

Index

Page numbers in **bold** (e.g., **123**) refer to figures; in **bold/italics** (e.g., **123**) refer to tables; in *italics* (e.g., *123*) refer to footnotes

- 23andMe, 8, 230
 classification, 137
- abstraction, assumptions and axioms, 77
Acrylic Genetics, 8, **9**
- adaptation, 192
 to extreme environments, 214
 and female orgasm, 238
 to freediving, 221
 genomic, local, 223
 medical implications, 224
 and natural selection, 70, 83, 195
 origin of, understanding, 169
 perspective of, 307
 phenotypic, spleen, 214
 spleen size, 221
- adaptationism, 194, 200, 261
- adaptationist
 explanation, trait variation, 215
 IQ explanation, 240
 methodological, 213
 paradigm, 195, 199, 261, 307
- adaptive scenario, 214
- adenosine triphosphate (ATP), 48
- Adult human genitalia, **250**
- Africa
 genomic variation, 171–176
 heterozygosity correlation with distance
 from, 187–188
 multiregionalism hypothesis, 42
 versus non-African nucleotide diversity,
 171–173
 Planet Unity, 176, 188
 sex-biased dispersal out of, 157
- Africa–East Asia–Europe genomic overlaps,
130
- agapasm (evolutionary love), 292
- age estimation, empirical method of
 molecular clock, 47
- allele under natural selection, An, **198**
- alleles, 20
 combinations, loss of, 122
 common and global distribution, 173
 common and private, 175
 dark and light skin, fixation, 211
 distribution, 171, 173–175
 global, Lewontin collection, **177**
 evolution, for lactase persistence, 192
 fitness, **198**
- frequencies, 23
 across continental regions, distinctness,
177
 change of, 10
 at different loci, 186
 differences in populations, 33
 differences, at different loci, 138
 distributions at neighboring loci, 211
 inferred and Hardy–Weinberg simple
 square expansion, 136
 parameters, estimation procedures
 (Weir), 162
 of *PDE10A*, 222
 in populations, estimation, 91
 at single loci, 148
 in variance partitioning, 144
- global distribution, 179
- incomplete dominance, 21
- microsatellite, geographic flow, 172
- per locus, and population diversity, 104
- and phenotype of individuals, 23
- pleiotropically causative, 212
- and population differentiation, 109
- presence profile of, 146
- rare and private distribution, 174

- recessive and dominant, under natural selection, **198**
- substitution, across mice and humans, 207–210
- substitution, average effect of, 240
- T4 production, upregulation, 219
- under selection, conditions, 210
- world map, schematic, **172**
- allelic lineages, **46**, 50
- Allentoft, M.E., on Eurasian genetic landscape, 35
- alternation of generations, 20
- amino acids, and codons, 204
- AMOVA methodology, 141
- analysis of variance (ANOVA). *See* ANOVA (analysis of variance)
- anacasm (determinism), 292
- Anatolian hypothesis, **36**
- anatomy, female genital, 255–257
- Ancestral recombination graph, **51**
- ancestral recombination graph (ARG), **51**
- ancestry kit, genetic, 134
- ancestry, tracing of, 33
- AncestryDNA, 8, 230
- Andreasen, R.O., on cladistic races, 126
- androgens, 251
- Ankeny, R., 76
- ANOVA (analysis of variance), 29, 78, 132, 139
- error domestication, 302
- phenotypic decomposition, 240
- variance decomposition and Lewontin's equations, 139–140
- anthropic principle, 287
- antideterminism versus indeterminism, epistemological (Dewey), 293
- antirealism, ontological stance toward biological races, 282
- antirealists, 126, 269
- biogenomic cluster/race, conceptions, 271, 278
- biological, ignoring biogenomic cluster/race debate, 278
- Edwards on, 273
- Hochman on human race, 275
- races, perspective on, 267
- ape evolution, 56–61, 61
- ape fossil record, 59
- “Apportionment of Human Diversity, The” (Lewontin), 118, 264
- Archaea, **0**, **310**
- ARG (ancestral recombination graph), **51**
- assumption archaeology, 82
- assumptions, questions about, 96
- of genetic variation, 101
- and population trichotomy, 95
- variance partitioning and clustering analysis explained, 133
- Ásta, conferralist framework, construction of categories, 279
- ATP (adenosine triphosphate), 48
- Auberger* gene, 177
- Australopithecus (Praeanthropus) afarensis*, 52, **53**, **72**
- autopoiesis, 34
- autosomal genes. *See* genes
- autosomes, 46
- averaging strategy, 78
- Avery, O., 24
- back to Africa migrations, 56
- badMIXTURE* (computer program), 95
- Bajau peoples
- allele prevalence, and upregulated T4 production, 219
- case study, value and outlook, 224
- distribution map, **216**
- freediving abilities, 214–224
- natural selection, shaping influence, 214
- and Saluan peoples, spleen size comparison, 219
- spleen size, 216–224, **217**
- Baldwin effect, 224
- bar plots, Lewontin calculation errors, **180**
- Bateson, W., 27
- Bayesian inference, in statistical modeling, 146
- Bayes's theorem, 26, 146
- Begun, D., 59
- on dryopithecines, 59–60
- Out of Europe hypothesis, 60
- Bell Beaker culture, **37**
- Bergström, A., on common and private alleles, 175
- Bernoulli, J., 26
- biallelic locus, **119**, 137
- genetic variance, decomposition at, 141
- in two populations, 107
- Biddanda, A., allele distribution, 174
- big data, genomic, 22, 25
- binomial distribution, 26
- “Biological Aspects” (Park), laboratory-experimental model in, 80

360 · Index

- biogenomic classification, of races, 267
 biogenomic clusters/races
 versus biological race distinction, 272–274
 constructivist conventionalism, 270, 276, 282
 conventionalism about, 282
 debates about, 278
 existence of, 269
 to one-to-one mapping, nonexistence, 272
 pernicious reification, 269
 realism, 264, 268, 275, 277, 282
 realist and antirealist conceptions, 271, 275
 and social races, 277
 biogenomic race concepts, 90
 biological disciplines, metrics and models
 context, **113**
 biological features, relevance to evolution of
 society, 29
 biological phenomena, and statistics, 27
 biological race, 264, 269
 biological racial realism, 268–269, 272
 and biogenomic cluster/racial realism, 275
 biology, aim of evolutionary, 74
 biology, and race determination, 278
 See also race
 biology, conservation. *See* conservation biology
 biomedicine, DNA and genomics context in,
 229
 biometrician versus Mendelian debate, 27, 76
 bonobos, 56, **65**
 bottlenecks
 genetic, 171, 175, 187
 populational, 88
 bottom-up modeling, 132, 147
 Boyle, R., 2
 brain expansion, example, 169
 branch reticulation topology, 126
 Branching life, **310**
Brave New World (Huxley), 30
 breeding, controlled, 29

 candidate genes, 214
 catarrhines, **63**, 308
 causal inference, from data, 303
 causation, philosophies of, 304–305
 Cavalli-Sforza, L.L., 24
 criteria, rank order of, 153
 probabilistic phylogenetic inference, 124
 on sampling protocol, aboriginal
 populations, 153
 cells
 differentiation, 11
 diploid, 20

 endosymbiotic events within, 311
 eukaryotic, 20, 48
 haploid, 20
 oxygenated red blood, storage, **217**, 217
 sperm, 46
 stem, 75, 85
 thyroid, 219
 census size, conflation, 86
 Center for Population Health Sciences
 (Stanford University), 235
 CEPH (Centre d'Étude du Polymorphisme
 Humain), 153
 See also Fondation Jean Dausset-CEPH
 cheetahs
 genetic diversity, 168
 populational bottlenecks, 88
 chimpanzees, 56, 171
 tool use, **170**
 chromosomes
 non-sex nuclear (autosomes), 46
 in offspring, 50
 See also X chromosomes; Y chromosomes
 cladism, 123
 phylogenetic theory of, 126
 cladistic methods, in phylogenetics, 124
 cladograms, phylogenetic, 124
 classifications, 134
 allele frequency differences across loci,
 across populations, 138
 biogenomic and social, mapping, 269
 in clustering analysis, 137–138
 cluster assignments, individuals, 147
 and continental regions, 147
 and consequences, ethics of, **103**
 Eurocentric racial, 154
 individual-level, 134, 137
 individuals, 185–186
 logic, thought experiment, **137**
 for medical predictions, 149
 of metrics and measures, genetic variation,
 101
 nested, 142
 of population concept, 74
 probability of false, **147**
 race (Lewontin), 120
 race, *Structure* analyses mimicking, 91
 taxonomic, 123
 classificatory ambiguity, **151**
 clines, representing Out of Africa migration,
 278
 clitoris
 importance, 249

