

Subject Index

Boldface numbers indicate definitions, descriptions, or important sections; *italic numbers indicate Figures.*

- a*, branch point in a key, 392
a, constant in allometry formula, 158
a, frequency in 2×2 table, 130
 a_{hk}, a_{ki}, a_{ij} , elements of W^{-1} matrix, 405
 a_i , number of OTU's for which character *i* is applicable, 181
 a_{iJ} , number of OTU's in taxon **J** with positive character state, 142, 241
 a_j, a_{jk} , number of characters applicable to OTU's, 181
 a_j , OTU **a** of taxon **J**, 382
A, $h \times n$ matrix, 483
A, group or taxon, 25, 382
 A_i , sum of scores for identification, 385
 A_{ij} , constant in identification scheme, 396
A-space, **116**, 122–123, 138, 139, 173, 175, 215, 395, 397, 414–415
 α_j, α_k , constants in combinatorial clustering, **215**, 218, 240
Absolute resemblance linkage, 226
Acari, *see* Mites
Achelia, 461
Achromobacter, 478–479
Acinetobacter, 476, 478–479
Actinocamax, 465
Actinomyces, 474
Actinomycetales, 472–474
Adansonian or neo-Adansonian taxonomy, 5, 14, 23
Adaptive and nonadaptive clustering methods, 212–214
Additive coding, 148, **150**, 152, 350
Adiantoid ferns, 471
Advancement index, 336, 341
Aedes, 101, 102, 155, 302, 463–464
Aegelaus phoeniceus, 460
Aegilops, 470
Aenictonia, 462
Aeromonas, 477, 479
Affinitätsrechnung, 14
Affinity, 28
Age of specimens, 157–161
Agglomerative clustering, 202–205, **214–245**
Agrobacterium, 478
Alcae, 459
Algae, 471–472
Alismataceae, 470
Alleles and allelic antigens, 186, 443
Allodape, 29
Allometry, **157–159**
 formulae, 158, 313–314
 growth gradients, 316–317
 of meristic characters, 159, 184
 in paleontology, 357
Alloplectus, 468
Allopolyploidy, 48, 54, 352
Alluroididae, 465
Aloineae, 470
Alternaria, 471
Amaranthaceae, 466
Amaryllidaceae, 470
Ambystoma mexicanum, 159
Amia calva, 83
Ammonites, 35
Ammonothea, 159, 461
Amphibia, 352, 438, 459–460
Anacardiaceae, 468
Anagenesis, 58
Analogy (*see also* Homology), 75, 86–87
Analysis of variance and covariance, 196, 374
Analyzed and unanalyzed entities, 20, 27
Ancestors
 reconstruction of characters of, 310, 322, 346
 inclusion in classification, 310–313
Ancestor function, 324, 325
Ancestral characters (*see also* Primitive character states), 50, 310, **328–346**
Anemia, 471
Angiospermae, angiosperms
 congruence between life forms and parts, 101–102
 key to families, 390–391
 taxometric studies on, 430, 458, 466–470
Angular similarity coefficients (*see also* Correlation coefficient), 120, **139**, 395
Animals, reviews and taxometric studies of, 458–465, 487
Annelida, 465
Anommatochara, 462
Anoplura, 462
Anteaters, 158
Antennaria, 466
Anthropoids, 183
Anthropology, 250, 443–445
Anura, 459
Apharyngostrigea, 465
Aphids, Aphididae, 188–189
Apis, 461
Apis mellifera, 412, 461–462
Apocynaceae, 466
Apocynum, 466
Apodemus, 459
Apodemus sylvaticus, 458, 459
Apomictic groups, 415–416
Aquilegia, 469
Arabidopsis thaliana, 466
Araneida, 463
Arccos transformation, 166
Arceuthobium, 467
Archaeology, 250, 288, 443–446
Arcsin transformation, 166
Arcostaphylos, 333
Argodrepana, 462, 464
Aristotelian logic, 19–20, 27, 201
Arithmetic average clustering, 228
Armoracia rusticana, 468
Arthrobacter, 475–476
Arthropoda, 460–464
Artificial organisms (*see also* Caminalcules), 288
Artiodactyla, 459–460
Arts and Humanities, 449–450
Asca, 461
Asclepiadaceae, 467
Association analysis, **203**, 385, 436–457, 482
Association coefficients (*see also* under S)
 coding and scaling for, 156
 confidence limits of, 165, 167
 definition, **119**, **129**
 formulae, for, **131–137**
 with multistate characters, 133–137
 negative matches in, 131
 symbolism for, 129–130
Attribute states, 71

- Attributes, 71–72
 Attributive matching, 77
Atriplex, 467
 Atypicality, 174–176, 175
 effect of standardization on, 156
 in ordinations, 252
 relation to taxonomic rank, 293
 Augochlorini, 461
 Authorship, disputed, 449–450
 Automation (*see also* Scanning)
 and efficiency, 11
 and the future of taxonomy, 452
 for identification, 387, 400
 in mapping, 380
 to give unit characters, 74
 Average differences, 122
 Average linkage clustering, 218–219, 228–240
 arithmetic, 228, 230–231, 234, 240
 centroid, 228, 234–240
 evolutionary rates and, 319
 usefulness of, 303, 358
 Average organism, 195
 Axolotl, 159
- b*, constant in allometry formula, 158, 314
b, frequency in 2×2 table, 130
B, group or taxon, 25, 382
B, $h \times n$ matrix, 483
B_k clustering, 208, 256
 β , constant in combinatorial clustering, 215, 218, 226, 227, 228, 240
Bacillus, 307, 472–476
Bacillus cereus, 475
 Bacteria
 bacteriophages derived from, 54
 characters for, 91, 105, 425
 coding of characters with, 151
 congruence in, 102
 distribution of similarity values in, 286, 305–306
 ecology of, 437
 exemplar method with, 184
 Gram-positive and Gram-negative, 472, 474–479
 hygiene and, 443
 homology in, 77, 81, 425
 identification methods for, 385, 390, 394–399
 negative matches in, 131
 nomenclature of, 411
 ordination and clustering of, 253
 phenetic patterns of, 373–374
 population studies on, 369, 371
 primary and secondary characters in, 180
 Q-R relations of, 258
 relevance in, 181
 susceptibility to, as characters, 95
 taxometric studies of, 260, 261, 424–425, 430, 443, 457–458, 472–479
 vigor and pattern in, 176–177
 Bacteriophage, 54, 95
 Bacteroidaceae, 476
 Ball-and-stick model, 260
 Ball cluster, 199
 Barley, 372, 470
 Basidiomycetes, 420, 471
 Basionym, 412–413
- Bats, 438, 459
 Bayesian methods, 387, 442
 Beans, 372
 Bees (*see also* *Apis*, Augochlorinae, *Hoplitis* complex, Meliponinae, Megachilidae)
 characters from, 288
 congruence in, 29, 100, 102, 282
 distribution of similarity coefficients in, 305
 exemplars of species in, 184, 368
 factor analysis of, 108, 248
 Q-R relations in, 258
 effects of standardization in, 155
 taxometric studies of, 276, 430, 461–462
 untrained workers finding characters of, 288
 Belemnitidae, 465
Betula, 466
 Betulaceae, 466
 Bias in choosing characters, 95
 Binary character, *see* Two-state character
 Binary coding, 150
 Binomial distribution, 132, 165
 Binominal nomenclature, 411, 416
 Biochemical corroboration of classifications, 297–302, 320
 Biogeography, 94–95, 438, 463
 Biological species concept, 18, 60, 70, 362, 364, 424
 Birds, 95, 430, 438, 458–460
 Birds of paradise, 423
 Bit (binary) of information, 73–74
 Blackflies, 320
Blatta, 162
 Blattaria, 461
 Blood groups, 327, 458–459
 Bonner's clustering program II, 207
 Botryology, 448
 Brachiopoda, brachiopods, 356, 465
 Bracket keys, 389, 392
 Bradytely, 47, 48, 313
 Branching structure of keys, 388, 389
Brassica, 466, 469
Brevibacterium, 474–475
 Bromeliaceae, 308, 469
 Bronze tools, 446
 Brooches, 445
 Bryozoa, 356, 360–361, 465
Bufo, 460
Bursera, 468
 Burseraceae, 468
 Butomaceae, 470
 Butterflies, 98, 100, 369, 438
- c*, frequency in 2×2 table, 130
C, chaining coefficient, 226
C, *C_i*, larger proportion of character states, 384
C, *C_i*, partition in clustering, 205
C, cophenetic matrix, 278
C_H², distance coefficient of Penrose, 170
Ch(*h*, *i*), number of extra steps for compatibility, 348
C_i, unit character consistency, 350
C_j, number of prior clustering steps of OTU, 218, 229
- C_J*, constant in identification scheme, 396
C_{JK}, cophenetic value, 278
C_P², shape coefficient of Penrose, 170, 171, 174
C_Q², size coefficient of Penrose, 126, 170–171, 171
C_Z², square of Zarapkin's coefficient, 170
CD_{JK}, coefficient of divergence, 126
C.R.L., coefficient of racial likeness, 13, 127, 185
CSD2, coefficient of Crovello, 186
CV, convenience value of character for key-making, 392
 Calhoun distance, 128
 Callimptaminae, 462
Callosobruchus, 375, 461
Calyptogea, 471
 Camin and Sokal's numerical cladistic method, 332–337, 338, 339–341, 486
 Caminalcules, 87, 88, 329–331, 332, 334, 337–340, 338, 342, 348
Campanula, 372
Campanula rotundifolia, 467
 Campanulaceae, 467
 Canberra metric, 125
Candida, 471–472
Canis, 33
 Canonical variates or vectors, 249, 406, 407, 486
Capsicum, 466
Capsicum baccatum, 466
 Carnivora, 460
Carya, 468
 Caryophyllaceae, 467, 469
Cassia, 467
 Categories of taxonomic rank, *see* Rank, taxonomic
 Categorization, 376–377
 Cats (*see also* Felidae), 123, 431
 Caulalideae, 467
 Caulobacteraceae, 479
 Center of cluster or taxon, 195–196, 396, 414
 Centroid of cluster or taxon, 195, 204, 207, 292, 395–396, 397, 401, 414
 Centroid clustering methods, 218, 228, 234–235, 437
 Centroid factor extraction, 247, 273–275
 Centrotype, 196, 396, 414
Cerion, 379
Cerion uva, 465
 Chaining, 220, 223, 226, 227, 442
 Characidae, 459
 Character complex evolution rate, 313, 315
 Character evolution rates, 313–314
 Character relevance, 181
 Character states, 71
 calculation for HTU's, 328, 329
 coding of, *see* Coding of characters derived, 42
 inapplicable, 115, 383
 missing, 115, 383
 overlap affecting identification, 385
 primitive, 37–39, 42, 333
 recoding in cladistics, 343, 343
 unknown, 115, 383
 as vectors, 334–336, 335

