

Epistemic Principle of a Congruence Maximization of a Phylogenetic Tree to External Classifications

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Abstract

A miscongruence of a phylogenetic tree to external classifications is proposed as a criterion of the quality of a phylogenetic tree. Since an established classification of biological objects is taxonomy, the computation of taxonomy miscongruence between a phylogenetic tree and a given taxonomy is described. The miscongruence with the NCBI taxonomy can be used as one number evaluating the quality of a phylogenetic tree. The computation of taxonomy miscongruence also can be used to assign taxonomy names to interior nodes of a tree. Taxonomy miscongruence is applied to comparing different phylogenetic trees, optimization of the parameters of a tree building, finding taxonomically misassigned type strains, and the analysis of the MLST clades of *Escherichia coli*.

Keywords— Phylogenetic tree, Tree congruence, Taxonomy, Taxonomy miscongruence, Type strain, *Escherichia coli*.

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1 Introduction

The problem of a phylogenetic tree reconstruction has a curse of lacking training sets because there are no observed phylogenetic trees, and yet there is a desire to reconstruct a most probable phylogenetic tree. As a possible solution the principle of maximum congruence estimation is proposed.

This principle needs an external tree or classification and a function of miscongruence. If a phylogenetic tree spans a large number of taxa, the taxonomy can be used as the reference tree and a taxonomy miscongruence function is described.

This way a single number, miscongruence, is assigned to a phylogenetic tree, which allows optimizing tree building parameters, comparing phylogenetic trees by quality or finding outlier objects.

2 Methods

2.1 Principle of maximum congruence estimation

This section describes the concept and properties of miscongruence in an informal way.

Consider a set of objects for which it is desired to build a phylogenetic tree and for which there exist external classifications. For example, an external tree is a set of external classifications.

Let phylogenetic trees on these objects and classifications of these objects be represented as vectors. Let vector \mathbf{t} be the vector representing an unknown true tree T , \mathbf{r} be the vector representing external classifications R , and \mathbf{x} be the vector representing an arbitrary tree X , then

$$|\mathbf{x} - \mathbf{r}|^2 = |(\mathbf{x} - \mathbf{t}) - (\mathbf{r} - \mathbf{t})|^2 = |\mathbf{x} - \mathbf{t}|^2 + |\mathbf{r} - \mathbf{t}|^2 - 2(\mathbf{x} - \mathbf{t})^t(\mathbf{r} - \mathbf{t}). \quad (1)$$

If the deviations of \mathbf{x} and \mathbf{r} from \mathbf{t} are independent, then on the average $(\mathbf{x} - \mathbf{t})^t(\mathbf{r} - \mathbf{t}) = 0$, and

$$\arg \min_{\mathbf{x}} |\mathbf{x} - \mathbf{r}|^2 = \arg \min_{\mathbf{x}} |\mathbf{x} - \mathbf{t}|^2$$

which is generalized as

$$\arg \min_{\theta \in \Theta} \Delta(X(\theta), R) = \arg \min_{\theta \in \Theta} \Delta(X(\theta), T),$$

where $X(\theta)$ is the tree built with parameters $\theta \in \Theta$, and $\Delta(T_1, T_2)$ is a *miscongruence* between trees or classifications T_1 and T_2 .

Minimizing the miscongruence of the tree $X(\theta)$ from external classifications R by selecting parameters $\theta \in \Theta$, in other words, maximizing the congruence between $X(\theta)$ and R , on the average minimizes the miscongruence of $X(\theta)$ from the true tree T .

Therefore, building a phylogenetic tree of high quality consists in selecting Θ and R and computing

$$\arg \min_{\theta \in \Theta} \Delta(X(\theta), R).$$

The miscongruence consists of the two parts:

$$\Delta(X(\theta), R) = \Delta_0 + \Delta_1,$$

where

- Δ_0 matches $|\mathbf{x} - \mathbf{t}|^2$ in (1), which is minimized with the minimization of the miscongruence;
- Δ_1 matches $|\mathbf{r} - \mathbf{t}|^2 - 2(\mathbf{x} - \mathbf{t})^t(\mathbf{r} - \mathbf{t})$ in (1), which is noise and creates a lower bound of the miscongruence.

The maximum congruence estimation is similar to the statistical maximum likelihood estimation, where the parameters are adjusted to minimize the discrepancy of model from data and the formula measuring the discrepancy follows from a probabilistic model. In the maximum congruence estimation external classifications R act as data.

Since it is required that the deviations of X and R from T should be independent, the tree X and the classifications R should be created by different methods and/or by using different characters.

2.2 Maximum parsimony miscongruence

This section describes how to compute miscongruence using the maximum parsimony method.

Consider two rooted trees T_1 and T_2 having the same set S as leaves. Let $L(y)$ be the leaves of the subtree rooted at node y of a tree.

For a set $Y \subseteq S$ define a Boolean attribute on the elements $y \in S$ which is 1 if $y \in Y$ and 0 otherwise. Then solve the maximum parsimony problem for this Boolean attribute in a tree T , and let $s_{\text{mp}}(Y|T)$ be the score of this solution. The maximum parsimony problem can be solved by the Sankoff algorithm in time $O(n)$, where $n = |S|$, see [3].

Let $y \in T$ mean that y is a node of the tree T .

Define the *maximum parsimony miscongruence* of trees T_1 and T_2 as

$$\Delta_{\text{mp}}(T_1, T_2) = \sum_{y \in T_1, L(y) \neq S} (s_{\text{mp}}(L(y)|T_2) - 1).$$

This formula is similar to the Robinson-Foulds distance between trees [3], where a set in $\{L(y) : y \in T_1\}$ is scored 1 if it is missing in $\{L(y) : y \in T_2\}$, whereas in $\Delta_{\text{mp}}(T_1, T_2)$ a set is scored 1 or greater if it is missing in $\{L(y) : y \in T_2\}$.

