

An Indexed Bibliography of Genetic Algorithms in Biosciences

compiled by

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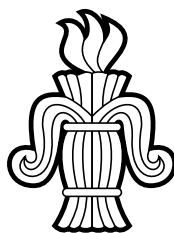
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Warning

While this bibliography has been compiled with the utmost care, the editor takes no responsibility for any errors, missing information, the contents or quality of the references, nor for the usefulness and/or the consequences of their application. The fact that a reference is included in this publication does not imply a recommendation. The use of any of the methods in the references is entirely at the user's own responsibility. Especially the above warning applies to those references that are marked by trailing '†' (or '*'), which are the ones that the editor has unfortunately not had the opportunity to read. An abstract was available of the references marked with '*'.

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Chapter 1

Preface

“Living organism are consummate problem solvers.
They exhibit a versatility that puts the best computer
programs to shame.”

John H. Holland [1]

The material of this bibliography has been extracted from the genetic algorithm bibliography [2], which when this report was compiled contained 10684 items and which has been collected from several sources of genetic algorithm literature including Usenet newsgroup `comp.ai.genetic` and the bibliographies [3, 4, 5, 6]. The following index periodicals have been used systematically

- ACM: *ACM Guide to Computing Literature*: 1979 – 1993/4
- BA: *Biological Abstracts*: July 1996 - Nov. 1997
- ChA: *Chemical Abstracts*: Jan. 1997 - Aug. 1998
- CA: *Computer Abstracts*: Jan. 1993 – Feb. 1995
- CCA: *Computer & Control Abstracts*: Jan. 1992 – Apr. 1998 (except May -95)
- CTI: *Current Technology Index* Jan./Feb. 1993 – Jan./Feb. 1994
- DAI: *Dissertation Abstracts International*: Vol. 53 No. 1 – Vol. 56 No. 10 (Apr. 1996)
- EEA: *Electrical & Electronics Abstracts*: Jan. 1991 – Apr. 1997
- P: *Index to Scientific & Technical Proceedings*: Jan. 1986 – Dec. 1997 (except Nov. 1994)
- A: *International Aerospace Abstracts*: Jan. 1995 – Mar. 1998
- N: *Scientific and Technical Aerospace Reports*: Jan. 1993 - Dec. 1995 (except Oct. 1995)
- EI A: *The Engineering Index Annual*: 1987 – 1992
- EI M: *The Engineering Index Monthly*: Jan. 1993 – Apr. 1998 (except May 1997)

1.1 Your contributions erroneous or missing?

The bibliography database is updated on a regular basis and certainly contains many errors and inconsistencies. The editor would be glad to hear from any reader who notices any errors, missing information, articles etc. In the future a more complete version of this bibliography will be prepared for the genetic algorithms in biosciences research community and others who are interested in this rapidly growing area of genetic algorithms.

When submitting updates to the database, paper copies of already published contributions are preferred. Paper copies (or ftp ones) are needed mainly for indexing. We are also doing reviews of different

aspects and applications of GAs where we need as complete as possible collection of GA papers. Please, do not forget to include complete bibliographical information: copy also proceedings volume title pages, journal table of contents pages, etc. Observe that there exists several versions of each subbibliography, therefore **the reference numbers are not unique and should not be used alone in communication**, use the key appearing as the last item of the reference entry instead.

Complete bibliographical information is really helpful for those who want to find your contribution in their libraries. If your paper was worth writing and publishing it is certainly worth to be referenced right in a bibliographical database read daily by GA researchers, both newcomers and established ones.

For further instructions and information see `ftp.uwasa.fi/cs/GAbib/README`.

1.1.1 How to cite this report?

The complete BiBTeX record for this report is shown below:

```
@TECHREPORT{gaBIObib,
  KEY = "BIO",
  ANNOTE = "*on,*FIN,bibliography /special",
  AUTHOR = "Jarmo T. Alander",
  TITLE = "Indexed Bibliography of Genetic Algorithms in Biosciences",
  INSTITUTION = "University of Vaasa, Department of Information Technology and Production Economics",
  TYPE = "Report",
  NUMBER = "94-1-BIO",
  NOTE = "(\ftp{ftp.uwasa.fi}{cs/report94-1}{gaBIObib.ps.Z})",
  YEAR = 1995
}
```

You can also use the BiBTeX file `GASUB.bib`, which is available in our ftp site `ftp.uwasa.fi` in directory `cs/report94-1` and contains records for all GA subbibliographies.

1.2 How to get this report via Internet?

Versions of this bibliography are available via anonymous ftp and www from the following sites:

<i>media</i>	<i>country</i>	<i>site</i>	<i>directory</i>	<i>file</i>
ftp	Finland	<code>ftp.uwasa.fi</code>	<code>/cs/report94-1</code>	<code>gaBIObib.ps.Z</code>
www	Finland	<code>http://www.cs.hut.fi</code>	<code>~ja/gaBIObib</code>	<code>gaBIObib.html</code>

Observe that these versions may be somewhat different and perhaps reduced as compared to this volume that you are now reading. Due to technical problems in transforming L^AT_EX documents into html ones the www versions contain usually less information than the corresponding ftp ones. It is also possible that the www version is completely unreachable.

The directory also contains some other indexed GA bibliographies shown in table 1.1.

1.3 Acknowledgement

The editor wants to acknowledge all who have kindly supplied references, papers and other information on genetic algorithms in biosciences literature. At least the following GA researchers have already kindly supplied their complete autobibliographies and/or proofread references to their papers: Dan Adler, Patrick Argos, Jarmo T. Alander, James E. Baker, Wolfgang Banzhaf, Helio J. C. Barbosa, Hans-Georg Beyer, Christian Bierwirth, Joachim Born, Ralf Bruns, I. L. Bukatova, Thomas Bäck, David E. Clark, Yuval Davidor, Dipankar Dasgupta, Marco Dorigo, J. Wayland Eheart, Bogdan Filipič, Terence C. Fogarty, David B. Fogel, Toshio Fukuda, Hugo de Garis, Robert C. Glen, David E. Goldberg, Martina Gorges-Schleuter, Hitoshi Hemmi, Vasant Honavar, Jeffrey Horn, Aristides T. Hatjimihail, Mark J. Jakiela, Richard S. Judson, Bryant A. Julstrom, Charles L. Karr, Akihiko Konagaya, Aaron Konstam, John R. Koza, Kristinn Kristinsson, D. P. Kwok, Gregory Levitin, Carlos B. Lucasius, Michael de la Maza, John R. McDonnell, J. J. Merelo, Laurence D. Merkle, Zbigniew Michalewics, Melanie Mitchell, David

<i>file</i>	<i>contents</i>
ga90bib.ps.Z	GA in 1990
ga91bib.ps.Z	GA in 1991
ga92bib.ps.Z	GA in 1992
ga93bib.ps.Z	GA in 1993
ga94bib.ps.Z	GA in 1994
ga95bib.ps.Z	GA in 1995
ga96bib.ps.Z	GA in 1996
ga97bib.ps.Z	GA in 1997
gaAIBib.ps.Z	GA in artificial intelligence
gaALIFEBib.ps.Z	GA in artificial life
gaARTBib.ps.Z	GA in art and music
gaAUSBib.ps.Z	GA in Australia
gaBASICSBib.ps.Z	Basics of GA
gaBIOBib.ps.Z	GA in biosciences including medicine
gaCADBib.ps.Z	GA in Computer Aided Design
gaCHEMPHYSBib.ps.Z	GA in chemistry and physics
gaCONTROLBib.ps.Z	GA in control
gaCSBib.ps.Z	GA in computer science (incl. databases and GP)
gaDBBib.ps.Z	GA in databases
gaECOBib.ps.Z	GA in economics and finance
gaENGBib.ps.Z	GA in engineering
gaESBib.ps.Z	Evolution strategies
gaFAR-EASTBib.ps.Z	GA in the Far East (Japan etc)
gaFRABib.ps.Z	GA in France
gaFTPBib.ps.Z	GA papers available via ftp
gaFUZZYBib.ps.Z	GA and fuzzy logic
gaGERBib.ps.Z	GA in Germany
gaGPBib.ps.Z	genetic programming
gaIMPLEBib.ps.Z	implementations of GA
gaISBib.ps.Z	immune systems
gaJOURNALBib.ps.Z	journal articles
gaLOGISTICSBib.ps.Z	GA in logistics
gaMANUBib.ps.Z	GA in manufacturing
gaMEDITERBib.ps.Z	GA in the Mediterranean
gaNNBib.ps.Z	GA in neural networks
gaNORDICBib.ps.Z	GA in Nordic countries
gaOPTIMIBib.ps.Z	GA and optimization (only a few refs)
gaOPTICSBib.ps.Z	GA in optics and image processing
gaORBib.ps.Z	GA in operations research
gaPARABib.ps.Z	Parallel and distributed GA
gaPOWERBib.ps.Z	GA in power engineering
gaPROTEINBib.ps.Z	GA in protein research
gaROBOTBib.ps.Z	GA in robotics
gaSABib.ps.Z	GA and simulated annealing
gaSIGNALBib.ps.Z	GA in signal and image processing
gaTHEORYBib.ps.Z	Theory and analysis of GA
gaTOP10Bib.ps.Z	Authors having at least 10 GA papers
gaUKBib.ps.Z	GA in United Kingdom
gaVLSIBib.ps.Z	GA in VLSI design and testing

Table 1.1: Indexed GA subbibliographies.

J. Nettleton, Volker Nissen, Ari Nissinen, Tomasz Ostrowski, Kihong Park, Nicholas J. Radcliffe, Colin R. Reeves, Gordon Roberts, David Rogers, Ivan Santibáñez-Koref, Marc Schoenauer, Markus Schwehm, Hans-Paul Schwefel, Michael T. Semertzidis, Moshe Sipper, William M. Spears, Donald S. Szarkowicz, El-Ghazali Talbi, Masahiro Tanaka, Leigh Tesfatsion, Peter M. Todd, Marco Tomassini, Andrew L. Tunson, Jari Vaario, Gilles Venturini, Hans-Michael Voigt, Roger L. Wainwright, D. Eric Walters, James F. Whidborne, Steward W. Wilson, Xin Yao, and Xiaodong Yin.

The editor also wants to acknowledge Elizabeth Heap-Talvela for her kind proofreading of the manuscript of this bibliography.

Chapter 2

Introduction

The table 2.1 gives the queries that have been used to extract this bibliography. The query system as well as the indexing tools used to compile this report from the BiBTeX-database [7] have been implemented by the author mainly as sets of simple `awk` and `gawk` programs [8, 9].

<i>string</i>	<i>field</i>	<i>class</i>
agriculture	ANNOTE	Agriculture
biology	ANNOTE	Biology
biochem	ANNOTE	Biochemistry
drug	ANNOTE	Pharmacy
evolution,	ANNOTE	Evolution
evolution /modeling	ANNOTE	Evolution modeling
pharmacy	ANNOTE	Pharmacy
DNA	ANNOTE	DNA
environmen	ANNOTE	Environmental sciences
pollution	ANNOTE	Environmental sciences
horticulture	ANNOTE	Agriculture
protein	ANNOTE	Proteins
medicine	ANNOTE	Medicine
medical	ANNOTE	Medicine
MEDLINE	ANNOTE	In MEDLINE database
psycholo	ANNOTE	Psychology

Table 2.1: Queries used to extract this subbibliography from the main database.

Chapter 3

Statistical summaries

This chapter gives some general statistical summaries of genetic algorithms in biosciences literature. More detailed indexes can be found in the next chapter.

References to each class (c.f table 2.1) are listed below:

- **Agriculture** 18 references ([10]-[27])
- **Biochemistry** 13 references ([28]-[40])
- **Biology** 34 references ([41]-[74])
- **DNA** 42 references ([75]-[116])
- **Environmental sciences** 25 references ([117]-[141])
- **Evolution** 28 references ([142]-[169])
- **In MEDLINE database** 13 references ([170]-[182])
- **Medicine** 107 references ([183]-[289])
- **Pharmacy** 11 references ([290]-[300])
- **Proteins** 192 references ([301]-[492])
- **Psychology** 3 references ([493]-[495])

Observe that each reference is included (by the computer) only to one of the above classes (see the queries for classification in table 2.1; query order gives priority for classes).

3.1 Publication type

This bibliography contains published contributions including reports and patents. All unpublished manuscripts have been omitted unless accepted for publication. In addition theses, PhD, MSc etc., are also included whether or not published somewhere.

Table 3.1 gives the distribution of publication type of the whole bibliography. Observe that the number of journal articles may also include articles published or to be published in unknown forums.

<i>type</i>	<i>number of items</i>
book	2
section of a book	2
part of a collection	19
journal article	239
proceedings article	192
report	15
manual	1
PhD thesis	12
MSc thesis	4
<i>total</i>	486

Table 3.1: Distribution of publication type.

3.2 Annual distribution

Table 3.2 gives the number of genetic algorithms in biosciences papers published annually. The annual distribution is also shown in fig. 3.1. The average annual growth of GA papers has been approximately 40 % during almost the last twenty years.

3.3 Classification

Every bibliography item has been given at least one describing keyword or classification by the editor of this bibliography. Keywords occurring most are shown in table 3.3.

3.4 Authors

Table 3.4 gives the most productive authors.

<i>year</i>	<i>items</i>	<i>year</i>	<i>items</i>
1967	2	1968	0
1969	0	1970	0
1971	0	1972	1
1973	1	1974	0
1975	0	1976	0
1977	1	1978	0
1979	1	1980	1
1981	0	1982	0
1983	0	1984	0
1985	4	1986	2
1987	1	1988	0
1989	3	1990	6
1991	11	1992	22
1993	64	1994	80
1995	81	1996	95
1997	90	1998	20
<i>total</i>			486

Table 3.2: Annual distribution of contributions.

protein folding	111
proteins	84
medicine	75
evolution	38
chemistry	36
image processing	35
biology	29
neural networks	24
DNA	23
comparison	22
medical imaging	20
hybrid	20
genetic programming	19
engineering	16
agriculture	16
simulation	14
population size	14
parallel GA	14
implementation	13
biochemistry	13
machine learning	12
macromolecules	11
environment	11
imaging	10
others	1088

Table 3.3: The most popular subjects.

total number of authors	890
Dandekar, Thomas	11
Moult, John	11
3 authors	8
3 authors	7
4 authors	6
12 authors	5
8 authors	4
45 authors	3
135 authors	2
677 authors	1

Table 3.4: The most productive genetic algorithms in biosciences authors.

3.5 Geographical distribution

The following table gives the geographical distribution of authors, when the country of the author was known. Over 80% of the references of the main database are classified by country.

<i>country</i>	<i>abs</i>	<i>%</i>
<i>Total</i>	486	100.00
United States	166	34.16
Japan	50	10.29
United Kingdom	46	9.47
Germany (incl. DDR)	42	8.64
Unknown country	37	7.61
Italy	13	2.67
The Netherlands	12	2.47
Australia	8	1.65
Canada	7	1.44
Finland	7	1.44
France	7	1.44
China (incl. Hong Kong)	5	1.03
Taiwan R.o.C.	5	1.03
Cyprus	3	0.62
India	3	0.62
Russia	3	0.62
Venezuela	3	0.62
Austria	2	0.41
Brazil	2	0.41
Denmark	2	0.41
Mexico	2	0.41
Poland	2	0.41
Switzerland	2	0.41
Belgium	1	0.21
Bulgaria	1	0.21
Czech Republic	1	0.21
Norway	1	0.21
Singapore	1	0.21
Slovak Republic	1	0.21
Spain	1	0.21

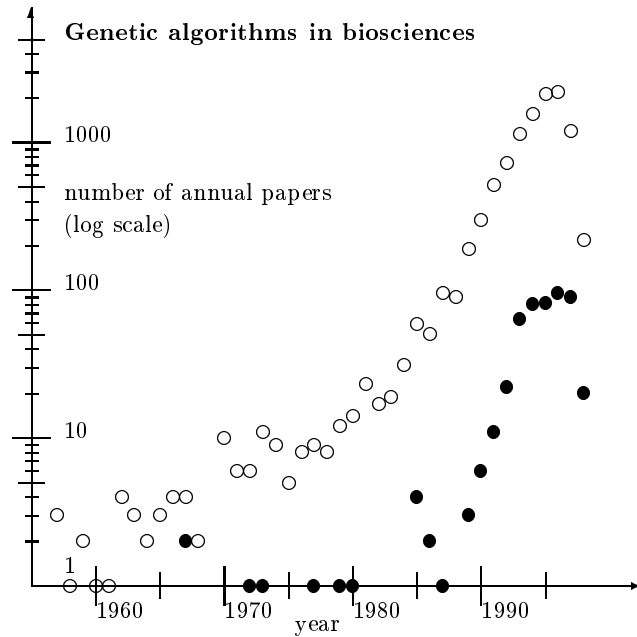


Figure 3.1: The number of papers applying **genetic algorithms in biosciences** (●) ○ = total GA papers. Observe that the last two years are most incomplete in the database.

Table 3.5: The geographical distribution of the authors.

3.6 Conclusions and future

The editor believes that this bibliography contains references to most genetic algorithms in biosciences contributions upto and including the year 1998 and the editor hopes that this bibliography could give some help to those who are working or planning to work in this rapidly growing area of genetic algorithms.

Chapter 4

Indexes

4.1 Books

The following list contains all items classified as books.

- Climbing Mount Improbable, [53]
The Origins of Order, Self-Organization and Selection in Evolution, [164]
total 2 books

4.2 Journal articles

The following list contains the references to every journal article included in this bibliography. The list is arranged in alphabetical order by the name of the journal.

