

# Bcheck Introdemo

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**Theoretical Biochemistry Group**

17-01-09

# Outline

## 1 Introduction

# Outline

1 Introduction

2 Method

# Outline

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3 Result

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1 Introduction

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3 Result

4 Demo

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1 Introduction

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4 Demo

5 Conclusion

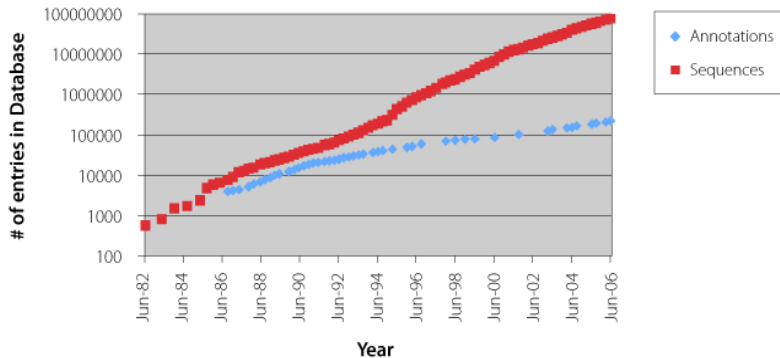
# Outline

- 1 Introduction
- 2 Method
- 3 Result
- 4 Demo
- 5 Conclusion
- 6 Outlook

# Sequencing Speed vs. Annotation Speed

- $841 - 728 = 113$

## Growth of sequences and annotations since 1982

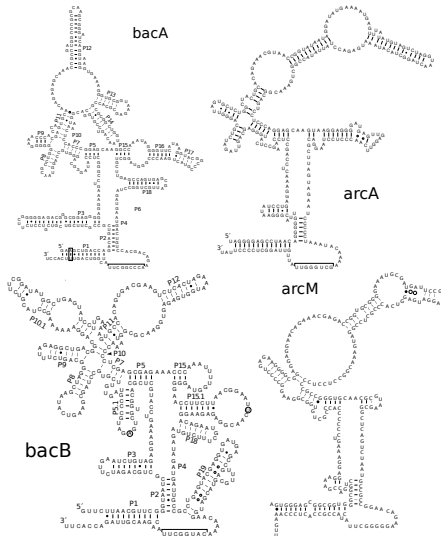




## Abundant ncRNAs

”nearly the entire genome may be represented in primary transcripts that extensively overlap and include many non-protein-coding regions.”

# Microevolution of ncRNA



# ncRNA Annotation Tools

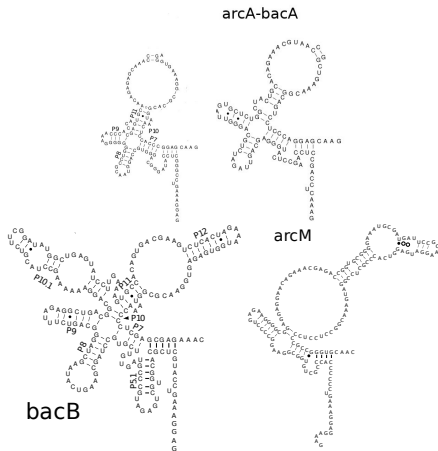
- conserved information  $\rightarrow$  search  $\rightarrow$  evaluate  $\rightarrow$  prediction
  - De novo: RNAz
  - General approaches
    - BLAST
    - infernal
    - rnabob
- Wrapper: tRNAscan-SE(1997)

# Wrappers for ncRNA Detection

- Tools
  - speed
  - accuracy
  - classification
- Applicable to ncRNA families
- Pipeline: patterns  $\rightarrow$  cm  $\rightarrow$  hit
  - evaluation: pipeline; E
- Conserved information
  - classification
  - sufficient and diverse testset

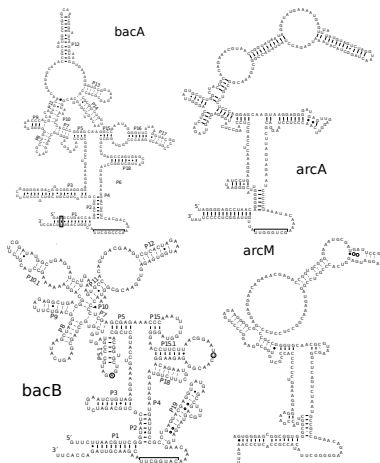
# Patterns

- classification: S-domain ss



## CMs

- classification: rnpB ss&seq

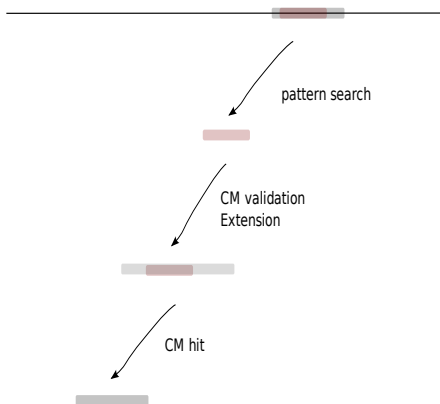


# Alignment

- Divide and manual alignment



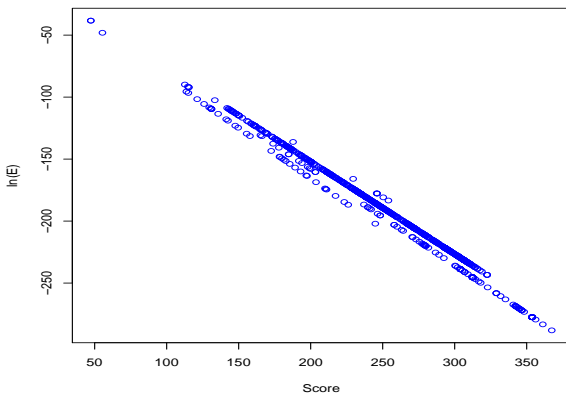
# Bcheck Workflow



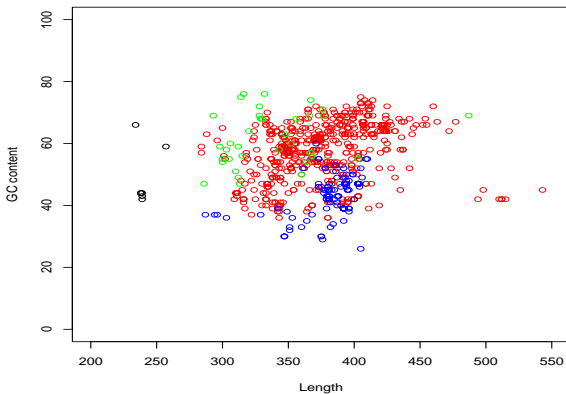


# Hits

- 814 out of 841
- 200min with 2.26GHz CPU



# GC & length of rnpB



# Bcheck Demo

Demo

# Conclusion

- Sensible classification for sensible conserved information
- Bcheck: speedy, accurate, makes classification

# Outlook

- Additional conserved information
- Rcheck

# Thanks!

- Ivo
- Richard
- Andy
- Christian
- TBI