T-BAS: Phylogeny-based placement of emerging pathogens
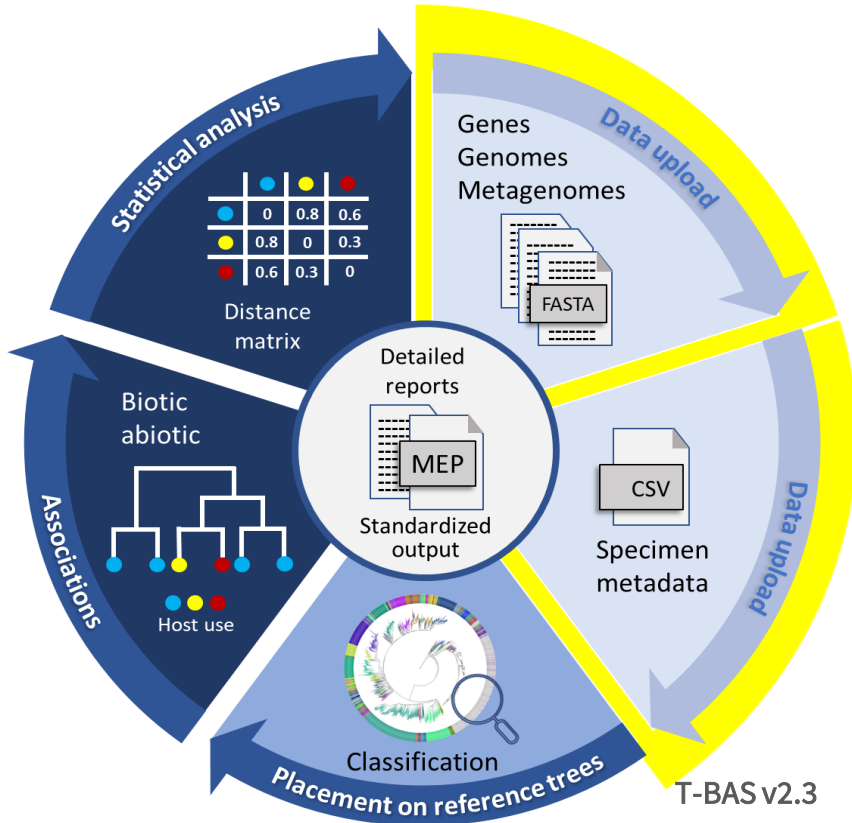
Ignazio Carbone and James White