- ACOUSTICA, [277]
Adaptive Behavior, [69]
Am. J. Math. Manage. Sci. (USA), [96]
Analytica Chimica Acta, [468]
Analytical Chemistry, [178, 36]
Artificial Life, [256]
Artificial Organs, [281]
Atmospheric Environment Part A General Topics, [137]
Behavioural Ecology and Sociobiology, [67]
Biochemistry, [403, 420]
Biochimica et Biophysica Acta – Protein Structure and Molecular Enzymology, [438]
Bioinformatics, [104, 39]
Biological Cybernetics, [47, 156, 158]
Biomedizinische Technik, [288]
Biophysical Chemistry, [172]
Biophysical Journal, [331, 341, 394]
Biophysics Journal, [33, 359]
Biopolymers, [422, 467]
Biosystems, [177]
BioSystems, [51]
Biosystems, [180]
BioSystems, [58, 63]
British Journal of Psychology, [493]
Canadian Journal of Fisheries and Aquatic Sciences, [46]
Cancer Letters, [240]
Chemical Physics Letters, [492]
Chemistry and Biology, [367]
Chemometrics and Intelligent Laboratory Systems, [407]
Chin. Sci. Bull., [434]
Chinese Chemical Letters, [412]
Complex Systems, [155]
Complexity (USA), [151]
Comput. Appl. Biosci., [182]
Comput. Chem. (UK), [374]
Comput. Electron. Agric., [12]
Computer, [120]
Computer Applications in the Biosciences (CABIOS), [327, 361]
Computer-Aided Innovation of New Materials, [478]
Computers and Electronics in Agriculture, [24, 25]
Computers in Biology and Medicine, [71]
Computers & Chemistry, [31]
Computers & Mathematics with Applications, [275]
Control Eng. Pract., [14]
Current Opinion in Structural Biology, [363, 390, 480]
Discrete Applied Mathematics (Netherlands), [85]
Drug Discovery Today, [295]
Electronics Letters, [200]
Endocytobiosis and Cell Research, [366]
Eng. Intell. Syst. Electr. Eng. Commun. (UK), [132]
Environmental Science & Technology, [122]
Evolutionary Computation, [494]
Expert Opinion on Therapeutic Patents, [297]

Folding and Design, [369, 439]
 Fortschrittsberichte der VDI-Zeitschriften, [269]
 Fujitsu Sci. Tech. J. (Japan), [86]
 Gaodeng Xuexiao Huaxue Xuebao, [410]
 Genome Inf. Ser., [377]
 Health Physics, [252]
 Huaxue Jinzhan, [298]
 IEEE Comput. Sci. Eng., [421]
 IEEE Eng. Med. Biol., [193]
 IEEE Expert, [48]
 IEEE Trans. Biomed. Eng. (USA), [249]
 IEEE Transaction on Neural Networks, [262]
 IEEE Transactions on Biomedical Engineering, [238, 282]
 IEEE Transactions on Evolutionary Computation, [154]
 IEEE Transactions on Medical Imaging, [242, 196, 215]
 IEEE Transactions on Neural Networks, [143, 247]
 IEEE Transactions on Power Systems, [134]
 IMA Journal of Mathematics Applied in Medicine and Biology, [91]
 Image and Vision Computing, [216]
 Information Processing Letters, [276]
 Int. J. Biomed. Comput. (Ireland), [220]
 International Journal of Biological Macromolecules, [379]
 International Journal of Control, [246]
 International Journal of Peptide and Protein Research, [170]
 International Journal of Quantum Chemistry, [460]
 J. Acoust. Soc. Am. (USA), [99]
 Joho Shori, [370, 381]
 Journal of Applied Physiology, [263]
 Journal of Biomolecular NMR, [352, 372, 92]
 Journal of Biomolecular Structure & Dynamics, [423, 489]
 Journal of Chemical Information and Computer Sciences, [302, 386, 397, 415, 440, 445, 448, 450, 451, 469]
 Journal of Chemical Physics, [416]
 Journal of Computational Chemistry, [346, 347, 358, 388, 400, 404, 414, 461, 462, 490]
 Journal of Computer-Aided Molecular Design, [32, 173, 354, 176, 428, 38]
 Journal of Economic Behaviour and Organization, [166]
 Journal of General Virology, [258]
 Journal of Global Optimization, [464]
 Journal of Japanese Society for Artificial Intelligence, [113]
 Journal of Medicinal Chemistry, [28, 345, 432, 437]
 Journal of Molecular Biology, [307, 174, 365, 396, 408, 417, 429, 477]
 Journal of Molecular Graphics, [181]
 Journal of Molecular Graphics and Modelling, [411, 444]
 Journal of Molecular Modeling, [402]
 Journal of Molecular Modelling, [406]
 Journal of Molecular Structure: THEOCHEM, [443]
 Journal of Neuroscience Techniques, [194]
 Journal of Physical Chemistry, [315, 30, 382]
 Journal of the American Chemical Society, [413]
 Journal of Theoretical Biology, [171, 179, 57, 59, 60, 161, 479]
 Lancet, [243]
 M. D. Comput. (USA), [237]
 Machine Learning, [83]
 Magn. Reson. Imaging (USA), [203]
 Measurement Science & Technology, [229, 190]
 Medical Engineering and Physics, [259]
 Medical Physics, [244, 248]
 Medical Physics (Woodbury), [260]
 Methods of Information in Medicine, [283]
 Molecular Simulation, [318, 418]
 Molecular Simulations, [446]
 Nature, [350]
 Nature Biotechnology, [431]
 Nature-Structural Biology, [291]
 Neural Computat. Appl., [433]
 Nippon Kikai Gakkai Ronbunshu C Hen, [251]
 Nucleic Acids Research, [175, 88]
 Opt. Rev. (Japan), [210]
 Pattern Recognit. (UK), [261]
 Pattern Recognition Letters, [209]
 Pharmaceutical Research, [442]
 Physica D, [145, 148, 64]
 Proceedings of the National Academy of Sciences of the United States of America, [303, 312, 349, 447]
 Proceedings of the Royal Society of London Series B Biological Sciences, [61]
 Protein Engineering, [319, 336, 368, 430, 435, 453]
 Protein Science, [306, 339, 391, 419, 441, 481, 487]
 Proteins, [323]
 Proteins: Structure, Function, and Genetics, [340, 356, 378, 395, 409, 424, 426, 436, 452]
 Quantitative Structure-Activity Relationships, [317, 329]
 SAR and QSAR in Environmental Research, [449]
 Seisan Gijyutsu, [105]
 Signal Processing, [206]
 Supramol. Chem., [357]
 THEOCHEM, [29]
 Trans. Inf. Process. Soc. Jpn., [360]
 Trans. Inf. Process. Soc. Jpn. (Japan), [89, 90]
 Transactions of the Institute of Electronics, Information and Communication Engineers A (Japan), [22]
 Transactions of the Society of Instrument and Control Engineers (Japan), [11]
 Trends in Biotechnology, [362]
 Wall Street Journal, [62]
 Water Research, [136]
 Water Resources Bulletin, [139]
 Water Resources Research, [118]

total 239 articles in 144 series

4.3 Theses

The following two lists contain theses, first PhD theses and then Master's etc. theses, arranged in alphabetical order by the name of the school.

4.3.1 PhD theses

Harvard University, [337]
The Pennsylvania State University, [465]
The University of Michigan, [230]
University of California, [290]
University of Louisville, [294]
University of Michigan, [66, 159, 40]
University of Minnesota, [272]
University of Paris 7, [322]
Utah State University, [15]
Wayne State University, [221]

total 12 thesis in 10 schools

4.3.2 Master's theses

This list includes also "Diplomarbeit", "Tech. Lic. Theses", etc.

Air Force Institute of Technology, [309]
Rice University, [187]
University of Kuopio, [257]
Wright-Patterson AFB, [343]

total 4 thesis in 4 schools

4.4 Report series

The following list contains references to all papers published as technical reports. The list is arranged in alphabetical order by the name of the institute.

Georgia Institute of Technology, [495]
Institute for New Generation Computer Technology, [77, 463, 111, 112]
Massachusetts Institute of Technology, [471]
Sandia National Laboratories, [300]
Santa Fe Institute, [70]
Tierärztliche Hochschule Hannover, [68]
University of California, [162]

University of Cambridge, [384]

University of Maryland, [472, 473]

University of Michigan, [106]

total 14 reports in 10 institutes

4.5 Patents

The following list contains the names of the patents of genetic algorithms in biosciences. The list is arranged in alphabetical order by the name of the patent.

- none

4.6 Authors

The following list contains all genetic algorithms in biosciences authors and references to their known contributions.

Abkevich, V. I.,	[447]	Bangalore, Arjun S.,	[178]	Brusic, Vladimir,	[39]
Accornero, N.,	[264]	Bansal, A.,	[91]	Bryson, James W.,	[376]
Acharya, R. S.,	[219, 228]	Barricelli, N. A.,	[161]	Burden, Frank R.,	[407]
Addis, Tom,	[488]	Barrios, Victor,	[265, 266]	Burks, Christian,	[83, 108, 109]
Adler, Dorit D.,	[248]	Barta, Zoltan,	[61]	Burnham, K. J.,	[231]
Aert, A. H. J. M. van,	[114]	Bartels, Christian,	[372]	Buydens, Lutgarde M. C.,	[374, 383, 92, 115, 468, 469]
Ahmed, M.,	[207]	Bartenstein, P.,	[232]	Cagnoni, S.,	[227]
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Chapter 5

Permuted title index

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- [436] **Ab initio** protein folding simulation with GAs: Simulations on the complete sequence of small proteins
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- [294] **actinomycin** Computer-assisted drug design: GAs and structures of molecular clusters of aromatic hydrocarbons and ● D-deoxyguanosine
- [30] – GAs for docking of ● D and deoxyguanosine molecules with comparison to the crystal structure of ● D-deoxyguanosine complex
- [136] **activated** Competitive adsorption of trichloroethylene and humic substances from groundwater on ● carbon
- [121] **active** Opt. , ● cntr. of oxides of nitrogen (NO_x) emissions from a nat. gas-fired burner using a simple GA
- [442] **activity** Pharmacological ● and membrane interactions of antiarrhythmics: 4-D QSAR/QSPR analysis
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- [73] **adaptability** Mutation and recombination effects on the ● of sexual and asexual organisms
- [159] **adaptation** Computer simulation of gen. ● Par. sub-component interaction in a multilocus model
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- [131] **Adaption** to a changing environment by means of the thermodynamical GA
- [487] **adaptive** A computer based simulation with artificial ● agents for predicting secondary structure from the protein hydrophobicity [Abstract]
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- [59] – Trans gene regulation in ● evol. : A GA model
- [136] **adsorption** Competitive ● of trichloroethylene and humic substances from groundwater on activated carbon
- [367] **AG-1343** Molecular recognition of the inhibitor ● by HIV-1 protease: conformationally flexible docking by EP
- [487] **agents** A computer based simulation with artificial adaptive ● for predicting secondary structure from the protein hydrophobicity [Abstract]
- [41] – GA-based method to design a primary screen for antirhinovirus ●
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- [286] **AIDS** Appl. of neural networks and GAs in the diagnosis of cancer, anorexia nervosa and ●
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- [300] **algorithm-based** A gen. ● method for docking flexible molecules
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- [167] **AntFarm** Towards simulated evol.
- [442] **antiarrhythmics** Pharmacological activity and membrane interactions of • 4-D QSAR/QSPR analysis
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- [293] **approximation** Cerius² Release 1.6, Drug Discovery Workbench QSAR+ User's Reference, Chapter 16: Introduction to gen. function •
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- [322] **artificielle** Développement de méthodes basées sur les mathématiques, l'informatique et l'intelligence • pour l'alignement de séquences et la prédiction de structures protéines [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure prediction]

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- [92] **calculations** Appl. of a GA in the conformational analysis of methylene-acetal-linked thymine dimers in DNA: Comparison with distance geometry •
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- [394] **center** Kinetic modeling of exciton migration in photosynthetic syst. . 3. Appl. of GAs to simulations of excitation dynamics in three-dimensional photosyst. I core antenna/reaction • complexes
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- [341] **cleavage** Peptide design in machina: Development of artificial mitochondrial protein precursor • sites by simulated molecular evol.
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- [19] **climate** Greenhouse • cntr. by evol. computation - GAs and evol. ary prog.
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- [420] **coagulation** Refinement of the NMR solution structure of the gamma-carboxyglutamic acid domain of factor IX using molecular dynamics simulation with initial Ca²⁺ positions determined by GA
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- [337] **computational** An evaluation of the GA as a tool in protein NMR
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- [322] **computing** Développement de méthodes basées sur les mathématiques, l'informatique et l'intelligence artificielle pour l'alignement de séquences et la prédiction de structures protéines [Development of mathematical, and artificial intelligence methods for the protein secondary structure prediction]
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- [371] **concepts** Use of GAs to learn ligand recognition Appl. to the GPCR superfamily
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- [388] **conformational** A comparison of a direct search method and a GA for • searching
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- [245] – Pareto opt. of the • of a cardiac assist device using multicriteria, rank and niche-based GAs hybridised with breeding and gradient methods
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- [126] – The appl. of GA and nonlinear fuzzy prog. for water pollution • in a river basin
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- [128] **coordinating** GA for economic load dispatch: • economy and environment objectives
- [419] **core** *De novo* design of the hydrophobic • of ubiquitin
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- [439] **cytotic** Molecular modeling of amoebapore and NK-lysin: A four-alpha-helix bundle of • peptides from distantly related organisms
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- [260] **Decision** theoretic steering and GA opt. : Appl. to stereotactic radiosurgery treatment planning
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- [255] **domain** An evol. appr. to simulate cognitive feedback learning in medical •
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- [495] **dynamic** Acquisition and production of skilled behavior in • decision-making tasks
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- [401] **elements** An alg. for prediction of structural • in small proteins
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- [209] **endothelial** Appl. of neural networks and GAs in the classification of • cells
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- [31] **GAME: GA for minimization of •** An interactive FORTRAN prog. for three-dimensional intermolecular interactions
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- [352] **ensembles** GA-based protocol for docking • of small ligands using experimental results
- [148] **entropy** Evol. , complexity, • and artificial reality
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- [47] **environmental** Evol. of biological regulation networks under complex • constraints
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- [275] **estimating** An approximate alg. for • treatment lags from right censored data
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- [91] – An • of appl. of the GA to the problem of ordering gen. loci on human chromosomes using radiation hybrid data
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- [63] **events** Evolve III: A discrete • model of an evol. ecosyst.
- [479] **evolution** A Darwinian evol. syst. – II. Experiments on protein • and evol. ary aspects of the gen. code
- [67] – A simulation appr. to evol. game theory: The • of time-sharing behavior in a dragonfly mating syst.
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- [86] • is promoted by asymmetrical mutations in DNA replication-GA with double-stranded DNA
- [155] • Learning, and Culture: Computational Metaphors for Adaptive Alg.
- [335] • of a computer prog. for classifying protein segments as transmembrane domains using gen. prog.
- [47] • of biological regulation networks under complex environmental constraints
- [69, 70] • of food foraging strategies for the Caribbean *Anolis* lizard using gen. prog.
- [43] • of metabolism for morphogenesis
- [409] • of model proteins on a foldability landscape
- [143] – Notes on the simulation of •
- [312] – Opt. sequence sel. in proteins of known structure by simulated •
- [308] – Opt. amino acid sequences by simulated molecular •
- [341] – Peptide design in machina: Development of artificial mitochondrial protein precursor cleavage sites by simulated molecular •
- [161] – Simulation of biological • and machine learning
- [375] – Structure formation of biopolymers is complex, their • may be simple
- [304] – Studying genotype-phenotype interactions: a model of the • of the cell regulation network
- [164] – The Origins of Order, Self-Organization and Sel. in •
- [331] – The rational design of amino acid sequences by artificial neural networks and simulated molecular • *De novo* design of an idealised leader peptidase cleavage-site
- [177] – The • of understanding: A GA model of the • of communication
- [434] – The • simulation of zinc finger domain sequence. Appl. of GAs in protein structure study
- [59] – Trans gene regulation in adaptive • A GA model
- [169] – Understanding • as a collective strategy for groping in the dark
- [329] – Variable sel. in QSAR studies 2. A highly efficient combination of syst. atic search and •
- [146] – Visualization of • of GAs
- [222] **evolution strategies** Fuzzy-set opt. in use of medical MR-image analysis based on •
- [281] **evolution strategy** Search for opt. frequencies and amplitudes of therapeutic electrical carotid sinus nerve stimulation by appl. of the •
- [289] – The applicability of the • to the cntr. of paralyzed limbs through fes
- [282] – The • - A search strategy used in individual opt. of electrical parameters for therapeutic carotid sinus nerve stimulation
- [479] **evolutionary** A Darwinian • syst. – II. Experiments on protein evol. and • aspects of the gen. code
- [101] – A DNA based impl. of an • search for good encodings for DNA computation
- [188] – A new • appr. for blood vessel detection on a transputer network
- [262] – A new • syst. for evolving artificial neural networks
- [67] – A simulation appr. to • game theory: The evol. of time-sharing behavior in a dragonfly mating syst.
- [134] – An • alg. for evaluation of emission compliance options in view of the Clean Air Act Amendments
- [303] – An • appr. to folding small alpha-helical proteins that uses sequence info and an empirical guiding fitness function
- [255] – An • appr. to simulate cognitive feedback learning in medical domain
- [42] – Appl. of • alg. to the structure-activity relationship
- [427] – Appl. of • alg. to protein folding prediction
- [235] – Appl. of • prog. to hypocenter determination
- [127] – Appl. of salqr and • alg. to opt. of graundwater bioremediation
- [56] – Biological consequences of • opt. s: mortality, variability, survival
- [233] – cntr. blood pressure during surgery using • prog.
- [457] – Determining protein folds by inverted and • protein folding alg.
- [344] – Docking conformationally flexible small molecules into a protein binding site through • prog.
- [63] – Evolve III: A discrete events model of an • ecosyst.
- [19] – Greenhouse climate cntr. by • computation - GAs and • prog.
- [17] – Greenhouse climate cntr. by • computation: GAs and • prog.
- [166] – Market, innovation, competition An • model of industrial dynamics
- [367] – Molecular recognition of the inhibitor AG-1343 by HIV-1 protease: conformationally flexible docking by • prog.
- [295] • and gen. methods in drug design
- [212] • CT image reconstruction
- [211] • CT image reconstruction by image partition
- [197] • CT image reconstruction by image partitioning
- [299] • drug discovery [Abstract of an invited lecture]
- [79] • opt. of a neural network-based signal processor for photometric data from an automated DNA sequencer

