-

# 16s

,

August 9, 2018

## 1

, — ,
. , , ,
. , , , ,
16s [?]. .
( , Infernal [?]), [?, ?, ?, ?, ?].
.
: , - , . -
. , , ,
- . ,
. ,
, .
, — 16s rRNA.
16s , - .

## 2

YARD [?], ECFG [?] .
.
?? , .
( , - ), ,
*stem_e*1<*s*>, .

## 3

- , .
, , , ,

| | |
|---|---|
| *any* | $A, U, C, G$. |
| $any^*[n..m]$ | $n$ $m$. |
| $stemN<s>$ | $N$ $s$ ( ). |
| $mk\_stem<s>$ | ( 0 $N$) $s$. |
| $stem\_e1<s>$ | , , , . |

Table 1:

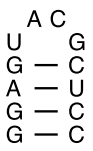
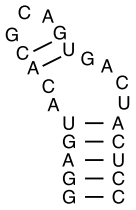
| | |
|---|---|
| $stem4<any^*[3..5]>$ | $mk\_stem<any^*[1..2]$ $stem2<any^*[3..4]>$ $any^*[2..5]>$ |
|  |  |

Table 2:

.

, , **??**.

16s Escherichia coli. - : $A, U, C, G$.

, . `inline`

, ,

.

: 16s 16s

. :

. — .

.

SILVA [**?**], 20 .

**??**, ’+’ — , ’-’ —

. , 98.16% , 16s ,

5’M — 63.13%. , , 5’M .

100 NCBI.

, . 5’M **??**.

NCBI, , 16s (Expected

Covered ), (FP-intervals), ,

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | + | - | + | - | + | - |
| | h19 | 17878 | 335 | 2153 | 3165 | 306 | 13 |
| 5'M | h3 | 11498 | 6715 | 64 | 5254 | 81 | 238 |

Table 3:

. . , 100
:

- 299, 221,54;
- 0,98 0,11.

, **??** 5'M .
. , , .

