

# INDEX

## A

### Algorithm

- expectation–maximization (EM) algorithm... 282, 285, 286, 289, 339, 342, 343, 367
- genetic algorithm ..... 239, 241, 242
- iterative signature algorithm (ISA)..... 88, 90–93, 95, 96

### Array

- ChIP-chip ..... 14, 168, 172, 276, 277, 294, 298, 307, 323, 324, 327, 328, 363–374, 377–386
- single nucleotide polymorphism (SNP) array ...10, 42, 57–71, 337, 338
- tiling array ..... 10, 42, 328, 369, 378

## B

### Bioconductor

- allele-specific copy number analysis of tumors (ASCAT) ..... 59, 62–64, 66–71
- gene answers ..... 101–111
- gene set analysis ..... 359–360
- qpgraph ..... 215–232

### Bioinformatics

- Bioinformatics for Next Generation Sequencing (BiNGS!) ..... 89–397

## C

- Cancer ..... 9, 30, 43, 57–71, 74, 82, 98, 101, 105, 106, 110, 119, 120, 136, 137, 158, 162–163, 177, 277, 283, 286, 294, 347, 357, 389–391, 394–397

- Chromatin immunoprecipitation (ChIP) ..... 10, 14, 48, 176, 254, 275–290, 294–296, 302, 305, 306, 308, 309, 312–314, 319–321, 323–333, 364, 378, 381, 383

- Coexpression ..... 158, 159, 161, 164–165, 169, 172

- Cross-platform ..... 11–12, 124, 141–143, 147–152, 347

- probe matching ..... 143, 150, 151

## D

### Data

- data consistency ..... 143, 147–148, 150, 152
- data integration
  - combinatorial algorithm for expression and sequence-based cluster extraction (COALESCE) ..... 160, 168–173

- microarray experiment functional integration technology (MEFIT) ..... 159, 164–168, 174

### data mining methods

- bicluster ..... 88–90
- Gaussian processes (GP) ..... 74, 75, 77, 78, 187

- gene set top scoring pairs (GSTSP) .. 345–360
- generalized profiling method ..... 187, 188, 190, 192, 195

- hidden Markov model (HMM) ..... 295, 297–298, 323, 337–344

- Kernel-embedding ..... 75, 84
- meta-analysis ..... 158–164, 176, 177, 385, 395

- model-based classification ..... 281–283
- top scoring pairs (TSP) ..... 345–360

### database

- Gene Expression Omnibus (GEO) ..... 11, 15, 41–52, 124, 142, 160, 220, 260, 363, 364

- Kyoto Encyclopedia of Genes and Genomes (KEGG) ..... 19–38, 93, 105, 108, 165, 290, 350, 351, 369

### Differential analysis

- false discovery rate (FDR) ..... 74, 162, 163, 269, 270, 282, 283, 286, 310, 312, 313, 315, 324, 337–344, 351, 352, 358, 371, 373, 374, 383, 395

- multiple comparisons ..... 113–120, 395
- multiple tests ..... 216, 218

### Differential equation ..... 185–196

- differential equation model ..... 235, 236

### Disease ..... 4, 10, 19–38, 50,

- 75, 76, 81, 83, 101, 105,

- 108, 111, 125, 136, 158,

- 174, 176, 268, 275, 280,

- 286, 337–343, 345–347, 357

- disease ontology ..... 102, 105, 107, 111

## E

### Epigenomics

- DNA methylation ..... 10, 87

- epigenetic modification ..... 377, 378

### histone modification

- differential histone modification site ..... 293–302

**G**

- Gene
  - gene ontology ..... 44, 93, 102, 105–111, 126, 128, 165, 167, 172, 219, 227–230, 232, 242, 290
- Genetic
  - genetic algorithm ..... 239, 241, 242
  - genetic regulation ..... 235–245
  - genome-wide association ..... 176, 337–344
- Genomics ..... 3, 5, 38, 168, 185, 186, 265, 389
  - functional genomics ..... 41–52, 153, 235, 345, 346

**I**

- Inference
  - Bayesian inference ..... 75, 77, 78, 201, 210
  - network inference ..... 102, 158, 160, 210, 217, 225

**K**

- KEGG, Kyoto Encyclopedia of Genes and Genomes
  - BRITE hierarchy ..... 20–33, 37, 38
  - KegArray ..... 20, 25–29, 35
  - KEGG API ..... 25, 36
  - KEGG Orthology (KO) ..... 21, 23–25, 37

**M**

- Microarray platform
  - one-dye ..... 7–8, 13, 15, 144, 150
  - two-dye ..... 7–8, 13, 15, 144, 146, 150
- Model
  - differential equation model ..... 235, 236
  - nonlinear model ..... 237–244
- Motif
  - motif analysis ..... 316, 318, 320
  - protein binding motif ..... 243–244
- mRNA isoforms ..... 113, 114, 266, 272

**N**

- Networks
  - network inference
    - Bayesian networks .... 165, 166, 174, 202, 235
    - dynamic Bayesian networks (DBNs) . 199–212
    - reverse engineering ..... 186
  - regulatory networks
    - biomolecular networks ..... 164
    - functional interaction networks ..... 165, 174
    - gene regulation network ..... 185–196
- Next-generation sequencing
  - ChIP-seq
    - peak calling ..... 254, 386

- RNA-seq ..... 101, 175, 250–256, 259–272, 381
- SL-seq ..... 389–397
- Non-linear
  - dynamic system ..... 19, 196, 347
  - non-linear model ..... 237–244
  - non-linear normalization ..... 280, 281, 283–285, 290
  - non-linear systems ..... 239

**O**

- Optimisation ..... 169, 188–189, 239, 343

**P**

- Pathway
  - biological pathway database ..... 124–126, 138
  - pathway analysis ..... 102, 111, 125, 286
  - pathway map ..... 21–26, 30, 32–36
- Protein
  - protein function prediction ..... 178
  - protein–DNA interaction ..... 10, 250, 275, 276, 307, 319, 363, 365

**Q**

- Quantitative real-time polymerase chain reaction (QRT-PCR) ..... 12, 14, 15, 149–151, 153

**R**

- Read mapping ..... 251, 263–267
- Regression ..... 74, 75, 116, 159, 160, 162, 187, 201, 203, 208, 270, 280, 284
  - regression model ..... 74, 75, 77, 162, 201, 202, 205

**S**

- Sampling method
  - Reversible jump Markov chain Monte Carlo (RJMCMC) ..... 201, 204, 206, 210–212
  - Monte Carlo methods ..... 224
  - non-rejection rate ..... 216–219, 222–228
- SNP
  - allelic bias ..... 64
  - aneuploidy ..... 58, 59, 62–64
  - variant detection ..... 250, 252, 256
- Spline smoothing ..... 191, 192
- Synthetic lethal screen
  - RNAi (RNA interference) ..... 389–391
  - short hairpin RNA (shRNA) ..... 389–392, 394, 395, 397

**Systems**

- dynamic system ..... 19, 196, 347
- systems biology ..... 138, 187, 199–212

**T**

Time-series ..... 84, 87–99, 199–202,  
 205–207, 210, 235–245  
 temporal module ..... 91, 94–97  
 Transcription factor  
 OCT4 ..... 302, 323–333  
 ZNF263

motif ..... 323–333  
 position weight matrix (PWM) ..... 324–333  
 transcription factor (TF)  
 binding site ..... 324  
 Tumor  
 intra-tumor heterogeneity ..... 59, 68, 70  
 morphogenesis ..... 200, 201, 207–210