NC STATE Center for Integrated Fungal Research
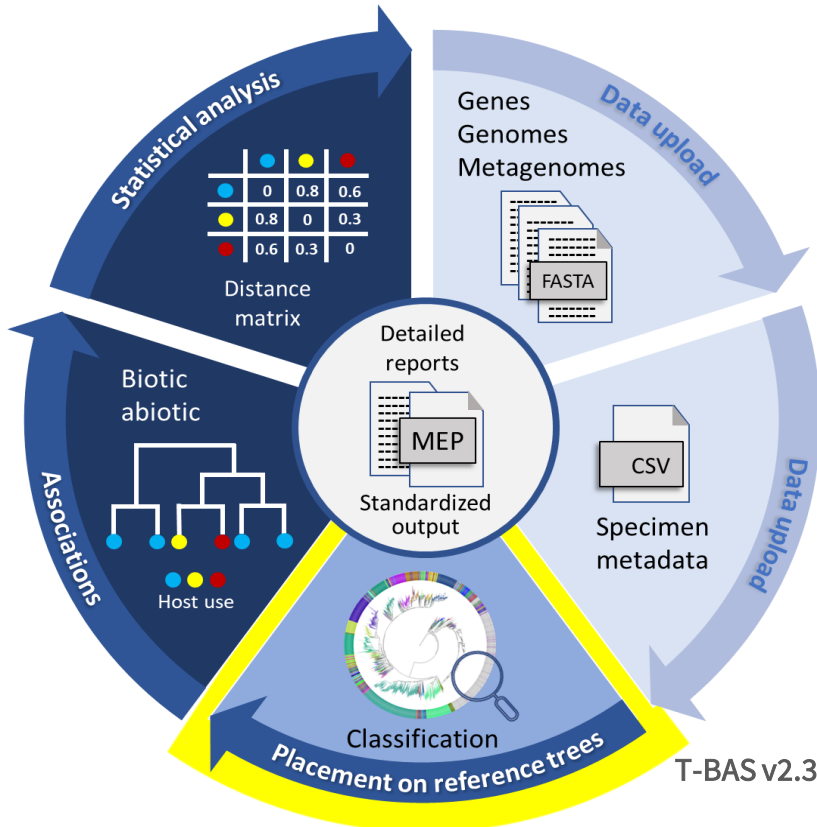
https://tbas.hpc.ncsu.edu/
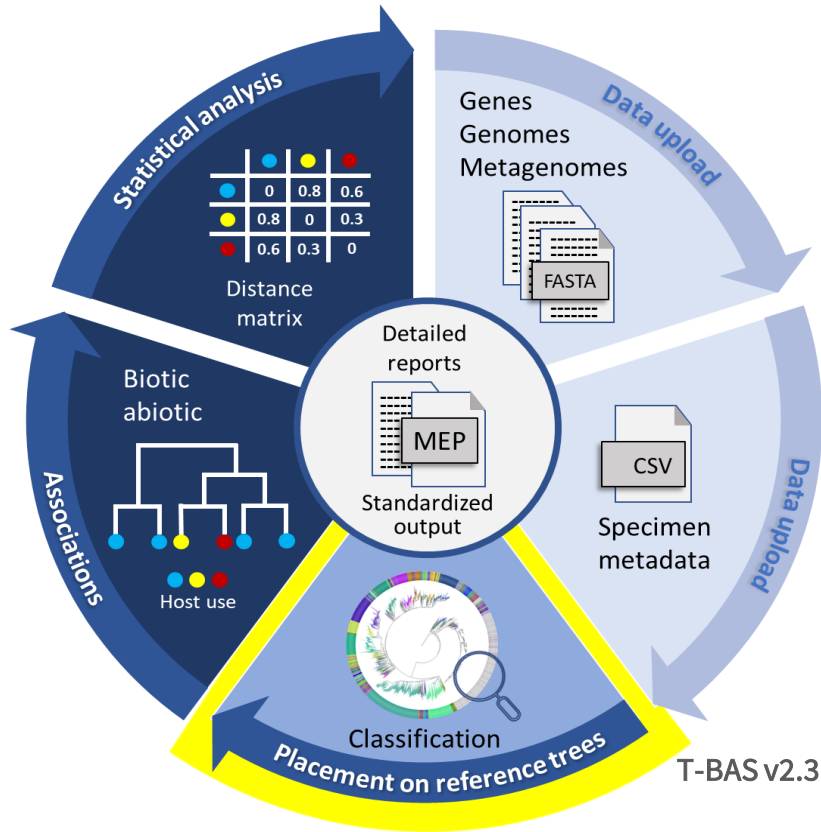
T-BAS: Data and metadata enriched analysis portal

> To track genes, genomes, and metagenomes as DNA or amino acid sequences and their metadata

T-BAS: Data and metadata enriched analysis portal

> To track genes, genomes, and metagenomes as DNA or amino acid sequences

> To better resolve species and facilitate species identification for monitoring and ecological studies