- Character state sets, 342
 Character state tree, 333, 333
 Characters, **71–72**
 adaptive and nonadaptive, 63
 adequacy of samples, 103, 423
 behavioral, 90
 chemical, 11, 90, **91–94**, 452
 choice for identification, 382–383, **384–385**, 388–389, 406
 choice for medical studies, 440
 choice for numerical taxonomy, 92, **95–103**, 425–427, 481
 classification of, *see* R technique
 compatibility between, 44, 46, 347–350
 correlation between, *see* Correlation between characters
 diagnostic or discriminatory, 20, 90, 384–386, 484
 ecological, 91, 94
 in ecology, 436
 empirically correlated, 105–106
 geographic distributions as, 91, 95
 inadmissible, **103–106**
 invariant, 105, 406
 kinds of, **90–96**
 logically correlated, 103–104
 meaningless, 103
 meristic, 159, 182, 184
 handling of mixed types, 135–136, 156
 morphological, 11, 90
 multistate, *see* Multistate characters
 new, 8, 107, 189, 289, 452
 number needed, 99, **106–109**, 168, 347, 351–353, 426, 481
 partially dependent, 104
 phenetically discrete or overlapping, 182, 184–185
 phylogeny of, **42–46**, 43, 45, 320, 333, 335, 348
 physiological, 11, 90, 425
 primary and secondary, 151–152, 179–180
 from published data, 103
 standardization of, *see* Standardization of characters
 two-state, *see* Two-state characters
 unit, **72–75**
 validity in psychology, 444
 weighting of, *see* Weighting of characters
 Cheilanthoid ferns, 471
 Chemical structure, 443, 449
 Chemotaxonomy
 analogue of size and shape in, 177
 corroboration of classifications by, 299
 discussion, **91–94**
 errors in, 167–168
 and genetics, 371–372
 taxometric studies with, 460–461, 466–473, 476
 Chenopodiaceae, 467
Chenopodium, 467
 Chi-square measure, 186
Chlorella vulgaris, 471
Chlorococcum, 471
Chlorodesmis, 471
 Chloroplasts, 55
Chlorops, 463
 Chonetacea, 465
 Chorological progression, 43
Chorthippus, 162
 Chromatography, 91
Chromobacterium, 102, 477–479
 Chromosome inversions, 319–320
 Chronistic relationship, 30
 Chronology of literary works, 450
Chrotogonus, 461
 Chrysobalanaceae, 468
Cicadellidae, 462
Cicindela, 464
Cirsium, 466
 Citharininae, 458
Citrobacter freundii, 398, 399
 Clade, 311
 Cladistic analysis, 42, 44, 46, **319–356**, 486
 Cladistic difference, 30
 Cladistic relationship, **29–30**, 37
 incongruence with phenetics of, 57, 57
 of manuscripts, 450
 based on phenetics, 10, 46, 319–320
 problems of estimating, **40–52**, 53
 Cladistics, 10, **29**, 53–60, 310
 numerical, 319, **323–356**, 432, 444–445
 taxometric studies of, 458–465, 471
 Cladogeny, 344–349, 345, 351–352
 Cladograms, **29**, 30, **58**, 260
 graphic output of, 260, 483
 as graphs, 324
 length of, 335–341
 number of possible, 44, 45, 324–325, 353, 354
 parsimony of, 44, 45, 111, 337, 341
 and rank, 296
 reconstruction of, **332–346**, 334, 338
 reliability of, 42, 60, 351
 Classification (*see also* Systematics, Taxonomy), **3**
 from above or below, 22–23, 68
 arbitrary or artificial, 19–20, 25
 of characters, *see* R techniques
 choice of a basis for, **53–60**
 contrasted with identification, **3**, 383–384
 evolutionary, 421–422
 in fields outside systematics, 435–450
 general and special, **25**, 31, 34
 horizontal, 61–62, 310
 of inanimate objects, 423
 isocratic, 109
 optimal, 190, **275–284**, 424, 428
 rationale of, 5
 stability of, 8, 108, 289
 vertical, 61–62
 Classification number in nomenclature, 413
 Clay, 447
 Clethrionomys glareolus, 458
 Clifford and Goodall's clustering method, 244
 Climate, 379, 433
 Clines and clinal variation, 378–379, 434
Cliona, 465
 Clones, 184–185
Clostridium tetani, 476
 Clumping, 202
Clupea finta, 83
 Cluster analysis (*see also* Clustering methods), **6–7**, **201–202**
 adaptive and nonadaptive, 212–214
 agglomerative, 202–205
 choice of methods, 189, 303
 combinatorial, **215**, 219, **226**, 231
 comparisons between, 218–219, 235, 240, 240, 280
 contrasted with ordination, 251–253, 357, 367–368, 436
 direct or iterative methods, 209–211
 divisive, 203–205
 in ecology, 436
 effect of different methods on phenetics, 31
 hierarchical and nonhierarchical, 205–207
 local or global criteria, 209
 monothetic, *see* Monothetic methods
 nonoverlapping and overlapping, 207–208
 pair-group methods, 216
 on populations, 367–370
 on reduced number of dimensions, 253
 reviews on, 487
 sequential and simultaneous, 208–209
 SAHN methods, **214–245**
 space-conserving and space-distorting, 215, 219, 303, 481
 variable group methods, 216
 weighted and unweighted, 211–212
 Clustering methods, **201–245**
 absolute resemblance linkage, 226
 adaptive and nonadaptive, 212–214
 association analysis, **203**, 385, 436–437, 482
 average linkage, *see* Average linkage
 clustering
 B_k methods, 208
 ball cluster method, 199
 Bonner's iterative method, 211
 Bonner's method II, 207
 Camin and Sokal's, 210, 336–341
 of Carmichael, George, and Julius, 211–212
 Clifford and Goodall's, 244
 complete linkage, 218, **222–228**, 224–225, 240
 curve-seeking, 213
 dissimilarity analysis, 205
 Edwards and Cavalli-Sforza's, 204
 Farchi's, 213
 Fitch and Margoliash's, 344
 flexible clustering strategy, 226, 227, 303
 furthest neighbor, 218, 222
 Goodall's probabilistic, 207
 group analysis, 204, 210
 Harrison's, 211
 Hartigan's, 210
 hierarchical mode analysis, 213
 Hyvärinen's, 211
 information analysis, 241–244
 integer link linkage, 226
 ISODATA, 210
 Jancey's, 213

- k*-means, 207
 McQuitty's hierarchic classification, 240
 McQuitty's linkage analysis, 223
 McQuitty's recursive method, 210–211
 maximum method, 218, 222
 median linkage, 226
 minimum method, 218
 multiple rank order typal analysis, 241
 nearest neighbor, 216, 218
 neighborhood limited, 213
 Orloci's, 204–205
 Ornstein's, 213
 proportional link linkage, 226
 rank order typal analysis, 223
 relative resemblance linkage, 226
 Rogers and Tanimoto's, 207
 Rohlf's generalized distance, 212–213
 Rubin's, 205, 210
 Shepherd and Willmott's, 213, 226
 single linkage, 213, **216–228**, 220, 240, 256, 358
 UPGMA, *see* UPGMA
 UPGMC, 218–219, **234–235**, 236–237, 240, 280
 Ward's, 204, 241, 283
 WISS, 341
 WPGMA, 218–219, **234**, 234, 240
 WPGMC, 219–219, **235**, 238–240
- Clusters, 194–200**
 of aberrant OTU's, 244
 ball, 199
 center of, 195–196, 396, 414
 of characters, *see* R techniques
 connectivity of, 198
 defined, **194–195**
 density, 196
 differences or distinctness of, 277, 285, 286, 287
 dimension, 197
 gaps between, 198, 290–291
 in geographic analysis, 379
 moat of, 198, 264, 266, 284
 number of members in, 198
 parameters of, 195–199
 radius of, 197
 statistical significance of, 252, 284–287, 428
 straggleness of, 198
 variance of, 196
 Coccinellids, 161
 Coccoidea, 461
Coccus hesperidum, 461
 Codes of Nomenclature, 409–410
 Codex Bezae, 450
 Coding of characters, **147–152**, 427, 482
 additive and nonadditive, 148, **150**, 152, 350
 binary, 147–150
 for cladistic analysis, 333, 343, 343, 350
 and correlation coefficients, 140
 and distance functions, 150
 mixed, 136, 156–157, 437
 in population studies, 368
 qualitative multistate, 149
 quantitative multistate, 148
 recommendations for, 157
 and weight of characters, 110, 151
Coefficient (of)
 Carmichael, Julius, and Martin, 186
 character state randomness, 349
 correlation, *see* Correlation coefficients
 Crovello, 186
 Dice, 131
 discrimination, 408
 dispersion, 194
 divergence, 126
 Edwards and Cavalli-Sforza, 186
 Gambaryan, 135
 generalized distance, *see* *D*, *D*²
 Gini, 407
 Gower, *see* *S_G*
 Hamann, 133
 Hiernaux, 186
 Jaccard, **131**, 136, 180
 mismatch of diagrams, *see* *d_h*
 Morisita, 137
 Mountford, 137
 pattern difference, 176
 racial likeness, 13, **127**, 185
 Rajski, 144
 rank order correlation, 139
 Rogers, 187
 Rogers and Tanimoto, 132, 134, 211
 Sanghvi, 186
 simple matching, *see* *S_{SM}*
 Smirnov, 134–135, 437
 Smith, 186
 Sneath, 186
 Stewart, 186
 taxonomic distance, *see* *d*, *d_{jk}*
 vigor difference, 176
 Yule, 133, 177
 Zarapkin, 126, 170
- Coefficients (of)**
 association, *see* Association coefficients
 dissimilarity, 6, 75, 116, 119, 191, 219
 distance, *see* Distance coefficients
 similarity or resemblance, *see* Similarity coefficients
 Coelacanth, 313, 315
Coelorrhachis, 469
 Coleoptera, 460–464
 Colonic diseases, 441
 Color, coding characters for, 78, 149
Columnnea, 468
 Combinatorial clustering procedures, **215**, 219, **226**, 230–231
 Communalities, 246–247
 Comparison of classifications, **275–283**
 Compatibility between characters, 44, 46, 347–350
 Compatibility of clustering methods, 215, 219
 Compatibility matrix, 347–349
 Complete linkage clustering, 218, **222–228**, 224–225, 240
 Complexity, 177
 Compositae, 393, 466–468
 Computation, time and quantity, **482–483**
Computers
 for contouring maps, 378
 in identification, 387, 390–391, 394, 397, 398, 399, 400, 442
 indexing by, 448
 to make keys, 392–393, 393
 in mapping, 380
 in medical diagnosis, 440, 442–443
 and nomenclature, 409, 412–413
 on-line, 387, 390–391, 394, 397, 400, 442
 in pattern recognition, 449
 programs for, 482–486
 for taxonomic data, 452–453
 techniques for, **481–487**
 visual displays from, 274
- Confidence limits**
 with intra-OTU variation, 185
 NC entries and, 180–181
 of similarity coefficients, 124, 125, 166–168
- Configuration, 193**
Congruence (see also Nonspecificity hypothesis), 97
 between chemotaxonomy and phenetics, 299, 301–302
 between cladistics and phenetics, 50–52, 315, 355, 360
 factor analysis and, 99
 between geography and phenetics, 369, 379
 in languages, 445
 between life stages and sexes, 31, 97–98, 102, 282, 431–432
 between means and ranges, 185
 methods for, 97–98, 100–102, **280**, 282
 numbers of characters and significance of, 102, 106
 between organs, 31, 97, 100–103, 432
 OTU's yielding least, 282
 as problem for phenetics, 31, 54, 429
 in population and genetic studies, 368, 370–372
 taxometric studies on, 459–464, 474, 476–478
 and taxonomic rank, 98
 as a test of taxonomies, 66
- Coniferales, conifers, 356, 438, 471
 Connection function, 324, 325
 Connectivity, 198, 226, **254**, 255, **283**
 Conodonts, 357, 465
 Consistency test, 46
 Contingency table, 130, 142, 349
 Continental drift, 438
 Contour diagram, 269, 270, 271
 Contour lines, 377–378
 Convergence and parallelism, **32–40**
 apparent, 34, 47–48, 47
 heterochronic, 39
 homology and, 34
 occurrence, 33
 organ, 32
 overall, 32, 35
 in paleontology, 360–361
 probability of, 50
 reticulate evolution and, 353
 similarity due to, 39–40, **38**
- Cophenetic correlation coefficient, 97**, 100–103, 252, **278–280**, 279, 281, 284, 304
Cophenetic value, 29, 278
 Coptotermoeiina, 462
 Corals, 465
 Coreidae, 463

