT) Program. In September 1992, the essential details of the Program were communicated through the distribution of a brochure to scientists and trainees associated with all four of the sponsoring agencies.

The first Peer Review Committee was named by the Management Committee in September 1992 and is chaired by Dr. Michael Gray of Dalhousie University. The Committee members, as well as invited participants in the first peer review meeting, are listed below.

Dr. Michael Gray, Chairman, Dalhousie University, Biochemistry  
Dr. Abbyann Lynch, Hospital for Sick Children, Bioethics  
Dr. David L. Nelson, Baylor College of Medicine (Houston), Molecular Genetics  
Dr. David Sankoff, Université de Montréal, Mathematics  
Dr. Michael Smith, University of British Columbia, Biotechnology  
Dr. Ed Southern, University of Oxford, Biochemistry  
Dr. Frank W. Tompa, University of Waterloo, Comp. Sci.  
Dr. Lap-Chee Tsui, Hospital for Sick Children, Genetics  
Dr. David C. Ward, Yale University, School of Medicine, Molecular Biophysics

## Invitees to the May 1993 meeting:

Dr. Alistair Brown, University of British Columbia, Biomedical Ethics  
Dr. Howard Bussey, McGill University, Biology  
Dr. Bruce Chapman, University of Toronto, Law  
Dr. Nathan Goodman, Whitehead Institute (Cambridge), Informatics  
Dr. Ben F. Koop, University of Victoria, Biology  
Dr. Ronald Pearlman, York University, Biology  
Dr. Steven Wood, University of British Columbia, Medical Genetics

From September to December 1992, the Program attempted to set administrative offices in Toronto. During this period, the Management Committee was ably assisted by Ms. Evie Gray (MRC) and Mrs. Andrea Vogel, who had several years experience in grants administration with NCIC. In December 1992, the decision was taken to establish the CGAT office in Ottawa, and in January 1993, Ms. Evie Gray was officially named Program Administrator. Shortly

after, the Program hired Ms. Genny Cardin as Program Officer and Dr. Karl Tibelius as Senior Scientist. Administratively, the CGAT Program falls under Dr. Lewis Slotin, Director of Programs at MRC.

The first competition received 110 letters of intent, of which 38 were invited to apply. Of 31 applications received, ten were selected by the Management Committee for funding. The selection was based entirely on ranking from the Peer Review Committee, with a cut-off chosen to give a \$6 million commitment over the first three years. This left \$16 million for subsequent competitions. All applicants not selected for funding were invited to re-apply in the second competition. The ten applications chosen for funding included:

Dr. A. Howard Bussey, Biology, McGill University: The sequencing of chromosomes I and XVI of the yeast *saccharomyces cerevisiae*, \$1,406,000  
Dr. Diane Cox, Medical Genetics, Hospital for Sick Children: An expressed sequence map of I4Q32 and radiation hybrids of chromosome 14, \$348,800  
Dr. W. Ford Dolittle, Biochemistry, Dalhousie University: Sequence of the Genome of *Sulfolobus Solfataricus*, \$1,035,873  
Dr. Michael R Hayden, Medical Genetics, University of British Columbia: Predictive testing for Huntington Disease, \$447,000  
Dr. B. Franz Lang, Biochemistry, Université de Montréal: The Organelle Genome Megasequencing Project, \$236,161  
Dr. Jerry Pelletier, Biochemistry, McGill University: Rapid Identification and Mapping of Transcription Initiation Sites, \$331,885  
Dr. David Sankoff, Mathematics and Statistics, Université de Montréal: Models and Algorithms for Genomic Evolution \$190,000  
Dr. Erwin A. Schurr, Medicine, Montreal General Hospital: Isolation of Contiguous Yac Clones Overlapping Human Chromosome 2, \$305,282  
Dr. Jeremy A. Squire, Pathology, Hospital for Sick Children: A human gene resource for fluorescence in situ hybridization, \$443,978  
Dr. Lap-Chee Tsui, Genetics, Hospital for Sick Children: Large-scale physical gene mapping of human chromosome 7Q, \$1,383,411

Funding requests for sponsorship of workshops/symposia and for travel to international genome workshops were considered by the Management Committee. Travel to meetings normally supported by regular grants was not eligible. A list of these grants can be found listed below by organizer, meeting, and amount.

Dr. Diane Cox, 1st Int. Chromosome 14 Workshop, \$20,000  
Dr. J. Miller, Symp. on Medical, Ethical, Legal, and Social Issues in the new Genetic Era, \$3,500

Dr. S.M. Schmutz, Workshop on Gene Mapping Technology, \$8,000  
Dr. S. Wood, 1st Int. Chromosome 18 Workshop, \$17,767

#### Travel Grants:

Listed by applicant, event, and amount

Dr. Diane Cox, Gene Mapping Workshop 11.5, \$3,567  
Dr. Diane Cox, 5 researchers of chromosome co-ord. cmte and human gene, Japan, \$8,700  
Dr. B. M. Knoppers, HUGO Yearbook on Genetics, Ethics, \$14,700

#### Law and Society meetings:

Dr. A. Robinson, cross Canada travel for interviews for article in Canada Medical Ass. J., \$3,500  
Dr. L.-C. Tsui, 1st Int. Chromosome 7 Workshop, \$1,500

The final activity of the CGAT Program for the first year of operation was a Retreat held in Toronto June 1-2, 1993. Respected genome scientists, social scientists, lawyers, informatics specialists, and others were invited from across Canada, with special guests from the U.S.A., Great Britain, and France. After two days of discussion, the Management Committee received a number of recommendations, including (1) greater emphasis on the ethical, legal, and social aspects of the Program, (2) development of Canadian resource centres for informatics, physical mapping resources, genetic mapping resources, etc., and (3) concentration of grant funds on a) very large-scale mapping/sequencing projects with well defined milestones and b) smaller short-term innovative projects that may result in new enabling technologies.

The Management Committee considers these recommendations as the cornerstone for the further development of the CGAT Program.

#### Footnote

As the Informatics member of CGAT, I have expressed my concern that, in addition to sequencing algorithms which have been contributed by informatics specialists (mathematicians and computer scientists) that Canada could also play a role in the conceptual modelling and development of genomic data bases and spin-offs from that research and also in the scientific visualization and molecular modelling for which Canada's informatics specialists are renowned. To further that effort, a list of all Canadian chairs of Computer Science Departments have been included as part of the mailing list for CGAT announcements. This is an opportunity for applications-minded Canadian computer scientists to apply and receive funding for interesting applications in the world-wide human genome project. Applications for informatics research in CGAT must be tightly coupled to other CGAT fundable projects and CGAT plans to spend 7.5% of available funding on informatics projects independent of the setting up of resource centres.



*Nick Cercone took a three-year leave of absence from Simon Fraser University in 1993 and is currently Associate Vice-President Research and Dean of Graduate Studies at the University of Regina, and international liaison officer. He received his undergraduate degree in engineering science from Pennsylvania's University of Steubenville, his Master's degree at Ohio State, and his PhD. in Computing Science from the University of Alberta. (See Issue No. 32, Summer 1993, of Canadian Artificial Intelligence magazine for a profile of Nick Cercone by Connie Bryson.)*

#### AAAI Calendar Notices

**AAAI Spring Symposium Series 1995**, sponsored by the American Association for Artificial Intelligence, March 27-29, 1995, Stanford University, California. Contact: Spring Symposium Series 1995, AAAI, 445 Burgess Drive, Menlo Park, CA 94025; 415-328-3123; FAX: 415-321-4457; electronic mail: sss@aaai.org.

**IJCAI '95, Fourteenth International Joint Conference on Artificial Intelligence** sponsored by the International Joint Conference on Artificial Intelligence Inc.; the American Association for Artificial Intelligence, and the Canadian Society for Computational Studies of Intelligence, August 20-25, 1995, Montreal, Canada. Contact: AAAI, 445 Burgess Drive, Menlo Park, CA 94025; 415-328-3123; FAX: 415-321-4457; electronic mail: ijcai@aaai.org.

**IAAI '95, Seventh Annual Conference on Innovative Applications of Artificial Intelligence** sponsored by the American Association for Artificial Intelligence, August 20-25, 1995, collocated with IJCAI-95, Montreal, Canada. Contact: IAAI-95, 445 Burgess Drive, Menlo Park, CA 94025; 415-328-3123; FAX: 415-321-4457; electronic mail: iaai@aaai.org.

**AAAI Fall Symposium Series 1995**, sponsored by the American Association for Artificial Intelligence, November 10-12, 1995, tentatively scheduled to be held at MIT, Massachusetts. Contact: Fall Symposium Series 1995, AAAI, 445 Burgess Drive, Menlo Park, CA 94025; 415-328-3123; FAX: 415-321-4457; electronic mail: fss@aaai.org.

# Current Canadian Projects

*Le grand nombre d'information qui s'accumule sur les bases de données en génome et molécule, fournit un domaine riche et stimulant pour l'application des résultats en recherche sur l'intelligence artificielle. Nous décrivons aussi les projets de recherche en cours qui se continuent à l'université de Toronto ainsi qu'à l'université Queen qui impliquent l'investigation sur les techniques d'intelligence artificielle pouvant être utilisées à résoudre les problèmes concernant le secteur de la biologie moléculaire.*

*The vast amount of information that is being accumulated in genome and molecular databases provides a rich and challenging domain for the application of AI research results. Following, we describe some ongoing research projects at The University of Toronto and Queen's University that involve the investigation of how techniques from AI can be used to address open problems in the area of molecular biology.*

## AI and Molecular Biology at the University of Toronto

### Genome Map Assembly

*Anthony Bonner, Gloria Kissin, and Eric Harley*

A major goal of the Human Genome Project is to construct detailed genome maps for humans and other model organisms. A genome map is an assignment of DNA fragments to their specific locations in a genome. In assembling a map, a genetics expert typically reasons about the experimental data and how it fits together. The problem is to construct a coherent picture of the genome from data that is imprecise, ambiguous, and often contradictory. For small-scale mapping projects, maps are often constructed manually, perhaps with the aid of a graphical editor. This is a tedious and time-consuming task. Large-scale mapping projects require better computational approaches to efficiently handle the large volumes of data and the explosive combinatorial growth in the search space of maps.

We propose to address a range of computational problems that are integral to large-scale mapping projects. Although progress has been made on each of these problems, much more remains to be done. In addition, no known computational approach deals with the full range of issues in an integrated manner. These issues include the following:

- reasoning with data that is imprecise, ambiguous, or contradictory;
- methods for visualizing, querying, and exploring genome maps;
- integrating many forms of mapping data, each arising from different types of laboratory experiments;
- integrating data from different laboratories;
- the computational complexity of map assembly.

To address these issues, we are developing a logic-based framework for genome map assembly and visualization [3]. This framework allows the easy integration of logical rules and algorithms for map assembly. Moreover, it provides a flexible and interactive yet rigorous approach. Interactive operation enables biologists to guide the map-assembly process. A flexible strategy can accommodate different kinds of mapping data, with various kinds of experimental error. A rigorous approach allows for the formal verification of correctness and efficiency. The goal

is to allow a biologist to rapidly develop and test new ideas for large-scale map assembly.

This research project involves close collaboration between biologists and computer scientists, and between computer scientists in different specialties, both within Canada and internationally.

