INDEX

A-optimality, 786
Aalen-Johansen estimator, 810
accelerated failure-time model, 622, 809
active antiretroviral therapy (ART), 846
active matrix flat-panel image (AMFPI), 253, 280
actuarial science, 802
acute radiation syndrome (ARS), 240
additive hazards model, 622
adjustment of treatment effect, 636
admixture mapping, 766
Affymetrix GeneChips, 401
aggregation, 506
AIDS survival studies, 803
alpha-spending method, 325
American Association of Medical Record Librarians, 818
American Association of Physicians in Medicine (AAPM), 261, 311
American Board of Radiology (ABR), 262
American Medical Association, 818
American Society of Hospital Pharmacists, 818
analysis of covariance (ANCOVA), 551
analysis of variance (ANOVA), 10, 448, 551
analytical approximations, 98
anchor-based methods, 617
Animal Pharmacology and Toxicology Studies, 823
ANOVA table, 11
antithetic variates, 98
apparent overdispersion, 1
area under the curve (AUC), 51
Armitage-Doll multistage model, 629
artifacts, 222
artificial intelligence, 276
as low as reasonably achievable (ALARA), 222
association analysis, 764
Asthma Quality of Life Questionnaire (AQLQ), 33
asymmetrical funnel plot, 602
Atomic Bomb Survivors Study, 132
Atomic Energy Act (AEA), 245
attenuation, 227
Australian Institute of Health and Welfare, 707
automatic exposure control, 311
availability, 277
availability bias, 598
balanced bootstrap, 98
balanced data, 17
bandit processes, 40
Bartlett correction, 154
baseline hazard, 808
Bayes' theorem, 545
Bayesian dose escalation, 56
Bayesian methods, 799
Bayesian predictive power, 105
Bayesian techniques, 628
BCa intervals, 86
Bernoulli distribution, 44
Bernoulli process, 417
Bernoulli sampling process, 430
Beta(α, β) distribution, 2
beta-binomial distribution, 2
between-subject variation (BSV), 340
bias, 64, 74
binary criterion, 740
binomial distribution, 1, 570
binomial test, 636, 663
biomarkers, 908
blinding, 399
block randomization design, 17
blocking, 399
bone mineral density (BMD), 853
Bonferroni adjustment, 441, 796
Bonferroni method, 441
Bonferroni-Holm procedure, 16
bootstrap sampling, 82
bootstrap, 62, 558
bootstrap t, 84
bootstrap confidence intervals, 62
bootstrap distribution, 64
bootstrap tilting, 155
bootstrap tilting intervals, 87
box-whisker plot, 557
bracketing design, 780
breast cancer screening, 710
Breslow estimator, 808
Brezzi and Lai's approximation, 432
Brownian motion, 108

Cardiac Arrhythmia Suppression Trial (CAST), 438
Carvedilol (Coreg) by the Cardiovascular and Renal Drugs Advisory Committee, 734
case series, 545
case-cohort, 908
case-control, 908
case-control studies, 623, 721
case-control study, 537
case-crossover design, 537
case-time-control design, 541
cathode ray tube (CRT), 278
cause of death, 693
cDNAs, 393
cell means hypotheses, 23
cell means model, 12
censored data, 120
censoring, 802
censoring at random, 314
center, 64
central limit theorem, 62
charge-coupled device (CCD), 253
chi-square, 371
chi-square distribution, 136
Chip-on-chip, 397
citation bias, 598
class differentiation analysis, 403
class discovery analysis, 403
class prediction analysis, 402
Clinical Coordinating Center (CCC), 903
Clinical Data Interchange Standard Consortium (CDISC), 383
clinical phase, 690
clinical significance, 617
clinical significance of the evidence, 597
clinical trial monitoring, 102
Clopper-Pearson interval, 574
cluster data, 490
cluster randomized trial, 533
clustered failure time data, 130
coarsening at random, 811
Cochrane reviews, 864
cochrane risk of bias tool, 865
Code of Federal Regulations, 245
cohort simulation, 707
cohort studies, 623, 721, 807
cohort study design, 537
COM-Poisson models, 6
commingling, 763
Committee On Publication Ethics (COPE), 866
comparing intersubject variabilities, 676
comparing intraindividual variabilities, 672
comparisowise error rate, 436
competing risk mortality rates, 904
competing risks, 803
competing risks model, 810
complementary metal oxide semiconductor (CMOS), 253
compliance-adjusted analyses, 320
compound Poisson, 507, 509
compound Poisson distribution, 169, 510
compound weighted Poisson distribution, 510
Compton electron, 231
Compton scatter (CS), 229
Compton scatter photon, 231, 258
Compton scatter radiation, 258
computed radiography (CR), 213, 279, 281
computed tomography (CT), 213, 292
computer-adaptive testing, 615
computer-assisted detection (CAD), 274
computer-assisted diagnosis (CAD), 264
computer-assisted testing, 615
computer-network security, 277
concomitants, 98
concordance correlation coefficient (CCC), 448
conditional logistic regression, 365, 539
conditional mean, 365
conditional power, 102, 175
conditional transition probabilities, 708
conditionally ignorable missing data, 315
confidence intervals, 702
confidentiality, 277
confounded, 377
Index

