

AN EMPIRICAL ASSESSMENT OF
THE BOOTSTRAP SUPPORT AS AN INDICATOR OF
ROBUSTNESS IN PHYLOGENETIC TREES

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ORIGINAL LITERARY WORK DECLARATION

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An empirical assessment of the bootstrap support as an indicator of robustness in phylogenetic trees (“this Work”)

Field of Study: Bootstrapping, Phylogenetics, Bioinformatics

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ABSTRACT

Bootstrapping is a de-facto standard for displaying the validity of a phylogenetic tree. However this may not be the case as bootstrapping assume that the random sequence exist within the genome. In order to examine whether bootstrapping is a valid process, it must be done empirically. Across multiple taxa there are minimal fully curated genomes but there are mitochondrion genomes available to test this. A widely accepted evolutionary tree is chosen with 6 taxa - *Pan paniscus* (bonobo), *Homo sapiens* (human), *Gorilla gorilla* (gorilla), *Pongo pygmaeus* (orangutan), *Hylobates lar* (common gibbon) and *Gallus gallus* (red junglefowl) as the outgroup. A comparison of topology and bootstrap support value is executed between the phylogenetic tree of the whole mitochondrial genome with trees built from all the genes in mitochondrial genome. The result shows that bootstrap support value tend to inflate and larger than the empirical estimate. This suggests that bootstrap support in phylogenetic trees must be interpreted cautiously and not casually accepted at face value.

ABSTRAK

Butstrap ialah piawai de facto untuk memaparkan kesahihan pokok evolusi. Walau bagaimanapun, ini tidak selalu berlaku kerana butstrap menganggap bahawa jujukan rawak wujud dalam genom. Untuk memeriksa sama ada butstrap adalah satu proses yang sah, ia mesti dilakukan secara empirikal. Terdapat minima genom yang dikemaskini dan dikurorkan merentasi beberapa taksa terdapat genom mitochondrion disediakan untuk menguji situasi ini. Pokok evolusi yang diterima secara meluas dipilih dengan 6 taksa - *Pan paniscus* (bonobo), *Homo sapiens* (manusia), *Gorilla gorilla* (gorila), *Pongo pygmaeus* (orangutan), *Hylobates lar* (siamang biasa) dan *Gallus Gallus* (ayam hutan merah) sebagai outgroup itu. Perbandingan nilai sokongan topologi dan bootstrap yang dimeterai antara pokok filogenetik seluruh genom mitokondria dengan pokok-pokok yang dibina dari semua gen dalam genom mitokondria. Hasil menunjukkan bahawa nilai sokongan butstrap cenderung untuk mengembung dan lebih besar daripada anggaran empirik. Ini menunjukkan bahawa sokongan butstrap dalam pokok evolusi mesti ditafsirkan dengan berhati-hati dan tidak bersahaja diterima pada nilai muka.

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TABLE OF CONTENTS

ORIGINAL LITERARY WORK DECLARATION	ii
ABSTRACT	iii
ABSTRAK	iv
ACKNOWLEDGEMENT	v
TABLE OF CONTENTS	vi
LIST OF FIGURES	vii
LIST OF TABLES	ix
LIST OF SYMBOLS AND ABBREVIATIONS	x
LIST OF APPENDICES	xi

Chapter	Pages
1. INTRODUCTION	
1.1. <i>Mitochondrion</i>	1
1.2. <i>Bootstrapping</i>	4
1.3. <i>Objective</i>	6
2. LITERATURE REVIEW	
2.1. <i>Mitochondrion in Evolution</i>	7
2.2. <i>Bootstrapping in Phylogenetic</i>	9
2.3. <i>Software</i>	10
3. METHODOLOGY	12
4. RESULT	15
5. DISCUSSION	27
6. CONCLUSION	31
7. SUPPLEMENTARY	
7.1 <i>Instrumentation</i>	32
7.2 <i>Appendix</i>	33
7.3 <i>Bibliography</i>	72

LIST OF FIGURES

		Pages
Figure 1.1	Struture of mitochondrion	2
Figure 1.2	Mitochondrion Genome of <i>Homo sapiens</i>	3
Figure 1.3	Mitochondrion Genome of <i>Gallus gallus</i>	3
Figure 1.4	Mitochondrion Genome of <i>Pan paniscus</i>	3
Figure 1.5	Bootstrapping includes column resampling and creating sequences	5
Figure 3.1	Major steps in execution of the study	12
Figure 4.1	Topology of the reference tree	13
Figure 4.2	Position of node A, B and C on the topology of the reference tree	14
Figure 4.3	Empirical estimate on the reference tree in MEGA	18
Figure 4.4	Empirical estimate of the reference tree in R	18
Figure 4.5	Histogram of frequency of bootstrap support for (a) Node A, (b) Node B and (c) Node C for protein and rRNA genes. The dotted line reflect the empirical estimate from all genes	20
Figure 4.6	The distribution of bootstrap values against sequence length for node A (represented by ○), node B (represented by ■) and node C (represented by +) using protein and rRNA genes	21
Figure 4.7	Histogram of frequency of bootstrap support for (a) Node A, (b) Node B and (c) Node C for tRNA genes. The dotted line reflect the empirical estimate from all genes	22

LIST OF FIGURES (continued)

		Pages
Figure 4.8	The distribution of bootstrap values against sequence length for node A (represented by ○), node B (represented by ■) and node C (represented by +) using tRNA genes only	23
Figure 4.9	Histogram of frequency of bootstrap support for (a) Node A, (b) Node B and (c) Node C for all genes. The dotted line reflect the empirical estimate from all genes	24
Figure 4.10	The distribution of the nodes from bootstrap value against sequence length for protein and rRNA (represented by ○) and tRNA (represented by ■) using all genes	26

LIST OF TABLES

		Pages
Table 4.1	Total Frequency of Node Appearance	17
Table 4.2	Empirical Bootstrap Support Value for Each Node	17
Table 4.3	Summary of bootstrap values in node A, B and C from MEGA	19

LIST OF SYMBOLS AND ABBREVIATIONS

APE	Analyses of Phylogenetics and Evolution
ATP	Adenosine Triphosphate
CDS	Coding Sequence
CI	Confidence Interval
GI	GenInfo Identifier
kbp	Kilo-base pair
MEGA5	Molecular Evolutionary Genetics Analysis version 5
ML	Maximum Likelihood
MSA	Multiple Sequence Alignment
mtDNA	Mitochondrion DNA
MUSCLE	Multiple Sequence Comparison by Log- Expectation
NADH	Nicotinamide adenine dinucleotide (reduced form)
NCBI	National Center for Biotechnology Information
ND	NADH dehydrogenase
NNI	Nearest-Neighbour-Interchange
PyCogent	Python the Comparative Genomic Toolkit
RNA	Ribonucleic Acid
rRNA	Ribosome Ribonucleic Acid
SD	Standard Deviation
SE	Standard Error
TN93	Tamura-Nei, 93
tRNA	Transfer Ribonucleic Acid
µm	Micrometer

LIST OF APPENDICES

Appendix A	Frequency of Node Appearance of Protein Coding Sequence
Appendix B	Frequency of Node Appearance of Ribosomal RNA Sequence
Appendix C	Frequency of Node Appearance of Transfer RNA Sequence
Appendix D	Topology of phylogenetics trees of MEGA5 for all genes including mitochondrial genome
Appendix E	Topology of phylogenetics trees of R for all genes including mitochondrial genome
Appendix F	PyCogent codes
Appendix G	R codes