TFAM 1.0: an online tRNA function classifier

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ABSTRACT

We have earlier published an automated statistical classifier of tRNA function called TFAM. Unlike tRNA gene-finders, TFAM uses information from the total sequences of tRNAs and not just their anticodons to predict their function. Therefore TFAM has an advantage in predicting initiator tRNAs, the amino acid charging identity of nonstandard tRNAs such as suppressors, and the former identity of pseudotRNAs. In addition, TFAM predictions are robust to sequencing errors and useful for the statistical analysis of tRNA sequence, function and evolution. Earlier versions of TFAM required a complicated installation and running procedure, and only bacterial tRNA identity models were provided. Here we describe a new version of TFAM with both a Web Server interface and simplified standalone installation. New TFAM models are available including a proteobacterial model for the bacterial lysylated isoleucine tRNAs, making it now possible for TFAM to correctly classify all tRNA genes for some bacterial taxa. First-draft eukaryotic and archaeal models are also provided making initiator tRNA prediction easily accessible genes to any researcher or genome sequencing effort. The TFAM Web Server is available at http://tfam.lcb.uu.se

INTRODUCTION

The vast majority of new tRNA gene sequence data accumulates today from analysis of genome sequences. The major tRNA gene-finders in use today, tRNAscan-SE (1) and ARAGORN (2), classify the functions of predicted tRNA genes by structurally locating and decoding their inferred anticodons according to an assumed genetic code. As a result, genome projects regularly misclassify initiator tRNAs in genomes from all three phylogenetic domains and lysylated isoleucine tRNA (kIle) genes from bacteria (described further below). These two types of tRNAs carry the same genetically templated anticodons as methionine elongators and hence cannot be distinguished from them by anticodon-based tRNA classifiers. It may also happen that these genes are entirely missing in the annotation of a complete genome. Because genome projects regularly verify the completion of their assemblies by checking for the presence of a complete set of tRNA gene classes in their genome data, the ability to identify these two additional classes of tRNA genes provides additional power for this important task [although in very rare cases the lysylated isoacceptor may be missing along with corresponding metabolic pathways (3)]. Furthermore, a method that uses entire sequence information to classify tRNA gene function is more robust to sequencing error, can correctly predict tRNA charging specificity in organisms with altered genetic codes, can predict the identity of suppressors, and can predict the potential or former charging identity of tRNA-like molecules and pseudotRNAs (in this article we loosely use “tRNA” to mean both tRNA and tRNA gene sequences).

We present here a new version (1.0) of such a method—an update to the TFAM statistical classifier of tRNA function published earlier (4). TFAM 1.0 is now available online as a Web Server requiring no installation. Version 1.0 of TFAM also provides eukaryotic and archaeal tRNA functional models for the purpose of identifying initiator tRNAs, and an expanded bacterial model that can predict some kIle tRNAs. For certain bacterial species such as proteobacteria and gram-positive bacteria, TFAM 1.0 can be expected to correctly annotate the function of all tRNAs with good confidence.

In bacteria, the cytidine in the CAU anticodons of lysylated isoleucine tRNAs are post-transcriptionally modified to lysidine (5). This modification simultaneously changes the codon reading specificity of this usually minor isoacceptor from AUG to AUA and its amino acid charging specificity from methionine to isoleucine in keeping with the genetic code. Because the unmodified (CAU) tRNA is charged with methionine (6) it cannot be expected that TFAM would recognize this tRNA as an isoleucine tRNA. However, the determinants that target this tRNA for post-transcriptional modification are themselves genetically templated in the tRNA gene (7,8), and it is possible for TFAM to distinguish this class of tRNA with fairly good confidence when suitably trained (3). Nonetheless, both experimental (8) and bioinformatic (3) evidence suggest that the determinants for this class have diverged in bacteria. Rather than iteratively acrering all
dissimilar sequences of the same apparent type into one model class (3), we have taken a different, perhaps more conservative approach of making smaller, more phylogenetically restricted models, in the hopes that this will allow us to study the evolution and diversification of tRNA identity determinants. Our ultimate aim is to model and understand the constellation of identity determinants that actually can or could function together in the same cellular context. In TFAM 1.0 we release a model of lysylated isoleucine tRNAs based only on proteobacterial data.

