

# ParsEvalMPI: comparison of gene structure annotations in parallel

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Bioinformatics and Computational Biology

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# Gene prediction (annotation)

## Input

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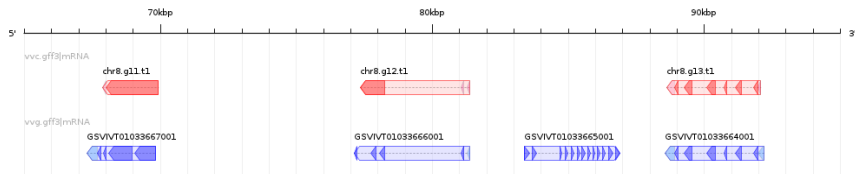
String representing DNA sequence

## Output

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Regions (coordinates) of sequence that correspond to genes and their structural components

# Comparing annotations



# Previous implementation

## ParsEval

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- written in Perl

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- serial execution: run time in minutes to hours

# New implementation

## ParsEvalMPI

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- written in C



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# Program overview

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- delegation

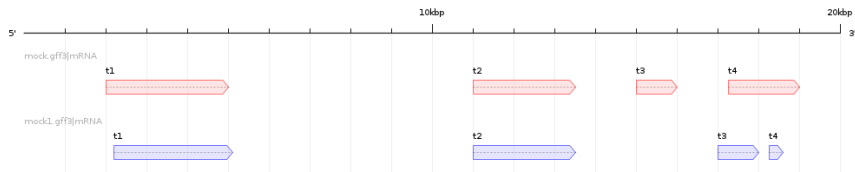
# Program overview

- delegation
- local analysis

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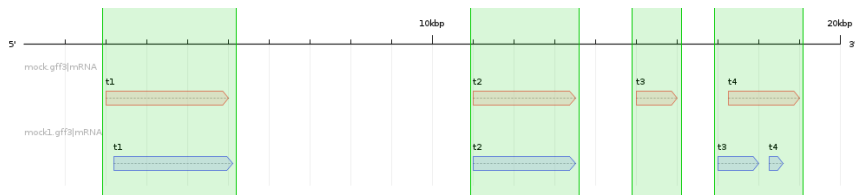
- delegation
- local analysis
- global analysis

# Delegation

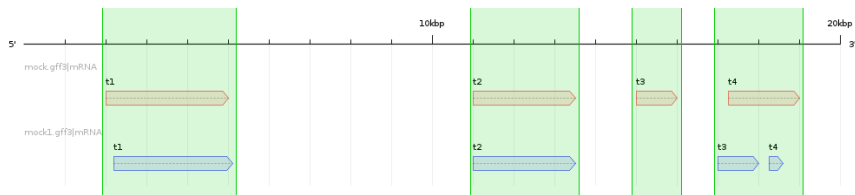




# Delegation

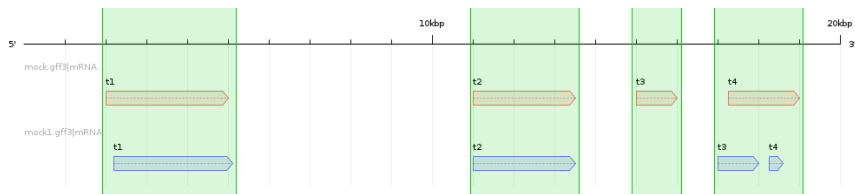


# Delegation



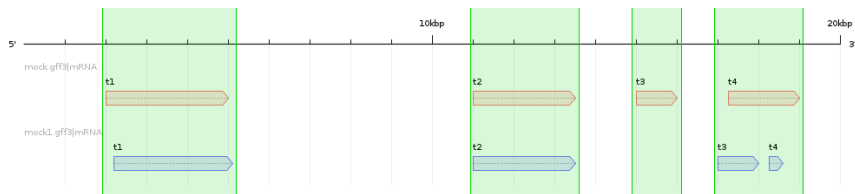
- 1 all data on all processors

# Delegation



- 1 all data on all processors
- 2 even distribution of DNA

# Delegation



- 1 all data on all processors
- 2 even distribution of DNA
- 3 even distribution of genes

