An Indexed Bibliography of Genetic Algorithms in Biosciences

compiled by

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Trademarks

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 inconsistences. 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:

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

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 LATEXdocuments 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

file	*contents*
`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. Tuson, 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].

string	*field*	*class*
`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.

type	*number of items*
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
total	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.

year	*items*	*year*	*items*
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
total			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.

3.4 Authors

Table 3.4 gives the most productive authors.

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.

country	*abs*	*%*
Total	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

Table 3.5: The geographical distribution of the authors.

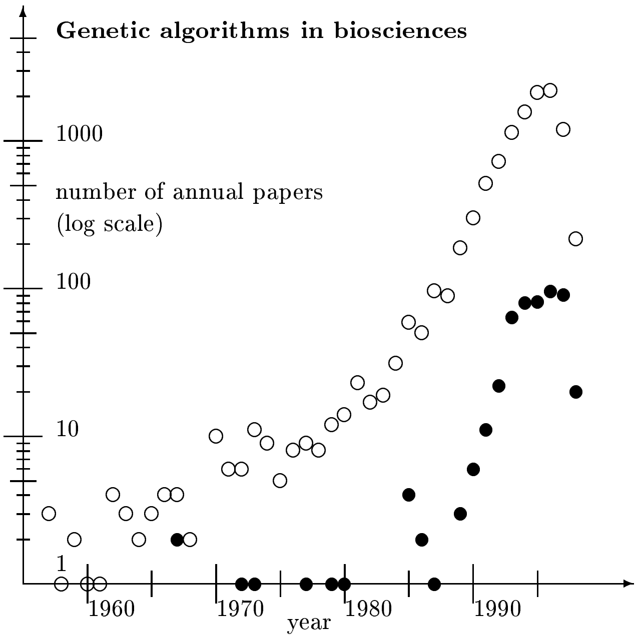

Figure 3.1: The number of papers applying **genetic algorithms in biosciences** (•) ∘ = total GA papers. Observe that the last two years are most incomplete in the database.

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.

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.

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 Gijutsu, [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]

Massachusets 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.

total 486 articles by 890 different authors

4.7 Subject index

All subject keywords of the papers given by the editor of this bibliography are shown next.

4.8 Annual index

The following table gives references to the contributions by the year of publishing.

1967, [161, 40]

1972, [66]

1973, [479]

1977, [269]

1979, [68]

1980, [281]

1985, [63, 159, 67, 277]

1986, [64, 288]

1987, [289]

1989, [215, 160, 168]

1990, [155, 136, 162, 114, 71, 488]

1991, [268, 273, 158, 165, 115, 278, 282, 72, 73, 169, 489]

1992, [264, 453, 454, 106, 270, 138, 216, 163, 460, 495, 69, 70, 166, 466, 467, 470, 279, 472, 473, 167, 483, 484]

1993, [142, 301, 265, 266, 267, 141, 137, 455, 107, 271, 456, 156, 457, 272, 65, 108, 109, 157, 458, 181, 459, 139, 274, 275, 461, 462, 300, 110, 463, 111, 112, 113, 276, 464, 465, 468, 469, 471, 474, 475, 476, 477, 478, 280, 217, 116, 480, 283, 284, 481, 482, 485, 486, 487, 182, 285, 286, 26, 490, 287, 491, 74, 492]

1994, [143, 302, 303, 75, 304, 218, 183, 305, 28, 306, 307, 219, 220, 221, 222, 223, 308, 309, 144, 310, 311, 290, 10, 312, 313, 314, 145, 315, 291, 41, 493, 29, 117, 224, 316, 317, 292, 318, 225, 319, 140, 320, 146, 11, 147, 170, 148, 118, 321, 322, 12, 42, 226, 119, 76, 323, 324, 77, 325, 227, 326, 184, 228, 327, 328, 43, 329, 185, 330, 44, 30, 331, 120, 332, 31, 333, 293, 334, 294, 335]

