TSEBRA

Integrating various extrinsic evidence sources for more accurate genome annotation with BRAKER

Plant and Animal Genomes XXIX
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Overview

1. BRAKER: Automated Whole-Genome Annotation

2. TSEBRA: Transcript Selector for BRAKER

3. Long-Read Integration Using GeneMarkS-T and TSEBRA

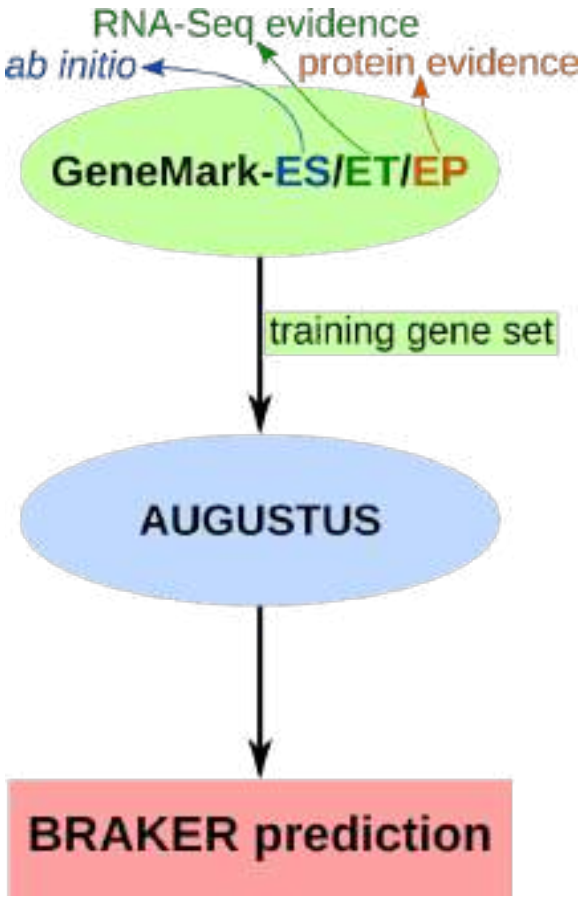
BRAKER - Overview

BRAKER

- Automated genome annotation of novel eukaryotic genomes
- Integrates extrinsic evidence from short-read RNA-Seq or homologous proteins

