

---

# Contents

<b>List of Code Challenges</b>	<b>xxv</b>
<b>Meet the Authors</b>	<b>xxxi</b>
Meet the Development Team . . . . .	xxxii
Meet our Adopting Institutions . . . . .	xxxiv
Acknowledgments . . . . .	xxxv
<b>1 Where in the Genome Does DNA Replication Begin?</b>	<b>2</b>
A Journey of a Thousand Miles. . . . .	3
Hidden Messages in the Replication Origin . . . . .	5
<i>DnaA</i> boxes . . . . .	5
Hidden messages in “The Gold-Bug” . . . . .	6
Counting words . . . . .	7
The Frequent Words Problem . . . . .	8
Frequent words in <i>Vibrio cholerae</i> . . . . .	10
Some Hidden Messages are More Surprising than Others . . . . .	11
An Explosion of Hidden Messages . . . . .	14
Looking for hidden messages in multiple genomes . . . . .	14
The Clump Finding Problem . . . . .	15
The Simplest Way to Replicate DNA . . . . .	16
Asymmetry of Replication . . . . .	19
Peculiar Statistics of the Forward and Reverse Half-Strands . . . . .	22
Lurking biological phenomenon or statistical fluke? . . . . .	22
Deamination . . . . .	24

---

The skew diagram . . . . .	25
Some Hidden Messages are More Elusive than Others . . . . .	27
A Final Attempt at Finding <i>DnaA</i> Boxes in <i>E. coli</i> . . . . .	31
Epilogue: Complications in <i>ori</i> Predictions . . . . .	32
Open Problems . . . . .	34
Multiple replication origins in a bacterial genome . . . . .	34
Finding replication origins in archaea . . . . .	36
Finding replication origins in yeast . . . . .	37
Computing probabilities of patterns in a string . . . . .	38
Charging Stations . . . . .	40
The frequency array . . . . .	40
Converting patterns to numbers and vice-versa . . . . .	42
Finding frequent words by sorting . . . . .	44
Solving the Clump Finding Problem . . . . .	46
Solving the Frequent Words with Mismatches Problem . . . . .	48
Generating the neighborhood of a string . . . . .	50
Finding frequent words with mismatches by sorting . . . . .	52
Detours . . . . .	53
Big-O notation . . . . .	53
Probabilities of patterns in a string . . . . .	53
The most beautiful experiment in biology . . . . .	58
Directionality of DNA strands . . . . .	60
The Towers of Hanoi . . . . .	61
The overlapping words paradox . . . . .	63
Bibliography Notes . . . . .	65
<b>2 Which DNA Patterns Play the Role of Molecular Clocks?</b>	<b>66</b>
Do We Have a “Clock” Gene? . . . . .	67
Motif Finding Is More Difficult Than You Think . . . . .	68
Identifying the evening element . . . . .	68
Hide and seek with motifs . . . . .	69
A brute force algorithm for motif finding . . . . .	71
Scoring Motifs . . . . .	73
From motifs to profile matrices and consensus strings . . . . .	73
Towards a more adequate motif scoring function . . . . .	75
Entropy and the motif logo . . . . .	76
From Motif Finding to Finding a Median String . . . . .	77

---

The Motif Finding Problem . . . . .	77
Reformulating the Motif Finding Problem . . . . .	78
The Median String Problem . . . . .	80
Why have we reformulated the Motif Finding Problem? . . . . .	82
Greedy Motif Search . . . . .	83
Using the profile matrix to roll dice . . . . .	83
Analyzing greedy motif finding . . . . .	86
Motif Finding Meets Oliver Cromwell . . . . .	87
What is the probability that the sun will not rise tomorrow? . . . . .	87
Laplace’s Rule of Succession . . . . .	88
An improved greedy motif search . . . . .	89
Randomized Motif Search . . . . .	92
Rolling dice to find motifs . . . . .	92
Why randomized motif search works . . . . .	94
How Can a Randomized Algorithm Perform So Well? . . . . .	97
Gibbs Sampling . . . . .	99
Gibbs Sampling in Action . . . . .	101
Epilogue: How Does Tuberculosis Hibernate to Hide from Antibiotics? . . . . .	105
Charging Stations . . . . .	108
Solving the Median String Problem . . . . .	108
Detours . . . . .	109
Gene expression . . . . .	109
DNA arrays . . . . .	109
Buffon’s needle . . . . .	110
Complications in motif finding . . . . .	113
Relative entropy . . . . .	113
Bibliography Notes . . . . .	115
<b>3 How Do We Assemble Genomes? . . . . .</b>	<b>115</b>
Exploding Newspapers . . . . .	117
The String Reconstruction Problem . . . . .	120
Genome assembly is more difficult than you think . . . . .	120
Reconstructing strings from $k$ -mers . . . . .	120
Repeats complicate genome assembly . . . . .	123
String Reconstruction as a Walk in the Overlap Graph . . . . .	124
From a string to a graph . . . . .	124
The genome vanishes . . . . .	127