- Corotocini, 462
- Correlation between characters
allometry and, 159
empirical, **105–106**, 160
evolution and, 308
in identification, 384, 386, 395–396,
399, 405, 407
logical, **103–104**, 149
partial logical, **104**
in soil classification, 440
taxa separated by, 23
transformation grids and, 160
- Correlation coefficients (see also r)
in association analysis, 203
cophenetic, 97, 100–103, 252, **278–280**
279, 281, 284, 304
in discriminant analysis, 405
discussed and described, 120, **137–140**
of pattern similarity, 124–125
product moment, see r
rank order, 139
for two-state characters, 133, 203
- Correspondences in homology, 76, **80**
compositional, 77, 84
multidimensional structural, 82–84
one-dimensional structural, 84
one-to-one, 80–84
structural, 77, 79, **82–84**
- Corynebacterium*, 476
- Corynebacterium pyogenes*, 433, 476
- Coryneform bacteria, 472–473, 475–476
- Cos η , cosine shape coefficient, 139, 172,
173, 174
- Cotoneaster, 467
- Cotton, 374
- CPCC, see r_{CS}
- Crinoidea, crinoids, 356, 465
- Criteria in clustering
for admission to a cluster, 211, 214–
216
local and global, 209
for variable group membership, 216
- Criteria of optimality of taxonomies,
64, 196, **277–284**
- Cron, 313
- Crop science, 372–373, 375
- Cross-association, 84, 107, 136, 447
- Cross-fertility, 320, 370
- Crotalaria*, 466
- Crovello's character state difference,
112
- Cruciferae, 466, 468–469
- Cucurbita*, 371, 466, 468
- Cucurbitaceae, 466, 468
- Culicidae, 461, 463
- Cultures, 444
- Cupressaceae, 470
- Curve-seeking method, 213
- Cyclothems, 447
- Cyrnus, 59
- Cyrtanthus*, 371, 470
- Cytherellidae, 463
- Cytochrome c, 86, 92, 314, 343–346,
345, 458
- Cytogenetic data, 319–320
- Cytopathology, 443, 452
- Cytophaga*, 477–479
- d, d_{jk} , coefficient of taxonomic distance,
123, **124**, 126
confidence limits of, 125
in ecology, 437
expected value of, 124, 125
effect of experimental error on, 168
in medicine, 442
partitioning of, 170
effect of standardization on, 155
variance of, 124
 d' , distance affected by errors, 168
 d' , frequency in 2×2 table, 130
 d_{CANB} (j, k), Canberra metric, 125
 d_h , dissimilarity between images, 75,
128, 173–174
 $d(h, i)$, Rajsiki's metric, 144, 241
 d_{jk} , distance to maintain monotonicity,
249
 \bar{d}_{jk} , mean distance to cluster centroid,
197
 d_{jk} , Rogers and Tanimoto's distance
measure, 145
 $d_m(j, k)$, mutation distance, 344
 $d_n(j, k)$, Minkowski metrics, 125
 $d_{\Sigma, n}$, distance of unknown from cen-
troid, 395
 $d_1(j, k)$, see Manhattan distance
 D , coefficient of Rogers, 187
 D^2, D_{jk}^2 , Mahalanobis' generalized
distance, **127–128**, **403–406**
computer program for, 486
contribution of characters to, 404
and discrimination space, 177–178,
249, 403–406, 405
in evolution rates, 315, 317
intra-OTU variation and, 185
Rohlf's modification, 212–213
sampling variance, 406
and significance of clusters, 287
and taxon radius, 197
 D , number of differences in protein
sequences, 300
 D , matrix of distances, 249
 D_j , deviant index, 176, 205, 244, 396
 D_{j-k} , Rohlf's generalized distance
function, 212
 D_p^2 , coefficient of pattern difference, 176
 D_p^2 , complement of S_{SM} , 176
 D_p^2 , coefficient of vigor difference, 176
 D -space, see Discrimination space
 $DS, DS_j, DS_k, DS_n, DS_{o,s}$, discrimi-
nant scores, 402–404, 402, 403
 DV , value of character for key-making,
392
 δ , scaling factor for diagrams, 483
 δ_i , element of vector of differences of
means, 404
 δ_{jk} , vector of differences of means,
127–128, 401–402, 404
 ΔI , information gain, 144, 241–244
 Δ_{jk} , Euclidean distance, **124**, 126
 $\hat{\Delta}_n$, measures of distortion, 280
Darwin, unit of evolutionary rate,
313–314
Darwinian theory of evolution, 40
Dasyurus, 163
Dayhoff and Eck's cladistic method, 346
Deer, 460
Definitions of terms in taxonomy, 2
Dendrograms, (see also Cladograms,
Phenograms), **58–60**, 66, 260
Dendrograph, 264, 486
Density of cluster, 196
Dental malocclusion, 442
Deposition of numerical taxonomic
data, 304–305
Derived character states, 38–39, 42
Derived patristic similarity, 38–40, 38
42
Dermatophytes, 471
Dermatophyta, 471
Dermestidae, 463–464
Deviant index, 176, 205, 244, 396
Diagnosis in medicine and psychiatry,
440, 442–443
Diaspididae, 461
Dicotyledones, dicotyledons, 430, 466
469
Dicyoptera, 461
Differentiation index, 316–317
Dimension of cluster, 197
Dip-intensity statistic, 200
Diptera (see also Blackflies, Mosquitoes,
319, 460–464
Direct clustering methods, 209–211
Directed graphs, 255, 324–325
Discrimination and taxonomic purpose,
67, 432
Discrimination space, 177–178, 405,
405–408
Discriminatory characters, **384–386**,
388–389
Discriminant analysis, 383–385, 395,
400–408, 402, 405
Discriminant functions, 13, **400–404**,
401–403
and generalized distance, 128, 403
identification and, 384
in medicine, 442–443
probabilistic nature of, 387, 404
Discriminant score, 402–404, 402, 403
Diseases, 440–443
Dissimilarity coefficients (see also
Distance coefficients), 6, 75, 116,
119, 191, 214
Dissimilarity analysis, 205
Distance coefficients (see also Distance
taxonomic; Dissimilarity coeffi-
cients; Metrics), 6, **119–128**, 122,
123, 139, 144–145
average difference, 122
Calhoun distance, 128
Canberra metric, 125
Coefficient of divergence, 126
Coefficient of mismatch of diagrams,
see d_h
Coefficient of racial likeness, 13, **127**
185
Coefficient of taxonomic distance
see d, d_{jk}
generalized, see D^2, D_{jk}^2
permitting intra-OTU variation,
185–187
Manhattan, see Manhattan distance
Mean character difference, **122–123**
125, 136, 150, 171
Rajsiki's metric, 144
recommendations on, 178
of Rogers and Tanimoto, 145

- topographic, 128
Zarapkin's, 126, 170
- Distances (see also d , d_{jk} , Dissimilarity coefficients, Distance coefficients, Metrics)
Euclidean, 119–125, 122–123, 248–249, 395, 405–406
and identification schemes, 386, 395–396, 397, 405–408, 405, 407
minimal mutation, 84, 300, 323, 343–344
and nomenclature, 415
relation of S_{SM} and S_C to, 132, 136
Distinctiveness, 174–176, 175
- Distortion of classifications, 249, 278–283, 304
- Distributions
chi-square, 141–142, 170, 176, 197
contagious, 199
multivariate normal, 128, 197, 284, 287, 307, 404
of organisms in phenetic space, 189, 305–308, 429
of OTU's from cluster center, 285, 286
random, 193–194, 194
regular, 193–194, 194
of similarity coefficients, 264, 265, 305
- Ditrigona*, 307, 464
- Divergence in evolution, 33, 36–37, 39, 317–319
- Divergenzanalyse, 14
- Diversity
indices, 433
species, 438
- Divisive clustering, 203–205
- DNA (deoxyribonucleic acid)
cladistics from, 320, 352
congruence with taxonomy, 66, 73, 302
evolution rates of, 314
GC ratios, 301–302
homology in, 86
information content of, 73, 91
matches asymptote and, 107
pairing, 94, 301
sequences in, 37, 54, 92, 428
taxometric studies on, 475–479
and taxonomic rank, 61, 296
- Document retrieval, 413, 448
- Drapetis*, 462
- Drepanidae, 464
- Drosophila*, 461, 464
- Drosophilidae, 100
- Durchschnittliche Differenz, 123
- e_{13} , ease of observation of character, 383–384, 395
- e_{jk} , transformed dissimilarity, 248
- e_j , vector of ease of observation of characters, 383
- E , ratio of sums of squares, 205
- E , transformed dissimilarity matrix, 248
- δ , expected value
of d , 124, 125
of d' , 168
of r , 139
of S'_{jk} , 167
- η , vector angle, 172, 173
- Ext Y*, extension Y in defining a taxon, 65
- Earth sciences, 446–448
- Earthworms, 430, 465
- Ease of observation of characters, 383–384, 391, 395
- Ecological niches, 375–376, 433–434
- Ecology
distributions in, 194, 199
hierarchies in, 200–201
numerical taxonomy in, 435–440
Q and R analyses, 116, 436
similarity coefficients in, 137, 141
- Economics, 449
- Edge (graph theoretic), 253–256
- EDP, Electronic data processing, 11–12, 67, 387, 412–413, 453
- Edwards and Cavalli-Sforza's cladistic methods, 326–327
- Edwards and Cavalli-Sforza's clustering method, 204
- Eigenvalues and eigenvectors, 245–246, 483
- Electrocardiography, 443
- Electron microscope, 452
- Electronic data processing, 11–12, 67, 387, 412–413, 453
- Electrophoresis, 91, 299, 371
- Empetraceae, 468
- Empetrum rubrum*, 468
- Empirical correlations, 105–106, 160
- Empirical findings of numerical taxonomy, 307–308, 425–427
- Empiricism, 5, 17, 362, 418, 421–422
- Enterobacteriaceae, 260, 472–473, 476–478
- Entropy, 141–142
- Environment
allometry and, 159
and geographic variation, 377
phenetics and, 103, 369, 373–376, 432
- Epacridaceae, 469
- Epicauta*, 463
- Epigaea*, 431
- Epilachna*, 461
- Episemantic molecules, 91
- Epistasis, 415
- Equal-weighting, see Weighting of characters
- Equidae, 458–459
- Erechtites*, 466
- Ericaceae, 476–469
- Ericales, 244, 426, 431
- Errors (see also Sampling errors)
affecting similarity coefficients, 165–168
of a classification, 287–288
experimental, 167–168
in geographic variation analysis, 377
in identification, 386, 388, 397–398
and missing entries, 180
of observation, 167–168, 426, 442
and standardization, 155
- Erwinia*, 478
- Escherichia coli*, 477
- Essence, in logic, 19, 27
- Essentialism, 421
- Etiology of disease, 440
- Eucalyptus camaldulensis*, 466
- Eulophia*, 470
- Euphorbiaceae, 468
- Euphydryas*, 461
- Euphydryas chalcidonea*, 369
- Euphydryas editha*, 369, 462
- Euschoengastia*, 464
- Euzerconidae*, 461
- Evolution
cost of, 314
divergent, 33, 36–37, 39, 317–319
and geographic variation, 380
minimum, 321, 323
mosaic, 315, 360
parsimony in, 44, 321–322, 337, 338, 353, 357
and phenetic patterns, 189, 305, 358–361, 367, 370–373
rates of, see Evolution rates
- Evolution rates, 313–319
constancy of, 317–319
locally constant, 343
and monophyly, 48–52, 57
from paleontology, 313, 361, 465
uniformity, 321
- Evolutionary hypothesis, 324
- Evolutionary order, of character states, 42–44, 45, 46, 320, 333, 333
- Evolutionary steps, 333, 336–337, 338
- Evolutionary tree (in graph theory), see also Phylogenetic tree, 324
- Exemplar method, 69–70, 167, 183–184
- Exogyra*, 465
- Experience in taxonomy, 287–288, 424, 434
- f , point in D-space, 405
- f_{ik} , frequency of character state, 142
- $f(j)$, ancestor function, 324
- f_{jk} , transformed dissimilarity, 248
- F , F_1 , F_2 , separation functions for key-making, 392
- F , transformed dissimilarity matrix, 248
- Factor analysis, 246–248
in congruence studies, 98–99
in ecology, 436–437, 440
and environment, 374
multiple, 247–248
number of characters and, 108
principal, 246
in psychology, 443–444
- Factor asymptote hypothesis, 106
- Fagaceae, 468
- Family names (surnames), 450
- Fanniinae, 461
- Farchi's clustering method, 213
- Feature, see Unit characters
- Federalist* papers, 449
- Felidae, 459
- Ferns, 35, 471
- Festuca ovina*, 371, 469
- Field-mice, 458–459
- Fishes
evolution rates in, 316
fossil, 83, 358–359, 358
homology in skulls of, 83, 357
red corpuscles of, 20
taxometric studies on, 458–460
- Flavobacterium*, 477
- Flavobacterium piscicida*, 477
- Flexible clustering strategy, 226, 227, 303

