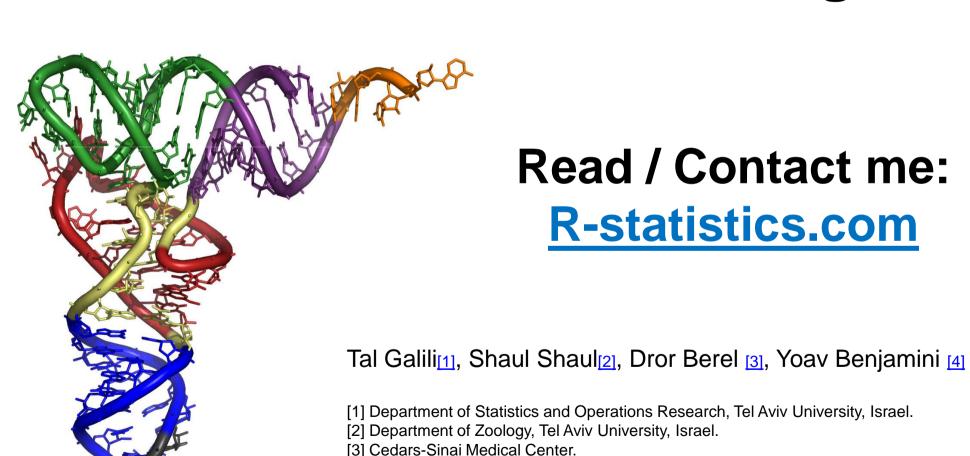
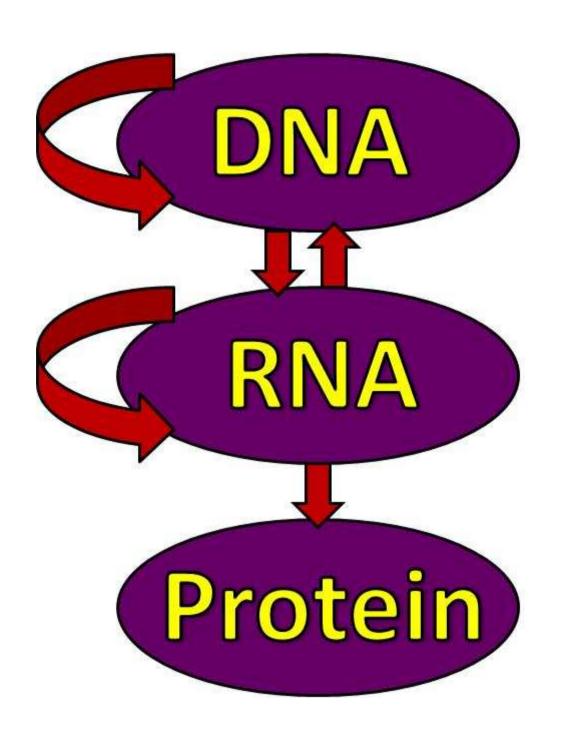
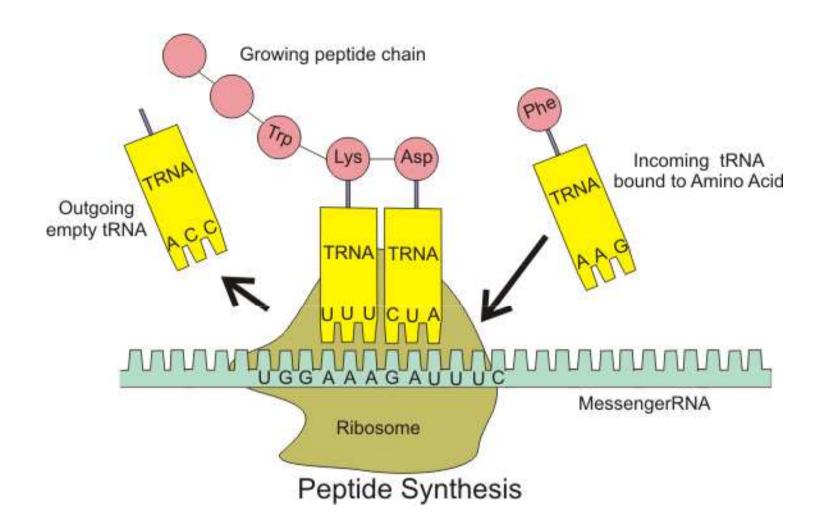
Analyzing the Operational RNA Code for Amino Acids - Using R

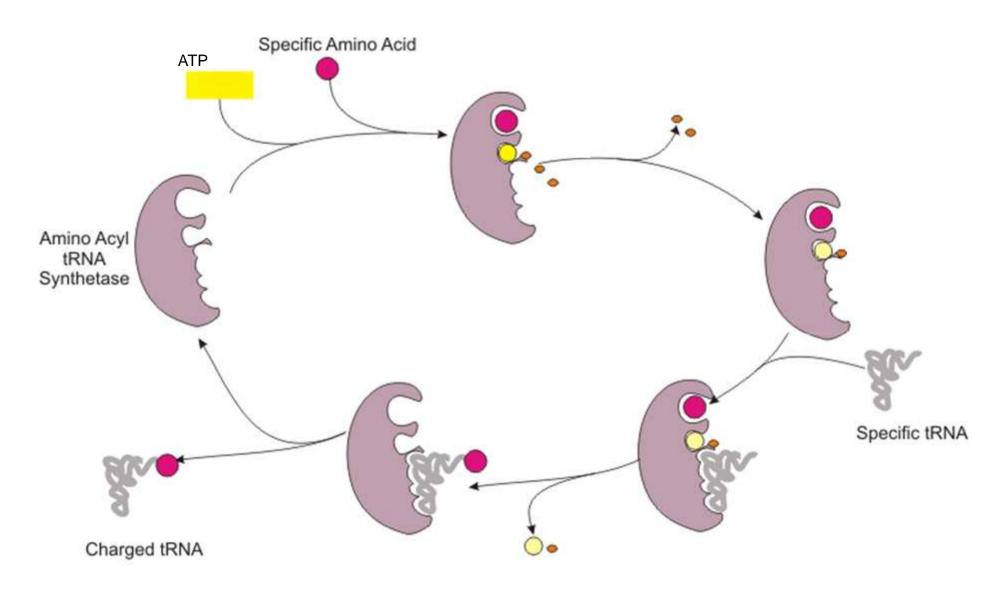


[4] Department of Statistics and Operations Research, Tel Aviv University, Israel.