The value $\Delta_{\text{mp}}(T_1, T_2)$ is not a distance.

$$\Delta_{\text{mp}}(T_1, T_2) \geq 0.$$

$$T_1 = T_2 \Leftrightarrow \Delta_{\text{mp}}(T_1, T_2) = 0.$$

The maximum parsimony score $s_{\text{mp}}(L(y)|T_2)$ is the number of nodes in T_2 where the Boolean attribute defined by $L(y)$ is gained or lost. Therefore, $\Delta_{\text{mp}}(T_1, T_2)$ can be decomposed into maximum parsimony scores $\Delta_{\text{mp}}(T_1, T_2, y)$ per node $y \in T_2$. This allows finding the most miscongruent interior nodes or leaves of T_2 .

2.3 Taxonomy miscongruence

In biology there is one distinguished classification which is the taxonomy. It is based mostly on phenotypic and rDNA characters. For prokaryotes the taxonomy tree can be extended below species by including phylogroups, serovars and MLST numbers.

Let \mathfrak{T} be the extended NCBI taxonomy tree [2]. Then define the *taxonomy miscongruence of a tree T* as

$$\tau(T) = \Delta_{\text{mp}}(\mathfrak{T}, T),$$

and the *taxonomy miscongruence of a node $y \in T$* as

$$\tau(y) = \Delta_{\text{mp}}(\mathfrak{T}, T, y),$$

see Section 2.2.

2.3.1 Computation of taxonomy miscongruence

Since some taxons are unknown (for example, *incertae sedis*), the Boolean attributes defining the maximum parsimony problem in Section 2.2 must have three values: 1, 0 or unknown. To compute $\tau(T)$ each of these 3-valued Boolean attributes should be assigned to each leaf of the tree T , so that the input data will have size $O(n^2)$ which is too much.

To simplify the input data, for each biological object only its taxonomic lineage is stored as a sequence of nominal attribute-value pairs *TaxonLevel:TaxonName*, for the detailed description see Appendix A. The set of nominal attributes is the same for each biological object. The nominal attributes are taxonomic ranks, e.g., kingdom, phylum, class, order, family, genus, species, together with *subranks*, which are the taxonomy levels between the ranks. The nominal attribute-value pairs are converted into 3-valued Boolean attributes, see Table 1. Since there is a limited number of taxonomy rank-subrank combinations, the input data size for the computation of taxonomy miscongruence is $O(n)$.

Value of <i>nom</i>	Variant	<i>nom:a</i>	<i>nom:b</i>	<i>nom:c</i>
<i>a</i>		<i>true</i>	<i>false</i>	<i>false</i>
<i>b</i>		<i>false</i>	<i>true</i>	<i>false</i>
<i>c</i>		<i>false</i>	<i>false</i>	<i>true</i>
unknown	1	unknown	unknown	unknown
unknown	2	<i>false</i>	<i>false</i>	<i>false</i>

Table 1: Conversion of a nominal attribute *nom* into three 3-valued Boolean attributes *nom:a*, *nom:b* and *nom:c*.

2.3.2 Assigning taxonomy names to interior nodes of a tree

The procedure for the computation of the taxonomy miscongruence described in Section 2.3 can be also used for an automatic assignment of taxonomy names to the interior tree nodes.

After the maximum parsimony problem is solved for each Boolean attribute, the binary assignment of each rank-subrank-taxonomic name is made to each node of the phylogenetic tree. A Boolean attribute is *gained* at a node, if it is *true* at the node, but *false* at its parent node. Then the *gained taxonomic names* of a node are the taxonomic names of the Boolean attributes which are gained in this node. These taxonomic names belong to different rank-subrank combinations, see the Lemma below, and therefore, can be ordered from the lowest to highest rank-subrank. The first and last taxonomic names in this ordering can be used as the name of the interior node in the format *name1/name2*, or just *name1* if the both names are the same.

To make the names more informative, the unknown taxons in a taxonomic lineage of an object are considered as novel taxonomic names unique to the object and they are not used in naming.

This method is used in the phylogenetic trees of [1].

Lemma: if Boolean attributes B_1 and B_2 represent different values of the same nominal attribute, the maximum parsimony problem is solved for each Boolean attribute independently, and Boolean assignments with more *false* nodes are preferred, then at no node B_1 and B_2 can be both gained.

Proof: by induction from tree leaves. Suppose the Lemma is proved for all tree depths greater than d . Then consider an interior node v at depth d where B_1 is gained. Let n_i be the number of the children of this node where $B_i = \text{true}$, and \bar{n}_i be the number of the children of this node where $B_i = \text{false}$. Then $n_1 > \bar{n}_1 \geq n_2$. If B_2 is also gained at the node v , then similarly $n_2 > n_1$, which is a contradiction.

2.3.3 Selection of the root of a phylogenetic tree

The procedure for the computation of the taxonomy miscongruence described in Section 2.3 can be also used for an automatic root selection of the phylogenetic tree.

After the maximum parsimony problem is solved for each Boolean attribute, for each tree node the number of the Boolean attributes having the *true* assignment can be computed. The node with the fewest number can be selected as the root.

2.3.4 Caveat: Filtering of objects can lower taxonomy miscongruence

Before a tree building the tree objects are usually filtered for contamination or taxonomic misassignment, which can be based on a separately built auxiliary phylogenetic tree. If the auxiliary phylogenetic tree is similar to the target phylogenetic tree then this procedure will artificially lower the taxonomy miscongruence of the target phylogenetic tree.

Consider two stable clades A and B and an object x located in the gray zone between A and B . Suppose that x is not a type strain, and that x is taxonomically assigned to clade A . This assignment may be an error and x may actually belong to B .

Different tree building methods will assign x to either A or B , so that all 4 cases are possible, see Table 2.

Case	Phylogenetic tree	True taxonomy	Current taxonomy	Taxonomy miscongruence
1	$(Ax)B$	$(Ax)B$	$(Ax)B$	0
2	$(Ax)B$	$A(xB)$	$(Ax)B$	0
3	$A(xB)$	$(Ax)B$	$(Ax)B$	1
4	$A(xB)$	$A(xB)$	$(Ax)B$	1

Table 2: Possible cases of placing an object x in the gray zone of stable clades A and B .

If a filtering procedure prefers cases 1 and 2 because they agree with the current taxonomy, the taxonomy miscongruence will be artificially lowered.

3 Results

3.1 Comparison of phylogenetic trees by quality

Different phylogenetic trees can be compared by quality using the taxonomy miscongruence. But these trees should contain the same objects. For a pair of trees the objects present only in one tree are removed, so that each reduced tree should contain only the objects common to the both trees, and then for these reduced trees the taxonomy miscongruences τ_1 and τ_2 are computed respectfully according to Section 2.3.