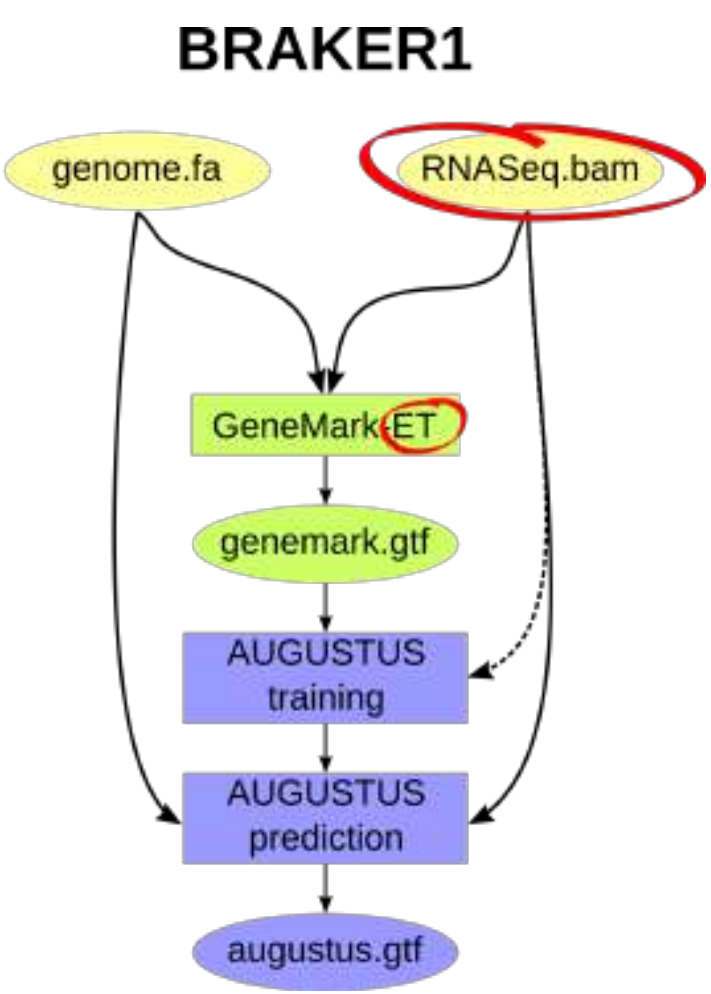
Gene Prediction Tools

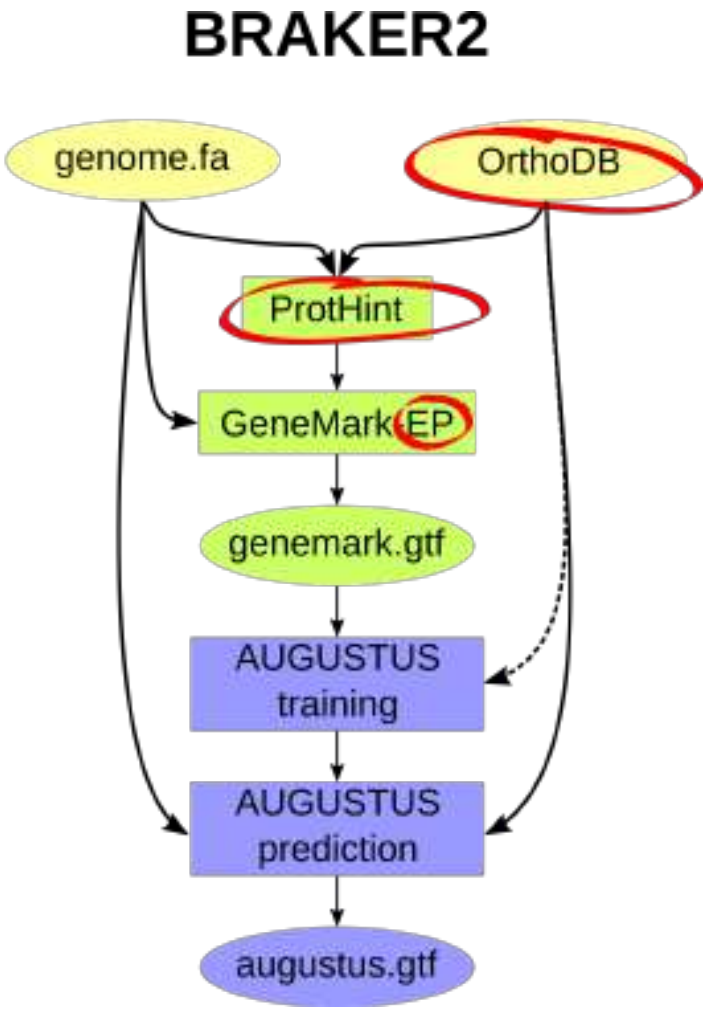
- **GeneMark**: suite of self-training methods
- **AUGUSTUS**: highly accurate method that requires a training gene set



Hoff et al. 2016. *Bioinformatics*. 32(5):767–9.
Brůna, Hoff et al. 2021. *NAR Genomics and Bioinform.* 3(1):lqaa108.

BRAKER - Genome Annotation Protocols

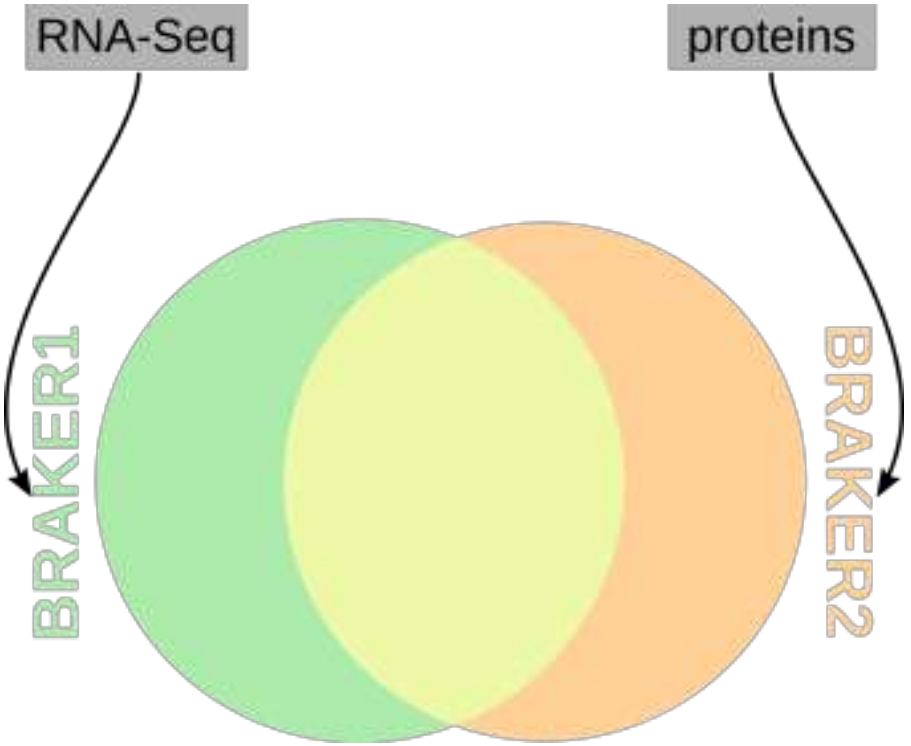




TSEBRA - Combiner for BRAKER

Goal

- BRAKER annotation with RNA-Seq and protein evidence
- Achieve higher accuracy than BRAKER1 and BRAKER2



Transcript set comparison for different gene predictions.

