

HybPhyloMaker software

				0a	0e	0f	1	2	3	3a	4a	4a2	4a3	4b	5	6	7	8a	8a2	8b	8c	8e	8f	8g	8h	8i	8j	8k	8l	8m	9	10	11	12	13	14		
		Install (yes/no)		Sample preparation	Create test dataset	Create plastome reference	Raw data processing	Read mapping	Generate psix	Full plastome alignment	Process psix	Select low heterozygosity	Trimming exons	Correct frame, translate	Missing data handling	Gene tree building	Root trees	ASTRAL	ASTRAL-IV	ASTRID	MRL	Concatenated FastTree	ExaML	BUCKy	Neighbour network	Dsuite	SuperQ network	Quartet sampling	SNaQ	PhyloNet	Update	Collapse trees & select	PhyParts	Exclude samples	DiscoVista	treePL	Reports	
Software	Source		Used command(s)																																			
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				x																										
BEDtools	https://github.com/arq5x/bedtools2	y	bedtools			x																																
BCFtools	https://samtools.github.io/bcftools/	y	bcftools									x																										
bam2fastq	https://github.com/dreamboatyz/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	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																								
seqtk	https://github.com/lh3/seqtk	y	seqtk comp			x									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											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/Smirab/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/Smirab/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														
PhyParts	https://bitbucket.org/blackrim/phyparts	y	java -jar phyparts-0.0.1																													x						