HybPhyloMaker software

Software	Source	Install (yes/no)	Used command(s)	0 Sample preparation	1 Raw data processing	2 Read mapping	3 Generate pslx	4a Process pslx	4a2 Selext low heterozygosity	4b Correct frame, translate	5 Missing data handling	6 Gene tree building	7 Root trees	8a ASTRAL	8b ASTRID	8c MRL	8e Concatenated FastTree	8f ExaML	8g BUCKy	9 Update	10 Collapse trees & select	Reports
GNU parallel	http://www.gnu.org/software/parallel/	y	parallel	x				x	x													
Bowtie2	http://bowtie-bio.sourceforge.net/bowtie2/index.shtml	y	bowtie2-build, bowtie2		x	x																
BWA	http://bio-bwa.sourceforge.net/	y	bwa mem			x			x													
SAMtools	http://samtools.sourceforge.net/	y	samtools		x	x			x													
BCFtools	https://samtools.github.io/bcftools/	y	bcftools						x													
bam2fastq	https://gsl.hudsonalpha.org/information/software/bam2fastq	y	bam2fastq		x																	
Trimmomatic	http://www.usadellab.org/cms/?page=trimmomatic	n	java -jar trimmomatic-0.33.jar		x																	
FastUniq	https://sourceforge.net/projects/fastuniq/	y	fastuniq		x																	
JDK/JRE	http://www.oracle.com/technetwork/java/javase/	y	java		x									x	x	x					x	
OCOCO	https://github.com/karel-brinda/ococo	y	ococo			x																
kindel	https://pypi.python.org/pypi/kindel	y	kindel			x																
ConsensusFixer	https://github.com/cbg-ethz/ConsensusFixer	n	java -jar ConsensusFixer.jar			x																
Perl	https://www.perl.org/	y	perl		x			x		x		x					x					
BLAT suite	https://genome.ucsc.edu/goldenpath/help/blatSpec.html	y	blat				x															
MAFFT	http://mafft.cbrc.jp/alignment/software/	y	mafft						x	x												
Python	https://www.python.org/	y	python					x						x	x							
Python3	https://www.python.org/download/releases/3.0/	y	python3			x			x	x												
AMAS	https://github.com/marekborowiec/AMAS/	n	python3 amas.py					x	x	x	x	x		x	x		x	x				
EMBOSS	http://emboss.open-bio.org/	y	transeq							x												
TrimAl	http://trimal.cgenomics.org/	y	trimal								x											
MstatX	https://github.com/gcollet/MstatX	y	mstatx								x											
FastTree	http://www.microbesonline.org/fasttree/	y	fasttree									x					x					
Newick Utilities	http://cegg.unige.ch/newick_utils	y	nw_reroot, nw_topology										x	x	x	x	x				x	
RAxML	http://sco.h-its.org/exelixis/web/software/raxml/index.html	y	raxmlHPC									x					x	x				
R	https://www.r-project.org/	y	R								x	x								x	x	x
ASTRAL	https://github.com/smirarab/ASTRAL	n	java -jar astral.5.6.1.jar											x								
ASTRID	https://github.com/pranjalv123/ASTRID	n	ASTRID												x							
p4	http://p4.nhm.ac.uk	y	p4											x	x							
mrpmatrix	https://github.com/smirarab/mrpmatrix	n	java -jar mrp.jar													x						
ExaML	http://sco.h-its.org/exelixis/web/software/examl/index.html	y	examl															x				
BUCKy	https://www.stat.wisc.edu/~ane/bucky/	y	mbsum, bucky																x			