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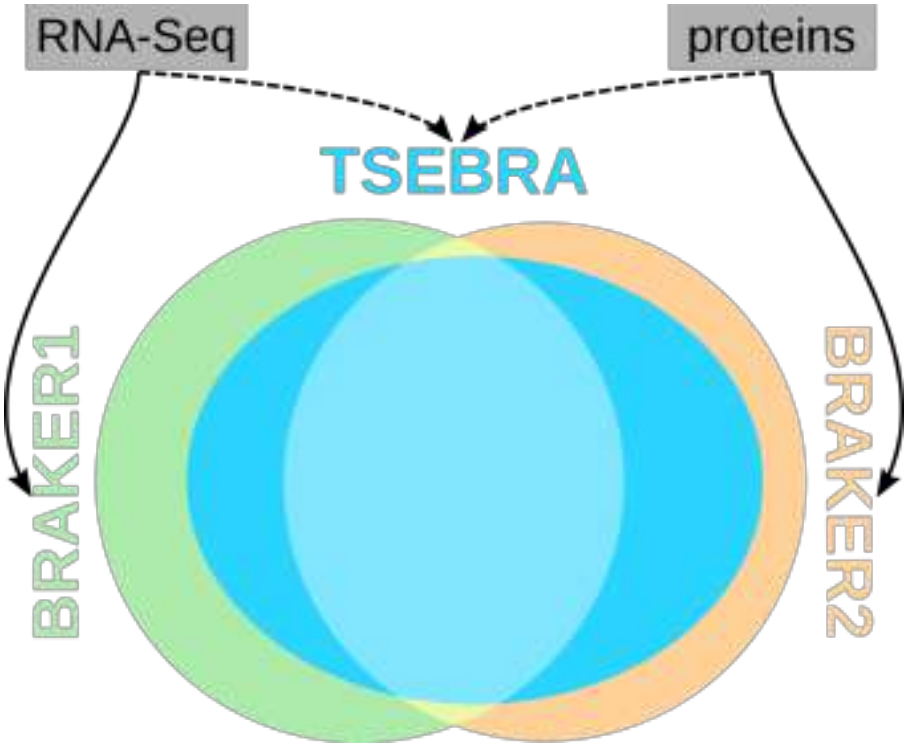
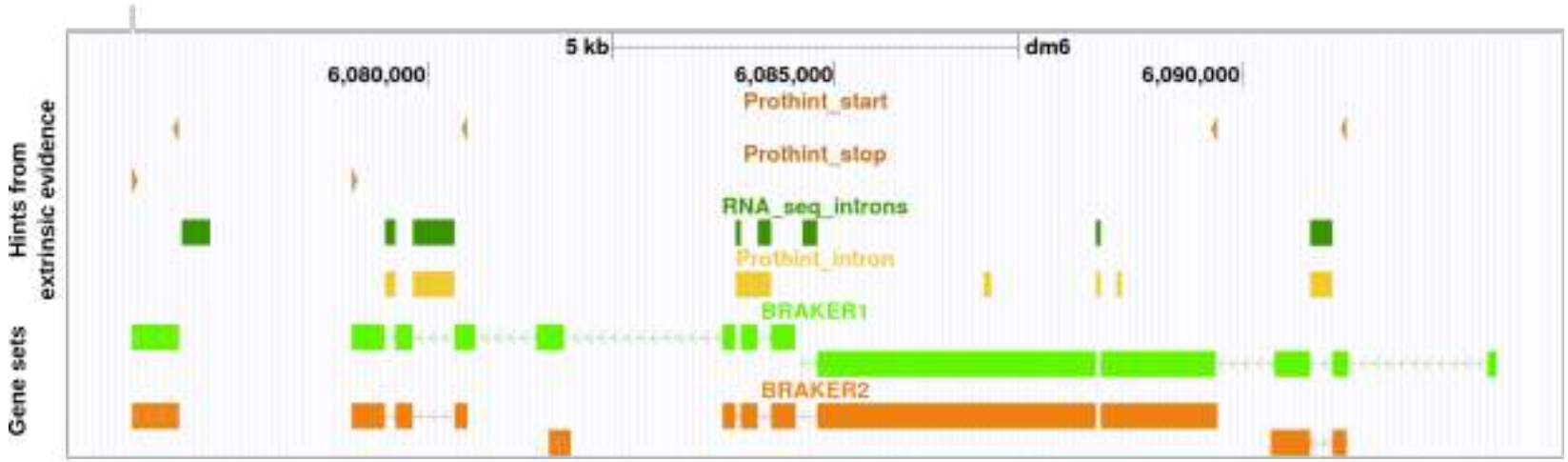


Transcript set comparison for different gene predictions.