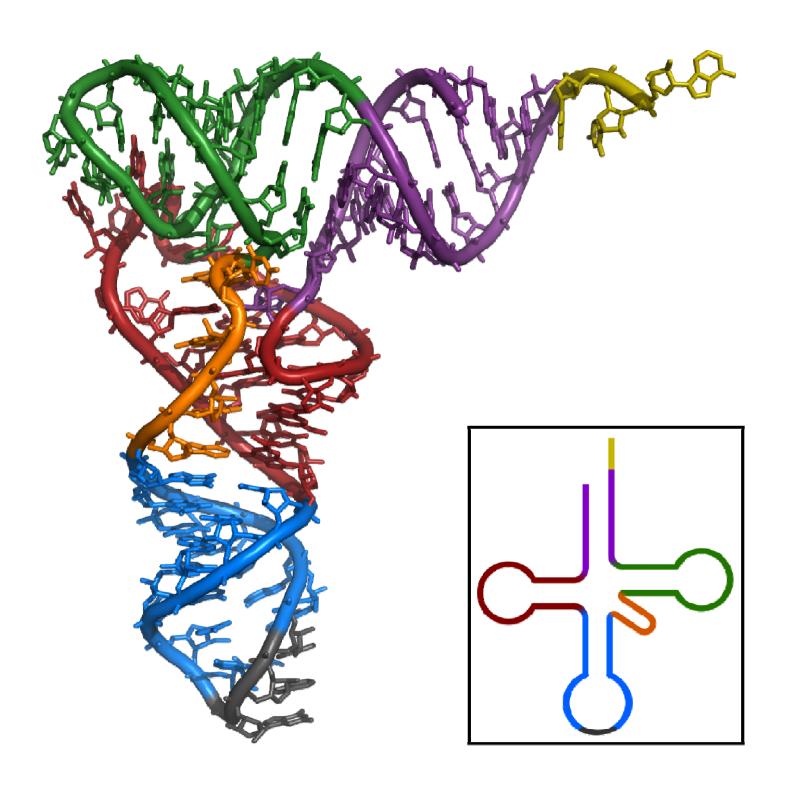
Story

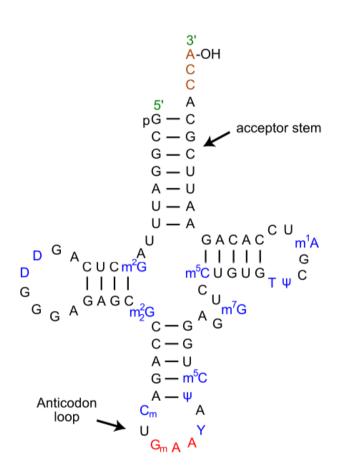


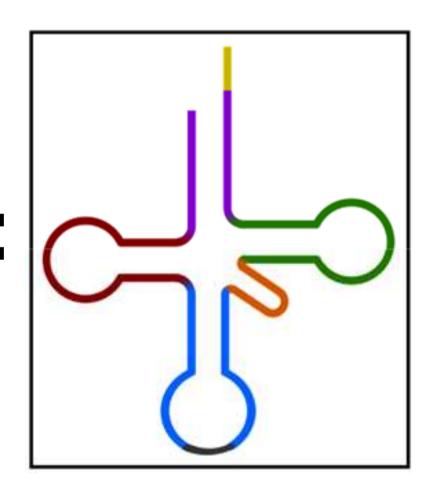


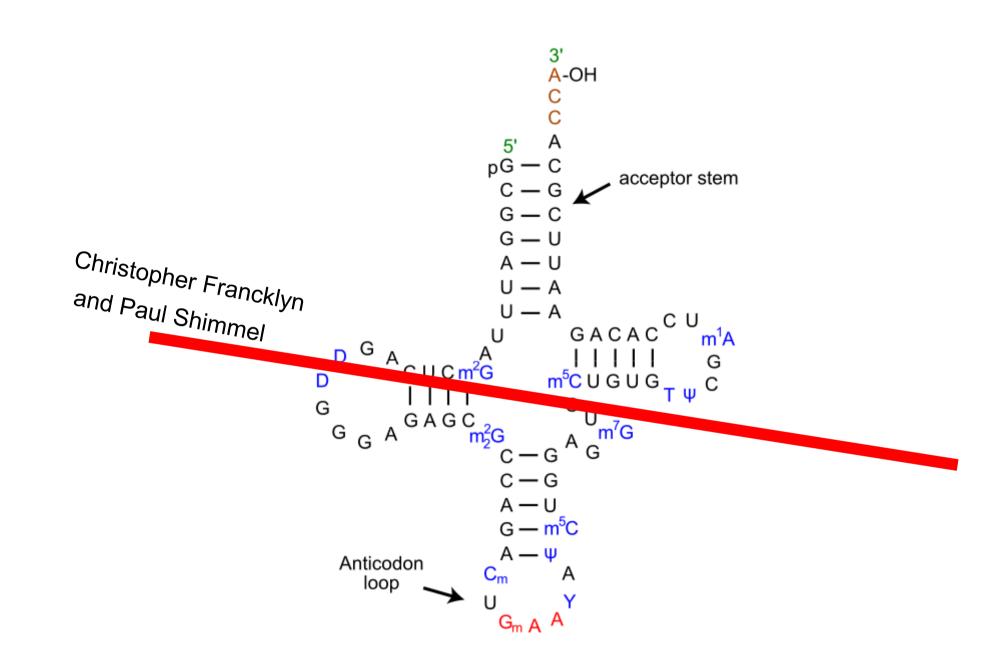


Loading a tRNA molecule

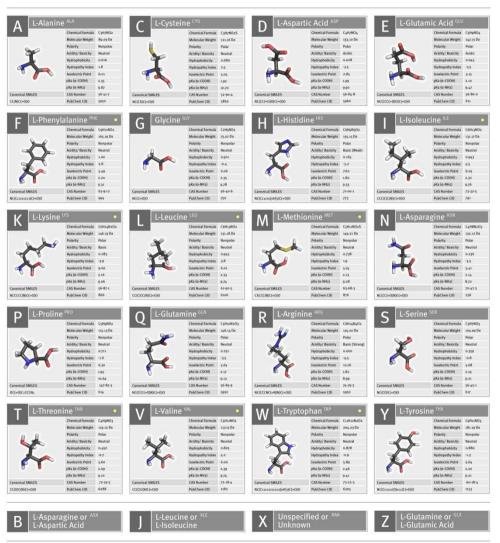








standard Amino Acids

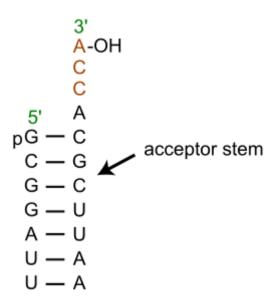


Essential amino acids are denoted with vellow soots. Polarity refers to Side Chain Polarity. Acidity/Basicity refer to Side Chain Acidity/Basicity

20 Structure Generation, 3D agrimmation: Chem Sacto 8.27 (ACD Labol) 3D Structure Bendering: PyMol opprof. (Decision Scientific) (Overlain Formula and Molecular Weight Calculations: Chem Sector 8.27 (ACD Labol) (Appropriately values, Most 1861, (1923) 33, 35 93, 25 2, 26 200 Cold Sector 8.27 (ACD Labol) (Page 1861) (Act 1861)

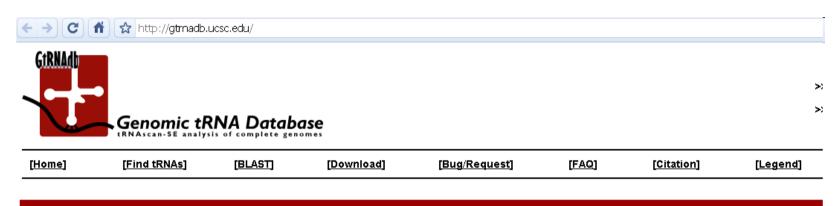
2007x259 Berk Zafer | MML.unc.edu | Questions, problems, and errors should be sent to berkzafergbunc.edu. The most recent version of this document can be found at www.unc.edu/~bzider/aminoacids.

Maintail



Data

Data source



Introduction

This genomic tRNA database contains tRNA gene predictions made by the program tRNAscan-SE (Lowe & Eddy, Nucl Acids Res 25: 955-964, 1997) on complete or nearly corotherwise noted, all annotation is automated, and has not been inspected for agreement with published literature.

Inevitably with automated sequence analysis, we find exceptions to general identification rules, isoacceptor type predictions (esp. due to variable post-transcriptional anticodon modi tRNA identifications (due to pseudogenes, SINES, or other tRNA-derived elements). We attempt to document all cases we come across, and welcome feedback (lowe @soe.ucsc unrecognized discrepancies. For a more detailed description of information in tables and the tRNA search algorithm, see the [Legend].

