

Subject Index

Particular organisms and characters are listed in the Organism and Trait index

- Adaptationist program, 4
Additive effect, 72-76, 85
 environment dependence, 683-685
Advanced intercross lines, 436
Affected pedigree-member test, 532-533
Affected sib-pair test, 525-529
AIC. *See* Akaike's information content
AII. *See* Advanced intercross line
Akaike's information content, 363
Allele, 51
 additive effect, 72-76, 79, 85
 average excess, 71-75, 79
 average effect of substitution, 66-68
 frequency, 52-53
 null, 289
Allelic effects
 distribution of, 236, 333-337
Allometry, 305-307, 653-655
Analysis of covariance, 633-636
Analysis of variance, 553
 factorial, 597
 mean squares, 556-558
 method of moments, 558
 nested, 571-579
 one-way, 554-570, 582-587
 power, 880-883, 885-889
 Satterthwaite's correction, 575-576
 sums of squares, 556-558, 846-848
 two-way, 598-610, 666-669, 672-678, 698-700
 unbalanced designs, 627-628
Aneuploidy, 289
Animal model, 755-758
ANOVA. *See* Analysis of variance
Antagonistic pleiotropy, 655-656
APM. *See* Affected pedigree-member
Ascertainment bias, 374
Associative overdominance, 288, 604-605
Associative underdominance, 288
Assortative mating, 153-161
 correlation between mates, 154
 effects on genetic covariance, 154-161
 effects on genetic variance, 154-157
 parent-offspring regression, 547-548
Asymmetry, 112
 antisymmetry, 112
 directional, 112
 fluctuating, 112-116
Atavisms, 10-11
Autosome, 52
Average effect of allelic substitution, 66-68
Average excess, 71-75, 79
Backcross design, 432
Balancer chromosomes, 104, 380
Bartlett's test, 356
Bateman-Mukai technique, 341
Bayes' theorem, 375, 864
Best linear unbiased estimation, 749
Best linear unbiased prediction, 745-778
Biometrical school, 7
Blending inheritance, 8-10
BLUE. *See* Best linear unbiased estimation
BLUP. *See* Best linear unbiased prediction
Bonferroni correction, 441
Bootstrap, 449, 570
Box-Cox transformation, 295
Breeders' equation, 47, 50, 175
Breeding value, 72-74, 78-79
 animal model, 755-758
 best linear unbiased prediction, 745-778
 dominance values, 767-769
Breeding value (*continued*),
 estimation, 745-778
 gametic mode, 1 758-759
 general mixed model, 746-755
 maternal effects, 773-774
 multiple traits, 774-778
 mutation, 766-767
 reduced animal model, 759-762
 repeated records, 769-772
 sire model, 758-759
 standard errors, 754
BSA. *See* Bulked segregant analysis
Bulked segregant analysis, 402-404
 χ^2 distribution, 878-879
Canalization, 309-314
 zone of, 310
Candidate locus, 327-328, 379, 418-425
 estimation of effects, 422-424
 Templeton and Sing's method, 424-425
 transmission/disequilibrium test, 419-422
Canonical transformation, 778
Castle-Wright estimator, 233-239
cDNA, 390-391
Central limit theorem, 27
Chebyshev's theorem, 813
Chromosomal assays, 380-381, 382
Chromosome length, 211
Cladogram, 424-425
Clones, 108
 broad-sense heritability, 594-595
 threshold characters, 735
 variance component analysis, 592-595
Cloning, 425-429
cM (centiMorgan). *See* Morgan
Coadapted gene complex, 223-226
Cockerham-Weir model, 605-610
Coefficient of coancestry, 135

- Coefficient of consanguinity, 135
 Coefficient of fraternity, 140
 Coefficient of kinship, 135
 Coefficient of variation, 23, 294
 fitness, 176
 sampling variance of, 819-821
 scale transformation, 294-295, 303-305
 Collateral relatives, 145
 Comparative mapping
 of QTLs, 428-429
 Comstock-Robinson model, 598-603
 Complex segregation analysis, 364-375
 common-family effects, 370-371
 hypothesis testing, 369-370
 likelihood functions, 366-375
 mixed models, 371
 polygenic background, 371-373
 regressive models, 373
 single major gene, 366-370
 transmission probabilities, 366-369
 Compensatory growth, 700-703
 Composite effects, 206-226
 estimation, 213-226
 Composite interval mapping, 433, 458, 463-469
 Conditional expectation, 36
 Confidence interval, 32, 812-813
 Consistent system of equations, 836-839
 Consistency, 836-839
 Contrasts, 838
 Correlation, 43-45
 intraclass, 540, 559, 573
 sampling variance of
 correlation coefficient, 819
 Cov. *See* Covariance
 Covariance, 35-38, 45
 between relatives. *See* Resemblance between relatives
 matrix, 179, 774-778
 of complex variables, 813
 of mean and moments, 815-816
 of variances and covariances, 816
 Crittenden-Falconer technique, 731-732
 Cross-classified designs, 597-628
 advantages over nested sib design, 627
 Cross-classified designs
 (*continued*),
 average degree of dominance, 603-605, 619-627
 Cockerham-Weir model, 605-610
 Comstock-Robinson model, 598-603
 diallels, 610-627
 general combining ability, 611-618
 Hayman-Jinks analysis, 619-627
 North Carolina Design II, 598-610
 North Carolina Design III, 624-626
 special combining ability, 611-618
 triple test cross, 626-627
 Cross-fostering experiments, 696-703
 crossing over, 58, 94-95, 325-328
 suppression, 395, 411-412
 Cytoplasmic transmission, 693-695
 D-test. *See* D'Agostino normality test
 D'Agostino normality test, 298
 Delta method, 807-813
 Dependent variable, 39
 Developmental homeostasis, 116-120, 309-313
 Lerner's hypothesis, 116-120
 Developmental map, 309-314
 DH. *See* Doubled haploids
 DHL (Doubled haploid line).