confounding, 538, 807
confounding bias, 539
consequences of poor reporting, 863
Consolidated Standards of Reporting Trials (CONSORT), 866
constrained Newton method, 5
contagion, 506
contingency table, 839
continuation set, 419
continuity correction, 575, 581
Contract Research Organization (CROs), 886
contrast, 202
control variates, 98
Conway-Maxwell-Poisson or COM-Poisson, 508
Cooperative Studies Evaluation Committee (CSEC), 881
cooperative studies program (CSP), 876
Cooperative Studies Program Guidelines, 877
copula models, 811
correlated frailty model, 171
cost bias, 598
cost utility analysis (CUA), 112
cost-effectiveness acceptability curve, 118
cost-effectiveness analysis, 111
cost-effectiveness plane, 115
count data, 1
count dispersion models, 508
count equidispersion property, 507
count explanatory models, 514
count time series models, 516
counting process, 2, 141
counting processes, 809
covariance, 553
covariates, 622
covariance probabilities, 572
Cox partial likelihood, 808
Cox regression model, 807
Cox's proportional hazards model, 543, 664, 667
Cox-type proportional hazards models, 126
Cramér-von Mises, 807
Cressie-Read statistic, 588
cRNAs, 393
Cronbach's coefficient, 614
cross-sectional design, 547
cross-validation, 565
crossover design, 653
cubic splines, 628
cumulative hazard function, 128, 905
cure model, 804
curse of dimensionality, 418
curve fitting, 470
D-efficiency, 787
D-optimality, 786
data and safety monitoring board (DSMB), 323, 734, 883, 905
data dredging, 16
data extraction, 401
data management, 752
data processors, 754
data storage and retrieval, 754
data suppression mechanisms, 597
data visualization, 754
deconvolution, 471
deep models, 592
delayed entry, 802, 803, 811
demography, 802
Department of Health and Human Services, 891
Department of Veterans Affairs (VA), 876
design effect, 113
design variables, 368
detector quantum efficiency DQE, 198
deterministic health effects, 235
Diabetes Control and Complications Trial (DCCT), 317
Diabetes Prevention Program, 318
Diabetes study, 137
Diabetic Retinopathy Study (DRS), 137
diagnostic trials, 483
dichotomous test, 837
differential attenuation, 233
diffusion tensor imaging (DTI), 213
digital filters, 272
digital fluoroscopy (DF), 279, 287
digital images, 266
digital mammography, 285
digital radiography (DR), 213, 279
digital smoothing filter, 272
digital subtraction angiography (DSA), 213, 287
digital tomosynthesis, 290
direct evidence of publication bias, 596
Dirichlet, 122
discordance probability, 106
discrete data, 1
discriminant validity, 614
dispersion parameter, 507
<table>
<thead>
<tr>
<th>Term</th>
<th>Page Numbers</th>
</tr>
</thead>
<tbody>
<tr>
<td>distinguishing between methodological and reporting issues</td>
<td>864</td>
</tr>
<tr>
<td>dose-response relationship</td>
<td>626</td>
</tr>