---

Two graph representations . . . . .	129
Hamiltonian paths and universal strings . . . . .	130
Another Graph for String Reconstruction . . . . .	131
Gluing nodes and de Bruijn graphs . . . . .	131
Walking in the de Bruijn Graph . . . . .	134
Eulerian paths . . . . .	134
Another way to construct de Bruijn graphs . . . . .	135
Constructing de Bruijn graphs from $k$ -mer composition . . . . .	137
De Bruijn graphs versus overlap graphs . . . . .	138
The Seven Bridges of Königsberg . . . . .	139
Euler’s Theorem . . . . .	142
From Euler’s Theorem to an Algorithm for Finding Eulerian Cycles . . . . .	146
Constructing Eulerian cycles . . . . .	146
From Eulerian cycles to Eulerian paths . . . . .	147
Constructing universal strings . . . . .	148
Assembling Genomes from Read-Pairs . . . . .	150
From reads to read-pairs . . . . .	150
Transforming read-pairs into long virtual reads . . . . .	152
From composition to paired composition . . . . .	153
Paired de Bruijn graphs . . . . .	155
A pitfall of paired de Bruijn graphs . . . . .	156
Epilogue: Genome Assembly Faces Real Sequencing Data . . . . .	158
Breaking reads into $k$ -mers . . . . .	159
Splitting the genome into contigs . . . . .	160
Assembling error-prone reads . . . . .	161
Inferring multiplicities of edges in de Bruijn graphs . . . . .	163
Charging Stations . . . . .	165
The effect of gluing on the adjacency matrix . . . . .	165
Generating all Eulerian cycles . . . . .	166
Reconstructing a string spelled by a path in the paired de Bruijn graph . . . . .	167
Maximal non-branching paths in a graph . . . . .	170
Detours . . . . .	171
A short history of DNA sequencing technologies . . . . .	171
Repeats in the human genome . . . . .	173
Graphs . . . . .	174
The icosian game . . . . .	176
Tractable and intractable problems . . . . .	177

---

From Euler to Hamilton to de Bruijn . . . . .	178
The seven bridges of Kaliningrad . . . . .	179
Pitfalls of assembling double-stranded DNA . . . . .	180
The BEST Theorem . . . . .	181
Bibliography Notes . . . . .	182
<b>4 How Do We Sequence Antibiotics? . . . . .</b>	<b>184</b>
The Discovery of Antibiotics . . . . .	185
How Do Bacteria Make Antibiotics? . . . . .	186
How peptides are encoded by the genome . . . . .	186
Where is Tyrocidine encoded in the <i>Bacillus brevis</i> genome? . . . . .	188
From linear to cyclic peptides . . . . .	190
Dodging the Central Dogma of Molecular Biology . . . . .	190
Sequencing Antibiotics by Shattering Them into Pieces . . . . .	192
Introduction to mass spectrometry . . . . .	192
The Cyclopeptide Sequencing Problem . . . . .	193
A Brute Force Algorithm for Cyclopeptide Sequencing . . . . .	195
A Branch-and-Bound Algorithm for Cyclopeptide Sequencing . . . . .	196
Mass Spectrometry Meets Golf . . . . .	199
From theoretical to real spectra . . . . .	199
Adapting cyclopeptide sequencing for spectra with errors . . . . .	200
From 20 to More than 100 Amino Acids . . . . .	203
The Spectral Convolution Saves the Day . . . . .	205
Epilogue: From Simulated to Real Spectra . . . . .	207
Open Problems . . . . .	210
The Beltway and Turnpike Problems . . . . .	210
Sequencing cyclic peptides in primates . . . . .	211
Charging Stations . . . . .	213
Generating the theoretical spectrum of a peptide . . . . .	213
How fast is CYCLOPEPTIDSEQUENCING? . . . . .	214
Trimming the peptide leaderboard . . . . .	216
Detours . . . . .	217
Gause and Lysenkoism . . . . .	217
Discovery of codons . . . . .	218
Quorum sensing . . . . .	219
Molecular mass . . . . .	219
Selenocysteine and pyrrolysine . . . . .	220