- Floristic studies, 436–437
 Foraminifera, 439
 Forest, 437
 Fossil record, 10, 42, 61, 76, 311, 312, 357
 Fossils
 allometry, 157
 and cladistics, 319
 ecology of, 438–439
 evolution rates in, 313, 361, 465
 in stratigraphy, 361
 taxometric studies on, 356–361, 432, 457–460, 463–465, 471
 trends in, 250
 Fourier series, 161
 Frame shift mutations, 346
Froelichia, 466
 Fully connected graph, 198, 254, 255
 Function, biological
 analogy and homology related to, 86–87
 and phenetic similarity, 28–29
 Fungi, 95, 151, 179, 250, 431, 433, 458, 471–472
 Furthest neighbor clustering, 218, 222–228, 224–225, 240
Fusarium, 472
 Fusulinidae, 464–465

 g, number of NC sites in a protein, 344
 g, point in D-space, 405
 g, state of a character, 141
 g(j), connection function, 324
 G, difference between character state frequencies, 384
 G, rotation matrix, 483
 γ, constant in combinatorial clustering, 215, 218
 Galliformes, 101, 301, 459
 Gambaryan's coefficient, 135
 Gaps between clusters or taxa (see also Moat of a cluster), 198, 290–291
 Gause's principle, 434, 438
 GC ratio, 301–302
 Gene frequencies
 cladistics from, 323, 326
 similarity coefficients from, 186–187
 General classifications, 25, 31
 General factor, 247
 General Index, 13
 Generalized distance, see D^2 , D_{JK}^2
 Generalized variance, 196, 212
 Genes
 cladogeny of, 346
 fine structure of, 73, 86, 92
 polythetic groups and, 21
 reduplications and, 73, 86
 similarity coefficients and, 147
 transfer of, 54, 86
 Genetics (see also Genes, Genome, Genotype), 432, 449
 Genome, 73, 96, 353
 Genospecies, 363
 Genotype, 96, 421, 432
 Geographic variation, 376–380, 407, 433, 458–460, 464, 466, 468, 471, 476
 Geography, 194, 445, 447–448
 Geology, 446–447
 Geraniaceae, 469
Geranium sanguineum, 469
 Gesneriaceae, 468
 Gini's synthetic coefficient, 407
Ginkgo, 313
Glabrocingulum, 465
Glycine wightii, 466
 Gomphocerinae, 462
 Goodall's probabilistic clustering method, 207
 Goodall's probabilistic similarity index, 140–141, 284, 396
 Goodness of fit
 of cladograms, 344
 of classification, see Distortion of classification
Gossypium, 467
 Gower's similarity coefficient, see S_G
 GRAFPAC graphic output subroutines, 483
 Graft chimera, 372
 Gramineae, 469–470
 Graphs and graph theory (see also Tree), 253–256
 connectivity, 198, 226, 254, 255, 283
 directed graphs, 255, 324, 325
 maximally and minimally connected graphs, 198, 254, 255
 use in taxonomy, 264, 267, 268
 Graphic output, 483
 Gravitational models, 159, 209, 213
 Gregg's Paradox, 62, 65
 Group analysis, 204, 210
 Group element potential, 204
 Group factor, 247
 Group methods of clustering, 228
 Growth, 157–161, 250, 432
Gryphea, 35
 Gymnospermae, 470–471

 h, a character, 115
 h, homological indistinctness, 104
 h, number of points on a diagram, 483
 h(j), $h(j_{a,b})$, advancement index, 336, 341
 H, coordinates in stereograms, 484
 H, $H(i)$, disorder or entropy, 141
 H, rotation matrix, 483
 $H(h, i)$, score of character state randomness, 349
 H_j , sum of Rogers and Tanimoto's distances, 145, 175
Haemaphysalis leporispalustris, 369, 378–379, 464
Halimeda, 472
 Hall's heterogeneity measure, 145
Hansenula, 472
Haplobasidium, 472
Haplopappus, 468
 Hartigan's measure of distortion, 281–282
 Heart disease, 441, 443
 Heincke's Law, 305–306
Helminthosporium, 471
Hemidactylus garnottii, 459
 Hemiptera, 159
 Hemoglobin, 86, 92, 314, 346, 458–459
 Hemorrhagic septicemia bacillus, 433
 Hepatitis, 441
 Herring, 13, 305
 Hesperioidea, 461, 463
 Heterochronic parallelism, 39
 Heterogeneity, measures of, 145
 Heterogeneity of column vectors, 138, 162
 Heteroptera, 63
 Heuristic aspects of numerical taxonomy, 418, 427, 429–434
 Hierarchical classification method of McQuitty, 240
 Hierarchical classification systems, 206, 207
 in ecology, 436
 in identification schemes, 388, 400
 logic of, 65
 merits of, 67, 200–201
 nomenclature and, 415
 at population level, 368
 and reticulate evolution, 59
 Hierarchic and nonhierarchic clustering, 205–207, 214–245
 Hierarchical grouping method of Ward, 204, 241, 283
 Hierarchical mode analysis, 213
 Hierarchy of characters, 62–63
Hirstionyssus, 461
 Hollow curve, 306–308
 Holography, 452
 Holomorph, 69, 442
 Holoophyletic groups, 49
 Hominoidia, hominoids, 280, 460
Homo sapiens (see also Man), 183, 185
 Homogeneity of dispersions of taxa, 404
 Homoiology, 39–40
 Homology, 75–90
 in bacteria, 77, 81, 425
 in electrophoretic patterns, 299
 in relation to convergence and parallelism, 34
 correspondences, see Correspondences in homology
 in cross-association, 137
 on defined unit characters, 85–87
 definitional phenetic, 85
 external and internal criteria for, 77, 79
 in fossils, 357
 general, 105
 genetic, 86
 geometric similarity and, 89
 in languages, 445
 matching diagrams and, 89, 160
 numerical, 80, 84–85
 operational, 78–82, 420–421, 428
 phenetic approaches to, 85–89
 phylogenetic, 18, 75
 in proteins, 300–301
 redefinitions of, 77–78
 in rock strata, 447
 scanning images and, 87, 88
 serial, 105
 similarity criterion of, 79, 85–89
 of skull bones, 83
 in soils, 439
 taxometric studies on, 459, 461
 traditional definitions of, 75–77, 80
 on undefined characters, 87–89
 Homonyms, 410, 413
 Homoplastic similarity, 37, 38, 39–40
 Homoptera, 461–462, 464
 Homostats, 222
 Honeybees (see also *Apis mellifera*), 407

- Hoplitis* complex, 90, 100, 102, 108, 155, 248, 276, 282, 305
- Hoplopleura*, 462
- Horizontal classification, 61–62, 310
- Horotely, 313–314, 316
- Horses, 314–315, 337, 343, 348
- Hotelling's T^2 ratio, 287, 404
- HTU, hypothetical taxonomic unit, 322, 324, 326–350, 329, 332, 415
- Humanities, 449–450
- Hybrid Index, 372
- Hybrids and hybridization (*see also* Cross-fertility), 352–353, 354–355, 371–372, 432, 460, 466–470
- Hydrobiology, 438
- Hymenoptera, 411, 461–464
- Hyperspace, *see* Space
- Hypothetical median organism, 195–196, 396, 414
- Hypothetical modal organism, 196
- Hypothetical taxonomic unit, 322, 324, 326–350, 329, 332, 415
- i*, a character, 115
- I*, information statistic, 142, 142–144, 241–244
- I*, Mountford's coefficient, 137
- \mathcal{I} , identification matrix, 382, 384–385
- $I(h, i)$, joint information, 143
- $I(h; i)$, mutual information, 143
- $I(X, Y)$, intermediate form, 414, 415
- INT, $INT(a, b)$, interval, 328
- I-space, 116
- Identification, 3, 12, 381–408
 - errors in, 386
 - general considerations on, 383–387
 - OTU's remaining unidentified, 386, 395
 - and pattern recognition, 449, 452
 - probability of correct, 384, 387, 393–394, 396–400, 404, 408
 - as process in A-space or D-space, 395–396, 397, 406
 - testing of schemes of, 304, 387
- Identification matrix, 382–383, 384–385, 395, 397
- Identification score, 398
- Identity, similarity value for, 191
- Inapplicable comparisons, 180–181, 383
- Incongruence, *see* Congruence
- Indented keys, 389, 392, 393
- Indexing of documents, 413, 448
- Individuals, choice of, 69–70
- Influenza virus, 480
- Information analysis, 241–244, 437
- Information content
 - of characters, 72–74
 - of cladistic groups, 57
 - of genome, 73, 91
 - in natural groups, 5, 22, 25–27, 64, 113
 - of proteins, 91
- Information statistic, 141–144
 - clustering by, 203, 241–244
 - from contingency table, 142–143
 - in ecology, 436
 - gain in, 144, 241–244
 - in identification, 385
 - size factors and, 174
 - relation to squared distances, 145
 - in taxonomy, 145
- Information storage and retrieval, 67, 413, 448–449, 451
- Information theory, 119, 141–145, 241–244, 388, 448
- Informational macromolecules, 91
- Infrared spectra, 299
- Intraspecific studies (*see also* Populations), 365–371, 376–380
- Insects
 - DDT resistance of, 34, 74
 - evolution rates in, 316
 - taxometric studies of, 458, 460–464
- Integer link linkage, 226
- Intelligence tests, 444
- Intelligent ignoramus, 166, 287–289
- Intermediate forms, 223, 414, 415
- International Plant Index, 413
- Internode (graph theoretic), 253, 255, 325, 327–329, 328–329, 331
- Interval (in a tree), 328
- Intra-OTU or intrataxon variation, 70, 182–187, 321, 385, 392
- Inverse analyses in ecology, 436
- Invertebrata (*see also* Arthropoda), 464–465
- Iridaceae, 470
- Iris, 470
- Isarithmic lines, 377
- Isocratic classifications, 109
- ISODATA clustering method, 210
- Isology, 76
- Isomorphic sets, 81
- Isophenes, 377
- Isopoda, 464
- Iterative clustering methods, 209–211
- Iterative optimization
 - in cladistics, 332, 337, 341–342, 350
 - in cluster analyses, 209–214
 - in ordination, 249, 251
- Ixodorhynchidae, 462
- j*, an OTU, 114, 214
- $j_{a,b}$, most recent common ancestor, 336
- j_j , OTU *j* of cluster or taxon *J*, 293, 382
- J*, a cluster of OTU's, or a taxon, 127, 214, 235, 382–383
- (*J*), (*J, K*), and (*JK, L*)-measures in clustering, 214, 219
- J*, reflection matrix, 483
- $J(a, b)$, rank in logical definition of taxon, 65
- Jancey's clustering method, 213
- Jigsaw puzzle, 449
- Joint information, 143
- Juglandaceae, 468
- Junipers, 378
- Juniperus ashei*, 470
- Juniperus virginiana*, 470
- Jurinea*, 393
- k*, number of dimensions of a character, 152
- k*, number of factors or reduced number of dimensions, 99, 245
- k*, number of parts or partitions in clustering, 195
- k*, number of subgroups in a key, 392
- k*, parameter in hierarchical mode analysis, 213
- k*, an OTU, 115, 214
- k_i , number of parts in *i*th partition, 205
- K*, constant in clustering, 226
- K*, Lubischew's coefficient of discrimination, 408
- K*, a cluster of OTU's or a taxon, 127, 214, 235, 401
- κ , constant in taxon radius, 197
- k*-clusters and *k*-dendograms, 208
- k*-means clustering method, 207
- Kendall's rank order correlation, 139
- Key communality cluster analysis, 250
- Keys, taxonomic, 12, 388–400
 - bracket, 389, 392
 - character weighting for, 12, 392
 - computer produced, 392, 393
 - dichotomous, 388, 389, 393
 - indented, 389, 392, 393
 - monothetic sequential, 389–391, 394
 - multiple entry, 390–391
 - number of characters required in, 386
 - on-line, 387, 390–391, 400
 - polythetic sequential, 391–394
 - probabilistic, 394
 - sequential, 388–394
 - simultaneous, 394–400
 - taxometric work yielding, 462, 467, 473–474
- Klebsiella ozaenae*, 398
- Knights*, 358, 460
- Kosmoceras*, 465
- l*, an OTU, 215
- l_i , patristic unit character length, 350
- L , joint likelihood, 398
- L , L_{max} , L_{min} , length of cladogram, 335–336
- L , level in clustering, 226
- L , a cluster of OTU's or a taxon, 214, 235, 401
- \mathcal{L} , transformed identification matrix, 395
- L_1 , L_{11} , coordinates in stereograms, 484
- $L(\theta)$, length of a tree, 327
- λ , eigenvalue, 245
- λ_1 , λ_2 , measure of diversity, 137
- Λ , diagonal matrix of eigenvalues, 245
- Labiatae, 466, 468
- Laburnocytisus*, 468
- Lactobacillaceae, 475
- Lactobacillus*, 474–476
- Laelaptoidea, 463
- Languages, 444–445, 448
- Large and small scale detail, 174
- Lari, 101, 459–460
- Larvae, congruence with adults, 29, 97–98, 102
- Latimeria*, 113
- Least squares additive tree model, 327
- Leguminosae, 466–469
- Length of edge, 255
- Lepidoptera (*see also* Butterflies), 365, 412, 430, 461–464
- Leucopengha*, 460
- Leukemia, 441
- Library science, 448
- Lichens, 471