<tr>
<td>dose-escalation study</td>
<td>53</td>
</tr>
<tr>
<td>dose-finding designs</td>
<td>51</td>
</tr>
<tr>
<td>dose-finding designs for cytotoxic agents</td>
<td>497</td>
</tr>
<tr>
<td>dose-finding designs for molecularly targeted agents</td>
<td>497</td>
</tr>
<tr>
<td>dose-limiting events (DLE)</td>
<td>51</td>
</tr>
<tr>
<td>drug development</td>
<td>566</td>
</tr>
<tr>
<td>dummy variables</td>
<td>368</td>
</tr>
<tr>
<td>duplication bias</td>
<td>598</td>
</tr>
<tr>
<td>dynamic de-escalating designs</td>
<td>498</td>
</tr>
<tr>
<td>dynamic programming</td>
<td>42, 429</td>
</tr>
<tr>
<td>econometrics</td>
<td>609</td>
</tr>
<tr>
<td>economic analysis plan</td>
<td>113</td>
</tr>
<tr>
<td>economic perspective</td>
<td>112</td>
</tr>
<tr>
<td>effect modification</td>
<td>540</td>
</tr>
<tr>
<td>effective dose (ED)</td>
<td>242</td>
</tr>
<tr>
<td>effectiveness</td>
<td>313</td>
</tr>
<tr>
<td>efficient score</td>
<td>326</td>
</tr>
<tr>
<td>electronic regulatory submission</td>
<td>382</td>
</tr>
<tr>
<td>eligibility and exclusionary criteria</td>
<td>903</td>
</tr>
<tr>
<td>EM algorithm</td>
<td>5</td>
</tr>
<tr>
<td>empirical likelihood methods</td>
<td>146</td>
</tr>
<tr>
<td>Enhancing the Quality of Informed Consent (EQUIC) program</td>
<td>892</td>
</tr>
<tr>
<td>entropy</td>
<td>155</td>
</tr>
<tr>
<td>equidispersion</td>
<td>506</td>
</tr>
<tr>
<td>equivalence tests</td>
<td>586</td>
</tr>
<tr>
<td>equivalent dose</td>
<td>242</td>
</tr>
<tr>
<td>European Public Health Information Network (EUPHIN), 917</td>
<td></td>
</tr>
<tr>
<td>excess risk</td>
<td>623</td>
</tr>
<tr>
<td>excess risks per 10,000 person years</td>
<td>911</td>
</tr>
<tr>
<td>exon array</td>
<td>396</td>
</tr>
<tr>
<td>expected number of deaths</td>
<td>803</td>
</tr>
<tr>
<td>experimental design</td>
<td>565</td>
</tr>
<tr>
<td>experimentwise error rate</td>
<td>436</td>
</tr>
<tr>
<td>exploration versus exploitation</td>
<td>41</td>
</tr>
<tr>
<td>exponential attenuation</td>
<td>227</td>
</tr>
<tr>
<td>exponential dispersion family</td>
<td>507</td>
</tr>
<tr>
<td>exponential distribution</td>
<td>44, 804, 807</td>
</tr>
<tr>
<td>exponential families</td>
<td>507</td>
</tr>
<tr>
<td>exponential model</td>
<td>664</td>
</tr>
<tr>
<td>exponentially weighted Poisson distribution</td>
<td>511</td>
</tr>
<tr>
<td>extensions to kappa</td>
<td>451</td>
</tr>
<tr>
<td>external validation</td>
<td>565</td>
</tr>
<tr>
<td>extreme value distribution</td>
<td>809</td>
</tr>
<tr>
<td>F distribution</td>
<td>344, 574</td>
</tr>
<tr>
<td>F-statistics</td>
<td>11</td>
</tr>
<tr>
<td>factorial design</td>
<td>135, 902</td>
</tr>
<tr>
<td>failure to report</td>
<td>861</td>
</tr>
<tr>
<td>false discovery rate (FDR)</td>
<td>404</td>
</tr>
<tr>
<td>false negative</td>
<td>690</td>
</tr>
<tr>
