Index

abstraction, 321
acquire domain knowledge, 292
acronym, 138
active site, 51
actor, 284
acyclic graph, 332
adjacency matrix, 143
AGAVE, 105, 107, 379
AlignACE, 106
alignment, 156
ambiguity, 321
amino acid, 50
antecedent, 52
antibody, 129
Apelon DTS, 141
API, 198
a posteriori distribution, 360
a priori distribution, 360
ASN.1, 45
aspect-oriented modeling, 310
assertion, 53
asterisk, 176
at-sign, 176, 182
attribute link, 38
authority matrix, 144
automated conceptual blending, 147
automated reasoner, 61
axiom, 53, 56
backtrack, 57
BankIt, 107
Bayes' law, 135, 327
Bayesian analysis, 328
Bayesian network, 331, 332, 369
  accuracy, 342
  causal inference, 338
  component, 347, 370
  consistency checking, 351
  decision node, 340
  design pattern, 349
  diagnostic inference, 338
  encapsulation, 346
  evidence, 335
  improving and optimizing, 352
  interface, 342, 346
  medical diagnosis, 333
  mixed inference, 338
  node, 376
  performance, 342, 347
  query, 335
  random variable, 332
  reliability, 351
  sensitivity, 351
  test cases, 351
  testing, 351
  training, 343
  translating, 352
  undirected cycle, 334

utility node, 340
validation, 351
value node, 340
Bayesian Web, 369
BDGP, 105
belief network, 334
Berkson's paradox, 353, 361
Berners-Lee, Tim, 61
BIND, 51
binding potential, 195
binding site, 51
biochemical reaction network, 102
BioCyc, 122
biology laboratory, 191
biomedical research, 149
biomedical terminology browser, 140
BioML, 9, 15, 69, 101, 260, 280, 289, 308, 310
BioPAX, 121
BioProspector, 106
bit score, 166
bl2seq, 168
BLAST, 107, 155
BLAT, 171
BLOCKS, 110, 157
BLOSUM, 110, 156
BMI, 343, 363
BN, 331
BNL, 111
Boolean constraint solvers, 58
brackets, 178
BRITE, 122
browsing, 130
BSML, 28, 100
butterfly effect, 191
BW, 369

C++, 203
cancer, 149
cardinality, 310, 314
CASE, 291
case distinctions, 138
catalysis, 52
CATH, 112
causality, 335
causal network, 334
CDATA, 308
CellML, 34, 103
cellular process, 104
central source, 144
CGAP, 124
chain rule of probability, 332
chemical hierarchies, 19
chi-square distribution, 364, 378
chi-square test, 364
chromatography, 187
classifier, 340
classifying documents, 138
closed world, 67, 83
Clustal, 110
ClustalW, 110
clustering, 21
CML, 6, 10, 67, 105
COG, 111
COMA, 202
combining information, 355
COMPEL, 116
computing the marginal distribution, 336, 360
concept combination, 146, 147, 365
conceptual blending, 147
conceptual integration, 147
conclusion, 52
conditional distribution, 376
conditional probability, 326
conditional probability distribution, 332
conditioning, 376
conjecture, 56, 184
connectionist network, 345
CONSENSUS, 106
consequent, 52
consistency checking, 56
constraints, 10

containment, 25
continuous information combination, 359
continuous meta-analysis, 359
continuous random variable, 325, 359
controlled vocabulary, 141
CORBA, 105
corpus, 129
correlation, 137, 139, 146
cosine similarity function, 137, 365
covariance, 360
coverage, 130, 149
CPD, 332
CPT, 376
creating an overview, 355
credibility, 325
crisp logic, 324
crisp statement, 324
critical evaluation, 355
crystallographic information, 105
cut and paste, 294
cytometry data, 105
CytometryML, 105

D-S theory, 365
DAG-Edit, 94, 118
Dali, 113
DAML, 27
DAML+OIL, 27
DARPA Agent Markup Language, 27
data-clustering, 21
database
  database schema, 4, 294
  database table, 204
data fusion, 355
data structure, 230, 304
data warehousing, 201
DAVID, 95
dbEST, 120
dbSNP, 123
DDBJ, 107
decision support system, 58
declarative programming, 52, 199
deductive reasoning, 321
Dempster's rule of combination, 366
Dempster-Shafer theory, 356, 365
de Saussure, F., 147
description logic, 57, 287, 347
design rationale, 283, 314
DIP, 114
directed graph, 142
directed graphical model, 334
directory structure, 10
discrete information combination, 356
discrete meta-analysis, 356
discrete random variable, 325, 356
disjoint classes, 302
disjointness, 314
dissemination of knowledge, 190
distribution, 326
DL, 57
DNA binding motif, 51, 106
DNA sequence, 43
document frequency, 132
DOM, 199
domain knowledge, 291
dot product, 136
double slash, 176, 177
Drosophila, 105
DTD, 6, 38, 286
DTD generator, 289
DUET, 291
Dutch book, 328