If a tree T_1 is better than a tree T_2 , in other words, $\tau_1 \leq \tau_2$, then the *quality difference* is

$$1 - \tau_1/\tau_2.$$

The phylogenetic trees of Table 3 have been compared by quality in Table 4.

Tree name	Tree file	Taxon	Tree object	Objects	Reference
ASTRAL	ASTRAL	prokaryota	assembly	10,575	[8]
GTDB-86	bac120_r86.1.tree	bacteria	assembly	27,372	[4]
GTDB-89	bac120_r89.tree	bacteria	assembly	23,458	[4]
NCBI bacteria	bacteria-R11	bacteria	assembly	415,761	[1]
NCBI bacteria-type	bacteria-R11t	bacteria	assembly, type strains	11,970	[1]
Budding Yeast	332_24080Gs_ time-calibrated_ phylogeny...	<i>Saccharomycotina</i>	assembly	332	[7]
NCBI fungi	fungi-R15	fungi	assembly	4,413	[1]
Silva	LTPs132.SSU	prokaryota	16S rRNA	13,867	[6]
NCBI 16S	prok-16S-R4	prokaryota	16S rRNA	20,975	[1]

Table 3: Phylogenetic trees whose quality is evaluated in Table 4.

Tree T_1 (better)	Tree T_2	Common objects	τ_1	τ_2	Quality difference
GTDB-86	NCBI bacteria	22,479	37,420	41,158	9.1%
GTDB-86	NCBI bacteria-type	6,885	11,239	11,584	3.0%
GTDB-89	NCBI bacteria	20,759	41,592	45,515	8.6%
GTDB-89	NCBI bacteria-type	7,170	13,394	13,694	2.2%
GTDB-86	GTDB-89	13,248	27,012	27,134	0.4%
ASTRAL	NCBI bacteria	8,422	17,686	20,264	12.7%
ASTRAL	NCBI bacteria-type	3,411	7,416	7,726	4.0%
ASTRAL	GTDB-86	6,685	15,083	15,387	2.0%
NCBI fungi	Budding Yeast	319	520	528	1.5%
NCBI 16S	Silva	12,501	16,494	19,110	13.7%

Table 4: Comparison of the quality of phylogenetic trees T_1 and T_2 by taxonomy miscongruences τ_1 and τ_2 of the common object trees.

The quality difference for the NCBI bacteria-type tree is much better than the for NCBI bacteria tree. A possible explanation is that in the GTDB and ASTRAL trees the contaminated genomes have been removed by the CheckM analysis [5] which itself uses a phylogenetic tree, see Section 2.3.4. This removal of contaminated genomes can artificially reduce the taxonomy miscongruence, but type strains are less likely to be affected by the contamination removal.

In comparing the GTDB-86 and GTDB-89 trees the common objects have been restricted to those which could be mapped to the NCBI assemblies.

The best current bacterial phylogenetic tree is ASTRAL followed by GTDB-86 followed by NCBI bacteria-type.

3.2 Achieving the best phylogenetic tree

The topology and, therefore, the taxonomy miscongruence of a phylogenetic tree depend on the following choices:

- object type: specific gene or genes, whole genome;
- parameters of multiple alignment or dissimilarity computation;
- tree building method (maximum likelihood, distance-based) and parameters of the method;
- outlier identification parameters;
- how good the optimization is: optimization criterion, number of optimization iterations;
- number of the objects used in the tree.

The tree building parameters of least squares distance trees of [1] have been optimized to achieve the minimum of taxonomy miscongruence for a random subset of 1000 objects. That is how the parameters in Appendix C of [1] have been chosen. The obtained parameters have been used to build the whole trees, see Table 5.

Taxon Object type	bacteria genome	fungi genome	protists genome	prokaryotes 16S rRNA	fungi ITS rRNA
Reservoir objects	473,130	4,670	635	21,137	11,025
Objects in the tree	415,761	4,413	581	20,975	10,428
Outliers, %	12.1%	5.5%	8.5%	0.8%	5.4%
Taxonomy miscongruence	156,076	3,557	747	30,907	26,141
Tax. misc. per object	0.38	0.81	1.29	1.47	2.51
Release	11	14	3	4	8
Data collection date	10 Jan 2020	10 Jan 2020	22 Apr 2019	29 Jun 2019	21 Oct 2019
Base file name	bacteria-R11	fungi-R14	protists-R3	prok-16S-R4	fungi-ITS-R8

Table 5: The GenBank global trees from [1] with taxonomy miscongruences

The improvement of the taxonomy miscongruence with the number of optimization iterations for the initial 3,000 objects of the Fungal ITS tree **fungi-ITS-R8** [1] is in Table 6. Given the variance of τ there is no improvement after 5 optimization iterations.

Number of optimization iterations	Absolute criterion	τ
0 (NNJ only)	590.87	9,969
1	43.18	9,385
2	42.90	9,139
3	42.88	9,146
4	42.88	9,093
5	42.88	9,117
6	42.88	9,084
7	42.88	9,093
8	42.88	9,051
9	42.88	9,075
10	42.88	9,024
15	42.88	9,075
20	42.88	9,074
30	42.88	9,087
50	42.88	9,101

Table 6: Improvement of the taxonomy miscongruence τ with the number of optimization iterations in the Fungal ITS tree [1].

When a tree is built incrementally the taxonomy miscongruence of the initial set of objects improves with the total number of objects. This is shown for the Fungal ITS tree [1] in Fig. 1.

