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. you have to restart your PC (computer). [^4] Appendix 3: Last published versions of the tools
===== 1) Free download of "*scipy" package* version 1.0.0 or
"*numpy" package* version 1.10.2. If a new version is released, it is not necessary to uninstall the previous version before
installing the new one. The user can delete the old folders and data on the hard disk. 2\)"phylip" package* version 3.3 or
earlier. This package comes with many programs, including SeqMan (search and align sequences), BioEdit (editing sequences),
BioSamples (tools for sample management), and DNAStar (software package). Phylip version 3.3.19 or earlier is not compatible
with the current version of SeqMan, so the user must uninstall it. 3) "*fasta" package* version 0.12.0 or earlier. The current
version is 2.1.0, and this package is not compatible with earlier versions. The user must delete the old folder and data before
installing the new one. 4) "*mafft" package* version 7.220 or earlier. The current version is 7.314, and this package is not
compatible with earlier versions. The user must delete the old folder and data before installing the new one. 5) "*phyml"
package* version 2.0.6 or earlier. The current version is 3.0.1. If a new version is released, it is not necessary to uninstall the
previous version before installing the new one. The user can delete the old folder and data on the hard disk. 6) "*bait" package*
version 2.0 or earlier. The current version is 3.0.1, and this package is not compatible with earlier versions. The user can delete
the old folder and data on the hard disk. 7) "*ClustalW" package* version 1.83 or earlier. The current version is 2.1.5. If a new
version is released, it is not necessary to uninstall the previous version before installing the new one. The user can delete the old
folder and data on the hard disk. 8) "*R" package* version 3.2.0 or earlier. The current version is 3.2. 82157476af

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