

# Deciphering the tRNA operational code - using R

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Keywords: tRNA, amino acids, operational RNA code, rpart, dendrogram

The talk will deal with the unique properties of the RNA code that governs the charging of the transfer-RNA (tRNA) molecule so that it will bring the appropriate amino-acid to the Ribosome.

The analysis was performed on 3936 tRNA sequences from 86 Archaea species using R. We employed various existing facilities for performing data importing (**Biostrings**, **XML**, **RCurl**), cleaning and preparation (**plyr**, **reshape**), classification and regression trees and cross-validation (**rpart**), clustering (**cluster**), visualization (**Graphics**, **lattice**, **seqLogo**, **colorspace**), reproducible research (**Sweave**, **knitr**, **xtable**, **Hmisc**, **installr**) etc.

In addition, we self-developed (or implemented) algorithms for manipulating dendrograms objects for tasks such as the comparing of hierarchical clusters and new plotting options (all of which are intended to be released in the near future in the **dendextend** package).

This talk is much-updated follow-up for the 2010 useR talk I gave on the same topic (see ref 1). In this talk I will provide the brief biological background that is needed in order to understand the relevant questions and discoveries, and present how we used R's various packages and statistical methods, while devising and implementing new methods, in order to support our investigation.

## References

1. Tal Galili, Shaul Shaul, Yoav Benjamini (2010), "Analyzing the Operational RNA Code for Amino Acids - Using R", a talk from useR2010 - <http://user2010.org/abstracts/Galili+Shaul+Benjamini.pdf>
2. Shaul S, Berel D, Benjamini Y, Graur D.(2010), "Revisiting the operational RNA code for amino acids: Ensemble attributes and their implications", RNA. 2010 Jan;16(1):141-53. Epub 2009 Dec 1.

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