- [302] • prog. appl. to the development of quantitative structure-activity relationship and quantitative structure-property relationships
- [25] • prog. for mix design
- [157] • wanderlust: Sexual sel. with directional mate preferences
- [39] – Prediction of MHC class II-binding peptides using an • alg. and artificial neural network
- [158] – Simulation of local • dynamics of small pop.
- [153] – Strategy of co-evol. of transposons and host genome: Appl. to • computations
- [55] – The appl. of • computation to selected problems in molecular biology
- [317] – Variable sel. in QSAR studies 1. An • alg.
- [458] **evolutionary programming** An introduction to the protein folding problem and the potential appl. of •
- [273] – Using • for arterial waveform discrimination
- [288] **Evolutionsstrategie** – ein Regelkonzept für die funktionelle Elektrostimulation gelähmter Gliedmaßen
- [68] $[\gamma', \lambda(\mu/\rho, \lambda)]$ -**Evolutionsstrategie** Untersuchung der evol. sstrategischen Bedeutung der nicht-genetischen Varianz mit Hilfe der •
- [68] **evolutionsstrategischen** Untersuchung der • Bedeutung der nicht-genetischen Varianz mit Hilfe der $[\gamma', \lambda(\mu/\rho, \lambda)]$ -ES
- [142] **evolutio** Laskennallinen • GAt ja keinoelämä [Computational evol. , GAs, and artificial life]
- [63] **Evolve** III: A discrete events model of an evol. ecosystem.
- [28] **evolved** Gen. • receptor models (GERM): A computational appr. to construction of receptor models
- [445] – PARM: a gen. • alg. to predict bioactivity
- [262] **evolving** A new evol. syst. for • artificial neural networks
- [49] – Biological metaphors for • artificial cognitive syst.
- [60] – Modelling • pop.
- [493] • facial composite with a GA
- [240] • neural networks for detecting breast cancer
- [189] • neural networks for medical appl.
- [239] • polydistributional mixtures for mammographic feature modeling and analysis
- [147] **exaptive** Simulation of • behaviour
- [394] **excitation** Kinetic modeling of exciton migration in photosynthetic syst. . 3. Appl. of GAs to simulations of • dynamics in three-dimensional photosyst. I core antenna/reaction center complexes
- [394] **exciton** Kinetic modeling of • migration in photosynthetic syst. . 3. Appl. of GAs to simulations of excitation dynamics in three-dimensional photosyst. I core antenna/reaction center complexes
- [84] **exons** Classifying nucleic acid sub-sequences as introns or • using gen. prog.
- [268] **experimental** An efficient classifier syst. and its • comparison with two representative learning methods on three medical domains
- [435] – Applying • data to protein fold prediction with the GA
- [352] – GA-based protocol for docking ensembles of small ligands using • results
- [406] – Improving protein structure prediction by new strategies: • insights and the GA
- [96] **experimental design** A case study in • appl. to GAs with appl. to DNA sequence assembly
- [479] **Experiments** A Darwinian evol. syst. – II. • on protein evol. and evolutionary aspects of the gen. code
- [236] **expert system** On rule checking and learning in an acupuncture diagnosis fuzzy • by GA
- [468] **expert-system** HIPs, A hybrid self-adapting • for nuclear-magnetic-resonance spectrum interpretation using GAs
- [370] **explanation** Stochastic models for the • of tertiary structures of protein
- [130] **Explorations** Artificial life and pollution cntr. : • of a GA syst. on the highly par. Connection Machine
- [404] **exploring** Development of a novel GA search method (GAP1.0) for • peptide conformational space
- [395] • the energy landscapes of molecular recognition by a GA: Analysis of the requirements for robust docking of HIV-1 protease and FKBP-12 complexes
- [471] **exposing** Synthesizing regularity • attributes in large protein databases
- [333] **exposure** The prediction of the degree of • to solvent of amino acid residues via gen. prog.
- [380] – The prediction of the degree of • to solvent of amino acid residues via gen. prog.
- [22] **extracting** Study on • the adaptive agricultural development area using GA with complex PTYPE
- [200] **extraction** Gen. appr. to select wavelet features for contour • in medical ultrasonic imaging
- [193] – Gen. appr. to select wavelet features for contour • in medical ultrasonic imaging
- [224] – Knowledge • from neural networks using GAs
- [89] – Signal pattern • from DNA sequences using hidden Markov model and GA
- [110] – Stochastic motif • using a GA with the MDL principle
- [493] **facial** Evolving • composite with a GA
- [420] **factor** Refinement of the NMR solution structure of the gamma-carboxyglutamic acid domain of coagulation • IX using molecular dynamics simulation with initial Ca²⁺ positions determined by GA
- [14] **factory** Opt. cntr. of physiological processes of plants in a green plant •
- [104] **family-specific** A GA for designing gene • oligonucleotide sets used for hybridization: the G protein-coupled receptor protein superfamily
- [320] **fast** Appl. of the par. • messy GA to the protein folding problem
- [239] **feature** Evolving polydistributional mixtures for mammographic • modeling and analysis
- [276] – GA for • sel. for par. classifiers
- [204] – Image • analysis for classification of microcalcifications in digital mammography - neural networks and GAs
- [248] – Image • sel. by a GA: Appl. to classification of mass and normal breast tissue
- [267] – Modified Kohonen's self-organizing • map and its appl. to automatic sleep cycle recognition
- [223] • sel. with distinction sensitive learning vector quantisation and GAs
- [201] **feature detection** Gen. prog. for • and image segmentation
- [242] **features** Analysis of mammographic microcalcifications using gray-level image structure •
- [200] – Gen. appr. to select wavelet • for contour extraction in medical ultrasonic imaging
- [193] – Gen. appr. to select wavelet • for contour extraction in medical ultrasonic imaging
- [411] – Ident. of common structural • in sets of ligands using a GA
- [199] – Use of GAs for computer-aided diagnosis of breast cancers from image •
- [444] – Using a GA to identify common structural • in sets of ligands
- [255] **feedback** An evol. appr. to simulate cognitive • learning in medical domain
- [257] **Female** Parameter Evaluation and Gen. -Based Rule Learning for the Differential Diagnosis of • urinary Incontinence
- [289] **fes** The applicability of the evol. strategy to the cntr. of paralyzed limbs through •
- [270] **Fetal** Non-invasive • Electrocardiograph Enhancement
- [214] **field** GA with modified elitism for RF coil NMR tomograph magnetic • homogeneity opt.
- [133] – Inverse modeling of • tracer data to characterize DNAPL contamination
- [122] **field-scale** Opt. • groundwater remediation using neural networks and GA
- [206] **filters** Designing texture • with GAs: An appl. to medical images
- [97] **finite-state machines** DNA impl. of •
- [303] **fitness function** An evol. appr. to folding small alpha-helical proteins that uses sequence info and an empirical guiding •
- [426] **FK506** Mean field analysis of FKBP-12 complexes with • and rapamycin: Implications for a role of crystallographic water molecules in molecular recognition and specificity
- [426] **FKBP-12** Mean field analysis of • complexes with FK506 and rapamycin: Implications for a role of crystallographic water molecules in molecular recognition and specificity
- [395] **FKBP-12 complexes** Exploring the energy landscapes of molecular recognition by a GA: Analysis of the requirements for robust docking of HIV-1 protease and •
- [29] **flexible** A GA based method for docking • molecules

- [32] — A GA for • molecular overlay and pharmacophore elucidation
- [300] — A GA-based method for docking • molecules
- [408] — Development and validation of a GA for • docking
- [344] — Docking conformationally • small molecules into a protein binding site through EP
- [358, 400] — Docking • molecules: A case study of three proteins
- [367] — Molecular recognition of the inhibitor AG-1343 by HIV-1 protease: conformationally • docking by EP
- [456] • docking of ligands to receptor sites using GAs
- [354] • ligand docking using a GA
- [347] • ligand docking without parameter adjustment across four ligand-receptor complexes
- [33] **flux** Gen. -alg. sel. of a regulatory structure that directs • in a simple metabolic model
- [435] **fold** Applying experimental data to protein • prediction with the GA
- [398] — Assessing the perf. of • recognition methods by means of a comprehensive benchmark
- [373] — Assigning a protein sequence to a three-dimensional • [Abstract of a poster]
- [447] — How evol. makes protein • quickly
- [396] — Identifying the tertiary • of small proteins with different topologies from sequence and secondary structure using the GA and extended criteria specific for strand regions
- [402] — The GA appl. as a modelling tool to predict the • of small proteins with different topologies
- [409] **foldability** Evol. of model proteins on a • landscape
- [376] **folded** Design of a three helix bundle with a “native-like” • state [Abstract of a poster]
- [338] **folding** An artificial life model for predicting the tertiary structure of unknown proteins that emulates the • process
- [303] — An evol. appr. to • small alpha-helical proteins that uses sequence info and an empirical guiding fitness function
- [441] — GENFOLD: A GA for • protein structures using NMR restraints
- [315] — Hierarchical alg. for computer modeling of protein tertiary structure: • of myoglobin to 6.2Å resolution
- [417] • simulation with GAs and a detailed molecular description
- [307] • the main chain of small proteins with the GA
- [349] — On constructing • heteropolymers
- [174] — The computer simulation of RNA • pathways using a GA
- [69, 70] **food** Evol. of • foraging strategies for the Caribbean *Anolis* lizard using gen. prog.
- [69, 70] **foraging** Evol. of food • strategies for the Caribbean *Anolis* lizard using gen. prog.
- [61] — Geometry for a selfish • group: A GA appr.
- [466] **form** Appl. of the GA to a simplified • of the phase problem
- [413] **formalism** Construction of 3-D QSAR models using the 4-D QSAR •
- [375] **formation** Structure • of biopolymers is complex, their evol. may be simple
- [31] **FORTTRAN** GAME: GA for minimization of energy, An interactive • prog. for three-dimensional intermolecular interactions
- [473] **foundations** Why GAs are suitable for protein folding analysis: The theoretical •
- [439] **four-alpha-helix** Molecular modeling of amoebapore and NK-lysin: A • bundle of cytotic peptides from distantly related organisms
- [325] **four-helix** Delineating the mainchain topology of • bundle proteins using the GA and knowledge based on the amino acid sequence alone
- [198] **fourier** GAs appl. to • descriptor based geometric models for anatomical object recognition in medical images
- [455] **fragment** DNA restriction • map assembly with GAs
- [83] — GAs operators, and DNA • assembly
- [356] **fragments** Ab initio structure prediction for small polypeptides and protein •
- [386] — Rebuilding connectivity matrices from two-atom • using the GA
- [269] **fremdenergetisch** Entwicklung und Anpassung eines vollständigen Ansteuersyst. für • angetriebene Ganzarmprothesen
- [281] **frequencies** Search for opt. • and amplitudes of therapeutic electrical carotid sinus nerve stimulation by appl. of the evol. strategy
- [24] **fruit-storage** An intelligent appr. for opt. cntr. of • process using neural networks and GAs
- [274] **function** Automatic registration of 3D images using a simple GA with a stochastic perf. •
- [293] — Cerius² Release 1.6, Drug Discovery Workbench QSAR+ User's Reference, Chapter 16: Introduction to gen. • approximation
- [217] — GA based input sel. for a neural network • approximator with appl. to SSME monitoring
- [326] — Gen. • approximation: A gen. appr. to building quantitative structure-activity relationship models
- [448] — Mining the NCI anticancer drug discovery databases: gen. • approximation for the QSAR study of anticancer ellipticine analogues
- [152] — On the usage of differential evol. for • opt.
- [464] **functions** The appl. of GAs to the minimization of potential energy •
- [288] **funktionelle** ES – ein Regelkonzept für die • Elektrostimulation gelähmter Gliedmaßen
- [246] **fuzzy** Hierarchical multivariable • cntr. for learning with GAs
- [236] — On rule checking and learning in an acupuncture diagnosis • expert syst. by GA
- [126] — The appl. of GA and nonlinear • prog. for water pollution cntr. in a river basin
- [52] **fuzzy logic** Using a hybrid GA and • for metabolic modeling
- [222] **Fuzzy-set** opt. in use of medical MR-image analysis based on evol. strategies
- [451] **GA-based** GA strategy for variable sel. in QSAR studies: • region selection for CoMFA modeling
- [251] • estimation method for human muscle parameter in elbow flexion
- [220] **GADELO** Opt. of simulation models with • a multi-pop. GA
- [377] **GAengine** Modeling proteins conformation in solution. Part I: a par. • for protein conformational space mapping
- [482] **GALB** GAs in biochemistry • learning protein folding pathways
- [67] **game** A simulation appr. to evol. • theory: The evol. of time-sharing behavior in a dragonfly mating syst.
- [145] — From gen. evol. to emergence of • strategies
- [31] **GAME** GA for minimization of energy, An interactive FORTRAN prog. for three-dimensional intermolecular interactions
- [420] **gamma-carboxyglutamic** Refinement of the NMR solution structure of the • acid domain of coagulation factor IX using molecularBLdynamics simulation with initial Ca²⁺ positions determined by GA
- [269] **Ganzarmprothesen** Entwicklung und Anpassung eines vollständigen Ansteuersyst. für fremdenergetisch angetriebene •
- [48] **GA-P** The • A GA and gen. prog. hybrid
- [404] **GAP1.0** Development of a novel GA search method • for exploring peptide conformational space
- [443] **GAPLS** GA strategy for variable sel. in QSAR studies: • and D-opt. designs for predictive QSAR model
- [372] **GARANT** Automated sequence-specific NMR assignment of homologous proteins using the prog. •
- [121] **gas-fired** Opt. , active cntr. of oxides of nitrogen (NO_x) emissions from a nat. • burner using a simple GA
- [288] **gelähmter** ES – ein Regelkonzept für die funktionelle Elektrostimulation • Gliedmaßen
- [104] **gene** A GA for designing • family-specific oligonucleotide sets used for hybridization: the G protein-coupled receptor protein superfamily
- [160] — GAs and info accumulation during the evol. of • regulation
- [59] — Trans • regulation in adaptive evol. : A GA model
- [382] **generalised** Minimising reduced-model proteins using a • hierarchical table-lookup potential function
- [305] **generated** GA refinement of structures • by a *de novo* design prog.
- [244] **generating** A generic GA for • beam weights
- [480] • and testing protein folds
- [71] — LINKERS: A simulation prog. syst. for • pop. with gen. structure
- [173] **generation** A GA for the automated • of molecules within constraints
- [244] **generic** A • GA for generating beam weights

- [162, 163] **GENESYS/TRACKER** Evol. as a thema in artificial life: The • syst.
- [28] **Genetically** evolved receptor models (GERM): A computational appr. to construction of receptor models
- [247] **Genetic-based** machine learning for the assessment of certain neuromuscular disorders
- [257] **Genetic-Based** Parameter Evaluation and • Rule Learning for the Differential Diagnosis of Female urinary Incontinence
- [76] **genetics** A hybrid GA appl. to a • sequencing problem
- [106] • and random keys for sequencing and opt.
- [350] • helping molecular dynamics
- [278] **Genetics-based-machine-learning** in clinical electromyography
- [441] **GENFOLD** A GA for folding protein structures using NMR restraints
- [74] **GENIE THE • PROJECT:** A GA appl. to a sequencing problem in the biological domain
- [153] **genome** Strategy of co-evol. of transposons and host • Appl. to evol. computations
- [109] **genomic** Stochastic opt. tools for • sequence assembly
- [304] **genotype-phenotype** Studying • interactions: a model of the evol. of the cell regulation network
- [261] **geometric** An appl. of GAs to • model-guided interpretation of brain anatomy
- [184] – GAs and deformable • models for anatomical object recognition
- [221] – Gen. and • opt. of three-dimensional radiation therapy treatment planning
- [198] **geometric-models** GAs appl. to fourier descriptor based • for anatomical object recognition in medical images
- [92] **geometry** Appl. of a GA in the conformational analysis of methylene-acetal-linked thymine dimers in DNA: Comparison with distance • calculations
- [61] • for a selfish foraging group: A GA appr.
- [28] **GERM** Gen. evolved receptor models • A computational appr. to construction of receptor models
- [288] **Gliedmaßen** ES – ein Regelkonzept für die funktionelle Elektrostimulation gelähmter •
- [290] **global** Adaptive • opt. with local search
- [50] • adaptive shifts in biological and trans-biological evol.
- [51] – The effects of variable biome distribution on • climate
- [292] – Using an annealing GA to solve • energy minimization problem in molecular binding
- [36] **glucose** GA-based protocol for coupling digital filtering and partial least-squares regression: Appl. to the near-infrared analysis of • in biological matrices
- [62] **gold** A scientist seeks • in a controversial drug patent
- [431] **GOLD** Evol. goes for • in silico
- [371] **GPCR superfamily** Use of GAs to learn ligand recognition concepts: Appl. to the •
- [190] **gradient** Design and evaluation of a transverse • set for magnetic resonance imaging of the human brain
- [203] – Design of a biplanar • coil using a GA
- [245] **gradient methods** Pareto opt. of the cntr. of a cardiac assist device using multicriteria, rank and niche-based GAs hybridised with breeding and •
- [127] **groundwater** Appl. of salqr and evol. alg. to opt. of • bioremediation
- [242] **gray-level** Analysis of mammographic microcalcifications using • image structure features
- [14] **green** Opt. cntr. of physiological processes of plants in a • plant factory
- [19] **Greenhouse** climate cntr. by evol. computation - GAs and evol. ary prog.
- [17] • climate cntr. by evol. computation: GAs and evol. ary prog.
- [27] – Opt. cntr. of • climate using GAs
- [169] **groping** Understanding evol. as a collective strategy for • in the dark
- [136] **groundwater** Competitive adsorption of trichloroethylene and humic substances from • on activated carbon
- [123] – Dynamic opt. -cntr. for • remediation management using GAs
- [122] – Opt. field-scale • remediation using neural networks and GA
- [125] – Opt. • remediation design using differential GA
- [118] – Using GAs to solve a multiple objective • pollution containment problem
- [61] **group** Geometry for a selfish foraging • A GA appr.
- [26] **Growth** opt. of plant by means of the hybrid syst. of GA and neural network
- [303] **guiding** An evol. appr. to folding small alpha-helical proteins that uses sequence info and an empirical • fitness function
- [423] **Haar transformation** Discrete • and protein structure
- [46] **habitats** Ecological appl. of GAs: predicting organism distribution in complex •
- [98] **Hamiltonian path** A heuristic appr. for • problem with molecules
- [250] **hard** A GA appr. to opt. for the radiological worker allocation problem - discussions on different • constraints
- [446] – Protein structure prediction as a • opt. problem: the GA appr.
- [418] – Protein structure prediction as a • opt. problem: the GA appr.
- [154] **hardware systems** A phylogen. , ontogenetic, and epigenetic view of bio-inspired •
- [249] **heating** An inverse method to optimize • conditions in RF-capacitive hyperthermia
- [379] **helical** Ab initio tertiary-fold prediction of • and non-helical protein chains using a GA
- [376] **helix** Design of a three • bundle with a “native-like” folded state [Abstract of a poster]
- [350] **helping** Gen. • molecular dynamics
- [263] **hemorrhagic** Prediction of • blood loss with a GA neural network
- [349] **heteropolymers** On constructing folding •
- [38] **heuristic** A comparison of • search alg. for molecular docking
- [98] – A • appr. for Hamiltonian path problem with molecules
- [77] **hidden** DNA sequence analysis using • Markov model and GA
- [89] – Signal pattern extraction from DNA sequences using • Markov model and GA
- [382] **hierarchical** Minimising reduced-model proteins using a generalised • table-lookup potential function
- [315] • alg. for computer modeling of protein tertiary structure: folding of myoglobin to 6.2Å resolution
- [246] • multivariable fuzzy cntr. for learning with GAs
- [156] – Opt. by • mutant production
- [468] **HIPS** A hybrid self-adapting expert-syst. for nuclear-magnetic-resonance spectrum interpretation using GAs
- [395] **HIV-1 protease** Exploring the energy landscapes of molecular recognition by a GA: Analysis of the requirements for robust docking of • and FKBP-12 complexes
- [367] – Molecular recognition of the inhibitor AG-1343 by • conformationally flexible docking by EP
- [214] **homogeneity** GA with modified elitism for RF coil NMR tomograph magnetic field • opt.
- [372] **homologous** Automated sequence-specific NMR assignment of • proteins using the prog. GARANT
- [153] **host** Strategy of co-evol. of transposons and • genome: Appl. to evol. computations
- [207] **human** 3D reconstruction of the • jaw from a sequence of images
- [91] – An evaluation of appl. of the GA to the problem of ordering gen. loci on • chromosomes using radiation hybrid data
- [190] – Design and evaluation of a transverse gradient set for magnetic resonance imaging of the • brain
- [251] – GA-based estimation method for • muscle parameter in elbow flexion
- [229] **human brain** Design by GA of a z gradient set for magnetic resonance imaging of the •
- [136] **humic** Competitive adsorption of trichloroethylene and • substances from groundwater on activated carbon
- [34] **hybrid** A • appr. to modeling metabolic syst. using GA and simplex method
- [76] – A • GA appl. to a gen. sequencing problem
- [20] – Developing a sugar-cane breeding assistant syst. by a • adaptive learning technique
- [26] – Growth opt. of plant by means of the • syst. of GA and neural network
- [468] – HIPS, A • self-adapting expert-syst. for nuclear-magnetic-resonance spectrum interpretation using GAs
- [35] • GA for the ident. of metabolic models
- [310] – Protein structure prediction using • AI methods
- [48] – The GA-P: A GA and gen. prog. •
- [52] – Using a • GA and fuzzy logic for metabolic modeling