Genomes								
[Eukarya]				[Archaea]				[Bacteria]
Eukarya								
	[<u>Echinozoa]</u> [<u>Tracheophyta]</u>	[Embryophyta] [Vertebrata]	[Fungi]	[<u>Haemosporida</u>]	[insecta]	[Leishmania]	[Rhabditida]	
Echinozoa (1 genome)								
Strongylocentrotus purpuratus (Sea urchitRNAs)	<u>in) (Version 2.1)</u> (106	5						
Embryophyta (3 genomes)								

>Aeropyrum pernix chr.trna3-AlaCGC (1-77) Ala (CGC) 77 bp Sc: 93.45 GGGCCGGTAGCTCAGCCTGGAAGAGCGCCGCCCTCGCACGGCGGAGGCCCCGGGTTCAAA TCCCGGCCGGTCCACCA

>Aeropyrum pernix chr.trna39-AlaGGC (1-77) Ala (GGC) 77 bp Sc: 88.60 GGGCCGGTAGCTCAGCCTGGAAGAGCGCCCGGTTGGCATCCGGGAGGCCCCGGGTTCAAA

TCCCGGCCGGTCCACCA

>Aeropyrum pernix chr.trna27-AlaTGC (1-77) Ala (TGC) 77 br Sc: 93.25 GGGCCGGTAGCTCAGGCTGGAAGAGCGCCCGGCTTGCACCCGGG<mark>AGGCCCCGGGTT</mark>CAAA TCCCGGCCGGTCCACCA

>Aeropyrum pernix chr trna18-ArgCCG (1-77) Arg (CCG) 77 bp Sc: 20.48 ATAAATGCAACACAGGTATTTATAGAGCGGGTCTCCGGAGCCGGAGGTCCCGGGTTCAAA TCCCGGCGGGCCCGCCA

>Aeropyrum pernix chr.trna2-ArgCCG (1-72) Arg (CCG) 72 bp Sc: 24.36 TGCAACGTGAGTATTTATAGCGTCGTTCTCCCGAGCCGGAGGTCCCGGGTTCAAATCCCG GCGGGCCCGCCA

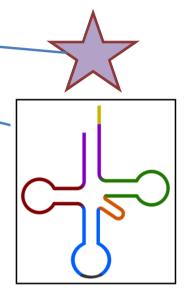
>Aeropyrum pernix chr.trna1-ArgCCG (78) Arg (CCG) 78 bp Sc: 92.70 GGGCCCGTAGCTCAGCCAGGATAGAGCGCCGGCCTCCGGAGCCGGAGGTCCCGGGTTCAA

ATCCCGGCGGGCCCGCCA

>Aeropyrum pernix chr.trna26-ArgCCT (1-78) Arg (CCT) 78 bp Sc: 91.62 GGGCCCGTAGCTCAGCCAGGATAGAGCGCCGGCCTCCTAAGCCGGTGCTCGGGGGTTCAA

ATCCCCCCGGGCCCGCCA

>Aeropyrum pernix chr.trna9-ArgGCG (1-79) Arg (GCG) 79 bp Sc: 92.86 GGGCCCGTAGCTCAGCCAGGACCAGAGCGCCGGCCTGCGGAGCCGGAGGTCCCGGCTTCA



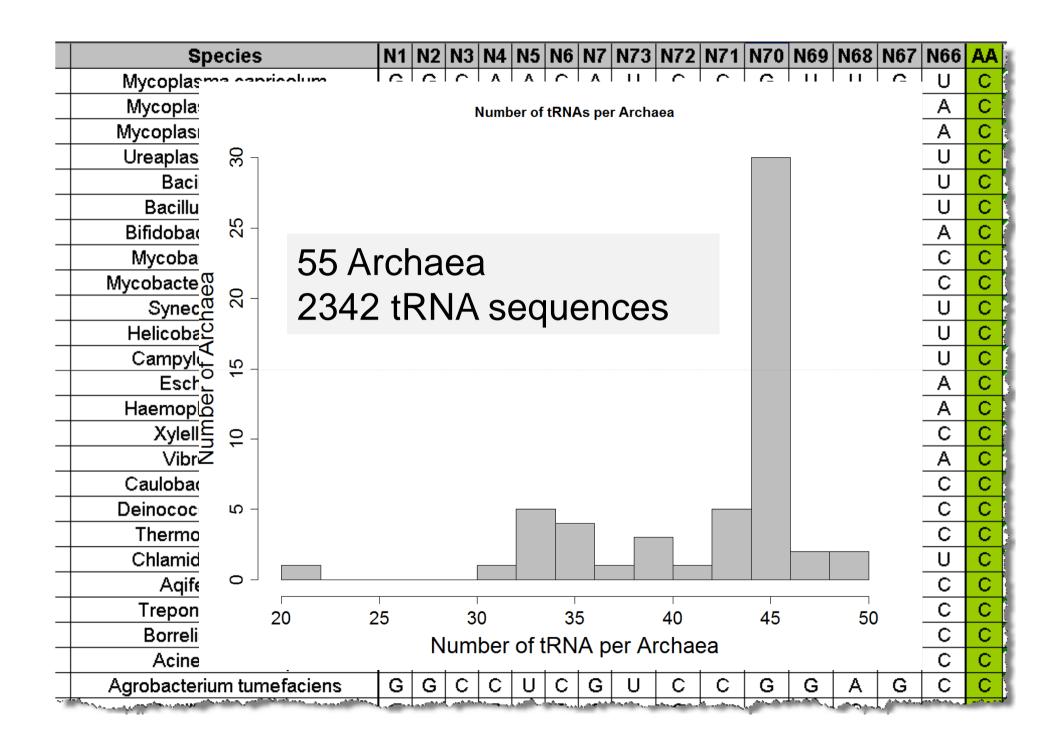
Species
Mycoplasma capricolum
Mycoplasma genitalium
Mycoplasma pneumoniae
Ureaplasma urealyticum
Bacillus subtilis
Bacillus halodurans
Bifidobacterium longum
Mycobacterium leprae
Mycobacterium tuberculosis
Synechocystis sp.
Helicobacter pylori J99
Campylcobacter jejuni
Escherichia coli

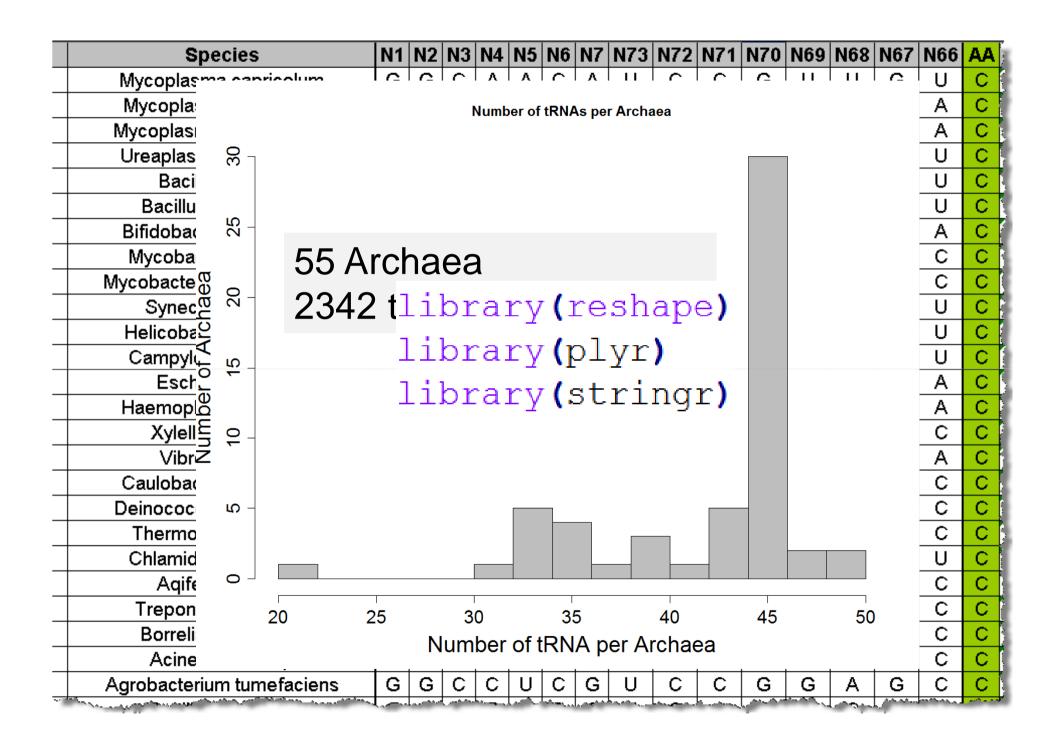
library(Biostrings)

readFASTA("http://gtrnadb....")