 See Doubled haploids
 Diallels, 597, 610-627
 complete, 618
 partial, 618
 Dichotomous characters, 521
 affected pedigree member tests, 532-533
 affected sib-pair tests, 525-529
 epistasis, 524-525
 exclusion mapping, 530-532
 genomic scanning, 529-530
 information content mapping, 530-532
 James' identity, 523-524
 mapping, 521-533
 recurrence risk, 523-524
 relative risk, 523-524
 Also see threshold characters
 Digenic descent coefficients, 146
 Diploid, 51
 Directional selection differential, 31, 45-46
 Disease susceptibility genes, 414, 522
 Distribution of effects, 385-386, 444
 Dizygotic twins, 581
 Dobzhansky-Muller model of speciation, 387-388
 Dominance, 62
 associative overdominance, 288-291
 average degree of, 283-284, 603-605, 619-627
 breeding values, 767-769
 chromosomal, 381-382
 directional, 257
 effect, 85
 fitness, 381-382
 inference with molecular markers, 287-288, 290-291
 mechanism of, 63-65
 of QTLs, 479, 484
 relationship matrix, 768
 scale transformation, 308
 variance, 570-579, 600-619, 624-625
 Double reduction, 58
 Doubled haploids, 242-243, 401
 DS genes. *See* Disease susceptibility genes
 DZ. *See* Dizygotic twins
 Ecovalence, 681
 Effective number of factors, 231-249
 Castle-Wright estimator, 233-239
 effect of linkage, 233-238
 effect of nonadditive effects, 237
 genotype assay technique, 246-249
 haploid analysis, 241-243
 inbred-backcross technique, 244-246
 leading factor, 238-241
 Wehrhahn-Allard estimator, 244-246, 406
 Zeng's estimator, 236-238
 EM. *See* Expectation-maximization

- Environmental correlation, 629
tests of significance, 641
- Environmental deviation, 47
- Environmental effects, 107
effects on phenotypic covariance, 162-170
general, 107, 123-127
special, 107, 111
repeatability, 121-123
within-individual, 112
- Environmental stress, 115
effects on heritability, 174
- Environmental variance, 107-127, 162-170, 681-682, 689-690
- Epistasis, 82-92
chromosomal, 381-382
dichotomous traits, 524-525
effects, 85-86, 212-213, 215
inbreeding depression, 257-259, 267-268
mutation effects, 347-348
of QTLs, 480, 485
- Equation of complete determination, 825
- Equivalence by descent, 146
- Equivalent linear models, 849-850
- Error
Type I, 869
Type II, 869
- Estimability
of fixed factors, 839-841
- Evolvability, 175-176
- Exclusion mapping, 530-532
- Exon trapping, 427
- Expectation-maximization method, 797-799, 863-867
- Expectations of complex variables, 808-810
expected value of a product, 817
expected value of a ratio, 818
expected value of square root, 808
functions of multiple variables, 809-810
- Explanatory variable, 177
- Extranuclear effects, 605-610
- F* distribution, 879-880
- F* test, 560-561, 574-576, 587, 602, 608, 617, 669, 880-883
power, 877-889
- FA. *See* Fluctuating asymmetry
- Fain's test, 356-358
- Falconer's mode of maternal effects, 706-711
- Fetal effects, 711-714
- Fisher information matrix, 789, 855-857
- Fisher's fundamental theorem, 176
- Fisher's scoring method, 795, 862
- Fitness, 46, 176, 180-182
coefficient of variation, 176
inbreeding effects, 253-257, 269-274
relationship with heterozygosity, 287-291
- Flanking-marker analysis, 433
- Fluctuating asymmetry, 112-116
- G test, 60-61, 859
- Gametic imprinting, 718-719
- Gametic model, 758-759
- Gametic phase disequilibrium, 94-106
drift-recombination equilibrium, 413-414
effects on dominance, 288-291
effects on genetic covariance, 150-153
estimation, 97-100
- Gaussian distribution. *See* Probability distribution
- GCA. *See* General combining ability
- Gene content, 65
- Gene conversion, 325
- Gene number. *See* Effective number of factors
- General combining ability, 611-618
- General mixed model, 746-755
estimability of fixed effects, 753-754
fixed vs. random effects, 748
mixed-model equations, 752
- Generalized inverse, 188, 835-839
Moore-Penrose inverse, 836
- Generalized least squares, 842-843
- Genetic correlation, 629
across environments, 660-665
across the sexes, 723-726
