

Index

- 16S and 23S rRNA, 136
- Aberer, Karl, 170
- Ackermann, Friedrich, 3
- adaptive combinatorial optimization, 384
- adaptive learning, 89
- algorithm, 215, 285
 - combinatorial, 170
 - dynamic programming, 107, 170
- alignment, 314, 341
 - structural, 107, 170
 - see also* sequence alignment
- Altman, Russ, 12
- amino acid
 - composition, 240
 - environments, 12
 - properties, 402
- annotation, 66
- APIC: A Generic Interface for Sequencing Projects*, 57
- APIC graphical interface, 57
- approximation, 285
- Arikawa, Setsuo, 359
- artificial immune system, 89
- ASN.1, 66
 - objects, 66
- automata, finite-state, 341
- Automata—Theoretic Models of Mutation and Alignment*, 341
- Automatic RNA Secondary Structure Determination with Stochastic Context-Free Grammars*, 136
- automatic programming, 162

- Babenko, V. N., 206
- Bagley, Steven, 12
- Bailey, Timothy L., 21
- Baldi, Pierre, 30
- Bergeman, Ellen R., 48
- Bisson, G., 249
- Bisson, Gilles, 57
- BONSAI Garden: Parallel Knowledge Discovery System for Amino Acid Sequences*, 359
- Brenner, Steven E., 66
- Brunak, Søren, 30
- Brutlag, Douglas L., 402
- Bryant, Stephen, 259
- Cary, Robert, 75
- Casadio, Rita, 81
- cds prediction, 249

- Characterizing Oriented Protein Structural Sites Using Biochemical Properties*, 12
- Chauvin, Yves, 30
- chemical graph, 259
- Cheng, Carol, 12
- classification, 309
- Classifying Nucleic Acid Sub-Sequences as Introns or Exons Using Genetic Programming*, 162
- cluster analysis, 170
- coding sequences, recognition of, 206
- combinatorial algorithms, 121
- combinatorial optimization, 75, 277
- comparative sequence analysis, 75
- Compiani, Mario, 81
- Computer Tool FUNSITE for Analysis of Eukaryotic Regulatory Genomic Sequences*, 197
- computer tools, 197
- conformational analysis, 300
- consensus, 249
- Constituting a Receptor-Ligand Information Base from Quality-Enriched Data*, 170
- constraint satisfaction, 121, 231, 268, 332
- Constraint-Based Assignment System for Automating Long Side Chain Assignments in Protein 2D NMR Spectra*, A, 231
- constraints, 215
- Cooke, Denise E., 89
- Cooperative Computer System For Genome Sequence Analysis*, 249
- correlation of classifications, 240
- covariance models, 75
- Craven, Mark W., 98

- Danchin, A., 249
- data-dependent pseudocounts, 188
- database, 127, 197
 - searches, 170
 - systems, 350
 - views, 48
- databases, object-oriented, 231
 - structure, 170
- decision tree, 359
- Dirichlet
 - mixture priors, 188
 - priors, 21
- discriminant analysis, 367
 - functions, 154
- Distance-Based Block Searching Algorithm*, A, 322