- Life stages, congruence between, 31, 97–98, 102, 431–432
- Likelihood, joint, 398
- Liliaceae, 470
- Limits of taxa, 61–62, 395, 414
- Limnanthaceae, 259, 466, 468
- Limulus*, 321
- Lingula*, 313
- Linkage analysis of McQuitty, 223
- Linkage diagrams, 264, 267
- Linnean system and nomenclature, 200, 295, 363, 366, 411, 416
- Liponyssoides*, 101
- Lirceus fontinalis*, 464
- Listeria*, 475
- Literary style, 449–450
- Lithophragma*, 468
- Liver disease, 442
- Liverworts, 438
- Lizards, 369, 459–460
- Lockhart and Hartman's clustering method, 240, 385
- Locusts, 374
- Logical model for taxonomy, 65
- Lotus*, 467
- Luciliini, 463
- Lumping and splitting, 7, 431
- Lungfishes, 316
- Lygaeoidea, 463
- m , number of alleles, 186
- m , number of matches, 130
- m , reduced number of characters in identification, 383–384
- m_i , number of states of character i , 141
- m_{jk} , mutation distance, 344
- $m(R)$, Lerman's measure of distortion, 283
- M , constant in stereograms, 484
- M , a cluster of OTU's, 215, 235
- M_j , average similarity, 283
- M_j , attraction of OTU j , 283
- $M.C.D.$, mean character difference, 122–123, 125, 136, 150, 171
- μ , parameter in distortion measure, 281
- μ , mean proportion, 133
- μ , an HTU, 328, 328, 329, 332
- Mahalanobis' generalized distance, *see* D^2 , D_{jk}^2
- Maize, 370, 374, 469–470
- Majority voting in cladistic analysis, 320, 346 in keys, 391
- Malacostraca, 464
- Mallophaga, 95
- Malvaceae, 467
- Mammalia, mammals, 25, 83, 113, 316, 438, 459–460
- Man, 92, 183, 185, 327, 458–459
- Mangifera*, 468
- Manhattan distance or metric, 125–126 and evolution, 317, 323, 327–331, 329, 333–337, 341–343 ordination with, 249 size and shape in, 171
- Manihota*, 468
- Manuscripts, 450
- Maps, estimating resemblance between, 447
- Mapping, automated, 380, 453
- Market research, 449
- Marsupialia, marsupials, 33, 163, 459
- Matches negative, 130–131, 135–136, 151, 179, 437, 445 probability of, 134 weighting of, 134, 135
- Matches asymptote hypothesis, 106–109, 289, 423
- Matching diagrams or images, 75, 89, 483
- Matrix, matrices of character correlations, 97–98, 245 compatibility, 347–349 data, 114–116 dissimilarity, 248 of eigenvalues, 245 fusion in clustering, 230, 242 identification, 382–383, 384–385, 395, 397 rank of, 245 of resemblances or similarities, 6–7, 119, 190–192, 260, 261, 298, 482 variance-covariance, 212, 383, 401
- Matrix correlations, 97–98, 100–102, 280, 282
- Maximally connected graph, 254, 255
- Maximum clustering, 218, 222
- Maximum likelihood method in cladistics, 326–327
- MDSCAL program, 250
- Mean character difference, 122–123, 125, 136, 150, 171
- Mean correlation coefficient, 407
- Means, vectors of, 207, 383, 401
- Median clustering, 218–219, 235
- Median linkage, 226
- Medicago*, 468
- Medicine, 440–443
- Megachilidae, 462–464
- Megascolecidae, 465
- Megathymidae, 464
- Melipona*, 462
- Meliponinae, 461
- Mentha*, 468
- Menziessa*, 467
- Meromyza*, 463
- Metasequoia*, 313
- Meteorology, 448
- Metrarabdotos*, 465
- Metrics, metric functions (*see also* Dissimilarity coefficients, Distances, Distance coefficients), 120–121 Canberra, 125 city-block, *see* Manhattan distance Euclidean, 140, 180 Manhattan, *see* Manhattan distance Minkowski, 125, 249–250, 281 Rajski's, 144
- Microbiology (*see also* Bacteria, Fungi) errors in, 167–168 size and shape analogues in, 176–177, 375 reticulate evolution in, 352 taxometric studies in, 430, 472–480, 487
- Micrococcaceae, 475–476
- Micrococcus*, 475–476
- Microspecies, 290, 365
- Milk, 443
- Milk fever, 441
- Millet, 432
- Minimal mutation distance, 84, 300, 323, 343–344
- Minimally connected graph, 198, 254, 255, 324, 325
- Minimum clustering, 218
- Minimum discrimination information statistic, 144
- Minimum evolution, principle of (*see also* Parsimony of evolution), 321, 323
- Minimum length directed tree, 255
- Minkowski metrics, 125, 249–250, 281
- Misclassification (*see also* Identification), 20, 23, 185
- Miscoding of characters, 34, 39–40, 44, 348
- Mismatches, number of, 130, 242
- Missing data (*see also* NC, Relevance), 178 in bacteria, 132 characters missing, 178 in coding characters, 148 in identification, 383, 392 organs missing, 179 practical problems with, 481–482
- Mites congruence in, 101 ecology, 437 exemplars of species in, 184, 368 taxometric studies of, 268, 270, 271, 275, 461–464
- Mixed coding of characters, 136, 156–157, 437
- Mixture problem, 199
- Moat of a cluster, 198, 264, 266, 284
- Models, 3-D taxonomic, 257, 260, 272, 274, 275, 276
- Moles, 33
- Mollusca, mollusks, 160, 316, 439, 465
- Monocotyledones, monocotyledons, 81, 469–470
- Monophyly, monophyletic groups, 40, 46–50
- Monothetic groups and classifications, 20–23, 203, 385, 391, 436
- Monothetic methods association analysis, 203 group analysis, 204 Lockhart and Hartman's method, 385 for procladograms, 336–341, 338
- Monotonicity of similarity coefficients, 118
- Moraxella*, 478–479
- Morisita's coefficient, 137
- Morphology, morphological trends, morphogenesis, 157–161, 250–251, 432
- Mosaic evolution, 315, 360
- Mosquitos congruence in, 101–102 distribution of similarity coefficients in, 305 elongate phenetic clusters in, 307 nonmetric multidimensional scaling of, 250 Q-R relations in, 258

- scanning of, 87–88
 serology and phenetics in, 302
 effects of standardization in, 155
 taxometric studies of, 269, 273, 274, 463
- Mosses, 472
- Mountford's coefficient, 137
- Mouse, 187, 317, 369–370, 458
- MTAM method, 248
- MULDIS computer routine, 128
- Multidimensional scaling, 249–250, 436
- Multiple comparisons tests, 378
- Multiple discriminant analysis, 405–406
- Multiple entry keys, 390–391
- Multiple factor analysis, 247–248
- Multiple rank order typal analysis, 241
- Multistate characters, 45, 133–134
 coding of, 148–152
 information statistics and, 241, 385
 qualitative, 115, 133, 149
 quantitative, 115, 133, 148
- Mus musculus*, 458, 460
- Musculature, 459
- Museums, 453
- Music, 450
- Mutations
 within clones, 185
 genetic analysis of, 449
 in proteins, 300, 343–344, 351
- Mutation value, 343
- Mutual information, 143–144
- Mycobacterium*, 473–474
- Mycobacterium chitae*, 474
- Mycobacterium fortuitum*, 474
- Mycobacterium novum*, 474
- Mycobacterium runyonii*, 474
- Mycobacterium terrae*, 474
- Mycoplasma*, 479
- Myrtaceae, 466
- Myxobacterales, 476–478
- n*, number of characters, 99, 114, 122, 130, 382
- n*, number of gene loci, 186
- n*, number of sites in a protein, 344
- n_i*, number of individuals of species *i* in stand **I**, 137
- N*, set of nodes, 324
- N_s*, sum of scores in cladistic analysis, 350
- N_I*, number of individuals in stand **I**, 137
- Natural group, classification or system, 18–27, 56, 64, 110, 113, 285, 410
- Naval studies, 449
- NC, "no comparison" (see also Missing data, Relevance), 115, 178 and coding of characters, 148, 150–151
 effect on metrics and similarity coefficients, 136, 180
 effect on ordinations, 249
 in protein sequences, 344
- Nearest neighbor clustering, 213, 216–228, 220, 240, 256, 358
- Negative matches, 130–131, 135–136, 151, 179, 437, 445
- "Neighborhood, rule of," 159
- Neighborhood limited classification, 213
- Neisseria*, 477
- Neimoniales, 471
- Nematoda, nematodes, 184, 464–465, 487
- Network, 255, 324
- "New Systematics," 16, 70, 364, 418
- New Testament manuscripts, 450
- Nexus hypothesis, 96, 423
- Niche, ecological, 375–376, 433–434
- "No comparison," see NC
- Nocardia*, 473–474
- Noda in ecology, 436, 440
- Node (graph theoretic), 255, 324, 326–327, 328–329, 333
- "Noise" (unwanted variation), 213, 288
- Nomenclature, 12–13, 365–366, 409–416
 codes of, 409–410
 of intermediate forms, 414, 415
 Linnean system and, 200, 295, 363, 366, 411, 416
 new proposals for, 411–413
 numerical, 412–413, 415
 numerical taxonomy and, 410–411, 414–416
 phenon, 8, 294–296, 295, 410–411
 stability, 410–413
- Nomenifer, 414
- Nomenspecies, 363
- Nominalism, 421–422
- Nonlinear discriminant methods, 408
- Nonmetric coefficient, 131, 437
- Nonmetric multidimensional scaling, 249–250, 436
- Nonoverlapping clustering methods, 207–208, 214–245
- Nonspecificity hypothesis (see also Congruence), 97–103, 106, 164, 166, 289, 423, 426
- Normal analyses in ecology, 436
- Normalization of vectors, 245, 248
- Nosology, 440
- Nototheniidae, 458–459
- Nucleic acids (see also DNA), 84, 94, 300–301, 323, 479–480
- Nucleotide minimum mutation distance, 84, 300, 323, 343–344
- Null hypotheses
 for clusters, 284
 for resemblances, 164
 for taxonomic structure, 193–194
- Number of characters required in ecology, 437
 in cladistics, 347, 351–353
 in identification, 385–386, 399
 in phenetics, 99, 106–109, 168, 426, 481
 in soil studies, 440
- Number of OTU's in a cluster, 198
 too large in a study, 70, 483
- Numerical cladistics, 319, 323–356, 432, 444–445
- Numerical homology, 80, 84–85
- Numerical taxonomy
 advantages, 11
 aims and principles, 1–15
 applications to biological systematics, 457–480
 applications outside biological systematics, 435–450
- criticisms, 417–427
 definition, 3–4
 fundamental positions, 5
 heuristic aspects, 429–434
 history of, 13–15, 23, 418–419
 recommendations for studies using, 302–305, 481–487
 reviews of special topics in, 487
 sequence of operations in, 5
 shortcomings of, 427–429
- Numerical, 412–413, 415
- NT-SYS computer programs, 128, 222, 224, 484
- Nutrition, 443
- O, O', origin of a space, 172–175
- O_j*, object stability, 283
- Oats, 433
- Object stability criterion, 205, 210, 283
- Objective function, Ward's, 241, 283
- Objectivity, 11
- Odocoileus virginianus*, 460
- Odontites*, 468
- Oenothera*, 468
- α*, number of clusterings, 205
- Onagraceae, 468
- Onciidiinae, 264, 266, 267, 470
- Ononis, 307, 467
- Ontogeny, 43, 442
- Operational homology, 78–82, 420–421, 428
- Operational taxonomic unit, see OTU
- Operationism, 9, 17–18, 80, 362, 364, 418
- Ophlitaspongia seriata*, 465
- Optical recognition method, 443
- Optimality criteria for classifications (see also Distortion of classifications), 190, 275–284, 424, 428
- Orangutan, 315
- Orchidaceae, 470
- Orchids, 264, 266, 267
- Ordination, 3, 201, 245–253
 as adjunct to clustering, 208, 244, 269
 computer programs for, 483–484, 486
 contrasted with clustering, 251–253, 357, 367–368, 436
 distortion of phenetics by, 209
 in ecology, 201, 436
 in geographic analysis, 379
 and graphs, 256, 257, 268
 and identification, 400
 nomenclature and, 415
 recommendations upon, 303–304
 representation of results, 269–275, 272–276
 size factors in, 173, 252
 multiple factor analysis, 247–248
 nonmetric multidimensional scaling, 249–250, 436
 pattern analysis, 250
 principal factor analysis, 246
 principal component analysis, see Principal component analysis
 principal coordinate analysis, 248–249, 252, 258, 286, 298, 303, 406
 seriation, 250–251, 251, 446, 482
 Tryon's key community cluster analysis, 250
- Oreodontidae, 459–460