EBI, 97, 105, 107
EcoCyc, 19, 122
ecology, 201
eigenvalue, 143
element node, 38
EM, 345, 352
EMBL, 49, 105, 107, 280
empty entity, 367
enforce style, 194
Ensembl, 124

entailed, 83, 184
entailment, 83
Entrez, 107
enzyme, 51, 129, 261
erythrocyte, 298
esophageal cancer, 352
event-based parsing, 198, 200
expectation maximization, 345, 352
experimental procedure, 187
expert system, 52, 61
exponential distribution, 378
EXPRESSION, 122
eXtensible Markup Language, 5
extensional uncertainty, 323
extrinsic property, 304, 306

F-test, 364
FASTA, 107, 110, 155, 159, 163
FatiGO, 95
Fauconnier, G., 147
F distribution, 378
featuritis, 301
fibronectin, 137
file folder structure, 10
Fischer, Emil, 51
FISH, 118
Fisherian, 344
FishProm, 121
Fitzhugh-Nagumo model, 33
fixed-column, 4
fixed-width, 4, 113, 205, 206, 210
Flow Cytometry Standard, 105
FlyBase, 105, 117
Forgy, Charles, 56
formal query language, 131
formal semantics, 38
frame-based language, 285
frequentism, 322
frequentist method, 344
FSSP, 113
fuzzy Bayesian network,, 324
fuzzy logic, 324
  possibility, 324

GAME, 105
gapped BLAST, 163
gap penalty, 156, 158
GDB, 118
GEML, 103
GenBank, 107, 118
GeneCards, 120
gene classification, 22
Gene Expression Markup Language, 103
gene families, 22
generative model, 334
gene regulation, 52
GENES, 122
GeneSNPs, 125
GenMAPP, 94
genus proximus, 292
Gibbs motif sampler, 106
GO, 64, 92
GOA, 97
GOAL, 95
Goguen, J., 147
GoMiner, 94
GONG, 98
Google, 142
GOTM, 96
graph-based language, 286

HapMap Project, 126
Harrell, 147
HEART-2DPAGE, 121
Heisenberg uncertainty principle, 322
HGVbase, 123
hierarchical structure, 139
  inflexibility, 195
hierarchy, 9, 20, 296
  uniformity, 300
HMMER, 110
Holmes, Sherlock, 358
homologous, 155

HPID, 114
HSC-2DPAGE, 121
HSP, 162
HTML, 61, 76, 191
htSNPs, 125
HTTP, 61
hub matrix, 144
human categorization, 147
human insulin gene, 8
hybrid BN, 340
hypertext link, 139
Hypertext Markup Language, 61, 191

IBM, 38
ICE syndrome, 80
identify theft, 61
IDF, 136
imperative programming, 53, 199
imported ontology, 295
inclusion of ontology, 294
incompatible observations, 358
inconsistent observations, 358
induced-fit model, 51
influence diagram, 340
influenza virus, 146
information broker, 98
information retrieval system, 130, 148
information transformation, 187
infoset, 38
inner product, 136
inositol lipid-mediated signaling, 93
integration point, 201
intensional uncertainty, 323
interchange format, 38
InterPro, 98, 110
intrinsic property, 304
iridocorneal endothelial syndrome, 80
IUPAC, 105

Java, 198, 203
joint probability distribution, 326, 331
JPD, 326, 331
Jumbo browser, 105

Kalman filter, 360
KEGG, 122
KGML, 122
KIF, 285
KL-ONE, 285
Kleinberg algorithm, 142
  Google, 145
Know-ME, 141
knowledge base, 53, 59
Koshland, Daniel E., Jr., 51
Krebs cycle, 74