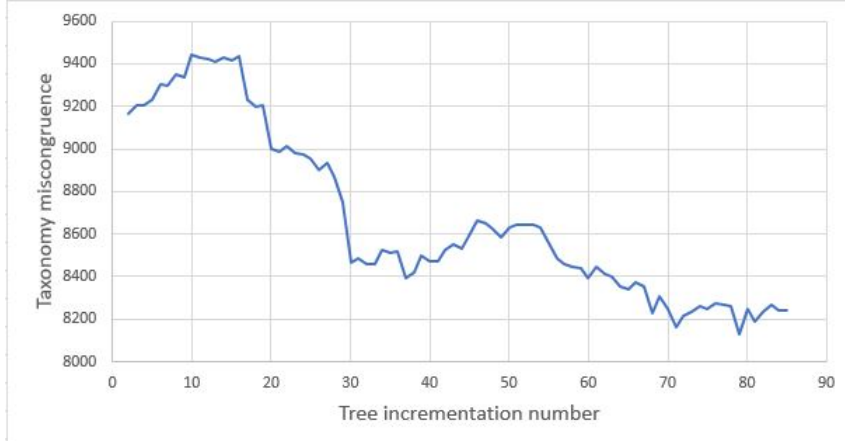


Figure 1: Improvement of the taxonomy miscongruence of the initial set of objects with the tree incrementation number in the Fungal ITS tree [1].

This suggests the following method to improve a phylogenetic tree for a set S of objects:

- add more objects to S making a superset S' : $S \subset S'$;
- build a tree for the superset S' ;
- remove the extra objects $S' \setminus S$ from the tree.

The resulting tree will contain the original set S of objects and will be on the average better than a tree built only from S .

3.3 Bacterial type strains with probably misassigned sequence

Type strain sequences are used as golden standard for taxonomic assignment of other sequences, but the whether the type strain sequences themselves are correct or their taxonomic lineages are correct remains a problem.

The bacterial genomes of type strains with taxonomic miscongruence $\tau \geq 32$ in the tree **bacteria-R12t** [1] have been manually checked, and 53 genomes which probably have been assigned to a type strain in error or where the taxonomic lineage of the type strain is incorrect are in Table 7.

The same manual analysis has been done for prokaryotic type strain 16S rRNA sequences using the tree **prok-16S-R4** [1], and 68 16S rRNA sequences which probably have been assigned to a type strain in error or where the taxonomic lineage of the type strain is incorrect, are in Table 8.

3.4 Analysis of the MLST clades of *Escherichia coli*

For the GenBank genomes assigned to *Escherichia coli* the 7-locus ST numbers have been identified using the data from http://enterobase.warwick.ac.uk/species/ecoli/download_data. And the obtained ST numbers have been used as taxonomy extension and assigned to the interior nodes of the phylogenetic tree of GenBank bacterial genomes [1] by the method described in Section 2.3.2.

Some ST numbers are polyphyletic, and some ST numbers are paraphyletic, in other words, their clades contain other ST numbers. The ST numbers with more than 50 genomes are in Table 9.