<td>false positive</td>
<td>690</td>
</tr>
<tr>
<td>familial aggregation</td>
<td>763</td>
</tr>
<tr>
<td>familiarity bias</td>
<td>598</td>
</tr>
<tr>
<td>family data</td>
<td>761</td>
</tr>
<tr>
<td>family-wise error rate (FWE)</td>
<td>16, 404, 436</td>
</tr>
<tr>
<td>fast-pivoting algorithm</td>
<td>425</td>
</tr>
<tr>
<td>fecal occult blood test (FOBT)</td>
<td>691</td>
</tr>
<tr>
<td>file drawer analysis</td>
<td>600</td>
</tr>
<tr>
<td>film mammography</td>
<td>250</td>
</tr>
<tr>
<td>filtered back-projection reconstruction</td>
<td>297</td>
</tr>
<tr>
<td>first-into-man (FIM) studies</td>
<td>51</td>
</tr>
<tr>
<td>first-order correct</td>
<td>83</td>
</tr>
<tr>
<td>first-order validation</td>
<td>708</td>
</tr>
<tr>
<td>Fisher exact test</td>
<td>531, 725</td>
</tr>
<tr>
<td>Fisher index of dispersion</td>
<td>510</td>
</tr>
<tr>
<td>Fisher's z-transformation</td>
<td>841</td>
</tr>
<tr>
<td>Fisher's exact test</td>
<td>570, 582, 663</td>
</tr>
<tr>
<td>Fisher's least significant difference</td>
<td>436</td>
</tr>
<tr>
<td>fixed effects model</td>
<td>553</td>
</tr>
<tr>
<td>Food and Drug Administration (FDA)</td>
<td>245, 313, 331</td>
</tr>
<tr>
<td>Food and Drug Administration (FDA) guidelines</td>
<td>880</td>
</tr>
<tr>
<td>Fourier transform</td>
<td>202</td>
</tr>
<tr>
<td>fourth-order validation</td>
<td>709</td>
</tr>
<tr>
<td>fractional factorial designs</td>
<td>782</td>
</tr>
<tr>
<td>frailty models</td>
<td>166</td>
</tr>
<tr>
<td>Framingham heart study</td>
<td>137</td>
</tr>
<tr>
<td>full design</td>
<td>779</td>
</tr>
<tr>
<td>full-field digital mammography (FFDM)</td>
<td>285</td>
</tr>
<tr>
<td>fully sequential test</td>
<td>327</td>
</tr>
<tr>
<td>functional MRI (fMRI)</td>
<td>213</td>
</tr>
<tr>
<td>funnel plot</td>
<td>600</td>
</tr>
<tr>
<td>futility</td>
<td>324</td>
</tr>
<tr>
<td>futility analysis</td>
<td>174</td>
</tr>
<tr>
<td>G-efficiency</td>
<td>787</td>
</tr>
<tr>
<td>gamma distribution</td>
<td>3, 44, 169</td>
</tr>
<tr>
<td>gatekeeping strategies</td>
<td>736</td>
</tr>
<tr>
<td>Gaussian time series</td>
<td>6</td>
</tr>
<tr>
<td>gene sampling</td>
<td>404</td>
</tr>
<tr>
<td>generalized additive model</td>
<td>628</td>
</tr>
<tr>
<td>generalized estimating equations</td>
<td>6, 811, 840</td>
</tr>
<tr>
<td>generalized linear mixed models</td>
<td>4</td>
</tr>
<tr>
<td>generalized linear models</td>
<td>507, 515</td>
</tr>
</tbody>
</table>
generalized proportion designs, 501
 genetic analysis, 762
genetic coding, 187
genetic maps, 762
genomics, 752
genotype data, 761
geospatial data, 381
Gittins index, 416, 418
global health situation analysis and projection, 918
glomerular filtration, 555
goodness of fit, 367
goodness-of-fit statistics, 2
Greenwood formula, 358
gridding/addressing, 401
group model, 554
group sequential trial, 327

