



# The Laboratory for RNA-Based Lifeforms

## **Problem #02:** INFERNAL Acceleration

INFERNAL ([eddylab.org/inferral](http://eddylab.org/inferral)) is an application for identifying RNA secondary structures using evolutionary covariation models. It is CPU-intensive and thus does not scale to ultra-large scale analysis efficiently.

By *any means necessary*, accelerate INFERNAL's single-core search for Delta Ribozyme (<https://rfam.org/family/RF00094>) on raw (fastq) sequence data, without a loss to sensitivity. Objective is to reach >10x acceleration.

- **Murray** Positive Control Dataset (SRR2136906)
- **Frank** Negative Control Dataset (ERR2756788)
- **Baseline Command** (INFERNAL v1.1.4)

```

```
# INFERNAL cmsearch "BASELINE"  
time cmsearch \  
-o "$OUTNAME.out" \  
-A "$OUTNAME.outA" \  
--cpu 1 -Z 1000 \  
--incE 0.1 \  
--tblout "$OUTNAME.outT" \  
$CM_MODEL \  
$QUERY_FQ
```

```