
Code Index

- algebraic manipulation
 - assignment and simplify (MAPLE), 526
 - expand and substitute (MAPLE), 523
- animation (MAPLE), 47
- applying a function to an array (mapping), 22
- calculating
 - a cumulative distribution, 61
 - a Jacobian, 134, 277
 - a matrix exponential, 311
 - combinations (MAPLE), 74
 - derivatives (MATLAB), 134
 - eigenvalues and eigenvectors, 56, 57, 134, 155, 312, 526
 - mean and median, 63, 64
 - permutations (MAPLE), 78
 - roots, 13, 345
 - the integer part of a number (MAPLE), 24
 - the number of terms in a sequence, nops() (MAPLE), 78
 - the power of a matrix, 456
 - variance and standard deviation, 64
- clearing
 - all variables with restart (MAPLE), 26
 - an individual variable (MAPLE), 21
- comparing a fit with the original data, 102
- computing a matrix
 - exponential, 57
 - power, 155
- creating
 - a phaseportrait plot, 44
 - a row of 1s (MATLAB), 23
 - an array, 21
 - sequences, 21
 - vectors and matrices, 34
- defining
 - column vectors (MATLAB), 21
 - row vectors (MATLAB), 21
 - variables from calculated results (MAPLE), 21
- direction field plot (MAPLE), 38
- Euler method for integrating a delay differential equation, 99, 128
- examining the type of an object, whattype() (MAPLE), 56
- extracting the result of a calculation for a later step (MAPLE), 101, 104
- formatted printing (MAPLE), 68
- graphing a slope to a curve, 275
- histogram plot, 185
- how to
 - end statements, 12
 - make comments, 12
- inverting a matrix, 311
- labeling plots (MATLAB), 21
- least squares, 21
 - fit, 23
 - exponential, 67
 - polynomial, 66
- limits at infinity, 16
- linear spline fit, 67
- log and log-log plots, 16

- making
 - a histogram plot, 60
 - a plotting sequence (MATLAB), 311
 - a “pulse” function, 315
- matrix–vector multiplication, 34
- metric conversion, 32
- multiple
 - graphs in a single plot, 14
 - statements per line, 64
- multiplying arrays, 20
- numerical
 - differentiation, 134
 - solution of a differential equation, 40, 130
- overlying plots, 14, 24, 125
- phaseportrait plot, 316
- piecing together differential equation
 - solutions, 318
- plotting
 - a function, 12
 - points, 21, 24, 102, 160
 - various components of a vector (MATLAB), 44
 - with color (MAPLE), 388
- programming
 - loops, 123, 160
 - subroutines or procedures, 411
- random number generation, 79
- resetting individual variables, 526
- root
 - finding, 452
 - solving
 - avoiding some solutions, 526
 - in rings (SINGULAR), 527
- setting
 - numerical precision, 155
 - plotting symbols, 21
 - titles, labels, and fonts in plots, 385
- solution of higher-order differential
 - equations (MATLAB), 46
- solving
 - a differential equation, 17
 - a system of differential equations, 43, 220, 392
 - with changing parameters, 387
 - an algebraic linear system, 51
 - multiple differential equations, 352
- specifying
 - numerical precision (MAPLE), 411
 - tickmarks and labeling (MAPLE), 268
- stitch together piecewise functions, 99
- stochastic simulation, 185
- summing an array, 20, 21
- symbolic differential equation solution
 - (MAPLE), 38
- symbolic differentiation (MAPLE), 526
- three-dimensional plot, 35
- transposing a matrix, 34
- units conversion, 15
- use of procedure, 52
- using
 - % to refer to previously calculated results (MAPLE), 21
 - rhs to extract the right-hand side of an expression (MAPLE), 17
 - unapply to create a function (MAPLE), 17