---

Pseudo-polynomial algorithm for the Turnpike Problem . . . . .	221
Split genes . . . . .	222
Bibliography Notes . . . . .	223
<b>5 How Do We Compare Biological Sequences?</b>	<b>224</b>
Cracking the Non-Ribosomal Code . . . . .	225
The RNA Tie Club . . . . .	225
From protein comparison to the non-ribosomal code . . . . .	226
What do oncogenes and growth factors have in common? . . . . .	227
Introduction to Sequence Alignment . . . . .	228
Sequence alignment as a game . . . . .	228
Sequence alignment and the longest common subsequence . . . . .	229
The Manhattan Tourist Problem . . . . .	231
What is the best sightseeing strategy? . . . . .	231
Sightseeing in an arbitrary directed graph . . . . .	234
Sequence Alignment is the Manhattan Tourist Problem in Disguise . . . . .	235
An Introduction to Dynamic Programming: The Change Problem . . . . .	238
Changing money greedily . . . . .	238
Changing money recursively . . . . .	239
Changing money using dynamic programming . . . . .	241
The Manhattan Tourist Problem Revisited . . . . .	243
From Manhattan to an Arbitrary Directed Acyclic Graph . . . . .	247
Sequence alignment as building a Manhattan-like graph . . . . .	247
Dynamic programming in an arbitrary DAG . . . . .	248
Topological orderings . . . . .	249
Backtracking in the Alignment Graph . . . . .	253
Scoring Alignments . . . . .	255
What is wrong with the LCS scoring model? . . . . .	255
Scoring matrices . . . . .	256
From Global to Local Alignment . . . . .	257
Global alignment . . . . .	257
Limitations of global alignment . . . . .	259
Free taxi rides in the alignment graph . . . . .	261
The Changing Faces of Sequence Alignment . . . . .	264
Edit distance . . . . .	264
Fitting alignment . . . . .	265
Overlap alignment . . . . .	266

---

Penalizing Insertions and Deletions in Sequence Alignment . . . . .	267
Affine gap penalties . . . . .	267
Building Manhattan on three levels . . . . .	269
Space-Efficient Sequence Alignment . . . . .	271
Computing alignment score using linear memory . . . . .	271
The Middle Node Problem . . . . .	272
A surprisingly fast and memory-efficient alignment algorithm . . . . .	276
The Middle Edge Problem . . . . .	278
Epilogue: Multiple Sequence Alignment . . . . .	280
Building a three-dimensional Manhattan . . . . .	280
A greedy multiple alignment algorithm . . . . .	283
Detours . . . . .	286
Fireflies and the non-ribosomal code . . . . .	286
Finding a longest common subsequence without building a city . . . . .	287
Constructing a topological ordering . . . . .	287
PAM scoring matrices . . . . .	288
Divide-and-conquer algorithms . . . . .	291
Scoring multiple alignments . . . . .	293
Bibliography Notes . . . . .	295
<b>6 Are There Fragile Regions in the Human Genome? . . . . .</b>	<b>296</b>
Of Mice and Men . . . . .	297
How different are the human and mouse genomes? . . . . .	297
Synteny blocks . . . . .	298
Reversals . . . . .	298
Rearrangement hotspots . . . . .	299
The Random Breakage Model of Chromosome Evolution . . . . .	301
Sorting by Reversals . . . . .	304
A Greedy Heuristic for Sorting by Reversals . . . . .	308
Breakpoints . . . . .	310
What are breakpoints? . . . . .	310
Counting breakpoints . . . . .	311
Sorting by reversals as breakpoint elimination . . . . .	312
Rearrangements in Tumor Genomes . . . . .	314
From Unichromosomal to Multichromosomal Genomes . . . . .	316
Translocations, fusions, and fissions . . . . .	316
From a genome to a graph . . . . .	317