| NCBI ID | Name | Expected | Covered | FP-intervals | Length(avg.) | Length SD |
|---|---|---|---|---|---|---|
| NZ_CP012959.1 | Aggregatibacter actinomycetemcomitans strain 624 | 6 | 6 | 164 | 614.6 | 246.4 |
| NC_014640.1 | Achromobacter xylosoxidans A8 | 3 | 3 | 556 | 586.9 | 244.9 |
| NC_005966.1 | Acinetobacter sp. ADP1 complete genome | 7 | 7 | 211 | 552.8 | 134.4 |
| NZ_CP009448.1 | Achromobacter xylosoxidans C54 | 3 | 3 | 598 | 579.1 | 201.6 |
| NC_013171.1 | Anaerococcus prevotii DSM 20548 | 4 | 3 | 245 | 584.6 | 256.0 |
| NZ_CP012590.1 | Actinomyces sp. oral taxon 414 strain F0588 | 3 | 3 | 363 | 591.5 | 196.8 |
| NZ_CP014060.1 | Achromobacter xylosoxidans strain FDAARGOS_147 | 3 | 0 | 741 | 614.1 | 266.0 |
| NZ_CP007502.1 | Aggregatibacter actinomycetemcomitans HK1651 | 6 | 6 | 113 | 569.8 | 173.6 |
| NZ_LT635457.1 | Actinomyces sp. Marseille-P2985 | 3 | 3 | 71 | 570.0 | 153.4 |
| NZ_CP012046.1 | Achromobacter xylosoxidans strain MN001 | 3 | 3 | 560 | 599.9 | 222.9 |
| NZ_LN831029.1 | Achromobacter xylosoxidans genome assembly NCTC10807 | 3 | 3 | 653 | 582.5 | 206.0 |
| NZ_CP015594.1 | Acinetobacter sp. NCu2D-2 | 7 | 7 | 125 | 544.1 | 117.1 |
| NC_012913.1 | Aggregatibacter aphrophilus NJ8700 | 6 | 6 | 157 | 551.2 | 147.7 |
| NZ_CP020468.1 | Actinomyces sp. pika_114 | 3 | 3 | 103 | 664.1 | 596.9 |
| NZ_CP014232.1 | Actinomyces oris strain T14V | 3 | 3 | 200 | 606.1 | 227.7 |
| NZ_CP015110.1 | Acinetobacter sp. TGL-Y2 | 7 | 7 | 234 | 561.9 | 173.1 |
| NZ_CP012608.1 | Acinetobacter sp. TTH0-4 | 7 | 7 | 204 | 575.3 | 169.6 |
| NZ_CP017812.1 | Actinomyces sp. VUL4_3 | 3 | 3 | 125 | 662.4 | 326.1 |
| NZ_CP012067.1 | Aggregatibacter aphrophilus strain W10433 | 6 | 6 | 162 | 551.3 | 119.0 |
| NZ_CP012072.1 | Actinomyces meyeri strain W712 | 3 | 3 | 197 | 631.5 | 313.8 |
| NC_000964.3 | Bacillus subtilis subsp. subtilis str. 168 chromosome | 10 | 10 | 278 | 558.2 | 154.3 |
| NZ_CP016852.1 | Bacillus subtilis subsp. subtilis strain 168G | 10 | 10 | 278 | 558.9 | 154.3 |
| NZ_CP009902.1 | Bacillus anthracis strain 2002013094 | 11 | 10 | 1352 | 656.2 | 269.3 |
| NZ_CP017763.1 | Bacillus subtilis strain 29R7-12 | 10 | 10 | 297 | 538.0 | 110.4 |
| NZ_CP010314.1 | Bacillus subtilis subsp. subtilis strain 3NA | 10 | 10 | 273 | 556.3 | 150.7 |
| NC_012659.1 | Bacillus anthracis str. A0248 | 11 | 11 | 1302 | 660.8 | 285.9 |
| NC_011835.1 | Bifidobacterium animalis subsp. lactis AD011 | 2 | 2 | 190 | 604.0 | 223.0 |
| NZ_CP009748.1 | Bacillus subtilis strain ATCC 13952 | 7 | 7 | 216 | 553.3 | 147.2 |
| NZ_CP009749.1 | Bacillus subtilis strain ATCC 19217 | 7 | 7 | 231 | 542.8 | 147.4 |
| NC_017834.1 | Bifidobacterium animalis subsp. animalis ATCC 25527 | 4 | 4 | 157 | 653.2 | 299.0 |
| NC_022523.1 | Bifidobacterium animalis subsp. lactis ATCC 27673 | 4 | 4 | 176 | 613.7 | 252.4 |
| NC_017866.1 | Bifidobacterium animalis subsp. lactis B420 | 4 | 4 | 192 | 605.1 | 243.0 |
| NZ_CP014227.1 | Capnocytophaga haemolytica strain CCUG 32990 | 4 | 4 | 405 | 681.3 | 312.6 |
| NZ_CP014230.1 | Desulfomicrobium orale DSM 12838 | 2 | 2 | 198 | 566.4 | 162.8 |
| NC_013162.1 | Capnocytophaga ochracea DSM 7271 | 4 | 4 | 161 | 613.1 | 184.1 |
| NZ_CP012475.1 | Bacillus clausii strain ENTPro | 7 | 7 | 350 | 555.3 | 147.7 |
| NZ_CP017037.1 | Dialister pneumosintes strain F0677 | 5 | 5 | 407 | 647.0 | 257.2 |
| NZ_CP012366.1 | Enterococcus durans strain KLDS6.0933 | 6 | 6 | 202 | 532.3 | 101.7 |