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*Anthony Bonner is an Assistant Professor of Computer Science at the University of Toronto. His research interests include knowledge representation, logic programming, database systems, and genome databases. In addition, he is currently working on intelligent computer systems for genome mapping and sequencing in collaboration with biologists and computer scientists in Toronto and internationally.*

*Gloria Kissin received her Ph.D. in Computer Science from University of Toronto. She was Assistant Professor at the Technion in Haifa, Israel, and at the University of Amsterdam. She was also Senior Scientist at the Centre for Math and Computer Science (CWI) in Amsterdam, The Netherlands. Dr. Kissin is currently a Research Scientist at the University of Toronto. She has lectured internationally on algorithms for VLSI design. She is currently applying her expertise in algorithmic design to problems in Genomic Mapping and sequencing.*

### Protein Structure Prediction

*Evan Steeg*

The protein structure prediction problem is a crucial one in the emerging field of computational molecular biology. In order to gain a comprehensive and deep understanding of the structure and evolution of biological organisms, and to make sense of the flood of sequence data — DNA, RNA, protein — produced by the Human and other Genome Projects, we must be able to infer the relationship between macromolecular sequences and 3D structures. In order to design (or artificially evolve) new, safer, and more effective drugs and vaccines that interact with particular targeted substances at the molecular level, we must understand how the insertion, deletion, or substitution of particular

subelements in a protein chain will affect the overall structure and function of the molecule. In order to achieve and to employ this understanding, we need fast and efficient methods for comparing, matching, displaying, and reasoning about sequences and structures.

Artificial intelligence and machine learning researchers can find in this domain several factors which make for challenging research: the high dimensionality of input and output representations, the huge size of some of the datasets (sequences) along with a severe paucity of other kinds of data (precisely-determined tertiary structures), and the tension between the syntactic nature of the domain objects and the geometric (vector space) nature of most adaptive pattern recognition and machine learning methods.

My current work, and my PhD thesis, concerns the application of neural network and other statistical learning methods to the prediction of protein secondary and tertiary structure from primary structure (amino acid sequence). Unlike much previous work in the field (including my own) [8], my current research does not aim to place the entire structure prediction task within a convenient machine learning engine (e.g., a neural network). Rather, I consider structure prediction as a multi-stage task requiring the integration of more standard methods (energy minimization, quantum, and classical physical simulation) with AI methods, and I use machine learning to discover good intermediate representations between sequence and final predicted structure.

My overall approach is based on an information-theoretic framework: Minimum Description Length (MDL) [7]. An MDL framework for representation of different levels of protein structure, combined with assumptions about the information-theoretic "costs" of particular components, lead to specific objective functions which must be optimized. A consideration of how best to optimize these objective functions in turn leads to particular learning algorithms. These algorithms are then used to find good (in some well-defined sense) representations for secondary structure [5, 6] and for complex, long-distance positional correlations across protein sequences [9].


This approach is suggested in part by other recent work in Prof. Geoffrey Hinton's research group at the University of Toronto, especially [4,1,10], and might be applied successfully to other difficult multi-stage "prediction" tasks like machine vision and speech recognition.

(My current projects involve collaborations with Alan Lapedes and Rob Farber of Los Alamos National Labs and the Santa Fe Institute, and Derek Robinson of Toronto. The research has been supported in part by LANL and SFI, and by NSERC and IRIS grants to my supervisor Geoffrey Hinton.)

## References

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*Evan W. Steeg is a Ph.D. candidate in the Department of Computer Science at the University of Toronto. Originally from the New York City area, he has degrees in Mathematics from Cornell University and Computer Science from the University of Toronto. His scientific interests include neural networks and pattern recognition, as well as evolution — biological, cultural, economic linguistics, etc.* 



## Overview of Ongoing Research Projects at Queen's Janice Glasgow

### Molecular Scene Analysis Project

The concept of "scene analysis" has been used in the context of machine vision to refer to the set of processes associated with the classification and understanding of complex images. By analogy, the Molecular Scene Analysis project at Queen's University is concerned with the processes associated with the reconstruction and interpretation of complex scenes involving molecular structures and molecular interactions.

The main goal of the Queen's group is to design and implement a knowledge-based system for protein structure determination. Fundamental to our approach is the development of knowledge representation and learning techniques that focus on the three-dimensional visual and spatial characteristics of molecular images. Applying techniques from computational imagery to the information accumulated in a crystallographic knowledge base provides the "intelligence" vital to the understanding of molecular structures and molecular recognition processes. In the emerging system, the process of protein structure determination is rephrased as an iterative and hierarchical scene analysis (see accompanying Figure 1) which is carried out through the integration of AI and direct methods strategies.

The Queen's project is being led by Janice Glasgow (Department of Computing and Information Science) and

Suzanne Fortier (Departments of Chemistry and Computing and Information Science). It involves collaboration with researchers at the Cambridge Crystallographic Data Centre (UK), the Faculties Universitaires Notre-Dame de la Paix (Belgium), the Oak Ridge National Laboratory (USA), the University of Alberta (Canada), the Medical Foundation of Buffalo, Inc., (USA) and the MIT AI Laboratory (USA).

Following is a brief abstract of the primary subprojects currently underway at Queen's University:

#### 1) Computational Imagery: (J. Glasgow, C. Yendt, P. Kalin)

At the core of our knowledge-based approach to Molecular Scene Analysis is the concept of imagery, that is, the ability to represent and reason with three-dimensional models of molecular structure. In order to provide a computational framework that captures the experts' visualization abilities, we are designing a knowledge representation scheme that makes explicit the fundamental spatial and visual characteristics of an image. This scheme includes primitive functions for constructing, transforming, and inspecting image representations.

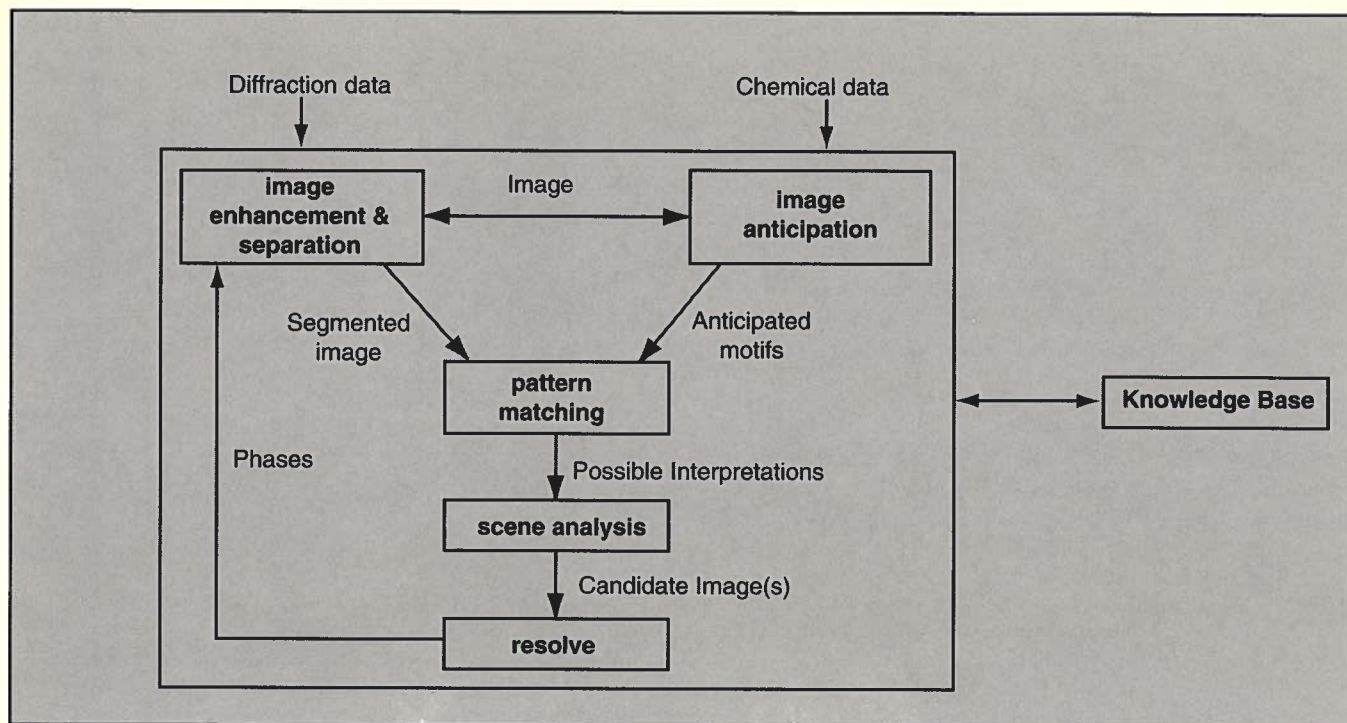


Figure 1. Processes for molecular scene analysis

2) Development of a Protein Structural Knowledge Base:  
(J. Glasgow, S. Fortier, C. Walmsley, S. Hara, D. Conklin)

This project involves the integration of comprehensive information on protein crystal structures into a knowledge base of molecular scenes. This ever-growing information base is organized according to the natural structural and conceptual hierarchies of molecules; it includes concepts and instances for proteins, secondary structures, residues, and atoms. Other intermediate levels are being considered, based on the application of machine learning techniques (see subproject 3) to the discovery of protein motifs. At each level of the hierarchy, prototypical visual and spatial representations are stored for the pattern matching and retrieval of molecular motifs.

3) Learning and Discovery in Molecular Databases:  
(D. Conklin, S. Fortier, J. Glasgow, F. Allen)

An approach to knowledge discovery in complex molecular databases has been developed and is currently being applied

implementation of a knowledge-based system for protein crystal structure determination. The proposed system integrates direct-methods mathematical techniques from crystallography with artificial intelligence strategies to rephrase the structure determination problem as an exercise in scene analysis. A general joint probability distribution framework, which allows the incorporation of isomorphous replacement, anomalous scattering, and partial structure information, forms the basis of the direct-methods strategies. The accumulated knowledge on crystal and molecular structures is exploited through the use of AI strategies, which include knowledge representation, search, and learning techniques (see subprojects 1 - 3).

5) Topological Analysis of Molecular Scenes  
(L. Leherte, K. Baxter, S. Fortier, J. Glasgow)

Methods to assist in the spatial and visual analysis of electron density maps (molecular images) are being developed as part of the Molecular Scene Analysis project.