- and penis, structural homology, 251
- phylogenetic tree, placement of, 256
- clockwork universe, law-governed, 285, 288
 - description, 286–287
 - perspective, 307
- Close-Up of Soup Universe*, 309
- cluster reification, 132, 159–160
- clustering
 - algorithm (*Structure*), 74, 85
 - $K = 5$ comparison, 155
 - of particular K , reliability, 160
- clustering analysis, 132
 - allele frequency differences across loci, 138
 - Bayesian form of, 132
 - clusters, construction, 136
 - constraints, 136
 - inference process, 144–147
 - inferences, 185–186
 - for medical predictions, 149
 - ontological interpretation, 132
 - and pernicious reification, 133
 - population- and individual-level
 - classification, distinction, 137
 - research programs, results, 156
 - results, interpretation, 132
 - sample sizes, basis for, 150
 - social science–theoretical components in
 - populations, 154
 - and variance partitioning, 132, 144
- clusters
 - Hardy–Weinberg expectations, 144
 - natural number, 160
 - overinterpretation, 159
 - pooling, 132
 - reification, 132, 160
- CNVs (copy number variants), 123, 167
- coalescent theory, 44, 45, 54
- Cockerham, C.C., 139
 - F -statistics and ANOVA framework,
 - connection, 140
- codons, 204
 - changes in first letter, 206–207
 - changes in second and third letters, 207
 - three letter nucleotide sequences, 205
- cognitive and genetic racial differences
 - debate, 274–275
- Collins, F., genetic variations and cancer risk, 232
- comparative anatomy, female genital, 255
- competition, interspecific, 83
- complexity
 - environmental and ecological, 43
 - evolution of, 307
 - gene sequence phenomena, management
 - of, 124
 - of genomic data, 123
 - and parameter estimation, 162
 - of reality and existence, 199
 - scientific and political, 242
 - of systems, 305
 - of theoretical machinery, 102
- conflation
 - of census size, 86
 - danger of, 90–95
 - de-reification, 96
 - pernicious, 277
 - of population types, 85
 - of populations, 75
 - statistic–parameter (Lewontin), 161
 - of *Structure* clusters, confused
 - interpretations, 94
- congenital adrenal hyperplasia, 251
- conscious universe
 - balanced, 285, 288
 - law and chance in, 293
 - perspective, 308
 - predictions and causal explanations,
 - 294–295
 - statistics in, 295–304
- consciousness
 - and complexity, 305
 - power and ubiquity of, 304
 - in statistics, 303
- conservation biology, 102
 - characterization, 122
 - connectivity versus single species, 115
 - and genetic diversity use, 127
 - genetic variation metrics, pertinence to, 111
 - metrics and models context, 113, 114–116
 - statistical measurements, value, 115
- conservation units below the species level,
 - role, 115
- constructivist conventionalism
 - defense of, 281
 - about race, 267
 - versus realism, biogenomic cluster/race,
 - 269, 277
- consumer genomics, uses, 232
- contextual influence, populations, 73
- continental aggregates
 - of populations, 138
 - racess, 132
- continental level aggregates, visualization of
 - variation apportionment, 132

362 · Index

- continuum determination, realist's
populations fit, 102
- conventionalism, about biogenomic clusters/
races, 270
- conventionalist perspective, reasons for
adoption, 126
- conventionalists versus realists, differences, 102
- copy number variants (CNVs). *See* CNVs
(copy number variants)
- Corded Ware culture, 35, **37**
- Cornfield, J., relative risks study, 233
- coronavirus pandemic, and absence of
adaptive responses to a virus, 204
- Crick, F., 24
- CRISPR, 233, 266
- crosscuts, of social Whole, 196
- cultural evolution theory, lactase persistence,
193
- Darwin, C.R., 19, 59, 123, 195, 200, 308
- Darwin's Finches* (Lack), 82–84
- data
choice, phylogenetic work influence by,
124–125
genetic, F_{ST} role in interpretation, 157
genomic, interpretation, 126
importance, 99
interpretation, 100
measurements and mathematics,
abstraction and idealization, 99
- data sources, effects, 154
- Dawkins, R., 7
- Dawood, K., twin study, 259
- de Waal, F., 67
- Deep Demography*, **49**
- demographic isopoint, **49**, 52
- Denisovans, 53
DNA in humans, 56
evolution, 54
population hybridization, 125
- Descent of Man, and Selection in Relation to Sex*,
The (Darwin), 59
- Design of Experiments, The* (Fisher), 28
- determinism
methodological, and error terms, 302
and necessity, epistemological critique
(Dewey), 292
versus absolute chance (Peirce), 292
- Development of human genitalia, **252**
- developmental bias, 10
- developmental interactionists, 7
- developmental systems theory, 34
- developmental–historical hypotheses, future
discussions, 258
- Dewey, J.
necessity and determinism,
epistemological critique, 292
philosophy is criticism, 4
“Dialectics” (Levins and Lewontin), 196
- dichotomy, 227
gene versus environment, variance
understanding, 228–229
importance of, 196
nature versus nurture, 13
- differentiation
genetic, 101
and diversity, 111
human history, inference, 264
metrics, 109
population similarity, measure of lack
of, 109
variation, measure of, 103
- metrics
populations, indication of dissimilarity,
111
probabilistic phylogenetic methods
using, 124
- dimensionality, curse of statistical, 30
- diploid cells, 20
- disease etiology, 266
Huntington's disease, 230
lung cancer, 233
- diseased ontologizing, 86
- diseases
and environmental effects, association,
234
genetic, examples, 236
outcome of genomic and environmental
factors, 236
- dispersal hypotheses, 38
- distinctions
dualism, 196
interpenetration, 261
metaphilosophy of, 195, 197
non-dualistic, 196
pairing of, 195–197
plurality of, 197
synthesis, 198
- distribution functions, probability, 26
- Distribution of Bajau Peoples*, **216**
- diversity
in Africa, genomic, 171

- apportionments, Lewontin's and true one, **178**
- averaged, 139
- genetic, 32, 101, 103–105
- below the species level, 115
 - and differentiation, 111
 - and differentiation, distinction, 111
 - genetic variation, a measure of, 101
 - and population-devastating apocalypse, 120–122
- Jost's *D*, 99, 104
- metrics, nonidentity of populations, 111
- nucleotide, 167, 171–173
- total, three levels apportionment (Lewontin), 139
- diving reflex, 217, 221
- dizygotic versus monozygotic twins, genetic similarity, 258
- DNA
- ancestry reports, geographic analysis, **135**
 - and biomedicine, context, 229
 - haplotype divergence, 141
 - molecular basis of genetics, 24
 - replication, 50, 206
- DNA ancestry report, **135**
- Dobzhansky, T., 84, 118, 200
- on genetic variation in nature, 105
- Doll, R., etiology of lung cancer study, 233
- Donnelly, P., *Structure* algorithm, 145
- double helix, discovery, 24
- drift. *See* random genetic drift
- Drosophila melanogaster*, four chromosomal pairs of, 23
- dryopithecines, 59
- Duffy, 176
- Dunn, J.M., population health perspective, 235
- Earth, life on, 308–311
- East African Rift System, The, 38, 40, **41**
- ecology, aim of, 74
- Edwards, A.W.F.
- biogenomic cluster/racial realism, defending, 273
 - and Lewontin, methodological and normative differences, 271
 - on “Lewontin's fallacy”, 147, 264
 - on moral equality and genetic similarity, 273
- probabilistic phylogenetic inference, 124
- eggs
- fecundity, **81**
 - formation of mother's, 50
 - implantation of fertilized, 256
 - law of segregation and gamete formation, 20
 - ostrich, 43
- eigenvalue, effective population size, 89
- Einstein, A., 4, 294
- embedded cuts, of the biological One, 196
- endosymbiotic theory, **310**, 311
- Entropy and Gini diversity, **119**
- ENU mutagen, male mouse treatment with, **9**
- epidemics, emergence of, 202
- epistemology, 296
- equality and freedom, path toward, 17, 313
- estimator, in statistics, 100, 107
- ethics, 296
- in evolution of *Homo sapiens* (Wrangham), 67
 - and power, tracking of, 229, 285
- ethnocentric origin myths, critiqued by genetic studies, 35
- Euclidean genetic distance, 110, **113**, 124, 141
- eugenics, 29, 77, 107, 201, 264
- discoveries, 5
 - eugenic views, political spectrum of, 6
 - eugenicists (Fisher), 77
- eukaryotic cells, 20, 48, **310**, **312**
- Euler, L., 26
- Eurasian genetic landscape, 35
- Eurocentric racial classification, 154
- Europe
- making of, **36**
 - Neanderthal fossil record, 54
- Europe 2, 35
- European peoples
- ancestral components, **37**
 - archaeogenetic components, **37**
 - origin, 34–37
- evidence approach, total, 125
- evolution
- analyses, usefulness of variance partitioning for, 149
 - change, variable rates of, 10
 - of complexity, 307
 - dynamics of, 90
 - genomic, adaptation against viruses, 202
 - of hominins, **58**
 - of *Homo sapiens*, **57**
 - mathematical models of (Fisher), 28
 - mechanisms, 126
 - natural selection, three conditions of, 192
- Evolution of hominins, **58**
- Evolution of *Homo sapiens*, **57**

