

---

# Index

## A

Accuracy, 86  
Across-strata shift, 194, 196, 200  
Affymetrix, 6, 30–32, 34, 35  
Agreement, 178  
    attributable to chance, 83–84  
    intraobserver, *see* Intrarater  
        reliability  
    interobserver, *see* Interrater  
        reliability  
    limits of, 96, 98  
    negative, 85, 87  
    overall, 85  
    perfect, 88, 92, 97, 102  
    positive, 85, 87  
    reversed, 92, 102  
Algorithms  
    clustering, 45  
    gene-shaving, 39  
    genetic, 46  
    geometrization, 23–25  
    labeling, 23–25  
    quantitation, 23–25  
    spotfinding, 24  
    statistical, 18–20  
Alignment, 9  
Amino acid, 3, 7  
Analytical engine, 22  
Angiosarcoma, 194, 196, 199, 200, 201  
ANOVA, 19, 24, 94, 104  
    robust, 38

## Array

    spotted, 31, 32

## Association

    disease-genotype, 144  
    gene-disease, 143–168  
    linear, 88, 104  
    nonlinear, 102  
    tests, 143–168

## Autorad, 15

Average negative agreement, 85

Average positive agreement, 85

## B

## Backbone

    Oracle, 24

## Background

    adjustment, 32  
    intensity, 32  
    level, 25  
    signal, 18, 27  
    threshold, 25, 32  
    value, 26, 32

## Basepair

    sequence, 4, 8, 31

## Batch effect, 95

Bayesian analysis, 12, 19, 25, 37, 40, 42, 43

## Bias, 12, 96

    constant, 99, 101  
    proportional, 99, 101

## Binary tree, 3

## Binomial distribution, 194

- Bioinformatics, 1, 9
- Biological pathway, 4, 5
- Biomarker, 3, 11–13, 81–106 (*see also* Marker)
  - continuous, 82, 88–104
  - definition of, 81
  - dichotomous, 82–88
  - examples of
    - chronic exposure to heavy metals and dioxins/furans, 104
    - colon cancer risk, 91, 92
    - environmental tobacco smoke exposure, 82, 101, 104
    - exposure to benzene, 96
    - exposure to toluene, 103
    - lung cancer, 82, 83, 86, 87
- Biometric modeling, 2
- Biometry, 2
- Biostatistics, 1, 2
- Bland-Altman method, 96, 106
- BLAST (Basic Local Alignment Search Tool), 8
  - GAPPED, 8
  - PSI-BLAST, 8
- Blinding, 82, 184
- Bonferroni adjustment, 152, 160, 180
- Bootstrapping, 36, 180, 192–196, 199, 200
- C**
- Calibration, 95
- Cancer, 29, 38
  - breast, 176–183
- Candidate genes, *see* Genes, candidate
- CAP, *see* College of American Pathologists
- Carcinogenesis, 7
- Case-control study, 104, 132, 134–135, 191, 194–196, 198, 200, 201
  - control selection in, 132
  - multistrata, 192
- Categorical data, 114
- CDF, 194
- Central Limit Theorem, 195, 197
- CERM (Cumulative exposure rank months), 200, 201
- Chi-square distribution, 44
- Chi-square test, *see* Tests, chi-square
- Classification, 40, 41, 65, 76
- Clinical importance, 96, 98, 174
- Clinical trials, 2, 11, 12, 106, 170, 172, 184, 185
- Clinical utility, 170–172, 184
- Closed testing 144–147
- Clustering, 39, 40, 41, 43, 65
  - algorithm, 45
  - hierarchical, 42–45
- Coefficient of variation, 37, 106
- Cohen's kappa, *see* kappa
- College of American Pathologists (CAP), 171, 183–185
- Computational biology, 1, 2, 3, 7, 9, 10, 12, 13
  - academic programs in, 9
- Computer models, 7
- Concordance
  - coefficient of, 91, 93, 96, 101, 128
- Confidence interval, 43, 106
- Conformity, 86
- Confounding, 95, 191
- Conditional likelihood, 200
- Consistency (of agreement), 26, 87, 103
- Consistency (of estimation), 192, 200
- Consistent statistical test, 112
- Constructionist philosophy, 10
- Continuity correction, 196
- Convergence in probability, 195
- Convolution, 196