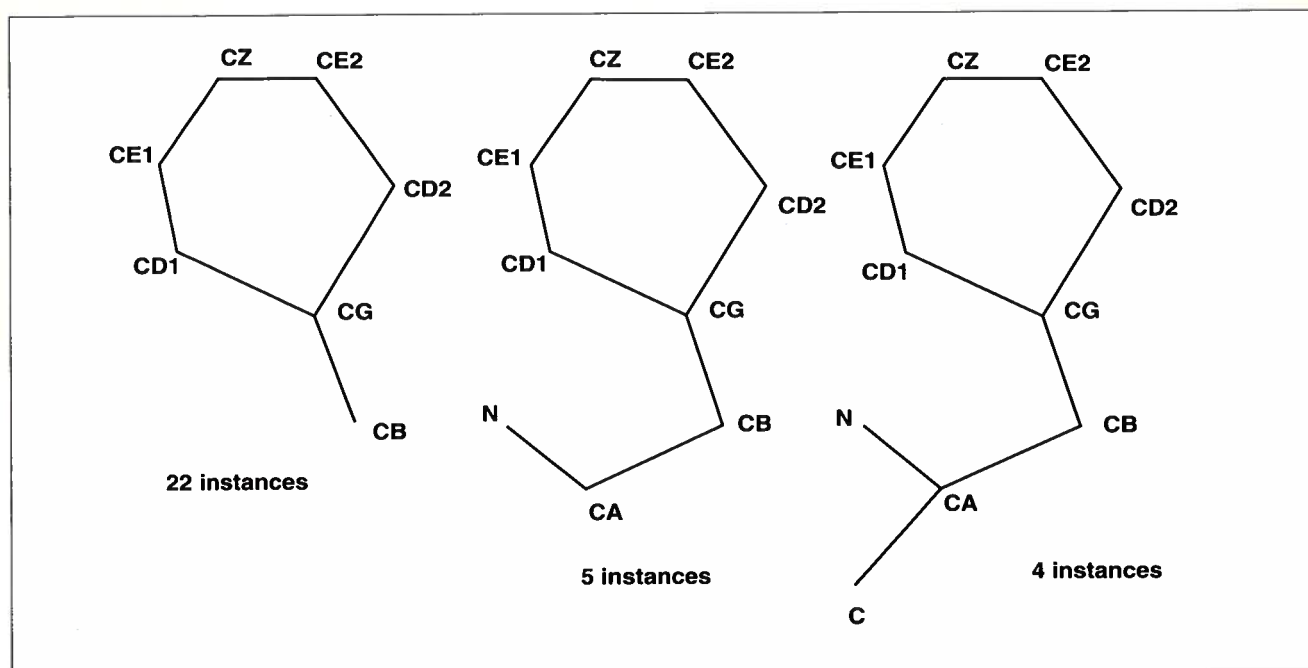


Figure 2. Discovered molecular motifs

to the discovery of protein structure motifs. The machine learning paradigm used in this work is structured concept formation, in which objects are clustered and organized in a knowledge base. Symbolic images are used to represent classes of molecular motifs. For example, Figure 2 illustrates three discovered phenylalanine motifs, ordered by subsumption.

4) Integrating AI and Direct Methods Strategies:  
(S. Fortier, T. Chiverton, S. Guo)

A major application in molecular scene analysis is the

In particular, a topological approach for the segmentation and interpretation of low and medium resolution maps of proteins has been applied. The implemented approach provides a global representation of the electron density distribution through the location, identification, and linkage of its critical points. Our studies have shown that the derived networks of critical points provide a useful segmentation of maps, tracing the protein main chains and capturing their conformation. In addition, these networks can be parsed in terms of secondary structure motifs, through a geometrical analysis of the critical points.

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*Janice Glasgow is a professor in the Department of Computing and Information Science at Queen's University. She received her B.Sc. from the University of Alberta and her M.Math and Ph.D degrees from the University of Waterloo. Dr. Glasgow's primary research interests are in the area of artificial intelligence. These interests include computational imagery, case-based*

*reasoning and machine learning. She has also been involved in research in programming languages and tools for artificial intelligence, and has led several projects for developing knowledge-based applications in business, science, and engineering. Dr. Glasgow has been a principal investigator in the Institute for Robotics and Intelligence Systems (IRIS), Federal Network of Centers of Excellence of Canada and a co-investigator in the Information Technology Research Corporation (ITRC) and the Manufacturing Research Corporation (MRCO) Provincial Centers of Excellence of Ontario.*

*As well, she is the Past President of the Canadian Society for Computational Studies of Intelligence (CSCSI).* ▲

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Intelligence  
Artificielle  
au Canada

# Alan Mackworth: Working With Constraints

Robert J. Woodham

## Sommaire

Alan Mackworth a reçu le prix de Service Distingué CSCSI 1994. Ce prix est présenté bisannuellement à un individuel qui a exceptionnellement contribué dans certains domaines de l'Intelligence artificielle tels que: service communautaire, recherche, formation aux étudiants, et interaction dans l'industrie et la recherche. La présentation se tenait à la conférence AI/GI/VI '94, du 16 au 20 mai à Banff, Alberta. Cet article parle des quelques contributions d'Alan, et essaie de souligner les qualités personnelles de ces contributions.

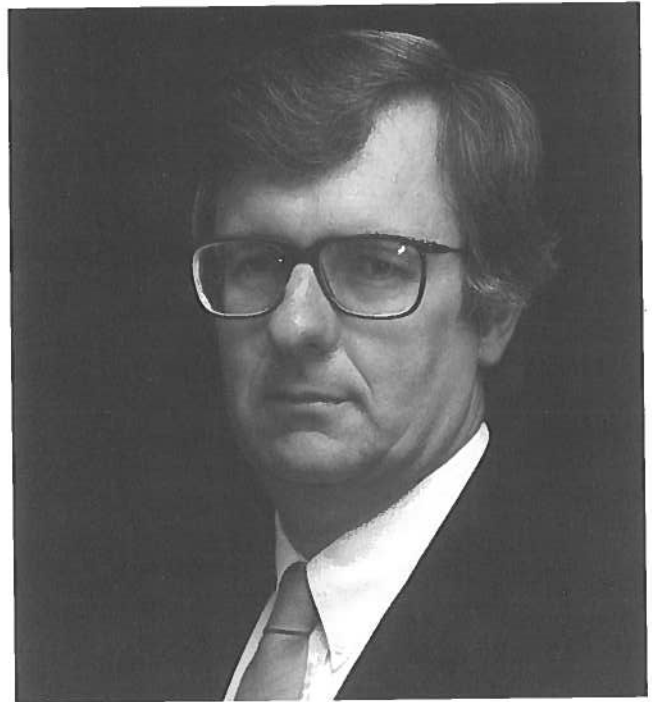
## Summary

Alan Mackworth is the recipient of the 1994 CSCSI Distinguished Service Award. This award is presented biennially to an individual who has made outstanding contributions to the Canadian AI community in one or more of the following areas: community service, research, training of students, and research/industry interaction. Formal presentation of the award took place at the AI/GI/VI '94 conferences, May 16-20, 1994, in Banff, Alberta. This article describes some of Alan's contributions and, in addition, tries to convey some sense of the personal qualities underlying those contributions.

## Introduction

The executive of the Canadian Society for Computational Studies of Intelligence chose Alan Mackworth as the recipient of the 1994 CSCSI Distinguished Service Award. Formal presentation of the award took place at the AI/GI/VI '94 conferences, May 16-20, 1994, in Banff, Alberta. Alan thus becomes the second recipient of the CSCSI Distinguished Service Award. This award is presented biennially to an individual who has made outstanding contributions to the Canadian AI community in one or more of the following areas: community service, research, training of students, and research/industry interaction.

I have known Alan since 1975 and we have been colleagues at the University of British Columbia (UBC) since 1978. I am pleased that the award provides me with the opportunity to write about Alan. I must be up-front, however, and confess my bias. I hold Alan in the highest possible regard as a friend, scientist, and colleague. Recent events at Concordia University and elsewhere have cast a shadow upon the entire scientific and engineering research community in



Canada. In contradistinction, Alan serves as an exemplar of what sound scholarship, research excellence, and effective collaboration mean (and ought to mean). Alan's service to the Canadian AI community is indeed distinguished.

The views I present in this article are personal. At the same time, I acknowledge comments received from several of Alan's Ph.D. graduates and other colleagues, in particular Jay Glicksman, Bill Havens, Alex Kean, Ron Lake, Farzin Mokhtarian, Jan Mulder, John Mylopoulos, Zenon Pylyshyn, and Ray Reiter. The subtext I have chosen for this article is "working with constraints." For those who already know Alan's research, this has the obvious technical meaning related to Alan's seminal contributions in the area of constraint satisfaction. But, I intend it also to be a metaphor for Alan's more general interactions with people, institutions, and events. Alan's talent has been to isolate key constraints and to envision new possibilities by questioning accepted constraints, and, where appropriate, by working to change the set of constraints to enhance what is possible.

Alan is outspoken and passionate about principles he believes to be important. He is forthright and substantive in his argument and generous of his energy in support of his colleagues and his discipline. Organizational and administrative tasks become opportunities rather than burdens. Alan really has been effective in influencing the way university administrations, granting agencies, and other government bodies respond to AI in particular (and to Computer Science in general). At the same time, Alan does not shy away from taking unpopular stands when he feels it is the necessary thing to do. Alan can be counted upon to

raise the important questions, even when those questions are not the ones that the majority of the community seems prepared to address.

One anecdote from the late 1960's helps to make the point. Ron Lake, Principal Engineer, MacDonald Dettwiler & Associates (MDA), recalls, "When I was in second year at the University of Toronto, I was a bit of a 'trouble maker.' One professor I knew said that he remembered another 'trouble maker' who had caused trouble in the department a few years before, one Alan Mackworth. I went to see Alan and found an immediate ally. He was someone who understood my own sense of alienation and who was willing to challenge the existing order of things. Mostly, he was someone who was open and supportive. Our 'trouble making' was simply to try to reform the engineering program so that it was more humane and more open to the rest of the world. Allowing engineering students to experience things like literature, poetry, and perceptual psychology was a radical idea at the time. Alan's breadth of interests and holistic view of engineering was for me a breath of much needed fresh air. Our mini-rebellion culminated in a face-to-face encounter with the Faculty of Engineering Science. The Faculty were arranged on one side. Alan and I were on the other. The result was a sort of grand debate with the students looking on. I will never forget the moment when Alan walked in with his long hair and flaming green bell bottoms. The other side knew we were serious customers."

This story would be interesting enough if it were merely about two students speaking out against the establishment of their day. The story becomes more telling, given that, at the time, Alan was not a student but a member of the Faculty. Alan had graduated from the University of Toronto with a B.A. Sc. in Engineering Science in 1966 but was, from 1967-1970, a lecturer in Industrial Engineering. I don't know at what point Alan developed the holistic view that Ron Lake cites. Perhaps one indication is that Alan spent the year, 1966-67, at Harvard University, where he received an A.M. (masters) degree in Applied Mathematics, pursuing a program in which he also included a number of courses in Psychology.

In 1970, Alan left Toronto and set out, with his wife Marian, to tour the world. I am told Alan and Marian were heading to India but, in fact, never made it past England. There, Alan encountered Max Clowes at Sussex University. At the time, Max was a preeminent computer vision researcher and a sufficiently kindred spirit to cause Alan to stay at Sussex to complete his D. Phil. in 1974. Unfortunately, Max Clowes died suddenly in 1981 well before his career potential could be realized. Pat Hayes wrote of Max, "Several generations of AI researchers were inspired by the passion, humour, and critical honesty which he brought to research work." Alan bears witness to this legacy.

Alan has been a faculty member in Computer Science at UBC since 1974. In the time I've known him, Alan has always been able to articulate a clear vision of AI research in Canada. As Canadian AI researchers, we do operate

under a different set of constraints than do our colleagues in other jurisdictions. In Alan's vision, this never need make us second rate. Instead, Alan has demonstrated, and continues to demonstrate, that our Canadian environment provides unique opportunities, including distinct advantages, to make our contribution on the world stage. This vision is manifest in Alan's own research. It also has been contagious among his colleagues, especially his students.

## Research

Alan's research excellence already has been recognized via a number of national and international awards. Since 1984, Alan has been a Fellow of the Canadian Institute for Advanced Research (CIAR) program in Artificial Intelligence and Robotics (AIR). He also was elected Fellow of the American Association for Artificial Intelligence (AAAI) in 1990. As such, he is one of approximately 150 researchers, including 5 Canadians, who share this honour. In 1991, Alan received the Information Technology Association of Canada (ITAC) NSERC award for Academic Excellence. The ITAC/NSERC award is given out each year to two Canadian academics for outstanding contributions to Canadian Information Technology. Alan was the first member of the Canadian AI community to receive this award.