- "Organ taxa", 85
 Organism evolution rates, 313, **315-319**
 Organisms (*see also* OTU's)
 different kinds studied by numerical taxonomy, 424-425, **457-480**
 information content of, 73
 Orloci's clustering method, 204-205
 Ornstein's clustering method, 213
 Orthogonal axes, 245, 247, 405-406
 Orthoptera, 162, 460-462
Oryza (*see also* Rice), 307, 470
Oryza perennis, 470
 Osmeridae, 460
 Ostracoda, ostracods, 356, 439, 462-463
 OTU, Operational Taxonomic Unit, **68-71**, 362
 aberrant, 156, 244, 282
 additional, 8, 258, **289-290**, 296
 in archaeology, 445
 choice of, 481-482
 effect of choice on R clusters, 258-259
 effect of choice on scaling, 155
 in ecology, 436
 higher taxa as, 183
 number, *see* Number of OTU's standard, 290
 unknown, for identification, 382
 variation within, 70, **182-187**
 OTU relevance, 181
 OTU by OTU relevance, 181
 Overall similarity (*see also* Resemblance, Similarity), 5, 24
 criticisms of, 28, 419, 427
 homology and, 76, 85
 Overdominance, 372, 415
 Overlap rules, 366
 Overlapping classifications, clusters or taxa
 in identification systems, 395-396, 397
 in information retrieval, 448
 methods for, 201, 205-208, 207
 nomenclature for, 415
 and taxonomic rank, 290
 Oysters, 35

p, proportion of errors, 167
p, scaling factor in discriminant analysis, 405
P_{ij}, *P_{klj}*, *P_{klj}*, proportion of character state *j*, 186-187, 385
P_{h,j}, *p_j*, proportion of state 1 in taxon J, 397
p_i, character weight in cladistics, 350
p_i, *p_{ik}*, proportion of character states, 133, 135, 141
p_x, proportion of quadrats containing *x*, 204
P, projected matrix of OTU's on principal axes, 246
 \mathcal{P} , transformed identification matrix, 397
P_i, probability of heterogeneity, 285
 φ , pair function, 120-121
 ϕ , phenetic vector, 375
 Pair-group clustering methods, 216
 Paired affinity, 299
 Paleontology, 97, 332, 356-361, 452, 457
 Paleospecies, 363
Panicum maximum, 470
 Papaveraceae, 466
Papilio, 412
 Papilionaceae, 391
 Papilionoidea, 461, 463
Paraleucophenga, 460
 Parallelism, *see* Convergence and Parallelism
Paramecium, 89
 Parametric similarity, 107
 Paraphyletic groups, 49
 Parasites
 as characters, 95
 congruence with hosts, 95
 congruence between life stages, 431-432
 as indicators of phylogeny, 46
 Parholaspididae, 462, 463
 Parsimony in evolution, 44, 321-322, 337, 338, 353, 357
 Partition (*see also* Cluster analysis), 201, 205-206
Parus, 460
Passer domesticus, 459
 Passeres, 458
Pasteurella, 476, 479
Pasteurella enterocolitica, 286
Pasteurella multocida, 479
Pasteurella pseudotuberculosis, 286
 Patristic similarity, **37-40**, 38
 derived, 38-40, 38, 42
 primitive, 37-38, 38, 40, 42
 Patristic unit character length, 350
 Pattern, **192-194**
 in character compatibility, 347
 character vector termed, 193
 coefficients of pattern similarity, 124-125
 of evolution, 358-361
 in microbiology, 176-177, 399
 of organisms in phenetic space, 189, 305-308, 429, 432
 in time and space, 367
 Pattern analysis, 250
 Pattern detection, 192-193
 Pattern recognition, 192-193, 448-449, 452
 PCA, *see* Principal component analysis
 Peculiarity index, 175-176, 205
 Peek-a-boo systems, 390, 400
 Pelycosauria, 459
Pemphigus populitransversus, 98, 369, 378, 379, 464
Penitella, 465
 Periposocidae, 464
 PFA, principal factor analysis, 246
Phalanger, 163
Phaseolus, 469
 Phenetic approach to homology, 85-89
 Phenetic patterns, 189, **305-308**, 429
 in ecological space, 369, 373, 375-376
 and evolution, 189, 305, 358-361, 367, 370-373
 future work needed, 432-434
 and geography, 379
 and identification schemes, 393
 and nomenclature, 415-416
 Phenetic relationship or similarity (*see also* Phenetics), **28-29**
 components of, **37-40**, 38, 146, **168-178**, 171, 173, 175
 distortion by cluster analysis, 66, 206-209, 247
 distortion in ordinations, 209, 247, 250, 256, 257
 of organs, 28-29, 85
 problems of estimating, **31-40**, 53, 168-169
 recommendations on, 178
 Phenetic space (*see also* Space)
 distribution of organisms in, 189, **305-308**, 429
 fullness of, 308
 Phenetic species concept, 364-365
 Phenetics (*see also* Phenetic relationship), **29**
 basis of cladistics, 10, 46, 50, 76-77, 319-321
 as basis for numerical taxonomy, 10, 53-60
 congruence with cladistics, 56-57, 57
 congruence with geography, 369
 criticisms of, 419-421
 response to environment, 373-376, 432
 of populations, **362-380**
 at species level, 365, 368
 and time dimension, 309-313
 Phenograms, 29, **58**, **260**, 262-263, 265-270
 graphic output of, 483
 nomenclature from, 411
 order of branches in, 261, 263, 264
 from probabilistic similarity coefficients, 141
 recommendations upon, 303
 reliability of, 264, 265, 284
 tests of goodness, 252, 278-284
 Phenome, 96
 Phenon nomenclature, 8, **294-296**, 295-410-411
 Phenotypic, 96, 421, 432
 Phenotypic plasticity, 374
Phialocephala, 471
Phlox, 467
 Phthiracaroida, 463
 Phyletic lineages, (*see also* Cladogeny, Cladograms) 50-51, 57-60, 310-311, 310-312, 313, 358-359, 360
 Phyllococe, 468
 Phyllococeae, 431
 Phyllota phlycooides, 467
 Phylogenetic or phyletic relationship (*see also* Cladistic relationship, Phenetic relationship), 8-9, **30**, **40-52**
 based on phenetics, 10, 46, 50, 76-77, 319-321
 as shown in dendrograms, 57-60, 57-310-312
 Phylogenetic taxonomy, 9-10, 53-55, 310, 419-421
 Phylogenetic trees, 57-60, 57, 310-311, 310-312, 313, 358-360
 Phylogeny, phyletics (*see also* Cladistics, Cladogeny)
 assumptions of, 17-18
 reviews of taxometrics in, 487
 study of, **309-361**
 taxometric studies on, 344, 346, 345, 358-361, 358-360, 458-465, 471

- Physical anthropology, 443, 445
 Phytoseiidae, 464
Picea, 471
Pichia, 472
 Pinaceae, 470–471
Pinus, 470–471
Pinus contorta, 471
Piricularia oryzae, 471
 Plant breeding, 371–373, 432
 Plants (see also Angiospermae, Bacteria)
 characters for, 91
 congruence studies on, 101–102
 crop, 372–373, 375
 evolution rates in, 316
 exemplar method with, 184
 phenotypic plasticity, 374
 population studies on, 369
 Q-R relations in, 258–259
 reticulate evolution, 48, 352
 reviews of taxometrics in, 487
 size and shape in, 172
 taxometric studies on, 458, 466–479
Platypalpus, 462
 Platystemonoidea, 466
Poecilozonites, 465
 Poetry, 450
 Polemoniaceae, 467
 Political science, 443–444
 Pollen grains, 394
 Pollination mechanisms, 29, 419, 429
 Pollution, 438
 Polycytemia, 442
 Polyphenic methods, 91
 Polyphyly, polyphyletic groups, 46–50
 Polyploidy, polyploid series, 184, 371
 Polythetic groups and classifications
 (see also Monothetic groups),
 20–23, 201, 308
 fully polythetic, 21–22
 homology and, 85
 philosophy and, 21, 448
 Populations, 362–380
 human, 445
 local interbreeding, 364, 366
 taxometric studies on, 367–370,
 458–461, 465, 467–470
 Portunidea, 464
 Predictive value of classifications,
 25–27, 56–57, 64, 188–189, 431
 Pregroup-exgroup problem, 52, 52
 Primates, 159, 458–460
 Primitive character states, 37–39, 42,
 322, 333
 Primitive patristic similarity, 37–38, 38,
 40, 42
 Principal axes, 246, 248
 Principal axes matrix, 246
 Principal component analysis, 245–246,
 257, 269, 272, 395
 computer programs for, 486
 distortion of phenetics by, 209, 280
 Q-R relations in, 258
 recommendations on, 303
 Principal component matrix, 245
 Principal coordinate analysis, 248–249,
 252, 258, 286, 298, 303, 406
 Principal factor analysis, 246
Principles of Numerical Taxonomy
 (Sokal and Sneath, 1963), xi–xiv,
 14–15, 23, 28, 50, 73, 75, 86, 91, 96,
 98, 101, 106, 117, 124, 126–127, 129,
 130, 132–134, 146–147, 186, 196,
 201, 207, 298, 314, 322, 368, 373,
 381, 418, 419, 430, 451, 457, 481,
 485, 487, 539
 Probabilistic classifications
 cluster methods for, 207, 241–245
 significance of clusters in, 284–285
 Probabilistic similarity coefficients, 118,
 120, 134, 140–145, 245
 of Gambaryan, 135
 of Goodall, 140–141, 284, 396
 Hall's heterogeneity measure, 145
 of Hyvärinen, 145
 information statistical, 141–145
 of Joly, 145
 Rajski's coefficient and metric, 144
 Rogers and Tanimoto's distance, 145
 of Smirnov, 134–135, 437
 Probability of correct identification,
 384, 387, 391, 393–394, 396–400,
 398–399, 404, 408
 Probability of genetic identity, 187
 Procladograms, 208, 336–337, 338
 Profile, 193
Propionibacterium, 474–476
 Proportional link linkage, 226
 Protein sequences (see also Cytochrome
 c, Hemoglobin), 92, 300–301
 and cladistics, 320, 327, 343–344, 346,
 345, 351
 complexity in resemblance and, 177
 convergence in, 37
 evolution rates in, 314, 317–318
 homology in, 84, 86, 300–301
 invariant characters in, 105
 and matches asymptote, 107
 and polythetic groups, 21
 relation to serology, 93–94
 significance tests and, 164
 similarity measure for, 136
 taxometric studies on, 344, 345,
 457–459
 and taxonomic rank, 61, 296–297, 481
 taxonomic significance of, 66, 73, 92,
 300
 Protein taxonomy, 92
Protesilaus, 462
 Provinces, biogeographic, 438
 Pseudometric functions, 121, 131, 145
 Pseudomonadaceae, 472–473, 477, 479
 Pseudomonadales, 477–478
Pseudomonas, 472, 477–479
Pseudomonas aeruginosa, 476
Pseudomonas bathycetes, 479
Pseudomonas piscicida, 477
 Pseudoscanning experiment, 74, 87–88,
 88, 421, 424
Pseudoschwagerina, 465
 Psocoptera, 461, 464
Psorophora, 101, 269, 273, 274, 461
 Psychiatry, 441–442
 Psychology, 223, 250, 441–444
 Psychology of perception, 287, 297, 434,
 444
 Ptercephaliidae, ptercephaliids,
 359–360, 463
Puccinia, 472
 Pycnogonida, pycnogonids, 159, 184,
 461
 Pylonephritis, 441
q, number of taxa, 293, 382
q_a, number of taxa at branch point of a
 key, 392
q_a, *q_b*, *q_z*, number of taxa with given
 combinations of character states,
 390
q_b, number of taxa in a subgroup of a
 key, 392
q_T, *q_F*, *q_V*, number of taxa for which
 leads are true, false, or variable,
 392
q₁, *q₀*, number of taxa with 1 or 0
 states, 385
Q, a taxon, 382
Q techniques, 115–116
 in ecology, 436
 in medicine, 440
 relation to R techniques, 256,
 258–259, 447
 representation, 269, 272, 274–275,
 272–275
 in social sciences, 445
 Qualitative multistate characters, 115,
 133, 149
 Quantitative multistate characters, 115,
 133, 148
Quercus, 468
r, *r_{jk}*^{*}, product moment correlation
 coefficient, 137–140, 139
 character coding for, 140
 relation to distinctiveness, 175
 in medicine, 442
 negative values of, 138, 155
 in principal component analysis, 245
 recommendations on, 178
 as a shape measure, 171–174
 effects of standardization on, 138–
 139, 155–156
r, *r_J*, radius of cluster or taxon, 197, 213,
 395, 397
r, rank of a matrix, 245
r_c, *r_{coph}*, see *r_{CS}*
r_{C₁C₂}, correlation between phenograms,
 97, 280
r_{CS}, cophenetic correlation coefficient,
 97, 100–103, 252, 278–280, 279,
 281, 284, 304
r_i, range of character states, 350
r_{p(jk)}, coefficient of pattern similarity,
 124–125
r_{S₁S₂}, matrix correlation, 97, 100–102,
 280, 282
R, matrix of character correlations, 245
R, matrix in matching diagrams, 483
R, radius, 140
R_i, character relevance, 181
R_i, range of character, 136
R_i, rank figure of character usefulness
 in identification, 385
R_J, OTU relevance, 181
R_{jk}, OTU by OTU relevance, 181
R₁, *R₁₁*, coordinates in stereograms, 484
r, parametric correlation coefficient,
 117, 138
R techniques, 115–116
 in ecology, 269, 272, 436
 factor analysis using, 182, 248, 259
 in medicine, 440