Correlation, 93, 96, 98, 104  
  inter-pixel, 43  
Correlation coefficient  
  intraclass, 89, 90, 92, 93, 95, 101, 105, 106  
  Pearson, 88, 89, 92, 93, 101, 102, 104  
  problems with, 88, 102  
  Spearman, 101, 102, 104, 106  
Correspondence analysis, 65  
Cost-benefit, 39  
Cox model, 133, 136, 138, 139, 179  
  hazard, 138  
  hazard ratio, 133, 138  
  prognostic index and, 138  
  sample size for, 174, 175  
  survival analysis and, 136  
Critical value, 194  
Cross-signal comparison, 24  
Cross-platform  
  applications, 22  
  independence, 21  
Cumulative distribution function,  
  *see* CDF  
Cut-points, 172, 173, 185  
  problems with, 173–174  
CV, *see* Coefficient of variation

## D

Data  
  analysis, 17–19  
  categorical, 114  
  dichotomous, 114  
  exploration, 22  
  numerical, 114  
  ordinal, 114  
  storage, 21  
  structure, 21  
Database, 21, 22  
  backbone, 21

Decision tree, 105  
Delta method, 199  
Deming regression, 99, 100, 106  
  weighted, 101  
Densitometry, 15  
Detectable level, 34  
DFS, *see* Disease-free survival  
Diagnostics, *see* Statistical  
  diagnostics  
Dichotomous data, 114  
Dichotomization, 191, 192  
Differential equations, 46  
Disagreement, 82, 84, 85, 93, 99, 101  
Discriminant analysis, 41  
Disease-free survival, 178, 179  
Distribution  
  binomial, 194  
  chi-square, 44  
  gamma, 37  
  hypergeometric, 200  
  logistic, 195  
  multivariate normal, 41  
  normal, 41, 42, 90, 96, 99, 104  
  statistical, 19  
DNA, 3–7, 29, 33, 34, 44, 94, 169  
Dominance, 149–150

## E

Effect size, 116–117, 174  
Efficiency, 191  
Electrophoresis, 3, 4, 7, 12, 15, 16, 53–55, 57  
Envelope of imaging, 17, 25, 26  
Environmental effects, 154–155  
Epistasis, 136, 153–154  
Error  
  measurement, 88  
  Type I, 173  
  Type II, 111

variance, 93, 100, 101  
     homogeneity of, 99, 101  
     ratio of, 100  
 Errors-in-variables model, 100  
 EST (expressed sequence tag), 30  
 Eugenics, 11  
 Evolutionary biology, 3, 11  
 Exceedance statistics, 196  
 Exchange matrix, 3, 8  
 Experimental design, 17, 30, 34  
 Exponential failure, 175  
 Exposure, 191  
     distribution, 193, 194, 198  
     index, 199, 200  
     markers of, 81, 82, 96, 102–104  
     occupational, 199, 200  
     rank-ordered, 191, 192, 199, 200  
     stratum-specific, 192, 194, 198, 201  
 Expression profile, 7  
 Extensibility, 22

## F

Factor  
     analysis, 65  
     loadings, 40  
     scores, 39, 40  
 Factorial experiment, 175  
 False discovery rate (FDR), 144  
 Familywise error rate (FER), 144  
 FDR, *see* False discovery rate  
 Feature  
     geometry, 18  
     imaging, 17  
     intensity, 35  
     with labels, 18  
 Feedback  
     mechanism, 18  
 FEW, *see* Familywise error rate  
 Filtering

background, 61–62  
     gel images, 59  
 Fluorescence, 30, 34  
 Fourier transform, 46

## G

Gamma distribution, 37  
 Gaussian, *see* Normal  
 Gel, 62–63, 69  
     electrophoresis, 57  
     images of, 70–75  
     master, 76  
     preparation, 55–57  
     staining and scanning, 57–58  
     synthetic, 64–65  
 Gel images  
     filtering, 59–60  
 Gene  
     blocks, 39  
     candidate, 132  
     classes  
         discriminatory power of, 42  
         latent, 42  
     clustering 40, 41  
     effects, 46  
     expression, 6, 12, 15, 16, 26, 29–33,  
         35–37, 39, 41, 42, 46, 160–164  
     differential, 37  
     intensity, 42  
     pattern, 46  
     periodic, 46  
     expression profile, 7  
     housekeeping, 33  
     interaction, 46  
     intensity, 42  
     modifier 136  
     networks, 46  
     prefiltering of, 44  
     products, 33–35, 42, 44