Index

- ab initio*, 464
- absorbed, 439
- accession number, 477
- acellular, 202
- acetylcholine, 210
 - esterase, 210
- acquired immunological tolerance, 334
- activation energy, 264
- active
 - site, 250
 - transport, 166
- adaptation, 143
- additive tree, 500
- affine functions, 519
- African trypanosomiasis*, 373
- age density, 150
- alignment
 - global, 485
 - local, 485
- all-or-none, 209
- Allee effect, 116
- alleles, 430
- allopatric speciation, 507
- Altschul
 - Karlin–Altschul equation, 492
 - parameters, 491
 - Stephen, 491
- alveoli, 291
- amebiasis, 372
- amebic dysentery, 372
- amino
 - acids, 305
 - group, 246
- ammonia, 305
- amnion, 288
- amniotic fluid, 287
- amoeboids, 372
- anaphase, 400, 422
 - promoting complex (APC), 400
- Anderson, Terry, 125
- anemia, 299
- angiogenesis, 402
- Anopheles*, 374
- antibodies, 252, 331
- anticodon, 253
- antigen, 252, 329
 - presenting cells, 331
- anus, 294
- aorta, 297
- apical complex, 374
- apomorphy, 503
- apoptosis, 145, 401, 404
- Arabidopsis*, 466, 467
 - thaliana*, 465
- arbitrary constant, 37
- arteminisin, 382
- asexual reproduction, 239
- asymptotic limit, 43
- ataxia telangiectasia mutated, 401
- autoimmune reactions, 334
- autonomous, 44
- auxiliary equation, 50
- average, 59
- axoplasm, 214
- Babesia microti*, 374

- babesiosis, 374
- background probabilities, 492
- bacterial artificial chromosome (BAC), 462, 466
- bacteriophage, 325
- balantidiosis, 373
- Balantidium coli*, 372
- BankIt, 477
- basin of attraction, 45
- B-cell, 329
- Bcl-2, 404
- benign, 402
- bilayer, 165
- binary, 500
- binomial, 171
- biocides, 116
- biological compartment, 284
- biotic potential, 94
- bit score, 493
- BLAST, 478, 489
- blastocyst, 287
- BLOSUM62, 489
- body-mass index, 31
- Bombyx mori*, 251
- bottleneck effect, 439
- boundary
 - conditions, 180
 - points, 520
- branches, 499
- Brown, Robert, 169
- Brownian motion, 169
- budding off, 327
- caecum, 372
- Caenorhabditis elegans*, 465
- Cantor
 - Charles, 508
 - Jukes–Cantor matrix, 510
- capillaries, 294
- capsid, 252, 324
- carbohydrate, 237
- carboxyl, 246
- carcinogenesis, 399
- carcinoma, 402
 - in situ, 402
- cardinality, 70
- carrier, 406
- carrying capacity, 110, 119
- cdf, 59
- cDNA, 470
- cell
 - cycle, 400
 - clock, 400
 - lines, 328
 - mediated, 331
- cellulose, 237, 294
- central
 - dogma of genetics, 239
 - limit theorem, 64, 65
 - nervous system, 203
- centromere, 422
- change of basis matrix, 53
- chaos, 52
- characters, 498
- chemically gated channels, 207
- chemoautotrophic, 87
- cherry, 532
- chloroplasts, 89
- chloroquine, 382
- choose, 74
- chromatids, 422
- chromosome, 420
 - sex, 438
- cilia, 202, 372
- ciliates, 202, 372
- Ciliophora*, 372
- Ciona intestinalis*, 466
- circulation
 - fetal, 303
 - lymphatic, 302
 - pulmonary, 300
 - systemic, 301
- circulatory system
 - closed, 297
 - open, 296
- cladistics, 498
- cladists, 499
- cladograms, 499
- cleavage divisions, 285
- climax community, 107, 118
- clonal
 - deletion, 334
 - selection, 335
- closed, 516
 - circulatory system, 297
- coding strand, 258
- codominance, 438
- codon, 257