NCBI assembly	Strain	τ	Taxonomic lineage	Phylogenetic lineage
GCA_000167375.1	ATCC 25662	200	Anaerorhabdus furcosa; Anaerorhabdus; Ba...	Erysipelotrichaceae; Clostridia; Terraba...
GCA_002934545.1	DSM 3808	198	Bacteroides xylanolyticus; Bacteroides <...	Lachnospiraceae; Lachnospiraceae; Clos...
GCA_003847445.2	X0209	194	Kroppenstedtia sanguinis; Kroppenstedtia...	Gordoniaceae/Gordonia <actinomycete>; Co...
GCA_000169515.1	Marseille-P3369	183	Varibaculum timonense; Varibaculum; Acti...	Tissierellaceae; Tissierella; Clostridi...
GCA_0006740705.1	NKC3-5	172	Salicibacter halophilus; Salicibacte...	Bacillaceae; ; Bacillales; Bacilli; Clos...
GCA_0003051055.1	DSM 5822	166	Agitococcus lubricus; Agitococcus; Carno...	Thiotrichales; ; Gammaproteobacteria; Pr...
GCA_002362315.1	ATCC 31363	148	Pseudomonas acidophila; Pseudomonas; Pse...	Paraburkholderia; Burkholderiaceae; Burk...
GCA_002894665.1	CB7	138	Salinivenuus iranica; Salinivenuus; Salini...	Bacteroidetes <phylum>/Rhodothermaceae; ...
GCA_000114705.1	ATCC 43154	126	Rugamonas rubra; Rugamonas; Pseudomonada...	Oxalobacteraceae; Burkholderiales; Betap...
GCA_000290205.1	Marseille-P4302	126	Anaerolactibacter massiliensis; Anaerola...	Erysipelotrichaceae; Clostridia; Terraba...
GCA_003254275.1	DSM 6779	103	Cytophaga xylanolytica; Cytophaga; Cytop...	Bacteroidia/Bacteroidales; Bacteroidetes...
GCA_007970665.1	BR7-21	100	Baekduia soli; Baekduia; Baekduiaceae; R...	Solirubrobacterales; Thermoleophilia; Ac...
GCA_000483165.1	ATCC 49900	90	Acholeplasma multilocale ATCC 49900; Ach...	Mesoplasma; Entomoplasmataceae; Entomopl...
GCA_000717315.1	NRRL B-24431	90	Actinospica acidiphila; Actinospica; Act...	Streptomyces/Streptomyces; Actinobac...
GCA_002529455.1	TRM 49117	90	Glycomyces fuscus; Glycomyces; Glycomyce...	Nocardiosis; Nocardiosis; Streptosp...
GCA_003052455.1	ATCC 31213	90	Sphaerisporangium cinnabarinum; Sphaeris...	Promicromonosporaceae/Cellosimicrobium...
GCA_000473895.1	KORDI 51-2	76	Rubidibacter lacunae KORDI 51-2; Rubidib...	Synechococcales; ; Cyanobacteria/Melaina...
GCA_000382325.1	DSM 17123	68	Woodsholea maritima DSM 17123; Woodshole...	Rhodobacterales/Hyphomonadaceae; Alphapr...
GCA_000688235.1	DSM 6293	68	Terasakiella pusilla DSM 6293; Terasakie...	Rhodospirillaceae; Rhodospirillales; Alp...
GCA_003725335.1	DSM 22242	68	Parvibacter caecicola; Parvibacter; Cori...	Eggerthellales/Eggerthellaceae; Coriobac...
GCA_000100455.1	930I	68	Roseospirillum parvum; Roseospirillum; R...	Rhodospirillaceae; Rhodospirillales; Alp...
GCA_003574215.1	TH-1	63	Hydrogenophilus thermoluteolus; Hydrogen...	Proteobacteria; Bacteria <prokaryotes>...
GCA_001855385.1	DSM 1989	62	Andreesenia angusta; Andreesenia; Gottsc...	Tissierella; Clostridiales; Clostridia;...
GCA_001274725.1	DSM 4	48	Sporosarcina globispora; Sporosarcina; P...	Bacillus <bacterium>; Bacillaceae; ; Bac...
GCA_000626075.1	Marseille-P8228	48	Clostridium transplantifacale; Clostrid...	Lachnospiraceae; Lachnospiraceae; Clos...
GCA_000102225.1	i6	44	Eubacterium pyruvativorans; Eubacterium;...	Clostridiales; Clostridia; Terrabacteria...
GCA_001443605.1	L21-Spi-D4	42	Salinivirga cyanobacteriivorans; Saliniv...	Bacteroidia/Bacteroidales; Bacteroidetes...
GCA_000155205.1	ATCC 29176	37	Ruminococcus lactaris ATCC 29176; Rumino...	Lachnospiraceae; Clostridiales; Clostrid...
GCA_000518685.1	ATCC 35991	37	Eubacterium xylanophilum ATCC 35991; Eub...	Lachnospiraceae; Clostridiales; Clostrid...
GCA_000167085.1	ATCC 17233	37	Eubacterium ruminantium; Eubacterium; Eu...	Lachnospiraceae; Clostridiales; Clostrid...
GCA_000167205.1	ATCC 51222	37	Eubacterium coprostanoligenes; Eubacteri...	Ruminococcaceae; Clostridiales; Clostrid...
GCA_000174415.1	AHT 1	34	Dethiobacter alkaliphilus AHT 1; Dethiob...	Clostridia; Terrabacteria group/Firmicut...
GCA_000374145.1	DSM 15528	34	Neomegalonema perideroedes DSM 15528; Ne...	Alphaproteobacteria; Proteobacteria; Bac...
GCA_000384415.1	PS-1	34	Cyclocasticus pugetii PS-1; Cyclocasti...	Gammaproteobacteria; Proteobacteria; Bac...
GCA_000422285.1	DSM 4660	34	Desulfatigibans anilini DSM 4660; Desulfa...	Proteobacteria/Deltaproteobacteria; Bact...
GCA_000620305.1	DSM 16504	34	Desulfatibacter alkalitolerans DSM 16504...	Clostridiales; Clostridia; Terrabacteria...
GCA_002088235.1	22II-S10r2	34	Oceanococcus atlanticus; Oceanococcus; E...	Gammaproteobacteria; Proteobacteria; Bac...
GCA_003148465.1	DSM 24906	34	Oceanotoga teriensis; Oceanotoga; Thermo...	Thermotogae <phylum>/Thermotogae <
GCA_003751635.1	DSM 100275	34	Immirania thermothiophila; Immirania; Ec...	Gammaproteobacteria; Proteobacteria; Bac...
GCA_009602465.1	2-36	34	Cumulibacter manganitolans; Cumulibact...	Actinobacteria <class>; Actinobacteria
GCA_000086705.1	Marseille-P2411	34	Massilibacillus massiliensis; Massilibac...	Negativicutes; Terrabacteria group/Firmi...
GCA_000101835.1	DSM 20475	34	Peptococcus niger; Peptococcus; Peptococ...	Clostridia; Terrabacteria group/Firmicut...
GCA_000129455.1	DSM 45627	34	Jatrophihabitans endophyticus; Jatrophih...	Actinobacteria <class>; Actinobacteria
GCA_004362405.1	DSM 25082	33	Kinneretia asaccharophila; Kinneretia; C...	Burkholderiales; Betaproteobacteria; Pro...
GCA_004362975.1	DSM 28287	33	Aminicella lysinitica; Aminicella; Eub...	Clostridiales; Clostridia; Terrabacteria...
GCA_007004765.1	GYP-15	33	Aliikangiella marina; Aliikangiella; Kan...	Oceanospirillales; Thiotrichales; ; Gamm...
GCA_000167975.1	DSM 25262	33	Ohtaekwangia koreensis; Ohtaekwangia; Cy...	Cytophagia/Cytophagales; Bacteroidetes <...

Table 7: Bacterial type strain genomes which probably have been assigned to a type strain in error or where the taxonomic lineage of the type strain is incorrect. The data are as of January 2020.