Alan's research has covered a wide range of topics and applications, with, at the same time, a consistent theme: the evolving cycle of theory, experimentation, and application. Alan's doctoral thesis introduced the gradient space representation for surface orientation and demonstrated how it could be used to exploit metric constraints in "blocksworld" scene analysis. At UBC, Alan led the development of multiple incarnations of Mapsee, his system for interpreting hand drawn sketch maps of geographical areas. Mapsee began as a study of the applicability of Huffman-Clowes-Waltz style constraint labeling techniques outside the blocksworld. It continued with a variety of algorithms for what now is referred to as constraint satisfaction problems. Mapsee also explored schema based knowledge representations and their interaction with constraint satisfaction. Formalizing these issues led, in turn, to joint work with Ray Reiter on the logic of depiction.

Most recently, Alan has been exploring various sensor-based robotic systems, including teams of mobile robots, with real-time visually-based control systems, for tasks like soccer playing. This has driven the development, with student Zhang Ying, of the on-line constraint net model as a framework for specifying, verifying, simulating, and implementing robotic systems. The constraint net model combines work with constraint satisfaction and dynamical systems. In the model, a robotic system is a dynamical system composed of a robot coupled symmetrically to its environment, while the robot consists of its controller coupled to its plant.

Alan has made a variety of other contributions, particularly in computational vision, and has published widely in the

appropriate journals and conferences. The journal *Artificial Intelligence* is considered by many to be the leading international journal in the field. To date, Alan has been the author or co-author of eight articles in *Artificial Intelligence*. Recently, Dan Bobrow edited a special issue of the journal as a retrospective celebration of its first fifty volumes [1]. An attempt was made to identify the landmark papers appearing in volumes one through fifty. The Science Citation Index and the Social Science Citation Index each were consulted to determine the fifty most cited papers in the five years following their publication. Two of Alan's papers [2,3] were included in the list of the most cited papers. Indeed, the second of the two [3] was among the 30 most cited. This example allows me to make some general comments about Alan's research contributions.

Today, increasing emphasis is placed on networking and collaborative research. To be effective, at least two ingredients are required: scientific ability and scientific integrity. The first requirement is obvious. The second, in my view, often is decisive. In addition to his specific technical skills, Alan possesses the rare ability to find common intellectual ground among the various disciplines and sub-disciplines related to AI. Alan's integrity also is renowned. His respect for proper scholarship, including the fair and accurate attribution of ideas, has made him a trusted research collaborator. This, in large measure, accounts for the spirit of collaboration within the UBC Laboratory for Computational Intelligence. It also has led to effective, long-term collaborations with researchers beyond UBC including Johan de Kleer, Gene Freuder, and Ray Reiter.

When asked for a comment, Ray Reiter described Alan simply as "stellar." Alan's collaboration with Gene Freuder is, I think, a good example. The history of their joint work is summarized in [4]. Alan had pioneered the development of network consistency algorithms. His earlier work [2] described a class of algorithms abstracted from the particular applications in which constraint satisfaction problems first appeared. One of the algorithms, known in computer vision as "Waltz filtering," was thought to be linear, although any conclusion based on empirical data was dubious, especially given the limited experimental data available. The complexity of the problem remained an important open issue.

Both Alan and Gene solved the problem independently in 1981. Clearly, this was to be a significant result. In comparable situations, I have seen animosity develop between researchers as to who discovered what first or, more destructively, who stole what from whom. To the credit of both Alan and Gene, the solution to them was obvious. They would collaborate and write up the results together. As mentioned, the resulting paper [3] is a landmark. It proved that arc consistency has time linear in the number of binary constraints. Further, if the constraint graph is planar, as is the case for Waltz filtering, then time also is linear in the number of variables. Finally, if the constraint graph is a strict tree, a solution to the constraint satisfaction problem will be found (or failure reported if there are no

solutions) also in linear time.

One of the practical consequences of this work has been to allow designers of constraint-based programming languages to include arc consistency algorithms as part of a basic inference mechanism, with confidence in the tractability of the result. Constraint programming now is used in a wide variety of applications including scheduling, simulation, diagnosis, and repair.

Alan went on to establish new connections between classes of constraint satisfaction problems and logical methods, leading to new insights into trade-offs between expressive power and tractability in logical representation and reasoning systems. With Ph.D. student, Zhang Ying, he also has been developing, and analyzing, parallel and distributed algorithms for constraint satisfaction. Clearly, work with constraints continues.

### **Community Service**

A cornerstone of Alan's distinguished service to the Canadian AI community has been service to the CSCSI itself. My earliest encounter with Alan was at a CSCSI/SCEIO Workshop on Computational Studies of Intelligence held in Ottawa in May, 1975. This workshop preceded the inaugural CSCSI conference and, it seemed to me, served to define the Canadian AI community. My memory of this first event has faded over the years. One strong recollection that remains, however, is of the leadership role Alan played. Subsequently, Alan was Program Chair of the first CSCSI/SCEIO National Conference held at UBC in 1976. This first conference began the tradition of strongly technical Canadian AI conferences which we all still enjoy and benefit from. Alan was a member of the CSCSI/SCEIO Executive Committee (1975-76), Vice-President (1978-80) and President (1980-82).

Alan also has been of distinguished service to the international AI community. Alan has been a member of the International Joint Conferences on Artificial Intelligence (IJCAI) Board of Trustees and Executive Committee since 1983. He chaired the IJCAI Board of Trustees from 1983-85. He was the driving force behind the successful proposal to hold IJCAI-81 in Vancouver. This event marked Canadian AI on the international map, where it has played a prominent role ever since. Alan also was General Chair of IJCAI-85 in Los Angeles. That conference was the largest IJCAI ever, with more than 5,000 registered participants.

Alan played seminal roles both in the creation of the CIAR AIR program and of the Institute for Robotics and Intelligent Systems (IRIS). The CIAR AIR program officially began July 1, 1984. Alan was active in the workshops and meetings that preceded the official start of the AIR program. Alan was a member of the original AIR Program Coordinating Committee (1984-87) and, since 1988, a member of its Program Development Committee. IRIS, funded by the federal Networks of Centres of Excellence (NCE) program, officially began July 1, 1990. The proposal

for IRIS was submitted in November, 1988. Alan served as the Area Coordinator for the Computational Perception component of IRIS and was a member of the IRIS Steering and Research Committees during the critical period 1988-90. Alan was Project Leader for IRIS phase 1 project A-1, "Vision systems for recognition, tracking, and navigation." Alan served as a member of the IRIS phase 2 Steering Committee, in 1993, and is Project Leader for IRIS phase 2 project ISDE-6, "Constraint-based visual robotic systems." Since its creation in 1990, Alan also has been a member of IPACC, the IRIS/PREARN/AIR Coordinating Committee. IPACC attempts to coordinate, and obtain maximum synergy between, university-based research in IRIS and the AIR program and industry-based research supported by PREARN.

Alan has played a wide range of other organizational and service roles, both nationally and internationally. The list really is too long to enumerate further here.

### Training Of Students

At UBC, Alan has supervised 18 masters and six doctoral theses. His students have gone on to play leadership roles in university, government, and industry, both nationally and internationally. In addition, Alan has been on numerous other thesis supervisory committees. Alan also is a gifted teacher. His graduate courses consistently have high enrolments and attract significant numbers of students from other disciplines. Alan has an extremely high reputation among graduate students and has always been in great demand at UBC as a thesis supervisor. Students, past and present, consistently comment on Alan's openness, breadth of knowledge, freshness of ideas, high standards, and integrity.

From Alan's early years at UBC, one student recalls, "Alan was still a long hair ex-grad student and it took him awhile to progress to the distinguished professor that we know him as today. We all thought he was great because he was approachable and one of us, but with one big difference. He knew so much about AI and computer vision. So he was a real delight from the grad student point of view."

Another student's comments are typical. "Alan's ability to manage grad students always impressed me. At one point he was having meetings with upwards of ten students and I noticed that he treated them very differently— always finding the right way to spur them on in their pursuit of an education and a degree. In my own case, he nudged me a little but was always available for guidance when I asked. Then at the right time, he told me he was going to end my research assistantship which provided the impetus for me to wrap up my dissertation and graduate. I've seen a lot of graduate advisors and Alan is definitely one of the best."

Alan's role as mentor also is evident. Another student, now a professor too, notes, "I truly feel proud to be one of Alan's students. I admire Alan a great deal. I have been influenced by him to the extent that I am beginning to speak

like him — I asked my recent Ph.D. student, 'Are you sure you want to do a Ph.D. degree?' Alan once used the word demi-god to describe a distinguished researcher. It's about time we use it to describe Alan. I personally like to describe him as the walking encyclopedia."

Yet another student describes Alan as, "... a man who has played a major role in my adult life. Although Alan has achieved great stature in his field, I have always found him to be down-to-earth and very approachable. His objectivity, openness, and enthusiasm make him a true scientist. It has been a pleasure and a privilege to be able to work with him, and I hope I have been a worthy student."

Finally, another student says, "As a supervisor he has been invaluable: personable, compassionate, always open to new ideas, but, at the same time, strict. The standards of his own work are also required of his students. His students greatly benefited from his reputation. Finding a job was facilitated if people found out you had been a student of Alan's. Personally, there have been two people in my life who have had a major influence in shaping my professional career. Alan has been one of them."

### Research/Industry Interaction

I would characterize Alan's contributions to research/industry interaction at two levels. First, Alan has pursued his own research in the context of applications that are the most significant, given Canada's economic base and the needs of its industrial sector. This has included both the development of cross-disciplinary environments (people, resources, and research projects) to facilitate technology transfer and the specific aspects of Alan's own technical work. Alan's earlier Mapsee work, for example, explored the domain of spatial reasoning in the context of remote sensing and geographical information systems, a technology area of clear importance to Canadian industry. More recently, Alan has built, with Peter Lawrence and student Jane Mulligan, a model-based vision system for monitoring the movements of the boom, stick and bucket of an excavator, as applicable to teleoperation in forest harvesting. The system now operates in real-time, at 10 Hz, using hybrid parallel architectures. Canadian industry participates in the development of the associated special purpose hardware. Under Alan's leadership, the UBC group has a strong, documented record of technology transfer, including ideas, students, software, and now also hardware.

Second, Alan has been active at the national policy level. As a country, we still are struggling to figure out how to achieve effective interaction among universities, governments, and industry. Alan's involvement with the CIAR and IRIS, including the IRIS/PREARN/AIR Coordinating Committee, already has been mentioned. Over the years, Alan has been involved in many national grant selection, policy, and other advisory boards and committees. In most cases, research/industry interaction was an issue addressed. Clearly, Canada still is a long way from having

an effective industrial R&D strategy. Organizational terms-of-reference and policy documents are not sufficient. Nevertheless, Alan's passion and willingness to participate have had a positive influence.

### Conclusion

In the introduction to [5], Alan wrote: "The proper study of artificial intelligence is the design of computational systems that represent, use, and acquire knowledge to perceive, reason, communicate, and act. Under that definition, knowledge representation is the heart of artificial intelligence. Past and future success in building systems for vision, problem solving, planning, and language depend critically on progress in knowledge representation. Workers in the field have been prolific in proposing and exploiting a variety of knowledge representation schemes such as grammars, semantic nets, programs, logics, schemas, rules, constraints, and neural nets. However, as we explore in the world of knowledge representation we need navigational tools: the analogs of chart, compass, log, and sextant."

