

Bioinfo Project

Bioinformatics should be a tool for biologist. The best way to learn it is by using it with the right motivation - “**learning by doing**”. Think of a problem that interests you and/or might be of relevance to you. Instead you can also pick a problem from the list of suggested ideas.

Bioinfo Project - Report structure

(a) Header - Title, date and name.

(b) Aim - Give a brief introduction into the system and describe the aim of the project. This is the biological part or the report.

(c) Application flow - What do you need and what are you going to use in order to answer your question. Work out a application flow and list all the program and database your are going to use.

**(d) Protocol - Start processing you data or writing your program. Include intermediate results,
write down application parameters, and/or describe problems.**

(e) Results and Discussion - Summarize your outcome(s) and talk about next steps.

Bioinfo Project - rRNA in Bacteria




Questions:

- a) number of complete rRNA sequences (16S-23S-5S) per genome
- b) size variation of the rRNA region (e.g. 16S, ITS1, 23S, ITS2, 5S)
- c) sequence variation of ITS1 and ITS2 region within a bacteria
- d) phylogenetic analysis using the 16S region

Source:

Use the CMR (Comprehensive Microbial Resource) database to obtain genome information.

Bioinfo Project - rRNA in Bacteria



Comprehensive Microbial Resource

Search for

[Home](#) [Genome Tools](#) [Searches](#) [Comparative Tools](#) [Lists](#) [Downloads](#) [Carts](#)

[CMR Manual](#) | [CMR FAQ](#) | [CMR Tutorial](#) | [Links](#)

Genome Search

Organism name:

Genome List

[View All CMR Genomes](#)

Gene Search

Search by:

Match: Exact Inexact

Keywords/Accession:

Data Summary

	Complete	Draft	Totals
Bacteria	608	64	672
Archaea	48	0	48
Viruses	3	0	3
Totals	659	64	723

Welcome to the Comprehensive Microbial Resource

The Comprehensive Microbial Resource (CMR) is a free website used to display information on all of the publicly available, complete prokaryotic genomes. In addition to the convenience of having all of the organisms on a single website, common data types across all genomes in the CMR make searches more meaningful, and cross genome analysis highlight differences and similarities between the genomes. A [CMR Mirror](#) site maintained by the Genome Encyclopedia of Microbes ([GEM](#)) in Korea is also available. [\[More Information\]](#) [\[Publication Information\]](#)

CMR Menu Bar Tools

CMR offers a wide variety of tools and resources, all of which are available off of our menu bar at the top of each page. Below is an explanation and link for each of these menu options. First time users can use our [CMR tutorial](#) to learn how to navigate this site.

- ▶ **Genome Tools**
Find organism lists as well as summary information and analyses for selected genomes.
- ▶ **Searches**
Search CMR for genes, genomes, sequence regions, and evidence.
- ▶ **Comparative Tools**
Compare multiple genomes based on a variety of criteria, including sequence homology and gene attributes. SNP data is also found under this menu.
- ▶ **Lists**
Select and download gene, evidence, and genomic element lists.
- ▶ **Downloads**
Download gene sequences or attributes for CMR organisms, or go to our FTP site.
- ▶ **Carts**
Select genome preferences from our Genome Cart or download your Gene Cart genes.

Additional Resources

- [CMR Web Usage Statistics](#)
- [CMR Updates Schedule](#)
- [JCVI Annotation SOPs](#)
- [Data Release Control](#)
- [History of CMR News](#)
- [JCVI Role Ids](#)
- [PANDA Release](#)

Announcements

Recent News

NEW! January 21, 2010
Data Release [24.0](#) is now available. 150 new genomes have been added to the CMR.

March 31, 2009 Data Release [23.0](#) is now available. 116 new genomes have been added to the CMR.