- rank, 25
- sequence, 7
- shaving, 39
- space, 39
- transcription, 5, 46
- translation, 46
- variation, 37
- Generalized linear model (GLM), 132
- Genetic epidemiology, 131
  - association studies in, 131
- Genetics, statistical, 2
- Genome
  - human, 15
  - scan, 144, 149, 159–160
- Genomics, 5, 9, 11
  - modeling, 11
- Geometry, 23
  - characterization, 27
  - feature, 18
  - storage, 24
- Geometrization,
  - algorithm, 23–25
- Gibbs sampling, 12
- Glass slides, 31
- Glutathione-S-transferase (GST), 131
- Gold standard, 82, 84–87, 89, 104, 173
- Golub et al. data set, 160–164
- Goodness-of-fit, 20, 193
- Graphical methods
  - data exploration and, 22
- GST, *see* Glutathione-S-transferase
- H**
- Hazard ratio, 133, 138, 175
- Hereditary traits, 11
- Heterogeneity of sample values, 88, 96
- Hierarchical clustering, 42–45
- Hierarchical model, 37
- Historical data, 200
- HLA, 148
- Hodges-Lehmann estimator, 196–198, 200
- Homogeneity, 36
- Human Genome Project, 6
- Hybridization, 30–32, 34, 36
  - differential, 43
- Hypergeometric distribution, 200
- Hypothesis testing
  - multiplicity in, 173, 180, 184, 185
- I**
- ICC, *see* Correlation coefficient, intraclass
- Image
  - acquisition, 18
  - alignment, 62–63
  - analysis, 2, 20
  - background, 17
  - composite, 22
  - data, 24
  - gel, 59
  - intensity, 32
  - master, 64
  - microarray, 22
  - processing, 22,
  - quantitation, 15–20, 23, 24, 35
  - warping, 62
- Imaging, 24, 25
  - envelope, 17, 18, 20, 25, 26
  - methods, 27
  - parameters, 25
  - variability, 25
- Immunoblotting, 15
- Independence, 98, 99
- Independent variables, 132
  - confounders, 132
  - covariates, 132
  - factors, 132

predictors, 139  
 Index of crude agreement, 83, 84, 105  
 Induction level, 39  
 Inference set, 18  
 Inheritance  
   bleeding, 11  
 Intensity  
   gene-specific, 42  
 Interaction effect, 90, 94, 173–175,  
   179, 180  
 Interchangeability, 82, 98  
 Internal controls, 33, 34  
 Intraclass correlation coefficient,  
   *see* Correlation coefficient,  
   intraclass  
 Isoelectric  
   focusing, 7, 16, 54, 56  
   point, 51, 54

## J

Jacob-Monod central dogma, 4  
 Java, 22  
   applets, 22  
   application, 21  
   code, 24

## K

Kaplan-Meier, 179  
 Kappa, 83–85, 87, 105, 106

## L

Labeling algorithms, 23–25  
 Lack-of-fit, 44, 47  
 Large-sample properties, 195  
 Latent class, 40–45, 47  
 Latent variable, 37, 41  
 Least squares, 35, 36, 40, 46  
   partial, 39, 40  
 Level of evidence (LOE), 171, 172  
 Level of measurement, 82

Limits of agreement, *see* Agreement,  
   limits of  
 Linear association, 88, 104  
 Linear regression, 132, 137  
 Linkage disequilibrium, 143  
 Lin's coefficient, *see* Concordance,  
   coefficient of  
 Local alternative, 193  
 Locally most powerful test, 193  
 LOE, *see* Level of evidence  
 Logistic distribution, 195  
 Logistic model, 134  
   conditional, 135  
   logit and, 134  
   log odds ratio and, 135  
   odds ratio and, 133, 134  
   unconditional, 135  
 Logistic regression, 179, 192, 200  
   ordered, 136–137  
 Logistic shift, 191–193, 195, 196,  
   199, 200  
 Log-rank test, 174

## M

Mapping tables, 22  
 Marginal likelihood, 193  
 Marker (*see also* Biomarker)  
   breast cancer, 176–182  
   clinical utility of, 170–172  
   dichotomization of, 178, 179  
   discretization of, 173  
   molecular, 169–185  
   predictive, 170  
   prognostic, 170, 172, 174, 175  
   studies, 171, 184  
   sample size for, 174  
   surrogate, 160  
   value of, 173, 185  
 Markov Chain Monte Carlo (MCMC), 42