- stop, 259
- termination, 259
- translation, 258
- coefficient, 11
- coelom, 288
- cohort, 147, 362
- colon, 294
- combinations, 74
- commensalism, 116
- common source, 381
- Commoner, Barry, 108
- community, 117
- commutative, 516
- compartment, 55
- competition
 - interspecific, 114
 - intraspecific, 115
 - model, 135
- complement, 331
- complementary, 241
 - DNA (cDNA), 470
- computational chemistry, 464
- concentration, 204
 - of oxygen in water, 176
- condensation, 237
- conditional probabilities, 443
- conjugation, 372
- connected, 499
- conservation of mass, 266
- constant, 11
 - of proportionality, 11
- contigs, 466
- continuity equation, 177
- contractile vacuoles, 372
- convergence, 504
- convergent evolution, 504
- convolution, 361
- covalent bond, 232
- critical points, 44, 525
- crossing over, 435, 465
- cumulative distribution function, 59
- cyclin, 400
 - dependent kinases (CDKs), 400
- cystic fibrosis (CF), 469
- cytokinesis, 422
- cytotoxic T-cell, 329
- D-2, 3-biphosphoglycerate (BPG), 188
- Dayhoff, Margaret, 471
- de novo*, 465
- death rate, 151
- definitive host, 373
- degree, 11, 499, 515
- delay, 98
 - differential equation, 98
- deletion error, 259
- delta F508, 469
- denatured, 242
- density
 - dependent, 110
 - independent, 109
- dentition, 292
- deoxyribonucleic acid (DNA), 240
 - complementary (cDNA), 470
- depolarization, 216
- depolarized, 207
- development, 425
- diabetes mellitus, 251, 306
- diaphragm, 291
- differential equation, 37
 - delay, 98
 - logistic, 119
- differentiation, 285, 425
- diffusion
 - coefficient, 174
 - equation, 177
- diffusivity, 174
- dihybrid cross, 432
- diploid, 426
- dipolar, 233
- directed, 500
- direction field, 38
- disease, 114
- disjoint, 70
- disposable soma model, 144
- dissimilarity map, 531, 532
- distribution, 58
- diversity threshold, 352
- divisions, 86
- DNA Data Bank of Japan (DDBJ), 477
- dock, 464
- domain
 - of definition, 37
 - space, 519
- dominant, 430
- double reciprocal plot, 29, 276
- doubling time, 97
- DOXP reductoisomerase, 470

- doxycycline, 382
- dropoff value, 490
- Drosophila*, 441
 - melanogaster*, 465
- ductus arteriosus, 303
- Duffy, 377
- dynamic programming, 485
- dysplasia, 402

- Eadie–Hofstee plot, 276
- early trophozoite, 377
- ecological niche, 114
- ecosystem, 108
- ectoderm, 287
- ectoparasite, 372
- edges, 443, 499
- effective lengths, 492
- eigenvalues, 53, 183
- eigenvector, 53
- Einstein, Albert, 169
- electrical charge, 204
- electrochemical equilibrium, 204
- electron sharing, 231
- Ellis–van Creveld syndrome, 440
- endocrine glands, 251
- endoderm, 287
- endoparasite, 372
- endoplasmic reticulum, 89
- energy landscape, 463
- ensemble average, 169
- Entamoeba histolytica*, 372
- Entrez, 477
- entropy, 231, 259
- envelopes, 324
- environmental resistance, 95, 107, 110
- enzymes, 247, 294
- epidemiology, 380
- epitopes, 331
- equally likely, 71
- equilibrium
 - points, 44
 - state, 248, 261
- erythrocytes, 187, 252, 298
- erythrocytic schizogonic phase, 377
- Escherichia coli*, 466, 467
- esophagus, 293
- eukaryotes, 89
- Euler’s method, 39

- European Molecular Biology Laboratory (EMBL), 477
- event, 70
 - tree, 443
- exflagellation, 377
- exoerythrocytic schizont, 377
- exons, 258, 476
- expect value, 480
- expected, 71
- exponential, 13
 - growth phase, 98
 - model, 28
- exponentially, 97
- exposure, 388
- expressed sequence tag (EST), 468, 477
- extrinsic, 501