| | | | | | | |
|---|---|---|---|---|---|---|
| NZ_CP012384.1 | Enterococcus durans strain KLDS 6.0930 | 6 | 6 | 203 | 532.0 | 101.4 |
| NC_006582.1 | Bacillus clausii KSM-K16 DNA | 7 | 7 | 369 | 559.0 | 176.2 |
| NZ_CP016923.1 | Klebsiella pneumoniae isolate 11 | 8 | 8 | 381 | 543.7 | 150.8 |
| NZ_CP008740.1 | Haemophilus influenzae 2019 | 6 | 6 | 132 | 545.0 | 107.4 |
| NZ_CP016926.1 | Klebsiella pneumoniae isolate 23 | 8 | 8 | 389 | 553.2 | 162.1 |
| NZ_CP011313.1 | Klebsiella pneumoniae subsp. pneumoniae strain 234-12 | 8 | 8 | 392 | 556.3 | 154.4 |
| NC_013721.1 | Gardnerella vaginalis 409-05 | 2 | 2 | 237 | 601.6 | 229.9 |
| NZ_CP007470.1 | Haemophilus influenzae strain 477 | 6 | 6 | 136 | 560.1 | 118.2 |
| NZ_CP007472.1 | Haemophilus influenzae strain 723 | 6 | 6 | 146 | 564.1 | 152.6 |
| NC_007146.2 | Haemophilus influenzae 86-028NP | 6 | 6 | 157 | 548.1 | 104.8 |
| NC_014644.1 | Gardnerella vaginalis ATCC 14019 chromosome | 2 | 2 | 267 | 597.4 | 190.2 |
| NC_003454.1 | Fusobacterium nucleatum subsp. nucleatum ATCC 25586 | 5 | 5 | 766 | 654.9 | 281.7 |
| NC_010376.1 | Finegoldia magna ATCC 29328 DNA | 4 | 4 | 339 | 645.8 | 335.1 |
| NC_018610.1 | Lactobacillus buchneri CD034 | 5 | 5 | 107 | 533.4 | 173.3 |
| NC_000908.2 | Mycoplasma genitalium G37 | 1 | 1 | 30 | 533.8 | 98.9 |
| NZ_CP019058.1 | Gardnerella vaginalis strain GV37 | 2 | 2 | 282 | 588.6 | 184.2 |
| NZ_CP012716.1 | Fusobacterium nucleatum subsp. nucleatum ChDC F3162 | 4 | 4 | 819 | 655.7 | 301.7 |
| NC_018498.1 | Mycoplasma genitalium M2288 | 1 | 1 | 32 | 519.3 | 92.5 |
| NC_018496.1 | Mycoplasma genitalium M6282 | 1 | 1 | 30 | 530.3 | 95.6 |
| NC_015428.1 | Lactobacillus buchneri NRRL B-30929 | 5 | 5 | 97 | 524.6 | 122.8 |
| NZ_CP019323.1 | Lactobacillus sp. WiKim39 | 4 | 4 | 443 | 605.1 | 206.9 |
| NZ_CP009531.1 | Lactobacillus sp. wkB8 | 4 | 4 | 108 | 555.3 | 162.9 |
| NC_014752.1 | Neisseria lactamica 020-06 complete genome | 4 | 4 | 176 | 643.8 | 294.6 |
| NZ_CP013696.1 | Pseudomonas aeruginosa strain 12-4-4(59) | 4 | 4 | 374 | 555.6 | 160.0 |
| NC_017534.1 | Propionibacterium acnes 266 | 3 | 3 | 197 | 605.1 | 270.4 |
| NZ_CP012889.1 | Porphyromonas gingivalis 381 | 4 | 4 | 105 | 520.1 | 78.0 |
| NC_017535.1 | Propionibacterium acnes 6609 | 3 | 3 | 195 | 609.4 | 279.5 |
| NZ_AP014839.1 | Pseudomonas aeruginosa DNA | 4 | 4 | 377 | 570.3 | 181.0 |
| NZ_CP011995.1 | Porphyromonas gingivalis strain A7436 | 4 | 4 | 98 | 540.6 | 151.9 |
| NZ_CP013680.1 | Pseudomonas aeruginosa AES-1R | 1 | 1 | 369 | 556.4 | 137.9 |
| NZ_CP015347.1 | Proteus mirabilis strain AOUC-001 | 7 | 7 | 261 | 550.1 | 176.0 |
| NZ_CP020052.1 | Proteus mirabilis strain AR_0059 | 7 | 7 | 259 | 557.6 | 152.2 |
| NZ_CP021694.1 | Proteus mirabilis strain AR_0155 | 7 | 7 | 281 | 565.3 | 171.6 |
| NC_017550.1 | Propionibacterium acnes ATCC 11828 | 2 | 2 | 183 | 583.6 | 210.5 |
| NZ_CP017149.1 | Pseudomonas aeruginosa strain ATCC 15692 | 4 | 4 | 377 | 556.7 | 159.6 |
| NZ_CP007726.1 | Neisseria elongata subsp. glycolytica ATCC 29315 | 4 | 4 | 179 | 655.0 | 324.3 |
| NC_010729.1 | Porphyromonas gingivalis ATCC 33277 DNA | 4 | 4 | 103 | 525.3 | 104.1 |
| NC_018707.1 | Propionibacterium acnes C1 | 3 | 3 | 206 | 598.5 | 265.6 |
| NZ_CP012830.1 | Pseudomonas fluorescens strain FW300-N2E3 | 6 | 6 | 433 | 564.4 | 158.7 |
| NZ_CP011117.1 | Pseudomonas fluorescens strain LBUM223 | 6 | 6 | 437 | 591.4 | 217.4 |
| NZ_CP012073.1 | Ottowia sp. oral taxon 894 strain W10237 | 3 | 3 | 269 | 636.5 | 258.7 |