The navigational tools metaphor perhaps originates from Alan's sailing experience, since sailing is indeed one of his non-academic passions. The metaphor is a good one. Alan has provided the Canadian AI community with navigational tools in all the relevant areas: research, community service, training of students, and research/industry interaction. Alan is a leader among his peers and an outstanding role model for younger researchers and graduate students alike.

When I first congratulated Alan for winning the 1994 CSCSI Distinguished Service Award, his response was that he felt the award was premature, given that distinguished service awards often are perceived as lifetime achievement awards. In the sense of lifetime achievement, I agree that the award is premature. Even if we reset Alan's distinguished service clock to zero, I anticipate that he will be a deserving candidate for another distinguished service award in the next 10-15 years.

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*Robert J. Woodham received the B.A. (Honours) degree in Mathematics from the University of Western Ontario in 1971. Subsequently, he attended the Massachusetts Institute of Technology (MIT) where he was a member of the Artificial Intelligence Laboratory. At MIT, he received the S.M. (masters) and E.E. (Engineer)*

*degrees in 1974 and the Ph.D. degree in 1977. He continued as a postdoctoral research scientist in the MIT AI Lab until July, 1978. Based in large measure on creative recruiting by Alan Mackworth, Woodham became a faculty member at UBC in August, 1978, appointed jointly in Computer Science and Forestry. In July, 1984, he was appointed a Fellow of the CIAR Artificial Intelligence and Robotics program. Woodham was a principal investigator in Mackworth's Project A-1 in phase 1 of IRIS, and continues as a principal investigator in Mackworth's IRIS, phase 2 project ISDE-6. Woodham also is project leader for IRIS 2 project IC-5. He now is Professor and Associate Head of the UBC Department of Computer Science. His principal research interest is computational vision, including shape from shading, photometric stereo, optical flow and orientation-based representations of shape. Applications range from robotics to remote sensing and geographic information systems. Woodham can be reached at:*

Laboratory for Computational Intelligence  
Department of Computer Science  
University of British Columbia  
Vancouver, BC  
V6T 1Z4

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# AI/GI/VI '94 Conference Report

by Alain Désilets, NRC

The AI/GI/VI '94 conference was held in Banff on May 16-20. It consisted of two days of workshops, followed by the conference itself.

The following topics were covered by the AI conference:

1. Distributed AI: 1 day workshop
2. Learning: 1 day workshop + 3 sessions
3. Natural Language: 1 session
4. Modelling Physical Systems (called "Problem Solving" in the conference proceedings): 1 session
5. Reasoning and Knowledge Representation: 2 sessions
6. Planning and Search: 2 sessions
7. Evolutionary Algorithms: 1/2 day tutorial

Learning was a dominant theme, taking up one full-day workshop and one third of the conference sessions. An interesting trend was a change in the application area for Machine Learning. Almost none of the applications presented were about extracting patterns from massive quantities of data. Instead, Machine Learning applications seemed to focus on what Bruce MacDonald calls instructable systems. These are systems that learn a user's intent or preferences by observation.

There were three invited speakers. Bonnie Weber of the University of Pennsylvania talked about using animated agents with a human-like appearance that can respond to commands, such as "Pour a glass of water," as a testbed for natural language understanding. Hector Levesque of the University of Toronto talked about a formalism for describing the knowledge of a cognitive robot. The formalism also allows the description of the robot's abilities and the consequences of its actions. Stephen Judd of Siemens Corporation Research presented material that was a little

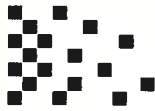
too technical for an invited talk. He presented a solution to a constraint satisfaction problem that he used to train a new artificial neural network architecture.

My favourite talk at the conference was Goldfarb, Abela, Bhavsar, and Kamat's "Are Vector Space Models Capable of Inductive Learning in a Symbolic Environment?" The talk presented a new model for inductive learning, called Evolving Transformation System (ETS). This model proposes a learning paradigm which differs significantly from Neural Nets and Tree Induction, which are the two paradigms I was most familiar with. Here, learning is achieved by applying certain basic transformations to data points, thereby collapsing them into smaller sets. The quality of the learning is determined by the ratio of the intra-class and inter-class distances. One advantage of this model is that you can choose basic transformation which is significant for the space where learning takes place. You can use character substitution, deletion, or insertion when points are strings, or you can use numerical operators when the points are numerical.

As a first time participant in an AI conference, I found the sessions interesting yet a bit too theoretical. I would like to hear less technical detail and more about applications to real-life problems. Nevertheless, the conference was stimulating and definitely worthwhile.

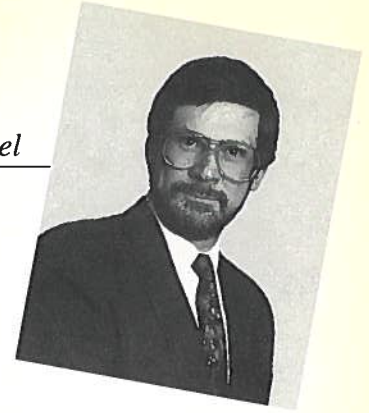
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*Alain Desilets is a research officer at the Knowledge Systems Laboratory of the National Research Council of Canada. His current research interests are in the application of Logic Programming and Constraint Satisfaction to finance, scheduling, and vehicle routing. He holds a Bachelors in Fundamental Mathematics and a minor in Education, both from University of Montreal, as well as a Masters in Management Sciences from the University of Waterloo. AI*



## PRECARN UPDATE NOUVELLES DE PRECARN

Jean-Claude Gavrel



### **Fourth Annual IRIS•PRECARN Conference**

"Emerging Opportunities" was the theme for this year's annual IRIS/PRECARN Conference, held in Toronto, on June 21-23. Over 400 delegates gathered to "see," "hear about" and "test" the technologies coming out of four years of research within the IRIS and PRECARN networks. Over 40 technologies were on display this year, either in the form of a live demonstration or a video, from a system for handwriting recognition to a spherically symmetrical walking robot. For the first time, non-members were invited to participate, and such companies took advantage of our offer.

The Conference opened with the Secretary of State and Minister for Science, the Honourable Jon Gerrard, remarking that: "... it is exciting to see what is happening, not only in the quality of the science, but in the excitement of the young people involved in the projects. It is also exciting to see the coupling and the partnerships between the universities and industry in this country, which present, in many areas, exciting possibilities not there before." Dr. Gerrard was then handed a pair of scissors by PRECARN's ARK robot to cut the Technology Exhibition ribbon, and officially open the Conference's Student Poster Area.

Once again this year, the students' participation in the Conference was one of the highlights, with over 100 posters vying for four prizes. This year's winners are:

#### **Computational Perception Area:**

Michael Kelly, Centre for Intelligent Machines, McGill University, "Extracting Perceptually Relevant Object Information Using Annular Symmetry Operators."

#### **Knowledge-Based Systems Area:**

Jinxin Lin, Department of Computer Science, University of Toronto, "Knowledge-Base Merging by Majority."

#### **Intelligent Robotics Area:**

Joseph Yan, Department of Electrical Engineering, University of British Columbia, "Design and Control of a Force-Reflecting Motion-Scaling Teleoperation System Using Magnetic Levitation."

#### **Technology Transfer Prize:**

Colin Carter, Department of Computer Science, University of Regina, "DBLearn and Knowledge Discovery From Large Databases."

By all accounts, this year's Conference was a success. The industrial participation was high, which was rewarding for the IRIS and PRECARN researchers who spent countless days and nights fine tuning their demonstrations and presentations. Another first this year was the extensive press coverage that we received through television coverage (CTV and CBC), and newspaper coverage (Toronto Star, Globe and Mail).

### **PRECARN's Strategic Plan**

In late June, PRECARN submitted its long-term Strategic Plan to the federal government. The Plan proposes a series of new research initiatives over the period 1995-1999. Some of these are:

- The Mining Automation Project; a five-year project to start in late 1994;
- A new competition for long-term research projects to start in 1995;
- A joint initiative with the Canadian Space Agency's STEAR Program;
- A new competition for short-term projects within the PERK program;
- A new program designed to interact with the IRIS Network.

Launching these exciting new initiatives will depend on the continued commitment of the federal government, as well as the support of PRECARN's Member companies. A decision by the federal government on the next phase of PRECARN is expected in the fall.

### **STEAR Program**

In mid-June, PRECARN issued its first Request for Research Proposals under its new joint initiative with the Canadian Space Agency's STEAR program. Organizations are invited to submit proposals in the areas of teleoperation, remote process control, human-machine interactions, and simulation and training. The program, to involve at least three PRECARN Member companies, will be carried out over a four-year period, including the feasibility study stage. At the time of writing, we expect to receive a large number of proposals by the deadline date, September 23, 1994. Copies of the RFP may be obtained from the PRECARN office.

To obtain more information on the PRECARN and IRIS networks, please contact Mrs. Lise McCourt, Manager of Corporate Affairs, at the following address:

PRECARN Associates Inc.

300-30 Colonnade Road, Nepean, Ontario  
K2E 7J6

Tel: (613) 727-9576, ext. 30 Fax: (613) 727-5672

E-Mail: precarn!iris!mccourt@ottawa.attmail.com





## BOOK REVIEWS

**Associative engines: Connectionism, concepts, and representational change** Andy Clark (University of Sussex) Cambridge, MA: The MIT Press, 1993, xiii+252 pp; hardbound, ISBN 0-262-03210-4, US\$29.95

Reviewed by  
Christopher D. Green  
York University

### "Fighting the good fight"

It goes without saying that connectionism is big in cognitive science these days. In fact, it is so big, that there are many — seemingly, most of the members of the Cognitive Science Society — who think that it just *is* cognitive science; that pretty well everything that goes by the names of experimental psychology, philosophy of mind, linguistics, and ("classical") AI is just so much alchemy, phlogiston, and . . . well, pick your favorite dead science.

It took connectionism a while to catch on, getting its start in the 1940's, going through some ups and down in the 1960's. After several technical innovations, the flame began to burn again in the early 1980's, bursting into a full-blown inferno soon after the publication of Rumelhart and McClelland's *Parallel distributed processing* in 1986. It is hard to believe that was less than a decade ago. Academic conferences, scholarly journals, and whole university departments have since sprung up dedicated to the proposition that connectionism constitutes the "proper treatment," to borrow Smolensky's famous phrase, of cognitive science.

The problem has been that, until very recently, much of this work has carried with it a "Gee whiz!" tone; the feeling that doing connectionist research is just so doggone much fun that it would be a shame to spoil it with sharp questions or incisive criticism. Although it is necessary, as philosopher of science Imre Lakatos said, to give new scientific research programs "breathing space," the grandness of the claims emanating from connectionist cognitive scientists rose to such dizzying heights in such short order that the old guard quickly came to the point where they felt it necessary to snap back, and hard. The best known of these counter-offensives was Fodor and Pylyshyn's (1988) "Connectionism and cognitive architecture," in which the authors argued that connectionist systems can only correctly model language (and thought itself) to the degree that they implement a traditional symbol processing system, and to the degree that they do that, the implemented symbol-processing model is

the cognitively interesting level of analysis. The Fodor and Pylyshyn paper "threw a scare into the field" as one connectionist (Chalmers, 1991) put it. Although many defenses of connectionism quickly followed, the celebratory tone ebbed somewhat, to be replaced by more sober and sophisticated thinking, not just about the networks themselves (the leading connectionists had always been technical wizards) but, more importantly, about the philosophical and theoretical issues involved. The real battle had just begun.