- facilitated transport, 166
- factorial, 74
- faculative, 371
- family, 86
- FASTA
 - file, 480
 - format, 480
- fat, 238
- fatty acids, 237
- fecal matter, 294
- fetal circulation, 303
- fibrin, 299
- Fick’s
 - first law, 176
 - second law, 177
- filial, 432
- first
 - gap phase, 400, 420
 - order, 37
- fitness, 88
- flagellates, 373
- flat file, 483
- flux, 176
- follicle stimulating hormone, 202
- founders effect, 439
- Fourier
 - analysis, 528
 - coordinates, 529
 - series, 183
 - transform, 529
 - transformation, 528
- free

- energy, 261
- oxygen, 189
- frequency, 212
- Fugu*, 466
- functional unit of heredity, 420
- fusion, 326
- G_1 , 400, 420
- G_2 , 420
- gametes, 426
- gametogenesis, 428
- gap phase
 - first, 400, 420
 - second, 400, 420
- gastrulation, 287
- Gause's law, 114
- Gaussian, 65
- geminin, 401
- GenBank, 477
- gene
 - locus, 420
 - therapy, 469
- generated by $\mathcal{F}$, 517
- genetic
 - code, 258
 - drift, 438
- genome, 461
 - survey sequence (GSS), 477
- genus, 86
- germ layers, 287
- germinal, 406
 - cells, 423, 426
- Gershgorin's circle theorem, 55
- Giardia lamblia*, 373
- giardiasis, 373
- gills, 291
- global, 45
 - alignment, 485
- globular proteins, 251
- glucose, 237, 306
- glycerol, 238
- glycogen, 237
- glycoproteins, 325
- granulocytes, 328
- growth factors, 400
- Haemophilus influenzae*, 467
- half-life, 97
- haploid, 426
- Hardin, Garrett, 116
- Hardy–Weinberg principle, 446
- Heaviside, 363
- helper T-cell, 329
- hemoglobin, 251, 298
- Hennig, William, 501
- hepatocyte (liver cell), 377
- Hessian, 526
- heterozygous, 432
- hidden Markov model, 521
- high
 - scoring segment pair (HSP), 490
 - throughput genome sequence (HTGS), 477
- histogram, 58
- hit, 490
- Hodgkin, Alan, 214
- homeostatic function, 306
- homologous pairs, 423
- homology, 466
- homozygous, 430
- hormones, 202, 251, 296
- host, 371
 - definitive, 373
 - intermediate, 373
 - reservoir, 373
- Human Genome Project (HGP), 461
- humoral, 331
- Huxley, Andrew, 214
- hydrocarbon, 165, 236
- hydrogen bonds, 233
- hydrolysis, 237
- hydrophilic, 164
- hydrophobic, 164
- hydroxyapatite, 304
- hyperplasia, 402
- hyperpolarized, 207
- hypersurface, 519
- hypnozoite, 377
- ideal, 516
- image, 528
- immunoglobulins, 252
- immunological specificity, 331
- implantation, 287
- implicit, 131
- in utero*, 334
- inactive, 329
- incident, 499

- incubation period, 359
- independent, 73
 - assortment, 432
- infected, 335
- infinitesimal generator, 509
- inhibitory, 212
 - pathway, 400
- initial
 - conditions, 180
 - value problem, 37
- insertion error, 259
- instructive mechanism, 335
- insulin, 251, 306
- intercept, 11
- intercostal, 291
- interior nodes, 499
- intermediate host, 373
- International Nucleotide Sequence Database
 - Collaboration (INSDC), 477
- interphase, 400, 420
- interspecific competition, 114
- interstitial fluid, 301
- intraspecific competition, 115
- intrinsic, 501
- introns, 258, 476
- invasion, 402
- isoclines, 224
- IUB/IUPAC nucleic acid codes, 481, 482
- Ixodes dammini*, 374

- Jacobian, 391
- Jordan canonical form, 54
- Jukes
 - Cantor matrix, 510
 - Thomas, 508

- K -strategists, 108, 110
- Karlin
 - Altschul
 - equation, 492
 - parameters, 491
 - Samuel, 491
- karyotype, 423
- Kelvin, 11
- keratin, 251
- Kimura-80 matrix, 510
- kingdoms, 86
- Kirkwood, Thomas, 144