- Matching, 192, 198, 200  
Match-mismatch, 34, 35  
MCMC, *see* Markov Chain Monte Carlo  
Mean square, 90, 91  
Measurement  
    error, 37, 88  
    level of, 82  
    scale of, 88, 96  
Median, 198, 199  
Meta-analysis, 19, 20, 22, 25, 26, 172, 176  
Metastasis, 29  
Method comparison studies, 93, 95  
Micelle, 54  
Microarray, 6, 13, 24, 25, 29–48, 169  
    analysis, 15–17  
    chip, 18, 31  
    data, 32, 38, 40, 42, 46, 47, 160–164  
        visualization of, 47  
    experiment, 42  
    image, 22, 31  
    instance, 29, 31, 33–36, 38, 41–43, 47  
        outliers in, 35  
    slide, 42  
    spotted, 36  
    studies, 23  
MIDAS (Mathematical-Modeling of Image Data Across the Sciences), 20–22, 24, 25, 27  
Minimum risk, 36  
Missing data, 185  
Model  
    statistical, 20  
Modifier genes, *see* Genes, modifier  
Molecular biology, 1–4, 10–13, 15, 24, 48, 173  
    training in, 6  
Molecular fingerprinting, 3, 13  
Molecular function and information  
    flow, 4  
Molecular marker, *see* Marker  
Molecular mass, 51  
Monotonic relationship, 102, 104  
Monte Carlo, 147  
Morphology  
    mathematical, 61, 62  
Motifs  
    sequence, 12  
MULTTEST, PROC, 143–168  
    closed Fisher combination  
        method and, 148  
    closed MinP-based Algorithm and, 146  
    closed Simes-Hommel method  
        and, 147  
    syntax for, 151, 154–156, 158, 165  
Multimedia data, 22  
Multiple testing, 143–168, 173, 180, 184, 185  
Multiplicity, *see* Multiple testing  
Multiplicity-adjusted p-values, 143–168  
Multiresolution analysis, 66–68, 69  
Mutation, 3, 8  
  
N  
National Surgical Adjuvant Breast and Bowel Project (NSABP), 177–179, 181, 183  
Negative agreement, index of ( $p_{\text{neg}}$ ), 85, 87, 105  
Negative binomial regression, 133, 136, 137  
    rate ratio (irr) and, 133, 136, 137  
Neural network, 10  
Noise  
    removal, 75–76  
Nonlinear association, 102

Nonparametric analysis, 36, 196  
 Normal approximation, 195, 196, 200  
 Normal distribution, 41, 42, 90, 96,  
     99, 104  
     multivariate, 41  
 Normal model, 42, 43  
 Northern blot, 4, 5, 15, 29  
 NSABP, *see* National Surgical  
     Adjuvant Breast and Bowel  
     Project  
 Numerical data, 114

## O

Odds ratio, 191  
 Oligonucleotide, *see* oligos  
 Oligos, 30, 32, 34–36  
     intensity of, 36  
     match-mismatch, 34  
 One-way analysis, 41–42  
 Oracle, 22, 24  
 Ordinal data, 114  
 Ordinal exposure, 191, 192, 194  
 Outcome, 135–137  
 Outliers, 35, 96, 164, 196  
 Overdispersion, 44, 138

## P

$P_{\text{neg}}$ , *see* Negative agreement, index of  
 $P_{\text{pos}}$ , *see* Positive agreement, index of  
 PABAK, *see* Prevalence-adjusted  
     and bias-adjusted kappa  
 Parameters  
     gene-specific, 35  
 Pattern recognition, 65  
 PCA, *see* Principal components  
     analysis  
 PCC, *see* Correlation coefficient,  
     Pearson  
 PCR, *see* Regression, principal  
     components

Penetrance, 157–159  
 Peptide, 3  
 Permutation test, 146, 147  
 Phenotype, 2–4  
 Phenotyping, 3, 7  
 Photolithography, 30  
 Pilot studies, 124–125  
 Pixel, 18, 33  
     correlation, 24, 43  
     intensity, 23, 25  
     kurtosis, 23  
     principal components of, 24  
     variance, 23  
 Plot  
     diagnostic, 48  
 PLSR, *see* Regression, partial least  
     squares  
 Poisson regression, *see* Regression  
     analysis, Poisson  
 Polyacrylamide gel electrophoresis,  
     *see* 2D-PAGE  
 Population stratification, *see*  
     Stratification, population  
 Positive agreement, index of ( $p_{\text{pos}}$ ),  
     85, 87, 105  
 Power, *see* Statistical power  
 Predictive factor, 182  
     definition of, 170  
 Prefiltering, 44  
 Prevalence-adjusted and bias-adjusted  
     kappa (PABAK), 84, 85, 87,  
     105, 106  
 Principal components analysis  
     (PCA), 24, 38, 39, 47, 48  
 Probe, 30, 34–36  
     weights, 35, 36  
 Problem domain, 21  
 PROC MULTTEST, *see*  
     MULTTEST, PROC