T-BAS: Data and metadata enriched analysis portal

Statistical analysis

Distance matrix

Biotic abiotic

Host use

Associations

Detailed reports

MEP

Standardized output

Data upload

Genes Genomes Metagenomes

FASTA

Data upload

CSV

Specimen metadata

Classification

Placement on reference trees

T-BAS v2.3
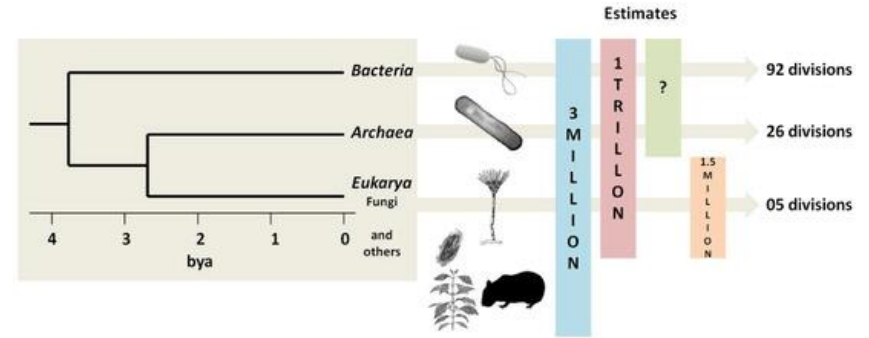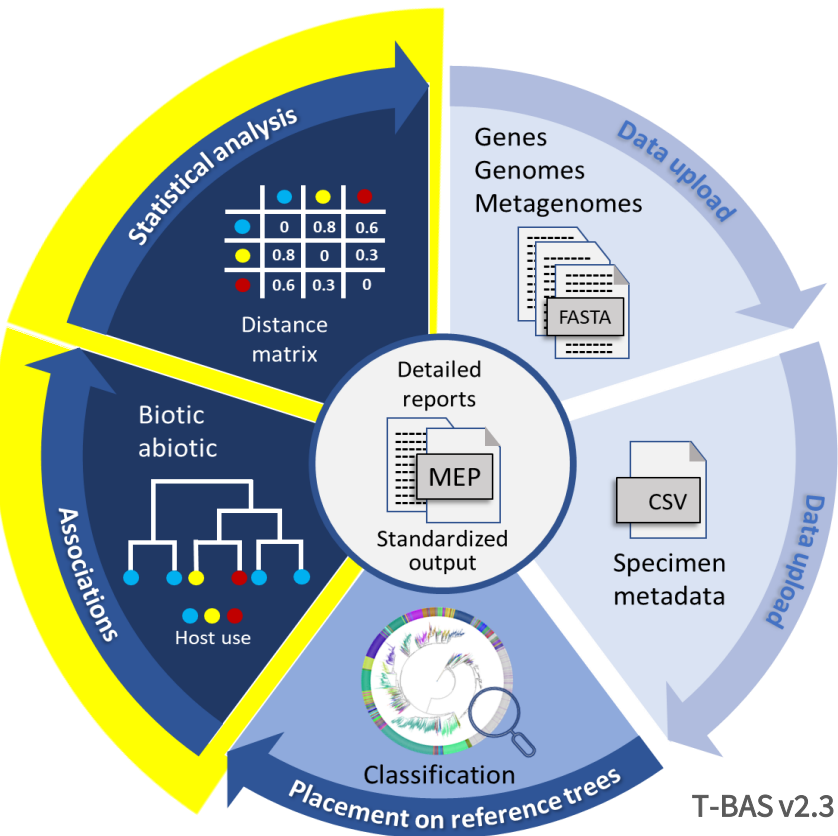
> To track genes, genomes, and metagenomes as DNA or amino acid sequences

> To better resolve species and facilitate species identification for monitoring and ecological studies

Less than 1% of microbial diversity is described

Vitorino LC, Bessa LA. Microbial Diversity: The Gap between the Estimated and the Known. *Diversity*. 2018; 10(2):46. https://doi.org/10.3390/d10020046

T-BAS: Data and metadata enriched analysis portal

> To track genes, genomes, and metagenomes as DNA or amino acid sequences

> To better resolve species and facilitate species identification for monitoring and ecological studies

> To test hypotheses of migration, genetic structure and hybridization within a robust phylogenetic framework

T-BAS: Data and metadata enriched analysis portal
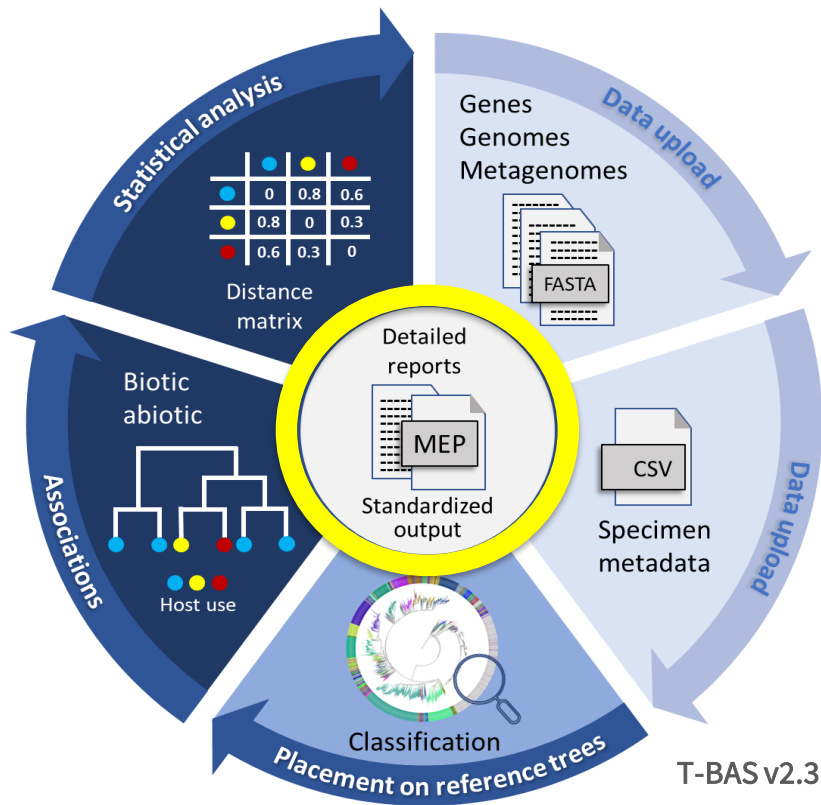