- large intestine, 294
- late trophozoite, 377
- latent period, 209
- latently, 347
- law of mass action, 266
- leading term, 517
- leaf, 499
- leakage currents, 216
- Leishmania*
 - braziliensis*, 374
 - donovani*, 374
 - tropica*, 374
- leishmaniasis, 373, 374
- Leslie matrix, 154
- leukemia, 402
- leukocytes, 299
- lexicographic monomial order, 517
- likelihood
 - function, 513
 - maximum, 512
 - variety, 525
- limit cycle, 316
- linear, 40
 - spline, 59
- linearizing the system, 132
- linearly related, 11
- Lineweaver–Burk equation, 29, 276
- linked, 435
- lipid, 238
- Lipman, David, 480
- ln, 13
- local alignment, 485
- log, 13
 - odds matrix, 475
- logistic
 - curve, 110
 - (differential) equation, 119
 - recurrence relation, 52
- Lotka, Alfred, 129
- lungs, 291
- lymph nodes, 303
- lymphatic
 - circulation, 302
 - fluid, 303
- lymphocytes, 252, 328, 329
- lymphoma, 402
- lysis, 327
- lysogenic, 327
- lytic, 327

- m*-dimensional simplex, 518
- M-phase promoting factor, 400
- macrogametes, 377
- macrogametocytes, 377
- macronucleus, 372
- macroparasites, 372
- macrophages, 328, 331
- malaria, 374
- malarone, 382
- malignant, 402
- Malthus, Thomas, 95
- map-based sequencing, 462
- Markovian, 471
- marrow, 304, 328
- mass action principle, 129
- mast years, 112
- mathematical ring, 515
- MAVID, 531
- maximum likelihood estimation, 512
- mean, 59, 65
 - square, 172
- median, 62
- mefloquine, 382
- meiosis, 426
- Mendel, Gregor, 430
- Mendelian ratios, 432
- merozoites, 377
- mesoderm, 287
- messenger RNA (mRNA), 245
- metal chelates, 306
- metaphase, 422
- metastasis, 402
- Methanococcus jannaschii*, 467
- metric, 532
- Michaelis–Menten
 - constant, 274
 - equation, 275
- microarray, 470
- microgametes, 377
- microgametocytes, 377
- micronucleus, 372
- microparasites, 372
- microvilli, 294
- mitochondria, 89
- mitosis, 92, 400
- mitotic arrest deficient, 402
- model, 28
- molecular
 - clock, 508
 - mimicry, 379
- monogenic diseases, 468
- monohybrid cross, 432
- monomial, 516
- monophyletic, 499
- mortality, 151
- morula, 287
- mutations, 259
- mutualism, 116
- myc*, 403
- National Center for Biotechnology Information (NCBI), 477
- Needleman
 - Saul, 485
 - Wunsch algorithm, 485
- neighbor, 489
 - joining algorithm, 533
- neoplasm, 402
- Nernst equation, 215
- nerve gases, 210
- neurons, 203
- neurotransmitter chemical, 210
- neutrally stable, 133
- NF-1, 403
- nodes, 212, 499
 - interior, 499
 - leaf, 499
- noise, 9
- nonpolar, 164
- normal, 65
- nucleotides, 239, 240
- obligate, 371
- odds ratio, 474
- oncogene, 402
- ontogeny, 502
- oocyst, 375, 378
- oogenesis, 428
- ookinete, 378
- open
 - circulatory system, 296
 - compartment, 308
- organogenetic, 334
- orthologs, 466, 494
- osmosis, 166
- osteoblasts, 304
- osteoclasts, 305
- outgroup, 504