LaTeX, 199, 271
leukemia, 149, 301
lexical space, 47
LIGAND, 122
linguistics, 147
Linnaeus, 302
local ranges, 309
lock-and-key model, 51
logic,, 321
logical inference, 369
logical language, 285
Logical structure, 191
lumbar puncture, 35, 292
lvg, 91

machine learning, 343
MAGE-ML, 103
MAGE-OM, 103
MAML, 103
MAP, 344
MAPPBuilder, 94
MAPPFinder, 94
markup languages, 9
Materials and Methods, 187
mathematical function, 307
mathematical logic, 27
MathML, 377
maximum a posteriori, 344

maximum cardinality, 310
maximum likelihood, 344
maxOccurs, 311
medical chart ontology, 283, 288, 293, 296, 308, 309, 314, 316
medical data exchange, 106
medical data storage, 106
medical diagnosis, 328
Medical World Search, 92
Medline, 36, 67, 91, 141, 176, 182, 304
MegaBLAST, 170
MeSH, 90, 140
  MeSH browser, 140
  MeSH thesaurus, 141
META, 90
meta-analysis, 355
MetaCyc, 117, 122
metadata, 4
MetaMap, 91
MetamorphoSys, 91
metaphor, 147
MGD, 117
MGED, 103
MIAME, 103
microarray data, 103, 261
microarray information, 195
minimum cardinality, 310
minOccurs, 311
MINT, 114
MIPS, 114
ML, 344
mmCIF, 109
MML, 106
model, 35, 82
monotonicity, 83, 184
MotifML, 106
motifs, 156
MPATH, 118
MPBLAST, 170
MSA, 110, 168
MSP, 166
MYCIN, 325
myGrid, 188

namespace, 28
namespace prefix, 28
NCBI, 90
NCBI BLAST, 161
NCBI Reference Sequences, 151
NCI, 125
NDB, 108
Needleman-Wunsch algorithm, 158
nested data structure, 230
NetAffx GO Mining Tool, 95
neural network, 345
NeuroML, 106
neuroscience, 106
NHLBI, 125
nitrous oxide, 37, 41, 87, 178, 184
NLM, 90, 140
NLP, 149
NMTOKEN, 308
noisy OR-gate, 349
nondeterminism, 321
nonorthogonal basis, 137
normal distribution, 334, 355, 359, 363, 378
normalization, 138, 326
normalized score, 166
normetanephrines, 132, 136

OBO, 98
olfactory receptor, 118
oligonucleotide probe, 129
one-hit, 162
online search engine, 130
Onto-Tools, 95
ontological commitment, 301
ontology, 4, 36
ontology development tool, 289
ontology editor, 289
ontology evolution, 315
ontology language, 38
ontology mediation, 201

ontology modification, 315
OOBN, 346
OONF, 347
ooTFD, 116
open world, 67, 83
ORDB, 118
ordered list, 76
overelaboration, 302
OWL, 27, 58, 79, 98, 99, 183, 371
  enumeration, 80
  interpretation, 82
  restriction, 81
  theory, 82
OWL-DL, 58, 79, 287, 347, 392
OWL editor, 290
OWL Full, 58, 79, 287
OWL Lite, 58, 79, 287
ozone, 116

PAM, 156
paramodulation, 79
parent-child link, 38
parsing, 198
partial function, 311
partitioning, 23
Pathbase, 118
PathBLAST, 170
PATHWAY, 122
Pathway Tools, 122
pattern-action paradigm, 52
PDB, 51, 102, 109–111
PDBML, 112
Pearl, J., 323
Peirce, Charles Sanders, 147
periodic table, 49
Perl, 181, 198, 203, 268, 275, 279, 323
Pfam, 109
PGA, 125
PHI-BLAST, 169
phylogeny, 106
Piaget, Jean, 307
PMMA-2DPAGE, 121
pooling of results, 355
prefix, 28
presentation format, 193
presentation style, 194
primate, 137
principal component analysis, 143
principal eigenvalue, 143
principal eigenvector, 143
PRINTS, 110, 111
prior distribution, 360
probabilistic inference, 327
probabilistic network, 334
probability density, 326
probability distribution, 325, 355
probability theory, 325, 365
procedural programming, 53, 199, 261
ProDom, 111
profiles, 156
project requirements, 283, 292
project scope, 283
ProML, 106
PROMPT, 202
proof, 56
propagation of uncertainty, 324
PROSITE, 109
protein, 50
Protein Data Bank, 102
protein sequence, 106
proteomics, 119, 120
Protista, 302
prototype theory, 22
PSI-BLAST, 168
PSSM, 156
PubMed, 107, 131, 137, 141
purpose of Bayesian network, 342
purpose of ontology, 36, 281, 282, 292, 306, 313