364 · Index

- evolutionary genomic theory, human, as an organism, 7–11
- evolutionary genomics, human
 adaptationist total explanation, components, 214
 answers to questions, our place in the world, 7
 causal analysis in, 286, 298
 disciplines in study of, 102, 113
 empirical patterns, 13, 165
 versus evolutionary genetics, 5
F-statistics, application and interpretation, 158, 276
 and *Homo sapiens*, history, 19
 intelligence and female orgasm, 237
 methodologies, 133, 163
 natural selection, emerging findings about, 191
 paradigms, 194, 261
 pernicious reification, statistical, 161
 and philosophy, intersection, 73
 political and politicized ways, 7
 political interpretations, 15, 136, 147, 211, 264
 population types, 75, 96
 purpose, 11
 statistics, 285, 296
 theoretical organism, explanatory, 10
- evolutionary history
 Bajau peoples, 222
 endosymbiosis, 311
 epidemics and pandemics, 202
 evolutionary genomics, human, 8
 hominins, 54
- evolutionary love (agapasm), 292
- evolutionary significant unit, conservation biology, 115
- evolutionary synthesis, extended, 10, 11
- evolutionary theory
 birth and progress, 5
 natural selection, centrality, 191
 research paradigms, 194
- Ewens, W.J., 87
- exclusive network, descent lineages, 50
- Excoffier, L.
 on genetic differentiation, populations, 161
 haplotype-based model, 142
 variance partitioning methodology, AMOVA, 132, 138, 141
 Φ -statistics, formulation, 142
- explanations, controversies about possibility of total, 294–295
- Fanon, F., social race, reality and consequences, 279
- Female and male orgasm cycles, 226
- Female genital comparative anatomy, 255
- female reproduction, phylogenetic distribution, 254
- Fisher, R.A., 6, 10
 allele frequencies, mathematical models, 23
 ANOVA methodology, tension between gene and environment, 227
 causal analysis, skepticism about, 304
 eugenic efforts, 29
 fertility differences, role in human families, 29
 populations, theoretical study of, 74
 questionnaires to nature, 30
 randomization protocols, 28
 statistics and genetics, integration of, 27–30
 on theoretical populations, 76–79
- Fisherian needle-eye, 29
- Fisher–Wright model, 79
- Fly Group, Morgan's. *See* Morgan's Fly Group
- Fondation Jean Dausset-CEPH, 153
See also CEPH (Centre d'Étude du Polymorphisme Humain)
- food web networks, 11
- Foot evolution, 55
- founder effect, migrating populations, 175, 278
- Four Gene Coalescent (Incomplete and Idealized)*, 45
- FOXP2*, 212
- Frankel, O.H., on saving specific subpopulations, 114
- Franklin, R., 24
- freediving physiology
 adaptations, Bajau peoples, 216, 237, 245
 case study, 214–224
 and large-spleen adaptation, 221
- Freedman, D.A., on regression model requirements, 303
- frequentist versus Bayesian, interpretations of probability, 26
- From Galápagos-Writ-Large to Planet Unity 1*, 18

- From Galápagos-Writ-Large to Planet Unity 2: Vitruvian Woman*, **98**
- F_{ST} . *See* Wright's F_{ST}
- F -statistics
 and ANOVA framework, connection (Cockerham), 141
 ANOVA interpretation, 139
 evolutionary genomics, application and interpretation, 158
 Excoffier mapping to Φ -statistics, 142
 of F_{IS} and F_{IT} , 106
 heterozygosity use in, 105, 148
 and Lewontin's variance partitioning equations, comparison, 140
 parameters, estimation procedures (Weir), 162
 and phylogenetic relationships, inference, 112
 and shifting balance theory development, 108
 and variance partitioning, 141
- g factor, 241
- Gaia paradigm, **41**, 311
- Galápagos finches, study of, 82–85
- Galápagos-Writ-Large
 genetic variation measures, 110
 and natural selection, signature of, 188
 overemphasis by political right, 136
 to Planet Unity, thought experiment, **18**, 30–33, 276
 subdivision determination, 102
- Galton, F., 26
 concept of correlation, 5, 227
 intelligence studies, 243
- gametes, 20, **46**
- GATA transcription factors, **203**
- Gaussian distribution, 26
- gene loss, and evolutionary change, 169
- gene pool
 and conservation biology, 114
 differences in human, 34
 diversity, loss of, 114
 and populations, 73
- genealogy, and Planet Unity, 43
- gene–culture coevolution, 223
- gene–organism–environment co–interaction, 34
- general linear model (GLM). *See* GLM (general linear model)
- general systems theory, 34
- generalization, mathematical structure, 77
- genes
 additive effect, 240
 allelic lineages, **46**
Auberger, 177
 autosomal, **45**
 Lewontin's distribution, 182
 variance component estimates, 182
 biallelic, 107, **119**, 139, 146, 159
 candidate, 214, 258
 and cognitive differences debate, 274–275
Duffy, 177
 and environment, tension between, 227
 exchange, 127, 187, 202
 for human cognition and behavior, 212
 individuation, 218
 informative and non-informative, paradox of, 311
 lactase (LCT), 193, **203**
 racial, questions about, 265–266
SLC24A5, 211
 versus environment distinction, 259–261
 versus environment in disease, 228–237
Xg, 177
- genetic and environmental categories, and therapeutic options, 229
- Genetic Basis of Evolutionary Change, The* (Lewontin), 118
- genetic code
 history, 24
 mandala, universal, **205**
 in RNA language, 206
- genetic correlations, statistical methods, 213
- genetic determinists, 7
- genetic diseases, examples, 236
- genetic distance
 AMOVA, use in, 141
 Euclidean metric, 110
 probabilistic phylogenetic inference, use in, 124
- genetic diversity. *See* diversity
- genetic drift, random. *See* random genetic drift
- genetic information, philosophical challenge, 228
- genetic isopoint, 52
- genetic mutation, nonrandom, 10
- genetic paradigm
 development, background for, 21
 emergence (19th century), 19–22
 evolutionary and ecological significance, 73

366 · Index

- importance to statistics, 26–27
 - See also* paradigms
- genetic reductionism, complementary
 - perspectives, 34
- genetic reductionists, 7
- genetic variance
 - additive, identical versus fraternal twins, 259
 - total, decomposition at a biallelic locus, 141
- genetic variants, traceability of, 33
- genetic variation
 - and biological populations, integration platform of statistics, 159
 - clinal nature, 278
 - evolutionary, molecular assessment of, 123
 - human, 64, 165–166
 - Lewontin's distribution, 176–185
 - Lewontin's measure, single population and world, 119
 - measures and metrics, 100, 103
 - classification, 101
 - comparison, 110–112
 - meanings, 112
 - philosophical and conceptual analysis, 101
 - and population classification, comparison, 151
 - total global, partitioning, 120
 - total, variance partitioning assessment, 134
 - within versus among human groups, 118
- genetic versus environmental effects (twins), estimation, 258–259
- Genetical Theory of Natural Selection, The* (Fisher), 29, 77–78
- geneticists, splitters and lumpers, 102
- genetics
 - material, 22
 - material basis, history, 23–25
 - and statistics, nineteenth and twentieth centuries, 5, 27
- genetics, evolutionary, 7
 - development, 86
 - mathematical, 22
 - and modern statistics, relation, 30
 - versus evolutionary genomics, 5
- genital tubercle, 251
- genomes
 - human
 - allelic variation, global, 164
 - clines, 278
 - natural selection, signature of, 201
 - medical conditions, assessment of human, 230
 - mitochondrial, size, 50
 - sequences, motivations for, 157
 - sequencing, whole, 174
 - structural variation, 169
 - genome-wide association studies (GWAS). *See* GWAS (genome-wide association studies)
 - genomic analyses
 - of the individual, 232
 - interpretations and applications, 165–166
 - metrics and measures, 103
 - models and methodologies, 131
 - of individuals and populations, family-level inference, 230–232
 - genomic data
 - databases, reliance on, 138
 - interpretation, 7, 16, 122
 - interpretation and racial classification, 265
 - Out of Africa evolution, evidence for, 188
 - genomic information, complemented by archaeology and paleoecology, 43
 - genomic research, 229–230
 - biomedical impact, 230
 - Genomic signature of lactase persistence, 203
 - genomic similarities, human and other primates, 21, 168, 171, 204
 - genomic technologies, revealing discoveries about humans, 229
 - genomic variation
 - across continents, comparative, 171
 - in Africa, 171
 - allele distribution, 173–175
 - diversity and differentiation, distinct measures, 111
 - empirical patterns of human, 165–166
 - of *Homo sapiens*, 32
 - intraspecies, 167–168
 - and Lewontin's distribution, implications to reality of race, 271
 - natural selection, findings about, 191
 - nucleotide diversity in different human populations, 171–173
 - overlaps, Africa–East Asia–Europe, 130
 - genomics
 - biomedical, 8
 - and biomedicine, context, 229
 - computational, 22
 - for conservation, 115
 - and human rights debate, 16