> To track genes, genomes, and metagenomes as DNA or amino acid sequences

> To better resolve species and facilitate species identification for monitoring and ecological studies

> To test hypotheses of migration, genetic structure and hybridization within a robust phylogenetic framework

> To provide standardization that integrates phylogeny, sequences, and metadata in a single compressed file

T-BAS: Tracking emerging *Phytophthora* species
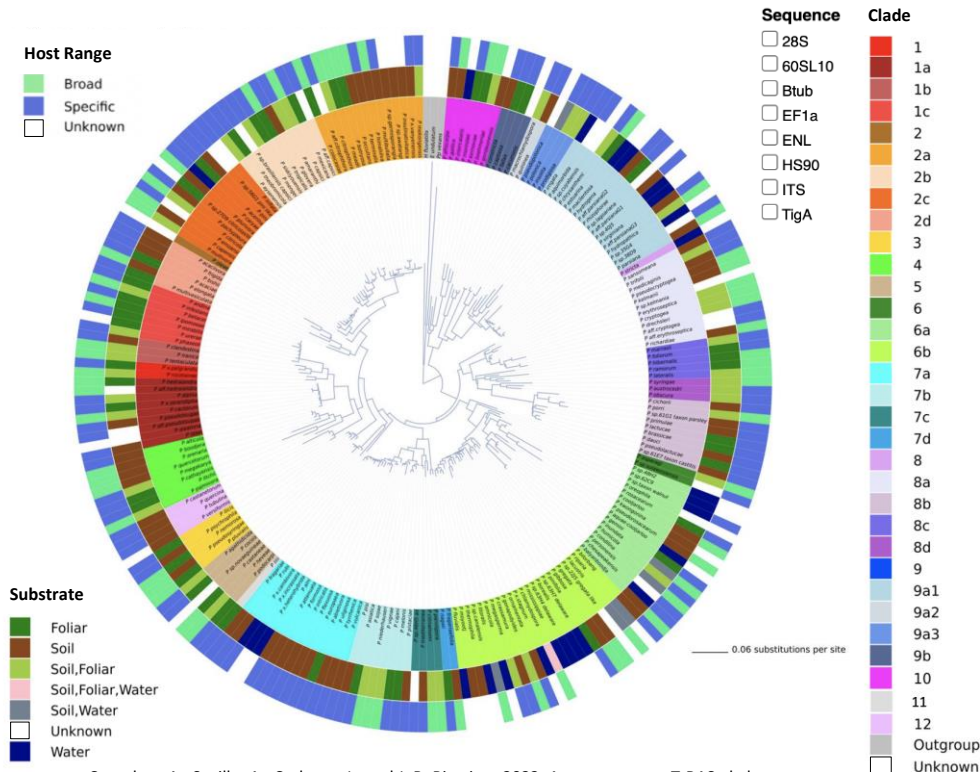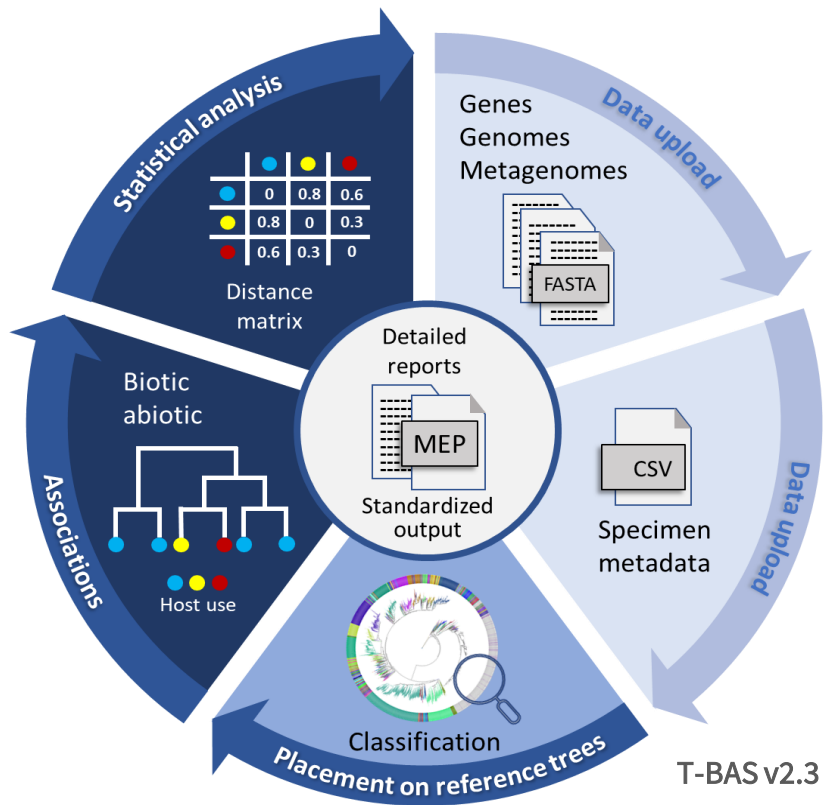
T-BAS v2.3

