Index

accuracy, 36, 136
advanced intercross lines, 38
AIL, 38
allele, 2, 13
allele dosage, 103
allogamy, 101
allopolyploid, 18, 22, 126
allosomes, 19
anchor locus, 117
ant colony optimization, 95
autogamy, 101
autopolyploid, 18
autosomes, 19
backcross, 4, 23
backcross inbred lines, 38
BC1, 4, 23
BIL, 38
biochemical technique, 4
bridge locus, 117
bridge marker, 107
brute force search, 87
cell division, 10
centimorgan, 2, 61
centromere, 11
chiasma, 11
chiasmata, 11
chi-square goodness-of-fit, 82, 135
chromatid, 11
chromatid interference, 15, 124
cis-configuration, 22
cM, 2, 61
codominance, 22
cold spots of recombination, 8
combinatorial optimization, 90
common logarithm, 49
coupling phase, 22, 31, 33, 34, 105
crossover, 11, 14, 124
crossover interference, 17, 62, 68, 72, 124
D, 49
degrees of freedom, 49
deletion, 125
device, 27, 49
DH, 4
dioecious species, 101
diploid, 9, 11
disomic, 18
distance geometry, 96
dominance, 4, 22, 23, 33, 36, 103, 127
dominant, 22
dominantly observed loci, 94
dosage, 103
double heterozygote, 31
doubled haploids, 4, 29
evergy cells, 10
EM algorithm, 31, 71, 110
epistasis, 22
ES, 94
evolution strategy, 94
evolutionary algorithm, 94
experimental population, 3
F1, 4, 13, 24
F2, 4, 29
F2 backcross, 24
F2 intercross, 29
F2-derived doubled haploids, 38
false positive linkage, 52, 54
Fisher information, 28
full-sib family, 102
G2, 47, 83
GA, 94
gamete, 10
generalized least squares, 67
genes, 2
genetic algorithm, 94
genetic linkage, 5, 45
genetic map, 2
genetic marker, 2
genetic recombination, 3, 9
genotype, 13, 22, 127
geometric map integration, 119
Gibbs sampling, 93, 116
global optimum, 90
graphical genotypes, 133
greedy algorithm, 91
grouping algorithm, 52
Haldane’s mapping function, 61, 68
haploid, 9, 11
haplotype, 13
haplotype combination, 22, 110
hermaphrodite species, 101
heterochromosomes, 19
heterogametic, 19
heterozygous, 3, 13
heuristic, 90
hierarchical cluster analysis, 53
homeologous, 18
homozygous, 3, 13
hot spots of recombination, 8
immortalized population, 4, 29, 38
inbred line, 3
inbreeding depression, 101
incomplete information, 32
independent assortment, 12, 13, 46
independent segregation, 46
insertion, 125
integrated map, 118
interchromosomal recombination, 13
interference, 15, 17, 62, 68, 72, 124
intron recombination, 14, 124
inversion, 117
iterative solution, 33
Kosambi’s mapping function, 62, 68
L, 26
ℓ, 26
least squares, 66
life cycle, 9
likelihood, 26, 78
likelihood function, 26
likelihood ratio, 27
likelihood ratio chi-square, 47
linear regression, 66, 118
linkage, 17
linkage analysis, 2
linkage group, 5, 45
linkage phase, 22, 102, 127
linkage phase combination, 111
linked, 17
local optimum, 91
loci, 2, 13
locus, 2, 13
LOD, 27
logarithm of odds, 27
log-likelihood, 26, 78, 95, 135
LR, 27
map function, 61
map integration, 117
mapping function, 61
marker, 2
mating types, 10
maximum likelihood, 26, 69, 110, 119
maximum likelihood mapping, 135
meiosis, 9
Mendel’s law of independent assortment, 12, 124
Mendel’s law of segregation, 13, 124, 130
Mendel’s laws, 12
Mendelian inheritance, 124
Mendelian ratio, 130
minimum spanning tree, 92
mitosis, 9, 10
mitotic cell division, 10
ML estimator, 27
model assumptions, 124
model fit, 135
molecular genetic marker, 2
molecular marker technique, 4
MST, 92
multinomial coefficient, 26
multipoint estimate, 71, 89
multipoint estimation, 116
multipoint maximum likelihood, 69, 71, 94, 116
N, 24
natural logarithm, 49
nearest neighbour algorithm, 91
nearest neighbour fit, 136
nearest neighbour stress, 134
non-recombinant haplotype, 14
non-sister chromatid, 11, 124
null-allele, 4, 33, 103
outbreeding species, 6, 23
P1, 24
P2, 24
pairwise estimate, 71
pairwise recombination frequency, 110, 131
parental haplotype, 14
parental specific recombination, 113
Pearson chi-square, 47, 130
phase combination, 111
phase type, 104
phenotype, 21, 127
phenotype probability, 133
physical distance, 18
physical linkage, 45
physical map, 7
physically linked, 5
plausible map orders, 136
ploidy level, 9
polyploid, 18
polysomic, 18
post-mapping diagnostics, 123, 132
pre-mapping diagnostics, 123, 129
principal coordinate analysis, 55, 130
pseudo-autosomal, 19
pseudo-testcross, 106
Punnett square, 29
pure line, 3, 23
Index

te, 17
R, 25
rate of recombination, 5, 17, 21
recessive, 22
recessive allele, 33
recombinant haplotype, 14
recombinant inbred lines, 4, 37
recombination fraction, 17
recombination frequency, 17, 21
regression mapping, 135
repulsion phase, 22, 32, 33, 35, 105
RF, 17
RI, 4
RIL, 4, 37
s, 30
S, 32
SA, 92
SA LOD, 80
ΣARF, 81
segregation distortion, 51, 130, 132
segregation ratio, 129, 132
segregation type, 102
self-fertilization, 101
self-incompatibility, 101
self-pollination, 101
self-sterility, 101
sex chromosomes, 19
sexes, 10
sex-linked, 19
simulated annealing, 92
single nucleotide polymorphism, 4
single seed descent, 37
sister chromatid, 11
skewed segregation, 130
smart search algorithms, 88
SNP, 4
spatial sampling, 93
spem cells, 10
spindle fibres, 11
spurious linkage, 52, 54, 55, 130
SSR, 82
stress, 134
strongest cross-link, 55
sum of adjacent recombination frequencies, 92, 93, 94, 95
synapsis, 11, 117
tabu search, 93
tetrasomic, 18
three-point testcross, 77
trans-configuration, 22
translocation, 117, 125
travelling salesman problem, 88
two-point estimate, 71
two-point recombination frequency, 131
two-way pseudo-testcross, 106
weighted least squares, 66
weighted linear regression, 91
X², 47
X-chromosome, 19
Y-chromosome, 19
zygote, 9