- oxygen
 - affinity, 187
 - consumption, 177
 - dissociation curve, 187
- p53, 401, 403
- PAM1 matrix, 472
- PAM250 scoring matrix, 475, 489
- paralogs, 466
- parameters, 11
- parasite, 371
 - ecto-, 372
 - endo-, 372
 - macro-, 372
 - micro-, 372
- parasitism, 113, 371
- parenchymal cell, 377
- partial
 - derivative, 19
 - fraction decomposition, 120
 - pressure, 187
- partition coefficient, 184
- passive, 166
- path, 499
- Pauling, Linus, 508
- Pearson, William, 480
- penicillamine, 307
- peptide bond, 246
- per capita growth rate, 94
- percutaneous, 295
- peristalsis, 294
- permeases, 163, 166, 251
- permutations, 74
- phagocytosis, 168, 372
- phase
 - plane, 42, 131, 224
 - portrait, 42, 131
- phenotype, 432
- photosynthesis, 261
- phyla, 86
- phylogenetic, 498
 - invariants, 528
- phylogenetic footprints, 467
- pinocytosis, 168
- placenta, 187, 288
- plasma, 298
 - cells, 331
- Plasmodium*, 374
 - falciparum*, 374
 - malariae*, 374
 - ovale*, 374
 - vivax*, 374
- platelet, 299
 - derived growth factor receptor alpha (PDGFR α), 470
- plesiomorphy, 503
- Pneumocystis carinii*, 342, 374, 375
 - pneumonia (PCP), 374
- point accepted mutation, 472
 - PAM1, 472
 - PAM250, 475, 489
- Poiseuille's equation, 180
- Poisson
 - distribution, 452, 491
 - process, 510
- polar, 164
 - bodies, 428
- polarity, 502
- polygonal graph, 59
- polymerase chain reaction, 461
- polypeptide, 246
- polyunsaturated, 237
- population, 441
- postsynaptic
 - membrane, 210
 - neuron, 210
- potential difference, 203
- power, 11
- predation, 112
- predator
 - pit, 124
 - prey
 - model with child care, 136
 - three-species problem, 135
- presynaptic
 - membrane, 210
 - neuron, 210
- primary structure, 463
- primitive streak, 287
- probability
 - density function, 77
 - generating function, 408, 449
- Proguanil, 382
- prokaryotes, 89
- proliferation rate, 344
- promoter, 467
- prophase, 422
- protein

- fibrous, 251
- folding, 463
- globular, 251
- transport, 163, 166, 251
- proteomics, 463
- protozoans, 202
- provirus, 327
- pseudocysts, 375
- pseudopod, 168, 372
- pulmonary circulation, 300
- pulse, 314
- Punnett square, 432
- query, 478
- r*-strategists, 108, 109
- radical, 232
- random walk, 439
- range, 519
 - space, 519
- Rankine, 11
- ras*, 403
- rate matrix, 509
- rational, 515
- reaction, 248
- recapitulation, 502
- recessive, 430
- recombinant, 435
- recovery rate, 384
- recurrence relations, 48
- relative entropy, 491
- repolarization, 216
- reproduction
 - asexual, 239
 - sexual, 240
- reservoir host, 373
- residue, 246
- resistance, 180
- respiration, 237, 262
- resting potential, 206
- reverse
 - transcriptase, 339
 - transcription, 339
- ribonucleic acid (RNA), 240
 - messenger (mRNA), 245
 - ribosomal (rRNA), 245
 - transfer (tRNA), 245
- ribosomal RNA (rRNA), 245
- ribosomes, 89, 253
- right-hand side, 40
- root
 - mean square (RMS), 172
 - node, 443, 500
- Runge–Kutta methods, 39
- S-phase promoting factor (SPF), 400
- Saccharomyces cerevisiae*, 465
- saltationism, 506
- saltatory conduction, 213
- sample space, 58
- sampling error, 439
- sandfly, 374
- Sanger, Frederick, 462
- Sarcodina*, 372
- sarcoma, 402
- saturated, 272
- Schwann cells, 212
- Scientific American*, 26, 340, 341
- score, 492
- scoring matrix, 475
 - PAM250, 475, 489
- second
 - gap phase, 400, 420
 - law of thermodynamics, 231, 260
- secondary
 - structure, 463
 - succession, 118
- seeds, 490
- semigroup, 509
- semilog plot, 14
- senescence, 141, 404
- separatrix, 226
- sequence tagged site (STS), 477
- Sequin, 477
- sex chromosomes, 438
- sexual reproduction, 240
- Seymouria*, 505
- sickle-cell
 - anemia, 259
 - trait, 378
- signum, 363
- SINGULAR, 526
- size, 499
- skeleton, 304
- slope, 11
- small
 - intestine, 294
 - trees website, 528

