

NemMitoMapper

An automated, heuristic, annotation tool for the complete mitochondrial genomes of Nematodes

Aaron Jex, Ross Hall, Robin Gasser

NemMitoMapper is an automated annotation tool for mitochondrial genomes of Nematodes. NemMitoMapper uses a number of search parameters to accurately and rapidly determine the identity, position and boundaries of all protein coding, ribosomal and transfer rRNA genes.

The boundaries for coding genes are determined by comparative linear alignment using a reference sequence representing the a published mitochondrial genome for one of the species listed below. Each coding gene is located using the inferred amino acid sequence of the corresponding gene from the reference species, and step-wise alignment searching of the queried genome in all six reading frames (3 forward and 3 reverse). Identity is determined by BLOSSUM identity score, and boundaries are determined initially by peptide length and then refined by identification of known Nematode mitochondrial genomic start and stop codons. Ribosomal RNA genes are identified using a similar approach, using nucleotide sequences only. Please note that the closer the evolutionary relationship is between the species from which the queried genome has been derived and the species used as a reference the more accurate the annotation is likely to be.

Transfer rRNA genes are determined by a three part process, combining predicted secondary structure, anti-codon identity and comparative alignment against a database representing all published nematode tRNA genes.

Sequences may be loaded (in FASTA format) into NemMitoMapper either using the text window below (copy and paste), or uploaded as a plain text file from the user's computer. Presently NemMitoMapper can analyse up to 200 mt genomes per job. Analysis time will be dependent upon the number of sequences. An average analysis time of approximately 2 minutes per genome should be expected.

Notification of a completed analysis will be sent to the user-specified email address. Results will be obtainable from a use-specific ftp site (assigned upon completion of the analysis). All data will be stored on a secure server for 48 hours.

Data output includes a FASTA sequence (rotated to cox1) of the queried mt genome, a SEQUIN table containing all gene boundaries, and graphic files for showing the secondary structure of each identified tRNA gene (in scalable vector graphics (.svg) and published document file (.pdf) format).

To view and manipulate .svg files, user's are directed to the free-ware program Inkscape.

Paste FASTA format sequence(s) here (Max 200). Please ensure each sequence is labelled with a unique 10 character code.

Or upload FASTA format sequence(s) as a plain text file (Max 200 sequences per file) directly

Browse

Email address (Email address will exclusively be used notify the user of the completion of their analysis)

Please select the most appropriate reference sequence from the list below

Ancylostoma caninum
Ancylostoma duodenale
Anisakis simplex
Ascaris suum
Bunostomum phlebotomum
Caenorhabditis elegans
Dictyocaulus filarial

Select

Change

Submit sequence(s)

Thank you for using NemMitoMapper. You will be notified when you analysis is complete.

In publications using NemMitoMapper, please cite:

Aaron Jex, Ross Hall, Robin Gasser (2010). "NemMitoMapper: an accurate and rapid heuristic annotation tool for the mitochondrial genomes of Nematodes. *Some Bioinformatic Journal*, xxx-xxx.

For technical support, please contact ajex@unimelb.edu.au