Coomber, A., Saville, A., Carbone, I., and J. B. Ristaino. 2022. An open-access T-BAS phylogeny for Emerging *Phytophthora* species. bioRxiv doi: https://doi.org/10.1101/2022.08.06.503053

T-BAS: Easily add new sequences and metadata

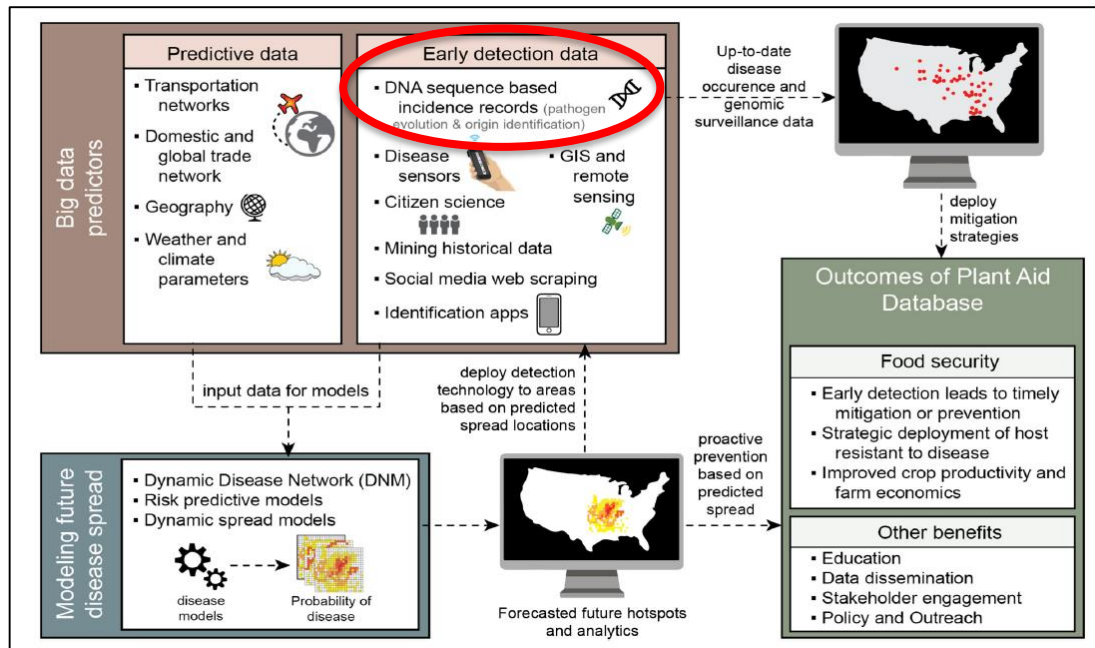Coomber, A., Saville, A., Carbone, I., and J. B. Ristaino. 2022. An open-access T-BAS phylogeny for Emerging *Phytophthora* species. bioRxiv doi: https://doi.org/10.1101/2022.08.06.503053
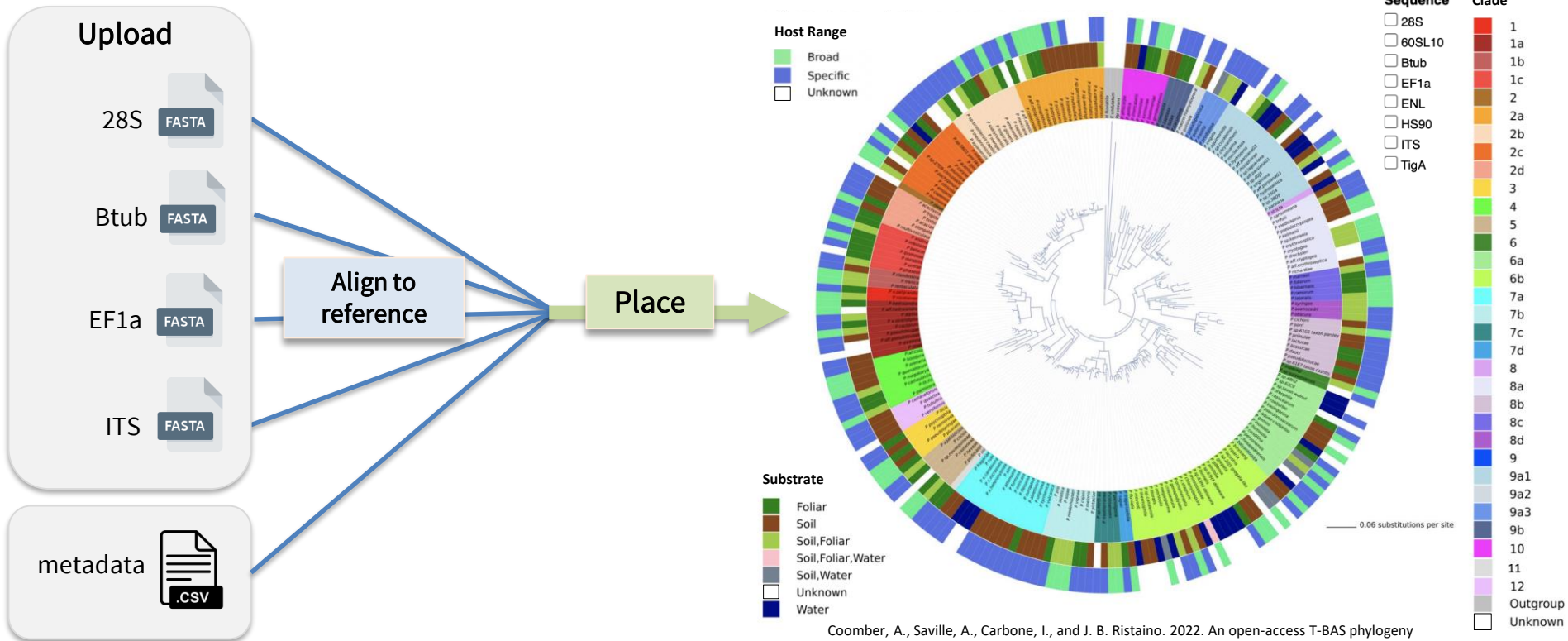
Integrate T-BAS and pathogen genomic surveillance on *P. infestans* into the Plant Aid Database (PAdb)

NSF PIPP Phase I: Real-time Analytics to Monitor and Predict Emerging Plant Disease

Senior Personnel	Position
Jean B. Ristaino (PI)	Director, Emerging Plant Disease Cluster
Ignazio Carbone (co-PI)	Director, Center for Integrated Fungal Research (CIFR)
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Qingshan Wei (Co-PI)	Chemical and Biomolecular Engineering (CBE)
Chris Jones (co-PI)	Research Scholar, Center for Geospatial Analytics (CGA)
Ross Meentemeyer	Director, Center for Geospatial Analytics (CBA)
Peter Ojiambo	Professor, Center for Integrated Fungal Research (CIFR)
Raju Vatsavai	Associate Director, Spatial Computing and Technology, CGA, Computer Science
Laura Tateosian	Associate Teaching Professor, Center for Geospatial Analytics (CGA)
Kelly Zering	Agriculture Resource Economics

T-BAS: Public online or local version with license

Journal Submission Data Repositories (free and open)

T-BAS is more than a data repository!

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https://decifr.hpc.ncsu.edu/license_options.php