- Divide and Conquer Approach to Multiple Alignment*, A, 107
- DNA, 30
 - computer analysis, 206
 - sequence analysis, 292
 - sequence assembly, 277
 - sequences., 114
- DNA Sequence Assembly and Genetic Algorithms — New Results and Puzzling Insights*, 277
- domain assignment, 376
- Dress, Andreas, 107
- drug design, 170, 300
- Dubchak, Inna, 240
- dynamic programming, 145, 215, 341, 367
- Eddy, Sean R., 114
- efficient
 - sequence search, 393
 - query processing, 350
- Elkan, Charles, 21
- empirical potentials, 154
- encoding cost, 188
- Engelbrecht, Jacob, 30, 292
- entropy, 188
- Enzyme and Metabolic Pathway Database*, 127
- escherichia coli, 292
- Evaluating Regularizers for Estimating Distributions of Amino Acids*, 188
- exon, 30
 - recognition, 367
- expectation maximization, 21
- experimental design, 277
- Farber, Rob, 154
- Fariselli, Piero, 81
- flexible docking, 300
- FlexX, 300
- fold classification, 240
- Fothergill, John E., 231
- Foucrault, Marielle, 121
- Füllen, Georg, 107
- FUNSITE, 197
- Gaasterland, Terry, 127
- Garreau, Alain, 57
- gene structure prediction, 367
- genetic algorithms, 162, 277
- genetic
 - map, 57
 - programming, 162
- genome mapping, 332
- genomics, 48
- Glasko, Galina, 309
- grammars,
 - attribute grammars, 215
 - stochastic context-free, 215
- graph representation, 48, 367
- graph theory, 75
- Graph-Theoretic Approach to RNA Modeling Using Comparative Data*, 75
- graphical interface, 57
- graphics, 66
- Grate, Leslie, 136
- Graves, Mark, 48
- Gray, Peter M. D., 231
- Gribskov average score, 188
- Grice, J Alicia, 145
- grid-based scoring, 3
- Grossman, Tal, 154
- Handley, Simon, 162
- Hauser, Loren J., 98
- Hegyi, Hedvig, 376
- Hemm, Klemens, 170
- Hendlich, Manfred, 170
- Herrmann, Grit, 3
- hidden Markov models, 30, 114, 215
- high quality databases
- Holm, Liisa, 170
- homology, 240
 - modeling, 259, 314
- Hubbard, Tim J. P., 66
- Hughey, Richard, 145
- Hunt, John E., 89
- Identification of DNA Sequences by Specific Oligonucleotide Sets—A Computer Tool and Application*, 206
- Identification of Protein Motifs Using Conserved Amino Acid Properties and Partitioning Techniques*, 402
- immune network, 89
- information theory, 292
- integrated database systems, 170
- intron, 30
 - exon problem, 162
- Investigations of Escherichia coli Promoter Sequences with Artificial Neural Networks: New Signals Discovered Upstream of the Transcriptional Startpoint*, 292
- Islam, Suhail A., 376
- Johnson, Mark E., 277
- Karplus, Kevin, 188
- Kel, A. E., 206
- Kel, Alexander, 197
- Kel, O. V., 197
- Knowledge representation, 3
 - object-oriented, 249
- Kolchanov, N. A., 197, 206
- Kolpakov, P. A., 197
- Kondrakhin, Y. V., 197
- Kramer, Bernd, 300
- Kriegel, Hans-Peter, 350
- Krogh, Anders, 30, 215
- Kuhara, Satoru, 359

Kummert, Franz, 3

Lapedes, Alan, 154

Lappe, Michael, 359

large RNA modeling, 136

Latkin, Evgeniy, 309

Lawrence, Charles B., 48, 367

Lefebvre, Fabrice, 215

Leishman, Scott, 231

Lengauer, Thomas, 300, 384

local shape index, 350

log-likelihood ratio, 154

logic programming, 127, 231

logical analysis, 240

Luo, Jingchu, 376

machine learning, 98, 240, 359

machine learning, induction, 162

macromolecular structure, annotating, 66

database, 259

viewers, 66

Major, Francois, 121

maximization, 309

Maximum Entropy Weighting of Aligned Sequences of Proteins or DNA, 215

Mayoraz, Eddy, 240

Medigue, Claudine, 249

MEME, 21

metabolism, 127

method integration, 249

Milanesi, L., 197

mime, 66

minimum length encoding, 136

Mitchison, Graeme, 215

mixture models, 21

Miyano, Satoru, 359

MMDB: An ASN.1 Specification for Macromolecular Structure, 259

modeling tasks and methods, 121

molecular

docking, 300

flexibility, 300

surface representation, 350

surfaces, 3

motif discovery, 21

databases, 121

motifs, 402

Muchnik, Ilya, 240

Multiple Alignment Using Hidden Markov Models, 114

multiple alignment, 136, 215, 384

multiple comparison, 322

multiple sequence alignment, 114

Mural, Richard J., 98

Murphy, Kevin P., 341

mutational spectrum, 309

mutual information, 136

nearest-neighbor classifiers, 98

neighborhood spheres, 154

Neural Net Representations of Empirical Protein Potentials, 154

neural nets, 154

neural networks, 98, 292,

radial basis function, 81

New Approach to Primer Selection in Polymerase Chain Reaction Experiments, A, 285

Neweyes: A System for Comparing Biological Sequences Using the Running Karp-Rabin Greedy String-Tiling Algorithm, 393

NP-completeness, 285

nuclear magnetic resonance, 231

nucleic acid sub-sequences, classification of

object-oriented

databases, 170

representation, 48

Ohkawa, Hitomi, 259

Okazaki, Takeo, 359

oligonucleotide hybridization, 206

Optimized Parsing Algorithm Well Suited to RNA Folding, An, 222

Ostell, James, 259

Parallel Sequence Alignment in Limited Space, 145

parallel

computation, 145

knowledge acquisition, 359

parser, 215

Parsons, Rebecca, 277

Parsons, Simon, 268

pattern recognition, 89

PCR experiments, 285

Pearson, William R., 285

Pedersen, Anders Gorm, 292

Periodic Sequence Patterns in Human Exons, 30

periodicity, 30

Perrey, Sören, 107

physical map, 57

planar graphs, 350

Posch, Stefan, 3

Predicting Free Energy Contribution to the Conformational Stability of Folded Proteins From the Residue Sequence with Radial Basis Function Networks, 81