| | | | | | | |
|---|---|---|---|---|---|---|
| NZ_CP019894.1 | Neisseria lactamica strain Y92-1009 | 4 | 4 | 177 | 603.6 | 195.8 |
| NZ_CP007241.1 | Streptococcus pyogenes strain 1E1 | 6 | 6 | 126 | 582.6 | 180.2 |
| NZ_CP016756.1 | Stenotrophomonas nitritireducens strain 2001 | 4 | 4 | 595 | 616.9 | 252.8 |
| NC_014498.1 | Streptococcus pneumoniae 670-6B | 4 | 4 | 257 | 591.7 | 199.0 |
| NC_012468.1 | Streptococcus pneumoniae 70585 | 4 | 4 | 246 | 598.4 | 201.2 |
| NC_002967.9 | Treponema denticola ATCC 35405 chromosome | 2 | 2 | 132 | 587.1 | 220.8 |
| NC_022246.1 | Streptococcus intermedius B196 | 4 | 4 | 304 | 586.0 | 198.7 |
| NC_022236.1 | Streptococcus constellatus subsp. pharyngis C232 | 4 | 4 | 267 | 588.4 | 213.5 |
| NZ_CP021181.1 | Sphingomonas sp. DC-6 | 2 | 2 | 478 | 558.8 | 153.8 |
| NC_013521.1 | Sanguibacter keddieii DSM 10542 | 4 | 4 | 302 | 583.3 | 208.9 |
| NC_013520.1 | Veillonella parvula DSM 2008 | 4 | 4 | 366 | 602.6 | 224.1 |
| NC_018089.1 | Streptococcus mutans GS-5 | 5 | 5 | 195 | 555.5 | 150.5 |
| NZ_AP012334.1 | Scardovia inopinata JCM 12537 DNA | 2 | 2 | 107 | 590.4 | 287.9 |
| NZ_CP018221.1 | Sphingomonas sp. JJ-A5 | 2 | 2 | 348 | 562.5 | 178.6 |
| NC_017768.1 | Streptococcus mutans LJ23 DNA | 5 | 5 | 203 | 572.1 | 172.1 |
| NZ_CP019511.1 | Sphingomonas sp. LM7 | 2 | 1 | 379 | 639.3 | 335.8 |
| NC_020561.1 | Sphingomonas sp. MM-1 | 2 | 2 | 475 | 594.1 | 254.4 |
| NZ_CP009227.1 | Treponema sp. OMZ 838 | 2 | 2 | 148 | 618.5 | 413.7 |
| NC_007492.2 | Pseudomonas fluorescens Pf0-1 | 6 | 6 | 484 | 573.8 | 178.3 |
| NC_014034.1 | Rhodobacter capsulatus SB 1003 | 4 | 4 | 722 | 650.8 | 328.0 |
| NZ_CP019721.1 | Veillonella parvula strain UTDB1-3 | 4 | 4 | 354 | 578.5 | 180.0 |

Table 4: (5'M )