haplotype analysis, 767
hazard function, 804
hazard rate function, 126
hazard ratio, 635
health-related quality of life (HRQoL), 26, 608
heterogeneity, 6, 166
Hinde–Demétrio model, 510
histogram equalization, 209
HRQoL assessment, 29
HRQoL instruments, 27
human and disease biology, 566
Human Genome Project, 187
Human Rights Committee (HRC), 880
human vision, 192
hypothesis testing, 91

ignoreable missing data, 314
image enhancement, 211
image noise, 196
image processing, 209
image quality (IQ), 222
image receptors (IR), 215
image restoration, 211
impact of CONSORT, 866
impact on knowledge syntheses, 863
importance sampling, 87
incidence, 536
incidence rates, 702, 722, 903
incremental cost-effectiveness ratio (ICER), 111, 115
incremental net benefit (INB), 111, 116
index approach, 447
indirect evidence of publication bias, 597

individualized maximum repeatable dose (iMRD), 500
information extraction, 401
information matrix, 808
information state, 430
informative noncompliance, 639
input-output model, 553
Institutional Review Board (IRB), 880
instrument selection, 615
integer-valued autoregressive moving average (INARMA) models, 517
integer-valued generalized autoregressive conditional heteroscedastic (IN-GARCH) models, 517
integrity, 277
intent-to-treat analysis, 318
intent-to-treat subset analysis, 318
intention-to-treat analysis, 313
intention-to-treat design, 316
intention-to-treat principle, 313
interaction, 538, 703
interaction effects, 623
interim analyses, 323
interim monitoring, 443
intermediate outcomes, 908
International Classification of Diseases, 915
International Committee of Medical Journal Editors (ICMJE), 866
International Conference on Harmonization (ICH) guidelines, 892
International Statistical Classification of Diseases and Related Health Problems (ICD), 916
intrarater reliability, 334
interval approach, 449
interval censoring, 811
interval estimation, 571
intraclass correlation coefficient, 447
intrarater reliability, 340
isotonic regression, 628
item banking, 615
item-level metadata, 386

James–Stein estimation, 799
Jeffreys interval, 573
just noticeable differences (JND), 195
Kaplan–Meier estimator, 803, 805
Kaplan–Meier estimator (K–M estimator), 357
Kaplan–Meier plot, 357
Kaplan–Meier survival curve, 95, 636
kappa, 450
kappa index, 836
Kendall's coefficient of concordance, 336
kernel density estimate, 52
Knox model, 713
Kolmogorov–Smirnov, 807
Kullback–Leibler distance, 155, 511
Kullback–Leibler distance, 88
kyphosis data, 75
Lagrangian Poisson, 507, 512
language bias, 598
large-sample theory, 807
largest-remaining-index algorithm, 420
least squares, 366
Lee–Wei–Amato (LWA) model, 130
left censoring, 811
left filtering, 811
left truncation, 512, 811
length bias, 722
length-biased sampling, 691
Lexis diagram, 803
life expectancies, 713
life table, 704, 802
light-emitting diodes (LED), 278
likelihood principle, 584
likelihood ratio statistic, 576, 581
likelihood ratio test, 128, 368, 557, 627, 807
Likert scale, 612
limited mortality analysis, 726
linear attenuation coefficient, 227
linear interpolation, 465
linear models, 15
linear rank tests, 806
linear regression, 68, 365
linkage analysis, 763