# Local and global analysis

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  - analyze local vector, print scores
- Global analysis



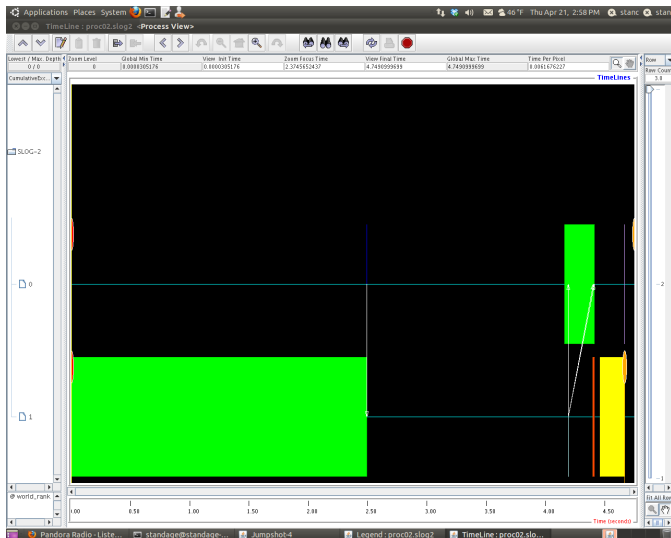
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- Local analysis
  - generate local model vector
  - send local vector to global vector on root processor
  - analyze local vector, print scores
- Global analysis
  - receive local vectors from each processor

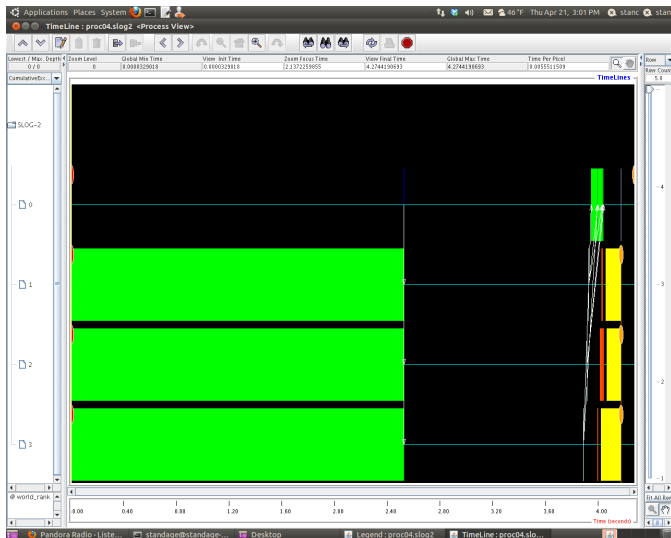
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- Local analysis
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  - analyze local vector, print scores
- Global analysis
  - receive local vectors from each processor
  - analyze combined global vector, print scores