bias due to selection, 644-647
- Genetic correlation (*continued*),
comparison across populations, 648-653
genetic covariance between relatives, 631
limitations of genetic interpretation, 633, 635
multiple comparison issues, 641
negative estimates, 635
nested analysis of covariance, 633-636
pairwise comparison of relatives, 632
path analysis model, 829-830
regression of family means, 636-637
resampling procedures, 650-653
sampling distribution, 642-644
standard error, 642-644
threshold characters, 739-741
- Genetic map, 211, 393-398
mapping functions, 394-396
relationship to physical distance, 395-396
- Genetic assimilation, 316-317
- Genetic variance, 69-71, 81
additive, 49, 69-71, 76-79
basis of, 321-352
disequilibrium, 100-106, 150-153, 322
dominance, 69-71
epistatic, 86-92
expressed, 100-106
hidden, 100-106, 150-153
in inbred population, 77
- Genome size, 396
- Genomic mismatch scanning, 393
- Genomic scanning, 529-530
- Genotype, 11, 52
frequency, 52-53
- Genotype-environment covariance, 47, 131
effects on phenotypic covariance, 164-168
- Genotype \times environment interaction, 107-111, 127-129, 308-309, 657-685
characterization of interaction effects, 672-678
correlation of family means, 664-665
cross-over interaction, 678-680
fixed vs. random effects, 666-669

- Genotype \times environment interaction (*continued*),
 genetic correlation across environments, 660-665
 influence on heritability, 669
 interpretative difficulties, 659, 666-669
 joint-regression analysis, 672-678, 682
 measures of stability and plasticity, 680-683
 of QTLs, 443, 487-489
 reaction norm, 658
 relation of correlation and ANOVA, 671-672
- Genotypic value, 47, 61-63, 65
- GLM (General linear model).
See Linear models
- GLS. *See* Generalized least squares
- GMS. *See* Genomic mismatch scanning
- Granddaughter design, 501-502
- Growth analysis, 831-833
- Haldane's mapping function, 394-395
- Haldane's rule, 389-390
- Haley-Knott regression, 453-457
- Hamilton's rule, 714
- Haplloid, 51
 genetic variance components, 92-93
- Hardy-Weinberg principle, 54-56
 age structure, 60
 polyploidy, 57-60
 sex-linked loci, 56
 test, 60-61
- Haseman-Elston regression, 513-520
- Hayman's procedure, 229-230
- Hayman-Jinks analysis, 619-627
- Heritability, 170-175
 biometric, 171
 broad-sense, 47, 584-587, 594-595
 character types, 174-175
 consistency of estimates, 171-174
 effects of environmental stress, 174
 heterogeneous environments, 669
 lab vs. field estimates, 172-174, 548-550
- Heritability (*continued*),
 narrow-sense, 50, 171
 natural populations, 800-803
 negative estimates, 563-564, 577-578
- Hessian matrix, 794-795, 855-857
- Heteroscedasticity, 42, 203
- Heterosis, 222-226, 251
- Heterozygosity,
 relationship with fitness, 287-291
- Heterozygote, 52
- Hexaploid, 52
- Historical background, 7
- Homoscedasticity, 42
- Homozygote, 52
- Hybrid sterility, 387
- Hybridity index, 206-207
- Identity by descent, 132-141, 511-517
 estimation with molecular markers, 516-517, 527-528
- Identity coefficients, 133-141
 coefficient of coancestry, 135-139
 coefficient of fraternity, 140-141
 condensed coefficients, 133-135
 digenic descent coefficients, 146-149
 equivalence by descent, 146
 estimation with molecular markers, 800
 full sibs, 136-138
 inbreeding coefficient, 133
 individual with self, 135
 parent and offspring, 135-136
 polyploidy, 162
 sex-linked loci, 720-722
- Identity in state, 132-133
- Imprinting, 718-719
- Inbred-line QTL mapping, 431-489
 advanced intercross lines, 436
 conditional probabilities of genotypes, 433-436
 detection with linear models, 442-444, 467-469
 detection with maximum likelihood, 445-456
 expected marker-class means, 437-439
 experimental designs, 432-433
 Haley-Knott regression, 453-457
- Inbred-line QTL mapping (*continued*),
 likelihood functions, 445-446, 450
 likelihood maps, 446-457
 marker-difference regression, 459-463
 recombinant inbred lines, 401-405, 436
- Inbreeding coefficient, 133