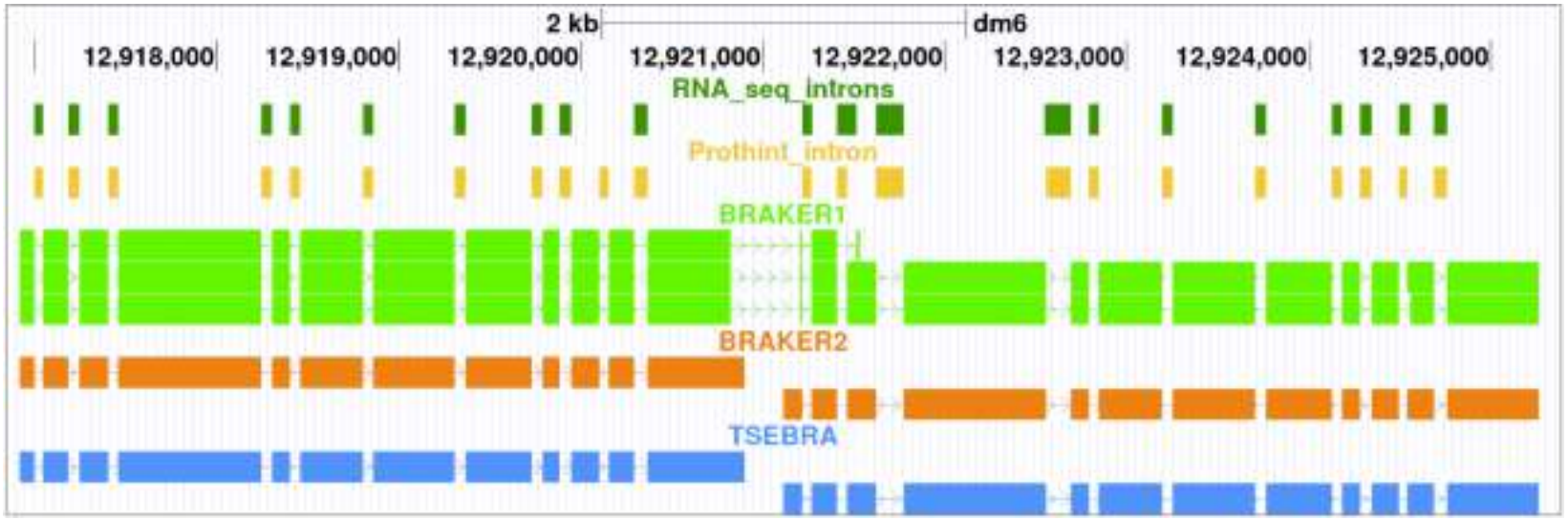
TSEBRA - Workflow

Input

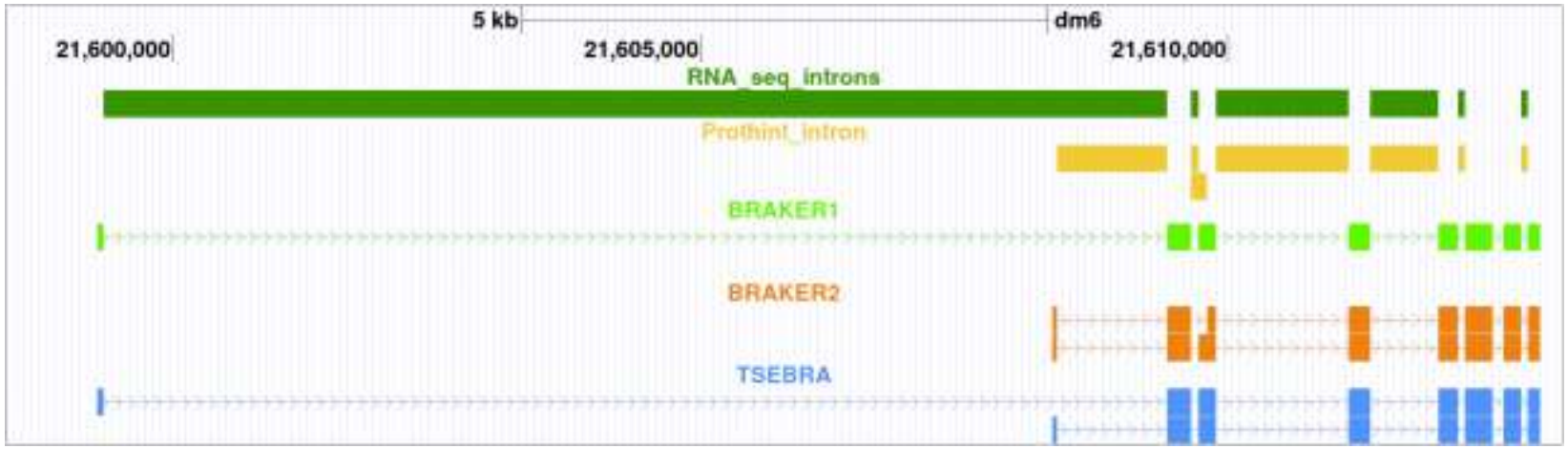
- Gene sets
- Hints from extrinsic evidence
- Configuration