linkage disequilibrium test, 765
liquid crystal display (LCD), 269, 278
LOCF analysis, 318
log odds, 373
log-normal distribution, 169, 464
log-rank test, 128, 669
log-rank test statistic, 667
log-scale odds ratio, 661
logarithmic interpolation, 465
logistic, 809
logistic model, 623
logistic regression, 75, 365, 715, 770
logit difference, 373
logit transformation, 365
loglinear model, 624
logrank test, 635, 725
longitudinal data, 616
longitudinal design, 547
lung study, 136
M-estimators, 5
magnetic resonance imaging (MRI), 188, 213
Mammography Quality Standards Act (MQSA), 245
Manhattan Project, 189
Mann–Whitney statistic, 483
Mann–Whitney U-test, 745
Mantel–Haenszel technique, 538
marginal rates, 842
Markov chain, 692
Markov chain Monte Carlo (MCMC), 584
Markov chain Monte Carlo method, 172, 628
Markov decision process (MDP), 41, 418
Markov decision programming, 42
Markov model, 122
Markov processes, 42, 804
matrixing design, 780
maximum concentration (C_{max}), 51
maximum likelihood, 366, 571
maximum tolerated dose (MTD), 496
maximum a posteriori (MAP) Bayesian estimation, 559
mean residence time (MRT), 469
measurement of cost, 114
measurement of effectiveness, 114
median survival time, 362
Medical Research Council Renal Cancer Collaborators, 327
memoryless property, 2
meta-analysis, 770
metadata, 380
method of moments, 571
Michaelis–Menten constant, 463
Michaelis–Menten kinetics, 459
microarray, 392
microarray quality control consortium (MAQC), 393
mid-P value, 576
minimal clinically important difference (MCID), 35
minimum important difference (MID), 618
minimum variance unbiased estimator, 571
Minnesota Colon Cancer Control Study, 691
MISCAN (Microsimulation SCreening ANalysis), 708
missing at random (MAR), 315
missing completely at random (MCAR), 314
missing data, 120, 540, 615, 616
missing responses, 613
mixed effects model, 553
mixed Poisson, 507, 508
mixed Poisson distribution, 509
mixed Poisson model, 3
mixed Poisson processes, 509
mixture model, 561
mixtures of likelihoods, 156
model checking, 809
model stability, 72
modulation transfer function (MTF), 198
molecular medicine, 191
molecularly targeted therapies, 496
Monte Carlo error, 96
Monte Carlo methods, 585
Monte Carlo simulation, 546
Monte Carlo variability, 96
Moolgavkar–Knudson two-stage model, 629
moral obligation to improve the reporting, 803
morbidity/mortality trials, 633
moving average, 911
MR angiography (MRA), 213
mRNA expression level, 392
multi-armed bandit, 416
multi-planar reformatting (MPR), 306
multicenter clinical trials, 876
multicenter trials, 121
multinomial contingency table, 570
multiple arms, 439
multiple comparison, 16, 436, 616
multiple end points, 440, 615, 616
multiple evaluators, 446
multiple event data, 129
multiple regression, 539
multiple scan average dose (MSAD), 309
multiple-sample one-way ANOVA, 648
multiple-sample Williams design, 650
multiple logistic regression model, 368
multiplicative model, 807
multiplicity, 616
multiplicity adjustment, 736
multistage theory of carcinogenesis, 624
multistate models, 804, 809
multivariate normal distribution, 488
multivariate survival, 811
multivariate frailty models, 170