---

2-breaks . . . . .	317
Breakpoint Graphs . . . . .	321
Computing the 2-Break Distance . . . . .	324
Rearrangement Hotspots in the Human Genome . . . . .	327
The Random Breakage Model meets the 2-Break Distance Theorem . . .	327
The Fragile Breakage Model . . . . .	328
Epilogue: Synteny Block Construction . . . . .	330
Genomic dot-plots . . . . .	330
Finding shared $k$ -mers . . . . .	330
Constructing synteny blocks from shared $k$ -mers . . . . .	334
Synteny blocks as connected components in graphs . . . . .	336
Open Problem: Can Rearrangements Shed Light on Bacterial Evolution? . . .	339
Charging Stations . . . . .	341
From genomes to the breakpoint graph . . . . .	341
Solving the 2-Break Sorting Problem . . . . .	343
Detours . . . . .	346
Why is the gene content of mammalian X chromosomes so conserved? .	346
Discovery of genome rearrangements . . . . .	346
The exponential distribution . . . . .	347
Bill Gates and David X. Cohen flip pancakes . . . . .	348
Sorting linear permutations by reversals . . . . .	349
Bibliography Notes . . . . .	351
<b>7 Which Animal Gave Us SARS? . . . . .</b>	<b>352</b>
The Fastest Outbreak . . . . .	353
Trouble at the Metropole Hotel . . . . .	353
The evolution of SARS . . . . .	353
Transforming Distance Matrices into Evolutionary Trees . . . . .	355
Constructing a distance matrix from coronavirus genomes . . . . .	355
Evolutionary trees as graphs . . . . .	357
Distance-based phylogeny construction . . . . .	359
Toward An Algorithm for Distance-Based Phylogeny Construction . . . . .	362
A quest for neighboring leaves . . . . .	362
Computing limb lengths . . . . .	364
Additive Phylogeny . . . . .	367
Trimming the tree . . . . .	367
Attaching a limb . . . . .	369



---

An algorithm for distance-based phylogeny construction . . . . .	369
Constructing an evolutionary tree of coronaviruses . . . . .	370
Using Least Squares to Construct Approximate Distance-Based Phylogenies .	372
Ultrametric Evolutionary Trees . . . . .	373
The Neighbor-Joining Algorithm . . . . .	377
Transforming a distance matrix into a neighbor-joining matrix . . . . .	377
Analyzing coronaviruses with the neighbor-joining algorithm . . . . .	381
Limitations of distance-based approaches to tree construction . . . . .	383
Character-Based Tree Reconstruction . . . . .	383
Character tables . . . . .	383
From anatomical to genetic characters . . . . .	384
How many times has evolution invented insect wings? . . . . .	385
The Small Parsimony Problem . . . . .	387
The Large Parsimony Problem . . . . .	392
Epilogue: Evolutionary Trees Fight Crime . . . . .	398
Detours . . . . .	401
When did HIV jump from primates to humans? . . . . .	401
Searching for a tree fitting a distance matrix . . . . .	401
The four point condition . . . . .	403
Did bats give us SARS? . . . . .	404
Why does the neighbor-joining algorithm find neighboring leaves? . . .	406
Computing limb lengths in the neighbor-joining algorithm . . . . .	411
Giant panda: bear or raccoon? . . . . .	412
Where did humans come from? . . . . .	413
Bibliography Notes . . . . .	415
<b>8 How Did Yeast Become a Wine Maker? . . . . .</b>	<b>416</b>
An Evolutionary History of Wine Making . . . . .	417
How long have we been addicted to alcohol? . . . . .	417
The diauxic shift . . . . .	418
Identifying Genes Responsible for the Diauxic Shift . . . . .	418
Two evolutionary hypotheses with different fates . . . . .	418
Which yeast genes drive the diauxic shift? . . . . .	419
Introduction to Clustering . . . . .	420
Gene expression analysis . . . . .	420
Clustering yeast genes . . . . .	422
The Good Clustering Principle . . . . .	424