Earlier versions of TFAM were only available for standalone compilation and installation on UNIX-like platforms and required complicated installations of prerequisites. The new web-based interface, besides obviating the installation burden, provides additional functionality over the standalone interface including color visualization and sorting of TFAM scores. Installation of the standalone version has also been simplified by the removal of dependencies.

MODELS

Both the Web Server and standalone interfaces to TFAM version 1.0 provide new models for tRNA classification. The bacterial model of earlier versions (earlier called 'MSDB' for 'Modified Sprinzl DataBase' and provided with TFAM versions 0.2 and 0.3, henceforth 'bacterial TFAM model 0.1') has been complemented and corrected by genomic tDNA sequences from 46 proteobacterial species classified on the basis of clustering to known methionine elongator, unmodified isoleucine elongator, initiator and lysylated isoleucine (kIle) elongator tRNAs. This data, generously provided by Paul Higgs and available here as Supplementary Data to this article, is an extension to the dataset analyzed in (9). These sequences and their classifications are a consistent subset of those provided in an independently made TFAM model (3). A full description of how we used these proteobacterial sequences to modify bacterial TFAM model 0.1 from (4) is provided as Supplementary Data here and at the TFAM Web Server. The model presented here is called 'bacterial TFAM model 0.2'.

Bacterial TFAM model 0.2 also provides the five selenocysteine sequences from the year 2000 release of the Sprinzl Search Server http://www.uni-bayreuth.de/departments/biochemie/trna/, that were removed in bacterial TFAM model 0.1. A leave-one-out cross-validation of bacterial TFAM model 0.2 without selenocysteine tRNAs misclassified 16 of 759 sequences (2.1%) of which 2 of 50 kIle tRNAs were misclassified (96% sensitivity) and 2 of 50 sequences classified as kIle were not kIle (96% specificity). These results were identical to those provided in an independently made TFAM model 0.1 from (4) is provided as Supplementary Data here and at the TFAM Web Server. The model presented here is called 'bacterial TFAM model 0.2'.

In TFAM 1.0 we introduce first-cut versions of eukaryotic and archaeal TFAM models, each given version numbers 0.1, with the main purpose of enabling convenient and automated initiator tRNA identification in all phylogenetic domains. Initiator tRNA determinants are highly conserved within phylogenetic domains (10). Both of these models were created from data downloaded on February 23, 2006 from the Sprinzl 2000 tRNA Search Server http://www.uni-bayreuth.de/departments/biochemie/trna/. For the eukaryotic TFAM model 0.1, redundant sequences were removed and no corrections were made to the identity annotations. The sensitivity of eukaryotic TFAM model 0.1 for detecting known initiator tRNAs in Drosophila melanogaster was verified to be perfect. Initiator tRNA predictions with eukaryotic TFAM model 0.1 in twelve Drosophila genomes have been released on the web at http://www.bioinf.manchester.ac.uk/bergman/data/ncRNA/tRNA/. Resubstitution analysis showed that all training data initiators from the Sprinzl 2000 dataset were correctly classified, including those from yeast, worm, flies, vertebrates and plants.

For the archaeal TFAM model 0.1, redundant sequences were removed and the identity annotations of three tRNAs were changed as described in Supplementary Data. The initiator tRNA sequences were verified to be consistent with other archaeal initiator identity determinants as described (11). We also verified the perfect performance of this model on two experimentally characterized archaeal initiator tRNA genes not included and differing in sequence from those in the model: those of Pyrococcus occultum (12) and Pyrococcus abyssi (13). The accuracy of the eukaryotic and archaeal TFAM models 0.1 for other tRNA type has not been verified or studied in any way.

RESULTS AND DISCUSSION

A user can input tRNA or tDNA sequences in multi-fasta format to the TFAM Web Server by cut-and-paste or file-upload, select a model with which to classify the input sequences, and then push a button to run the server. The browser window will wait while the computation takes place, after which the output is loaded in tabular format. A computation on 514 human tRNA sequences from the Genomic tRNA Database (GtRDB, http://lowelab.ucsc.edu/GtRNAdb/) took ~50s. The maximum input size is currently set to 200 KB, which accommodates more than 1300 tRNA sequences at once.