- Profiling, 3
- Prognostic factor, 172–174, 176, 179, 182, 184, 185  
definition of, 170  
phase I–III, 184  
ranking of, 171  
studies, 184
- Prognostic value, 173
- Proportional hazards model, *see* Cox model
- Protein, 4, 6, 8, 13, 16, 51, 54, 56  
Data Bank, 8  
expression 15  
folding, 7, 12  
labels, 23  
sequence, 4  
structure, 7, 8  
taxonomy, 3  
STAT, 5
- Proteome, 6, 16, 51
- Proteomics, 6, 9, 16–18, 23, 24, 51–80
- Publication guidelines, 185
- P-values  
adjustment of, 143–168, 174, 180
- Q**
- QTL, *see* Quantitative trait loci
- Quality control, 24, 35, 47
- Quantitation, 25  
algorithms, 23–25  
quality control and, 35,  
results, 24
- Quantitative trait loci (QTL), 144
- R**
- Random effects model, 90, 94, 95
- Random sample, 90, 95
- Random variation, 93
- Randomization, 174
- Ranked data, 101, 102
- Rank of exposure, 191, 192, 199
- Rare disease, 191–193
- Recessivity, 151–152
- Recombination, 159
- Reductionist philosophy, 10
- Reference method, 99
- Region of interest (ROI), 16
- Regression analysis, 24, 34, 39, 96, 101, 184  
negative binomial, 133, 136–138  
partial least-squares, 39, 40  
Poisson, 137, 138  
principal components, 39, 40
- Relative frequency, 84, 85
- Reliability, 172, 178, 184  
assessment of, 82–86, 89–93, 100, 104, 106  
definition of, 81  
intrarater, 81–83, 90, 91  
interrater, 81–86, 90, 91
- Repeatability (*see also* Reliability)  
within subject, 96, 98
- Repeated measures, 41
- Replicates, 90, 93, 94, 101
- Reproducibility, *see* Reliability
- Residuals, 44  
analysis of, 44  
overdispersion of, 44  
plot, 44
- Residue exchange matrix, 3, 8
- Retrospective study, 172–174, 183
- Risk, 132, 135–138  
factor, 191
- RNA, 4, 6, 7, 12, 15, 16, 29, 30, 34, 42, 46
- Robustness, 47, 196, 200
- S**
- SAGE (Statistical Analysis for Genetic Epidemiology), 11

- Sample preparation, 57
- Sample size, 93, 111-130, 171, 174, 175, 191, 192, 194, 196, 200
  - calculation of, 117-119
  - formulas, 120
  - grant applications and, 125
  - interaction effects and, 175
  - marker studies and, 174, 184
  - nomograms, 122
  - simulation and, 123
  - software, 121
  - tables, 122
  - too large, 119
  - too small, 120
- Scalability, 22
- Scale of measurement, 191
- Scatterplot, 48, 88, 96, 98, 99, 101
- SCC, *see* Correlation coefficient, Spearman
- SDS-PAGE, 7, 16, 18
- Selection bias, 185
- Sensitivity and specificity, 85, 86, 173, 178
- Sequence
  - alignment, 9, 12
  - motifs, 12
  - pairs
    - high-scoring, 8
  - searching, 9
- Shift, 196, 199, 201 (*see also* Logistic shift)
  - percentile, 199, 201
- Shrinkage estimator, 37
- Signal
  - background, 18
  - comparison, 24
  - intensity, 37
  - location, 24
  - primary, 23
  - threshold, 18, 27
  - variability, 23
- Signal-to-noise ratio, 17, 18
- Significance level, 194
- Simulation
  - computer, 123, 195, 196, 200
- Slice, 77-78
- SNP, 143, 144, 149, 159
- Software, 138
  - HERMeS, 59
  - MELANIE, 59
  - MINISNAP, 99, 101, 106
  - Oracle, 22, 24
  - PEPI, 106
  - sample size, 121
  - SAS, 106, 143-168
  - S-Plus, 22, 24
  - Stata, 133, 136, 139
  - statistical, 18
  - stepwise selection of predictors
    - and, 139
- Southern blot, 4
- Spatial modeling, 32
- Spectroscopy, mass, 58
- Spike, 34
- Splines, 174
- Spline smoother, 46
- Spot, 33
  - characterization, 32
  - detection, 60
  - identification, 58
  - intensity, 34, 37, 42
  - matching, 63-64
  - quantification, 62
- Spotfinding algorithm, 24
- Spotted array, 31, 32
- Spotters, ink-jet, 31
- Spotting, 30
  - doughnut, 32