Andy Clark's latest book, *Associative Engines: Connectionism, Concepts, and Representational Change*, is from this second generation of connectionist work. It is thoughtful and intelligent in its attempts to grapple with some of the central problems of cognition, more particularly with the significant criticisms that have been sent connectionism's way since its arrival as a major player in cognitive science. His command of the connectionist literature is masterful. He includes a great deal of recent work — some *very* recent work — emanating from sources such as "hot" new journals like *Connection Science*, unpublished technical reports, and even Internet discussions. Perhaps even more importantly, his command of the literature *critical* of connectionism is masterful as well. Straw men are few, though some do turn up to advance the narrative flow.

This does not mean that the book is non-partisan. Despite Clark's claim to being "ecumenical" at the outset, the overall thrust of the book is that connectionism has (or soon will) overcome most every gauntlet that has been thrown in its path, and those difficulties that it has failed to redress have not yet been solved by the "classical" (i.e., serialist, symbol-processing) approach either. Jerry Fodor, not surprisingly, plays the part of Grendel in Clark's story but, as Clark is far more considerate than was Beowulf, Fodor is depicted more even-handedly and with more respect, even if it is clear from the start that he is destined to fail in the epic struggle that ensues. There is mention of a "Copernican revolution" in cognitive science, and many points where opponents' view of the connectionist Truth is obscured by their "infection" (as he calls it at one point) by the classical paradigm. In short, the book is a spirited, but valuable and intelligent, defense of connectionist cognitive science.

*Associative Engines* is divided into two parts, entitled "Melting the inner code" and "From code to process," respectively. The first section opens with a chapter that sets out the main distinctions between classical ("anti-developmental," "text-based," "folk-psychological") and connectionist ("developmental," "process-based," "non-folk-

psychological”) orientations. The most interesting feature is Clark’s rejection of the common assumption — advanced mainly by Stich and the Churchlands — that connectionism leads naturally to the elimination of the whole folk-psychological vocabulary (beliefs, desires, etc.). He argues that, “the legitimacy and the value of the folk solids [e.g., concepts, propositions, attitudes] are independent of the truth of the [Fodorian] Syntactic Image as an empirical model of mind” (p. 8). Thus, he has carved out an interesting position for himself, abandoning folk psychology as the basis of cognitive theory, but pulling up short of the precipice of eliminativism.

Chapter 2 is an unabashed advertisement for the “unique selling point(s)” of connectionism. These include the superposition and distribution of representations which, it is argued, result in a natural account of the semantic relatedness of representations. The use of “semantic” is somewhat idiosyncratic here. What Clark has in mind is that, in a network representing the shapes of letters, the pattern of activation representing “E” will be more similar to that for “F” than to that for “C” because they have more physical features in common. Interestingly, this leads one to think that one is about to get an account of how to interpret units in a distributed representation (surely, in the above example, the representations are distributed with respect to letters, but not with respect to the component line segments of letters, an ambiguity in “distributed representation” that has long bothered me). This is not to be, however. Uninterpretability of individual units turns out to be an almost necessary feature of successful connectionist models. In any case, the argument continues that connectionist virtues such as “automatic prototype extraction,” “generalization” (to new cases), “flexibility,” and, most importantly, “context sensitivity” are among the benefits conferred by distributed representation.

The last of these gets special attention, as it has been often been put to connectionists that, below the level of the global representation, the individual units must be constitutive of local representations (albeit ones that are difficult to interpret) and, thus, the difference between connectionist and classical systems is more apparent than real. The response seems to be that as one travels down from the level of the representation to the level of the units, one finds *more* context sensitivity rather than less; that, indeed, normal concepts such as COFFEE come at the *end* of the process, only as a sort of amalgamation of individual coffee-contexts (and, in turn, their derivative contexts), not as the starting point from which the contexts are developed.

Chapters 3 and 4 address, respectively, the questions of what connectionist network can and cannot be said to “know.” It is here that the account of what such a network might be said to *explain*, from a scientific perspective, is addressed. This is an important question, for many critics have charged that even if a network could simulate *all* human behaviour, it would be of, at best, limited scientific use as an *explanation*

of human behaviour. Clark argues for an inversion of the traditional explanatory process. The classical move, he explains, is to begin with a high-level description that specifies the kinds of abstract principles that generate the surface phenomena (Chomskyan linguistics is taken as the exemplar), and then to try to discover what kinds of increasingly concrete mechanisms (e.g., computational, then physiological, then molecular, etc.) could carry out the abstract ones. The connectionist vision is said to reverse this process: attend only to the surface phenomena of the domain itself (assume no underlying abstract principles), and then (dropping immediately to the “bottom” level) try to get a connectionist network to simulate them. Finally, through multivariate statistical processes such as cluster analysis and principal components analysis (PCA), work your way back “up” to find out what abstract principles describe the networks performance. As intriguing as this account of explanation is, one is forced to wonder, however, why one would assume, *a priori*, that the “bottom” level must be connectionist if one were not already a partisan. Is it now to be considered a methodological failing not to assume so?

Clark offers a number of important caveats about not treating the statistical analyses as being the “real” explanation, primarily because, useful as they may be, they fail to capture a number of important facts concerning the dynamic nature of the systems under study. This is all true, and a number of critics of connectionism have stumbled on this point in the past (although, he doesn’t discuss Hinton’s unsupervised learning networks which, as I understand them, actually do cluster analysis and PCA in order to produce their representations). Chapter 4 also includes discussions of Cussin’s notion of “non-conceptual content,” and the relevance of Karmiloff-Smith’s studies of the developmental aspects of picture-drawing to the development of expertise in connectionist systems.

Chapter 5, the last of Part I, goes over the same fairly old psychological material on concepts, categories, and prototypes. Whereas the rest of the book is notable for the recency of the material it contains, this one is something of a disappointment. Clark’s fluency with the psychological literature does not match that fluency he has with the connectionist. He calls prototype theory “an increasingly popular account,” whereas it seems that prototype theory in psychology is on the wane after having been very prominent from the mid-1970’s through to the mid-1980’s. What *is* true in Clark’s account is that connectionist networks have a natural affinity with theories of cognition in which prototypes (for all their problems) figure prominently, and have, thus, been picked up by a number of connectionist researchers. If they can revive the area — and I fear Clark’s arguments here are at their weakest, though still worth considering — then more power to them.

In the second part of the book, Clark explores a series of applications of recent connectionist research to long-standing problems in connectionism and, as the section progresses, in

cognitive science more generally. In chapter 6, he critically examines the notions of compositionality (i.e., the fact that what sentences mean is a function of what their component words mean) and explicitness of representation. Following van Gelder, and using examples from research by Smolensky and by Chalmers, he argues that systems can behave in ways that are *functionally compositional* even if they do not obviously concatenate symbols (as the sentences of language do). Then, following Kirsh, he argues that the explicitness of a representation is in the eye of the beholder — i.e., what may not seem explicit to us (e.g., the structure of representations in a connectionist network) may be perfectly obvious to a system designed to extract information stored in such a way (viz., the network itself). Transferring such knowledge to new domains has been a problem for connectionists — with context-sensitivity comes context-dependence, but even here, Clark argues, “progress has been made,” namely in the form of self-modularizing systems.

Chapter 7 explores explicitly the problems that several researchers have encountered getting their networks to generalize to new inputs. Of particular interest here is Elman’s attempts to teach a net the grammar of natural language. The featured solution to such problems is “phased training,” in which the training schedule of the network is customized such that it “sees” only the easiest, or most “central,” cases first, followed by a regime of gradual increase in the level of difficulty. This keeps the network from “search[ing] wildly” as Clark puts it, and getting, “lost in space(s).” All this is said to lead to a “forced union” (p. 145) between connectionism and developmental psychology. It seems far from clear, however, that children are given “phased training” in language. They hear all kinds of language all the time, and the current evidence is that the presence of simple “care-giver language” (a.k.a. “motherese”) — which I take to be the analog to the first phase of training — has *no impact at all* on the speed or ease with which children learn language.

The chapter closes with an explicit response to the famous Fodor-Pylyshyn systematicity argument. Why, asks Clark, should we assume that minds are preset to be systematic in their thinking just because they ultimately turn out that way? “Instead of treating [systematicity] as a property to be directly induced by a canny choice of basic architecture,” he argues, “it may be fruitful to try to treat it as intrinsic to the knowledge we want a system to acquire” (p. 148). And later, “although systematicity (in mature, adult human thought) is indeed pervasive, it need not be traced directly to the nature of the underlying cognitive architecture. Instead, it may be fruitful to try thinking of systematicity as a knowledge-driven achievement” (p. 150).

Chapter 8 focuses on a series of simulations in which stage-wise learning behaviour, reminiscent of that exhibited by children, is exhibited as a natural property of the networks’ learning procedure. Chapter 9 features the “artificial life”

research of Nolfi and Parisi, showing how connectionist networks can escape the criticism of being helpless hostages of their input sets. Through simulated evolution, new networks “come into the world” with initial weight sets that, while falling far short of the strong nativism advocated by Fodor, are predisposed to deal effectively with their input “environments.” Clark calls this endowment “minimal nativism.”

Chapter 10, for my part, is the most interesting. It is here, more than in any other part of the book, that Clark shows his estimable talents at Good Old Philosophy Of Mind (GOPhOM?). Here he returns to detail and defends the interesting claim made at the beginning of the book that one can be a connectionist without having to reject the vocabulary of Folk Psychology wholesale. He begins with a review of the considerations that drove Stich to eliminativism. At the risk of streamlining the story too much, Stich argues that if all our beliefs are stored in a superposed form (i.e., in a connectionist network), then no sense can be made of the claim that any one of them was responsible for a particular action. Since the activity of the *whole* net went into producing the output, *all* of our beliefs must be equally responsible. Thus, “belief” turns out to be a notion of little explanatory value. Skipping a lot of very interesting discussion in the interests of brevity, Clark’s response, in essence, is that although beliefs are not, in any straightforward way, the *causes* of our actions, they still play a role in explanations of our behaviour. By way of analogy, he points out that the claim, “the match lit because it was struck,” does not describe the causal microstructure of combustion, but it does give us a good counterfactual-supporting explanation (i.e., if the match hadn’t been struck, *ceteris paribus*, it wouldn’t have lit). Consequently, the fact that individual beliefs are not isolable in the network has little consequence for their ontological status or explanatory value: “the folk explanations,” Clark insists, “simply occupy a different arena” (p. 207). If this sounds suspiciously similar to the position Gilbert Ryle advanced in the 1940’s, it is, and Clark admits it is. But then this is not surprising, given that he explicitly aligns himself (almost) with Daniel Dennett, who (I believe) was a student of Ryle’s. Where Clark differs is where he, almost as an afterthought, declares that a True Believer (i.e., a being that can truly be said to have beliefs) must have the ability to evaluate the rationality of its past cognitive performance, and must have consciousness. About this he, unfortunately, says precious little else. Finally, there is a short chapter reviewing the main threads of argument woven throughout the book.

To wrap up: This is a very good book on a number of counts. It reviews the best of the most recent work in connectionist cognitive science. It carries out this task in a vigorously partisan, but by no means blind or unthinking way. It also does it in an entirely non-mathematical way (this will, of course, be an advantage for some, a frustration for others). It responds to the major criticisms of the connectionist

paradigm with interesting, informed, well-argued points. It shows how one might accept connectionism without having to embrace eliminativism in one and the same gesture. It is appropriate for a wide range of audiences: those professional cognitive scientists actively engaged in the battle and eager to hear the "latest word" from the connectionist camp, as well as those wanting to do a little "catching up." Graduate students who are just getting their first serious exposure to the promise of connectionist research in cognitive science will benefit from it as well. This book will go a long way.