 regular systems of mating, 259
- Inbreeding depression, 251-291
 (A+B)/A ratio, 283-284
 average degree of dominance, 283-286
 directional dominance, 257, 284-287
 dominance hypothesis, 253-256, 283-291
 effects of environment, 273-274
 effects of epistasis, 257-259, 267-268
 evidence, 269-274
 general model, 256-259
 lethal equivalents, 276-283
 linearity, 255, 257-259, 272
 maternal effects, 272-273
 methodology, 259-269
 multigenerational analysis, 262-266
 overdominance hypothesis, 254-256, 283-291
 purging inbreeding depression, 274-276
 relationship to heterosis, 258
 Ritland's method, 266-267
 single generation analysis, 260-262
t test for, 261
 variance in inbreeding depression, 268
- Incidence matrix, 746
- Inconsistent system of equations, 835
- Independent variable, 39
- Infinitesimal model, 141
- Information content mapping, 530-532
 informativeness, 492-495
 polymorphism information content, 493-495
 proportion of fully informative matings, 493-495
- Interference, 394
- Interval mapping, 433, 450-451, 518-521

- Intraclass correlation, 540, 559, 573
- Inversions, 381
- Isoallele, 322
- Jackknife, 569-570
- James' identity, 523-524
- Joint-regression analysis, 672-678, 682
- Kascser-Burns model, 63-65
- Kin selection, 711-714
- Kleckowski's transformation, 300-301
- Kluge-Kerfoot phenomenon, 305
- Kosambi mapping function, 395
- Kronecker product, 792
- Kur. *See* Kurtosis
- Kurtosis, 28, 298
- Large-sample variance, 33
- LD mapping. *See* Linkage disequilibrium mapping
- Leading factors, 238, 240
- Least squares regression
generalized, 202-204, 842-843
ordinary, 39-41, 200-202
weighted, 203-204, 540-542
- Leptokurtosis, 29
- Lerner's hypothesis, 116-120
- Lethal equivalents, 276-283
detrimental equivalent, 276
detrimentals vs. lethals, 279-281
estimation of numbers, 276-283
observations, 278-283
- Liability, 377-378, 730
- Likelihood maps, 446-457
discontinuities in, 505
- Likelihood ratio test, 362-363, 400, 446, 530, 857-861
- Linear models, 177-182, 192-194, 198-204, 835-852
equivalency, 849-850
hypothesis testing, 848-849
likelihood-ratio tests, 860-861
- Line-cross analysis, 205-249
composite effects, 206-226
effective number of factors, 231-249
effects of linkage, 208-213
epistasis test, 215
estimation of gene number, 231-249
- Line-cross analysis (*continued*),
expected line means, 208-210
Hayman's procedure, 229-230
hybridity index, 206-207
hypothesis testing, 215-221
joint-scaling test, 215-221
segregational variance, 227
source index, 206-208
variance within lines, 226-231
- Linkage, 94
disequilibrium. *See* Gametic phase disequilibrium
drag, 409-411
effects on genetic covariance, 146-149
effects on line-cross analysis, 208-213
- Linkage disequilibrium
mapping, 413-418
disease genes in expanding populations, 414-418
- Local adaptation, 225
- LOD (likelihood of odds) scores, 447-448
- Logarithmic transformation, 293-299
- Logistic function, 378
- LR (Likelihood ratio). *See* Likelihood ratio tests
- Major genes, 322, 353-378
ascertainment bias, 374
Bartlett's test, 356
complex segregation analysis, 364-375
departures from normality, 355
discrete characters, 375-378
estimating individual genotypes, 374-375
Fain's test, 356-358
major-gene indices, 357
mixture models, 359-364
nonparametric tests, 358-359
select-and-backcross method, 354
sibship variance tests, 355-357
testing for, 354-378
- Major vs. minor gene effects, 231, 322-323, 353-378, 481-483
- Mapping function
Haldane, 210, 395-396
Kosambi, 395-396
- Marker-based analysis, 379-429
bias from population stratification, 420-421
- Marker-based analysis (*continued*),
bias from segregation distortion, 422
chromosomal assay, 380-390
classical approaches, 379-390, 398
comparative mapping, 428
distance to random QTL, 397
heritability in natural populations, 800-803
inbred lines
see inbred-line mapping
number of necessary markers, 397-398
populations under selection, 404-405
- Marker-difference regression, 458, 459-463