TSEBRA - Workflow

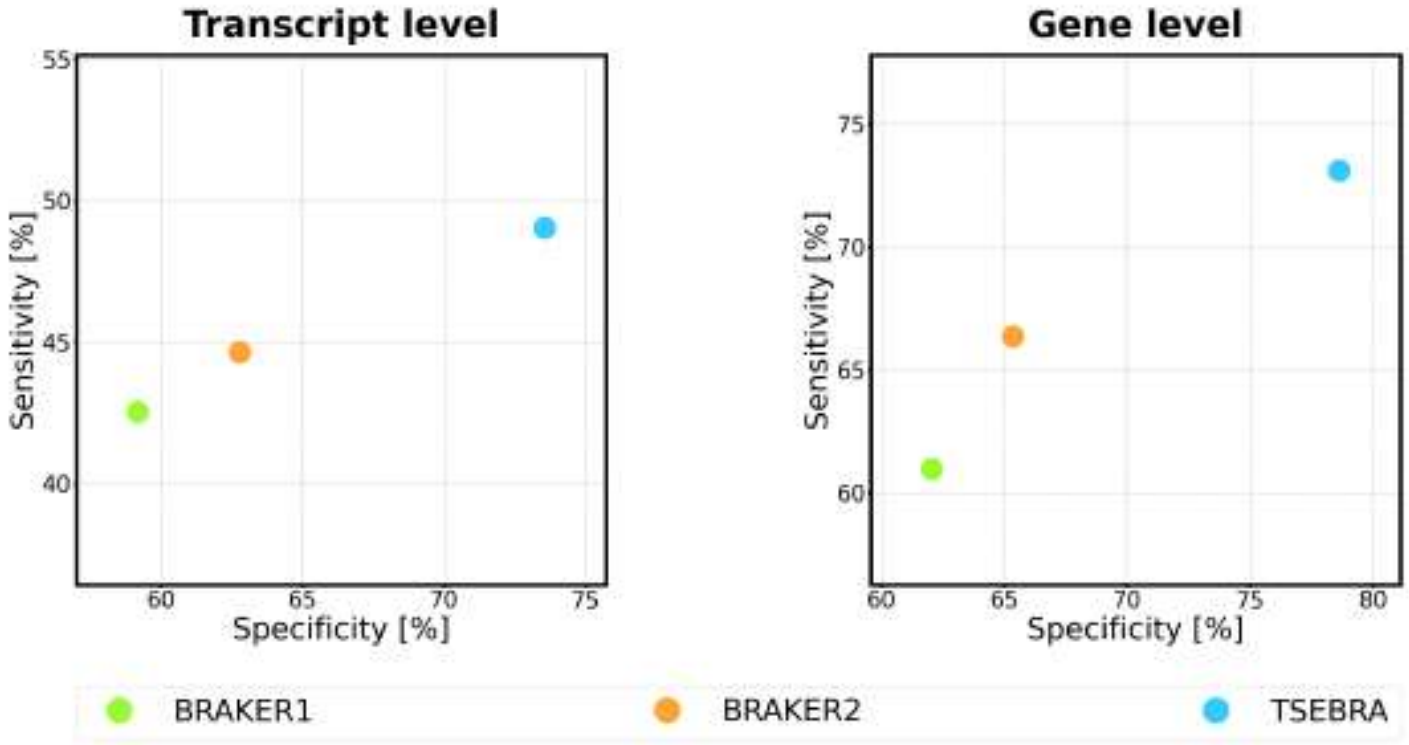


TSEBRA - Workflow



TSEBRA - Prediction Accuracy

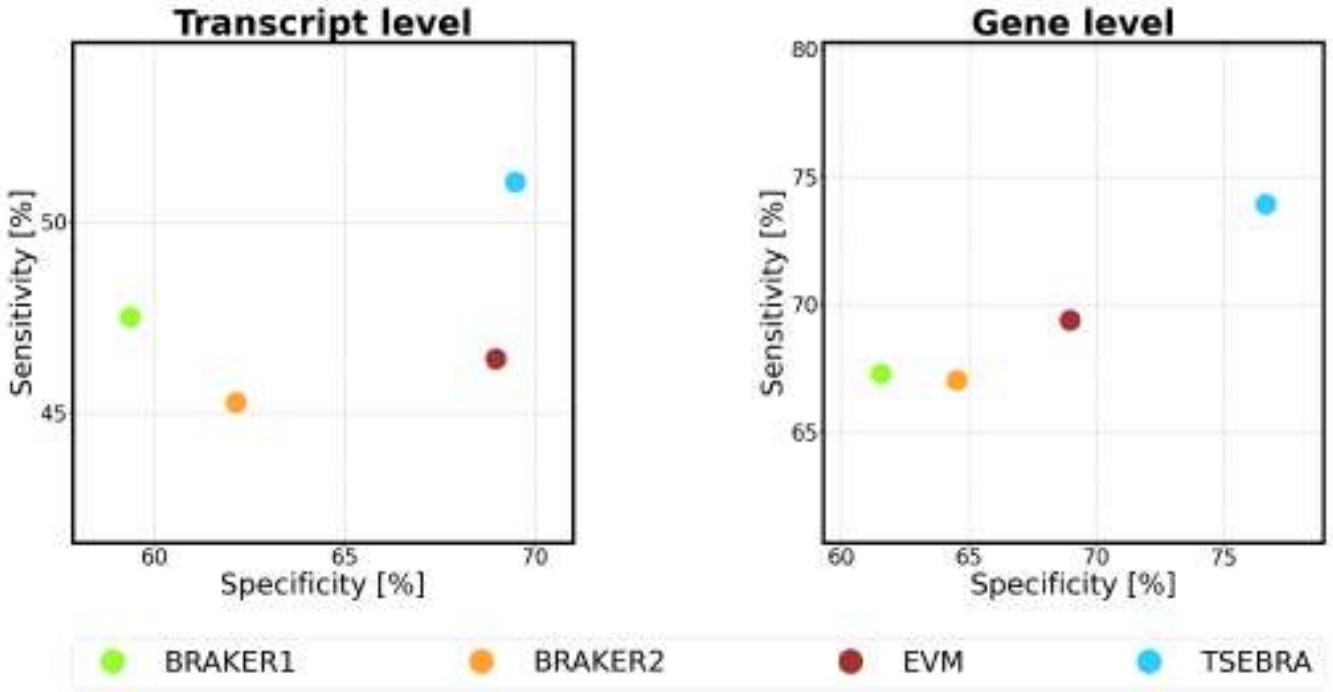
Average prediction accuracy for *A. thal.*, *C. ele.* and *D. mel.*



Gabriel et al. 2021. *BMC Bioinformatics* 22, 566.