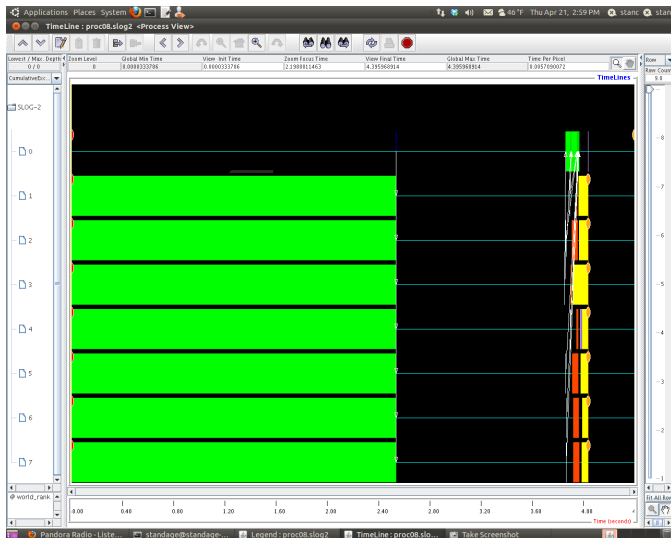
# Load balancing



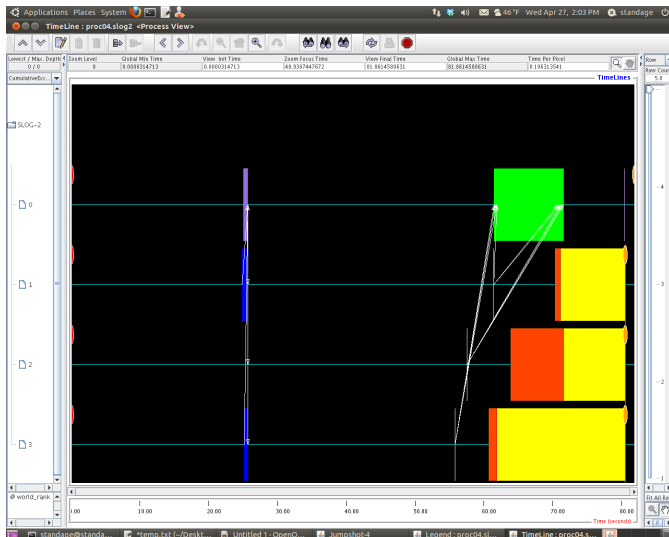
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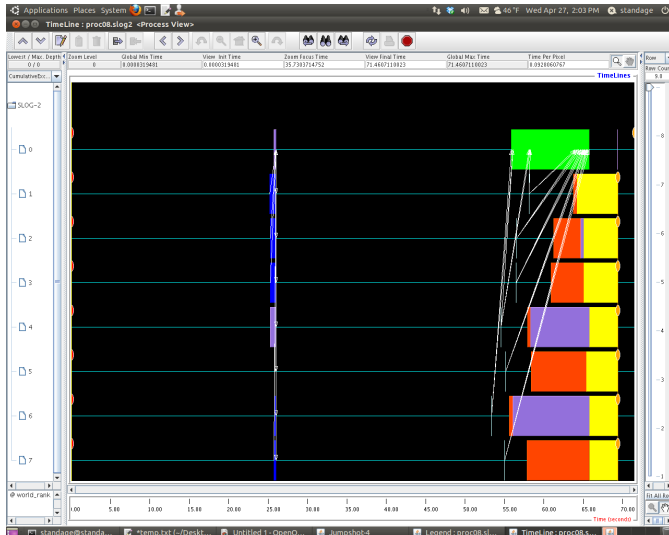
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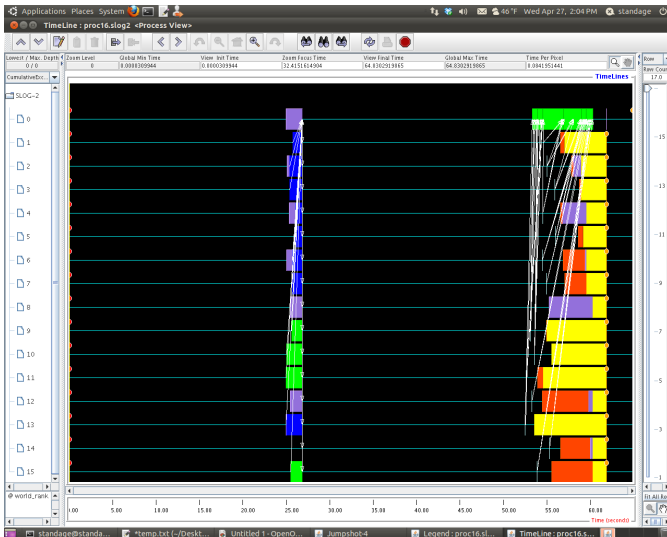
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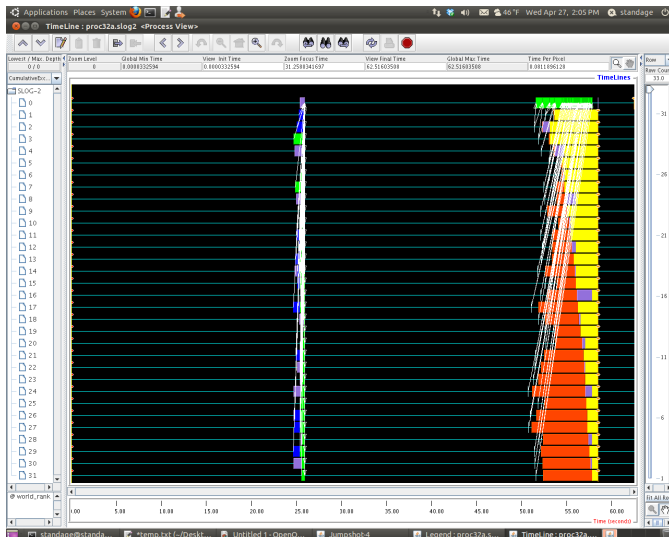