- ontological lines, and race, 267
- and politics, 282
- and race, 264, 278
- and statistics, 7
- study of populations, 7–11
- See also evolutionary genomics, human
- genotype-by-environment interaction, 78, 240
- genotype-environment covariance, 78, 240
- genotype-phenotype map, causal, 219
- genotyping, electrophoretic, **9**, 123
- GeoGenetics Center (University of Copenhagen), 217
- Geography of Genetic Variants Browser (Novembre), 174
- Gibbs sampler, 145
- Gini diversity and entropy, 118, **119**
- glans clitoris and glans penis, receptor numbers, 244
- GLM (general linear model), 298
 - determinism and indeterminism synthesis, 286
 - spring example, and assumptions, 298–302
 - three-universe thought experiment, 301
- global human genetic diversity projects, 24
- Goodall, J., chimpanzees, primatology research of, 38
- goodness paradox, the, 66
- gorillas, 56, 168, 171
- Gould, S.J., 252
 - on intelligence and genetic variance, 7
- Grant, P., study of Galápagos finches, 84
- Grant, R., 84
- Great Rift Valley, 38
- GRCh38, 167
- Griesemer, J., 76
- group selectionists, 7
- groups, hierarchical aggregation of populations, 134
- Gurche, J., **53**, **55**, **66**, **72**
- GWAS (genome-wide association studies), 8, 123, 233, 242, 303
 - genes and intelligence variation, association, 241
- habitat loss, 114
- Hacking, I., 296
 - looping effect, 295
 - on Peirce, 292
- Hahn, M.H., on positive selection, 202
- Haldane, J.B.S., 5, 10, 29
 - allele frequencies, mathematical models, 23
- Han Chinese peoples, 136, 150, 173, 218
- haplogroups, 46
- haploid cells, 20
- haploids, genome size, 167
- haplotypes, 46, 141
- Hardy-Weinberg
 - assumptions, 93, 132
 - equilibrium, 91, 94, 140, 145
 - expectations, 106, 144, 146
 - heterozygosity
 - under random mating, 106
 - subpopulations, proportions within, 106
 - simple square expansion, 136
- Harvey, W., 2
- Hayes, M.V., population health perspective, 235
- Hegel, G.W.F., 198
- Hennig, W., 123
- hereditarians, Lewontin's critiques, 272
- hereditary system, and statistical investigation, 27
- heredity, material basis, history, 23–25
- heritability
 - of cognitive traits, 238
 - and total phenotypic variance, 240, 259
- heritable factors (Mendel), 20
- hermaphroditic species, in theoretical populations, 87
- hermeneutic frames, 165
- heterozygosity
 - average, of multiple populations, 107
 - biogenomic racial taxonomic efforts, use for, 264
 - decline, Out of Africa model, 188
 - expected, 88
 - genetic, 101, 105–109
 - genetic variation, metric and measure of, 101
 - genomic, 175
 - inbreeding effect on, 106
 - measures, 99
 - metrics and measures
 - taxonomic conclusions, 112
 - use of allele frequencies, 105
 - observed (H_i), reduction relative to H_S , 105–106
 - outbreeding effect on, 106
 - reduction, 106
 - of subpopulation, 105
 - Weir's D metric, 105
- Heterozygosity to distance from eastern Africa global pattern, **187**

368 · Index

- heterozygotes versus homozygotes, 105
heterozygous individual, 20
HGDP (Human Genome Diversity Project), 24, 153, **156**
HGDP-CEPH cell line laboratory populations, 76
Hill, A.B., etiology of lung cancer study, 233
historicism, populations and species, 194
Hochman, A., on race, 275
homeostasis, organismic, 11
Hominin time spiral, **53**
Hominini split, 60
hominins
 apes, evolution, 61
 in East African Rift System, **41**
 evolutionary history, 54, **58**
 fossils, discovery, 40
 and Galápagos-Writ-Large, 31
 species, differences, 53
 time spiral, **53**
 Vitruvian, **66**
Homo erectus, 52, **53**, **66**
Homo heidelbergensis, 52, **53**
Homo sapiens
 emergence of, 33
 evolution, **57**
 representation, diversity, 125
 key events, 61, **62**
 expansion from Africa, 38
 heterozygosity, average, 168
 nested classification, 143
 nucleotide map, 229
 nucleotide variation, 167
 phylogenetic relationships among, **57**
 population hybridization, 125
 population structure, 127, 138
 selection on, political and ethical ramifications, 201
homozygosity
 average, of multiple populations, 108
 excess, 107, 139, 148
 haplotype, increased, 211
homozygotes versus heterozygotes, 105
Hooke, R., 2
hormones
 and mechanisms of PDE10A, **220**
 and neurotransmitters, sameness across species, 258
Houle, D., 100
How to Argue with a Racist (Rutherford), 14
H_S (subpopulation), 105
 reduction relative to *H_T*, 106–108
H_T (total population), heterozygosity of, 105
Hublin, J.-J., African *Homo sapiens* fossils, 54
human ancestry, shared, 50
Human Diversity (Lewontin), 120
Human Diversity: The Biology of Gender, Race, and Class (Murray), 15
human equality and justice, legal frameworks and moral justifications, 267
human evolution
 dynamics, 126
 explanation, limits, 193
 key events, **62**
 moral and behavioral, 67
 Out of Africa scenario, 188
human evolutionary genomic theory, 7–11
human evolutionary genomics. *See* evolutionary genomics, human
human genitalia
 adult, **250**
 development, **252**
 developmental process, function of genes and androgens, 251
Human Genome Diversity Project (HGDP). *See* HGDP (Human Genome Diversity Project)
Human Genome Project, 229
human history, natural selection impact on (lactase persistence), 192
human origins
 evolutionary and genomic information, knowledge of, 65
 regions, inferences about, 188
human population structure, thought experiment, **18**
human populations. *See* populations
human species history, reconstruction, 127
humans
 biological connection, 67
 fundamental identity, questions of, 1–2
 the goodness paradox, 66
 identities, threats to, 2
 injecting human intentionality, process of adaptation and selection, 203
 stewardship, 311
human-to-human transmission of pathogens, 203
Hume, D., causal analysis skepticism, 304
Huntington's disease
 dominant allele, 236