TSEBRA - Comparison to EVidenceModeler

Average prediction accuracy for *A. thal.*, *C. ele.* and *D. mel.*

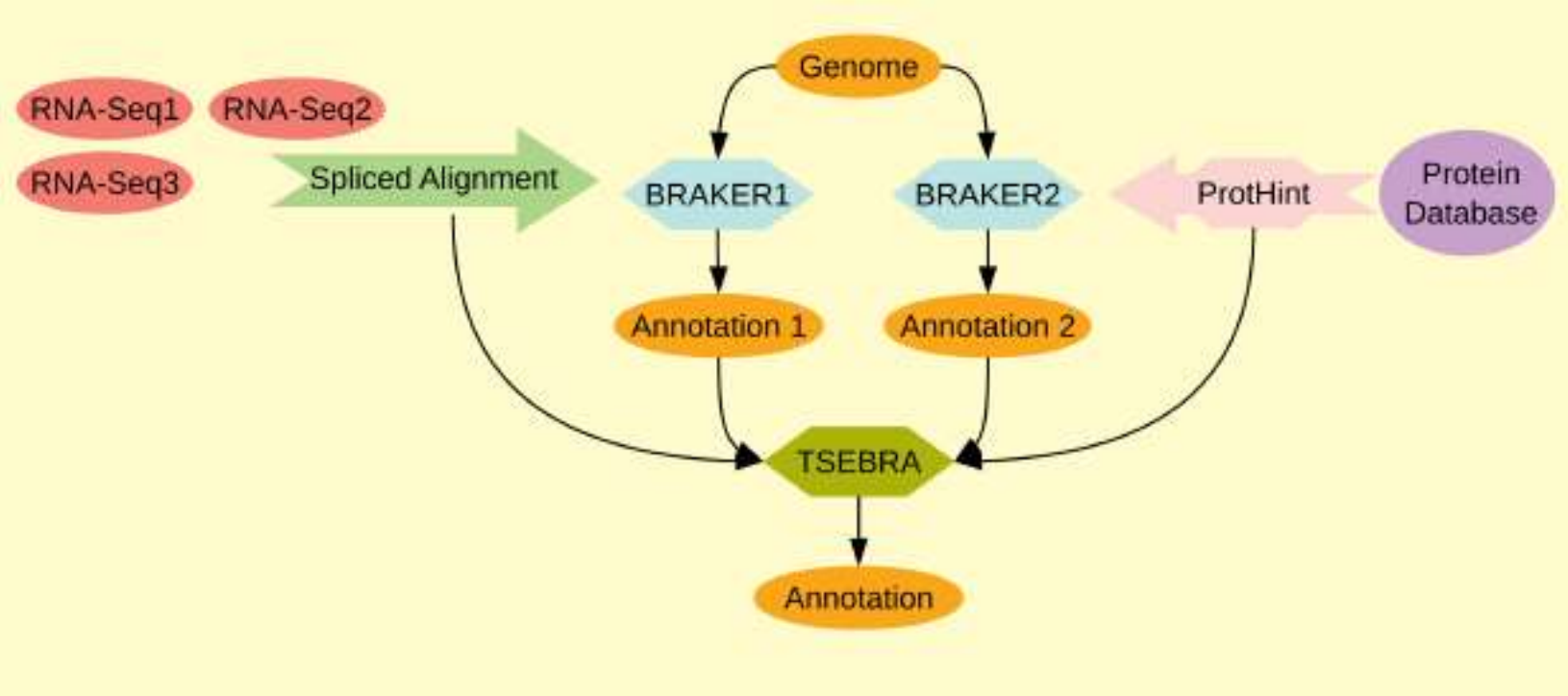


Average runtime

EVM : 35.28 min
TSEBRA : 0.37 min
* executed in parallel on 28 multi-core processor

Haas et al. 2008. *Genome biology* 9.1: 1-22.
Gabriel et al. 2021. *BMC Bioinformatics* 22, 566.

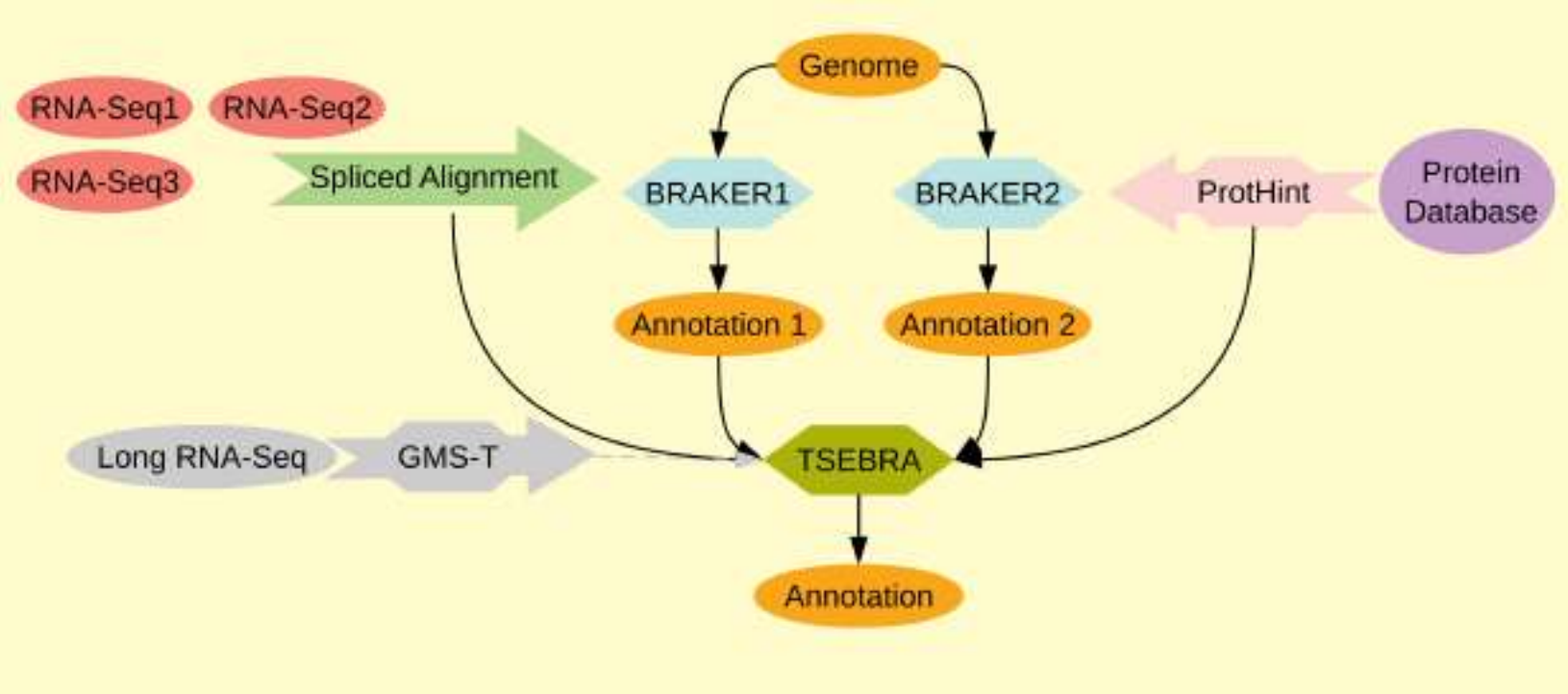
TSEBRA - Summary



Availability

- `https://github.com/Gaius-Augustus/BRAKER`
- `https://github.com/Gaius-Augustus/TSEBRA`