RefSeq accession	GenBank accession	τ	Taxonomic lineage	Phylogenetic lineage
NR_044819.1	X55406	231	Filifactor alocis; Filifactor; Peptostre...	Fusobacterium; Fusobacteriaceae; Fusobac...
NR_115176.1	AY230768	231	Paenibacillus sanguinis; Paenibacillus; ...	Lysobacter; Xanthomonadaceae; Xanthomona...
NR_104743.1	FR733681	226	Ilyobacter delafieldii; Ilyobacter; Fuso...	Clostridium; Clostridiaceae; Clostridial...
NR_104899.1	HF558386	226	Bacteroides xylanolyticus; Bacteroides <...	Lachnospirillum; Lachnospiraceae; Clos...
NR_104962.1	JX986959	226	Flavobacterium acidificum; Flavobacteriu...	Pantoea; Erwiniaceae; Enterobacterales; ...
NR_104868.1	HE582776	204	Agitococcus lubricus; Agitococcus; Carno...	Pseudomonadales/Moraxellaceae; Gammaprot...
NR_118671.1	L34614	203	Clostridium combesii; Clostridium; Clost...	Acidipropionibacterium; Propionibacteria...
NR_104948.1	JN175353	129	Prolinoborus fasciculus; Prolinoborus; N...	Acinetobacter; Pseudomonadales/Moraxella...
NR_117112.1	FR733683	129	Cytophaga xylanolytica; Cytophaga; Cytop...	Marinilabiliaceae; Marinilabiliales; Bac...
NR_041304.1	AB210824	118	Sharpea azabuensis; Sharpea; Lactobacill...	Firmicutes/Erysipelotrichaceae; Terrabac...
NR_104915.1	HM038005	118	Rugamonas rubra; Rugamonas; Pseudomona...	Oxalobacteraceae; Burkholderiales; Betap...
NR_112167.1	AB073978	118	Fucophilus fucoidanolyticus; Fucophilus;...	Puniceococcales/Puniceococcaceae; Opitut...
NR_144718.1	LN713275	118	Beduini massiliensis; Beduini; Clostridi...	Firmicutes/Erysipelotrichaceae; Terrabac...
NR_104836.1	GU269544	116	Lactobacillus rogosae; Lactobacillus; La...	Lachnospiraceae; Clostridiales; Terrabac...
NR_147732.1	LC055729	105	Filobacterium rodentium; Filobacterium; ...	Chitinophagia/Chitinophagaceae; Bacteroi...
NR_113504.1	AB663439	100	Halostagnicola alkaliphila; Halostagnico...	Halosimplex carlsbadense; Halosimplex; H...
NR_041204.1	AB184754	95	Streptomyces gardneri; Streptomyces; Str...	Nocardia; Nocardiaceae; Corynebacteriale...
NR_043396.1	D14125	95	Halorubrum trapanicum; Halorubrum; Halor...	Natrinema; Natrialbales/Natrialbaceae; H...
NR_044137.1	EF178675	95	Actinoalloteichus cyanogriseus; Actinoal...	Streptomyces; Streptomycetales/Streptomy...
NR_104535.1	EU693576	95	Prauserella marina; Prauserella; Pseudon...	Streptomyces griseus group/Streptomyces ...
NR_115779.1	DQ442518	95	Streptomyces libani; Streptomyces; Strep...	Arthrobacter; Micrococcaceae; Micrococca...
NR_117484.1	GU269552	95	Pilimelia columellifera subsp. pallida; ...	Streptomyces; Streptomycetales/Streptomy...
NR_042487.1	AM183347	90	Rheinheimera perlucida; Rheinheimera; Ch...	Alteromonadales/Alishewanella; Chromatia...
NR_104657.2	M22351	88	Asteroleplasma anaerobium; Asteroleplasm...	Terrabacteria group/Clostridia; bacteria...
NR_117160.1	FR749963	82	Thermohydrogenium kirishense; Thermohyd...	Thermoanaerobacterium; Thermoanaerobacte...
NR_042960.1	AY538169	79	Acholeplasma multilocale; Acholeplasma; ...	Entomoplasmataceae; Entomoplasmatales/Sp...
NR_112013.1	AB006157	79	Parvopolsyspora pallida; Parvopolsyspora; ...	Actinomadura; Thermomonosporaceae; Stre...
NR_025605.1	AJ578476	68	Woodsholea maritima; Woodsholea; Cauloba...	Hyphomonadaceae; Rhodobacterales; Rhizob...
NR_041955.1	AJ011919	68	Roseospirillum parvum; Roseospirillum; R...	Rhodospirillaceae; Rhodospirillales; Alp...
NR_116378.1	EU588727	68	Oceanotoga teriensis; Oceanotoga; Thermo...	Petrotogales/Petrotogaceae; Thermotogae ...
NR_1156875.1	KF022043.1	68	Haloactinomyces albus; Haloactinomyces; ...	Pseudonocardiaceae/Pseudonocardiaceae; Ac...
NR_118544.1	KC188660	60	Keratinibaculum paraultunense; Keratinib...	Tissierellales; Tissierellia; Clostridia...
NR_028816.1	AF349724	59	Turcibacter sanguinis; Turcibacter; Er...	Terrabacteria group/Clostridia; bacteria...
NR_041385.1	AB245479	55	Sulfurivirga caldicurii; Sulfurivirga;...	Chromatiales; Gammaproteobacteria; Oligo...
NR_113738.1	KP178167	55	Alkalimarinus sediminis; Alkalimarinus; ...	Oceanospirillales; Gammaproteobacteria; ...
NR_042854.1	AY345990	53	Entomoplasma melaleuca; Entomoplasma; E...	Entomoplasmatales/Spiroplasma; Tenericut...
NR_112008.1	AB004752	53	Serratia liquefaciens; Serratia; Yersini...	Klebsiella; Enterobacteriaceae; Enteroba...
NR_112014.1	AB006170	53	Sphaerimonospora mesophila NBRC 14179 = ...	Thermobifida; Nocardiopsaceae; Streptos...
NR_119056.1	X74709	53	Moritella marina ATCC 15381; Moritella m...	Pseudoalteromonas; Pseudoalteromonadacea...
NR_104808.1	FR749965	50	Thermohydrogenium kirishense; Thermohyd...	Thermoanaerobacterium; Thermoanaerobacte...
NR_117161.1	FR749964	50	Thermohydrogenium kirishense; Thermohyd...	Thermoanaerobacterium; Thermoanaerobacte...
NR_024683.1	AB018184	48	Eubacterium multiforme; Eubacterium; Eub...	Clostridium; Clostridiaceae; Clostridial...
NR_028884.1	AJ132943	48	Micrococcus lacustris; Micrococcus; Pr...	Nocardioidaceae/Friedmanniella; Propioni...
NR_074975.1	CP000482	48	Pelobacter propionicus; Pelobacter; Desu...	Geobacteraceae/Geobacter; Desulfuromonad...
NR_115528.1	D16278	48	Bacillus racemolactis; Bacillus <bact...	Sporolactobacillaceae/Sporolactobacillus...
NR_104905.1	HM037993	46	Vitreoscilla filiformis; Vitreoscilla; N...	Burkholderiales; Betaproteobacteria; Gam...
NR_134756.1	HF947551	46	Limisphaera ngatamariensis; Limisphaer...	Verrucomicrobia; PVC group; bacteria; pr...
NR_029181.1	U16758	45	Mycoplasma feliminutum; Mycoplasma; Myco...	Tenericutes/Mollicutes; Terrabacteria gr...
NR_113170.1	AB558581	43	Oligosphaera ethanolica; Oligosphaera; O...	bacteria; prokaryotes...
NR_137400.1	JF304644	43	Chitinispirillum alkaliphilum; Chitinisp...	bacteria; prokaryotes...
NR_149251.1	LN833202	43	Longimicrobium terrae; Longimicrobium; L...	bacteria; prokaryotes...
NR_040915.1	AB078062	42	Hughenoltzia roseola; Hughenoltzia; Bern...	Microscillaceae; Cytophagia/Cytophagales...
NR_111998.1	AB004691	42	Pantoea agglomerans; Pantoea agglomerans...	Enterobacteriaceae; Enterobacterales; Ga...
NR_152675.1	LM999900	42	Balneicella halophila; Balneicella; Baln...	Marinilabiliales; Bacteroidia; Bacteroid...
NR_041036.1	AB175654	40	Azomonas macrocytogenes; Azomonas; Azoto...	Pseudomonas; Pseudomonadales/Pseudomonad...
NR_024661.1	AB008552	37	Eubacterium ruminantium; Eubacterium; Eu...	Lachnospiraceae; Clostridiales; Terrabac...
NR_027579.1	L76602	37	Ruminococcus lactaris ATCC 29176; Rumino...	Lachnospiraceae; Clostridiales; Terrabac...
NR_104737.1	FR733672	37	Eubacterium oxidoreducens; Eubacterium; ...	Lachnospiraceae; Clostridiales; Terrabac...
NR_104931.1	JN175336	37	Carbophilus carboxidus; Carbophilus; Rhi...	Aminobacter; Mesorhizobium; Phyllobacter...
NR_115118.1	AY026916	37	Lutibacterium anuloederans; Lutibacteriu...	Erythrobacter; Altererythrobacter; Eryth...
NR_116306.1	EU401907	37	Beijerinckia fluminensis; Beijerinckia; ...	Rhizobium/Agrobacterium group/Rhizobium;...
NR_116747.1	FJ611794	37	Ruminococcus faecis JCM 15917; Ruminococ...	Lachnospiraceae; Clostridiales; Terrabac...
NR_118670.1	L34421	37	Eubacterium ventriosum; Eubacterium; Eub...	Lachnospiraceae; Clostridiales; Terrabac...
NR_118674.1	L34623	37	Eubacterium ramulus ATCC 29099; Eubacter...	Lachnospiraceae; Clostridiales; Terrabac...
NR_118676.1	L34628	37	Eubacterium xylanophilum; Eubacterium; E...	Lachnospiraceae; Clostridiales; Terrabac...
NR_134741.1	KJ023821	37	Hafnia psychrotolerans; Hafnia; Hafniace...	Yersiniaceae; Enterobacterales; Gammapro...
NR_135890.1	KF982858	35	Aestuariicella hydrocarbonica; Aestuari...	Cellvibrionaceae; Cellvibrionales; Gamma...
NR_159172.1	LN651200.1	35	Gellertiella hungarica; Gellertiella; Rh...	Rhizobium/Agrobacterium group/Rhizobium;...