- genetic basis, 231
- original pedigree, **231**
- Huxley, A., 30, 83
- Huxley, J., 83
- IBD (identity by descent), 211
- idealization of representations, reasoning about, 77
- identity by descent, **46**, 106
- IGSR (International Genome Sample Resource), 153
- Ilardo, M.
 - investigations, consequences of, 224
 - PDE10A* and spleen development, link, 219
 - PDE10A* and spleen size, investigation, 220
 - Saluan and Bajau populations, migration, 222
 - signature of selection, identification techniques, 221
 - SNP frequency, comparison with Saluan peoples, 218
 - spleen size in Bajau peoples, investigation, 216–224
- inbreeding
 - and F_{IS} (Wright), 106
 - and effective population size, 89
 - heterozygosity reduction, 106
 - subpopulation, and allele “recycling”, 106
- inclusive network, demographic, 50–52
- individuals, importance of relationships, 73
- inference procedure, individual-level, 134
- inference, probabilistic phylogenetic, 123
- inferential reliability, 147, 160
- Infinifree of Life*, **260**
- intelligence, 238–243
 - as a legitimate scientific concept, debate, 6
 - evolution, interplay between genetic influence and environment, 237
 - g* factor, 241
 - genetic basis, 241
 - genetic correlations, 241
 - genetics of, statistical background, 241
 - genomic effects on, evidence, 241
 - measurement, 241
 - research possibilities, skepticism about, 242
 - studies, past and future, 242
 - superior (Laplace), 289
 - three topics, 238
 - varieties of, **239**
- intercourse–female orgasm gap, 249
- International Genome Sample Resource (IGSR), 153
- interpenetration, 276
 - determinism and chance, GLM, 299
 - in nature of a distinction, 196
 - of distinctions, 261
 - of poles, 199, 276
- interspecies comparisons, genomic similarities and differences, 167–171
- Inuit adaptations, medical implications, 224
- IQ
 - adaptationist explanation, 240
 - advocates versus skeptics debate, 240
 - genomic effects on, evidence, 241
 - measure of intelligence, 238
 - wars, 6
- Jebel Irhoud, discovery of early *Homo sapiens*, 54
- Jensen, A., 6
- Jensen’s inequality, 108
- Jost, L., 99, 114
- Jost’s *D*
 - in conservation, 115
 - diversity measure, 99
 - formal metric, 104
- Journey of Man, The* (Wells), 14
- Judson, O., on female orgasmic experience variation, 258
- $K = 5$ clustering comparison, **155**
- Kant, I., on causation, 304
- Kern, A.D., on positive selection, 202
- Khoikhoi peoples, descendance, 40
- Kimura, M., 200, 213
- Kittles, R.A., on F_{ST} measure interpretation, 117
- Klein, R., on evolutionary history of hominins, 54
- Kohler, R., on lab–field cultural border in biology, 84
- laboratory populations
 - definition, 75
 - distinction, 74, 84, **85**
 - models, limitations and advantages (Neyman), 81–82
 - and natural populations, compared, 82
 - in *Structure* analyses, 91
 - use of (Park), 79

370 · Index

- laboratory-experimental models, of
populations, 80–82
- Lack, D.
on natural populations, 82–85
populations, natural domain studies, 74
- lactase
gene (*LCT*), **203**
gene enhancer, **203**
persistence, 193
evolution of alleles for, 192
genomic signature, **203**
Old World distribution, **190**
selection signature, 204
production, **203**
- lactose, 193
- Laplace, P.-S., 26
laws and determinism, statement on, 289
- Laplace's demon, 289
- largely genetic traits, 228
- last universal common ancestor (LUCA). *See*
LUCA (last universal common
ancestor)
- Law of Frequency of Error (Galton), 293,
302
- law of independent assortment (Mendel),
20–22
- law of linkage, third law of genetics, 22
- law of segregation (Mendel), 20–21
- laws
dynamic, 292
statistical, 294
- laws of behavior genetics, defense of
(Turkheimer), 242
- Leakey family, African fieldwork, 38
- Leakey, L., on African multiregionalism
model of human evolution, 43
- Leonelli, S., 76
- Lewontin (1972) versus Lewontin (1974),
influence comparison, 179
- Lewontin (1974), error correction, 179
- Lewontin, R.C., 7
1972 study, 108, 118–122, 138, 271
allele distributions, results, 177
analysis, diversity- and heterozygosity-like,
119
apportionments, averaged, 140
data sources, 176
and Edwards, methodological and
normative differences, 271
experimental population genetics,
question of, 118
genetic data, criteria external to, 151
genetic variation, occurrence in nature, 105
heterozygosity-like measures, 139
heterozygosity-like metrics, interpretation,
108
on intelligence and genetic variance, 7
measures, 119, 139
percentages, observations regarding
diversity components, 182
on racial classification, 120, 271
racial classifications and populations used,
152
racially averaged diversity, 139
results, correction of 1972 (Winther), 179
Shannon information measure,
assumptions and contexts, 120
statistic-parameter conflation, 161
and theoretical evolutionary genomics, 200
variance partitioning strategy, 139
- Lewontin's distribution
Edwards's critique, 147, 271
genetic variation, 120, 166
variance and diversity components,
176–185, 274
- Lewontin's fallacy (Edwards), 147, 185
- Lewontin–Winther bar plots, **180**
- Lewontin–Winther scatter plots, **181**
- life
branching, **310**
connection of all, 311
cycle stages, animals, 194
on Earth, 308–311
symbiotic, **312**
- lineage signatures, diversity of incongruous
gene, 125
- lineages
descent, alternative, 50
mitochondrial, 44
tracing of, 33
Y chromosome, 44
- linkage disequilibrium, 145, 211
- linkage groups, 23
- Linnaeus, C., **1**
- Lloyd, E.A.
conceptual carving of total genetic
adaptationist explanation, 215
female orgasm, cultural and biological
influences on, 253
female orgasm, definition, 245
- localist view, author's, 11
- Loci hitchhiking, 211

- logic
 causal, 285
 law of linkage, application to gene pair
 distance calculation, 23
 of statistical inference, 296
 of variance partitioning, 134
 thought experiment, explaining
 classification, 137
- Long, J.C., 94
 on F_{ST} measure interpretation, 117
 human F_{ST} values, interpretation, 276
- looping effect, 295
- Lovelock, J., **41**, 311
- LUCA (last universal common ancestor), 310
- Lucy's species, traversing a forest (Gurche), **72**
- lumpers, 277
 evolutionary geneticists, 102
 genetic diversity, lack of, 121
 and racial gene, 265
 See also splitters
- lung cancer, 236
 etiology of, 233
 and smoking graph, **234**
- Major components of the *Tribolium* model, **81**
- Making Europe, **36**
- “Male Nipples and Clitoral Ripples”
 (Gould), 252
- management unit, conservation biology, 115
- map pluralism, 195
- map projections, and complexity of reality, 199
- Markov chain Monte Carlo (MCMC)
 method. *See* MCMC (Markov chain
 Monte Carlo) method
- Marks, J., 15
- mass extinction, sixth, 115
- Masters and Johnson, four-phase model, 246
- material genetics, 22
- mathematical modeling process, The, **133**
- mathematical models
 and GLM, 298
 conflation and confusion, 132, 277
 of populations, 80
 selection, and data, 99
 strategies, variance partitioning and
 clustering analysis, 131
- matrilines, 44, 48, **49**
- matrilocal groups, 185
- maximum likelihood estimation (MLE)
 method. *See* MLE (maximum
 likelihood estimation) method
- McDonald–Kreitman test, 209
- MCMC (Markov chain Monte Carlo)
 method, 145, 161
- mean fitness, 108
- measure, 101
 convexity, role of, 108
 defined, 100
 and metric, compared, 100
- measurements, understanding of, 100
- measure–metric distinction, and statistic–
 parameter distinction, 162
- mechanism, of a system, 194
- Mechanisms of PDE10A action, **220**
- MegAlign Pro (software), **206**
- meiosis, 20, 50
- meiotic drive, 11
- Mendel, G.
 laws of independent assortment and of
 segregation, 20
 principles of, 19–22
- Mendelians versus biometricians debate, 27
- Metamorphosis* (Ovid), 243
- metaphilosophy of distinctions, 195, 197
- metaphysics, 296, 304
- metric
 defined, 100
 and measure, compared, 100
- metrics and measures
 in evolutionary genetics, 101
 of genetic variation, 99
 ontological interpretations, 102
- microsatellites, 123, 159, 171, 174, 182, 187
- migration, 11, 35, 195, 222, 271, 278
 concept of, 187
 importance of, 197
 Out of Africa, **39**
- Mills, C.
 racial contract, 280
 taxonomy of race existence, positions on,
 279
- Millstein, R., 76
- misclassification, probability of, 147, 147
- mitochondria, 50, 125, 204
- mitochondrial DNA (mtDNA), 43–47
 and age estimation, 47
 diversity component estimates, among
 continents, 183
 genetic variance and autosomal genes,
 among continents component
 comparison, 183–185
 matrilineal, **49**, 123