1995, [336, 229, 171, 337, 172, 338, 45, 230, 46, 78, 339, 47, 340, 186, 187, 32, 341, 342, 343, 344, 33, 173, 79, 174, 231, 345, 80, 346, 48, 49, 13, 121, 347, 232, 188, 122, 348, 349, 350, 351, 352, 353, 14, 175, 354, 81, 355, 356, 357, 358, 15, 359, 233, 16, 234, 360, 82, 361, 176, 362, 235, 34, 363, 123, 364, 365, 366, 50, 367, 236, 237, 83, 238, 368, 124, 239, 35, 84, 177, 189, 240]

1996, [369, 125, 370, 371, 190, 178, 372, 373, 374, 179, 85, 375, 376, 377, 241, 126, 17, 191, 378, 51, 379, 242, 243, 149, 18, 192, 86, 380, 19, 381, 87, 193, 127, 382, 20, 52, 383, 128, 384, 385, 129, 244, 386, 245, 180, 246, 387, 130, 194, 388, 131, 88, 389, 150, 295, 247, 195, 390, 36, 391, 392, 296, 248, 151, 196, 21, 152, 393, 132, 394, 249, 395, 250, 89, 22, 197, 396, 397, 198, 398, 199, 399, 251, 200, 400, 90, 401, 37, 27, 201, 202, 252, 23, 402, 135]

1997, [403, 404, 253, 254, 203, 91, 494, 92, 405, 204, 205, 93, 406, 53, 94, 206, 54, 407, 55, 408, 95, 56, 409, 255, 410, 411, 412, 413, 414, 415, 416, 417, 256, 418, 57, 58, 257, 419, 420, 421, 207, 422, 297, 24, 423, 59, 424, 425, 133, 426, 427, 428, 258, 60, 96, 429, 97, 208, 430, 259, 209, 431, 298, 153, 134, 432, 98, 25, 433, 38, 210, 99, 100, 260, 211, 434, 61, 435, 101, 102, 436, 103, 437, 261, 262, 212, 438, 213, 439, 154]

1998, [104, 440, 441, 442, 299, 443, 105, 444, 445, 263, 446, 447, 448, 449, 214, 450, 451, 39, 452, 62]

4.9 Geographical index

The following table gives references to the contributions by country.

Chapter 5

Permuted title index

The words of the titles of the articles are shown in the next table arranged in alphabetical order. The most common words have been excluded. The key word is shown by a disk (•) in the title field with the exception that it is omitted when appearing as the first word of the title after shown keyword. The other abbreviation used to compress titles are shown in appendix A.

[436] ***Ab initio*** protein folding simulation with GAs: Simulations on the complete sequence of small proteins

[487] **Abstract** A computer based simulation with artificial adaptive agents for predicting secondary structure from the protein hydrophobicity •

[296] **Abstract** Appl. of GAs to *de novo* design of therapeutic peptides • of a poster]

[373] – Assigning a protein sequence to a three-dimensional fold • of a poster]

[376] – Design of a three helix bundle with a "native-like" folded state • of a poster]

[299] **Abstract** Evol. drug discovery • of an invited lecture]

[385] **Abstract** Resolving water-mediated and polar ligand recognition using GAs • of a poster]

[160] **accumulation** GAs and info • during the evol. of gene regulation

[420] **acid** Refinement of the NMR solution structure of the gamma-carboxyglutamic • domain of coagulation factor IX using molecularBLdynamics simulation with initial Ca2+ positions determined by GA

[403] – Role of γ-carboxyglutamic • in the calcium-induced structural transition of conantokin G, a conotoxin from the marine snail *Conus geographus*

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[347] **complexes** Flexible ligand docking without parameter asjustment across four ligand-receptor •
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[337] **computational** An evaluation of the GA as a • tool in protein NMR
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[275] **estimating** An approximate alg. for • treatment lags from right censored data
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[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] **evoluutio** Laskennallinen • GAt ja keinoelämä [Computational evol. , GAs, and artificial life]
[63] **Evolve** III: A discrete events model of an evol. ecosyst.
[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 nucleid 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 molecularBLdynamics 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 microcalfications 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