---

Clustering as an Optimization Problem . . . . .	426
Farthest First Traversal . . . . .	428
<i>k</i> -Means Clustering . . . . .	430
Squared error distortion . . . . .	430
<i>k</i> -means clustering and the center of gravity . . . . .	432
The Lloyd Algorithm . . . . .	433
From centers to clusters and back again . . . . .	433
Initializing the Lloyd algorithm . . . . .	435
<i>k</i> -means++ Initializer . . . . .	436
Clustering Genes Implicated in the Diauxic Shift . . . . .	437
Limitations of <i>k</i> -Means Clustering . . . . .	438
From Coin Flipping to <i>k</i> -Means Clustering . . . . .	440
Flipping coins with unknown biases . . . . .	440
Where is the computational problem? . . . . .	443
From coin flipping to the Lloyd algorithm . . . . .	444
Return to clustering . . . . .	445
Making Soft Decisions in Coin Flipping . . . . .	446
Expectation maximization: the E-step . . . . .	446
Expectation maximization: the M-step . . . . .	448
The expectation maximization algorithm . . . . .	449
Soft <i>k</i> -Means Clustering . . . . .	449
Applying expectation maximization to clustering . . . . .	449
Centers to soft clusters . . . . .	450
Soft clusters to centers . . . . .	451
Hierarchical Clustering . . . . .	452
Introduction to distance-based clustering . . . . .	452
Inferring clusters from a tree . . . . .	455
Analyzing the diauxic shift with hierarchical clustering . . . . .	457
Epilogue: Clustering Tumor Samples . . . . .	459
Detours . . . . .	460
Whole genome duplication or a series of duplications? . . . . .	460
Measuring gene expression . . . . .	460
Microarrays . . . . .	461
Proof of the Center of Gravity Theorem . . . . .	462
Transforming an expression matrix into a distance/similarity matrix . . . . .	463
Clustering and corrupted cliques . . . . .	464
Bibliography Notes . . . . .	467

---

<b>9</b>	<b>How Do We Locate Disease-Causing Mutations?</b>	<b>468</b>
	What Causes Ohdo Syndrome? . . . . .	469
	Introduction to Multiple Pattern Matching . . . . .	470
	Herding Patterns into a Trie . . . . .	471
	Constructing a trie . . . . .	471
	Applying the trie to multiple pattern matching . . . . .	473
	Preprocessing the Genome Instead . . . . .	475
	Introduction to suffix tries . . . . .	475
	Using suffix tries for pattern matching . . . . .	475
	Suffix Trees . . . . .	479
	Suffix Arrays . . . . .	482
	Constructing a suffix array . . . . .	482
	Pattern matching with the suffix array . . . . .	483
	The Burrows-Wheeler Transform . . . . .	484
	Genome compression . . . . .	484
	Constructing the Burrows-Wheeler transform . . . . .	485
	From repeats to runs . . . . .	487
	Inverting the Burrows-Wheeler Transform . . . . .	488
	A first attempt at inverting the Burrows-Wheeler transform . . . . .	488
	The First-Last Property . . . . .	490
	Using the First-Last property to invert the Burrows-Wheeler transform . . . . .	493
	Pattern Matching with the Burrows-Wheeler Transform . . . . .	496
	A first attempt at Burrows-Wheeler pattern matching . . . . .	496
	Moving backward through a pattern . . . . .	497
	The Last-to-First mapping . . . . .	499
	Speeding Up Burrows-Wheeler Pattern Matching . . . . .	502
	Substituting the Last-to-First mapping with count arrays . . . . .	502
	Getting rid of the first column of the Burrows-Wheeler matrix . . . . .	503
	Where are the Matched Patterns? . . . . .	505
	Burrows and Wheeler Set Up Checkpoints . . . . .	506
	Epilogue: Mismatch-Tolerant Read Mapping . . . . .	508
	Reducing approximate pattern matching to exact pattern matching . . . . .	508
	BLAST: Comparing a sequence against a database . . . . .	510
	Approximate pattern matching with the Burrows-Wheeler transform . . . . .	511
	Charging Stations . . . . .	514
	Constructing a suffix tree . . . . .	514
	Solving the Longest Shared Substring Problem . . . . .	517