| NCBI ID | Name | Expected | Covered | FP-intervals | Length(avg.) | Length SD |
|---|---|---|---|---|---|---|
| NZ_CP012959.1 | Aggregatibacter actinomycetemcomitans strain 624 | 6 | 6 | 35 | 954.4 | 175.2 |
| NC_014640.1 | Achromobacter xylosoxidans A8 | 3 | 0 | 41 | 976.6 | 232.5 |
| NC_005966.1 | Acinetobacter sp. ADP1 complete genome | 7 | 7 | 14 | 974.8 | 207.5 |
| NZ_CP009448.1 | Achromobacter xylosoxidans C54 | 3 | 0 | 43 | 932.7 | 146.0 |
| NC_013171.1 | Anaerococcus prevotii DSM 20548 | 4 | 3 | 29 | 1174.6 | 609.3 |
| NZ_CP012590.1 | Actinomyces sp. oral taxon 414 strain F0588 | 3 | 3 | 28 | 1033.9 | 356.2 |
| NZ_CP014060.1 | Achromobacter xylosoxidans strain FDAARGOS_147 | 3 | 0 | 79 | 1024.9 | 343.2 |
| NZ_CP007502.1 | Aggregatibacter actinomycetemcomitans HK1651 | 6 | 6 | 17 | 884.0 | 64.0 |
| NZ_LT635457.1 | Actinomyces sp. Marseille-P2985 | 3 | 3 | 5 | 1120.8 | 217.2 |
| NZ_CP012046.1 | Achromobacter xylosoxidans strain MN001 | 3 | 0 | 56 | 953.9 | 206.3 |

Table 5: (5'M + )

# 4

,
. .

- , ,
.
-
-
.

# References


[1] Nawrocki E. P., Eddy S. R. Infernal 1.1: 100-fold faster RNA homology searches //Bioinformatics. – 2013. – . 29. – №. 22. – . 2933-2935.

[2] Dowell R. D., Eddy S. R. Evaluation of several lightweight stochastic context-free grammars for RNA secondary structure prediction //BMC bioinformatics. — 2004. — . 5. — №. 1. — . 1.

[3] Eddy S. R. A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure //BMC bioinformatics. — 2002. — . 3. — №. 1. — . 1.

[4] Yogev S., Milo N., Ziv-Ukelson M. StemSearch: RNA search tool based on stem identification and indexing //Bioinformatics and Biomedicine (BIBM), 2013 IEEE International Conference on. — IEEE, 2013. — . 145-152.

[5] Eddy S. R. Homology searches for structural RNAs: from proof of principle to practical use //RNA. — 2015. — . 21. — №. 4. — . 605-607.

[6] Anderson J. W. J. et al. Evolving stochastic context–free grammars for RNA secondary structure prediction //BMC bioinformatics. — 2012. — . 13. — №. 1. — . 78.

[7] Hemerik K. Towards a Taxonomy for ECFG and RRPG Parsing //Language and Automata Theory and Applications. – 2009. – . 410-421.

[8] Quast C. et al. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools //Nucleic acids research. – 2012. – . 41. – №. D1. – . D590-D596.

[9] YARD language description. Online. `http://yaccconstructor.github.io/YaccConstructor/yard.html`

[10] Rehakova K. et al. Variation in secondary structure of the 16S rRNA molecule in cyanobacteria with implications for phylogenetic analysis //Fottea. – 2014. – . 14. – . 161-178.