Long-Read Integration



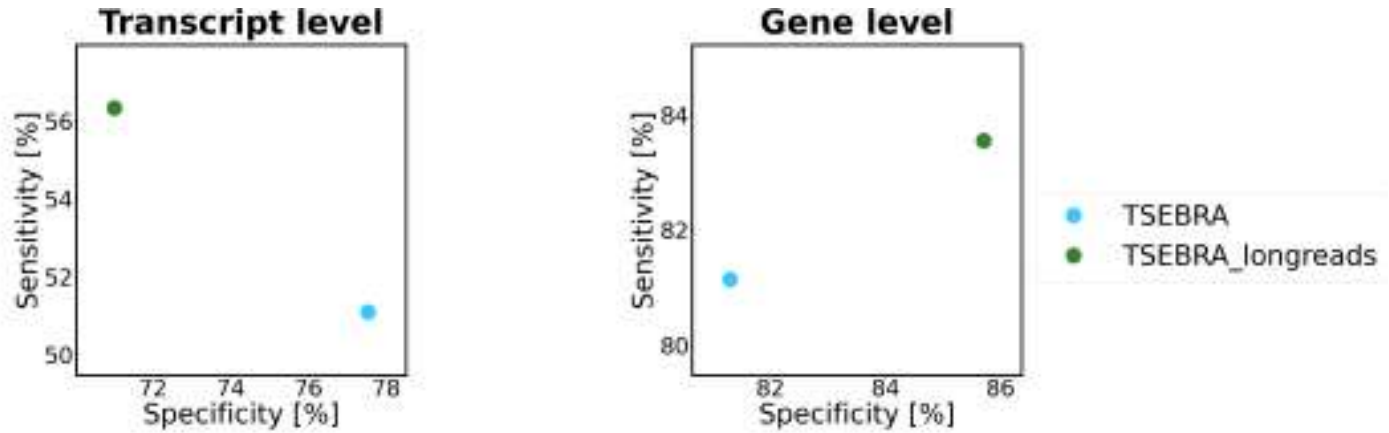
GeneMarkS-T

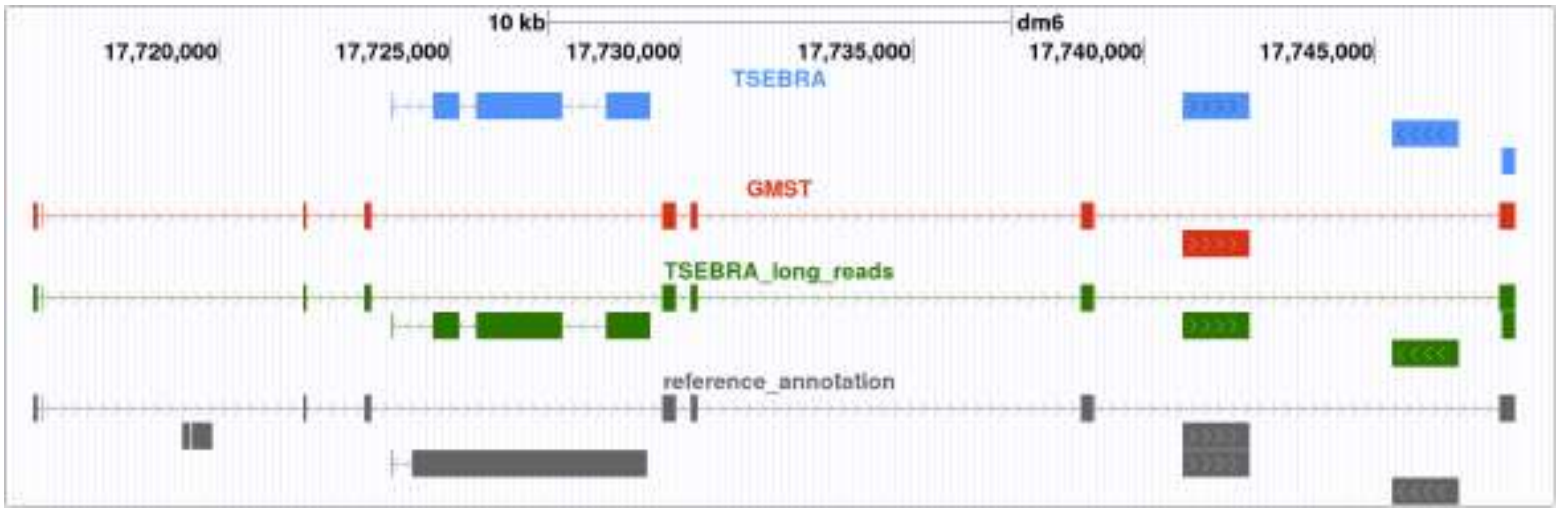
- Identifies protein-coding regions in assembled transcripts

Tang et al. 2015. *Nucleic acids research* 43.12:e78-e78.

