
Contents

1	Introduction	1
1.1	Strategic Considerations	1
1.2	Notations	4
1.3	Preparing the Computer	5
1.3.1	Installations	5
1.3.2	Configurations	7
2	First Steps in R for Phylogeneticists	9
2.1	The Command Line Interface	9
2.2	The Data Structures	11
2.2.1	Vector	11
2.2.2	Factor	14
2.2.3	Matrix	15
2.2.4	Data Frame	16
2.2.5	List	17
2.3	The Help System	18
2.4	Creating Graphics	19
2.5	Saving and Restoring R Data	20
2.6	Using R Functions	20
2.7	Repeating Commands	21
2.7.1	Loops	21
2.7.2	<i>Apply</i> -Like Functions	22
2.8	Exercises	23
3	Phylogenetic Data in R	25
3.1	Phylogenetic Data as R Objects	25
3.1.1	The Class "phylo" (ape)	26
3.1.2	The Class "phylog" (ade4)	27
3.1.3	The Class "matching" (ape)	27
3.1.4	The Class "treeshape" (apTreeshape)	28
3.2	Reading Phylogenetic Data	28

3.2.1	Phylogenies	28
3.2.2	Reading Internet Tree Databases	30
3.2.3	Molecular Sequences	30
3.3	Writing Data	33
3.4	Manipulating Data	35
3.4.1	Basic Tree Manipulation	35
3.4.2	Rooted <i>Versus</i> Unrooted Trees	36
3.4.3	Dichotomous <i>Versus</i> Multichotomous Trees	37
3.4.4	Summarizing and Comparing Trees	38
3.4.5	Converting Objects	39
3.4.6	Manipulating DNA Data	40
3.5	Generating Random Trees	44
3.6	Case Studies	46
3.6.1	<i>Sylvia</i> Warblers	46
3.6.2	Phylogeny of the Felidae	50
3.6.3	Snake Venom Proteome	52
3.6.4	Mammalian Mitochondrial Genomes	55
3.6.5	Butterfly DNA Barcodes	62
3.7	Exercises	64
4	Plotting Phylogenies	65
4.1	Simple Tree Drawing	65
4.1.1	Annotating Trees	71
4.1.2	Showing Clades	80
4.2	Combining Plots	83
4.3	Large Phylogenies	89
4.4	Perspectives	92
4.5	Exercises	94
5	Phylogeny Estimation	95
5.1	Distance Methods	96
5.1.1	Calculating Distances	96
5.1.2	Simple Clustering and UPGMA	99
5.1.3	Neighbor-Joining	100
5.2	Maximum Likelihood Methods	100
5.2.1	Substitution Models: A Primer	101
5.2.2	Estimation with Molecular Sequences	106
5.2.3	Finding the Maximum Likelihood Tree	110
5.2.4	DNA Mining with PHYML	111
5.3	Bootstrap Methods and Distances Between Trees	112
5.3.1	Resampling Phylogenetic Data	113
5.3.2	Bipartitions and Computing Bootstrap Values	115
5.3.3	Distances Between Trees	118
5.3.4	Consensus Trees	118
5.4	Molecular Dating	119

5.5	Case Studies	121
5.5.1	<i>Sylvia</i> Warblers	121
5.5.2	Phylogeny of the Felidae	125
5.5.3	Butterfly DNA Barcodes	129
5.6	Perspectives	131
5.7	Exercises	131
6	Analysis of Macroevolution with Phylogenies	133
6.1	Phylogenetic Comparative Methods	133
6.1.1	Phylogenetically Independent Contrasts	135
6.1.2	Phylogenetic Autoregression	138
6.1.3	Autocorrelative Models	139
6.1.4	Multivariate Decomposition	142
6.1.5	Generalized Least Squares	144
6.1.6	Generalized Estimating Equations	147
6.1.7	Mixed Models and Variance Partitioning	149
6.1.8	The Ornstein–Uhlenbeck Model	151
6.1.9	Perspectives	153
6.2	Estimating Ancestral Characters	154
6.2.1	Continuous Characters	155
6.2.2	Discrete Characters	156
6.3	Analysis of Diversification	160
6.3.1	Graphical Methods	161
6.3.2	Birth–Death Models	163
6.3.3	Survival Models	167
6.3.4	Goodness-of-Fit Tests	169
6.3.5	Tree Shape and Indices of Diversification	170
6.4	Perspectives	172
6.5	Case Studies	173
6.5.1	<i>Sylvia</i> Warblers	173
6.5.2	Phylogeny of the Felidae	176
6.6	Exercises	180
7	Developing and Implementing Phylogenetic Methods in R	183
7.1	Features of R	183
7.1.1	Object-Orientation	183
7.1.2	Variable Definition and Scope	185
7.1.3	How R Works	186
7.2	Writing Functions in R	187
7.3	Interfacing R with Other Languages	189
7.3.1	Simple Interfaces	189
7.3.2	Complex Interfaces	190
7.4	Writing R Packages	192
7.4.1	A Minimalist Package	192
7.4.2	The Documentation System	193

7.5 Performance Issues and Strategies	193
References	199
Index	209