Species	N1	N2	N3	N4	N5	N6	N7	N73	N72	N71	N70	N69	N68	N67	N66	AA
Mycoplasma capricolum	G	G	С	Α	Α	С	Α	U	C	C	G	U	U	G	U	С
Mycoplasma genitalium	G	G	U	G	С	С	U	U	С	С	Α	С	G	G	Α	С
Mycoplasma pneumoniae	G	O	U	G	O	C	С	U	O	O	Α	O	G	G	Α	O
Ureaplasma urealyticum	G	O	U	G	O	O	Α	U	O	O	Α	O	G	G	С	С
Bacillus subtilis	G	G	С	G	G	C	Α	U	C	C	G	C	U	G	U	С
Bacillus halodurans	G	G	С	G	G	C	Α	U	O	O	G	O	С	G	С	С
Bifidobacterium longum	G	O	U	G	G	G	U	U	O	С	Α	С	C	С	Α	O
Mycobacterium leprae	G	G	U	G	G	Α	G	U	O	O	Α	C	С	U	C	С
Mycobacterium tuberculosis	G	G	U	G	G	Α	G	U	O	O	Α	C	С	U	O	С
Synechocystis sp.	G	O	С	G	G	C	Α	U	O	O	G	O	C	G	С	C
Helicobacter pylori J99	G	G	С	G	Α	С	Α	U	C	C	G	C	U	G	U	С
Campylcobacter jejuni	G	G	С	G	Α	С	Α	U	C	C	G	C	U	G	С	С
Escherichia coli	G	O	С	G	O	G	С	U	O	O	O	O	G	С	Α	C
Haemophilus influenzae	G	G	С	G	כ	G	U	U	O	O	G	O	Α	С	Α	С
Xylella fastidiosa	G	G	С	С	J	G	G	U	C	C	G	G	Α	С	С	С
Vibro cholerae	G	O	С	G	O	G	С	U	O	O	O	O	G	С	Α	C
Caulobacter crescentus	G	G	С	С	O	G	G	U	O	O	G	G	G	С	O	С
Deinococcus radiodurans	G	G	С	G	O	U	G	U	O	C	G	C	G	Α	С	С
Thermotoga maritima	G	O	С	G	G	C	G	U	O	C	G	O	C	G	O	C
Chlamidia trachomatis	G	O	U	G	G	C	Α	U	O	O	Α	O	С	G	С	C
Aqifex aeolicus	G	G	С	G	Α	C	G	U	C	C	G	C	U	G	С	С
Treponema pallidum	G	O	С	G	O	C	G	U	O	O	G	O	G	G	O	С
Borrelia burgdorferi	G	G	С	G	С	U	G	U	С	С	G	С	G	Α	С	С
Acinetobacter sp	G	G	С	G	ø	G	G	J	O	O	G	O	С	U	С	С
Agrobacterium tumefaciens	G	G	С	С	J	С	G	U	C	C	G	G	Α	G	C	С

Species	N1	N2	N3	N4	N5	N6	N7	N73	N72	N71	N70	N69	N68	N67	N66	A/
Mycoplasma capricolum	G	G	C	Α	Α	O	Α	U	С	С	G	U	U	G	C	С
Mycoplasma genitalium	G	G	J	G	С	O	כ	U	С	С	Α	С	G	G	Α	С
Mycoplasma pneumoniae	G	G	כ	G	C	O	כ	U	С	С	Α	C	G	G	Α	С
Ureaplasma urealyticum	G	G	כ	G	С	O	A	U	С	С	Α	C	G	G	U	С
Bacillus subtilis	G	G	O	G	G	O	Α	U	С	С	G	С	U	G	C	С
Bacillus halodurans	G	G	С	G	G	O	Α	U	С	С	G	С	С	G	С	С
Bifidobacterium longum	G	G	U	G	G	G	U	U	С	С	A]	С	С	С	Α	С
Mycobacterium leprae	G	G	U	G	G	Α	G	U	С	С	A.	С	С	U	C	С
Mycobacterium tuberculosis	G	G	U	G	G	Α	G	U	С	С	Α	С	С	U	С	С
Synechocystis sp.	G	G	С	G	G	O	Α	U	С	С	G	С	С	G	U	C
Helicobacter pylori J99	G	G	С	G	Α	O	Α	U	С	С	G	С	U	G	U	C
Campylcobacter jejuni	G	G	С	G	Α	O	Α	U	С	С	G	С	U	G	U	(
Escherichia coli	G	G	С	G	С	G	U	U	С	С	G	С	G	С	Α	C
Haemophilus influenzae	G	G	С	G	U	G	U	U	С	С	G	С	Α	С	Α	(
Xylella fastidiosa	G	G	С	С	U	G	G	U	С	С	G	G	Α	С	С	(
Vibro cholerae	G	G	С	G	С	G	U	U	С	С	G	С	G	С	Α	(
Caulobacter crescentus	G	G	С	С	С	G	G	U	С	С	G	G	G	С	С	(
Deinococcus radiodurans	G	G	С	G	С	C	G	U	С	С	G	С	G	Α	С	(
Thermotoga maritima	G	G	С	G	G	O	G	U	С	С	G	С	С	G	С	(
Chlamidia trachomatis	G	G	U	G	G	O	Α	U	С	С	Α	С	С	G	U	(
Aqifex aeolicus	G	G	С	G	Α	O	G	U	С	С	G	С	U	G	С	(
Treponema pallidum	G	G	С	G	С	O	G	U	С	С	G	С	G	G	С	(
Borrelia burgdorferi	G	G	С	G	С	C	G	U	С	С	G	С	G	Α	С	(
Acinetobacter sp	G	G	С	G	G	G	G	U	С	С	G	С	С	U	С	(
Agrobacterium tumefaciens	G	G	С	С	U	С	G	U	С	С	G	G	Α	G	С	



