

## 10.6: R, DNA and evolution

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In biology, majority of research is now related with DNA-based phylogenetic studies. R is aware of these methods, and one of examples (morphological though) was presented above. DNA phylogeny research includes numerous steps, and the scripting power of R could be used to automate procedures by joining them in a sort of workflow which we call Ripeline.

Book supplements contain archived folder [ripline.zip](#) which includes R scripts and data illustrating work with DNA tabular database, FASTA operations, DNA alignment, flank removal, gapcoding, concatenation, and examples of how to use internal and external tree estimators.

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