- [245] **hybridised** Pareto opt. of the cntr. of a cardiac assist device using multicriteria, rank and niche-based GAs • with breeding and gradient methods
- [104] **hybridization** A GA for designing gene family-specific oligonucleotide sets used for • the G protein-coupled receptor protein superfamily
- [94] – Info transfer through • reactions in DNA based computing
- [343] **hybridized** Appl. of • GAs to the protein folding problem
- [139] **hydraulic** Determination of • conductivity tensor using a nonlinear least squares estimator
- [91] **hydrid** An evaluation of appl. of the GA to the problem of ordering gen. loci on human chromosomes using radiation • data
- [294] **hydrocarbons** Computer-assisted drug design: GAs and structures of molecular clusters of aromatic • and actinomycin D-deoxyguanosine
- [419] **hydrophobic** *De novo* design of the • core of ubiquitin
- [339] – *De novo* design of • cores of proteins
- [487] **hydrophobicity** A computer based simulation with artificial adaptive agents for predicting secondary structure from the protein • [Abstract]
- [249] **hyperthermia** An inverse method to optimize heating conditions in RF-capacitive •
- [235] **hypocenter** Appl. of EP to • determination
- [331] **idealised** The rational design of amino acid sequences by artificial neural networks and simulated molecular evol. : *De novo* design of an • leader peptidase cleavage-site
- [35] **identification** Hybrid GA for the • of metabolic models
- [411] • of common structural features in sets of ligands using a GA
- [424] **identifies** Structural consensus in ligand-protein docking • recognition peptide motifs that bind streptavidin
- [444] **identify** Using a GA to • common structural features in sets of ligands
- [396] **Identifying** the tertiary fold of small proteins with different topologies from sequence and secondary structure using the GA and extended criteria specific for strand regions
- [378] **identity** Towards meeting the Paracelcus challenge: The design, synthesis, and characterization of paracelcin-43, an alpha-helical protein with over 50-percent sequence • to all-beta protein
- [39] **II-binding** Prediction of MHC class • peptides using an evol. alg. and artificial neural network
- [243] **ill** Prediction of outcome in critically • patients using artificial neural network synthesised by GA
- [242] **image** Analysis of mammographic microcalcifications using gray-level • structure features
- [212] – Evol. CT • reconstruction
- [225, 185] – Medical • mapping using collaborative GA
- [216] – Model-based • interpretation using GAs
- [204] • feature analysis for classification of microcalcifications in digital mammography - neural networks and GAs
- [248] • feature sel. by a GA: Appl. to classification of mass and normal breast tissue
- [284] – Region merging in medical • segmentation and interpretation
- [199] – Use of GAs for computer-aided diagnosis of breast cancers from • features
- [186] **image processing** Using “biological” GAs to solve the TSP with appl. in medical •
- [211] **image reconstruction** Evol. CT • by • partition
- [197] – Evol. CT • by • partitioning
- [215] **image registration** Adaptive search space scaling in digital •
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- [183] – Appl. of gen. opt. to medical •
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- [190] **imaging** Design and evaluation of a transverse gradient set for magnetic resonance • of the human brain
- [229] – Design by GA of a z gradient set for magnetic resonance • of the human brain
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- [200] – Gen. appr. to select wavelet features for contour extraction in medical ultrasonic •
- [78] **immune system** Recognising promoter sequences using an artificial •
- [101] **implementation** A DNA based • of an evol. search for good encodings for DNA computation
- [397] – A par. GA for polypeptide three dimensional structure prediction. A transputer •
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- [257] **Incontinence** Parameter Evaluation and Gen. -Based Rule Learning for the Differential Diagnosis of Female urinary •
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- [271] **in-diffusion** GA-based reconstruction • tomography
- [282] **individual** The evol. strategy - A search strategy used in • opt. of electrical parameters for therapeutic carotid sinus nerve stimulation
- [166] **industrial** Market, innovation, competition An evol. model of • dynamics
- [387] **inference** Protein phylogen. • using maximum likelihood with a GA
- [440] **infinite** Prediction of • dilution activity coefficients of organic compounds in aqueous solution from molecular structure
- [463, 113] **information** A stochastic appr. to gen. • processing
- [303] – An evol. appr. to folding small alpha-helical proteins that uses sequence • and an empirical guiding fitness function
- [160] – GAs and • accumulation during the evol. of gene regulation
- [94] • transfer through hybridization reactions in DNA based computing
- [374] – Par. processing of chemical • in a local area network III. Using GAs for conformational analysis of biomacromolecules
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- [367] **inhibitor** Molecular recognition of the • AG-1343 by HIV-1 protease: conformationally flexible docking by EP
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- [24] **intelligent** An • appr. for opt. cntr. of fruit-storage process using neural networks and GAs
- [460] – Do • configuration search techniques outperform random search for large molecules?
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- [392] **interactions** Gen. prog. for improved data mining: An appl. to the biochemistry of protein •
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- [45] – Predator-prey • in a simulated world
- [429] – Predicting conserved water-mediated and polar ligand • in proteins using a K-nearest-neighbors GA
- [31] – GAME: GA for minimization of energy, An interactive FORTRAN prog. for three-dimensional intermolecular •

- [304] – Studying genotype-phenotype • a model of the evol. of the cell regulation network
- [227] **Interactive** segmentation of multi-dimensional medical data with contour-based appl. of GAs
- [31] – GAME: GA for minimization of energy, An • FORTRAN prog. for three-dimensional intermolecular interactions
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- [31] **intermolecular** GAME: GA for minimization of energy, An interactive FORTRAN prog. for three-dimensional • interactions
- [261] **interpretation** An appl. of GAs to geometric model-guided • of brain anatomy
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- [196] – Knowledge-based • of MR brain images
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- [458] **introduction** An • to the protein folding problem and the potential appl. of evol. prog.
- [293] – Cerius² Release 1.6, Drug Discovery Workbench QSAR+ User's Reference, Chapter 16: • to gen. function approximation
- [84] **introns** Classifying nucleid acid sub-sequences as • or exons using gen. prog.
- [249] **inverse** An • method to optimize heating conditions in RF-capacitive hyperthermia
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- [450] – Rational comb. library design 2. Rational design of targeted combinatorial peptide libraries using chemical similarity probe and the • QSAR appr.
- [407] **inversion** Predicting maximum bioactivity by effective • of neural networks using GAs
- [457] **inverted** Determining protein folds by • and evol. protein folding alg.
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- [299] **invited** Evol. drug discovery [Abstract of an • lecture]
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- [21] **irrigation** Gen. learning of the • cycle for water flow in cropped soils
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- [207] **jaw** 3D reconstruction of the human • from a sequence of images
- [142] **keinoelämä** Laskennallinen evoluutio, GAt ja • [Computational evol. , GAs, and artificial life]
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- [394] **Kinetic** modeling of exciton migration in photosynthetic syst. . 3. Appl. of GAs to simulations of excitation dynamics in three-dimensional photosyst. I core antenna/reaction center complexes
- [279] **K-means** Neural networks, GAs and the • alg. : in search of data classification
- [429] **K-nearest-neighbors** Predicting conserved water-mediated and polar ligand interactions in proteins using a • GA
- [325] **knowledge** Delineating the mainchain topology of four-helix bundle proteins using the GA and • based on the amino acid sequence alone
- [224] • extraction from neural networks using GAs
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- [275] **lags** An approximate alg. for estimating treatment • from right censored data
- [322] **l'alignement** Développement de méthodes besées sur les mathématiques, l'informatique et l'intelligence artificielle pour • de séquences et la prédiction de structures protéines [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure prediction]
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- [142] **Laskennallinen** evoluutio, GAt ja keinoelämä [Computational evol. , GAs, and artificial life]
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- [331] **leader** The rational design of amino acid sequences by artificial neural networks and simulated molecular evol. : *De novo* design of an idealised • peptidase cleavage-site
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- [299] **lecture** Evol. drug discovery [Abstract of an invited •
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- [450] **libraries** Rational comb. library design 2. Rational design of targeted combinatorial peptide • using chemical similarity probe and the inverse QSAR appr.
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- [354] **ligand** Flexible • docking using a GA
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- [429] – Predicting conserved water-mediated and polar • interactions in proteins using a K-nearest-neighbors GA
- [385] – Resolving water-mediated and polar • recognition using GAs [Abstract of a poster]
- [371] – Use of GAs to learn • recognition concepts: Appl. to the GPCR superfamily

- [424] **ligand-protein** Structural consensus in • docking identifies recognition peptide motifs that bind streptavidin
- [347] **ligand-receptor** Flexible ligand docking without parameter adjustment across four • complexes
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- [289] **limbs** The applicability of the evol. strategy to the cntr. of paralyzed • through fes
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- [322] **l'informatique** Développement de méthodes basées sur les mathématiques, • et l'intelligence artificielle pour l'alignement de séquences et la prédiction de structures protéines [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure prediction]
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- [374] **local area network** Par. processing of chemical info in a • III. Using GAs for conformational analysis of biomacromolecules
- [290] **local search** Adaptive global opt. with •
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- [91] **loci** An evaluation of appl. of the GA to the problem of ordering gen. • on human chromosomes using radiation hybrid data
- [341] **machina** Peptide design in • Development of artificial mitochondrial protein precursor cleavage sites by simulated molecular evol.
- [230] **machine learning** A comparison of GAs and other • syst. on a complex classification task from common disease research
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- [190] **magnetic resonance** Design and evaluation of a transverse gradient set for • imaging of the human brain
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- [325] **mainchain** Delineating the • topology of four-helix bundle proteins using the GA and knowledge based on the amino acid sequence alone
- [256] **malaria** Modeling • as a complex adaptive syst.
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- [123] **management** Dynamic opt. -cntr. for groundwater remediation • using GAs
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- [455] **map** DNA restriction fragment • assembly with GAs
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- [107] **mapping** An investigation of DNA • with GAs – Preliminary results
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- [403] **marine** Role of γ -carboxyglutamic acid in the calcium-induced structural transition of conantokin G, a conotoxin from the • snail *Comus geographus*
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- [248] **mass** Image feature sel. by a GA: Appl. to classification of • and normal breast tissue
- [191] **Matching** images for radiotherapy verification using GAs
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- [322] **mathématiques** Développement de méthodes basées sur les • l'informatique et l'intelligence artificielle pour l'alignement de séquences et la prédiction de structures protéines [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure prediction]
- [12] **mathematical** Automating the parametrization of • models using GAs
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- [272] – Relapse from tobacco smoking cessation: • and computer micro-simulation modelling including parameter opt. with GAs
- [67] **mating** A simulation appr. to evol. game theory: The evol. of time-sharing behavior in a dragonfly • syst.
- [36] **matrices** GA-based protocol for coupling digital filtering and partial least-squares regression: Appl. to the near-infrared analysis of glucose in biological •
- [386] – Rebuilding connectivity • from two-atom fragments using the GA
- [437] **matrixes** Three-dimensional quantitative structure-activity relationships from molecular similarity • and gen. neural networks.1. Appl.
- [432] – Three-dimensional quantitative structure-activity relationships from molecular similarity • and gen. neural networks.1. Method and validations
- [44] **maximum** Determination of • common 3D substructures using a GA
- [407] – Predicting • bioactivity by effective inversion of neural networks using GAs
- [387] – Protein phylogen. inference using • likelihood with a GA
- [105] **maximum likelihood** Search for • phylogen. tree using a GA
- [110] **MDL** Stochastic motif extraction using a GA with the • principle
- [426] **Mean field** analysis of FKBP-12 complexes with FK506 and rapamycin: Implications for a role of crystallographic water molecules in molecular recognition and specificity
- [268] **medical** An efficient classifier syst. and its experimental comparison with two representative learning methods on three • domains
- [255] – An evol. appr. to simulate cognitive feedback learning in • domain

- [218] – Appl. of gen. opt. to • image segmentation
- [183] – Appl. of gen. opt. to • image segmentation
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- [189] – Evolving neural networks for • appl.
- [222] – Fuzzy-set opt. in use of • MR-image analysis based on evol. strategies
- [200] – Gen. appr. to select wavelet features for contour extraction in • ultrasonic imaging
- [193] – Gen. appr. to select wavelet features for contour extraction in • ultrasonic imaging
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- [284] – Region merging in • image segmentation and interpretation
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- [198] **medical images** GAs appl. to fourier descriptor based geometric-models for anatomical object recognition in •
- [378] **meeting** Towards • the Paracelcus challenge: The design, synthesis, and characterization of paracelcin-43, an alpha-helical protein with over 50-percent sequence identity to all-beta protein
- [442] **membrane** Pharmacological activity and • interactions of antiarrhythmics: 4-D QSAR/QSPR analysis
- [284] **merging** Region • in medical image segmentation and interpretation
- [320] **messy** Appl. of the par. fast • GA to the protein folding problem
- [33] **metabolic** Gen. -alg. sel. of a regulatory structure that directs flux in a simple • model
- [35] – Hybrid GA for the ident. of • models
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- [34] **metabolic systems** A hybrid appr. to modeling • using GA and simplex method
- [43] **metabolism** Evol. of • for morphogenesis
- [49] **metaphors** Biological • for evolving artificial cognitive syst.
- [155] – Evol. , Learning, and Culture: Computational • for Adaptive Alg.
- [29] **method** A GA based • for docking flexible molecules
- [300] – A GA-based • for docking flexible molecules
- [462] – An analysis of the GA • of molecular conformation determination
- [249] – An inverse • to optimize heating conditions in RF-capacitive hyperthermia
- [425] – Development of a GA • especially designed for the comparison of molecular models: Appl. to the elucidation of the benzodiazepine receptor pharmacophore
- [404] – Development of a novel GA search • (GAP1.0) for exploring peptide conformational space
- [178] – GA-based • for selecting wavelenghts and model size for use with partial least-squares regression: Appl. to near-infrared spectroscopy
- [41] – GA-based • to design a primary screen for antirhinovirus agents
- [414] – New opt. • for conformational energy calculations on polypeptides: conformational space annealing
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- [100] – The effects of combination of DNA coding • with Pseudo-Bacterial GA
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- [383] **methodology** The effectiveness of recombination in the GA • A comparison to simulated annealing
- [268] **methods** An efficient classifier syst. and its experimental comparison with two representative learning • on three medical domains
- [398] – Assenssing the perf. of fold recognition • by means of a comprehensive benchmark
- [438] – Computational • for the prediction of protein folds
- [461] – Conformation searching • for small molecules II: A GA appr.
- [322] – Développement de méthodes besées sur les mathématiques, l’informatique et l’intelligence artificielle pour l’alignement de séquences et la prédiction de structures protéines [Development of mathematical, computing and artificial intelligence • for the protein secondary structure prediction]
- [295] – Evol. and gen. • in drug design
- [129] – Probabilistic • in life-cycle design
- [310] – Protein structure prediction using hybrid AI •
- [92] **methylene-acetal-linked** Appl. of a GA in the conformational analysis of • thymine dimers in DNA: Comparison with distance geometry calculations
- [95] **metric** A new • for DNA computing
- [39] **MHC** Prediction of • class II-binding peptides using an evol. alg. and artificial neural network
- [242] **microcalcifications** Analysis of mammographic • using gray-level image structure features
- [204] **microcalcifications** Image feature analysis for classification of • in digital mammography - neural networks and GAs
- [272] **micro-simulation** Relapse from tobacco smoking cessation: Mathematical and computer • modelling including parameter opt. with GAs
- [394] **migration** Kinetic modeling of exciton • in photosynthetic syst. . 3. Appl. of GAs to simulations of excitation dynamics in three-dimensional photosyst. I core antenna/reaction center complexes
- [280] **minimal** GAs for • source reconstructions
- [422] **minimalist** Protein folding: optimized sequences obtained by simulated breeding in a • model
- [382] **Minimising** reduced-model proteins using a generalised hierarchical table-lookup potential function
- [346] **minimization** Energy • of peptide analogues using GAs
- [328] – GAs codings used in protein structure prediction by energy •
- [319] – Protein structure comparisons using a combination of a GA, dynamic prog. and least-squares •
- [31] – GAME: GA for • of energy, An interactive FORTRAN prog. for three-dimensional intermolecular interactions
- [464] – The appl. of GAs to the • of potential energy functions
- [292] – Using an annealing GA to solve global energy • problem in molecular binding
- [448] **Mining** the NCI anticancer drug discovery databases: gen. function approximation for the QSAR study of anticancer ellipticine analogues
- [415] **minireceptor** Molecular design using the • concept
- [341] **mitochondrial** Peptide design in machina: Development of artificial • protein precursor cleavage sites by simulated molecular evol.
- [25] **mix** EP for • design
- [239] **mixtures** Evolving polydistributional • for mammographic feature modeling and analysis
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- [443] – GA strategy for variable sel. in QSAR studies: GAPLS and D-opt. designs for predictive QSAR •
- [178] – GA-based method for selecting wavelenghts and • size for use with partial least-squares regression: Appl. to near-infrared spectroscopy
- [33] – Gen. -alg. sel. of a regulatory structure that directs flux in a simple metabolic •
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- [10] – Opt. layout • for pressure irrigation syst. using GAs
- [422] – Protein folding: optimized sequences obtained by simulated breeding in a minimalist •
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- [304] – Studying genotype-phenotype interactions: a • of the evol. of the cell regulation network
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- [266] **Model-based** epicardial boundary detection using GAs
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- [261] **model-guided** An appl. of GAs to geometric • interpretation of brain anatomy