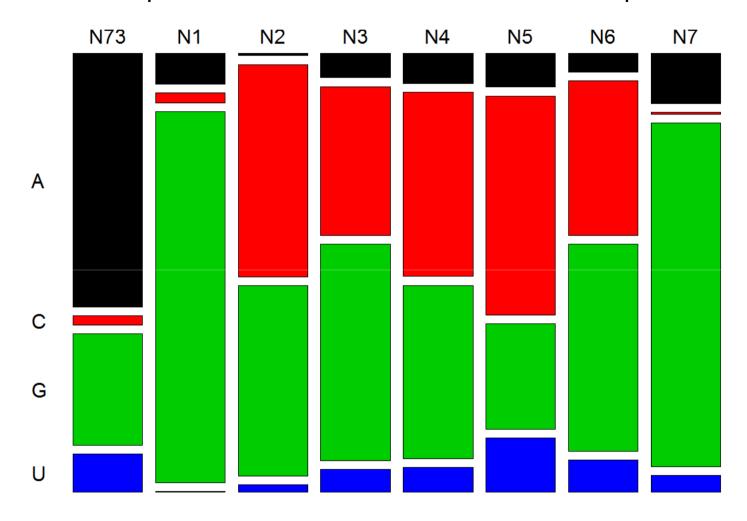


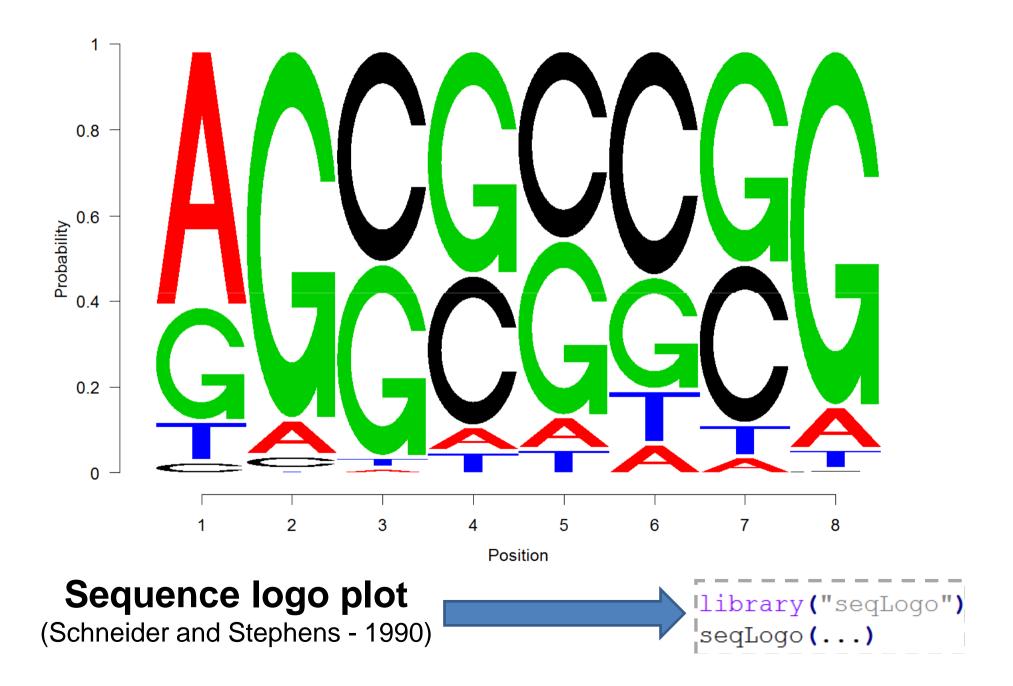
Visualize

N1 N2 N3 N4 N5 N6 N7 N73 I **Species** G Mycoplasma capricolum С Α U G Mycoplasma genitalium G С U U Mycoplasma pneumoniae G G G С U U Ureaplasma urealyticum G G U U Α G Bacillus subtilis G G G Α U Bacillus halodurans G G G G U G G G U U Bifidobacterium longum G G G G Α G U Mycobacterium leprae G U Mycobacterium tuberculosis G G G G G G Α U Synechocystis sp. Helicobacter pylori J99 G G G U U Campylcobacter jejuni G G Escherichia coli

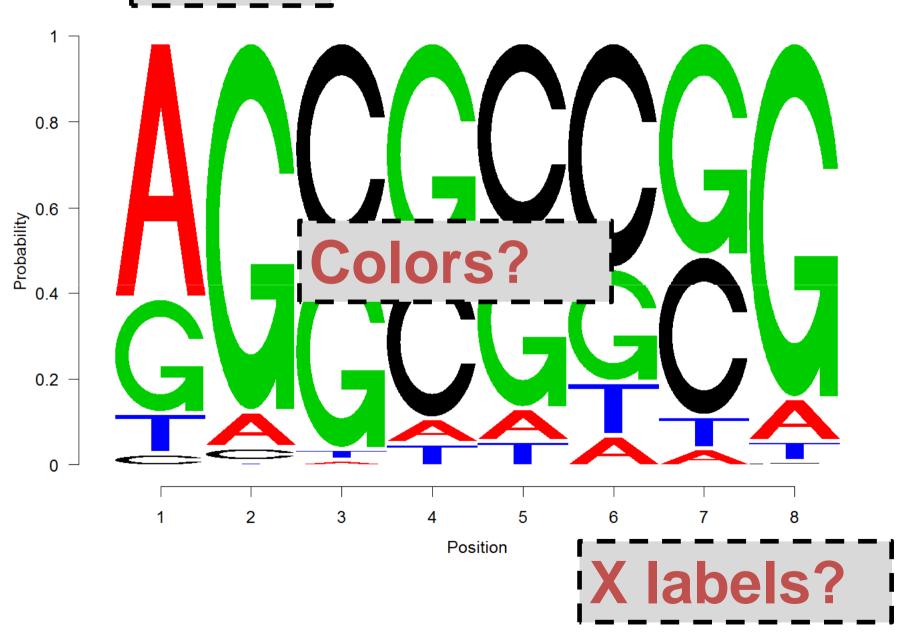
2342 — Data rows

Mosaic plot: nucleotide distribution in tRNA acceptor stem





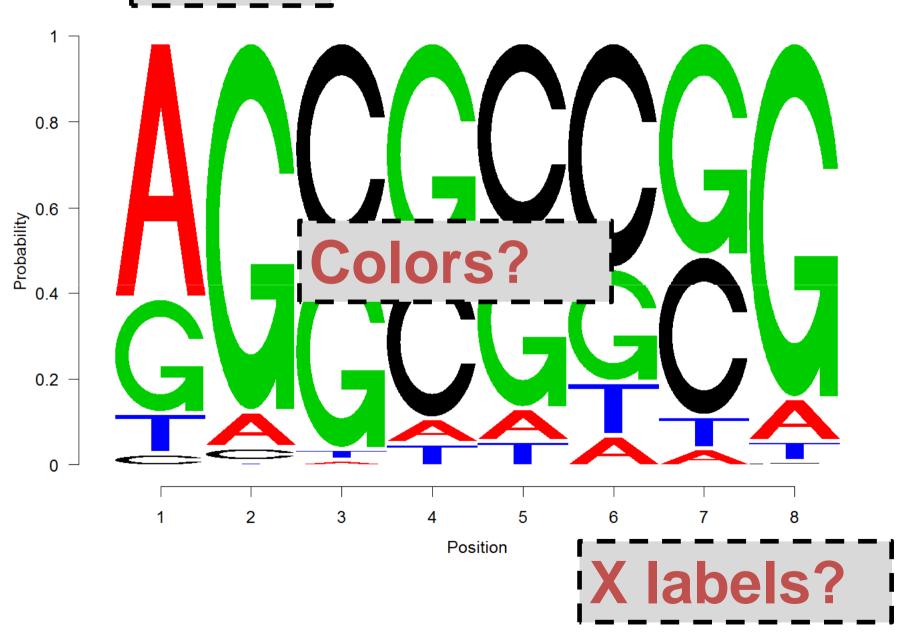
Title ?



```
|library(debug) |
|mtrace(seqLogo)|
|seqLogo(pwm) |
|mtrace.off()
```

```
R Console
                                                  _ 0 %
                                                                                                           - - X
                                                                74 seqLogo(1)
File Edit Misc Packages Windows Help
                                                                            if( class(pwm) == "pwm") {
                                                                     2:
                                                                                pwm <- pwm@pwm }
D(1)>
                                                                     3:
                                                                            else if ( class (pwm) == "data.frame") {
[1] TRUE
                                                                                pwm <- as.matrix(pwm) }</pre>
                                                                            else if ( class (pwm) != "matrix") {
D(1)>
                                                                     6:
                                                                                stop ("pwm must be of class matrix or
                                                                     7:
                                                                            if (any(abs(1 - apply(pwm, 2, sum)) > 0)
A 0.61739130 0.077391304 0.006956522 0.05043478 0.069565s
                                                                     8:
                                                                                stop ("Columns of PWM must add up to
C 0.02260870 0.024347826 0.509565217 0.36521739 0.452173$
                                                                     9:
                                                                            chars <- c("A", "C", "G", "T")
G 0.27217391 0.895652174 0.467826087 0.53739130 0.425217$
                                                                    10:
                                                                            letters <- list(x = NULL, y = NULL, id =
T 0.08782609 0.002608696 0.015652174 0.04695652 0.053043$
                                                                    11:
                                                                            npos <- ncol(pwm)
                                                                    12:
                                                                            if( ic.scale) {
A 0.093913043
                                                                    13:
                                                                                vlim <- 2
                                                                    14:
                                                                                ylab <- "Information content"
C 0.003478261
                                                                    15:
                                                                                facs <- pwm2ic(pwm) }
G 0.863478261
T 0.039130435
                                                                            else
                                                                    16:
                                                                                vlim <- 1
                                                                    17:
                                                                                vlab <- "Probability"</pre>
D(1)>
                                                                    18:
                                                                                facs <- rep(1, npos) }
 [1] FALSE
                                                                    19:
                                                                            wt <- 1
                                                                    20:
                                                                            x.pos <- 0
D(1)>
                                                                    21:
                                                                            for( j in 1:npos ) {
 [1] "A" "C" "G" "T"
                                                                                column <- pwm[, j]
                                                                    23:
                                                                                hts <- 0.95 * column * facs[j]
D(1)>
                                                                    24:
                                                                                letterOrder <- order(hts)
 $x
                                                                    25:
                                                                                y.pos <- 0
NULL
                                                                                for( i in 1:4 ) {
                                                                    26:
                                                                    27:
                                                                                    letter <- chars[letterOrder[i]]</pre>
 $y
                                                                    28:
                                                                                    ht <- hts[letterOrder[i]]
```