372 · Index

- variance component estimates, among continents, 183
- Mitochondrial Eve, 43–47, 52, 54
- mitochondrial genome, size, 50
- mitochondrial lineages, 44
- mitochondrion, 48, 50
- MLE (maximum likelihood estimation) method, 29, 124, 207
- modeling strategies
 - causal, 241
 - differentiation, productive use versus pernicious reification, 163
 - phylogenetics, 124
 - power of, 149
 - SMEO-*P* model, 127
 - variance partitioning and clustering analysis, 131, 144, 148
- models
 - and empirical patterns, differences, 165
 - genetic, library of population, 261
 - genomic, of human commonalities, 32
 - uses of false, 82
- molecular clock, 47
- monozygotic versus dizygotic twins, genetic similarity, 258
- Morgan, T.H., 22
- Morgan's Fly Group, 22–23
- Morrison, M., 76
- most recent common ancestor (MRCA). *See* MRCA (most recent common ancestor)
- MRCA (most recent common ancestor), 44, 49, 52
- mtDNA. *See* mitochondrial DNA (mtDNA)
- Muller, H.J., 200
- multiallelic microsatellites, effect on F_{ST} values, 159
- multilocus genotypes, 132, 137, 146, 161, 186
- multilocus information, clustering analysis, 144
- Murray, C., 15
- mutations
 - evolution by natural selection, variation for, 197
 - frameshift, 208, 209
 - genetic, nonrandom, 10
 - nonsynonymous, 207
 - point, 206, 208, 209
 - rate, 166–167
 - single site, types, 208
 - synonymous, 206
 - traceability of, 33
- National Cancer Institute, 233
- Natural Inheritance* (Galton), about normal distribution, 293
- natural phenomena, models illuminating, 80
- natural populations
 - definition, 75
 - delineation (Millstein), 76
 - determination, 134
 - distinction, 74, 84, 85
 - distinction from theoretical, 74
 - F_{ST} , accuracy, 157–159
 - Galápagos finches study (Grant), 84
 - genetic variation in, studies (mid-century), 84
 - geographic isolation, identification by, 83
 - Lack on, 82
 - migrating, genetic bottlenecks, 175
 - in *Structure* analysis, 91–95
 - and theoretical populations, distinction, 86–90
- natural sciences
 - and drawing boundaries, 86
 - and philosophy, crossroads, 5
 - and understanding of the world, 3
- natural selection. *See* selection
- Natural Theology* (Paley), 195
- Nature Timespiral*, 290–291
- nature/nurture binary, 227
- Neanderthal Cave*, 64
- Neanderthals, 53
 - DNA in humans, 56
 - evolution of, 54
 - population hybridization, 125
- Nei's G_{ST} , 105, 107
- neither–nor thinking, 197
- Neolithic, 35, 36, 192
- neuroendocrine mechanism, 255
- Newton, I., 2, 4
- niche construction, 10, 34
 - and peoples in extreme environments, 223
 - theory, lactase persistence, 193
- Nielsen, R., detecting the signature of natural selection, 207
- NIH (National Institutes of Health), 233
- nomenclature
 - gene names versus protein products, 178
 - statistical, 100

- nonsynonymous substitutions, variability
 across genes, 209
- Novembre, J., 174
- nucleotide codons, three-letter, **205**
- nucleotide diversity, African versus
 non-African, 171–173
- nucleotide sequences
 binding, transcription factors, **203**
 humans and other great apes, differences,
 169
 information for medical conditions, 230
 as targets of data analysis, 123
 technologies, 24
- Nyanzapithecus*, skull of, 59
- objective constructivist position on race
 (Mills), 279
- Old World distribution of lactase persistence,
190
- “On the Mathematical Foundations of
 Theoretical Statistics” (Fisher), 27
- On the Origin of Species* (Darwin), 195
- ontogeny, of individuals, 34
- ontological interpretation
 by conventionalists or constructivists, 102
 and population structure, understanding
 of, 127
 by realists versus conventionalists, 102
- ontology, inference of, 147
- oocyte, primary, 50
- organism aggregates, abstracted and idealized,
 77
- orgasm cycles, **226**
- orgasm, female
 and associated hormonal profiles,
 nonprimate species, 257
 byproduct account, 251–253
 classifications, 246
 copulation and ovulation, connecting
 mechanism, 255
 developmental–historical explanation,
 249–258
 and evolutionary fitness, lack of link, 247
 and evolutionary fitness, noncorrelation,
 249
 evolution, interplay between genetic
 influence and environment, 237
 evolutionary explanation, 245
 frequency, experienced, **248**
 genetic and environmental influence,
 research, 259
 genetic basis, establishment, 258
 versus male, 244
 nonadaptation, 245–249
 nonadaptiveness, 251
 reductionist descriptions, 245
 origin narratives, social and political
 functions, 34
 origin of species, understanding, 169
- Original Huntington’s disease pedigree, **231**
- Original lung cancer and smoking graph,
234
- Our cousins 1: Bonobos, **65**
- Our cousins 2: Chimpanzees, **170**
- Out of Africa
 clines representing migration, 278
 human evolution, model of, 188
 hypothesis, evolutionary effects, 173
 migrations, 16, 38
 model, and genomic heterozygosity
 decline, 188
 richest genomic variation, pattern, 175
- Out of Africa global migrations, **39**
- Out of Europe
 Begun’s hypothesis, 60
 migrations, 16
 paradigm (Begun), 59
 primates, ancient, 61
- outbreeding, of populations, 106
- oversampling, effect, 154
- ovulation
 male-induced, 256
 spontaneous, 256
 triggers, 256
- Pagani, L., on genomic analyses and fossil
 record in Africa, 40
- Paley, W., 195
- Pan-African Cultural Patchwork (Scerri), 42,
 188
- pandemics, emergence of, 202
- paradigms
 adaptationist, 307
 and complexity of reality, 199
 explanatory, integration, 295, 305–307
 pluralism, importance, 195, 224–225
See also genetic paradigm
- parameters, inference of fundamental, 162
- Park, T.
 on laboratory populations, 74, 79–82
- parsimony method, 124
- patrilines, 44, 48, **49**

374 · Index

- patrilocal groups, 185
 patterns, empirical
 in Africa, 188
 of human genomic variation, 165
 of human genetic variation, quantitative
 features, 166
 importance of, 189
 and models, differences, 165
 understanding of, 166
 Pavličev, M., vestigial trait account, 253–257
 PCA (principal component analysis), 148
PDE10A gene
 allelic causal variant, 218
 expression, 219
 link to spleen development in humans,
 219
 PDEs (phosphodiesterases), action, **220**
 Pearson, K., 5, 26
 Peirce, C.S., on power of chance, 289
 pernicious reification, 14, 86, 133, 163, 293
 about biogenomic cluster/race or
 biological race, 269
 blocking and overcoming, 149
 of clusters, 132, 160
 and *F_{ST}* uses, 132, 158
 and genetic information, 228
 occurrence, 163
 of populations, 132, 150
 potential occurrence, 150
 of race approach, 277
 statistical, 160, 163
 statistic–parameter, 132, 160
 of *Structure* output, 94
 types, 132
 phenotypes
 lactase persistence, distribution Africa and
 Eurasia, **190**
 production from genes, mechanisms, 214
 phenotypic correlations, statistical methods,
 213
 phenotypic decomposition model (Fisher),
 78
 phenotypic plasticity, 10
 phenotypic traits, 214
 emergence in humans, 228
 explanatory and predictive models of
 changes in, 28
 genetic correlation between, 213
 individuation, 220
 uniqueness to a population, 222
 phenotypic variation, causes, 27
 philosophers of race, 264
 Philosophical Essay on Probabilities, A (Laplace),
 289
 philosophy
 and natural science, crossroads, 5
 and questions of identity and connection,
 3–5
 Phylogenetic distribution of mammalian
 female reproduction, **254**
 phylogenetic inference
 genetic differentiation use in, 127
 metrics and models context, **113**, 124
 population pairs rank order implications,
 110
 phylogenetic methods, tree building, 47
 phylogenetic relationships
 among hominoids, **63**
 among *Homo sapiens*, **57**
 among populations, 112
 prokaryotes and eukaryotes, **310**
 phylogenetic studies, and *Structure* clusterings,
 93
 phylogenetic theory, of cladism, 126
 phylogenetic trees, 111–112
 building of, 47
 clitoris placement, 256
 of great apes, splitting, 60
 modeling, lineages for, 123
 ontological interpretation, 122
 and plant stem, **0**
 phylogenetics, 102
 cladistic and probabilistic methods in, 124
 genetic differentiation metric, pertinence
 to, 111
 genomic data for, 123
 metrics and models context, **113**,
 122–126
 phylogenies
 inference methods, 124
 insights, 93
 Pinker, S., 7
 Planet Unity, **18**, 31, **98**, 168
 continuum determination, 102
 and Galápagos–Writ–Large, thought
 experiment, **18**, 30–33, 276
 genetic variation measures, 110
 population similarity, 136
 Plant Perception 2, **0**
 plants, self-fertilization, 106
 pluralistic view, author’s, 11
 Poisson distribution, 26