Latest Releases

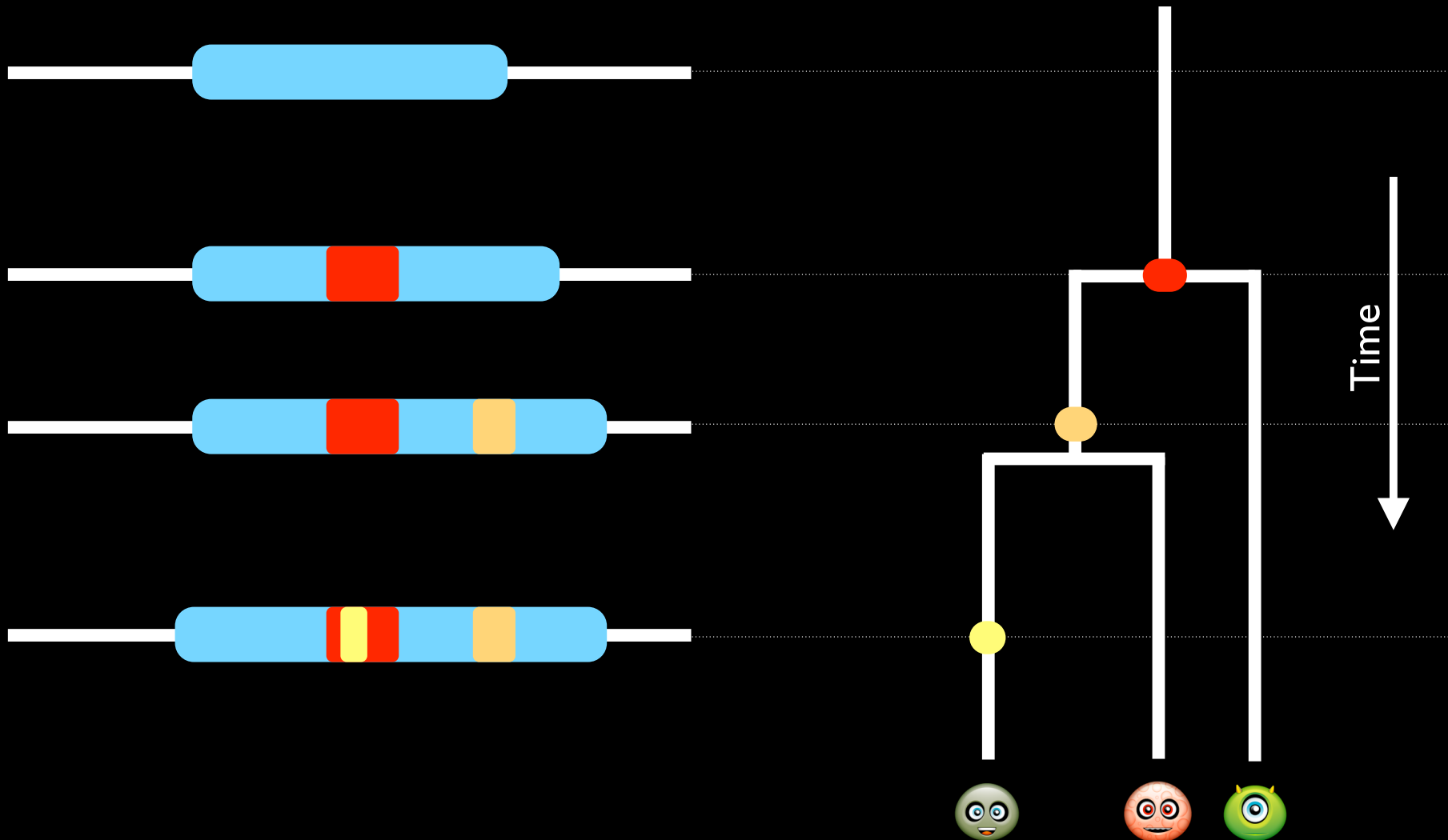
Data Release: [23.0](#)
Website Release: [3.0](#)

Contact Us

Can't find what you are looking for on the site? Want to alert us to new news or tools? Please [contact us](#).

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Bioinfo Project - TEs




Bioinfo Project - TEs

- a) Download for example the human TRF1 gene sequence and run RepeatMasker to determine the location and variation of TEs. Compare the results with a genome browser.**

- b) Find a group of TEs (e.g. LINE) in primates and compare their history with that one of the hosts.**

Bioinfo Project - Molecular Biology

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- a) Develop a way to estimate the number of cutting sites for a (bacteria) genome.
 - b) Find rare cutters for a particular genome.
 - c) Find microsatellite motives in a published genome and design sets of primers.

Bioinfo Project - Genome Evolution

- a) Compare a genome region from two species. For example find well conserved genes and compare gene orientation and intergenic region between the two genomes.**
- b) Compare two genes/regions that are next to each other on the chromosome and compare divergence. For example use a telomere associated gene and the neighboring gene in the Drosophila genome.**
- c) Choose a gene from the database. You download the coding region of the gene for two individuals (e.g. human and macaque). You align the sequences and compare the differences at different codon positions.**
- d) Find duplicated genes in genomes and try to find ways to determine their history.**