- Marker-trait associations, 398-424
likelihood functions, 399-400
variances and higher moments, 439-441
- Maternal effects, 123-127, 687-714
age-specific, 124
cross-fostering experiments, 696-703
cumulative Lansing effects, 126-127
cytoplasmic transmission of organelles, 683-685
effects on covariance between relatives, 162-170, 605-610, 615-618, 689-714
estimation, 773-774
extension to other types of relative effects, 711-714
Falconer's model, 706-711
nested analysis of variance, 703-706
postpollination reproductive traits, 695-696
Willham's model, 687-688
- Matrix algebra, 177-204, 835-852
addition, 183
basic notation, 182-183
bilinear form, 193
covariance of transformed variables, 193-194
derivatives of vectors and matrices, 851-852
design, 199, 746
determinant, 188-190
diagonal matrix, 188

- Matrix algebra (*continued*),
 estimability of fixed factors,
 839-841
 expectations of vectors and
 matrices, 192-193
 Fisher information matrix, 789,
 855-856
 full column rank, 839
 generalized inverse, 188, 835-
 839
 generalized least squares, 842-
 843
 Kronecker product, 792
 identity matrix, 187
 incidence matrix 199, 746
 inverse, 187-192
 minor, 188
 Moore-Penrose inverse, 836
 multiplication, 184-186
 multiple regression, 177-182,
 188-189
 nonsingular matrix, 187
 partitioned matrix, 183
 quadratic forms, 193, 843-848
 singular systems of equations,
 835-841
 solutions of systems of
 equations, 187
 square root of a matrix, 841
 subtraction, 183
 trace, 785
 transposition, 186-187
 vector, 182
- Maximum likelihood, 853-867
 asymptotic normality and
 efficiency, 855
 consistency, 854
 comparison to REML, 780-784
 estimation of variance
 components, 784-788
 estimate of mean, 854
 expectation-maximization
 method, 863-867
 Fisher information matrix, 789,
 855-856
 Fisher's scoring method, 862
 G test, 859
 iterative methods for solving,
 861-867
 invariance, 855
 large sample properties, 854-
 855
 likelihood ratio test, 362-363,
 400, 446, 530, 857-861
 Newton-Raphson method, 861-
 862
 score, 853
- Maximum likelihood (*continued*),
 standard errors of estimates,
 788-789
 support, 853
- Maximum LOD score
 linkage test, 526-527
- McNemar's test, 421
- MDR. *See* Marker-difference
 regression
- Measured-genotype approach,
 74
- Mendelian-Biometrician clash, 7
- Meiosis, 54-55
- Meristic characters, 19
- Metric characters, 19
- MGI (Major-gene indices). *See*
 Major genes
- Midparental value, 531
- Microsatellites, 392-393, 421-422
- Mixed model. *See* General
 mixed model
- Mixed model equations, 752
- Mixture models, 356-364
 distribution, 360
 hypothesis testing, 361-364
 parameter estimation, 360-361
- ML. *See* Maximum likelihood
- ML interval mapping, 450-453
- MLE (Maximum likelihood
 Estimate). *See* Maximum
 likelihood
- MLH (Multilocus hetero-
 zygosity). *See* Heterozygosity
- MLS. *See* Maximum LOD score
- MME. *See* Mixed model
 equations
- Modifier locus, 322
- Molecular markers, 390-393
- Moments, 22, 25
 kurtosis, 28, 298
 mean, 22
 quadratic forms, 843
 skewness, 24
 standard deviation, 23
 variance, 22-23
- Monomorphic, 51
- Monozygotic twins, 581
- Moore-Penrose inverse, 836
- Morgan, 395
- Most probable error, 32
- Multigene family, 327-328
- Multiple-factor hypothesis, 10
- Multiple regression, 177-182,
 200-204
 partial regression coefficients,
 178-182, 188-189
- Multiple test significance levels,
 441-444, 452, 641
- Multipoint mapping, 433
- Multivariate distribution, 19-20
 multivariate normal, 194-198
- Mutation
 Bateman-Mukai technique, 341
 between-line divergence, 330-
 333
 deleterious effects, 340-352
 distribution of effects, 236,
 333-337, 339, 343-352
 epistasis, 347-348
 estimates from natural
 populations, 348-352
 mutation rate, 337-352
 mutational heritability, 330,
 335-338
 mutational variance, 328-340
 persistence time, 351-352
 within-line variance, 328-329
- Mutation-selection balance, 253-
 254, 351-352
- MVN. *See* Multivariate distribu-
 tion