- [175] **modeling** A GA based molecular • technique for RNA stem-loop structures
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- [451] – GA strategy for variable sel. in QSAR studies: GA-based region selection for CoMFA •
- [315] – Hierarchical alg. for computer • of protein tertiary structure: folding of myoglobin to 6.2Å resolution
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- [394] – Kinetic • of exciton migration in photosynthetic syst. . 3. Appl. of GAs to simulations of excitation dynamics in three-dimensional photosyst. I core antenna/reaction center complexes
- [439] – Molecular • of amoebapore and NK-lysin: A four-alpha-helix bundle of cytotoxic peptides from distantly related organisms
- [256] • malaria as a complex adaptive syst.
- [377] • proteins conformation in solution. Part I: a par. GAengine for protein conformational space mapping
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- [60] **Modelling** evolving pop.
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- [402] – The GA appl. as a • tool to predict the fold of small proteins with different topologies
- [12] **models** Automating the parametrization of mathematical • using GAs
- [413] – Construction of 3-D QSAR • using the 4-D QSAR formalism
- [425] – Development of a GA method especially designed for the comparison of molecular • Appl. to the elucidation of the benzodiazepine receptor pharmacophore
- [184] – GAs and deformable geometric • for anatomical object recognition
- [326] – Gen. function approximation: A gen. appr. to building quantitative structure-activity relationship •
- [28] – Gen. evolved receptor • (GERM): A computational appr. to construction of receptor •
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- [345] – Receptor surface • 2. Appl. to quantitative structure-activity relationships studies
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- [214] **modified** GA with • elitism for RF coil NMR tomograph magnetic field homogeneity opt.
- [267] • Kohonen's self-organizing feature map and its appl. to automatic sleep cycle recognition
- [38] **molecular** A comparison of heuristic search alg. for • docking
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- [32] – A GA for flexible • overlay and pharmacophore elucidation
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- [462] – An analysis of the GA method of • conformation determination
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- [90] – Construction of • phylogen. trees using a GA
- [425] – Development of a GA method especially designed for the comparison of • models: Appl. to the elucidation of the benzodiazepine receptor pharmacophore
- [395] – Exploring the energy landscapes of • recognition by a GA: Analysis of the requirements for robust docking of HIV-1 protease and FKBP-12 complexes
- [417] – Folding simulation with GAs and a detailed • description
- [492] – GA: a new appr. to the prediction of the structure of • clusters
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- [75] – GA for • sequence comparison
- [362] – GAs in • recognition and design
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- [415] • design using the minireceptor concept
- [439] • modeling of amoebapore and NK-lysin: A four-alpha-helix bundle of cytotoxic peptides from distantly related organisms
- [365] • recognition of receptor sites using a GA with a description of desolvation
- [367] • recognition of the inhibitor AG-1343 by HIV-1 protease: conformationally flexible docking by EP
- [181] • recognition using a binary gen. search alg.
- [308] – Opt. amino acid sequences by simulated • evol.
- [341] – Peptide design in machina: Development of artificial mitochondrial protein precursor cleavage sites by simulated • evol.
- [440] – Prediction of infinite dilution activity coefficients of organic compounds in aqueous solution from • structure
- [176] – PRO-LIGAND: An appr. to de novo • design. 3. A GA for structure refinement
- [421] – STALK: an interactive syst. for virtual • docking
- [331] – The rational design of amino acid sequences by artificial neural networks and simulated • evol. : *De novo* design of an idealised leader peptidase cleavage-site
- [437] – Three-dimensional quantitative structure-activity relationships from • similarity matrixes and gen. neural networks.1. Appl.
- [432] – Three-dimensional quantitative structure-activity relationships from • similarity matrixes and gen. neural networks.1. Method and validations
- [292] – Using an annealing GA to solve global energy minimization problem in • binding
- [55] **molecular biology** The appl. of evol. computation to selected problems in •
- [170] **molecular dynamics** Characterisation of the solution conformation of a cyclic RGD peptide analogue by NMR spectroscopy allied with a GA appr. and constrained •
- [350] – Gen. helping •
- [420] **molecularBldynamics** Refinement of the NMR solution structure of the gamma-carboxyglutamic acid domain of coagulation factor IX using • simulation with initial Ca2+ positions determined by GA
- [29] **molecules** A GA based method for docking flexible •
- [173] – A GA for the automated generation of • within constraints
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- [344] – Docking conformationally flexible small • into a protein binding site through EP
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- [217] **monitoring** GA based input sel. for a neural network function approximator with appl. to SSME •
- [182] **Monte Carlo** APLOGEN: an object-oriented GA performing • opt.
- [357] • alg. for docking to proteins
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- [56] **mortality** Biological consequences of evol. opt. s: • variability, survival
- [110] **motif** Stochastic • extraction using a GA with the MDL principle
- [424] **motifs** Structural consensus in ligand-protein docking identifies recognition peptide • that bind streptavidin
- [53] **Mount** Climbing • Improbable

- [58] **movements** Simulation of large-scale tropical tuna • in relation with daily remote sensing data: The artificial life appr.
- [340] **moves** Local • An efficient alg. for simulation of protein folding
- [196] **MR** Knowledge-based interpretation of • brain images
- [234] – Knowledge based interpretation of • brain images
- [287] – Neural inhabitants of • and echo images segment cardiac structures
- [222] **MR-image** Fuzzy-set opt. in use of medical • analysis based on evol. strategies
- [245] **multicriteria** Pareto opt. of the cntr. of a cardiac assist device using • rank and niche-based GAs hybridised with breeding and gradient methods
- [227] **multi-dimensional** Interactive segmentation of • medical data with contour-based appl. of GAs
- [360] **multi-group** Protein sequence analysis using a • par. GA
- [159] **multilocus** Computer simulation of gen. adaptation: Par. subcomponent interaction in a • model
- [194] **Multiple** source localization using GAs
- [220] **multi-population** Opt. of simulation models with GADELO: a • GA
- [246] **multivariable** Hierarchical • fuzzy cntr. for learning with GAs
- [251] **muscle** GA-based estimation method for human • parameter in elbow flexion
- [470] **mutagenesis** Recursive ensemble • - A comb. opt. technique for protein eng.
- [156] **mutant** Opt. by hierarchical • production
- [73] **Mutation** and recombination effects on the adaptability of sexual and asexual organisms
- [478] **mutations** Effect of • on the perf. of GAs suitable for protein folding simulations
- [474] – Effects of • on the perf. of GAs suitable for protein-folding simulations
- [86] – Evol. is promoted by asymmetrical • in DNA replication-GA with double-stranded DNA
- [187] **Myoelectric** signal recognition using gen. prog.
- [315] **myoglobin** Hierarchical alg. for computer modeling of protein tertiary structure: folding of • to 6.2Å resolution
- [355] **native** A standard GA appr. to • protein conformation prediction
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- [47] **networks** Evol. of biological regulation • under complex environmental constraints
- [23] – Improved GAs appr. in management of irrigation • syst.
- [287] **Neural** inhabitants of MR and echo images segment cardiac structures
- [283] **neural network** A GA to improve a • to predict a patients response to Warfarin
- [366] – Amino acid sequence analysis and design by artificial • and simulated molecular evol. – An evaluation
- [217] – GA based input sel. for a • function approximator with appl. to SSME monitoring
- [26] – Growth opt. of plant by means of the hybrid syst. of GA and •
- [263] – Prediction of hemorrhagic blood loss with a GA •
- [39] – Prediction of MHC class II-binding peptides using an evol. alg. and artificial •
- [243] – Prediction of outcome in critically ill patients using artificial • synthesised by GA
- [79] **neural network-based** Evol. opt. of a • signal processor for photometric data from an automated DNA sequencer
- [262] **neural networks** A new evol. syst. for evolving artificial •
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- [286] – Appl. of • and GAs in the diagnosis of cancer, anorexia nervosa and AIDS
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- [407] – Predicting maximum bioactivity by effective inversion of • using GAs
- [433] – The prediction of protein secondary structure with a cascade correlation learning architecture of •
- [331] – The rational design of amino acid sequences by artificial • and simulated molecular evol. : *De novo* design of an idealised leader peptidase cleavage-site
- [437] **neural networks.1** Three-dimensional quantitative structure-activity relationships from molecular similarity matrixes and gen. • Appl.
- [432] – Three-dimensional quantitative structure-activity relationships from molecular similarity matrixes and gen. • Method and validations
- [488] **Neurons** Symbols versus •
- [210] **neutron** GAs appl. to • penumbral imaging
- [202] – Reconstruction of • penumbral images by a constrained GA
- [245] **niche-based** Pareto opt. of the cntr. of a cardiac assist device using multicriteria, rank and • GAs hybridised with breeding and gradient methods
- [68] **nicht-genetischen** Untersuchung der evol. sstrategischen Bedeutung der • Varianz mit Hilfe der $[\gamma', \lambda(\mu/\rho, \lambda)]$ -ES
- [121] **nitrogen** Opt. , active cntr. of oxides of • (NO_x) emissions from a nat. gas-fired burner using a simple GA
- [439] **NK-lysin** Molecular modeling of amoebapore and • A four-alpha-helix bundle of cytotoxic peptides from distantly related organisms
- [337] **NMR** An evaluation of the GA as a computational tool in protein •
- [372] – Automated sequence-specific • assignment of homologous proteins using the prog. GARANT
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- [420] – Refinement of the • solution structure of the gamma-carboxyglutamic acid domain of coagulation factor IX using molecularBLdynamics simulation with initial Ca^{2+} positions determined by GA
- [170] **NMR spectroscopy** Characterisation of the solution conformation of a cyclic RGD peptide analogue by • allied with a GA appr. and constrained molecular dynamics
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- [140] **nonlinear programming** Aquifer remediation design: • and GAs
- [121] **NO_x** Opt. , active cntr. of oxides of nitrogen • emissions from a nat. gas-fired burner using a simple GA
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- [410] **numeric** Nonlinear PLS improved by • GA for QSAR modeling
- [247] **neuromuscular** Gen. -based machine learning for the assessment of certain • disorders
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- [353] **object oriented** An • environment for artificial evol. of protein sequences: The example of rational design of transmembrane sequences
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- [118] **objective** Using GAs to solve a multiple • groundwater pollution containment problem
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- [391] **operator** Improved GA for the protein folding problem by use of a Cartesian combination •
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- [172] **optimal** A GA to search for • and subopt. RNA secondary structures
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- [16] **optimising** New techniques for • the design and sch. for irrigation syst.
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- [446] **optimization problem** Protein structure prediction as a hard • the GA appr.
- [56] **optimizations** Biological consequences of evol. • mortality, variability, survival
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- [440] **organic** Prediction of infinite dilution activity coefficients of • compounds in aqueous solution from molecular structure
- [405] **organic-molecules** Search for native conformations of • by GAs
- [46] **organism** Ecological appl. of GAs: predicting • distribution in complex habitats
- [439] **organisms** Molecular modeling of amoebapore and NK-lysin: A four-alpha-helix bundle of cytotoxic peptides from distantly related •
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- [164] **Origins** The • of Order, Self-Organization and Sel. in Evol.
- [243] **outcome** Prediction of • in critically ill patients using artificial neural network synthesised by GA
- [460] **outperform** Do intelligent configuration search techniques • random search for large molecules?
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- [32] **overlay** A GA for flexible molecular • and pharmacophore elucidation
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- [378] **paracelcin-43** Towards meeting the Paracelcus challenge: The design, synthesis, and characterization of • an alpha-helical protein with over 50-percent sequence identity to all-beta protein
- [378] **Paracelcus challenge** Towards meeting the • The design, synthesis, and characterization of paracelcin-43, an alpha-helical protein with over 50-percent sequence identity to all-beta protein
- [72] **paradigm** Biological evol. as a • for performance-driven search
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- [320] – Appl. of the • fast messy GA to the protein folding problem
- [130] – Artificial life and pollution cntr. : Explorations of a GA syst. on the highly • Connection Machine
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- [374] **Parallel processing** of chemical info in a local area network III. Using GAs for conformational analysis of biomacromolecules
- [289] **paralyzed** The applicability of the evol. strategy to the cntr. of • limbs through fes
- [393] **PARAM** Par. GAs on • for conformation of biopolymers
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- [272] – Relapse from tobacco smoking cessation: Mathematical and computer micro-simulation modelling including • opt. with GAs
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- [282] **parameters** The evol. strategy - A search strategy used in individual opt. of electrical • for therapeutic carotid sinus nerve stimulation
- [389] **parametric** Protein-protein docking using • surface Rep.
- [12] **parametrization** Automating the • of mathematical models using GAs
- [321, 330] **Parametrizing** GAs for protein folding simulation
- [245] **Pareto optimisation** of the cntr. of a cardiac assist device using multicriteria, rank and niche-based GAs hybridised with breeding and gradient methods
- [445] **PARM** a gen. evolved alg. to predict bioactivity
- [412] • a new QSAR research method based on GA
- [178] **partial** GA-based method for selecting wavelenghts and model size for use with • least-squares regression: Appl. to near-infrared spectroscopy
- [36] – GA-based protocol for coupling digital filtering and • least-squares regression: Appl. to the near-infrared analysis of glucose in biological matrices
- [211, 197] **partition** Evol. CT image reconstruction by image •
- [62] **patent** A scientist seeks gold in a controversial drug •
- [482] **pathways** GAs in biochemistry (GALB): learning protein folding •
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- [283] **patiens** A GA to improve a neural network to predict a • response to Warfarin
- [243] **patients** Prediction of outcome in critically ill • using artificial neural network synthesised by GA
- [89] **pattern** Signal • extraction from DNA sequences using hidden Markov model and GA
- [334] **patterns** Automated discovery of detectors and iteration-performing calculations to recognize • in protein sequences using gen. prog.
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- [316] – Recognizing • in protein sequences using iteration-performing calculations in gen. prog.
- [210] **penumbral** GAs appl. to neutron • imaging
- [202] – Reconstruction of neutron • images by a constrained GA
- [331] **peptidase** The rational design of amino acid sequences by artificial neural networks and simulated molecular evol. : *De novo* design of an idealised leader • cleavage-site
- [404] **peptide** Development of a novel GA search method (GAP1.0) for exploring • conformational space
- [346] • Energy minimization of • analogues using GAs
- [341] • design in machina: Development of artificial mitochondrial protein precursor cleavage sites by simulated molecular evol.
- [450] – Rational comb. library design 2. Rational design of targeted combinatorial • libraries using chemical similarity probe and the inverse QSAR appr.
- [424] – Structural consensus in ligand-protein docking identifies recognition • motifs that bind streptavidin
- [359] **peptides** A GA that seeks native states of • and proteins
- [296] – Appl. of GAs to *de novo* design of therapeutic • [Abstract of a poster]
- [439] – Molecular modeling of amoebapore and NK-lysin: A four-alpha-helix bundle of cytotic • from distantly related organisms
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- [37] **performance** A high • syst. for molecular dynamics simulation of biomolecules using a special-purpose computer
- [398] – Assenssing the • of fold recognition methods by means of a comprehensive benchmark
- [274] – Automatic registration of 3D images using a simple GA with a stochastic • function
- [478] – Effect of mutations on the • of GAs suitable for protein folding simulations
- [474] – Effects of mutations on the • of GAs suitable for protein-folding simulations
- [182] **performing** APLOGEN: an object-oriented GA • Monte Carlo opt.
- [442] **Pharmacological** activity and membrane interactions of antiarrhythmics: 4-D QSAR/QSPR analysis
- [32] **pharmacophore** A GA for flexible molecular overlay and • elucidation
- [425] – Development of a GA method especially designed for the comparison of molecular models: Appl. to the elucidation of the benzodiazepine receptor •
- [466] **phase** Appl. of the GA to a simplified form of the • problem
- [179] **phenotypic** The consequences of • plasticity in cyclically varying environments: A GA study
- [467] **photodimer** Conformational analysis of a dinucleotide • with the aid of the GA
- [79] **photometric** Evol. opt. of a neural network-based signal processor for • data from an automated DNA sequencer
- [394] **photosynthetic** Kinetic modeling of exciton migration in • syst. . . 3. Appl. of GAs to simulations of excitation dynamics in three-dimensional photosyst. I core antenna/reaction center complexes
- [394] **photosystem** Kinetic modeling of exciton migration in photosynthetic syst. . . 3. Appl. of GAs to simulations of excitation dynamics in three-dimensional • I core antenna/reaction center complexes
- [154] **phylogenetic** A • ontogen. , and epigenetic view of bio-inspired hardware syst.
- [387] – Protein • inference using maximum likelihood with a GA
- [105] **phylogenetic tree** Search for maximum likelihood • using a GA
- [90] **phylogenetic trees** Construction of molecular • using a GA
- [65] **physical** A GA for assembling chromosome • maps
- [14] **physiological** Opt. cntr. of • processes of plants in a green plant factory
- [399] **pieces** Puzzle • defined: locating common packing units in tertiary protein contacts