QMR-DT, 332
quality of a citation, 144
quantitative research synthesis, 355
query, 129, 198

query discovery, 201
query modification, 142

random variable, 376
RDF, 26, 64, 286, 371
  annotating resources, 72
  anonymous resources, 68
  blank node, 68
  class hierarchy, 67
  collection, 76
  data model, 183
  defining resources, 72
  domain constraint, 71
  Domain rule, 73
  graph, 67
  inference, 66, 72
  inheritance, 72
  link, 67
  many-to-many relationship, 66
  node, 67
  property, 67
  property hierarchy, 305
  range constraint, 71
  Range rule, 74
  reference, 65
  referring, 72
  sequence container, 75
  Subclass rule, 73
  subClass rule, 72
  Subproperty rule, 73
  triple, 69
RDF editor, 290
RDF graph, 68, 82
RDFS, 70
RDF Schema, 70
RDF semantics, 65
reasoning, 53
reasoning context, 59
REBASE, 113
recall, 130
reconciling terminology, 201
reduce effort, 194
redundancy of information, 191
reference, 26, 130
RefSeq, 151
RefSNPs, 123
regulatory transcription factor, 51
reification, 316
relational database, 52, 56, 131, 149, 175, 183
relational database table, 32
relational query, 52
relationship, 36
relationship link, 38
relationships, 25
relevance, 321
relevance diagram, 340
repackaging, 197
representing knowledge, 36
REPRODUCTION-2DPAGE, 121
repurposing, 197
research, 129
resource, 63
Rete algorithm, 56
reuse, 28
rhodopsin, 83
ribosome, 119
RiboWeb, 119
RNA interaction, 105
RNAML, 104
RNA sequence, 104
root node, 38
RPS-BLAST, 170
rule, 52, 149
rule-based inferencing, 52, 53
rule-based programming, 199, 261
rule-based system, 53, 323
rule-based systems, 324
rule-based transformation, 200
rule engine, 53, 184, 335
  backward-chaining, 55
  business rule system, 58
  forward-chaining, 54
  goal, 55

rule invocation, 53
rule translator, 58

sample statistics, 364
SAX, 198
SBML, 28, 102
schema, 4
schema integration, 201
schema integration tool, 202
schema matching, 202
scientific reasoning, 321
SCOP, 112
scope creep, 301
scoring matrix, 156
search intermediary, 130
SeattleSNPs, 125
second-class properties, 310
selection bias, 353
self-describing, 5, 17
self-organizing map, 23
semantics, 35
Semantic Web, 61, 64, 183, 369
  architecture, 371
  query language, 183
semiotics, 35, 147
sensitivity, 130
sensitivity analysis, 351
separating concerns, 191
Sequin, 107
set constructor, 81
SF, 376
SGD, 116
sharing information, 36
SIENA-2DPAGE, 121
simple API for XML, 198
SKAT, 202
SKIP, 92, 150
SKIP Knowledge Browser, 141
SMART, 109
SN, 90
SNP, 123
SNP500Cancer, 124
SNP ontology, 318
Source content, 191
SPECIALIST, 90
species density, 201
SpiD, 114
SQL, 130, 175, 181
  FROM, 181
  SELECT, 182
  WHERE, 181
SRS, 107, 116
SSDB, 122
Stanford Medical Informatics, 202, 290
statistical computations, 204
statistically independent, 139, 327
stochastic function, 332, 376
stochastic inference, 331, 360, 362, 369
stochastic model, 326, 331
stop word list., 132
striping, 25, 65
structural blending, 147
structural integration, 147
STS, 118
style file, 199
stylesheet, 194, 200
subcellular process, 104
subclass, 22, 73, 297
subjective probability, 328
subjectivity, 322
subproperty, 305
subroutine, 222
substrate, 51
substring, 207
suppressed details, 321
survey article, 144
SWISS-2DPAGE, 121
SWISS-PROT, 98, 108, 110, 111, 118
syntactic variations, 35
syntax, 35
Systems Biology Markup Language, 28

