

# Infernal-1.1.2

## Rationale:

Infernal ("INFERence of RNA ALignment") is for searching DNA sequence databases for RNA structure and sequence similarities. It is an implementation of a special case of profile stochastic context-free grammars called covariance models (CMs). A CM is like a sequence profile, but it scores a combination of sequence consensus and RNA secondary structure consensus, so in many cases, it is more capable of identifying RNA homologs that conserve their secondary structure more than their primary sequence.

1. Input data:
  - a. Fasta file

## Test run:

Please run Infernal app with the test data located at Community Data > iplantcollaborative > example\_data > Infernal (/iplant/home/shared/iplantcollaborative/example\_data/Infernal)

1. Input data:
  - a. Fasta file: mrum-genome.fa

Please work through the documentation and add your comments on the bottom of this page, or click the intercom button on this page.

## References

- <http://eddylab.org/infernal/>