# A 16S YARD,

```
inline any: A | U | G | C
inline any_1_2: any*[1..2]
inline any_1_3: any*[1..3]
inline any_2_3: any any_1_2
inline any_2_4: any*[2..4]
inline any_3_4: any*[3..4]
inline any_3_5: any any_2_4
inline any_5_7: any any any_3_5
inline any_4_6: any any_3_5
inline any_6_8: any any_5_7
inline any_9_11: any*[9..11]
inline any_4 : any any any any

stem1<s>:
      A s U
    | U s A
    | C s G
    | G s C
    | G s U
    | U s G
    | A s G
    | G s A

stem2<s>: stem1<stem1<s>>
stem4<s>: stem2<stem2<s>>
stem6<s>: stem4<stem2<s>>
stem8<s>: stem4<stem4<s>>

mk_stem<s>:
      A mk_stem<s> U
    | U mk_stem<s> A
    | C mk_stem<s> G
    | G mk_stem<s> C
    | G mk_stem<s> U
    | U mk_stem<s> G
    | G mk_stem<s> A
    | A mk_stem<s> G
    | s

stem<s>: mk_stem<stem4<s>>
```

```
stem_2<s>: mk_stem<stem2<s>>

stem_e1<s> : stem_2<(any stem_2<s> | stem_2<s> any)> | stem<s>
stem_e2<s> : stem_2<(any stem_e1<s> any | any stem_e1<s>
             | stem_e1<s> any)> | stem<s>
stem_4: stem_2<any_4>

[<Start>]
full: middle_part_root

head_part_root: h3
middle_part_root:  h19
tail_part_root: h28 any_3_5 h44 any_3_5 h45

head_middle_folded: stem2<(any_6_8 h3 any_9_11 h19 any_1_2 h27 any_2_4)>
full_size_root: h3 any_9_11 h19 any_1_2 h27 any*[7..9] tail_part_root

(* 5'M domain *)
h3: stem_e2<(any_1_2 h4 any_1_3 h16 any_3_5
    (h17 | any*[1..6]) any*[2..5] h18 any_1_2)>
h4: stem_e1<(h5 h15 any?)>
h5: any_5_7 stem_e2<(any_1_3 h6 any_5_7
    stem_2<(any_5_7 h7 any? h11 any_1_3 h12 any?)>
    any_1_2 h13 any_1_2 h14 any_2_4)> any_3_5

h6: stem_e2<stem_e2<stem_e2<stem_e2<any_3_4>>>>
h7: stem_e2<(any_2_4 stem<(any_1_2 h8 any_4_6 h9 any_3_5 h10 any_1_2)>
             any_1_3)>
h8: stem_2<(any_3_5 stem_4 any_3_5)>
h9: stem_2<any_3_5>
h10: stem_e2<any_3_5>
h11: stem_2<(any_2_4 stem_e2<any_6_8> any_3_5)>
h12: stem<(any? stem_2<any_3_5> any_2_4)>
h13: stem<any_9_11>
h14: stem_2<any_3_5>

h15: stem_e1<(any_2_4 stem2<any_4> any?)>
h16: stem_2<(any_5_7 stem_2<any_2_4> any_4_6)>
h17: stem<(any*[6..9] stem_2<any*[7..11]> any_6_8)>
h18: stem<(any_5_7 stem<(any_4_6 stem_2<any_3_5> any_6_8)>)>

(* Central domain *)
h19: stem_2<(any_5_7 h20 any_3_5 h25 any*[9..12] h26 any_1_2)>
h20: stem_2<( any_3_4 stem_2<( any_1_2 h21 any_2_4 h22 any_2_4 )> any_3_4 )>
h21: stem_e2<( any_3_5 stem_e2<(any_3_5 stem_e1<any*[5..6]> any_2_4)> any_3_5 )>
```

```
h22: stem_e2<( any_1_3 stem<(any_3_4 h23 any*[10..12] stem_2<( any any A any )>
               any_1_2)> any_1_3 )>
h23: stem<(any_2_4 stem_2<any*[5..6]> any_5_7)>
h25: stem<(any*[7..11] stem<any*[8..10]> any*[4..7])>
h26: stem_e1<(any_1_2 stem_e2<any_4_6> any_3_5 stem_4 any_3_5 )>
h27: stem_2<(any_5_7 stem_4 any_3_5)>

(* 3'M domain *)
h28: stem_e2<(any h28_a any_2_4)>
h28_a: stem<(any_1_3 h29 any_4_6 h43 any_4_6)>
h29: stem<(h30 any_2_4 h41 any_5_7 h42 any_4_6)>
h30: stem_e1<(any_3_5 h31 any*[7..9] h32 any_2_4)>
h31: stem<any*[7..9]>
h32: stem<(any_4_6 h33 any_1_2 h34 any_3_5)>
h33: stem<(any_1_3 stem<any_4> any_1_3 stem<any_4> any_1_3)>
h34: stem_e1<(any_1_2 stem<(stem_e2<(any_2_4 h35
     any_4_6 h38 any_3_5)> any_2_4)>)>
h35: stem<(h36 any_2_3 h37 any_2_3)>
h36: stem<any_4>
h37: stem<any_5_7>
h38: stem<(any_1_2 h39 any_1_3 h40 any_4_6)>
h39: stem<(any_2_4 stem<(any_1_3 stem<any_4_6>)> any_2_4)>
h40: stem<any_4>
h41: stem<(any_4_6 stem<(any_1_3 stem<(any_2_4 stem<any_4> any_2_4)>
           any_3_5)> any_4_6)>
h42: stem<(any_3_4 stem<any*[7..9]> any_3_4)>
h43: stem<any*[7..9]>


(* 3'm domain *)
h44: stem<(any_1_3 stem<(any_2_4 stem<(any_1_3 stem<(any_3_5
     stem_e1<(any_1_3 stem<any_4>)> any_2_4)> any_1_3)> any_3_5)> any_2_3)>
h45: stem<any_4>
```