- poles
 distinction
 thirdness, 197
 of a larger whole, 198
 dualistic, 197
 interpenetration, 196, 199
 mutually constitutive, 196
 polygenic trait risk scores, 233
 population genetic models, library of, 261
 population groups, genomic versus conventional categories, 266
 population health, 235–236
 population of *Australopithecus (Praeanthropus) afarensis*, A, 72
 population size, effective, 86
 and census population size, differences, 89
 consequence of use, 90
 perniciously reified, 90
 translation into field census size, 88
 use in empirical studies, 89
 Wright's concept, 88
 population-level phenomena, 8, 115
 populations
 aggregation, hierarchical, 134, 143
 ancestral and contemporary, inference example, 185
 biological, integration platform of statistics, 159
 census size, 88
 clustering, 185–186
 coalescent, ideal original, 47
 concept of, 73–74
 conflation of, 75, 85
 diseases with more environmental etiology, 233–237
 effective size, concept, 74, 86, 166
 in endless retreat, decline, 115
 founder, 175
 genetic differentiation, 95, 149, 184
 genetic diversity, need for, 88
 genetic theory, 10, 118, 162
 genetic variation in, 83–84
 genetics, flexible theoretical organism, 11
 group existence, circularity in proving, 133
 HGDP-CEPH cell line laboratory, 76
 human
 determination of existence, 127
 individualized, existence, 64
 origin within Africa, 38
 infinite and hypothetical (Fisher), 79
 laboratory-experimental models, 80–82
 local base, 138
 mathematical models, 80
 matrilocal groups, 185
 mean fitness, 108
 membership, 186, 268
 models, 131
 contrasts, 85
 integration, 84
 theoretical properties, 89
 theoretical to natural fitting, parameter estimates, 90
 natural selection, 192
 origins of, 37–43
 parameters, 100
 and sample statistics, distinction, 161
 patrilocal groups, 185
 phenomena, characteristics, 80
 philosophical and conceptual analysis, 101
 races, as subspecies, 117
 racially averaged diversity, 139
 rank order of total set of pairs, 110
 realist's fit, subdivision or continuum determination, 102
 reification, 132, 150–157
 characterization, 150
 data input, reliability, 150–151
 possibility of, 156
 seeds of, 151
 and samples, statistical distinction, 79
 social science—theoretical components in, 153
 trichotomy, 74
 assumption archaeology, tool for, 95
 and *Structure* analyses, 91
 true phylogenetic relationships, history, 92
 types, 74
 boundaries, management of fluidity, 85, 86
 conflation and confusion, errors, 85
 and philosophy, 76
 viciously abstract imposition, on genetic data, 163
 See also laboratory populations; natural populations; theoretical populations
 post-racial future, 270, 280–281
 genomic findings, and precision medicine, 232
 precision medicine, 232–233
 principal component analysis (PCA), 148

376 · Index

- Pritchard, J.
 Bayesian form of clustering analysis, 132
 modeling assumptions, 145
Structure algorithm, 145
 probabilistic thinking, sources for, 25
 probability theory, history, 25–26
 probability, scientific success story, 296
 propagation, differential, 29
 Proto-Germanic languages, emergence, 35
 Proto-Slavic languages, emergence, 35
 Punnett squares, 20–21
- race
 biogenomic, realism versus antirealism, 267
 biological, existence, 269
 classifications and populations (Lewontin), 152
 concepts, 263, 266
 biogenomic cluster/racial realism, 268
 biological and biogenomic, 90
 biological racial realism, 268
 and discourses, 270
 social racial realism, 268
 and *Structure*, 91
 conceptual analysis, future, 266
 constructivist conventionalism, genomic
 research context, 267
 entities, biologically real, 126
 existence, 117, 138, 149
 genomic differences and social races,
 mapping, 272
 genomic studies, analyses and
 interpretations, 263–264
 genomics and, 264
 human, single overarching, 168
 levels of, 264
 ontological lines surrounding, 267
 ontology, phylogenetically based, 126
 philosophers on, 264
 in post-racial futures, 280
 reality of, 182, 270, 283
 as a social category (Ásta), 279
 social construction, 280
- Race*, 262
 racial categorization, 266
 Lewontin on, 271
 redefinition, 279
 racial conundrum, small percentage, 274
 racial gene, questions about, 265–266
 racial realism, biological, 279
 racism, systemic judgments and prejudices, 263
 random genetic drift, 11, 87, 187, 195
 loss due to, 176
 and natural selection, 196–197, 200
 randomized controlled trials (RCTs). *See*
 (RCTs) randomized controlled trials
 randomized experiments, and statistical
 analysis, 297
 RCTs (randomized controlled trials), 28
 real planet of the apes, *The: Out of Europe*,
 63
 realists
 versus conventionalists, differences, 102
 ontological interpretations by, 102
 populations, biologically legitimate, 276
 social race, ignoring biogenomic cluster/
 race debate, 278
 Reardon, J., on Lewontin's anti-racist work,
 273
 recombination, chromosomal pairs, 21–22
 region mapping, genetic, 9
 regression models
 derivation (Freedman), 304
 GLM, 286, 299
 spleen size, Bajau versus Saluan, 218, 219,
 221
 spring example, 299
 variables and relationships, reasonableness,
 306
 Reich, D., 14
 reification. *See* pernicious reification
 reliability, inferential, 147, 160
 Renfrew's Anatolian hypothesis, 37
 reproductive comparative anatomy, female,
 256
 Rosenberg, N.
 Bayesian form of clustering analysis, 132
 on unlinked or loosely linked loci, 47
 variance partitioning and classification, 137
 Rostand, J., 73
 Rothamsted Experimental Station, 28–29
 Russell, B.
 causal analysis, skepticism about, 304
 on philosophy, 4
 Rutherford, A., 14
 sameness, of hormone and neurotransmitter
 profiles, across species, 258
 Sami peoples, 107, 136, 150

- sample statistics, and population parameters (distinction), 160–161, 163, 300
- San peoples, descendance, 40
- scatter plots, Lewontin's calculation errors, **181**
- Scerri, E.M.L., 42
- Schematic allele world map, **172**
- scientific inquiry, philosophical arguments, 163
- Scientific Revolution (1660s), British and French academies of sciences, 2
- selection
- in the aggregate, effects of, 77
 - coefficient, 166, **198**, 200
 - debate, levels of, 196
 - human evolution, phenotypic targets, 214
 - laws, and gas laws (thermodynamics) compared, 77
 - levels of, 34
 - natural, 11, 192
 - action on human genome, 213
 - and adaptationist paradigm, 261
 - alleles, recessive and dominant under, **198**
 - Bajau peoples, shaped by, 214
 - evidence, 215
 - in extreme environments, importance of demography, 222
 - findings and politics, 211
 - fundamental theorem of, 78
 - genomic signature of, 199–201
 - genomic signature, investigations in extreme environments, 214
 - historical action, statistical methods, 192
 - impact on human history, example, 192
 - and Mercator projection, functional likeness, 195
 - modes of action, on human genetic variation, 200
 - molecular signature of, 202
 - mutation, 197
 - as philosophical case study, 194
 - and population variation (Grant), 83
 - principle of, 23
 - and random genetic drift, as dualistic poles, 197
 - selective environment, 193
 - and sickle-cell allele, 236
 - signature, 207
 - political and ethical ramifications of, 201
 - signature
 - Ilardo's identification techniques, 221
 - lactase persistence, 204
 - measurement methods, 204, 206
 - statistical tests, reliance on mutation type, 207
- Selection during the life cycle, **194**
- selective sweeps, identification, 211
- self-fertilization, 106
- self-organization, 34
- sequences. *See* nucleotide sequences
- Sesardić, N., on biological racial realism, 275
- Sewall Wright effect, 83
- sex ratio, 79
- sexual selection, 83, 192
- Shannon information measure, 118
- calculation of, 139
 - heterozygosity-like, 118–119, 139, 143
 - Lewontin's use and interpretation, 120
 - theoretic, 99
- shifting balance theory, 108, 199
- short tandem repeats (STRs). *See* STRs (short tandem repeats)
- sickle-cell anemia, 236
- signature of selection
 - Ilardo's identification techniques, 221
 - lactase persistence, 204
 - measurement methods, 204, 206
 - natural, 207
- single-nucleotide polymorphisms (SNPs). *See* (SNPs) single-nucleotide polymorphisms
- skin color variation, and politics, 211
- SMEO-P* model, 127
- SNPs (single-nucleotide polymorphisms), 123, 173, 218, 233
- variants, geographic distribution, **131**
- social race, 264
- existence of, 269
- social racial realism, 268
- and post-racial society, 270, 279–281
- Soup Universe (Unstructured Change)*, **284**
- soup universe, disordered, **284**, 285
- close-up, **309**
 - description, 287–288
 - perspective, 308
- Spearman, C., general intelligence factor (g factor), 241
- speciation, variable rates of, 10
- species barcoding, 115