Smith

- Temple, 487
- Waterman algorithm, 487
- sodium/potassium pumps, 206
- solution, 37
- somatic, 406, 423
- Southern, H. N., 111
- space clamp, 219
- spatial summation, 212
- species, 86
- spermatogenesis, 428
- spin pairing, 232
- sporoblasts, 378
- sporozoans, 374
- sporozoite, 377
- standard deviation, 63, 65
- starch, 237
- stationary points, 44, 119
- steady state, 183
- stem cells, 304, 328
- stimulatory pathway, 400
- Stirling's formula, 173
- stomach, 293
- stop codons, 259
- strategists
 - K*-, 108, 110
 - r*-, 108, 109
- stratum corneum, 295
- subject, 478
- substitution matrix, 509
- substrate, 250
- subtree, 499
- succession, 118
- sugar, 237
- summation, 212
 - spatial, 212
 - temporal, 212
- supply rate, 343
- survival rates, 152
- survivorship curve, 109
- symbiotic, 116
- synapomorphy, 500
- synapse, 210
- synapsis, 426
- syncytia, 340
- synteny, 465
- synthesis phase, 400
- systemic circulation, 301
- target
 - organs, 202
 - tissues, 251
- TATA-box, 467
- taxa, 499
- T-cell, 329
 - cytotoxic, 329
 - helper, 329
 - inactive, 329
- telomeres, 404
- telophase, 422
- template, 244
- temporal summation, 212
- tension, 195
- termination codons, 259
- tertiary, 463
- test-cross, 435
- testicular feminization, 203
- testosterone, 203
- tetrads, 426
- tetrodotoxin, 231
- three-species predator–prey problem, 135
- threshold, 489
 - diversity, 352
- tongue, 293
- topological closure, 520
- Toxoplasma gondii*, 375
- toxoplasmosis, 374, 375
- trace, 511
- traceback, 487
- trachea, 293
- tracheal tubes, 291
- trajectory, 224
- transcription, 253
 - factors, 467
- transfer RNA (tRNA), 245
- transformational, 506
- transforming growth factor beta, 403
- transition state, 264
- translational term, 11
- transport proteins, 163, 166, 251
- tree, 499
 - additive, 500
 - metric, 500, 532
 - sub-, 499
- triangle inequality, 532
- Trichomonas vaginalis*, 373
- trichomoniasis, 373
- triglyceride, 238

- trophozoite, 372
 - early, 377
 - late, 377
- true breeding, 430
- Trypanosoma brucei*
 - gambiense*, 373
 - rhodesiense*, 373
- tsetse fly, 374
- tumor, 402
 - benign, 402
 - malignant, 402
 - suppressor genes (TSG), 403
- 2-cycle, 52
- ubiquitin, 401
- umbilical cord, 288
- uniform, 77
- uninfected, 340
- universal
 - Boltzmann's constant, 169
 - set, 501
- universe, 70
- unlinked, 432
- unsaturated, 237
- urine, 306
- uterus, 287
- valence, 232
- variables, 11
- variance, 63
- variety, 518, 519
- vector, 373, 466
- velocity, 274
- ventricles, 300
- Verhulst, Pierre, 119
- vertices, 499
- villi, 294
- voltage
 - clamp, 216
 - gated channels, 207
- Volterra, Vito, 129
- von Baer, Karl, 502
- Von Foerster equation, 159
- Waterman
 - Michael, 487
 - Smith–Waterman algorithm, 487
- wave equation, 223
- whole genome shotgun (WGS), 462
- wobble hypothesis, 258
- Woese, Carl, 498
- words, 489
- Wunsch
 - Christian, 485
 - Needleman–Wunsch algorithm, 485
- X-ray crystallography, 463
- Young's modulus, 11
- Zoomastigina*, 373
- Zuckerkindl, Emile, 508
- zygote, 285, 428