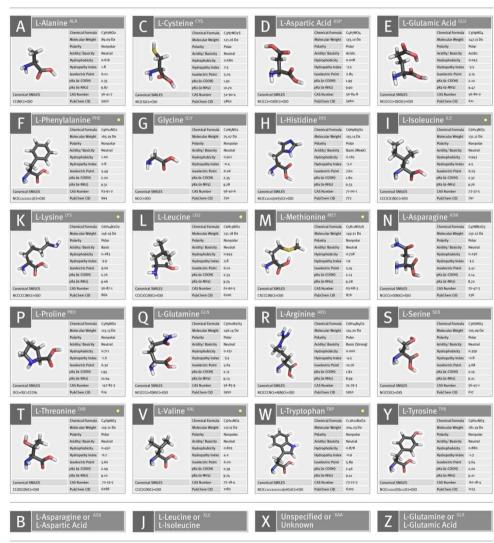
Title ?



Logo plot: Codon distribution in tRNA acceptor stem 8.0 Probability 9.0 0.4 0.2 -0 _ N4 N1 N2 N3 N5 N73 N6 N7

Position

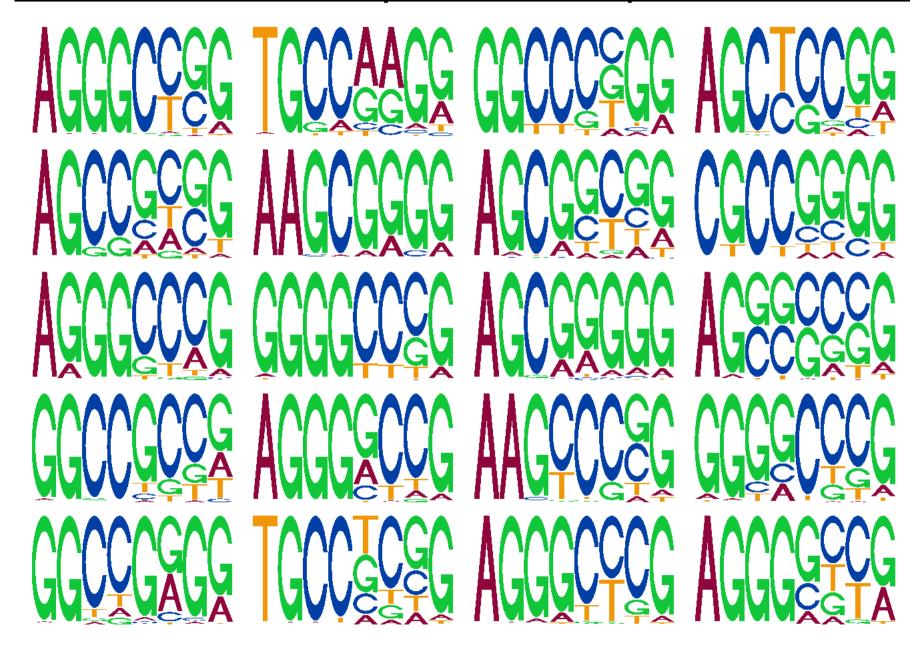
standard Amino Acids



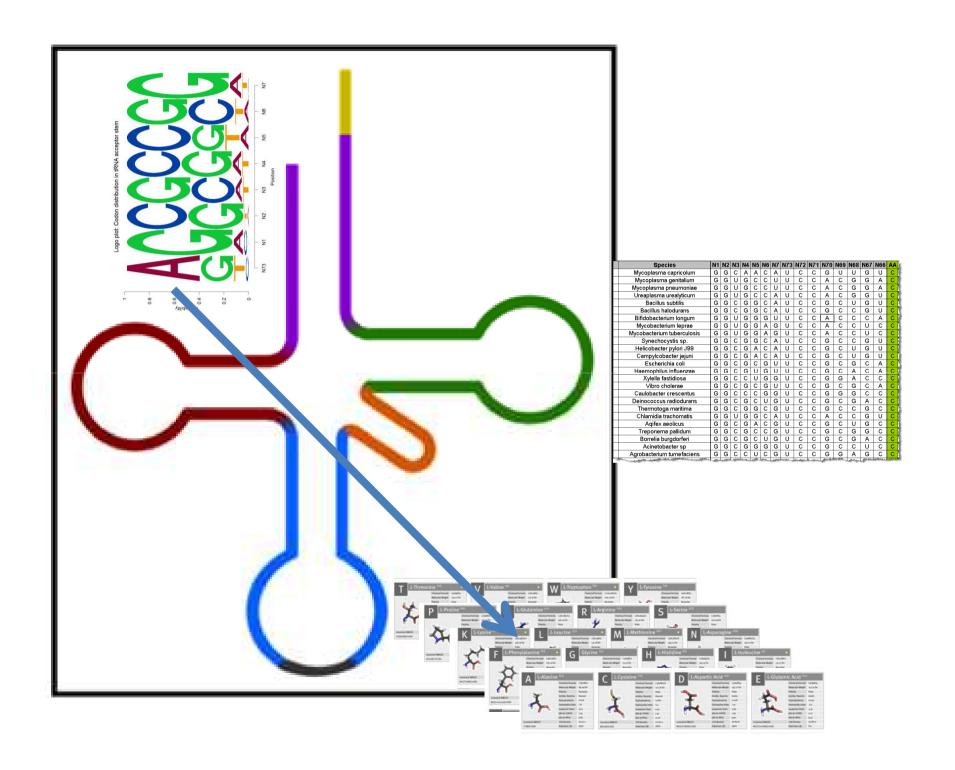
Essential amino acids are denoted with vellow soots. Polarity refers to Side Chain Polarity. Acidity/Basicity refer to Side Chain Acidity/Basicity

2007;239 Berk Zafer | MMLunc.edu | Questions, problems, and errors should be sent to berkzafergbunc.edu. The most recent version of this document can be found at waw unc.edu (-) builder (aminoacids.

Codon distribution, per location, per Amino Acid

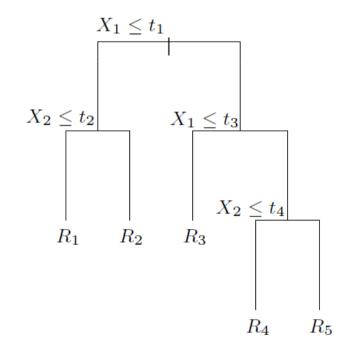


Analyze

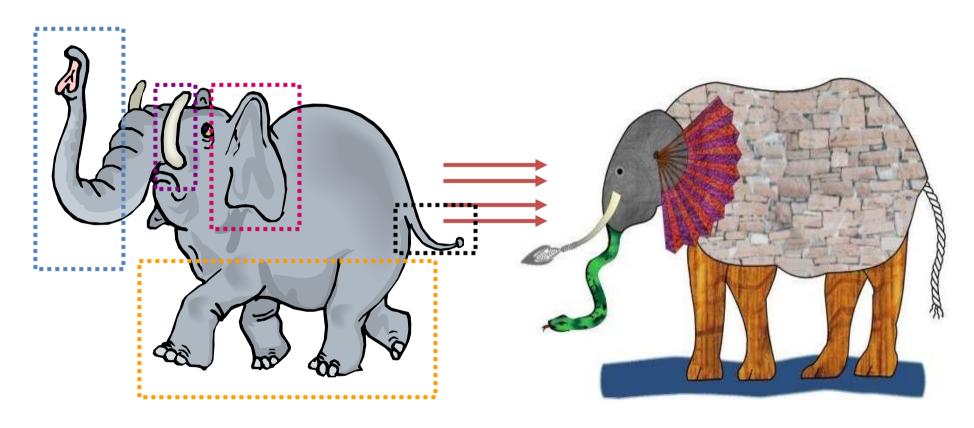


CART (Classification and regression trees)