378 · Index

- species determination, by individual genes, 168
- species–area relationships, 11
- Spleen, **217**
- spleen size
- in Bajau peoples, **217**
 - in Bajau and Saluan peoples, difference, 219
 - causal model, 221
 - and freediving, 217
 - and selection, direct, 222
 - variation, 218, 219–222
- splitters, 277
- evolutionary geneticists, 102
 - population structure, preservation, 122
 - and racial gene, 265
 - See also* lumpers
- spring example
- description, 298–302
 - explanatory paradigms, 305
 - role in GLM, 298
- statistical analysis, and randomized experiments, 297
- statistical inference, historical introduction to phylogenetics, 124
- statistical tools and thinking, roles, 296
- statistic–parameter and measure–metric distinctions, 162
- statistic–parameter reification, 132, 160–162
- statistics
- as a bridging tool, 6, 25
 - and consciousness, 303
 - development and interaction with genetics, nineteenth and twentieth centuries, 5
 - and evolution, nineteenth and twentieth centuries, 27–29
 - importance to genetic paradigm, 25
 - integration platform, 159
 - politics and ethics of, 303
 - rise of, 26
 - utility of, 285
- Statistics: A Very Short Introduction* (Hand), on statistics in a conscious universe, 297
- stem hominoids, 59
- Stephens, M., *Structure* algorithm, 145
- STRs (short tandem repeats), 123
- structural variation
- humans, 169
 - scope, 169
- Structure* (clustering algorithm), 74, 85
- algorithm, description, 145
 - cluster reification, 160
 - clustering, hypothetical results, **93**
 - clusters, conflation, 94
 - erring, systematically, 93
 - inferential errors, possibility of, 91–95
 - inferred clusters, 94
 - limitations (Weiss and Long), 94
 - model output, 160
 - pernicious reification of output, 94
 - and population trichotomy, 91
 - population memberships, estimation, 91
 - and race classification, 90
 - and shared ancestry, 93
 - three clusters, 92
- Structure* ontologizes, **93**
- subdivision determination, realist's populations fit, 102
- subpopulation, heterozygosity of, 105
- subspecies, criterion for nonhuman (Templeton), 117
- substitution rates, humans versus rodents or artiodactyls, **210**
- summary statistic, 100
- superorganisms, 197
- Symbiotic life, **312**
- symbiotic mergers, **312**
- Symons, D., on nonadaptiveness of female orgasm, 251
- synonymous substitutions, temporal rate calculation, 209
- synthesis, 197–199
- extended, 10–11, 34
 - grand, 11
 - modern, 83
- T4 production, 219
- Taming of Chance, The* (Hacking), 296
- taxonomic groupings, 112
- taxonomy, 102
- biogenomic racial, 264
 - characterization, 122
 - and conservation biology (Lewontin), 118–122
 - of existence of races, positions, 279
 - of *Homo sapiens* population structure, 117
 - human populations, Templeton's analysis, 117
 - metrics and models context, **113**, 116–117
 - subspecies, heterozygosity metrics use, 127
- Tay–Sachs disease, 236

- Templeton, A., on subpopulation recognition, 116
- Templeton's taxonomic analysis, 117
- teraSTRUCTURE* (computer program), 95
- Tesla, N., brain wave decipher attempts, 1
- theoretical populations
 and biometrician versus Mendelian debate, 76
 bottom-up building of, 147
 and clusters, 136
 conflating and confusing, 93
 definition, 75
 determination, 134
 distinction, 74, 84, **85**
 distinction from natural, 74
 Fisher on, 76–79
F_{ST}, accuracy, 157–159
 and natural populations, distinction, 86–90
 notion of, 77
 in *Structure* analyses, 91–95
- theory and model selection, assumptions and values, 100
- thirdness, from two poles of distinction, 197
- three-universe, thought experiment, 285–288, 294
 causality and statistics, 288
 perspective, 307
- thyroid hormones, production (T3, T4), 219, **220**
- Thyroid Stimulating Hormone (TSH), **220**
- Tibetan adaptations, medical implications, 224
- Tomberg, K., 8
 phenotypic target for genetic screen, **9**
- top-down modeling, 132, 147
- topology choice
 genealogical, 125
 for *Homo sapiens* evolution, 125
- traits
 additive genetic variance, identical versus fraternal twins, 259
 characterization, 228
 cognitive, heritability, 238
 genetic basis and natural selection, 258
 individuation, 217
- transects, 142
- transmission of pathogens, human-to-human, 203
- transmission routes, pathogen, 202
- transmission, genetic and cultural, 223
- tree of life, connections, **0**, 113
- trellis (network), **113**, 125–126
- Tribolium* flour beetle laboratory system, 79–81
- Tribolium* model, Major components, **81**
- true history, The, **92**
- TSH (Thyroid Stimulating Hormone). *See* Thyroid Stimulating Hormone (TSH)
- Turkheimer, E., on causal modeling in behavior genetics, 242
- Two types of single-site DNA mutations, **208**
- tychasm (absolute chance), 292
- Universal Genetic Code Mandala*, **205**
- universal laws, critique of possibility, 295
- universe, multiple perspectives approach, 306
- UPGMA (unweighted pair group method with arithmetic mean), 124
- urogenital anatomy, female, 256
- vaccines, planned immune responses, 203
- Van Valen, L., on evolution control, 10
- variance components
 estimates, autosomal genes, 182–183
 hierarchical (Cockerham), 140–142
 mtDNA and Y chromosome variance component estimates, comparison with autosomal genes, 183–185
- variance partitioning, 131
 allele frequency differences, across loci, 138
 assessment, total genetic variation, 134
 and clustering analysis, consistency and aims, 132, 144, 148–149
 empirical results (Lewontin), 136, 176–185
 empirical starting point, 151
 methodologies, 138
 methodology complications and multiplicities, 134–136
 modeling strategies, summary, 143–144
 ontological interpretation, 132
 and pernicious reification, 133
 population-level methodologies of, 134
 ranges and standard errors, of point estimates, 182
 studies, *Homo sapiens* classification, 143
 at three population levels, 138
 usefulness for evolutionary analyses, 149
- variance, effective population size, 89

380 · Index

- variation levels
 inequalities of Shannon information
 measures (Lewontin), 139
Varieties of Intelligence, 239
 Varnus, H., genetic variations and cancer
 risk, 232
 Venezuelan Huntington's disease, 230, 231
 vestigial trait account
 evidence, 256–258
 female orgasm evolution, 253
 viral exchanges, Neanderthals and modern
 humans, 202
 viruses and genomic evolution, interaction,
 202
Vitruvian Hominins, 66
- Wade, N., on *Structure* analysis, 95
 Wagner, G., vestigial trait account, 253–257
 Wahlund effect, 107, 108, 139–140
 Wahlund, S., 107
 Watson, J., 24
 Weir, B.S., 105
 ANOVA interpretation of F -statistics, 142
 estimation procedures, allele frequency
 and F -statistics, 162
 F_{ST} uses, 157
 on genetic distance measures, 110
 Weir's D , 105
 Weiss, K.M., 94
 Wells, S., 14
 phylogenetic method, analogy, 47
 West-Eberhardt, M.J., genetic
 accommodation, 224
When Maps Become the World (Winther), 163,
 195
 cartopower, 229
 post-racial societal future, 280
Who am I?
 answers to, 7, 275
 fundamental question, 2
 and genomic knowledge, 268
 life and mind, relation to, 4
 origins and human genome, 263
 relationship between individuals, 227
 and *Who are we?*, 32
Who are we?, 32
 answers to, 275
 human evolutionary genomics and
 philosophy, intersection, 73
 relationship between populations, 227
- Willerslev, E., 217
 Wilson, D.S., 7
 winner's curse, 241
 Winther, R.G.
 bar and scatter plots, 180, 181
 on Wahlund effect, 108
World of Allelic Color, A, 164
 Wrangham, R., on the goodness paradox,
 66
 Wright, S., 10, 79, 105, 200
 allele frequencies, mathematical models,
 23
 shifting balance theory, 108, 199
 Wright–Fisher model, 79
 effective population size, 88
 and natural population description, 90
 theoretical population, assumptions,
 87
 Wright's F_{IS}
 inbreeding, 106
 mating system within populations,
 properties of, 157
 Wright's F_{ST} , 99
 assumptions, 109, 275–276
 and genetic heterozygosity, 105
 heterozygosity reduction, measure of,
 106–108
 mathematical factors, dependence on,
 158
 pemicious reification, 132, 157–159
 population structure, 144
 role of, 159
 uses (Holsinger and Weir), 157
 Wright's F -statistics. *See F*-statistics
- X chromosomes, 46
 X_g gene, 177
- Y chromosomes, 43, 125
 and age estimation, 47
 genetic variance and autosomal genes,
 among continents component
 comparison, 183–185
 patrilineal, 49, 123
 variance component estimates, among
 continents, 183
 Yamnaya hypothesis, 35, 37
 Yang, R.-C., F -statistics, ANOVA
 interpretation, 139
 Y-Chromosomal Adam, 43–47, 52, 54