[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
[405] – Search for ● conformations of organic-molecules by GAs
[359] **native states** A GA that seeks ● of peptides and proteins
[376] **native-like** Design of a three helix bundle with a ● folded state [Abstract of a poster]
[121] **natural** Opt. , active cntr. of oxides of nitrogen (NO_x) emissions from a ● gas-fired burner using a simple GA
[448] **NCI** Mining the ● anticancer drug discovery databases: gen. function approximation for the QSAR study of anticancer ellipticine analogues
[178] **near-infrared** GA-based method for selecting wavelenghts and model size for use with partial least-squares regression: Appl. to ● spectroscopy
[36] – GA-based protocol for coupling digital filtering and partial least-squares regression: Appl. to the ● analysis of glucose in biological matrices
[117] **needs** Development ● for diverse GA design
[286] **nervosa** Appl. of neural networks and GAs in the diagnosis of cancer, anorexia ● and AIDS
[188] **network** A new evol. appr. for blood vessel detection on a transputer ●
[304] – Studying genotype-phenotype interactions: a model of the evol. of the cell regulation ●
[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 patiens 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 ●
[24] – An intelligent appr. for opt. cntr. of fruit-storage process using ● and GAs
[209] – Appl. of ● and GAs in the classification of endothelian cells
[286] – Appl. of ● and GAs in the diagnosis of cancer, anorexia nervosa and AIDS
[327] – Artificial ● and simulated molecular evol. are potential tools for sequence-oriented protein design
[240] – Evolving ● for detecting breast cancer
[189] – Evolving ● for medical appl.
[204] – Image feature analysis for classification of microcalfications in digital mammography - ● and GAs
[224] – Knowledge extraction from ● using GAs
[361] – LGANN: a par. syst. combining a local GA and ● for the prediction of secondary structure of protein
[279] ● GAs and the K-means alg. : in search of data classification
[264] ● trained by a GA for visual-field diagnosis
[122] – Opt. field-scale groundwater remediation using ● and GA
[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 cytotic 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
[214] – GA with modified elitism for RF coil ● tomograph magnetic field homogeneity opt.
[441] – GENFOLD: A GA for folding protein structures using ● restraints
[420] – Refinement of the ● solution structure of the gamma-carboxyglutamic acid domain of coagulation factor IX using molecularBLdynamics simulation with initial Ca2+ 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
[379] **non-helical** Ab initio tertiary-fold prediction of helical and ● protein chains using a GA
[270] **Non-invasive** Fetal Electrocardiograph Enhancement
[139] **nonlinear** Determination of hydraulic conductivity tensor using a ● least squares estimator
[238] – Gen. design of optimum linear and ● QRS detectors
[410] ● PLS improved by numeric GA for QSAR modeling
[126] – The appl. of GA and ● fuzzy prog. for water pollution cntr. in a river basin

[439] **related** Molecular modeling of amoebapore and NK-lysin: A four-alpha-helix bundle of cytotic 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** Cerius^2 • 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 patiens • 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 ancupuncture 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 wed-building behaviour with • simulations and GAs

[213] **rules** Learning diagnostic • from a urological database using GA

[88] **SAGA:** sequence alignment by GA

[186] **salesman** Using "biological" GAs to solve the travelling • problem with appl. in medical image processing

[127] **salqr** Appl. of • and evol. alg. to opt. of graundwater bioremediation

[416] **Sampling** protein conformations using segment libraries and a GA

[215] **scaling** Adaptive search space • in digital image registration

[16] **scheduling** New techniques for optimising the design and • for irrigation syst.

[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

[490] – A critical comparison of • alg. appl. to the protein side-chain conformations

[101] – A DNA based impl. of an evol. • for good encodings for DNA computation

[172] – A GA to • for opt. and suboptimal RNA secondary structures

[135] – A GA with variable range of local • for tracking changing environments

[72] – Biological evol. as a paradigm for preformance-driven •

[404] – Development of a novel GA • method (GAP1.0) for exploring peptide conformational space

[181] – Molecular recognition using a binary gen. • alg.