- R techniques *continued*
 relation to Q techniques, 256, 258–259, 447
 in social sciences, 445
 Rabbit tick, 369, 378–379
 Radius of taxon or cluster, 197, 213, 395, 397
 Rajski's coherence coefficient, 144
 Rajski's metric, 144, 241
Rana, 56
 Range of character states
 intra-OTU variation and, 184
 scaling by, 153
 similarity coefficients dependent on, 126, 136
 Rank, taxonomic, 60–63, 290–297
 absolute criteria for, 61, 296
 of ancestral forms, 310
 categories of, 8, 294–297
 convergence and parallelism in relation to, 33
 and evolution rates, 316–317
 identification at high, 389
 logical formulation, 65
 measures of, 291–294
 and nomenclature, 294–296, 295, 410–412
 numerical taxonomy at different levels of, 424
 and ordination, 252
 phenetic basis of, 61, 290–291
 Rank difference, 292–293
 Rank of a matrix, 245
 Rank order
 in clustering, 219
 correlation coefficient, 139
 in nonmetric multidimensional scaling, 249
 in scaling characters, 154
 Rank order typal analysis, 223
 Rankit, 154
 Ranunculaceae, 469
 Rates of evolution, *see* Evolution rates
Rattus, 290
 Reallocation of OTU's in clustering, 204–205, 207, 210–211, 483, 486
 Recapitulation, law of, 43
 Recursive computation of a similarity matrix, 210–211
 Reduction of dimensionality, 189, 245–250
 Redundancy in characters, 103–104, 259, 394
 Reference number in nomenclature, 413
 Relational matching, 77
 Relationship, 3, 27–30
 chronistic, 30
 cladistic, *see* Cladistic relationship
 genetic, 320, 370–373
 and nomenclature, 410–411
 phenetic, *see* Phenetic relationship
 phylogenetic, *see* Phylogenetic relationship
 Relative resemblance linkage, 226
 Relevance, 181–182
 Repeatability, 11
 Reptiles, 459
 Resemblance (*see also* Similarity, Dissimilarity, Phenetic relationship)
 coefficients of, *see* Similarity coefficients
 estimation of, 5–6, 116–117
 Resemblance matrix, 6–7, 190–192, 260, 261, 298, 482
 Reticulate evolution, 48, 50, 59, 325, 352–356, 354–355, 444–445
 Reversals
 in character evolution, 322, 327, 333, 342–343, 343
 in clustering, 66, 205, 235, 237, 239, 279, 344
 Rhipidistia, 459
 Rhipiphorid beetles, 426
Rhizobium, 95, 467, 472–473, 477–478
Rhynchosia, 469
Rhytachne, 469
 Rice (*see also* *Oryza*), 250, 320, 370–371
 Robustness of numerical taxonomy (*see also* Stability), 81, 117–118, 146, 181
 Rocks, classification of, 446–447
 Rodents, 184, 458
 Rogers and Tanimoto's association coefficient, 132, 134, 211
 Rogers and Tanimoto's distance measure, 145
 Rogers and Tanimoto's clustering method, 207
 Rohlf's generalized distance, 212–213
 Root (graph theoretic), 255, 324, 352
 Rosaceae, 467
 Rotation
 of factor axes to simple structure, 247–248
 of stems in phenograms, 261, 264, 263
 Rotifers, 375
 Rubin's clustering method, 205, 210
Ruminococcus, 475
 Rye grass, 433
 s , standard deviation of a taxon, 292–293
 s_i , $s_{i, \text{within}}$, pooled within-cluster standard deviation of a character, 112, 405, 408
 $s_{i,j}$, standard deviation of character i in cluster J , 127, 186
 s_{ijk} , score in Gower's similarity coefficient, 135
 $s_{y,x}$, scatter in allometric plots, 158
 S , coefficient of Stewart, 186
 S , S_{jk} , general symbol for a similarity coefficient, 191
 S , measure of stress, 249
 S^* , linking level in clustering, 283–284
 S , matrix in matching diagrams, 483
 \mathcal{E} , \mathcal{E}_{jk} , coefficient of Zarapkin, 126, 170
 S_D , coefficient of Dice, 131
 S_G , Gower's similarity coefficient, 135–136
 as a Manhattan metric, 126
 for protein sequences, 300
 relevance and, 181
 S_H , coefficient of Hamann, 133
 $S(h, i)$, Rajski's coherence coefficient, 144
 S_i , S_{joint} , separation figure for diagnostic characters, 385, 390
 S_j , coefficient of Jaccard, 131, 136, 180
 S_{jk} , error-affected S value, 167
 S_p , pattern similarity, 177
 S_ϕ , phi coefficient, 133
 S_{RT} , coefficient of Rogers and Tanimoto, 132, 134, 211
 S_S , simple matching coefficient (*see* S_{SM}), 132
 S_{SM} , simple matching coefficient, 132–133
 effect of experimental error on, 167
 in identification, 394
 effect of NC entries on, 180
 with overlapping characters, 184
 vigor and pattern components of, 176–177
 S_y , Yule coefficient, 133, 177
 S_1 , S_2 , S_3 , levels in clustering, 226
 S_2 , variance-covariance matrix, 212
 σ_s^2 , σ_e^2 , error variance, 165, 168
 S matrix, *see* Resemblance matrix
Saccharomyces, 471
Sagina apetala, 467
 SAHN methods, 214–245
 comparisons between 220, 224–225, 227, 231, 234, 235, 240, 236–240
 distortions produced by, 247
 general considerations on, 214–216
 table of formulae and properties, 218–219
 Salicaceae, 466
 Salish Indians, 445
Salix, 102, 184, 466
Salmonella, 478
 Salps, 432
Salvia, 425, 430, 466
 Sampling errors (*see also* Errors)
 of characters, 108, 165–166
 of correlation coefficient, 139
 of OTU's, 167
 Sanghvi's chi-square measure, 186
Sarcina, 475
Sarcostemma, 101, 467
Satyrum, 470
Saxifraga, 467
 Saxifragaceae, 467–468
 Scaling of characters (*see also* Coding of characters, Transformation), 147, 152–157
 of diagrams, 160
 and evolution rates, 314
 in geology, 446–447
 recommendations on, 157
 to equalize size, 152–153, 157, 170
 to equalize variation, 153
 in relation to weights of characters, 110, 153
 Scanning
 automatic, 400, 452
 of images in relation to homology, 87–89, 88, 421
 pseudoscanning experiment, 74, 87–88, 88, 421, 424
Scellus, 461
Schistosoma haematobium, 465
 Scoring of characters, 114–115
 Scrophulariaceae, 468
 Seals, 33
Secale, 469–470
 Sediments and sedimentary rocks, 44*

- Self-comparisons, 186, 191–192
 Semantic molecules, 91
 Semaphore, 69
 Sematophyllaceae, 472
 Semimetric functions, 121, 131, 145
 Separation functions in identification, 385, 390, 392
 Sequential agglomerative hierarchic nonoverlapping clustering methods, *see* SAHN methods
 Sequential clustering methods, 208–209, 214–245
 Sequential identification methods, 386, 388–394
 Seriation, 250–251, 251, 446, 482
 Serology
 congruence with phenetics, 93, 301–302
 corroboration of classifications by, 297–299
 evolution rates and, 93, 318
 similarity coefficients for, 298
 taxometric studies with, 459–461, 471, 476, 480
 and taxonomy, 66, 93
Serratia, 477
Serratia marcescens, 477
 Serum proteins, 443
 Sexes
 congruence between, 97
 and exemplar method, 184
 Shape, *see* Size and shape
 Shape coefficients
 cosine, 139, 172–173, 173
 d_s as, 173
 of Penrose, 170–172, 171, 174–175
 r , as, 171–174
 effect of transformations on, 173–174
 Shell form, 160, 308
 Shepherd and Willmott's clustering method, 213, 226
 Shortest spanning tree, 159, 222, 255–256, 257, 326, 350, 359
 Sibling species, 62, 323, 423, 429
 Significance, statistical
 of clusters, 252, 284–287, 428
 of contour lines, 377
 of discriminant functions, 403–404
 of similarity coefficients, 118, 162–165, 428
Silene, 467
 Similarity (*see also* Dissimilarity, Distance, Resemblance)
 Sneath's name for coefficient of Jaccard, 131
 and homology, 79, 85–89
 geometric, 89
 homoplastic, 37, 38, 39–40
 overall, *see* Overall similarity
 patristic, *see* Patristic similarity
 use of term, 114
 Similarity among diversity, 353
 Similarity coefficients (*see also* Association coefficients, Correlation coefficients, Distance coefficients, Probabilistic similarity coefficients; *for individual coefficients, see entries at* Coefficient (of) . . .), 6, 116–121
 additivity of, 317
 for cladistics, 316–317, 323, 333, 343–344
 coding and scaling for, 147–153
 comparison of, 117–118, 146–147
 in ecology, 137, 437
 effect of errors on, 165–168
 for identification schemes, 394
 allowing intra-OTU variation, 185–187
 (J), (J, K), and (JK, L) measures, 214
 matrix of, 6–7, 119, 190–192, 260, 261, 298, 482
 missing data and, 180
 for mixed types of characters, 136, 157
 need for, 119
 parametric values of, 117–118
 phenetics affected by different, 31, 146–147, 169
 recommendations on, 147, 178
 invariance under rotation, 125
 invariance under scaling, 173–174
 statistical significance of, 118, 162–165, 428
 two-way scattergrams, 280, 281–282
 types of, 119–120
 Similarity matrix. *see* Resemblance matrix
 Simple matching coefficient. *see* S_{SM}
 Simplex structure, 250
 Simuliidae, 463
 Simultaneous clustering methods, 208–209
 Simultaneous identification methods, 386, 394–408
 Simultaneous test procedures, 378
Sinapis, 469
 Single linkage clustering, 213, 216–228, 220, 240, 256, 358
 Sirenians, 33
 Size, size factor, (*see also* Size and Shape. Size coefficients), 169–170
 of diagrams, 173
 in discriminant analysis, 406–407
 in medicine, 442
 in ordinations, 173, 252
 removing effect of, 153, 170, 178
 in soils, 439
 effect of standardization on, 156, 172
 taxonomic discrepancies commonly due to, 431
 Size and shape (*see also* Size, Size coefficients, Shape coefficients), 140, 169–174
 generalized distance and, 406
 geographical variation and, 379
 in geology, 446
 Size coefficients
 of Penrose, 170–171, 171, 175
 effect of transformations on, 173–174, 303
 vector, 172, 173
 Skulls, 83, 89, 163, 280, 407, 458–460
 Skyline plot, 264, 266
 Sliding matches, 84, 107, 136, 447
 Smirnov's similarity coefficient, 134–135, 437
Smittium, 471
 Snails, 86, 379
 Social anthropology, 443–445
 Social sciences, 443–446
 Soils, 437, 439–440
 Solanaceae, 466–468
Solanum, 371, 467–468
Sorghum, 470
 Space (phenetic or taxonomic hyper-space), *see also* Discrimination space, 6
 A- or attribute, 116, 122–123, 138, 139, 173, 175, 215, 395, 397, 414–415
 in ecology, 375
 Euclidean, 120, 122, 123, 132, 136, 209
 1- or individual, 116
 identification, 386, 395–396, 397, 405–408
 space conserving, distorting, dilating, contracting cluster methods, 215, 219, 222, 226, 303,
 Sparrows, 369, 378–379, 459
 Spearman's sums of variables method, 235
 Species
 concepts and definitions, 362–367
 and ecological diversity, 433
 level or rank, 290, 362, 424
 nomenclature, 415–416
 Specimens, selection of, 68–69, 182–183, 370
 Sponges, 465
 Standard deviation (*see also* Variance)
 of chi-square distribution, 197
 of distances from centroid, 197
 as criterion of cladograms, 344
 in discriminant analysis, 404–405
 as measure of taxonomic rank, 291–294
 Standard errors of similarity coefficients, 165–168
 Standardization of characters, 154–156
 in geology, 446
 in principal component analysis, 245
 recommendations on, 157, 178
 and significance tests, 138, 163
 effects on similarity coefficients and size and shape, 155–156, 172, 175
 with two-state characters, 156, 437
Staphylococcus, 475–476
 Steiner minimal tree, 326–327
Stellaria, 469
 Stereograms, 274, 276, 484
 Straggleness (*see also* Chaining), 198, 218, 220
 Stratified classifications, 206
 Stratigraphy, 136, 357–361, 447
 Strepsiptera, 426
Streptococcus, 472, 474–476
Streptococcus faecalis, 474–475
Streptomyces, 473–474
 Streptomycetes, 429
 Stress measures in classifications, 249, 278–283, 304
 Strongylidae, 465
Stylosanthes, 467
 Subspecies, 365–366, 371, 416
 Sums of squares criterion, 204–205
 Symmetry of resemblance matrices, 191, 250, 298
 Symplesiomorphy, *see* Primitive patristic similarity