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**Christopher D. Green** is with the History and Theory of Psychology Program at York University. His doctoral dissertation was entitled Reasoning and the connectionist modelling of deduction (University of Toronto, 1992). His related publications include "Cognitivism: Whose party is it anyway?" Canadian Psychology, 1994 and "Fodor, functions, physics, and fantasyland: Is AI a Mickey Mouse discipline?" (Journal of Experimental and Theoretical AI, in press).

### **The Phenomenon of Commonsense Reasoning: Nonmonotonicity, Action, and Information**

*Dimitrios Thanassas* (Philips Research Laboratories, Redhill, Surrey) Chichester: Ellis Horwood (Ellis Horwood series in artificial intelligence, edited by John Campbell), 1992, x+254 pp; hardbound, ISBN 0-13-663634-9, no price listed

Reviewed by  
Craig Boutilier

Department of Computer Science  
University of British Columbia

The study of nonmonotonic reasoning has become something of a small industry over the last twelve years. The supposed justification for the intense research on the topic is the ubiquity of the phenomenon, that nonmonotonicity pervades all aspects of commonsense reasoning. In *The Phenomenon of Commonsense Reasoning*, Dimitrios Thanassas attempts to put this perspective to good use by developing what might generously be called a "theory of everything" related to common sense reasoning. Some of the knowledge representation and reasoning theories

in which nonmonotonicity arises include theories of action, planning, causal reasoning, frames, scripts, analogical reasoning, and production systems. Thanassas proposes a nonmonotonic logic called *typicality logic*, which underlies his reconstruction of all of these theories. The sheer number and scope of the theories involved ensures this is a formidable task. It is further complicated by the diversity of the theories involved — it is hard to fathom a system that does a reasonable job of formally encompassing relatively precise, formal theories of action as well as more general, procedural notions such as scripts. While the goal is laudable, one should expect any attempt to unify "everything" — at this point in the development of AI — to be unsuccessful and even uninformative. Thanassas's proposal lives up to this expectation. The proposal is far too ambitious and attempts to incorporate far too much. As a result, no single topic is treated in a serious way and the result is an unconvincing, unifying framework with serious foundational difficulties and very superficial embeddings of notions such as scripts and frames within it. Had the research been focused on one or two of the individual topics here, the results might have been more interesting.

Before discussing the content in more detail, it should be noted that the book is based on the author's PhD thesis (Imperial College). It has the unfortunate look of an unedited thesis. It is fraught with stylistic, grammatical, and typographical errors that are sometimes amusing, mostly annoying, and consistently distracting. The notation and definitions use a strange mix of formal, semi-formal, and informal symbolism, perhaps reflecting the influence of the disparate topics addressed.

Chapter 1 is entitled "A Critique of Artificial Intelligence" and consists of a series of facile observations about how the wild claims of early AI research damaged the reputation and ultimate "marketability" of AI. Thanassas claims that AI researchers have "hid themselves within the barricades that they built around their beloved science," and that the key to successful AI research is the development of products and (of course) marketing. These arguments are familiar and tired and Thanassas's discussion adds nothing new. What this has to do with the rest of the book and its research program is not exactly clear.

It is best to think of the book as beginning with Chapter 2. Here, several theories of "common sense reasoning" are reviewed. Unfortunately, it is here that the structure of the book begins to break down. The theories reviewed are quite varied, and without a proper introduction, the reader has no idea why these *component* theories are important for common sense reasoning, nor how they should fit together in a general framework. The reader is left to fill in most of the motivation as examples in later chapters are encountered. First, several theories of default reasoning are mentioned, including predicate completion, default logic, and other classic systems. No motivation for the different approaches is provided, and it is not made clear what advantages one approach has over

another. Logical notation is used from the outset without introduction (or even a disclaimer that the reader is assumed to be familiar with predicate calculus notation and semantics). Next, theories of action are briefly reviewed, including Allen's interval logic and Shoham's temporal system. The situation calculus is surprisingly absent from the survey. Finally, "cognitive theories" of knowledge representation are reviewed. This is quite a grab-bag of systems, including frames and conceptual graphs, scripts, and analogical reasoning. Also thrown in is Newell and Simon's GPS, which is directly followed up (according to this survey) by Korf's work on heuristic search. The survey provides no detail about any of these theories, and does not give a very good sense of how these theories might be used or of their potential importance.

The survey chapter sets an unfortunate tone for the rest of the book and the theory the author sets forth. The survey presents an almost random collection of work from a number of different areas of AI, mixing some very formal work with some more general, procedural, or vague ideas. The theme that unifies this work is the inherent nonmonotonicity of the concepts they address — but this link can only be seen as the rest of the book is read. The research presented in the subsequent chapters has the same character, a somewhat undirected and unsatisfying blend of semi-formal and informal ideas.

Thanassas introduces *typicality logic* in Chapter 3, which serves as the formal foundation for the rest of the book. Intuitively, typicality logic is based on the idea of identifying and marking a set of assertions as *typicality sentences*. These are used in proofs of other sentences in the usual way, but any conclusions derived from a typicality sentence are also marked. Because such conclusions might conflict, a mechanism for retracting conclusions is assumed. Roughly, preference criteria for typicality sentences are supposed to exist and those conclusions based on less-preferred assumptions are retracted in the case of conflict. To call this a logic is a bit far-fetched. First, the mechanism for resolving conflicts is spelled out in little more detail than presented here, and surprisingly there is no discussion of truth maintenance systems. Second, the notion of preference is left entirely unanalyzed. Indeed, throughout the book, specific preference criteria are given in English (e.g., "Tweety is a bird and Tweety is a penguin, therefore Tweety flies and Tweety does not fly, but we prefer to conclude that Tweety does not fly because this is a monotonic conclusion whereas the conclusion that Tweety flies is a typicality (default) conclusion"). A semantics for typicality logic is provided, but it is not clear how to make sense of the proposal. While the concept of a model is left unelaborated, the semantics is based on the idea of submodels: one model is a submodel of another if the first satisfies fewer sentences than the second. Certainly, this notion cannot be applied to models in the classical sense, for any two distinct models are incomparable by this measure. Thus it is not clear what the semantic

definitions are intended to convey. The formal foundations of typicality logic are exceedingly shaky, and the rest of the book suffers because of it.

Chapter 4 studies typicality logic in more detail. The Yale shooting problem is studied in depth and a rather reasonable solution is proposed. The method is very reminiscent of that set forth by Delgrande (1987) in the context of conditional logic. Unfortunately, Thanassas dismisses conditional logic as not relevant to present concerns, even though it seems that of all default reasoning methods, this bears the most similarity (in motivation) to typicality logic. Some rather unconvincing theorems relating typicality logic to default logic, Poole's Theorist system, and Touretzky's inheritance system are given.

Causation is the subject of Chapter 5, and typicality is used to give a formal account of causal reasoning. This is a very difficult subject and a 15-page treatment cannot be satisfactory. The treatment is similar to Shoham's (1988) theory of causation, which is compared here. The key distinction is Thanassas's mechanism for reasoning from effects to causes, something missing in a number of logical accounts of causation. However, much work on causation in AI, especially causal network approaches and their logical counterparts, also provide such a facility. This chapter would benefit from a deeper and more comprehensive examination of other theories of causation. One weakness of the proposed theory is the fact that causes cannot have unknown exceptions. One cannot say A causes B and have A occur without B unless there is an explicitly stated exception to this causal rule and the exception is known to hold. Thus any defeasibility associated with causation is buried in the known exceptions. Nonmonotonicity arises only when the causal theory is "revised."

Chapter 6 deals with reasoning about action, and provides a theory of frames and scripts. Scripts and actions (or events) are related by virtue of the fact that a script is taken to be a prototypical sequence of events. The chapter starts with a very confused discussion trying to distinguish events from facts. The confusion seems to arise only because Thanassas wants to interpret events as objects that have truth-values. Again, the rest of the chapter gets bogged down in sloppy and (to my mind) incomprehensible distinctions. The formal definitions of scripts, frames, and inheritance are very hard to follow. A script is a sequence of events, and when one event occurs the next in the sequence is assumed to occur by default (thus the application of typicality logic). If exceptions arise, the entire script (from the point of the last known event) is aborted and no conclusions can be reached about subsequent events. Chapter 7 continues in this vein, discussing planning using scripts (where scripts reduce search, much in the spirit of macro-operators), as well as causal and analogical reasoning. It is not clear what benefit Thanassas's formalization of scripts and inheritance provides. It is very hard to understand, and is no more (perhaps less) precise than current theories.

Chapter 8 presents an extended example of a marketing knowledge-base system using scripts, frames, and typicality logic. The types of inference demonstrated by this example are fairly standard. Finally, Chapter 9 (unsurprisingly) shifts gears yet again to propose infodynamics, a “physical theory of knowledge and information,” partly motivated it seems by a fear that connectionists will start doing symbolic AI better than symbolic AI researchers. Infodynamics is claimed to be a start toward a theory that brings everything together. The aim is to describe the knowledge inherent in a logical system using notions such as entropy. Despite Thanassas’s denials, the definitions presented are much in the style of standard probability and information theory. The upshot is the unsurprising conclusion that a system that “jumps to conclusions” (though defined in a way that doesn’t apply to most formalisms) might have information increases and decreases as premises are added, while a monotonic system cannot. This picture has some rather startling implications for the nature of life, the Universe and God, according to Thanassas.

I have difficulty trying to find an audience to which I can recommend this book. It is not suitable for a general audience without a background in logic and AI. It is certainly not suitable for someone wishing to learn about common sense reasoning for the purposes of starting research in the area due to the relatively little attention given to individual theories and the style of presentation. Finally, I think researchers in the various areas touched on by this book will find little of interest here, unless their mailing address is in Santa Fe — and even then I’m skeptical.

## References

- Delgrande, James P. (1987). “An approach to default reasoning based on a first-order conditional logic.” *Artificial Intelligence*, 36, 63-90.
- Shoham, Yoav (1988). *Reasoning about Change*. Cambridge, MA: The MIT Press.

*Craig Boutilier is an Assistant Professor with the Department of Computer Science at the University of British Columbia. His research interests lie within the area of knowledge representation and reasoning: in particular, default reasoning, belief revision, probabilistic inference, explanation, reasoning about action, planning, decision theory, reinforcement learning, and philosophical logic.*

**Recent advances in qualitative physics** *Boi Faltings and Peter Struss (editors)* (Swiss Federal Institute of Technology and Siemens Corporate Research and Development) Cambridge, MA: The MIT Press (Artificial intelligence series, edited by J. Michael Brady, Daniel Bobrow, and Randall Davis), xii+449 pp; hardbound, ISBN 0-262-06142-2, US\$39.95

Reviewed by  
Rob Wylie  
National Research Council

## Overview

*Recent Advances in Qualitative Physics* is a collection of 28 papers drawn from the 3rd and 4th International Workshops on Qualitative Physics (Stanford, 1989 and Lugano, Switzerland, 1990). These workshops have served as an important forum for presenting and debating ideas within the QP research community, and the papers contained in this book reflect that fact. They provide an interesting but incomplete view of activities in QP during this period (with some quite noticeable gaps; for example, there is no mention of qualitative phase plane analysis).