Preliminary Results: Model Species

Species: ***Drosophila melanogaster*** (fruit fly)



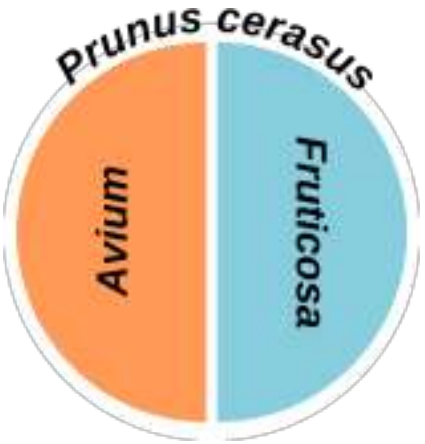


Preliminary Results: Novel Genome

Prunus cerasus (sour cherry)

- 2 subgenomes (*P. avium*, *P. fruticosa*)
- Extrinsic evidence:
  short+long read RNA-Seq data
  protein database (OrthoDB + *Prunus fruticosa*)

Morphology of *P. cerasus* L.. (a) mature tree habitus, (b) leaves, (c) inflorescence, (d) fruits.



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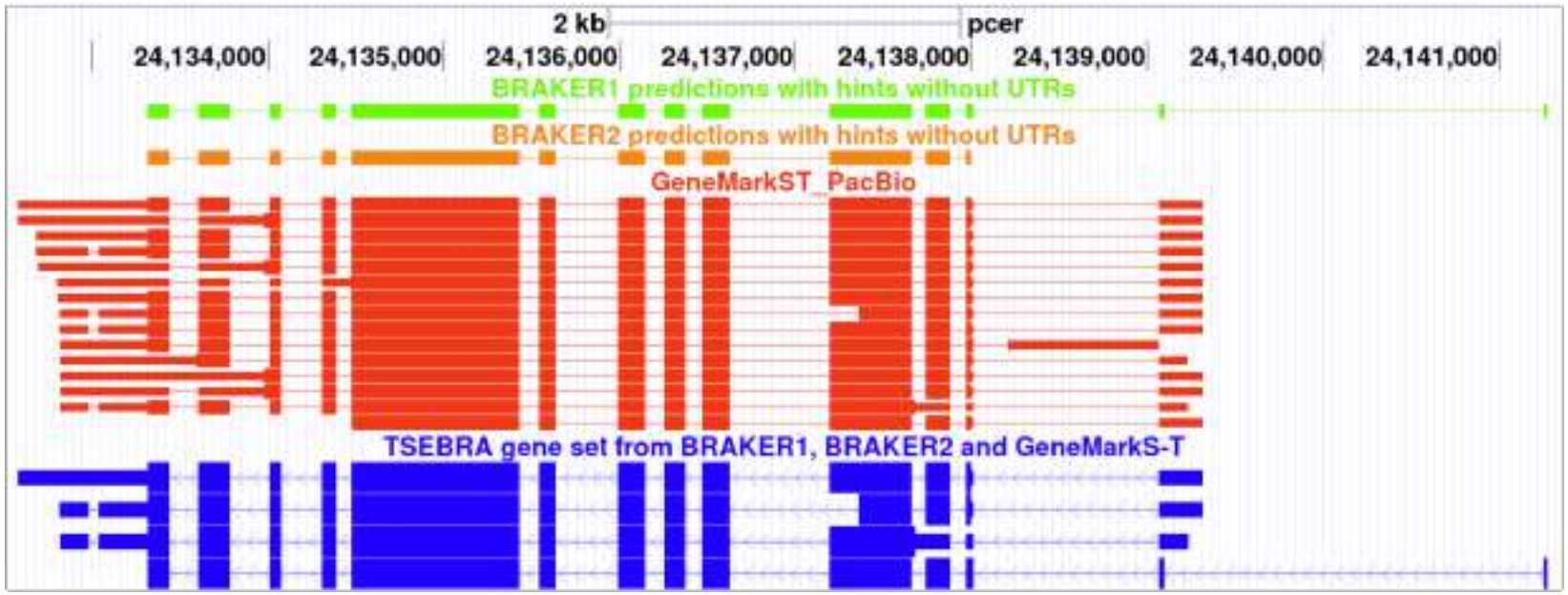
Preliminary Results: Novel Genome

Prunus cerasus (sour cherry)

- BUSCO: 99.3% completeness
- Annotation: 63,132 genes; 110,062 transcripts
  49,807 transcripts from PacBio long-reads



Hoff et al. 2019. *Genomics, proteomics & bioinformatics* 17.5: 546-549.

Summary

BRAKER Annotation with Extrinsic Evidence

- BRAKER1: short-read RNA-Seq
- BRAKER2: homologous proteins
- GMS-T Protocol: long-read RNA-Seq
- TSEBRA: short(+long)-read RNA-Seq and homologous proteins

Availability

- `https://github.com/Gaius-Augustus/TSEBRA`
- `https://github.com/Gaius-Augustus/BRAKER`
  - `http://exon.gatech.edu/GeneMark/license_download.cgi`
  - `https://github.com/Gaius-Augustus/Augustus`
  - `https://github.com/gatech-genemark/ProtHint`

Acknowledgements

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Alexandre Lomsadze

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Co-Authors

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Brůna et al. ”BRAKER2: Automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database.” NAR genomics and bioinformatics 3.1 (2021): lqaa108.

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