- MZ. *See* Monozygotic twins
- Nearly isogenic lines, 405-413
 flanking marker selection, 411-
 413
 linkage drag, 409-411
 proportion of donor genome,
 406, 409-411
 select-and-backcross procedure,
 406-407
- Neutral model, 329-331
- Newton-Raphson method, 861-
 862
- NIL. *See* Nearly isogenic line
- Nonsegregational mutational
 variance, 329
- Normal distribution. *See*
 Probability distribution
- North Carolina Design I. *See* Sib
 analysis, Full-sib design
- North Carolina Design II, 598-
 610
- North Carolina Design III, 624-
 626
- Null allele, 289

- One-sided tests, 870-872
- One-lod support intervals
for QTL mapping 448-449
- Optimization theory, 4
- Order statistics, 240-241
- Organelle inheritance, 683-685
- Outbreak of variation, 11-12
- Outbred-population mapping, 491-533
dichotomous characters, 521-533
full-sib analysis, 502-505
general pedigrees, maximum likelihood, 510-512
granddaughter design, 501-502
half-sib analysis, 496-500
Haseman-Elston regression, 513-520
identity by descent, 511-517
interval mapping, 518-521
joint estimation of position and effect, 518-521
marker contrast within sibship, 496-498, 502-504
multipoint interval mapping, 520-521
power, 500-502, 517-518
relationship to nested ANOVA, 499-500, 505
linear models, 495-505
maximum likelihood, 505-510
- Outbreeding depression, 222-226
- Outbreeding effects, 205-249
recombination loss, 224
- Overdominance, 254-256, 283-291
- Parent-offspring regression, 8, 48-50, 197, 537-552
assortative mating, 547-548
balanced design, 538-539
confidence interval, 543
linearity, 550-552
midparent, 48-50, 538, 540, 543
multiple offspring, 539
natural populations, 548-550
optimum design, 543-547
power, 547, 874-875
regression vs. correlation, 539
sampling variance, 542-543
sex-specific differences, 542
unequal family sizes, 539-542
- Paternal effects, 605-610, 615-618, 711-714
- Path analysis, 823-833
equation of complete determination, 825
maternal effects, 687-688
resemblance between relatives, 163-170, 827-829
- Path coefficient, 825-825
- Path diagram, 823
- PCR. *See* Polymerase chain reaction
- Penetrance, 375-376, 522
- Permutation test, 441-442, 466, 570
- PFIM (Proportion of fully informative matings). *See* Information content mapping
- Phenocopy, 324, 522
- Phenotype, 11
covariance, 131-132
linear model, 108, 163
- Phenotypic correlation, 629
as estimates of genetic correlation, 639
components, 637-639
polychotomous characters, 727, 736-739
test of significance, 641
- Phenotypic plasticity, 680-683
- Phenotypic similarity, 800
- Phenotypic stability, 680-683
- PIC (Polymorphism information content). *See* Information content mapping
- Playtkurtosis, 29
- Pleiotropy, 322, 629, 655-656
life-history evolution, 655-656
- Polygenes, 321-352
- Polygenic balance model, 103
- Polygenic mutation. *See* mutation
- Polymerase chain reaction, 391
- Polymorphic, 51
- Polymorphism information content, 493-495
- Polyploidy, 51, 57
effects on genetic covariance, 161-162
genetic variance components, 93-94
genotype frequency, 58-60
- Population prevalence. *See* Prevalence
- Population stratification, 420
- Positional cloning, 426-429
- Positional candidates, 427
- Postpollination reproductive traits, 695-696
- Power of statistical tests, 869-889
analysis of variance, 880-883
normally distributed test statistics, 870-877
one-sided tests, 870-872
two-sided tests, 872-873
Type I and II errors, 869
- prb. *See* Probit transformation
- Predictor variable, 39, 177
- Prevalence
population, 376-377, 523-524
- Probability density function, 21, 35
- Probability distribution, 20
 χ^2 distribution, 878-879
conditional, 196
F distribution, 879-880
log-normal distribution, 294-295
multivariate normal distribution, 194-198
negative exponential distribution, 21
normal (Gaussian) distribution, 26, 28, 194-198, 293-299
truncated normal distribution, 29-31
- Probands, 374
- Probit transformation, 296, 310-313
- Progeny testing, 401
- Propositi, 730