Predicting Protein Folding Classes without Overly Relying on Homology, 98

primer selection, 285

probability, 268

prokaryotic promoter recognition, 89

promoters, 292

Protein Docking: Combining Symbolic Descriptions of Molecular Surfaces and Grid-Based Scoring Functions, 3

protein, 66, 154
 classes, 402
 classification, 98
 coding regions, 89
 data bank (PDB), 66
 docking, 3, 350, 350
 folding classes, 98
 folding problem, 240
 sequences, 402
 structure prediction, 314
 structure, 12, 240, 376
 taxonomy, 376
 threading, 384
 topology, 268
 pseudocounts, 188

qualitative and quantitative relations, 332

Rarey, Matthias, 300
 receptor ligand interaction, 170, 300
Recognising Promoter Sequences Using An Artificial Immune System, 89
 recognition of coding sequences, 206
 recognition of promoters, 197
Reconstruction of Metabolic Networks Using Incomplete Information, 127
Recursive Dynamic Programming for Adaptive Sequence and Structure Alignment, 384
 recursive algorithm, 384
 regularizers, 188
Relation Between Protein Structure, Sequence Homology and Composition of Amino Acids, 240
 remote homologues, 314
 RNA, 215
 models, 75
 secondary structure, 136
 structure prediction, 121
 Robins, Gabriel, 285
 Rogozin, Igor, 309
 Romashenko, A. G., 197
 Rost, Burkhard, 314
Running Karp-Rabin Greedy String Tiling, 393
 Russell, Robert B., 376

Sagerer, Gerhard, 3
 Sagot, Marie-France, 322
 Salamov, Asaf, 367
 Sander, Chris, 170
 Schmeltzer, Olivier, 332
 Schomburg, Dietmar, 3
 scientific discovery, 359
 search, 215, 231
 Searls, David B., 341
 secondary structure, 170, 215, 314
 segmentation, 3
 Seidl, Thomas, 350
 SELEX, 75

Selkov, Evgeni, 127
 SEM algorithm, 309
 sequence alignment, 145
 multiple, 107
 near-optimal, 107
 and structure alignment, 384
 sequence analysis, 57, 127, 249, 402
 sequence
 comparison, 145
 databases, 21
 motifs, 121
 profiles, 215
 similarities, 249
 weighting, 215
 sequential structure, 30
 serine proteases, 12
 set covering problem, 240
 Shimozone, Shinichi, 359
 Shindyalov, I. N., 206
 Shinohara, Ayumi, 359
 Shinohara, Takeshi, 359
 Shoudai, Takayoshi, 359
 similarity model, word-based relation of, 322
 simulated annealing, 114
 method, 114
Softening Constraints in Constraint-Based Protein Topology Prediction, 268
 Soldano, Henri, 322
 Solovyev, Victor, 367
Solvent Accessible Surface Representation in a Database System for Identification of Human Gene Structure Using Linear Discriminant Functions and Dynamic Programming, 367
Solvent Accessible Surface Representation in a Database System for Protein Docking, 350
 solvent accessibility, 314
Specification for Defining and Annotating Regions of Macromolecular Structures, A, 66
 Speck, Don, 145
 STAMP algorithm, 376
 statistics, 12
 Sternberg, Michael J. E., 376
 stochastic context-free grammars, 136
 Stormo, Gary, 75
 structural
 comparison, 376
 representation, 154
 structure
 analysis, 12
 motif, 170
 validation, 259
Subclass Approach for Mutational Spectrum Analysis, 309
 subclass approach, 309
 suboptimal sequence alignment, 114
 substitution matrices, 188
 surface approximation, 350

Symbolic Generation and Clustering of RNA 3-D Motifs,
121

tasks representation, 249

Temporal Reasoning for Genome Map Assembly, Using,
332

temporal reasoning, 332

Thiele, Ralf, 384

threading, 314

Three-Dimensional Lookup: Fast Protein Structure

Database Searches at 90 % Reliability, 179

three-dimensional structure databases, 170

*Time-Efficient Docking of Flexible Ligands into Active
Sites of Proteins*, 300

*TOPITS: Threading One-Dimensional Predictions Into
Three-Dimensional Structures*, 314

Towards an Intelligent System for the Automatic

Assignment of Domains in Globular Proteins, 376

traceback, 145

transcription, 197

Uberbacher, Edward C., 98

Uchida, Tomoyuki, 359

user interface, 249

valuation systems, 268

*Value of Prior Knowledge in Discovering Motifs with
MEME*, The, 21

Vermat, T., 249

Viari, Alain, 249, 322

*Viewing Genome Data as Objects for Application
Development*, 48

Vishnevsky, O. V., 206

visual programming, 341

Vivarelli, Francesco, 81

Wei, Liping, 12

Wingender, E., 197

Wise, Michael J., 393

word wide web (WWW), 66

Wrege, Dallas E., 285

Wu, Thomas D., 402

Zhang, Tongtong, 285

Zimmer, Ralf, 384