## Load balancing

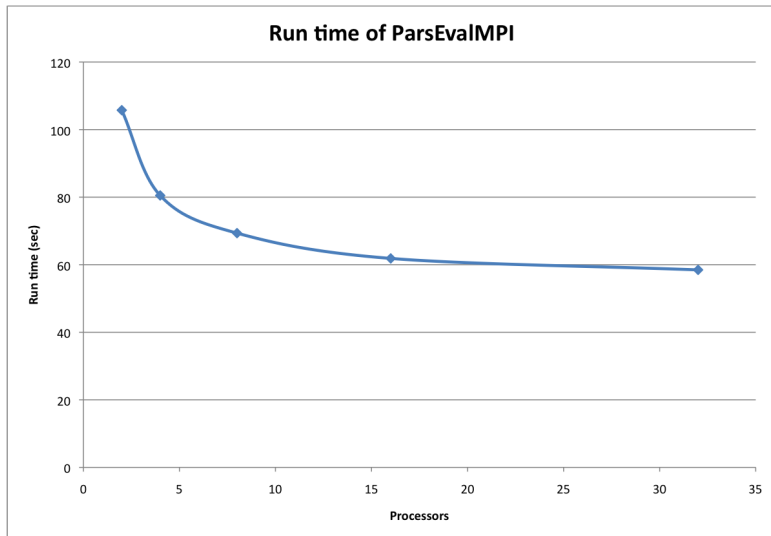




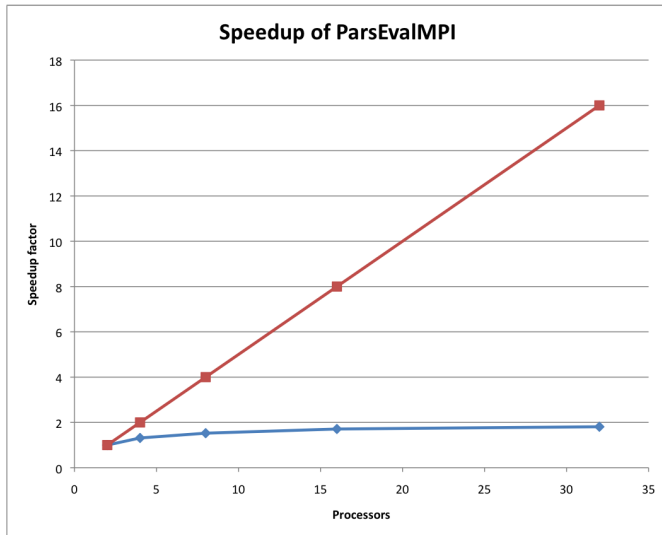
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# Scalability



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# Serial optimization

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  - static arrays

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  - pointers, dynamic arrays
  - dynamic data structures

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  - static arrays
- Bad
  - pointers, dynamic arrays
  - dynamic data structures
- Ugly
  - copying data

# Conclusions



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- Very poor scaling properties
  - maximum scaling factor of 2?!?!?
  - perhaps try OpenMP
- Significant improvement