- QTL. *See* Quantitative-trait locus
- Quadratic forms, 843-848
moments, 843
sums of squares expressed as, 846-848
- Quantitative-trait locus, 322
biased estimates of effects, 475-476, 484-486
bias from multiple QTLs, 457-458
cladistic analysis, 424-425
cloning, 425-429
conditional probabilities of genotypes, 433-436
detection of epistasis, 443, 485-486

- Quantitative-trait locus
(*continued*),
detection with linear models,
442-444, 467-469
detection with maximum
likelihood, 445-456
estimation of effects from
marker-class means, 437-439
expected marker-class means,
437-439
genotype-environment
interactions, 443, 487-489
Haley-Knott regression, 453-
457
inbred-line mapping, 431-489
informativeness, 492-495
joint estimates of effects and
map position, 439, 440-441,
459-462, 467-469
likelihood functions, 399-400,
445-446, 450, 507-510, 865-
867
likelihood maps, 446-457, 505-
506
mapping, 399-424, 431-489
marker contrast within sibship,
496-498, 502-504
marker-difference regression,
459-463
mixed model analysis, 750-751
molecular nature, 323-328
multiple-QTL analysis, 457-469
number of markers vs. number
of individuals, 473
outbred-population mapping,
491-533
precision of map position
estimates, 448-449
power of tests, 873, 876, 883-
885
repeatability, 474-476, 487
sample sizes required for
detection, 469-476
significance levels with
multiple tests, 441-444, 451-
453
- RAM. *See* Reduced animal
model
- RAPD. *See* Random amplified
polymorphic DNA
- Random amplified polymorphic
DNAs, 391-392
- RDA. *See* Representational dif-
ference analysis
- Reaction norm, 658
quantitative-genetic models,
683-685
- Reciprocal-effects model,
Griffing's diallel, 616
- Reciprocal general combining
ability, 615
- Reciprocal specific combining
ability, 615
- Recombinant inbred lines, 401-
405
- Recombination fraction, 94-95,
147, 394
average in genome, 210-211,
236
estimates from disease
associations, 416-418
modifiers, 395
repeated crossing, 436
- Recombination loss, 224
- Recurrence risk, 523-524, 727
- Reduced animal model, 759-762
- Regression, 39, 45
generalized least-squares, 202-
204, 842-843
logistic, 378
multiple, 65, 177-182, 188-189,
200-204
ordinary least-squares, 39-41,
200-202
residual variance, 44
sampling variance of
regression coefficient, 819
through origin, 201
towards mediocrity, 8
weighted least-squares, 203-
204, 540-542
- Regressive models
of complex segregation
analysis, 373
- Regulatory loci, 324
QTL mapping of, 478-479
- Relatedness, 132-141
- Relationship matrix
additive, 756
dominance, 768
methods for computing, 762-
767
- Relative risk, 523-524
- REML. *See* Restricted maximum
likelihood
- Repeatability, 121-123
- Replication slippage, 325
- Representational difference
analysis, 393
- Resampling procedures, 569-570
- Resemblance between relatives,
131-176
cytoplasmic transmission, 693-
695
effects of assortative mating,
153-161
effects of linkage, 146-149
effects of gametic phase
disequilibrium, 150-153
effects of polyploidy, 161-162
environmental covariance, 162-
170
genetic covariance, 141-162
maternal effects, 690-693
sex linkage, 719-724
sexual dimorphism, 719-724
- Residual variance, 44
- Response to selection, 9, 11, 50
- Response variable, 39, 177
- Restricted maximum likelihood,
779-784, 789-803
comparison with maximum
likelihood, 780-784
derivative-based methods, 794-
796
EM methods, 797-799
estimation of variance
components, 789-799
Fisher's scoring method, 795
multiple characters, 792
populations under selection,
792-793
Thompson-Shaw method, 799
- Restriction enzymes, 390
- Restriction fragment length
polymorphism, 390
- RFLP. *See* Restriction fragment
length polymorphism
- RCGA. *See* Reciprocal general
combining ability
- RSGA. *See* Reciprocal specific
combining ability
- RIL. *See* Recombinant inbred
line
- Risk function, 728-730
- Ritland's method, 800-803
- Robertson-Price identity, 45-47
- Roginskii-Yablokov effect, 303-
305
- Satterthwaite's correction, 575-
576
- SCA. *See* Special combining