- [18] **piped** GA design of • irrigation syst.
- [260] **planning** Decision theoretic steering and GA opt. : Appl. to stereotactic radiosurgery treatment •
- [231] – GA appl. to radiotherapy treatment •
- [221] – Gen. and geometric opt. of three-dimensional radiation therapy treatment •
- [228] – Opt. radiation therapy • using GAs
- [219] – Opt. radiation-therapy • using GAs
- [26] **plant** Growth opt. of • by means of the hybrid syst. of GA and neural network
- [14] – Opt. cntr. of physiological processes of plants in a green • factory
- [14] **plants** Opt. cntr. of physiological processes of • in a green plant factory
- [179] **plasticity** The consequences of phenotypic • in cyclically varying environments: A GA study
- [410] **PLS** Nonlinear • improved by numeric GA for QSAR modeling
- [429] **polar** Predicting conserved water-mediated and • ligand interactions in proteins using a K-nearest-neighbors GA
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- [137] **pollution** Analysis of the distribution of airborne • using GAs
- [130] – Artificial life and • cntr. : Explorations of a GA syst. on the highly par. Connection Machine
- [126] – The appl. of GA and nonlinear fuzzy prog. for water • cntr. in a river basin
- [118] – Using GAs to solve a multiple objective groundwater • containment problem
- [239] **polydistributional** Evolving • mixtures for mammographic feature modeling and analysis
- [397] **polypeptide** A par. GA for • three dimensional structure prediction. A transputer impl.
- [356] **polypeptides** Ab initio structure prediction for small • and protein fragments
- [414] – New opt. method for conformational energy calculations on • conformational space annealing
- [318] – The GA and the conformational search of • and proteins
- [60] **populations** Modelling evolving •
- [71] – LINKERS: A simulation prog. syst. for generating • with gen. structure
- [40] – Simulation of gen. • with biochemical properties
- [158] – Simulation of local evol. dynamics of small •
- [420] **positions** Refinement of the NMR solution structure of the gamma-carboxyglutamic acid domain of coagulation factor IX using molecularBLdynamics simulation with initial Ca²⁺ • determined by GA
- [323] **potential** A simplified amino acid • for use in structure prediction of proteins
- [458] – An introduction to the protein folding problem and the • appl. of evol. prog.
- [327] – Artificial neural networks and simulated molecular evol. are • tools for sequence-oriented protein design
- [453] • of GAs in protein folding and protein eng. simulations
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- [382] **potential function** Minimising reduced-model proteins using a generalised hierarchical table-lookup •
- [306] **potentials** De-novo protein design using pairwise • and a GA
- [124] **power** Environmentally constrained electric • dispatch with GAs
- [85] – On the computational • of DNA
- [322] **prédiction** Développement de méthodes basées sur les mathématiques, l'informatique et l'intelligence artificielle pour l'alignement de séquences et la • de structures protéines [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure prediction]
- [341] **precursor** Peptide design in machina: Development of artificial mitochondrial protein • cleavage sites by simulated molecular evol.
- [45] **Predator-prey** interactions in a simulated world
- [283] **predict** A GA to improve a neural network to • a patients response to Warfarin
- [445] – PARM: a gen. evolved alg. to • bioactivity
- [402] – The GA appl. as a modelling tool to • the fold of small proteins with different topologies
- [487] **predicting** A computer based simulation with artificial adaptive agents for • secondary structure from the protein hydrophobicity [Abstract]
- [338] – An artificial life model for • the tertiary structure of unknown proteins that emulates the folding process
- [46] – Ecological appl. of GAs: • organism distribution in complex habitats
- [429] • conserved water-mediated and polar ligand interactions in proteins using a K-nearest-neighbors GA
- [407] • maximum bioactivity by effective inversion of neural networks using GAs
- [309] • protein structure using GAs
- [80] • whether or not a nucleic acid sequence is an *E. coli* promoter region using gen. prog.
- [356] **prediction** Ab initio structure • for small polypeptides and protein fragments
- [379] – Ab initio tertiary-fold • of helical and non-helical protein chains using a GA
- [401] – An alg. for • of structural elements in small proteins
- [171] – An APL-prog. GA for the • of RNA secondary structure
- [427] – Appl. of evol. alg. to protein folding •
- [435] – Applying experimental data to protein fold • with the GA
- [438] – Computational methods for the • of protein folds
- [322] – Développement de méthodes basées sur les mathématiques, l'informatique et l'intelligence artificielle pour l'alignement de séquences et la prédiction de structures protéines [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure •
- [492] – GA: a new appr. to the • of the structure of molecular clusters
- [384] – GAs appl. to protein structure •
- [390] – GAs for protein structure •
- [332, 483, 485, 486] – GAs for protein tertiary structure •
- [406] – Improving protein structure • by new strategies: experimental insights and the GA
- [314] – Incremental • of side-chain conformation of proteins by a GA
- [361] – LGANN: a par. syst. combining a local GA and neural networks for the • of secondary structure of protein
- [263] • of hemorrhagic blood loss with a GA neural network
- [440] • of infinite dilution activity coefficients of organic compounds in aqueous solution from molecular structure
- [39] • of MHC class II-binding peptides using an evol. alg. and artificial neural network
- [243] • of outcome in critically ill patients using artificial neural network synthesised by GA
- [446] – Protein structure • as a hard opt. problem: the GA appr.
- [310] – Protein structure • using hybrid AI methods
- [418] – Protein structure • as a hard opt. problem: the GA appr.
- [481] – Reduced Rep. model of protein structure • Statistical potential and GAs
- [430] – Secondary structure • using segment similarity
- [342] – Simple GA parameter sel. for protein structure •
- [465] – The appl. of the GA to protein tertiary structure •
- [433] – The • of protein secondary structure with a cascade correlation learning architecture of neural networks
- [333] – The • of the degree of exposure to solvent of amino acid residues via gen. prog.
- [380] – The • of the degree of exposure to solvent of amino acid residues via gen. prog.
- [443] **predictive** GA strategy for variable sel. in QSAR studies: GAPLS and D-opt. designs for • QSAR model
- [157] **preferences** Evol. wanderlust: Sexual sel. with directional mate •
- [72] **performance-driven** Biological evol. as a paradigm for • search
- [10] **pressure** Opt. layout model for • irrigation syst. using GAs
- [41] **primary** GA-based method to design a • screen for antirhinovirus agents
- [176] **PRO_LIGAND** An appr. to de novo molecular design. 3. A GA for structure refinement
- [129] **Probabilistic** methods in life-cycle design
- [450] **probe** Rational comb. library design 2. Rational design of targeted combinatorial peptide libraries using chemical similarity • and the inverse QSAR appr.

- [250] **problem** A GA appr. to opt. for the radiological worker allocation • - discussions on different hard constraints
- [252] - A GA appr. to opt. for the radiological worker allocation •
- [98] - A heuristic appr. for Hamiltonian path • with molecules
- [76] - A hybrid GA appl. to a gen. sequencing •
- [91] - An evaluation of appl. of the GA to the • of ordering gen. loci on human chromosomes using radiation hybrid data
- [458] - An introduction to the protein folding • and the potential appl. of evol. prog.
- [253] - Appl. of GAs to the • of new clustering of psychological categories using real clinical data sets
- [466] - Appl. of the GA to a simplified form of the phase •
- [320] - Appl. of the par. fast messy GA to the protein folding •
- [391] - Improved GA for the protein folding • by use of a Cartesian combination operator
- [418] - Protein structure prediction as a hard opt. • the GA appr.
- [74] - THE GENIE PROJECT: A GA appl. to a sequencing • in the biological domain
- [292] - Using an annealing GA to solve global energy minimization • in molecular binding
- [186] - Using "biological" GAs to solve the travelling salesman • with appl. in medical image processing
- [118] - Using GAs to solve a multiple objective groundwater pollution containment •
- [99] **problems** Solving ray acoustic • with a DNA computer
- [55] - The appl. of evol. computation to selected • in molecular biology
- [338] **process** An artificial life model for predicting the tertiary structure of unknown proteins that emulates the folding •
- [24] - An intelligent appr. for opt. cntr. of fruit-storage • using neural networks and GAs
- [14] **processes** Opt. cntr. of physiological • of plants in a green plant factory
- [463, 113] **processing** A stochastic appr. to gen. info •
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- [495] **production** Acquisition and • of skilled behavior in dynamic decision-making tasks
- [156] - Opt. by hierarchical mutant •
- [369] **profiles** A study of combined structure/sequence •
- [119] **programming** A cross-platform par. GA • environment
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- [233] - cntr. blood pressure during surgery using evol. •
- [344] - Docking conformationally flexible small molecules into a protein binding site through evol. •
- [69, 70] - Evol. of food foraging strategies for the Caribbean *Anolis* lizard using gen. •
- [302] - Evol. • appl. to the development of quantitative structure-activity relationship and quantitative structure-property relationships
- [25] - Evol. • for mix design
- [120] - Gen. -alg. • environments
- [367] - Molecular recognition of the inhibitor AG-1343 by HIV-1 protease: conformationally flexible docking by evol. •
- [319] - Protein structure comparisons using a combination of a GA, dynamic • and least-squares minimization
- [71] - LINKERS: A simulation • syst. for generating pop. with gen. structure
- [126] - The appl. of GA and nonlinear fuzzy • for water pollution cntr. in a river basin
- [15] **project planning** Decision support for irrigated • using a GA
- [74] PROJECT THE GENIE • A GA appl. to a sequencing problem in the biological domain
- [86] **promoted** Evol. is • by asymmetrical mutations in DNA replication-GA with double-stranded DNA
- [80] **promoter** Predicting whether or not a nucleic acid sequence is an *E. coli* • region using gen. prog.
- [78] - Recognising • sequences using an artificial immune syst.
- [40] **properties** Simulation of gen. pop. with biochemical •
- [322] **protéines** Développement de méthodes basées sur les mathématiques, l'informatique et l'intelligence artificielle pour l'alignement de séquences et la prédiction de structures • [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure prediction]
- [487] **protein** A computer based simulation with artificial adaptive agents for predicting secondary structure from the • hydrophobicity [Abstract]
- [490] - A critical comparison of search alg. appl. to the • side-chain conformations
- [479] - A Darwinian evol. syst. - II. Experiments on • evol. and evolutionary aspects of the gen. code
- [104] - A GA for designing gene family-specific oligonucleotide sets used for hybridization: the G protein-coupled receptor • superfamily
- [489] - A new appr. to the rapid determination of • side chain conformations
- [356] - Ab initio structure prediction for small polypeptides and • fragments
- [379] - Ab initio tertiary-fold prediction of helical and non-helical • chains using a GA
- [337] - An evaluation of the GA as a computational tool in • NMR
- [435] - Applying experimental data to • fold prediction with the GA
- [327] - Artificial neural networks and simulated molecular evol. are potential tools for sequence-oriented • design
- [373] - Assigning a • sequence to a three-dimensional fold [Abstract of a poster]
- [428] - Comparison of • surfaces using a GA
- [306] - De-novo • design using pairwise potentials and a GA
- [322] - Développement de méthodes basées sur les mathématiques, l'informatique et l'intelligence artificielle pour l'alignement de séquences et la prédiction de structures protéines [Development of mathematical, computing and artificial intelligence methods for the • secondary structure prediction]
- [344] - Docking conformationally flexible small molecules into a • binding site through EP
- [335] - Evol. of a computer prog. for classifying • segments as transmembrane domains using gen. prog.
- [103] - From DNA to • transformations and their possible role in linkage learning
- [384] - GAs appl. to • structure prediction
- [454] - GAs as a new tool to study • stability
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- [332, 483, 485, 486] - GAs for • tertiary structure prediction
- [392] - Gen. prog. for improved data mining: An appl. to the biochemistry of • interactions
- [441] - GENFOLD: A GA for folding • structures using NMR restraints
- [315] - Hierarchical alg. for computer modeling of • tertiary structure: folding of myoglobin to 6.2Å resolution
- [447] - How evol. makes • fold quickly
- [336] - Improved GA-based • structure comparisons: pairwise and multiple superpositions
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- [361] - LGANN: a par. syst. combining a local GA and neural networks for the prediction of secondary structure of •
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- [360] • sequence analysis using a multi-group par. GA
- [319] • structure comparisons using a combination of a GA, dynamic prog. and least-squares minimization
- [446] • structure prediction as a hard opt. problem: the GA appr.
- [310] • structure prediction using hybrid AI methods
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- [341] - Peptide design in machina: Development of artificial mitochondrial • precursor cleavage sites by simulated molecular evol.
- [309] - Predicting • structure using GAs
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- [481] - Reduced Rep. model of • structure prediction: Statistical potential and GAs
- [416] - Sampling • conformations using segment libraries and a GA
- [342] - Simple GA parameter sel. for • structure prediction
- [370] - Stochastic models for the explanation of tertiary structures of •
- [471] - Synthesizing regularity exposing attributes in large • databases
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- [434] – The evol. simulation of zinc finger domain sequence. Appl. of GAs in • structure study
- [433] – The prediction of • secondary structure with a cascade correlation learning architecture of neural networks
- [378] – Towards meeting the Paracelsus challenge: The design, synthesis, and characterization of paracelcin-43, an alpha-helical • with over 50-percent sequence identity to all-beta •
- [377] **protein conformational** Modeling proteins conformation in solution. Part I: a par. GAengine for • space mapping
- [355] **protein conformation prediction** A standard GA appr. to native •
- [453] **protein engineering** Potential of GAs in protein folding and • simulations
- [470] – Recursive ensemble mutagenesis - A comb. opt. technique for •
- [476] **protein folding** A GA for 3D • simulations
- [368] – A simple • alg. using a binary code and secondary structure constraints
- [458] – An introduction to the • problem and the potential appl. of evol. prog.
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- [320] – Appl. of the par. fast messy GA to the • problem
- [457] – Determining protein folds by inverted and evol. • alg.
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- [422] • optimized sequences obtained by simulated breeding in a minimalist model
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- [473] – Why GAs are suitable for • analysis: The theoretical foundations
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- [438] **protein folds** Computational methods for the prediction of •
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- [353] **protein sequences** An object oriented environment for artificial evol. of • The example of rational design of transmembrane sequences
- [334] – Automated discovery of detectors and iteration-performing calculations to recognize patterns in • using gen. prog.
- [459] – Automated learning of a detector for α -helices in • via gen. prog.
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- [423] **protein structure** Discrete Haar transformation and •
- [418] • prediction as a hard opt. problem: the GA appr.
- [328] **protein structure prediction** GAs codings used in • by energy minimization
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- [474] **protein-folding** Effects of mutations on the perf. of GAs suitable for • simulations
- [389] **Protein-protein** docking using parametric surface Rep.
- [359] **proteins** A GA that seeks native states of peptides and •
- [323] – A simplified amino acid potential for use in structure prediction of •
- [401] – An alg. for prediction of structural elements in small •
- [338] – An artificial life model for predicting the tertiary structure of unknown • that emulates the folding process
- [303] – An evol. appr. to folding small alpha-helical • that uses sequence info and an empirical guiding fitness function
- [363] – Automated assignment of nuclear magnetic resonance assignments for •
- [372] – Automated sequence-specific NMR assignment of homologous • using the prog. GARANT
- [325] – Delineating the mainchain topology of four-helix bundle • using the GA and knowledge based on the amino acid sequence alone
- [358, 400] – Docking flexible molecules: A case study of three •
- [436] – *Ab initio* protein folding simulation with GAs: Simulations on the complete sequence of small •
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- [409] – Evol. of model • on a foldability landscape
- [307] – Folding the main chain of small • with the GA
- [396] – Identifying the tertiary fold of small • with different topologies from sequence and secondary structure using the GA and extended criteria specific for strand regions
- [314] – Incremental prediction of side-chain conformation of • by a GA
- [382] – Minimising reduced-model • using a generalised hierarchical table-lookup potential function
- [377] – Modeling • conformation in solution. Part I: a par. GAengine for protein conformational space mapping
- [357] – Monte Carlo alg. for docking to •
- [312] – Opt. sequence sel. in • of known structure by simulated evol.
- [429] – Predicting conserved water-mediated and polar ligand interactions in • using a K-nearest-neighbors GA
- [469] – Sequential assignment of 2D-NMR spectra of • using GAs
- [318] – The GA and the conformational search of polypeptides and •
- [402] – The GA appl. as a modelling tool to predict the fold of small • with different topologies
- [484] **Proteintertiärstrukturen** Genetische Algorithmen zur Vorhersage von •
- [36] **protocol** GA-based • for coupling digital filtering and partial least-squares regression: Appl. to the near-infrared analysis of glucose in biological matrices
- [352] – GA-based • for docking ensembles of small ligands using experimental results
- [100] **Pseudo-Bacterial** The effects of combination of DNA coding method with • GA
- [253] **psychological** Appl. of GAs to the problem of new clustering of • categories using real clinical data sets
- [22] **PTYPE** Study on extracting the adaptive agricultural development area using GA with complex •
- [399] **Puzzle** pieces defined: locating common packing units in tertiary protein contacts
- [81] **puzzling** DNA sequence assembly and GAs – New results and • insights
- [238] **QRS** Gen. design of optimum linear and nonlinear • detectors
- [293] **QSAR+** Cerius² Release 1.6, Drug Discovery Workbench • User's Reference, Chapter 16: Introduction to gen. function approximation
- [413] **QSAR** Construction of 3-D • models using the 4-D • formalism
- [451] – GA strategy for variable sel. in • studies: GA-based region selection for CoMFA modeling
- [443] – GA strategy for variable sel. in • studies: GAPLS and D-opt. designs for predictive • model
- [448] – Mining the NCI anticancer drug discovery databases: gen. function approximation for the • study of anticancer ellipticine analogues
- [410] – Nonlinear PLS improved by numeric GA for • modeling
- [412] – PARM: a new • research method based on GA
- [450] – Rational comb. library design 2. Rational design of targeted combinatorial peptide libraries using chemical similarity probe and the inverse • appr.
- [317] – Variable sel. in • studies 1. An evol. alg.
- [329] – Variable sel. in • studies 2. A highly efficient combination of syst. atic search and evol.
- [442] **QSAR/QSPR** Pharmacological activity and membrane interactions of antiarrhythmics: 4-D • analysis
- [302] **quantitative** EP appl. to the development of • structure-activity relationship and • structure-property relationships
- [326] – Gen. function approximation: A gen. appr. to building • structure-activity relationship models