Table 8: Bacterial type strain 16S rRNA sequences which probably have been assigned to a type strain in error or where the taxonomic lineage of the type strain is incorrect. The data are as of June 2019.

ST number	Number of genomes	Number of genomes in main clade	Number of clades	Clades of other ST numbers in the main clade (with numbers of genomes in parentheses, ≥ 10)
ST10	2062	1811	20	ST34(17) ST34(96) ST43(42) ST44(15) ST167(149) ST227(22) ST378(13) ST617(105) ST744(83) ST1060(11) ST1091(13) ST1284(15)
ST11	1594	1594	1	
ST12	171	171	1	
ST14	91	91	1	ST1193(71)
ST16	220	211	2	ST1792(13)
ST17	313	313	1	ST1967(37)
ST20	86	46	3	
ST21	785	785	1	ST723(23)
ST23	344	339	4	ST410(233)
ST29	1031	1021	4	ST21(785) ST723(23) ST765(15)
ST32	270	270	1	
ST33	76	76	1	
ST34	113	96	2	ST227(22) ST378(13)
ST38	253	219	3	
ST40	57	57	1	ST200(17)
ST48	330	325	4	ST4(36) ST1312(25) ST2353(17) ST5276(17)
ST58	97	95	2	
ST59	50	45	4	
ST69	394	394	1	
ST73	399	399	1	
ST88	157	87	4	ST90(26)
ST93	166	100	4	
ST95	462	438	3	ST421(14)
ST101	267	267	1	ST359(33)
ST117	213	211	2	ST5935(14)
ST127	118	118	1	
ST137	287	287	1	ST32(270)
ST141	57	35	2	
ST154	55	51	2	
ST155	170	79	3	
ST156	126	126	1	ST348(14)
ST162	70	26	6	
ST165	248	244	3	ST100(22) ST189(59) ST301(85)
ST167	155	149	4	
ST173	81	81	1	ST5305(28)
ST189	59	59	1	
ST206	115	114	2	
ST224	107	59	2	
ST245	68	62	2	
ST278	117	98	3	ST328(46)
ST297	63	63	1	
ST301	85	85	1	
ST342	88	88	1	
ST349	56	56	1	
ST354	57	57	1	
ST357	58	58	1	
ST398	59	56	2	
ST399	69	69	1	ST635(29)
ST405	181	164	4	
ST410	240	233	3	
ST442	109	105	3	
ST443	122	115	2	
ST448	54	54	1	ST94(15)
ST453	61	61	1	
ST457	76	76	1	
ST517	71	71	1	
ST542	60	49	2	
ST602	73	73	1	
ST617	105	105	1	ST1284(15)
ST641	180	180	1	ST86(11) ST453(61) ST877(10)
ST648	136	122	4	
ST655	163	153	2	
ST678	91	91	1	
ST744	85	83	3	
ST746	97	97	1	
ST1193	71	71	1	
ST2332	101	101	1	

Table 9: The *Escherichia coli* 7-locus MLST numbers with more than 50 genomes.

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Availability of data and materials

The source code for the algorithms described in this paper is written in C++ and `bash` scripts for UNIX and is available at <https://github.com/ncbi/tree-tool>.

License: Freely available to the public for use.

The documentation for this code is available at <https://github.com/ncbi/tree-tool/wiki>.

Authors contributions

Not applicable.

Competing interest

Authors declare that they have no competing interests.

Consent for publication

Not applicable.

Ethics approval and consent to participate

Not applicable.

Appendices

A Encoding of taxonomical lineage for maximum parsimony problem

The NCBI taxonomy as of 01/09/2020 is used. There are 30 ranks in the NCBI taxonomy. The *subranks* are taxons between ranks. See Table 10.