National Heart, Lung, and Blood Institute (NHLBI), 886, 904
National Institute on Deafness and Other Communication Disorders (NIDCD), 895
National Study of Breast Cancer Screening in Canada, 723
National Surgical Breast and Bowel Project (NSABP), 178
natural exponential family, 507
naturalistic sampling, 749
negative binomial, 3
Nelson–Aalen estimator, 128, 805
nested case–control studies, 809
neural networks, 276
New Drug Applications (NDAs), 331
Newton–Raphson method, 128
Neyman’s minimum modified chi-square, 580
Neyman–Pearson lemma, 147
nominal scale score, 348
nominal standard errors, 72
non-informative censorship, 133
noncentral $\chi^2$ distribution, 649
noncompartmental analysis, 457
noninferiority, 586
nonlinear regression, 465
nonparametric bootstrap, 559
nonparametric maximum likelihood estimator, 805
nonparametric models, 518
nonparametric ROC analysis, 483
nonparametric tilting, 155
nonrandomized study, 537
nonstationary Markov process model, 637
nontochastic noise, 260
normal distribution, 1, 44, 464
normal quantile plot, 68
nuisance parameter, 578
Nyquist sampling theorem, 269

O’Brian–Fleming boundary, 853
O’Brien–Fleming procedure, 108
objective function, 558
observational study (OS), 539, 721, 901
observed Fisher’s information, 327
odds, 373, 546
odds ratio, 373, 770
Office of Protection from Research Risks (OPRR), 891
on-line algorithms, 428
one-way classification, 12
optimal biological dose (OBD), 498
ordered responses, 612
ordinal and interval score data, 353
ordinal data, 451
organic light-emitting diode (OLED), 278
outcome bias, 598
overall mortality analysis, 725
overdispersed binomial model, 2
overdispersed Poisson model, 2
overdispersion, 1, 506
p-values, 1
pairwise comparison, 648
panel counts, 3
parallel design with replicates, 673, 677
parallel designs without replicates, 680
parameter variability, 555
parametric models, 802
parsimonious model, 622
partial likelihood, 623
partial likelihood function, 127
partnerships and coordination in epidemiology, statistics, and trend assessment, 918
Pearson's chi-square, 580
Pearson's goodness of fit, 575
per-comparison error rate, 436
percentile intervals, 84
permutation distribution, 529
permutation test, 91, 527
pharmacodynamics, 551
pharmacoepidemiology, 536
pharmacological efficacy, 313
phase I clinical trial, 496
phase I studies, 51
phase II efficacy studies, 496
Phase II trial, 855
phase III trial, 174, 323, 855
photoelectric absorption (PA), 229
picture archiving and communications system (PACS), 274
Pitman efficiency, 581
Planck–Einstein relationship, 218
planning clinical trials, 92
plug-in principle, 64
Poisson distribution, 507, 703
Poisson model, 1
Poisson process, 2, 725
Poisson random processes, 259
Poisson regression, 543, 809
population pharmacokinetics, 551
positive clinical trials, 797
positive stable distribution, 169
positron emission tomography (PET), 188, 213
posterior distribution, 799
power, 577, 704
power calculations, 770
power-divergence statistics, 576
prediction discrepancy, 563
prediction intervals, 70
predictive checks, 563
predictive value, 728
predictive value of a negative test (PVN), 742
predictive value of a positive test (PVP), 742
prescription data, 546
prevalence, 541, 702
prevalence-adjusted bias-adjusted kappa (PABAK) statistic, 842
prevention of publication bias, 598
prevention trials, 723
primary end point, 732
primary X-ray image, 215, 234
product-integral, 806
profile likelihood function, 128
prognosis, 622
prognostic factors, 807
progressive type II censoring, 133
proportion designs, 501
proportional hazards, 622
proportional hazards model, 168, 797
proportional hazards regression model, 807
prospective sampling, 749
Prostate, Lung, Colorectal, and Ovarian Cancer (PLCO) Screening Trial, 724
protein arrays, 398
prothrombin complex activity (PCA), 563
pseudo-partial likelihood function, 131
psychometrics, 609
publication bias, 595
qualitative interaction, 443, 796
quality assurance (QA), 222, 245
quality assurance program, 910
quality of life (QoL), 608
quality-adjusted life years (QALYs), 610
quality-of-life scales, 115
quantitative interaction, 443
quantum detection efficiency, 196
quasi-random sampling, 98
radiation safety, 245
Index 933