ability

- Scale, 293-317
 allometric equations, 305-307
 Box-Cox transformation, 295
 interaction effects, 307-309
 Kleckowski's transformation, 300-301
 log-normal distribution, 294-299
 normal probability plot, 296-299
 probit transformation, 296-299
 stabilizing the variance, 295, 300-305
 transformation to normality, 293-299
- SD. *See* Standard deviation
- Score function, 853-854
- SE. *See* Standard error
- Segregation distortion, 422
- Segregation index, 232-233
- Segregational variance, 227
 haploids, 242
- Select-and-backcross procedure, 354, 406-407
- Selection, 180-182
 canalization, 314-317
 direct, 180-182
 indirect, 180-182
 mutational contribution, 332-335
- Selection differential, 31, 45-47, 50, 175, 180-182, 816-817
- Selective genotyping, 401, 474
- Sex chromosome, 52
 speciation, 387-390
- Sex-linked loci, 715-726
 dosage compensation, 715-718
 genotype frequency, 56-57
- Sexual dimorphism, 542, 718-726
 genetic variation, 724-726
- Shapiro-Wilk normality test, 298
- Sheppard's correction, 24-25, 303
- Sib analysis, 553-579
 common environmental effects, 570
 comparison with maximum likelihood, 567
 comparison with parent-offspring analysis, 565
 confidence intervals of estimates, 562-563
 dominance, 570
 full-sib design, 570-579
 half-sib design, 554-570
- Sib analysis (*continued*),
 hypothesis testing, 560-561, 574-576
 negative heritability estimates, 563-564, 577-578
 North Carolina Design II, 598-610
 optimal design, 564-566, 577-578
 power, 887-889
 resampling procedures, 569-570, 576
 sampling variance of estimates, 561-562, 567, 576-577
 unbalanced design, 566-567
 variance component estimation, 558, 571
- Sire effect, 199-200
- Sire model, 758-759
- Sire variance, 571-572
- Skewness, 24
- Source index, 206-207
- Special combining ability, 611-618
- Speciation, 205, 387-390
 Dobzhansky-Muller model, 387-388
 Haldane's rule, 389-390
 hybrid sterility, 387
- Standard deviation, 23
- Standard error, 33, 812
- Standard normal deviate, 28
- Sums of squares, 846-848
- Support function, 853
- t test, 871-873
- Targeted growth, 304, 700-703
- Taylor expansion, 807-809
- TDT. *See* Transmission/disequilibrium test
- Templeton and Sing's method, 424-425
- Tetraploid, 52
- Thoday's method, 381-384
- Thompson-Shaw method, 799
- Threshold characters, 727-744
 clonal analysis, 735
 Crittenden-Falconer technique, 731-732
 heritability on the observed scale, 741-744
 heritability on the underlying scale, 730-738
 genetic correlation, 739-741
- Threshold characters (*continued*),
 liability, 730
 multiple thresholds, 736-739
 risk function, 728-730
- Trace of a matrix, 785
- Transgression. *See* Transgressive segregation
- Transgressive segregation, 235, 477-478
- Transmission/disequilibrium test, 419-422
- Transposition, 325-328
- Transposon tagging, 405, 425-426
- Triple test cross, 626-627
- Trow's formula, 394
- Truncation selection, 29
- Twins, 581-595
 broad-sense heritability, 584-587
 classical approach, 582-587
 monozygotic-twin half-sib method, 587-592
 monozygotic vs. dizygotic environment, 586
 sex-chromosome effects, 590
- Two-sided tests, 872-873
- Type I and II errors, 869
- Unequal crossing-over, 325
- Univariate distribution, 19
- Var. *See* Variance
- Variance, 22-23, 33
 ML vs. REML estimates, 781-784
 of coefficient of variation, 819-821
 of complex variables, 810-813
 of mean, 811-812, 855
 of moments, 815
 of products, 817-818
 of ratios, 818
 of regression and correlation coefficients, 818-819
 of square root, 820
 of standard deviation, 820
 of variance and covariance, 813-817, 845-846
 unbiased estimator, 810, 844
- Variance components
 environmental, 107-129
 genetic, 81-106

Variance components (*continued*),
ML estimation, 779-789
REML estimation, 779-784,
789-803

W-test. *See* Shapiro-Wilk
normality test
Wehrhahn-Allard estimator, 244-
246, 406
Willham's model of maternal
effects, 687-688

Zeng's estimator, 236-238
Zoo blotting, 427
Zygote, 54