In fact, this period in the history of QP is very interesting. It was around this time that the field widened from its original focus on qualitative simulation to include a range of other issues such as model construction and selection, hybrid qualitative-quantitative reasoning, and qualitative formulations of other analytical techniques. (Anyone interested in the motivation behind this shift of focus should check out the “Taking Issue” section of the May 1992 issue of *Computational Intelligence*.)

In the foreword, the editors state two objectives: to make available some unpublished and hard-to-find material from these workshops; and to update and complement the 1989 collection *Readings in Qualitative Physics* edited by Weld and de Kleer. By definition, the book satisfies the first of these (though most of the research reported on in this book is in fact documented elsewhere and is easily accessible). However, the book only partially succeeds with respect to its second goal. By including only papers presented at the QP Workshops, a lot of important material from this period has been missed. Also, the papers included in the book are often neither the primary nor the most comprehensible reference for a particular piece of research. These factors significantly reduce the book’s value as a reference volume.

## Some details

The book consists of four sections corresponding to the topics modelling and simulation, ontologies, computational issues, and qualitative analysis and design. Each section is introduced by a very brief summary of the papers it contains. I believe the book would have benefited from a more concerted attempt by the editors to overview the papers and place the research in context.

The papers in the first section are concerned with issues of modelling: model construction and reasoning with multiple models. Also (somewhat anomalously), three papers are included here that describe extensions of QP to exploit more expressive types of knowledge (fuzzy or quantitative representations of state).

Model construction and reasoning from multiple models continue to be very active areas of research. The papers by



Iwasaki, by Weld and Addanki, and by Forbus and Falkenhainer (all concerned with the problem of choosing model granularity and scope) form part of the foundation for the work going on today. Perhaps the most interesting paper for me in this section was Weld and Addanki's paper "Query-directed approximation" which discusses abstraction in QP and suggests a strategy for automatically constructing adequate, simple models specialized to particular queries.

Integrating qualitative and quantitative analysis is a very important practical problem, and there are many possible approaches. The paper by Forbus and Falkenhainer presents a scheme for using a qualitative simulation of a system to guide construction and control of a numerical simulation model. Berleant and Kuipers present a representation scheme and simulation engine capable of handling mixed models. In the paper by Shen and Leitch is a discussion of the use of fuzzy sets (instead of intervals) in QP. Two other papers on the integration of qualitative and quantitative reasoning are to be found in the final section of the book.

The second section is concerned with specialized methods for modelling different classes of physical system. Development of these 'ontologies' makes up a significant part of QP research. Especially entertaining is the short paper by Nypelseer, "Qualitative change waves: The automatic detection of highway traffic incidents." It is at once a practical solution to a real problem, and an example of the innovative application of QP ideas to a domain with unusual 'laws.'

The third section includes papers on computational aspects of QP. This is really a grab bag. One nice paper in this section is by Hamilton; it discusses the problem of building systems that can perform time-constrained qualitative reasoning. Another nice paper (by Doyle et al.) presents some interesting ideas about how to focus attention when trying to interpret large volumes of sensor data.

Finally, the section on qualitative analysis and design contains quite a few interesting papers. Brian William's paper on design is very interesting (though you may want to read one of his earlier papers on symbolic manipulation of mixed qualitative and quantitative expressions first). There are two papers discussing the use of qualitative models to guide numerical analysis (for some reason the editors failed to include a very nice paper by Sacks on this topic which was presented in the 3rd QP Workshop). There is a paper on determining causal orderings of variables in QP models (discussions of 'causality' are ubiquitous in the QP literature). Finally there are papers on the use of teleological information and on the use of abstractions ('thought experiments') to focus qualitative analysis.

### Conclusion

The papers in this book are of a reasonably high calibre and present interesting material. However, most of the material is covered by papers published elsewhere. Unless you have very specialized needs, you would probably be as

well served by reading the QP sections of the major AI conferences from the same period.

Finally, I feel some obligation to make the following broader observation. *Recent Advances in Qualitative Physics* is the third in a series of collections of QP papers targeted at an audience of AI researchers (the first was *Qualitative Physics*, edited by Bobrow in 1985). My introduction to QP consisted of reading the first of these, and I have found the second to be an extremely valuable reference book. The failure (in my opinion) of the third is at least partially due to the maturity of the field; QP has grown too large to be usefully represented by an unstructured collection of papers. What the field needs are decent syntheses of the work to date. It is to be hoped that in the near future we will see books that digest the (large volume of) QP research and present it in a coherent fashion to various audiences. The two books that I look forward to the most are a textbook suitable for senior undergraduate or graduate engineers, and a review of fielded QP applications.

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*Rob Wylie has worked at the National Research Council of Canada for twelve years. In the Divisions of Building Research and Energy he built simulation tools and conducted lab and field studies of the performance of heat-pump and solar-thermal systems. More recently, in the Institute for Information Technology he has been building knowledge-based systems to support engineering decision-making (especially as it pertains to the process industry). He holds bachelor's and master's degrees from the Department of Systems Design Engineering, University of Waterloo.*

## BRIEFLY NOTED

**The Soar papers** Paul S. Rosenbloom, John E. Laird, and Allen Newell (editors) (Information Sciences Institute, University of Michigan, and Carnegie Mellon University) Cambridge, MA: The MIT Press (Artificial intelligence series), 1993, xli+1438 pp in two volumes; hardbound, ISBN 0-262-68071-8, US\$95.00; paperbound, ISBN 0-262-68071-8, US\$65.00

"The Soar project is an attempt to develop and apply a unified theory of human and artificial intelligence," begins the introduction to this enormous collection. In the ten years since its inception, Soar has grown to become an enormous project, involving 90 people in many locations. Here, 68 papers are presented, covering Soar since its inception. Anyone interested in the architecture of cognition needs to know about Soar, and will find this collection to be a valuable resource. —G.H.

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Books marked with a + in the list below will be reviewed in a future issue. Reviewers are sought for books marked with a \*. Readers who wish to review books for *Canadian Artificial Intelligence* should write, outlining their qualifications, to the book review editor, Graeme Hirst, Department of Computer Science, University of Toronto, Toronto, Canada M5S 1A4, or send electronic mail to gh@cs.toronto.edu or gh@cs.utoronto.ca. Obviously, we cannot promise the availability of books in anyone's exact area of interest.

Authors and publishers who wish their books to be considered for review in *Canadian Artificial Intelligence* should send a copy to the book review editor at the address above. All books received will be listed, but not all can be reviewed.

**Artificial intelligence in perspective** *Daniel G. Bobrow (editor)* (Xerox Palo Alto Research Center) First published as a special issue of *Artificial Intelligence*, 59(1-2), 1993. Cambridge, MA: The MIT Press, 1994, 462 pp; paperbound, ISBN 0-262-52186-5, US\$35.00

\* **Thinking between the lines: Computers and the comprehension of causal descriptions** *Gary C. Borchardt* [MIT] Cambridge, MA: The MIT Press (Artificial intelligence series, edited by Michael Brady, Daniel Bobrow, and Randall Davis), 1994, xii+298 pp; hardbound, ISBN 0-262-02374-1, US\$35.00

**Statistical language learning** *Eugene Charniak* (Brown University) Cambridge, MA: The MIT Press (A Bradford book), 1993, xx+170 pp; hardbound, ISBN 0-262-03216-3, US\$25.00

**Natural language processing for Prolog programmers** *Michael A. Covington* (University of Georgia) Englewood Cliffs, NJ: Prentice-Hall, 1994, xvi+348 pp; hardbound, ISBN 0-13-629213-5, no price listed

**Constraint-based reasoning** *Eugene C. Freuder and Alan K. Mackworth (editors)* (University of New Hampshire and University of British Columbia) First published as a special issue of *Artificial Intelligence*, 58(1-3), 1993. Cambridge, MA: The MIT Press, 1994, 403 pp; paperbound, ISBN 0-262-56075-5, US\$34.95

**Readings in philosophy and cognitive science** *Alvin I. Goldman* (University of Arizona) Cambridge, MA: The MIT Press (A Bradford book), 1993, xi+860 pp; paperbound, ISBN 0-262-57100-5, US\$29.95

**Speech-to-speech translation: A massively parallel memory-based approach** *Hiroaki Kitano* (Carnegie Mellon University and Sony Computer Science Laboratory, Tokyo) Boston: Kluwer Academic Publishers (The Kluwer international series in electrical engineering and computer science; natural language processing and machine translation, edited by *Jaime Carbonell*), 1994, xvii+193 pp; hardbound, ISBN 0-7923-9425-9, US\$85.00

+ **Decision-analytic intelligent systems: Automated explanation and knowledge acquisition** *David A. Klein* (Boston University) Hillsdale, NJ: Lawrence Erlbaum Associates, 1994, xi+220 pp; hardbound, ISBN 0-8058-1105-2, US\$49.95

**Natural language processing** *Fernando C. N. Pereira and Barbara J. Grosz* (AT&T Bell Laboratories and Harvard University) First published as a special issue of *Artificial Intelligence*, 63(1-2), 1993. Cambridge, MA: The MIT Press, 1994, 531 pp; paperbound, ISBN 0-262-66092-X, US\$35.00

+ **Hybrid neural network and expert systems** *Larry R. Medsker* (The American University) Boston: Kluwer Academic Publishers, 1994, x+240 pp; hardbound, ISBN 0-7923-9423-2, US\$87.50

\* **A symbolic and connectionist approach to legal information retrieval** *Daniel E. Rose* (Apple Computer Inc) Hillsdale, NJ: Lawrence Erlbaum Associates, 1994, xvi+314 pp; hardbound, ISBN 0-8058-1388-8, US\$59.95

\* **Inside case-based explanation** *Roger C. Schank, Alex Kass, and Christopher K. Riesbeck (editors)* [Northwestern University] Hillsdale, NJ: Lawrence Erlbaum Associates (Artificial intelligence series), 1994, xviii+416 pp; hardbound, ISBN 0-8058-1028-5, US\$59.95; paperbound, ISBN 0-8058-1029-3, US\$22.50

**Reversible grammar in natural language processing** *Tomek Strzalkowski (editor)* (New York University) Boston: Kluwer Academic Publishers (The Kluwer international series in electrical engineering and computer science; natural language processing and machine translation, edited by *Jaime Carbonell*), 1994, xxi+454 pp; hardbound, ISBN 0-7923-9416-9, US\$130.00

\* **Autologic** *Neil Tennant* (The Ohio State University) Edinburgh University Press (Edinburgh Information Technology Series), 1992, xiii+239 pp; hardbound, ISBN 0-7486-0358-1, no price listed

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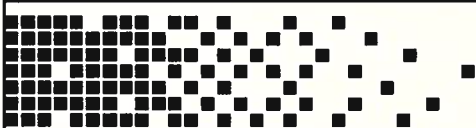
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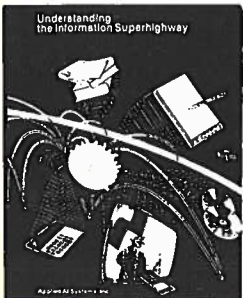
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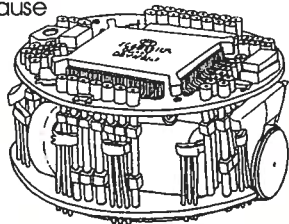
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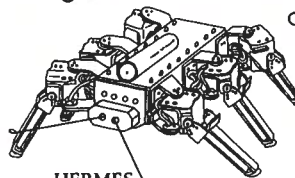
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