- Goal predict target variable
- •<u>Method</u>: recursively partition explanatory variables

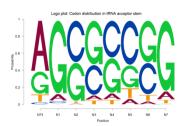


CART (Classification and regression trees)



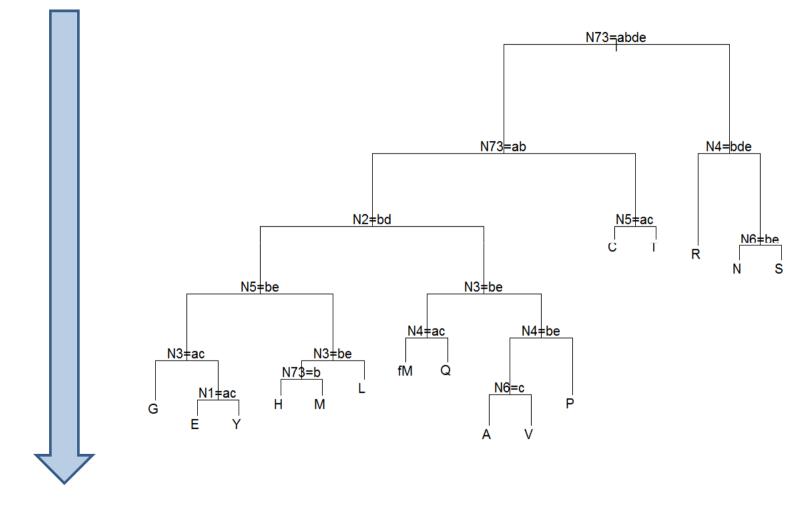
It was six men of Indostan; To learning much inclined, Who went to the Elephant; (Though all of them were blind), That each by observation; Might satisfy his mind etc

-- "The Blind Men and the Elephant" by John Godfrey Saxe (1816-1887)



CART

with default values

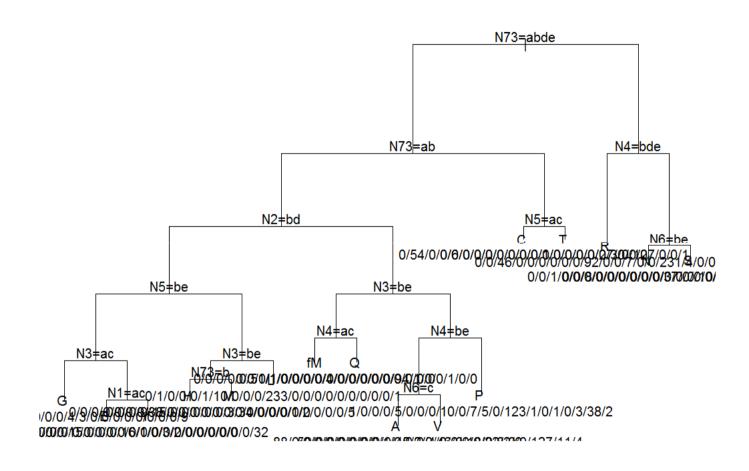




Library(rpart)

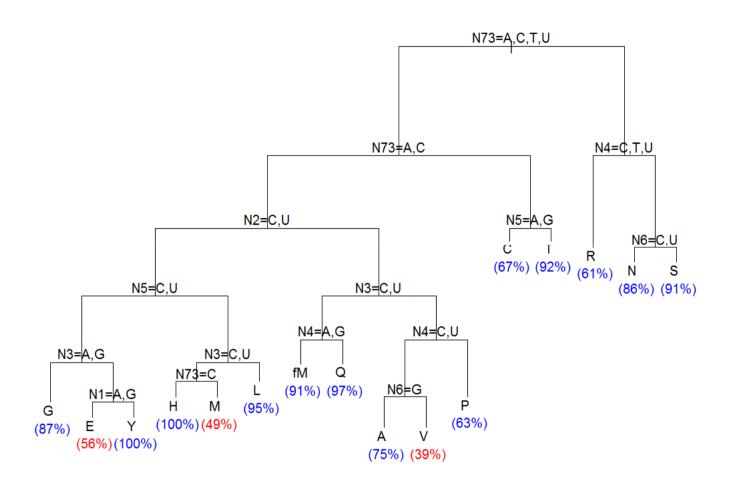
CART

Predictive success ? (use.n = T)