Rank name	Rank number	Max. number of subranks
superkingdom	0	5
kingdom	1	5
subkingdom	2	1
superphylum	3	0
phylum	4	3
subphylum	5	6
superclass	6	11
class	7	7
subclass	8	3
infraclass	9	3
cohort	10	8
subcohort	11	1
superorder	12	1
order	13	6
suborder	14	3
infraorder	15	4
parvorder	16	2
superfamily	17	1
family	18	3
subfamily	19	4
tribe	20	1
subtribe	21	1
genus	22	3
subgenus	23	2
species group	24	1
species subgroup	25	1
species	26	4
subspecies	27	2
varietas	28	1
forma	29	0

Table 10: Ranks in the NCBI taxonomy

The greatest number of subranks between two consecutive ranks is 11 for rank “superclass”, see Table 11. A taxonomical lineage is encoded as a sequence of lines of the format:

rank_number.subrank_number:tax_name

If some ranks or subranks are missing in the lineage, they are represented in the encoding by borrowing the **tax_name** from the previous line.

The unknown taxons are recognized by the following keywords in their taxonomic names: unclassified, unassigned, unidentified, candidate phyla, incertae sedis, symbionts, sp. (but not f. sp. which is forma speciales), taxa, taxon, uncultured, bacterium, actinobacterium, proteobacterium.

The unknown taxons are encoded by **tax_name = _OTHER_**.

For example, the lineage of taxid 2315236 is “cellular organisms; Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; unclassified Burkholderiales; Burkholderiales Genera incertae sedis; Aquabacterium; Aquabacterium pictum”. The lineage encoding is in Listing 1.

```

00-00: Bacteria <prokaryotes>
00-01: Bacteria <prokaryotes>
00-02: Bacteria <prokaryotes>
00-03: Bacteria <prokaryotes>
00-04: Bacteria <prokaryotes>
00-05: Bacteria <prokaryotes>
01-00: Bacteria <prokaryotes>
01-01: Bacteria <prokaryotes>
01-02: Bacteria <prokaryotes>
01-03: Bacteria <prokaryotes>
01-04: Bacteria <prokaryotes>
01-05: Bacteria <prokaryotes>
02-00: Bacteria <prokaryotes>
02-01: Bacteria <prokaryotes>
03-00: Bacteria <prokaryotes>
04-00: Proteobacteria
04-01: Proteobacteria
04-02: Proteobacteria
04-03: Proteobacteria
05-00: Proteobacteria
05-01: Proteobacteria
05-02: Proteobacteria
05-03: Proteobacteria
05-04: Proteobacteria
05-05: Proteobacteria
05-06: Proteobacteria
06-00: Proteobacteria
06-01: Proteobacteria
06-02: Proteobacteria
06-03: Proteobacteria
06-04: Proteobacteria
06-05: Proteobacteria
06-06: Proteobacteria
06-07: Proteobacteria
06-08: Proteobacteria
06-09: Proteobacteria
06-10: Proteobacteria
06-11: Proteobacteria
07-00: Betaproteobacteria
07-01: Betaproteobacteria
07-02: Betaproteobacteria
07-03: Betaproteobacteria
07-04: Betaproteobacteria
07-05: Betaproteobacteria
07-06: Betaproteobacteria
07-07: Betaproteobacteria
08-00: Betaproteobacteria
08-01: Betaproteobacteria
08-02: Betaproteobacteria
08-03: Betaproteobacteria
09-00: Betaproteobacteria
09-01: Betaproteobacteria
09-02: Betaproteobacteria
09-03: Betaproteobacteria
10-00: Betaproteobacteria
10-01: Betaproteobacteria
10-02: Betaproteobacteria
10-03: Betaproteobacteria
10-04: Betaproteobacteria
10-05: Betaproteobacteria
10-06: Betaproteobacteria
10-07: Betaproteobacteria
10-08: Betaproteobacteria
11-00: Betaproteobacteria
11-01: Betaproteobacteria
12-00: Betaproteobacteria
12-01: Betaproteobacteria
13-00: Burkholderiales
13-01: .OTHER_
13-02: .OTHER_
13-03: .OTHER_
13-04: .OTHER_
13-05: .OTHER_
13-06: .OTHER_
14-00: .OTHER_
14-01: .OTHER_
14-02: .OTHER_
14-03: .OTHER_
15-00: .OTHER_
15-01: .OTHER_
15-02: .OTHER_
15-03: .OTHER_
15-04: .OTHER_
16-00: .OTHER_
16-01: .OTHER_
16-02: .OTHER_
17-00: .OTHER_
17-01: .OTHER_
18-00: .OTHER_
18-01: .OTHER_
18-02: .OTHER_
18-03: .OTHER_
19-00: .OTHER_
19-01: .OTHER_
19-02: .OTHER_
19-03: .OTHER_
19-04: .OTHER_
20-00: .OTHER_
20-01: .OTHER_
21-00: .OTHER_
21-01: .OTHER_
22-00: Aquabacterium
22-01: Aquabacterium
22-02: Aquabacterium
22-03: Aquabacterium
23-00: Aquabacterium
23-01: Aquabacterium
23-02: Aquabacterium
24-00: Aquabacterium
24-01: Aquabacterium
25-00: Aquabacterium
25-01: Aquabacterium
26-00: Aquabacterium pictum
26-01: Aquabacterium pictum
26-02: Aquabacterium pictum
26-03: Aquabacterium pictum
26-04: Aquabacterium pictum

```

Listing 1: Encoded lineage for *Aquabacterium pictum*.

NCBI taxon id	Taxon name	Rank name	Rank number	Subrank number
8287	<i>Sarcopterygii</i>	superclass	6	0
1338369	<i>Dipnotetrapodomorpha</i>	-	-	1
32523	<i>Tetrapoda</i>	-	-	2
32524	<i>Amniota</i>	-	-	3
8457	<i>Sauropsida</i>	-	-	4
32561	<i>Sauria</i>	-	-	5
1329799	<i>Archelosauria</i>	-	-	6
8492	<i>Archosauria</i>	-	-	7
436486	<i>Dinosauria</i>	-	-	8
436489	<i>Saurischia</i>	-	-	9
436491	<i>Theropoda</i>	-	-	10
436492	<i>Coelurosauria</i>	-	-	11
8782	<i>Aves</i> (birds)	class	7	0

Table 11: Example of a taxonomic lineage with subranks: birds.

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