[279] – Neural networks, GAs and the K-means alg. : in • of data classification

[105] • for maximum likelihood phylogen. tree using a GA

[405] • for native conformations of organic-molecules by GAs

[281] • for opt. frequencies and amplitudes of therapeutic electrical carotid sinus nerve stimulation by appl. of the evol. strategy

[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

[329] – Variable sel. in QSAR studies 2. A highly efficient combination of syst. atic • and evol.

[215] **search space** Adaptive • scaling in digital image registration

[460] **search techniques** Do intelligent configuration • outperform random search for large molecules?

[388] **searching** A comparison of a direct search method and a GA for conformational •

[461] – Conformation • methods for small molecules II: A GA appr.

[487] **secondary structure** A computer based simulation with artificial adaptive agents for predicting • from the protein hydrophobicity [Abstract]

[368] – A simple protein folding alg. using a binary code and • constraints

[171] – An APL-prog. GA for the prediction of RNA •

[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 methods for the protein • prediction]
[396] – Identifying the tertiary fold of small proteins with different topologies from sequence and • using the GA and extended criteria specific for strand regions
[361] – LGANN: a par. syst. combining a local GA and neural networks for the prediction of • of protein
[258] • of the 3'-untranslated region of yellow fever virus
[430] • prediction using segment similarity
[433] – The prediction of protein • with a cascade correlation learning architecture of neural networks
[172] **secondary structures** A GA to search for opt. and suboptimal RNA •
[359] **seeks** A GA that • native states of peptides and proteins
[62] – A scientist • gold in a controversial drug patent
[287] **segment** Neural inhabitants of MR and echo images • cardiac structures
[416] – Sampling protein conformations using • libraries and a GA
[430] – Secondary structure prediction using • similarity
[227] **segmentation** Interactive • of multi-dimensional medical data with contour-based appl. of GAs
[284] – Region merging in medical image • and interpretation
[335] **segments** Evol. of a computer prog. for classifying protein • as transmembrane domains using gen. prog.
[200] **select** Gen. appr. to • wavelet features for contour extraction in medical ultrasonic imaging
[193] – Gen. appr. to • wavelet features for contour extraction in medical ultrasonic imaging
[55] **selected** The appl. of evol. computation to • problems in molecular biology
[178] **selecting** GA-based method for • wavelenghts and model size for use with partial least-squares regression: Appl. to near-infrared spectroscopy
[157] **selection** Evol. wanderlust: Sexual • with directional mate preferences
[223] – Feature • with distinction sensitive learning vector quantisation and GAs
[451] – GA strategy for variable • in QSAR studies: GA-based region • for CoMFA modeling
[443] – GA strategy for variable • in QSAR studies: GAPLS and D-opt. designs for predictive QSAR model
[217] – GA based input • for a neural network function approximator with appl. to SSME monitoring
[276] – GA for feature • for par. classifiers
[33] – Gen. -alg. • of a regulatory structure that directs flux in a simple metabolic model
[248] – Image feature • by a GA: Appl. to classification of mass and normal breast tissue
[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.
[317] – Variable • in QSAR studies 1. An evol. alg.
[329] – Variable • in QSAR studies 2. A highly efficient combination of syst. atic search and evol.
[468] **self-adapting** HIPS, A hybrid • expert-syst. for nuclear-magnetic-resonance spectrum interpretation using GAs
[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
[58] **sensing** Simulation of large-scale tropical tuna movements in relation with daily remote • data: The artificial life appr.
[223] **sensitive** Feature sel. with distinction • learning vector quantisation and GAs
[207] **sequence** 3D reconstruction of the human jaw from a • of images
[366] – Amino acid • analysis and design by artificial neural network and simulated molecular evol. – An evaluation
[303] – An evol. appr. to folding small alpha-helical proteins that uses • info and an empirical guiding fitness function
[373] – Assigning a protein • to a three-dimensional fold [Abstract of a poster]
[325] – Delineating the mainchain topology of four-helix bundle proteins using the GA and knowledge based on the amino acid • alone
[77] – DNA • analysis using hidden Markov model and GA
[436] – *Ab initio* protein folding simulation with GAs: Simulations on the complete • of small proteins
[87] – GA for DNA/RNA • comparison
[75] – GA for molecular • comparison
[108] – GAs for DNA • assembly
[396] – Identifying the tertiary fold of small proteins with different topologies from • and secondary structure using the GA and extended criteria specific for strand regions
[312] – Opt. • sel. in proteins of known structure by simulated evol.
[381] – Par. opt. processing appl. to protein • analysis
[80] – Predicting whether or not a nucleic acid • is an *E. coli* promoter region using gen. prog.
[360] – Protein • analysis using a multi-group par. GA
[109] – Stochastic opt. tools for genomic • assembly
[434] – The evol. simulation of zinc finger domain • Appl. of GAs in protein structure study
[378] – Towards meeting the Paracelcus challence: 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
[353] **sequences** An object oriented environment for artificial evol. of protein sequences: The example of rational design of transmembrane •
[308] – Opt. amino acid • by simulated molecular evol.
[422] – Protein folding: optimized • obtained by simulated breeding in a minimalist model
[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
[106] – Gen. and random keys for • and opt.
[74] – The Genie Project: A GA appl. to a • problem in the biological domain
[469] **Sequential** assignment of 2D-NMR spectra of proteins using GAs
[190] **set** Design and evaluation of a transverse gradient • for magnetic resonance imaging of the human brain
[229] – Design by GA of a z gradient • for magnetic resonance imaging of the human brain
[104] **sets** A GA for designing gene family-specific oligonucleotide • used for hybridization: the G protein-coupled receptor protein superfamily
[232] – Automatical registration of brain volume data •
[411] – Ident. of common structural features in • of ligands using a GA
[444] – Using a GA to identify common structural features in • of ligands
[157] **Sexual** Evol. wanderlust: • sel. with directional mate preferences
[73] – Mutation and recombination effects on the adaptability of • and asexual organisms
[66] **shifts** Adaptive behavior of simulated bacterial cells subjected to nutritional •
[50] – Global adaptive • in biological and trans-biological evol.
[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
[314] – Incremental prediction of • conformation of proteins by a GA
[187] **signal** Myoelectric • recognition using gen. prog.
[89] • pattern extraction from DNA sequences using hidden Markov model and GA
[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.
[430] – Secondary structure prediction using segment •