T-Coffee, 110
t-norm, 324
t-test, 364
tableaux, 57
TAMBIS, 98
taxonomy, 19
t distribution, 364, 378
Template Toolkit, 249
term frequency, 132
text file, 204
text node, 38
TFD, 116
TFIDF, 137
theorem, 56
theorem prover, 56, 184
  constraint solver, 57
  description logic, 57
The SNP Consortium, 126
TIGRFAMs, 111
TML, 106
TMTOWTDI, 203
transcription factor, 52
transcriptomics, 119
TRANSFAC, 115
transformation process, 192
transformation program, 287
transformation task, 184, 203, 287
tree-based processing, 199, 200
TrEMBL, 98, 108, 111
TRRD, 115
TSC, 126
Turner, 147
two-hit, 162
Type I error, 134
Type II error, 134

UML, 102, 284, 291, 310
UMLS, 36, 90, 140, 141, 146, 149
UMLSKS, 92
uncertainty analysis, 351
uniform data, 204
uniform distribution, 326, 378
uniform style, 191
unmodeled variables, 322
unnormalized Bayesian network, 332
unnormalized distribution, 332, 359
unordered container, 76
unreification, 316
usage example, 292, 305, 314
use case, 284

validation of ontology, 313
value space, 47
variable-width, 205, 206
vector space model, 132, 146, 365
  document frequency, 136
  inverse document frequency, 136
  term frequency, 136
  term weight, 132
vector space retrieval, 132
viewing the results of research, 355
virtual data integration, 201
visual appearance, 191, 197
vocabulary, 9

Webin, 107
Web Ontology Language, 27, 58, 64, 98
webpage content, 191
website maintenance, 190
wild card, 176
WORLD-2DPAGE, 121
World Wide Web Consortium, 61, 64
WormBase, 120
WU-BLAST, 161
WU-BLAST2, 170

XBN, 370, 372
XEMBL, 105, 107
XER, 45
Xerlin, 10, 34
XIN, 114
XML, 5, 46, 192, 204
  ATTLIST, 11
  attribute, 5, 304

CDATA, 6
changing attribute names, 197
changing attributes to elements, 198
changing element names, 197
changing elements to attributes, 198
child element, 9, 66
combining element information, 198
content, 11
content model, 11, 297
default value, 6
DOCTYPE, 274
ELEMENT, 11
element, 5, 304
entering data, 6, 10
ENTITY, 11
entity, 295
fragment, 38
hierarchy, 9
IDREF, 381
implicit class, 70
merging documents, 198
NMTOKEN, 379
order of attributes, 40
order of elements, 39, 66, 74
parent element, 9, 66
root, 9
sibling elements, 9
special character, 7
splitting documents, 198
syntax, 38
text content, 16
updating data, 6, 10
viewing data, 10
XML::DOM, 236
XML::Parser, 236
XML::XPath, 236
XML Belief Network format, 370
XML editor, 34, 289, 290
XML Schema, 42, 286
bounds, 48
canonical, 47
complex data type, 42
date, 47
facets, 47
ordered, 47
simple data type, 42
XML Spy, 34, 289
XML Stylesheet Language, 261
XML Topic Maps, 77, 286
association, 77
scope, 77
topic, 77
XML Transformation Language, 261
XPath, 175
ancestor element, 177
attribute, 177
axis, 177
child element, 177
descendant element, 177
element, 176
node, 176
numerical operations, 178
parent element, 177
root element, 177
step, 176
string operations, 178
text, 177
XQuery, 175, 180, 183
corpus, 181
database, 181
document, 180
for, 181, 182
let, 182
return, 181
where, 181
XSD, 42
xsdasn1, 45
XSL, 261
XSLT, 180, 261
accumulator, 276
and, 179

apply-templates, 266
asterisk, 179
attribute, 268
ceiling, 179
conditionals, 270
context, 263, 265
count, 179
digestion metaphor, 264
disable-output-escaping, 273
div, 179
document, 274
document order, 266
floor, 179
for-each, 266
format-number, 271
formatting, 271
indentation, 271
iterator, 276
last, 179
match, 262
maximum, 270
minimum, 270
mod, 179
navigation, 268
not, 179
numerical computations, 267
or, 179
output format, 272
position, 179
procedure, 275
procedures, 275
round, 179
select, 263, 268
starts-with, 179
string-length, 179
substring, 179
sum, 179
template, 261
transform, 261
transformation program, 261
value-of, 268
variable evaluation, 275
variables, 275
verbatim, 273
wild card, 262
XTM, 77

Zadeh, L., 324, 358
zebrafish, 98