Radiological Society of North America (RSNA), 311
radiology information system (RIS), 274
random censorship, 133
random effect, 811
random error, 546
random noise, 222
randomization, 399, 527, 581
randomization inference, 527
randomized block design (RBD), 347
randomized clinical trials (RCT), 174, 721
randomized controlled trials (RCTs), 536, 691, 860
randomized discontinuous designs, 855
randomized study of antenatal corticosteroids, 179
Rasch model, 148, 613
receiver operating characteristic (ROC) curve, 483
receiver operator characteristic (ROC), 742
reduced design, 780
reference nonsequential test (RNST), 102
region of interest (ROI), 485
regulatory science, 566
relative biological effectiveness (RBE), 241
relative likelihood, 546
relative risk, 67, 536, 622, 808
relative risk modeling, 622
relative risk—crossover design, 561
relative risk—parallel design, 659
reliability, 690
repeated significance tests, 325
replicated 2 x 2 crossover design, 685
replicated crossover design, 674, 678
replication, 399
reproducibility probability, 651
repulsion, 506
residual error model, 556
residual unidentified variability (RUV), 555
residuals, 503
resolution, 222, 255
response-adaptive clinical trials, 40
responsiveness, 614
restart formulation, 429, 431
retrospective (case-control) sampling, 750
reverse transcription polymerase chain reaction (RT-PCR), 396
Rhinoconjunctivitis Quality of Life Questionnaire (RQLQ), 34
right censoring, 802
right truncation, 811
risk assessment, 539
risk factors, 908
risk models, 622
risk set, 803
robust covariance estimator, 130
robust estimates, 477
Rose model, 205
rpg120 HIV Vaccine Study, 442
S-PLUS, 545
sample size determination, 344, 577
sample size review, 323
Saskatchewan Asthma Epidemiologic Project, 542
score statistic, 575
score test, 128
screen-film radiography, 248
screening, 689
screening trials, 721
seasonal allergy rhinitis (SAR), 34
second-order correct, 83
second-order validation, 709
secondary analyses, 727
secondary efficacy end points, 731
secondary end point, 732
seemingly unrelated regression, 122
segmentation, 401
segregation analysis, 763
selective reporting, 861
semiparametric Poisson, 507, 513
semiparametric regression, 804
sensitivity, 690, 727
sequential conditional probability ratio test (SCPRT), 106
serial correlation, 6
shared frailty model, 170
shelf life estimation, 788
signal-to-noise ratio (SNR), 196, 257
significance level, 324
significance testing, 324
Simpson's rule, 136
simultaneous comparison, 649
single binary test, 740
single photon emission computed tomography (SPECT), 188
single-photon emission computed tomography (SPECT), 213
size-biasing, 512
skewness, 62, 64
slope designs, 501
slope height area moment analysis (SHAM analysis), 457
Slusky's theorem, 605
SNP-chip, 397
spatial resolution, 198
spatial smoothing, 272
Spearman–Brown projection, 337
specificity, 690, 728
spending function, 443
spin in the interpretation, 862
splicing array, 396
spline functions, 545
spread, 64
stability protocol, 788
stability study designs, 778
standard 2 × 2 crossover design, 684
Standard Protocol Items: Recommendations for Interventional Trials [SPIRIT], 870
Stanford Heart Transplantation Study, 171
state-elimination algorithm, 421
statistics for lamivudine, 328
stepwise regression, 70
stochastic curtailment, 175
stochastic health effects, 235
stochastic simulation, 565
stopping rules, 324
stopping set, 419
Strategies for Management of Anti-Retroviral Therapy (SMART), 847
stratification, 539, 622
stratified Cox model, 808
stratified population, 128
stratified sampling, 87
strengthening country health information, 918
structural equation modeling, 614
structurally missing data, 319
Student's t distribution, 92
Student's t-test, 585
subgroup analyses, 442
subgroup analysis, 793
subject sampling, 404
subject variability, 553
sufficient statistic, 430
superposition methods, 471
support reduction algorithm, 5
surface models, 692
surrogate end points, 704
surveillance of disease, 914
survival analysis, 664, 802
survival function, 358
symmetrical funnel plot, 602
systematic errors, 82
2 × 2 crossover design, 672
2 × 2m crossover design, 676
t intervals, 83
t-test, 527
teratogenic health effects, 235
termination time, 2
test for equality, 645
test for equivalence, 644, 646
test for noninferiority/superiority, 645
therapeutic TI studies, 850
therapeutic vaccine trials, 854
third-order validation, 709
tied data, 131
tiling array, 397
time-dependent covariates, 132
time-to-disease progression, 357
time-to-event data, 134, 357
tomosynthesis, 292
transformation invariant, 83
transition probability, 122
translation/cross-cultural validation, 615
transmission disequilibrium test, 765
transmission imaging, 216
trapezoidal method, 465
treatment effect parameter, 326
treatment interruption, 846
treatment switches, 120
trial monitoring, 728
trial registration, 870
triangularization algorithm, 423
truncation, 802
two-arm trial, 723
two-by-two table, 838
two-sample crossover design, 646
two-sample parallel design, 645
two-stage sampling, 749
two-way ANOVA, 336
two-way crossed classification, 17
type I error, 324
type II censoring, 133

U.S. Department of Veterans Affairs Cooperative Studies Program, 876
U.S. Food and Drug Administration (FDA), 382, 650, 778
U.S. National Institutes of Health (NIH), 329
unbalanced data, 17
uncertainty, 552
underdispersion, 2, 508
unit variance function, 508
unplanned subgroup analysis, 794
US Nuclear Regulatory Commission (NRC), 245

VA health care system, 887
validation, 613
validation studies, 612
value-level metadata, 386
variable-level metadata, 384
variance reduction, 98
Veterans Integrated Service Networks (VISNs), 887
vital statistics, 862

Wald confidence interval, 570
Wald test, 128, 368
Weber–Fechner law, 195
Weibull distribution, 807
weight-average conditional power, 105
weighted distribution, 507
weighted empirical distribution, 93
weighted kappa, 450
weighted kappa index, 839
weighted log-rank statistics, 105
weighted logrank test, 638
weighted Poisson, 507, 510
weighted Poisson models, 6
Whittle’s approximation, 432
wild bootstrap, 74
Williams design, 643
Wilson interval, 573
within-subject variation (WSV), 340
Women’s Health Initiative, 901
World Association of Medical Editors (WAME), 866
World Health Organization (WHO), 608, 914
worst rank analyses, 319

X-ray imaging, 213

Z-transformation, 448
zero-inflated models, 6
zero-inflated Poisson models, 5
zero-modification, 512