---

Partial suffix array construction . . . . .	519
Detours . . . . .	520
The reference human genome . . . . .	520
Rearrangements, insertions, and deletions in human genomes . . . . .	520
The Aho-Corasick algorithm . . . . .	521
From suffix trees to suffix arrays . . . . .	522
From suffix arrays to suffix trees . . . . .	524
Binary search . . . . .	527
Bibliography Notes . . . . .	528
<b>10 Why Have Biologists Still Not Developed an HIV Vaccine?</b>	<b>530</b>
Classifying the HIV Phenotype . . . . .	531
How does HIV evade the human immune system? . . . . .	531
Limitations of sequence alignment . . . . .	533
Gambling with Yakuza . . . . .	534
Two Coins up the Dealer’s Sleeve . . . . .	536
Finding CG-Islands . . . . .	537
Hidden Markov Models . . . . .	538
From coin flipping to a Hidden Markov Model . . . . .	538
The HMM diagram . . . . .	540
Reformulating the Casino Problem . . . . .	540
The Decoding Problem . . . . .	543
The Viterbi graph . . . . .	543
The Viterbi algorithm . . . . .	546
How fast is the Viterbi algorithm? . . . . .	547
Finding the Most Likely Outcome of an HMM . . . . .	548
Profile HMMs for Sequence Alignment . . . . .	550
How do HMMs relate to sequence alignment? . . . . .	550
Building a profile HMM . . . . .	552
Transition and emission probabilities of a profile HMM . . . . .	555
Classifying proteins with profile HMMs . . . . .	559
Aligning a protein against a profile HMM . . . . .	559
The return of pseudocounts . . . . .	560
The troublesome silent states . . . . .	561
Are profile HMMs really all that useful? . . . . .	568
Learning the Parameters of an HMM . . . . .	569
Estimating HMM parameters when the hidden path is known . . . . .	569

---

Viterbi learning . . . . .	571
Soft Decisions in Parameter Estimation . . . . .	573
The Soft Decoding Problem . . . . .	573
The forward-backward algorithm . . . . .	574
Baum-Welch Learning . . . . .	577
The Many Faces of HMMs . . . . .	579
Epilogue: Nature is a Tinkerer and not an Inventor . . . . .	580
Detours . . . . .	582
The Red Queen Effect . . . . .	582
Glycosylation . . . . .	582
DNA methylation . . . . .	582
Conditional probability . . . . .	583
Bibliography Notes . . . . .	585
<b>11 Was <i>T. rex</i> Just a Big Chicken?</b>	<b>586</b>
Paleontology Meets Computing . . . . .	587
Which Proteins Are Present in This Sample? . . . . .	588
Decoding an Ideal Spectrum . . . . .	589
From Ideal to Real Spectra . . . . .	593
Peptide Sequencing . . . . .	596
Scoring peptides against spectra . . . . .	596
Where are the suffix peptides? . . . . .	598
Peptide sequencing algorithm . . . . .	600
Peptide Identification . . . . .	601
The Peptide Identification Problem . . . . .	601
Identifying peptides in the unknown <i>T. rex</i> proteome . . . . .	602
Searching for peptide-spectrum matches . . . . .	603
Peptide Identification and the Infinite Monkey Theorem . . . . .	605
False discovery rate . . . . .	605
The monkey and the typewriter . . . . .	606
Statistical significance of a peptide-spectrum match . . . . .	608
Spectral Dictionaries . . . . .	610
<i>T. rex</i> Peptides: Contaminants or Treasure Trove of Ancient Proteins? . . . . .	614
The hemoglobin riddle . . . . .	614
The dinosaur DNA controversy . . . . .	616
Epilogue: From Unmodified to Modified Peptides . . . . .	617
Post-translational modifications . . . . .	617

---

Searching for modifications as an alignment problem . . . . .	618
Building a Manhattan grid for spectral alignment . . . . .	620
Spectral alignment algorithm . . . . .	623
Detours . . . . .	626
Gene prediction . . . . .	626
Finding all paths in a graph . . . . .	627
The Anti-Symmetric Path Problem . . . . .	628
Transforming spectra into spectral vectors . . . . .	629
The infinite monkey theorem . . . . .	630
The probabilistic space of peptides in a spectral dictionary . . . . .	631
Are terrestrial dinosaurs really the ancestors of birds? . . . . .	632
Solving the Most Likely Peptide Vector Problem . . . . .	633
Selecting parameters for transforming spectra into spectral vectors . . . . .	634
Bibliography Notes . . . . .	636
<b>Appendix: Introduction to Pseudocode</b>	<b>639</b>
What is Pseudocode? . . . . .	639
Nuts and Bolts of Pseudocode . . . . .	641
The <b>if</b> condition . . . . .	642
The <b>for</b> loop . . . . .	643
The <b>while</b> loop . . . . .	645
Recursive algorithms . . . . .	646
Arrays . . . . .	647
<b>Glossary</b>	<b>649</b>
<b>Bibliography</b>	<b>671</b>
<b>Image Courtesies</b>	<b>683</b>