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[508] Pavel Ošmera, editor. *Proceedings of the 3rd International Mendel Conference on Genetic Algorithms, Optimization problems, Fuzzy Logic, Neural networks, Rough Sets (MENDEL'97)*, Brno (Czech Republic), 25.-27. June 1997. Technical University of Brno. `ga97Brno`.

[509] *Proceedings of the Second IEEE Conference on Evolutionary Computation*, Perth (Australia), November 1995. IEEE, New York, NY. `ga95ICEC`.

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[511] Jarmo T. Alander, editor. *Proceedings of the Third Nordic Workshop on Genetic Algorithms and their Applications (3NWGA)*, Helsinki (Finland), 18.-22. August 1997. Finnish Artificial Intelligence Society (FAIS). (available via anonymous `ftp` site `ftp.uwasa.fi` directory `cs/3NWGA` file `*.ps.Z`) `ga97NWGA`.

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[513] John R. Koza, Kalyanmoy Deb, Marco Dorico, David B. Fogel, Max Garson, Hitoshi Iba, and Rick L. Riolo, editors. *Genetic Programming 1997: Proceedings of the Second Annual Conference*, Stanford, CA, 13.-16. July 1997. Morgan Kaufmann, San Francisco, CA. †(prog) `ga97GP`.

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

Appendix B

Bibliography entry formats

footnotesize This documentation was prepared with LaTeX and reproduced from camera-ready copy supplied by the editor. The ones who are familiar with BibTeX 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 BibTeX 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.