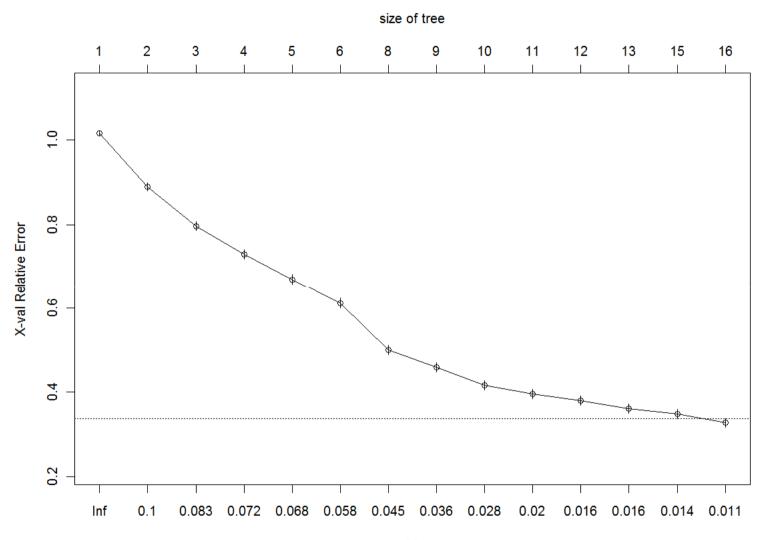


CART

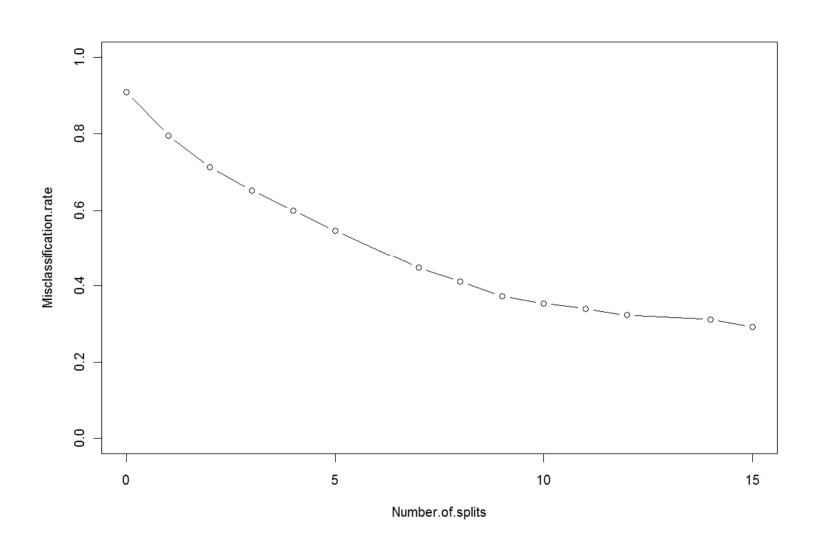
Percent of success in prediction



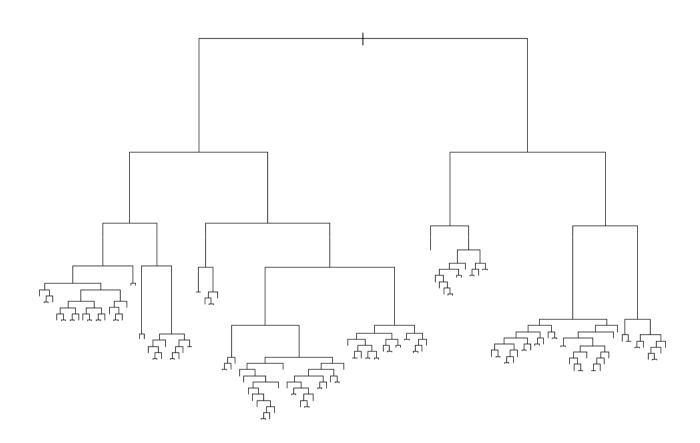
Cross validation – Relative error



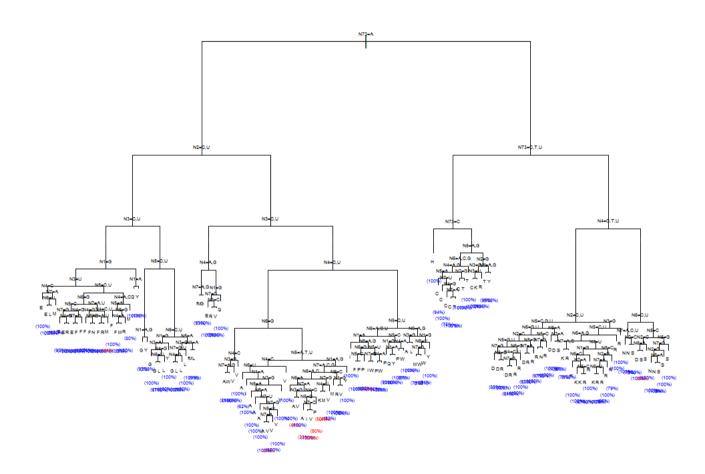
Cross validation – Misclassification rate



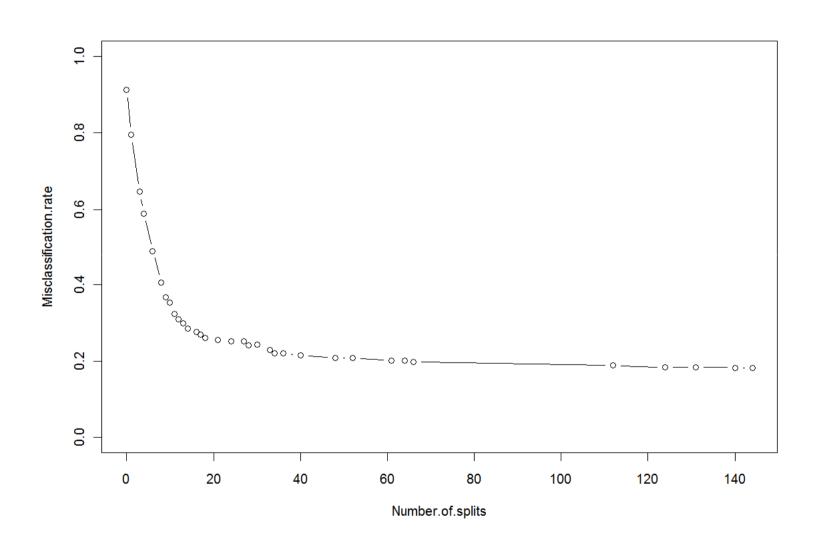
Bigger tree?



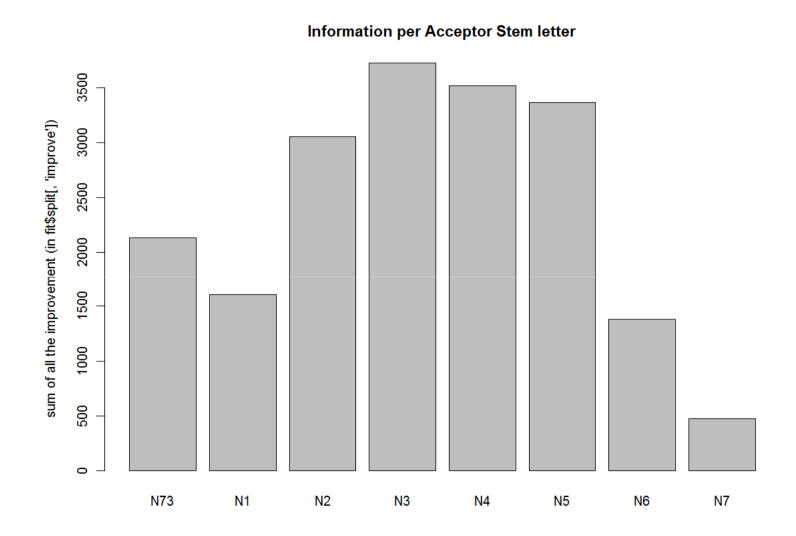
Bigger tree?



Cross validation – Misclassification rate

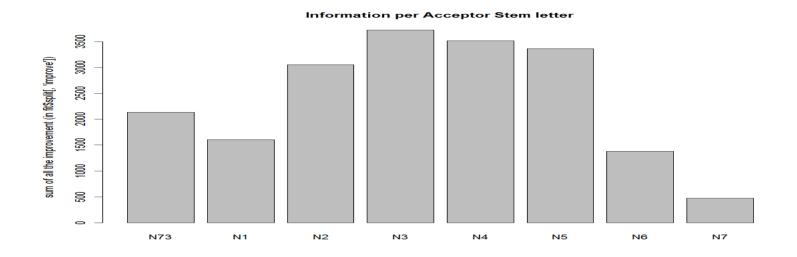


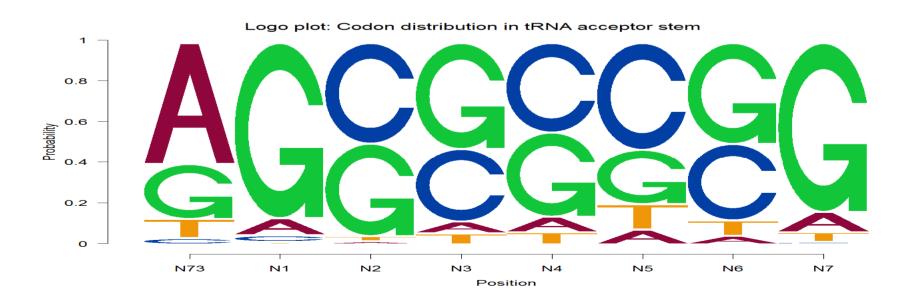
Relative importance for each letter in the model



(Sum of information gain in the use of each letter in the model)

Relative importance for each letter in the model



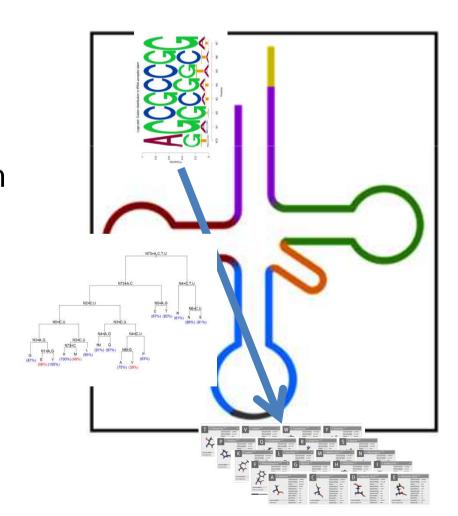


Results

- •20% misclassification in prediction
- •Same acceptor stem RNA can code for for different Amino Acids
 - •In different Archaeas
 - •In the same Archaea

Conclusions

- •There is code in the acceptor stem
- •It is not enough





Tal Galili₁₁, Shaul Shaul₂₁, Yoav Benjamini₁₃₁, Dror Berel₄₁

- [1] Department of Statistics and Operations Research, Tel Aviv University, Israel.
- [2] Department of Zoology, Tel Aviv University, Israel.
- [3] Department of Statistics and Operations Research, Tel Aviv University, Israel.
- [4] Cedars-Sinai Medical Center.