- Synapomorphy, *see* Derived patristic similarity
- Synonyms, 413
- Syrphidae, syrphid flies, 183, 463
- Systematics, 2
- explanatory role in biology, 55–56
- future of, **451–453**
- history of, 19–20, 23–24
- t , number of OTU's, 6, 114
- t_j , t_k , t_l , number of OTU's in cluster or sample, 127, 197, 214
- $t_{j,1}$, constant in identification scheme, 396
- t^* , number of nodes in a tree, 327
- $t_{1,2}$, coefficient of Smirnov, 134–135
- t_j , OTU t of taxon J , 382
- T , evolutionary tree in numerical cladistics, 324
- T^2 , coefficient of Sanghvi, 186
- T^2 , Hotelling's ratio, 287, 404
- T , time, 313, 317
- T , trend similarity coefficient, 161
- T_j , typicality coefficient of Hyvärinen, 175
- θ , arc cos r , 140
- τ , Kendall's rank order correlation coefficient, 139
- Tachyelic evolution, 313
- Taximetrics, 4
- TAXOCRIT experiment, 434
- Taxometric map, 268
- Taxometrics, 4
- Taxometrics* (newsletter), 485–487
- Taxon, taxa, 4, 65, 421
- center of, 195–196, 396, 414
- envelope and volume models of, 395, 397, 408, 415
- high-ranking, 70, 481
- limits of, 61–62, 414
- relations to phenons, 294
- rankless, 290
- variability within, 70, **182–187**, 321, 385, 392
- Taxonomic distance, *see* d , d_{jk}
- Taxonomic process, 2, 434
- Taxonomic relationship, *see* Relationship
- Taxonomic structure, 6–8, 188–190
- representation of, **259–275**, 260–263, 265–268, 270–276
- significance of, 277, 284–285, 287
- Taxonomy (*see also* Classification, Systematics), 3
- desirable properties of, **63–67**
- empirical, 5, 9, 17–18, 19
- numerical, *see* Numerical taxonomy
- operational, 9, 17–18, 19
- phenetic, *see* Phenetics
- phylogenetic, 9–10, 53–55, 310, 419–421
- principles of, 5, 17–67
- purposes of, 24, 55, **63–67**, 188, **200–201**
- Taxospecies, 363
- Teeth, 460
- Teldenia, 464
- Termitodiscus, 462
- Termitopaedini, 462
- Thalia democratica*, 464
- Thallosys*, 290
- Thiobacillus*, 478
- Thylacine wolf, 33
- Thymus drucei*, 269
- Thyroid disease, 442
- Tiarella*, 468
- Ties in clustering, 215, 221–223
- Time
- for computation, 482–483
- in evolution, 29–30, 326
- and phenetic variation, **309–313**
- Time-trends, 288, 378, 446
- Tissue typing, 443
- Topological stress measures, 283
- Tornados, 448
- Training in taxonomy, 452–453
- Transformation
- arcsin, 166
- arccos, 166
- of character state values, 115, 152–154
- cosine, 186
- of correlations, 139–140, 230
- to discriminant space, 402, 406
- linear, 152
- logarithmic, 152–154, 314
- effect on size and shape, 173–174
- to stabilize variances, 166, 186
- z , 139, 166
- Transformation grids, 160–161, *161–163*
- Tree, graph theoretic, **198**, **254–256**
- in cladistic analysis, **324–332**
- directed, 255, 324
- length of, 210, 327, 335–336
- minimum length, 255, 321–323, 326–327, 341
- number of alternatives, 324–325, 341
- rooted, 324, 332
- shortest spanning, 159, 222, 255–256, 257, 326, 350, 359
- Steiner minimal, 326–327
- Wagner, 321, 324, 332, 341–342
- Tree-ring research, 448
- Trellis diagram, 260, 261
- Trematoda, 465
- Trend surface analysis
- in geography and ecology, 377–378, 437, 447
- in study of homology, 89
- residuals, 161, 174
- of transformation grids, 160–161
- Trichodorus*, 464
- Trichodorus christiei*, 464
- Trifolium*, 467–468
- Trifolium repens*, 269
- Trilobites, 359–360, 359–360, 463
- Trioza*, 462
- Triticum*, 469–470
- Tudora*, 379
- Tudora megacheilos*, 465
- Tunicata, 464
- Twin species, 430
- Twins, 370, 422
- Two-state characters (0, 1 characters), **115**, **148**
- atypicality coefficients from, 175–176
- cladistic compatibility between, 349–350
- by recoding of multistate, 148–151
- distortions of distances by, 372
- identification using, 383–386, 390, 396–397, 406
- intra-OTU variation and, 184
- standardization of, 156, 437
- symbolism for, 115, 129, 148
- 2×2 frequency table, 129–130, 143, 203, 349
- Type specimen, 196, 414
- Types
- nomenclatural, 12, 410–411, 414
- in psychology, 211, 223, 240–241
- statistical, 9, 13
- Typology, 9, 421
- u , number of mismatches, 130
- u , vector of an unknown to be identified, 382, 395–396, 397
- U , utility of a classification, 285
- U , U_{jk} , dissimilarity coefficient, 214, 248, 343
- U , dissimilarity matrix, 248
- U , matrix in matching diagrams, 483
- Ultrametric functions, **121**
- and dendrograms, 65–66, 279
- evolution rates and, 318
- and reticulate evolution, 353
- reversals in clustering and, 66, 230, 235
- Umbelliferae, umbellifers, 244, 467
- Uncertainty principle, 287
- Uninominal nomenclature, 411–412
- Unique character state, 333
- Uniquely derived characters, 349–351
- Uniqueness, 246
- Unit character consistency, 350
- Unit characters **72–75**
- from complex characters, 179, 427
- homology and, 85
- weight of, 109
- Unknown OTU for identification, **382**
- Unwarranted comparisons, **178–182**
- Unweighted centroid clustering, 218–219
- Unweighted clustering methods, 211–212, 228
- Unweighted pair-group arithmetic average clustering, *see* UPGMA
- Unweighted pair-group centroid clustering, *see* UPGMC
- UPGMA, unweighted pair-group arithmetic average clustering, 230–234, 231
- in cladistic analysis, 318–319
- compared with other methods, **286**
- and cophenetic correlation, 279
- and evolution rates, 318
- properties, 218–219, 240
- of protein sequences, 318
- UPGMC, unweighted pair-group centroid clustering, 218–219, **234–235**, 236–237, 240, 280
- Uta stansburiana*, 460
- Utility of a classification, 285
- v , eigenvector, 245
- v_1 , v_2 , environmental vectors, 375
- V , matrix in matching diagrams, 483
- V , principal axes matrix, 245
- V_x , mean number of species in quadrats containing x , 204

- Vaccinium*, 468
- Variable-group clustering methods, 216
- Variance (see also Generalized variance, Variance-covariance matrix, Standard deviation)
- of a cluster, 196
 - of d , 124
 - of d' , 168
 - of D^2 , 406
 - of diagram as size factor, 173
 - of principal axes, 246
 - of S'_{jk} , 167
 - of S_{SM} , 132–133, 165
 - of samples of OTU's, 127
 - stabilizing transformations, 166, 186
 - as weights in cladistics, 350
 - of z , 139
- Variance-covariance matrix (see also Generalized variance), 212, 246, 383, 401
- Variation within OTU's and taxa, 182–187, 321, 385, 392
- Varimax rotation, 486
- Vector angle as shape coefficient, 172, 173, 446
- Vector size, 172, 173
- Vegetation studies, 436–438, 440
- Veigaia*, 461
- Verbenaceae, 466
- Vertebrata, vertebrates
- evolution rates in, 316
 - homologies in, 80, 83
 - subspecies in, 365
 - taxometric studies of, 458–460
- Vertex, (graph theoretic), 253–255, 324
- Verticicladiella*, 471–472
- Verticillium*, 472
- Vibrio*, 476–477, 479
- Vibrio paraaerolyticus*, 478
- Vigor (in microbiology), 176–177, 399
- Viruses
- gene transfer by, 86
 - host specificity as a character, 95
 - information content of, 73
 - nomenclature, 411
 - phylogeny, 33, 54
 - taxometric studies of, 479–480
- Viscaceae, 467
- w , w_j , weight of character, 104, 112, 135
- w , vector of character weights, 383
- w_k , w_j , weight of characters in cladistics, 350
- w_{ijk} , weight of character in S_G , 135
- w_{ij} , w_{ijk} , weight of character in identification, 383, 395
- w_j , weight of OTU in clustering, 218, 229
- w_{jk} , weight for OTU's in measure of distortion, 281
- W , tree in numerical cladistics, 324
- W , within-groups variance-covariance matrix, 127, 401
- W_k , group element potential, 204
- Wagner network, 324, 327–332, 329, 332, 356
- Wagner trees, 321, 324, 332, 341–342
- Ward's clustering method, 204, 241, 283
- Weevils, 369, 375
- Weighted centroid clustering, 218–219
- Weighted clustering methods, 211–212, 228, 229, 341
- Weighted invariant step strategy, see WISS
- Weighted pair-group arithmetic average linkage clustering, see WPGMA
- Weighted pair-group centroid clustering, see WPGMC
- Weighting of characters, 109–113
- a priori and a posteriori, 5, 109, 111
 - of character complexes, 109
 - for cladistics, 111, 321, 323, 347–351
 - from different coding and scaling schemes, 110, 151, 153
 - in ecology, 437
 - equal, Adansonian practice, 5–6, 14, 23, 29, 109–110, 112–113, 423
 - from factor analysis, 99
 - for identification, 12, 109, 383–384, 391–392, 395, 400, 406
 - by intra-OTU variation, 185
 - in medicine, 441
 - for partial logical correlations, 104
 - by rarity, 111, 134–135, 141, 156
- Weighting of dimensions in clustering, 211–212
- Weighting of OTU's
- in clustering, 211–212, 228, 229, 244
 - in key-making, 392
 - in representing taxa, 183
- Weighting of serological information, 298
- Wheat, 469
- WISS, weighted invariant step strategy, 341
- Wood structure, 471
- Worthenia*, 465
- WPGMA, weighted pair-group arithmetic average linkage clustering, 218–219, 234, 234, 240
- WPGMC, weighted pair-group centroid clustering, 218–219, 235, 238–240
- Wroclaw diagram, 269
- Wroclaw taxonomy, 14
- \bar{x} , \bar{x}_j , centroid of taxon or cluster, 195, 293, 395, 397
- \bar{x} , centroid of all OTU's of one or all clusters, 174, 293
- $\|\bar{x}'_j\|$, atypicality measure, 174, 175
- $\|\bar{x}_j\|$, $\|\bar{x}_k\|$, vector size, 172, 173
- \bar{x}_j , \bar{x}_k , vector of means, 212
- X , standard measure in allometry, 158
- X , X_L , X_R , stereogram axis and coordinates, 484
- X' , transformed score, 115, 153, 174
- X , standardized $n \times t$ matrix, 245
- X , a taxon, 415
- X^2_{ij} , X^2 statistic from 2×2 tables, 203
- \bar{X}_j , \bar{X}_k , sample mean, 127, 174
- X_{ij} , score of OTU j on character i , 114
- X_{ijk} , value of i th character of j th OTU of taxon K , 382
- X_{in} , character state of OTU for identification, 382
- X_{max} , X_{min} , in range of character, 153
- X_I , X_{II} , X_{III} , coordinates in ordinations, 484
- X^2 -statistic, 203
- Xanthomonas*, 477–478
- Xiphinema*, 465
- Y , character value in allometry, 158
- Y , Y_L , Y_R , stereogram axis and coordinates, 484
- Y , a taxon, 415
- Yeasts, 86, 92, 471–472
- Yersinia*, 476, 479
- z , Fisher's transformation, 139, 166
- z , number of combinations of character states, 390
- z , z_{jk} , discriminant function, 400–401
- z_1 , z_2 , z_i , z_m , weights in discriminant function, 401–402, 404
- ζ , coefficient of distinctiveness, 174, 175
- 0, 1 characters, see Two-state characters
- Zinnia*, 371, 467