A sample output on bacterial tRNA sequences is shown in Figure 1. Scores are visualized with a color scheme increasing from dark purple for negative numbers of large magnitude to bright red for large positive numbers. The table can be sorted by any column making it easy to find sequences with properties of interest. In addition, TFAM can indicate when its prediction conflicts with an annotated function. To get this functionality, the user may either name sequences with identifiers from which the annotated sequence can be parsed by TFAM, or TFAM can auto-detect anticodons and use these to annotate identity. A table of recognized sequence identifier formats is shown in Supplementary Data as well as in the Web-Server documentation. TFAM recognizes the format of identifiers from the GtRDB and the Sprinzl database (14) from which sequences may be pasted directly.
As described more fully in (4), TFAM works by structurally aligning the input sequences with the trusted model sequences using COVE software (15) and tRNA covariance models from (1). It then makes profiles of each model class and scores each input sequence according to the log-odds of belonging to a specific functional class versus belonging to any of the others. This log-odds computation is repeated for every functional class represented in the model. A positive score indicates a match to a particular functional class. The TFAM classification of a tRNA sequence is the functional class against which it has the highest score.

All results of TFAM computations are available for download from the Web Server including a structural alignment of their sequences (in aligned multi-fasta format) with TFAM classifications in the description line. The user is also provided a job ID with which she may return to the server for some unspecified time after visiting the Web Server and recover the results of their computation. Job IDs are not in any way public, so only users with a specific job ID in hand can recover results from that job. Jobs may be stored on the server for some unspecified time and then deleted, therefore it is safest to download results after computation. For more data privacy, the user may completely delete the data from our server after downloading their results. We log user-statistics but do not store any data input to the server for private use.

The tRNA structural alignment service of the TFAM Web Server may be useful in its own right. If the TFAM Web Server is used exclusively for this purpose users should additionally cite COVE software (15) and the tRNA covariance models from (1).

Figure 1. Sample output of the TFAM Web Server for tRNA genes from Escherichia coli K12. Colors indicate the magnitude and sign of the scores of each sequence to different tFAM models. Initiator tRNAs are sorted to the top of the table by clicking on the ‘iMet’ column header.
Currently the Web Server does not support uploading of custom tRNA classification models or the exclusion of certain positions from scoring such as the anticodon. However, these functionalities are available in the standalone version which is available free for download and obtainable through http://tfam.lcb.uu.se

TFAM results should not be used blindly. We emphasize that TFAM classifications are statistical and depend on the quality of trusted classifications that are used to make the models. Different models and even different ‘tfams’ for different functional classes vary in their statistical power and generality. We have provided a guide to the intended use of every component of every model available at the TFAM Web Server, and we also refer to earlier provided statistical results (4). To briefly summarize here, TFAM is not strong at distinguishing alanine and valine tRNAs in bacteria. The selenocysteine model is not very general and can fail to recognize true Sel-Cys tRNAs, nonetheless, the model is useful to distinguish falsely predicted Sel-Cys tRNAs such as called by tRNAscan-SE for firmicutes with an altered genetic code (data not shown). The kIle model is proteobacterial and does not score well for kIle tRNAs from Cyanobacteria, Bacteroidetes, Aquificae, Actinobacteria, Chlamydia/Verrucomicrobia group, Planctomycetes or Thermotogae [data not shown, but see also (3)]. This is probably because the determinants for this class are divergent in bacteria, the subject of our current research. Finally, the eukaryotic and archaeal TFAM 0.1 models are provided only for the purpose of initiator tRNA identification.

We plan major refinements and expansions of the TFAM models, including specializing them to more narrow phyla, towards the goal of general models that nonetheless accurately represent the actual constellation of identity determinants and antideterminants that function together in the context of a specific translational system. In the meantime, we believe that the model quality and ease of use of the TFAM 1.0 Web Server can promote practical improvements in the annotation of tRNA genes in genome projects and encourage computational biological research in tRNA structure, function and evolution already today.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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