- Standardization, 33, 36, 47, 200
- Standard method, 82, 86, 87, 99
- STAT (signal transducers and activators of transcription), 5
- Statistical algorithm, 18–20
- Statistical diagnostics, 22
- Statistical genetics, 2
  - history of, 10–11
- Statistical models, 20
- Statistical power, 12, 111–130, 171,
  - 173–175, 184, 185, 192, 194, 195
  - achieved, 123, 200, 201
  - conventional values of, 113
  - ethics and, 113
  - grant applications and, 125
  - local, 193
  - post-hoc, 124
- Statistical tests, *see* Tests
- Stratification, 154–156, 175, 184,
  - 191, 199, 200
  - population, 139
- Stratum-specific statistic, 192, 193,
  - 196, 199
- Strike's method, 99–101, 106
- Study design, 184–185
- Supergenes, 39
- Supervised methods, 33
- Surrogate marker, 106
- Survival analysis
  - alternatives to, 176
- Susceptibility, 132–135
- SVD, 40
- Symmetry, 198
- T**
- TDT, *see* Transmission disequilibrium test
- Test method, 99
- Tests
  - chi-square, 131, 134, 149
  - closed permutation, 160
  - closed minP method, 145–147
  - Cochran-Armitage, 155, 157
  - Fisher combination, 148
  - Fisher's exact, 104, 149, 155
  - Kruskal-Wallis, 104
  - Mann-Whitney-Wilcoxon test, 104
  - Mantel-Haenszel, 154
  - permutation, 146, 149–151
  - Sidak, 160
  - significance, 100, 105, 106
  - Simes-Hommel, 147
  - stepdown, 151–152, 157, 159
  - Student's *t*, 104
- Tests for
  - epistatic effects, 153–154
  - gene-disease association, 143–168
  - microarray data, 160–164
- Ties, 194
- TMUGS, *see* Tumor Marker Utility Grading System
- Tolerance parameters, 25
- Top-hat transform, 61
- Transcriptomics, 6, 9
- Transformation, 42, 47, 96
- Translation alternatives, 192
- Transmission disequilibrium test (TDT), 139
- Treatment effect, 193, 199, 200
- Truth table, 86
- Tumor Marker Utility Grading System (TMUGS), 171
- Two-way analysis, 42
- 2×2 Table, 82, 83, 85–87
- 2D-PAGE, 51, 52, 55
- Type I error, *see* Error, Type I
- Type II error, *see* Error, Type II

**U**

Unbiased estimation, 198  
User interface, 21  
U-statistic, 195

**V**

Validity, 85, 93, 172, 173, 184  
    assessment of, 86–88, 95–104, 106  
    concurrent, 104  
    construct, 104  
    criterion, 103  
    definition of, 81  
    predictive, 103, 104  
Variability, 19, 24  
    analytical, 81, 93, 94  
    between rater, 82  
    between specimen, 89, 90  
    inter-laboratory, 173, 184  
    inter-observer, 12  
    inter-subject, 81, 93–95  
    intra-laboratory, 184  
    intra-observer, 12  
    intra-subject, 81, 93–95  
    laboratory, *see* Variability,  
        analytical  
    measurement, 81, 93, 94  
    signal, 23

    sources of, 58–59  
    unrecognized, 26  
    within rater, 82  
    within specimen, 89, 90

Variable selection

    stepwise, 139

Variance, 93, 99–101

Variance components, 90, 94

Variance-inflation factor, 175

Vinyl chloride, 200, 201

**W**

WADP, *see* Weighted average  
    discrepant pairs statistic

Wavelets, 66–69, 75–76

Weighted average discrepant pairs  
    statistic (WADP), 45

Weighted statistic, 193

Weighted sum, 35

Weights

    oligo-specific, 36

    probe-specific, 35, 36

Wilcoxon statistic, 192

    stratum specific, 193, 199

Workflow, 18

    diagram, 18, 19

Work history, 200