- [345] – Receptor surface models 2. Appl. to • structure-activity relationships studies
- [437] **quantitative structure-activity relationships** Three-dimensional • from molecular similarity matrixes and gen. neural networks.1. Appl.
- [432] – Three-dimensional • from molecular similarity matrixes and gen. neural networks.1. Method and validations
- [144] **Quark** The • and the Jaguar
- [447] **quickly** How evol. makes protein fold •
- [91] **radiation** An evaluation of appl. of the GA to the problem of ordering gen. loci on human chromosomes using • hybrid data
- [228] – Opt. • therapy planning using GAs
- [221] **radiation therapy** Gen. and geometric opt. of three-dimensional • treatment planning
- [219] **radiation-therapy** Opt. • planning using GAs
- [195] **radiographs** Detection of patterns in • using ANN designed and trained with the GA
- [250] **radiological** A GA appr. to opt. for the • worker allocation problem - discussions on different hard constraints
- [252] – A GA appr. to opt. for the • worker allocation problem
- [260] **radiosurgery** Decision theoretic steering and GA opt. : Appl. to stereotactic • treatment planning
- [231] **radiotherapy** GA appl. to • treatment planning
- [191] – Matching images for • verification using GAs
- [106] **random** Gen. and • keys for sequencing and opt.
- [460] **random search** Do intelligent configuration search techniques outperform • for large molecules?
- [135] **range** A GA with variable • of local search for tracking changing environments
- [245] **rank** Pareto opt. of the cntr. of a cardiac assist device using multicriteria, • and niche-based GAs hybridised with breeding and gradient methods
- [426] **rapamycin** Mean field analysis of FKBP-12 complexes with FK506 and • Implications for a role of crystallographic water molecules in molecular recognition and specificity
- [353] **rational** An object oriented environment for artificial evol. of protein sequences: The example of • design of transmembrane sequences
- [450] • comb. library design 2. • design of targeted combinatorial peptide libraries using chemical similarity probe and the inverse QSAR appr.
- [331] – The • design of amino acid sequences by artificial neural networks and simulated molecular evol. : *De novo* design of an idealised leader peptidase cleavage-site
- [99] **ray** Solving • acoustic problems with a DNA computer
- [94] **reactions** Info transfer through hybridization • in DNA based computing
- [253] **real** Appl. of GAs to the problem of new clustering of psychological categories using • clinical data sets
- [148] **reality** Evol. , complexity, entropy and artificial •
- [386] **Rebuilding** connectivity matrices from two-atom fragments using the GA
- [93] **Recent** developments in DNA-computing
- [104] **receptor** A GA for designing gene family-specific oligonucleotide sets used for hybridization: the G protein-coupled • protein superfamily
- [425] – Development of a GA method especially designed for the comparison of molecular models: Appl. to the elucidation of the benzodiazepine • pharmacophore
- [456] – Flexible docking of ligands to • sites using GAs
- [28] – Gen. evolved • models (GERM): A computational appr. to construction of • models
- [365] – Molecular recognition of • sites using a GA with a description of desolvation
- [345] • surface models 2. Appl. to quantitative structure-activity relationships studies
- [364] – What do we do when there's no • crystal structure? Using a GA to construct atomistic models of • binding sites
- [78] **Recognising** promoter sequences using an artificial immune syst.
- [398] **recognition** Assessing the perf. of fold • methods by means of a comprehensive benchmark
- [395] – Exploring the energy landscapes of molecular • by a GA: Analysis of the requirements for robust docking of HIV-1 protease and FKBP-12 complexes
- [184] – GAs and deformable geometric models for anatomical object •
- [362] – GAs in molecular • and design
- [426] – Mean field analysis of FKBP-12 complexes with FK506 and rapamycin: Implications for a role of crystallographic water molecules in molecular • and specificity
- [267] – Modified Kohonen's self-organizing feature map and its appl. to automatic sleep cycle •
- [365] – Molecular • of receptor sites using a GA with a description of desolvation
- [367] – Molecular • of the inhibitor AG-1343 by HIV-1 protease: conformationally flexible docking by EP
- [181] – Molecular • using a binary gen. search alg.
- [187] – Myoelectric signal • using gen. prog.
- [385] – Resolving water-mediated and polar ligand • using GAs [Abstract of a poster]
- [424] – Structural consensus in ligand-protein docking identifies • peptide motifs that bind streptavidin
- [371] – Use of GAs to learn ligand • concepts: Appl. to the GPCR superfamily
- [334] **recognize** Automated discovery of detectors and iteration-performing calculations to • patterns in protein sequences using gen. prog.
- [316] **Recognizing** patterns in protein sequences using iteration-performing calculations in gen. prog.
- [73] **recombination** Mutation and • effects on the adaptability of sexual and asexual organisms
- [383] – The effectiveness of • in the GA methodology. A comparison to simulated annealing
- [207] **reconstruction** 3D • of the human jaw from a sequence of images
- [212] – Evol. CT image •
- [271] – GA-based • in-diffusion tomography
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- [280] **reconstructions** GAs for minimal source •
- [470] **Recursive** ensemble mutagenesis - A comb. opt. technique for protein eng.
- [481] **Reduced** Rep. model of protein structure prediction: Statistical potential and GAs
- [382] **reduced-model** Minimising • proteins using a generalised hierarchical table-lookup potential function
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- [305] **refinement** GA • of structures generated by a *de novo* design prog.
- [420] • of the NMR solution structure of the gamma-carboxyglutamic acid domain of coagulation factor IX using molecularBLDynamics simulation with initial Ca²⁺ positions determined by GA
- [176] – PRO-LIGAND: An appr. to de novo molecular design. 3. A GA for structure •
- [288] **Regelkonzept** ES – ein • für die funktionelle Elektrostimulation gelähmter Gliedmaßen
- [451] **region** GA strategy for variable sel. in QSAR studies: GA-based • selection for CoMFA modeling
- [284] • merging in medical image segmentation and interpretation
- [80] – Predicting whether or not a nucleic acid sequence is an *E. coli* promoter • using gen. prog.
- [258] – Secondary structure of the 3'-untranslated • of yellow fever virus
- [13] **regional** GAs in the role of intelligent • adaptation agents for agricultural support syst.
- [274] **registration** Automatic • of 3D images using a simple GA with a stochastic perf. function
- [232] – Automatical • of brain volume data sets
- [178] **regression** GA-based method for selecting wavelenghts and model size for use with partial least-squares • Appl. to near-infrared spectroscopy
- [36] – GA-based protocol for coupling digital filtering and partial least-squares • Appl. to the near-infrared analysis of glucose in biological matrices
- [471] **regularity** Synthesizing • exposing attributes in large protein databases
- [47] **regulation** Evol. of biological • networks under complex environmental constraints
- [160] – GAs and info accumulation during the evol. of gene •
- [59] – Trans gene • in adaptive evol. : A GA model
- [33] **regulatory** Gen. -alg. sel. of a • structure that directs flux in a simple metabolic model
- [272] **Relapse** from tobacco smoking cessation: Mathematical and computer micro-simulation modelling including parameter opt. with GAs

- [439] **related** Molecular modeling of amoebapore and NK-lysin: A four-alpha-helix bundle of cytotoxic peptides from distantly • organisms
- [58] **relation** Simulation of large-scale tropical tuna movements in • with daily remote sensing data: The artificial life appr.
- [42] **relationship** Appl. of evol. alg. to the structure-activity •
- [302] – EP appl. to the development of quantitative structure-activity • and quantitative structure-property relationships
- [326] – Gen. function approximation: A gen. appr. to building quantitative structure-activity • models
- [302] **relationships** EP appl. to the development of quantitative structure-activity relationship and quantitative structure-property •
- [345] – Receptor surface models 2. Appl. to quantitative structure-activity • studies
- [293] **Release** Cerius² • 1.6, Drug Discovery Workbench QSAR+ User's Reference, Chapter 16: Introduction to gen. function approximation
- [140] **remediation** Aquifer • design: nonlinear prog. and GAs
- [123] – Dynamic opt. -cntr. for groundwater • management using GAs
- [122] – Opt. field-scale groundwater • using neural networks and GA
- [125] – Opt. groundwater • design using differential GA
- [58] **remote** Simulation of large-scale tropical tuna movements in relation with daily • sensing data: The artificial life appr.
- [86] **replication-genetic** Evol. is promoted by asymmetrical mutations in DNA • alg. with double-stranded DNA
- [389] **representation** Protein-protein docking using parametric surface •
- [481] – Reduced • model of protein structure prediction: Statistical potential and GAs
- [268] **representative** An efficient classifier syst. and its experimental comparison with two • learning methods on three medical domains
- [395] **requirements** Exploring the energy landscapes of molecular recognition by a GA: Analysis of the • for robust docking of HIV-1 protease and FKBP-12 complexes
- [230] **research** A comparison of GAs and other machine learning syst. on a complex classification task from common disease •
- [412] – PARM: a new QSAR • method based on GA
- [333] **residues** The prediction of the degree of exposure to solvent of amino acid • via gen. prog.
- [315] **resolution** Hierarchical alg. for computer modeling of protein tertiary structure: folding of myoglobin to 6.2Å •
- [385] **Resolving** water-mediated and polar ligand recognition using GAs [Abstract of a poster]
- [283] **response** A GA to improve a neural network to predict a patients • to Warfarin
- [441] **restraints** GENFOLD: A GA for folding protein structures using NMR •
- [116] **restriction** Construction of • maps using a GA
- [455] – DNA • fragment map assembly with GAs
- [214] **RF** GA with modified elitism for • coil NMR tomograph magnetic field homogeneity opt.
- [249] **RF-capacitive** An inverse method to optimize heating conditions in • hyperthermia
- [170] **RGD peptide** Characterisation of the solution conformation of a cyclic • analogue by NMR spectroscopy allied with a GA appr. and constrained molecular dynamics
- [275] **right** An approximate alg. for estimating treatment lags from • censored data
- [126] **river** The appl. of GA and nonlinear fuzzy prog. for water pollution cntr. in a • basin
- [175] **RNA** A GA based molecular modeling technique for • stem-loop structures
- [172] – A GA to search for opt. and suboptimal • secondary structures
- [171] – An APL-prog. GA for the prediction of • secondary structure
- [174] – The computer simulation of • folding pathways using a GA
- [395] **robust** Exploring the energy landscapes of molecular recognition by a GA: Analysis of the requirements for • docking of HIV-1 protease and FKBP-12 complexes
- [103] **role** From DNA to protein: transformations and their possible • in linkage learning
- [13] – GAs in the • of intelligent regional adaptation agents for agricultural support syst.
- [426] – Mean field analysis of FKBP-12 complexes with FK506 and rapamycin: Implications for a • of crystallographic water molecules in molecular recognition and specificity
- [403] • of γ -carboxyglutamic acid in the calcium-induced structural transition of conantokin G, a conotoxin from the marine snail *Conus geographus*
- [11] **route** Creation of opt. • for agricultural vehicle and construction machinery by using a GA
- [324] **RSNR** A comparison of GA and • docking
- [236] **rule** On • checking and learning in an acupuncture diagnosis fuzzy expert syst. by GA
- [257] – Parameter Evaluation and Gen. -Based • Learning for the Differential Diagnosis of Female urinary Incontinence
- [57] **rule-based** Analysing spider web-building behaviour with • simulations and GAs
- [213] **rules** Learning diagnostic • from a urological database using GA
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- [62] **scientist** A • seeks gold in a controversial drug patent
- [41] **screen** GA-based method to design a primary • for antirhinovirus agents
- [38] **search** A comparison of heuristic • alg. for molecular docking
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- [172] – A GA to • for opt. and suboptimal RNA secondary structures
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- [72] – Biological evol. as a paradigm for performance-driven •
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- [282] – The evol. strategy - A • strategy used in individual opt. of electrical parameters for therapeutic carotid sinus nerve stimulation
- [318] – The GA and the conformational • of polypeptides and proteins
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- [460] **search techniques** Do intelligent configuration • outperform random search for large molecules?
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- [487] **secondary structure** A computer based simulation with artificial adaptive agents for predicting • from the protein hydrophobicity [Abstract]
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- [172] **secondary structures** A GA to search for opt. and suboptimal RNA •
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- [312] – Opt. sequence • in proteins of known structure by simulated evol.
- [342] – Simple GA parameter • for protein structure prediction
- [164] – The Origins of Order, Self-Organization and • in Evol.
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- [61] **selfish** Geometry for a • foraging group: A GA appr.
- [164] **Self-Organization** The Origins of Order, • and Sel. in Evol.
- [267] **self-organizing** Modified Kohonen's • feature map and its appl. to automatic sleep cycle recognition
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- [223] **sensitive** Feature sel. with distinction • learning vector quantisation and GAs
- [207] **sequence** 3D reconstruction of the human jaw from a • of images
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- [436] – *Ab initio* protein folding simulation with GAs: Simulations on the complete • of small proteins
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- [312] – Opt. • sel. in proteins of known structure by simulated evol.
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- [434] – The evol. simulation of zinc finger domain • Appl. of GAs in protein structure study
- [378] – Towards meeting the Paracelcus challenge: The design, synthesis, and characterization of paracelcin-43, an alpha-helical protein with over 50-percent • identity to all-beta protein
- [88] **sequence alignment** SAGA: • by GA
- [327] **sequence-oriented** Artificial neural networks and simulated molecular evol. are potential tools for • protein design
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- [308] – Opt. amino acid • by simulated molecular evol.
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- [78] – Recognising promoter • using an artificial immune syst.
- [331] – The rational design of amino acid • by artificial neural networks and simulated molecular evol. : *De novo* design of an idealised leader peptidase cleavage-site
- [372] **sequence-specific** Automated • NMR assignment of homologous proteins using the prog. GARANT
- [76] **sequencing** A hybrid GA appl. to a gen. • problem
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- [104] **sets** A GA for designing gene family-specific oligonucleotide • used for hybridization: the G protein-coupled receptor protein superfamily
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- [157] **Sexual** Evol. wanderlust: • sel. with directional mate preferences
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- [489] **side chain** A new appr. to the rapid determination of protein • conformations
- [490] **side-chain** A critical comparison of search alg. appl. to the protein • conformations
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- [241] **signal analysis** Electrocardiographic • using GAs (GAs)
- [79] **signal processor** Evol. opt. of a neural network-based • for photometric data from an automated DNA sequencer
- [431] **silico** Evol. goes for GOLD in •
- [450] **similarity** Rational comb. library design 2. Rational design of targeted combinatorial peptide libraries using chemical • probe and the inverse QSAR appr.
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- [437] – Three-dimensional quantitative structure-activity relationships from molecular • matrixes and gen. neural networks. I. Appl.
- [432] – Three-dimensional quantitative structure-activity relationships from molecular • matrixes and gen. neural networks. I. Method and validations
- [34] **simplex method** A hybrid appr. to modeling metabolic syst. using GA and •
- [323] **simplified** A • amino acid potential for use in structure prediction of proteins
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- [66] **simulated** Adaptive behavior of • bacterial cells subjected to nutritional shifts
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- [167] – AntFarm: Towards • evol.
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- [341] – Peptide design in machina: Development of artificial mitochondrial protein precursor cleavage sites by • molecular evol.
- [45] – Predator-prey interactions in a • world
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- [331] – The rational design of amino acid sequences by artificial neural networks and • molecular evol. : *De novo* design of an idealised leader peptidase cleavage-site
- [383] **simulated annealing** The effectiveness of recombination in the GA methodology. A comparison to •
- [487] **simulation** A computer based • with artificial adaptive agents for predicting secondary structure from the protein hydrophobicity [Abstract]
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- [67] – A • appr. to evol. game theory: The evol. of time-sharing behavior in a dragonfly mating syst.
- [159] – Computer • of gen. adaptation: Par. subcomponent interaction in a multilocus model
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- [476] **simulations** A GA for 3D protein folding •
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- [474] – Effects of mutations on the perf. of GAs suitable for protein-folding •
- [436] – *Ab initio* protein folding simulation with GAs: • on the complete sequence of small proteins
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- [456] **sites** Flexible docking of ligands to receptor • using GAs
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- [403] **snail** Role of γ -carboxyglutamic acid in the calcium-induced structural transition of conantokin G, a conotoxin from the marine • *Conus geographus*
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- [377] – Modeling proteins conformation in solution. Part I: a par. GAengine for protein conformational • mapping
- [414] – New opt. method for conformational energy calculations on polypeptides: conformational • annealing
- [37] **special-purpose** A high perf. syst. for molecular dynamics simulation of biomolecules using a • computer
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- [426] **specificity** Mean field analysis of FKBP-12 complexes with FK506 and rapamycin: Implications for a role of crystallographic water molecules in molecular recognition and •
- [469] **spectra** Sequential assignment of 2D-NMR • of proteins using GAs
- [178] **spectroscopy** GA-based method for selecting wavelnghts and model size for use with partial least-squares regression: Appl. to near-infrared •
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- [139] **squares** Determination of hydraulic conductivity tensor using a nonlinear least • estimator
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- [481] **Statistical** Reduced Rep. model of protein structure prediction: • potential and GAs

- [260] **steering** Decision theoretic • and GA opt. : Appl. to stereotactic radiosurgery treatment planning
- [175] **stem-loop** A GA based molecular modeling technique for RNA • structures
- [260] **stereotactic** Decision theoretic steering and GA opt. : Appl. to • radiosurgery treatment planning
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- [463, 113] **stochastic** A • appr. to gen. info processing
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- [69, 70] **strategies** Evol. of food foraging • for the Caribbean *Anolis* lizard using gen. prog.
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- [451] **strategy** GA • for variable sel. in QSAR studies: GA-based region selection for CoMFA modeling
- [443] – GA • for variable sel. in QSAR studies: GAPLS and D-opt. designs for predictive QSAR model
- [153] • of co-evol. of transposons and host genome: Appl. to evol. computations
- [282] – The evol. strategy - A search • used in individual opt. of electrical parameters for therapeutic carotid sinus nerve stimulation
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- [424] **streptavidin** Structural consensus in ligand-protein docking identifies recognition peptide motifs that bind •
- [141] **strings** The appl. of GA to two-dimensional • The source appointment problem
- [401] **structural** An alg. for prediction of • elements in small proteins
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- [424] • consensus in ligand-protein docking identifies recognition peptide motifs that bind streptavidin
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- [356] **structure** Ab initio • prediction for small polypeptides and protein fragments
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- [309] – Predicting protein • using GAs
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- [481] – Reduced Rep. model of protein • prediction: Statistical potential and GAs
- [420] – Refinement of the NMR solution • of the gamma-carboxyglutamic acid domain of coagulation factor IX using molecularBLdynamics simulation with initial Ca²⁺ positions determined by GA
- [71] – LINKERS: A simulation prog. syst. for generating pop. with gen. •
- [342] – Simple GA parameter sel. for protein • prediction
- [434] – The evol. simulation of zinc finger domain sequence. Appl. of GAs in protein • study
- [364] – What do we do when there's no receptor crystal • Using a GA to construct atomistic models of receptor binding sites
- [397] **structure prediction** A par. GA for polypeptide three dimensional • A transputer impl.
- [323] – A simplified amino acid potential for use in • of proteins
- [42] **structure-activity** Appl. of evol. alg. to the • relationship
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- [326] – Gen. function approximation: A gen. appr. to building quantitative • relationship models
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- [302] **structure-property** EP appl. to the development of quantitative structure-activity relationship and quantitative • relationships
- [175] **structures** A GA based molecular modeling technique for RNA stem-loop •
- [294] – Computer-assisted drug design: GAs and • of molecular clusters of aromatic hydrocarbons and actinomycin D-deoxyguanosine
- [322] – Développement de méthodes besées sur les mathématiques, l'informatique et l'intelligence artificielle pour l'alignement de séquences et la prédiction de • protéines [Development of mathematical, computing and artificial intelligence methods for the protein secondary structure prediction]
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- [287] – Neural inhabitants of MR and echo images segment cardiac •
- [370] – Stochastic models for the explanation of tertiary • of protein
- [369] **structure/sequence** A study of combined • profiles
- [159] **subcomponent** Computer simulation of gen. adaptation: Par. • interaction in a multilocus model
- [66] **subjected** Adaptive behavior of simulated bacterial cells • to nutritional shifts
- [172] **suboptimal** A GA to search for opt. and • RNA secondary structures
- [84] **sub-sequences** Classifying nucleic acid • as introns or exons using gen. prog.
- [136] **substances** Competitive adsorption of trichloroethylene and humic • from groundwater on activated carbon
- [44] **substructures** Determination of maximum common 3D • using a GA
- [20] **sugar-cane** Developing a • breeding assistant syst. by a hybrid adaptive learning technique
- [478] **suitable** Effect of mutations on the perf. of GAs • for protein folding simulations
- [474] – Effects of mutations on the perf. of GAs • for protein-folding simulations
- [473] – Why GAs are • for protein folding analysis: The theoretical foundations
- [104] **superfamily** A GA for designing gene family-specific oligonucleotide sets used for hybridization: the G protein-coupled receptor protein •
- [336] **superpositions** Improved GA-based protein structure comparisons: pairwise and multiple •

- [452] **supersecondary** Protein folding simulation with GA and • structure constraints
- [13] **support** GAs in the role of intelligent regional adaptation agents for agricultural • syst.
- [389] **surface** Protein-protein docking using parametric • Rep.
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- [428] **surfaces** Comparison of protein • using a GA
- [233] **surgery** ctnr. blood pressure during • using EP
- [56] **survival** Biological consequences of evol. opt. s: mortality, variability, •
- [488] **Symbols** versus Neurons?
- [378] **synthesis** Towards meeting the Paracelsus challenge: The design, • and characterization of paracelcin-43, an alpha-helical protein with over 50-percent sequence identity to all-beta protein
- [243] **synthesised** Prediction of outcome in critically ill patients using artificial neural network • by GA
- [471] **Synthesizing** regularity exposing attributes in large protein databases
- [329] **systematic** Variable sel. in QSAR studies 2. A highly efficient combination of • search and evol.
- [382] **table-lookup** Minimising reduced-model proteins using a generalised hierarchical • potential function
- [450] **targeted** Rational comb. library design 2. Rational design of • combinatorial peptide libraries using chemical similarity probe and the inverse QSAR appr.
- [230] **task** A comparison of GAs and other machine learning syst. on a complex classification • from common disease research
- [495] **tasks** Acquisition and production of skilled behavior in dynamic decision-making •
- [16] **techniques** New • for optimising the design and sch. for irrigation syst.
- [139] **tensor** Determination of hydraulic conductivity • using a nonlinear least squares estimator
- [338] **tertiary** An artificial life model for predicting the • structure of unknown proteins that emulates the folding process
- [396] – Identifying the • fold of small proteins with different topologies from sequence and secondary structure using the GA and extended criteria specific for strand regions
- [399] – Puzzle pieces defined: locating common packing units in • protein contacts
- [370] – Stochastic models for the explanation of • structures of protein
- [332, 483, 485, 486] **tertiary structure** GAs for protein • prediction
- [315] – Hierarchical alg. for computer modeling of protein • folding of myoglobin to 6.2Å resolution
- [465] – The appl. of the GA to protein • prediction
- [379] **tertiary-fold** Ab initio • prediction of helical and non-helical protein chains using a GA
- [54] **test** The emergence of emergence distributions: Using GAs to • biological theories
- [480] **testing** Generating and • protein folds
- [206] **texture** Designing • filters with GAs: An appl. to medical images
- [162, 163] **thema** Evol. as a • in artificial life: The GENESYS/TRACKER syst.
- [260] **theoretic** Decision • steering and GA opt. : Appl. to stereotactic radiosurgery treatment planning
- [473] **theoretical** Why GAs are suitable for protein folding analysis: The • foundations
- [54] **theories** The emergence of emergence distributions: Using GAs to test biological •
- [67] **theory** A simulation appr. to evol. game • The evol. of time-sharing behavior in a dragonfly mating syst.
- [64] – Computing the • of evol.
- [296] **therapeutic** Appl. of GAs to *de novo* design of • peptides [Abstract of a poster]
- [281] – Search for opt. frequencies and amplitudes of • electrical carotid sinus nerve stimulation by appl. of the evol. strategy
- [282] – The evol. strategy - A search strategy used in individual opt. of electrical parameters for • carotid sinus nerve stimulation
- [228] **therapy** Opt. radiation • planning using GAs
- [131] **thermodynamical** Adaption to a changing environment by means of the • GA
- [371] **three-dimensional** Assigning a protein sequence to a • fold [Abstract of a poster]
- [221] – Gen. and geometric opt. of • radiation therapy treatment planning
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- [437] • quantitative structure-activity relationships from molecular similarity matrixes and gen. neural networks.1. Appl.
- [432] • quantitative structure-activity relationships from molecular similarity matrixes and gen. neural networks.1. Method and validations
- [31] – GAME: GA for minimization of energy, An interactive FORTRAN prog. for • intermolecular interactions
- [92] **thymine** Appl. of a GA in the conformational analysis of methylene-acetal-linked • dimers in DNA: Comparison with distance geometry calculations
- [67] **time-sharing** A simulation appr. to evol. game theory: The evol. of • behavior in a dragonfly mating syst.
- [248] **tissue** Image feature sel. by a GA: Appl. to classification of mass and normal breast •
- [272] **tobacco smoking** Relapse from • cessation: Mathematical and computer micro-simulation modelling including parameter opt. with GAs
- [214] **tomograph** GA with modified elitism for RF coil NMR • magnetic field homogeneity opt.
- [271] **tomography** GA-based reconstruction in-diffusion •
- [337] **tool** An evaluation of the GA as a computational • in protein NMR
- [454] – GAs as a new • to study protein stability
- [402] – The GA appl. as a modelling • to predict the fold of small proteins with different topologies
- [327] **tools** Artificial neural networks and simulated molecular evol. are potential • for sequence-oriented protein design
- [109] – Stochastic opt. • for genomic sequence assembly
- [396] **topologies** Identifying the tertiary fold of small proteins with different • from sequence and secondary structure using the GA and extended criteria specific for strand regions
- [402] – The GA appl. as a modelling tool to predict the fold of small proteins with different •
- [325] **topology** Delineating the mainchain • of four-helix bundle proteins using the GA and knowledge based on the amino acid sequence alone
- [133] **tracer** Inverse modeling of field • data to characterize DNAPL contamination
- [135] **tracking** A GA with variable range of local search for • changing environments
- [195] **trained** Detection of patterns in radiographs using ANN designed and • with the GA
- [264] – Neural networks • by a GA for visual-field diagnosis
- [59] **Trans** gene regulation in adaptive evol. : A GA model
- [50] **trans-biological** Global adaptive shifts in biological and • evol.
- [94] **transfer** Info • through hybridization reactions in DNA based computing
- [103] **transformations** From DNA to protein: • and their possible role in linkage learning
- [403] **transition** Role of γ -carboxyglutamic acid in the calcium-induced structural • of conantokin G, a conotoxin from the marine snail *Conus geographus*
- [353] **transmembrane** An object oriented environment for artificial evol. of protein sequences: The example of rational design of • sequences
- [335] – Evol. of a computer prog. for classifying protein segments as • domains using gen. prog.
- [153] **transposons** Strategy of co-evol. of • and host genome: Appl. to evol. computations
- [188] **transputer** A new evol. appr. for blood vessel detection on a • network
- [397] – A par. GA for polypeptide three dimensional structure prediction. A • impl.
- [190] **transverse** Design and evaluation of a • gradient set for magnetic resonance imaging of the human brain
- [186] **travelling** Using “biological” GAs to solve the • salesman problem with appl. in medical image processing
- [275] **treatment** An approximate alg. for estimating • lags from right censored data
- [260] – Decision theoretic steering and GA opt. : Appl. to stereotactic radiosurgery • planning

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- [136] **trichloroethylene** Competitive adsorption of • and humic substances from groundwater on activated carbon
- [58] **tropical** Simulation of large-scale • tuna movements in relation with daily remote sensing data: The artificial life appr.
- [58] **tuna** Simulation of large-scale tropical • movements in relation with daily remote sensing data: The artificial life appr.
- [386] **two-atom** Rebuilding connectivity matrices from • fragments using the GA
- [141] **two-dimensional** The appl. of GA to • strings: The source appointment problem
- [419] **ubiquitin** *De novo* design of the hydrophobic core of •
- [277] **Ultraschall-wandlern** Simulation von •
- [200] **ultrasonic** Gen. appr. to select wavelet features for contour extraction in medical • imaging
- [193] **ultrasonic imaging** Gen. appr. to select wavelet features for contour extraction in medical •
- [169] **Understanding** evol. as a collective strategy for groping in the dark
- [177] – The evol. of • A GA model of the evolution of communication
- [399] **units** Puzzle pieces defined: locating common packing • in tertiary protein contacts
- [338] **unknown** An artificial life model for predicting the tertiary structure of • proteins that emulates the folding process
- [68] **Untersuchung** der evol. sstrategischen Bedeutung der nicht-genetischen Varianz mit Hilfe der $[\gamma', \lambda(\mu/\rho, \lambda)]$ -ES
- [257] **urinary** Parameter Evaluation and Gen. -Based Rule Learning for the Differential Diagnosis of Female • Incontinence
- [213] **urological** Learning diagnostic rules from a • database using GA
- [152] **usage** On the • of differential evol. for function opt.
- [408] **validation** Development and • of a GA for flexible docking
- [432] **validations** Three-dimensional quantitative structure-activity relationships from molecular similarity matrixes and gen. neural networks.1. Method and •
- [56] **variability** Biological consequences of evol. opt. s: mortality, • survival
- [135] **variable** A GA with • range of local search for tracking changing environments
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- [68] **Varianz** Untersuchung der evol. sstrategischen Bedeutung der nicht-genetischen • mit Hilfe der $[\gamma', \lambda(\mu/\rho, \lambda)]$ -ES
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- [421] **virtual** STALK: an interactive syst. for • molecular docking
- [264] **visual-field** Neural networks trained by a GA for • diagnosis
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- [269] **vollständigen** Entwicklung und Anpassung eines • Ansteuersyst. für fremdenergetisch angetriebene Ganzarmprothesen
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- [283] **Warfarin** A GA to improve a neural network to predict a patiens response to •
- [426] **water** Mean field analysis of FKBP-12 complexes with FK506 and rapamycin: Implications for a role of crystallographic • molecules in molecular recognition and specificity
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- [178] **wavelengths** GA-based method for selecting • and model size for use with partial least-squares regression: Appl. to near-infrared spectroscopy
- [200] **wavelet** Gen. appr. to select • features for contour extraction in medical ultrasonic imaging
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- [57] **wed-building** Analysing spider • behaviour with rule-based simulations and GAs
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- [80] **whether** Predicting • or not a nucleic acid sequence is an *E. coli* promoter region using gen. prog.
- [293] **Workbench** Cerius² Release 1.6, Drug Discovery • QSAR+ User's Reference, Chapter 16: Introduction to gen. function approximation
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- [45] **world** Predator-prey interactions in a simulated •
- [291] **years** Structure-based drug design ten • on
- [258] **yellow fever virus** Secondary structure of the 3'-untranslated region of •
- [449] **yopological** Comparison of benzodiazepine-like compounds using • analysis and GAs
- [434] **zinc finger** The evol. simulation of • domain sequence. Appl. of GAs in protein structure study

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Notations

†(ref) = the bibliography item does not belong to my collection of genetic papers.
(ref) = citation source code. ACM = ACM Guide to Computing Literature, EEA = Electrical & Electronics Abstracts, BA = Biological Abstracts, CCA = Computers & Control Abstracts, CTI = Current Technology Index, EI = The Engineering Index (A = Annual, M = Monthly), DAI = Dissertation Abstracts International, P = Index to Scientific & Technical Proceedings, BackBib = Thomas Bäck's unpublished bibliography, Fogel/Bib = David Fogel's EA bibliography, etc
* = only abstract seen.
? = data of this field is missing (BiBTeX-format).

The last field in each reference item in **Teletype** font is the BiBTeXkey of the corresponding reference.



Appendix A

Abbreviations

The following other abbreviations were used to compress the titles of articles in the permutation title index:

AI	= Artificial Intelligence	Int.	= International
Alg.	= Algorithm(s)	ImPr	= Image Processing
AL	= Artificial Life	JSS	= Job Shop Scheduling
ANN(s)	= Artificial Neural Net(work)(s)	ML	= Machine Learning
Appl.	= Application(s), Applied	Nat.	= Natural
Appr.	= Approach(es)	NN(s)	= Neural Net(work)(s)
Cntr.	= Control, Controlled, = Controlling, Controller(s)	Opt.	= Optimization, Optimal, = Optimizer(s), Optimierung
Coll.	= Colloquium	OR	= Operation(s) Research
Comb.	= Combinatorial	Par.	= Parallel, Parallelism
Conf.	= Conference	Perf.	= Performance
CS(s)	= Classifier System(s)	Pop.	= Population(s), Populational(ly)
Distr.	= Distributed	Proc.	= Proceedings
Eng.	= Engineering	Prog.	= Programming, Program(s), Programmed
EP	= Evolutionary Programming	Prob.	= Problem(s)
ES	= Evolutionsstrategie(n), = Evolution(ary) strategies	QAP	= Quadratic Assignment Problem
Evol.	= Evolution, Evolutionary	Rep.	= Representation(s), Representational(ly)
ExS(s)	= Expert System(s)	SA	= Simulated Annealing
FF(s)	= Fitness Function(s)	Sch.	= Scheduling, Schedule(s)
GA(s)	= Genetic Algorithm(s)	Sel.	= Selection, Selectionism
Gen.	= Genetic(s), Genetical(ly)	Symp.	= Symposium
GP	= Genetic Programming	Syst.	= System(s)
Ident.	= Identification	Tech.	= Technical, Technology
Impl.	= Implementation(s)	TSP	= Travel(l)ing Salesman Problem

Appendix B

Bibliography entry formats

footnotesize This documentation was prepared with L^AT_EX and reproduced from camera-ready copy supplied by the editor. The ones who are familiar with B^IB^TE^X may have noticed that the references are printed using `abbrv` bibliography style and have no difficulties in interpreting the entries. For those not so familiar with B^IB^TE^X are given the following formats of the most common entry types. The optional fields are enclosed by "[]" in the format description. Unknown fields are shown by "?". † after the entry means that neither the article nor the abstract of the article was available for reviewing and so the reference entry and/or its indexing may be more or less incomplete.

Book: Author(s), *Title*, Publisher, Publisher's address, year.

Example

John H. Holland. *Adaptation in Natural and Artificial Systems*. The University of Michigan Press, Ann Arbor, 1975.

Journal article: Author(s), Title, *Journal*, volume(number): first page – last page, [month,] year.

Example

David E. Goldberg. Computer-aided gas pipeline operation using genetic algorithms and rule learning. Part I: Genetic algorithms in pipeline optimization. *Engineering with Computers*, 3(?):35–45, 1987. †.

Note: the number of the journal unknown, the article has not been seen.

Proceedings article: Author(s), Title, editor(s) of the proceedings, *Title of Proceedings*, [volume,] pages, location of the conference, date of the conference, publisher of the proceedings, publisher's address.

Example

John R. Koza. Hierarchical genetic algorithms operating on populations of computer programs. In N. S. Sridharan, editor, *Eleventh International Joint Conference on Artificial Intelligence (IJCAI-89)*, pages 768–774, Detroit, MI, 20.-25. August 1989. Morgan Kaufmann, Palo Alto, CA. †.

Technical report: Author(s), Title, type and number, institute, year.

Example

Thomas Bäck, Frank Hoffmeister, and Hans-Paul Schwefel. Applications of evolutionary algorithms. Technical Report SYS-2/92, University of Dortmund, Department of Computer Science, 1992.