

# From Research to Surveillance: Leveraging the State of Whole Genome Sequencing for Precision Public Health in a High-Burden Tuberculosis Setting



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## Background and Aim

- **Brazil** is listed by the WHO as a **high-burden tuberculosis (TB)** and a **multidrug-resistant TB** country.
- In this context, **Whole-genome sequencing (WGS)** emerges as a valuable asset for TB surveillance in the realm of precision public health by facilitating the pinpointing of individuals involved in recent TB transmission chains.
- Thus, we aimed **to assess all *Mycobacterium tuberculosis* complex genomes isolated in Brazil that are publicly accessible to evaluate TB transmission and drug resistance in the context of the GEMIBRA database (Genomes of Mycobacteria from Brazil).**

## Methods

### 1. Literature Review



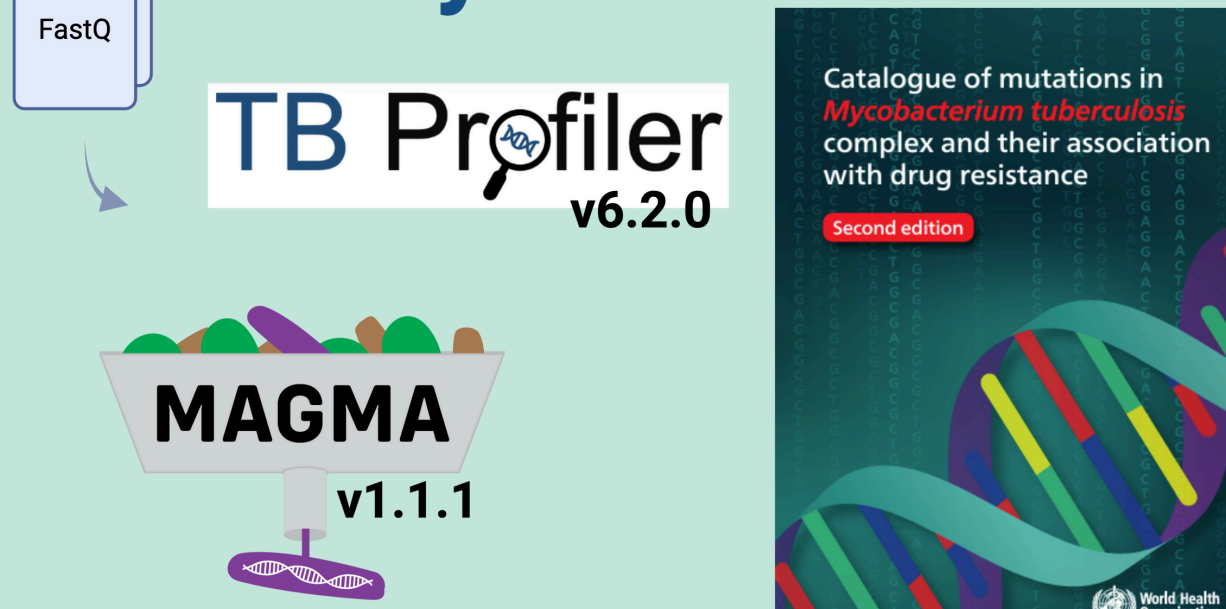
(TB AND Brazil AND WGS)

### 2. Database development



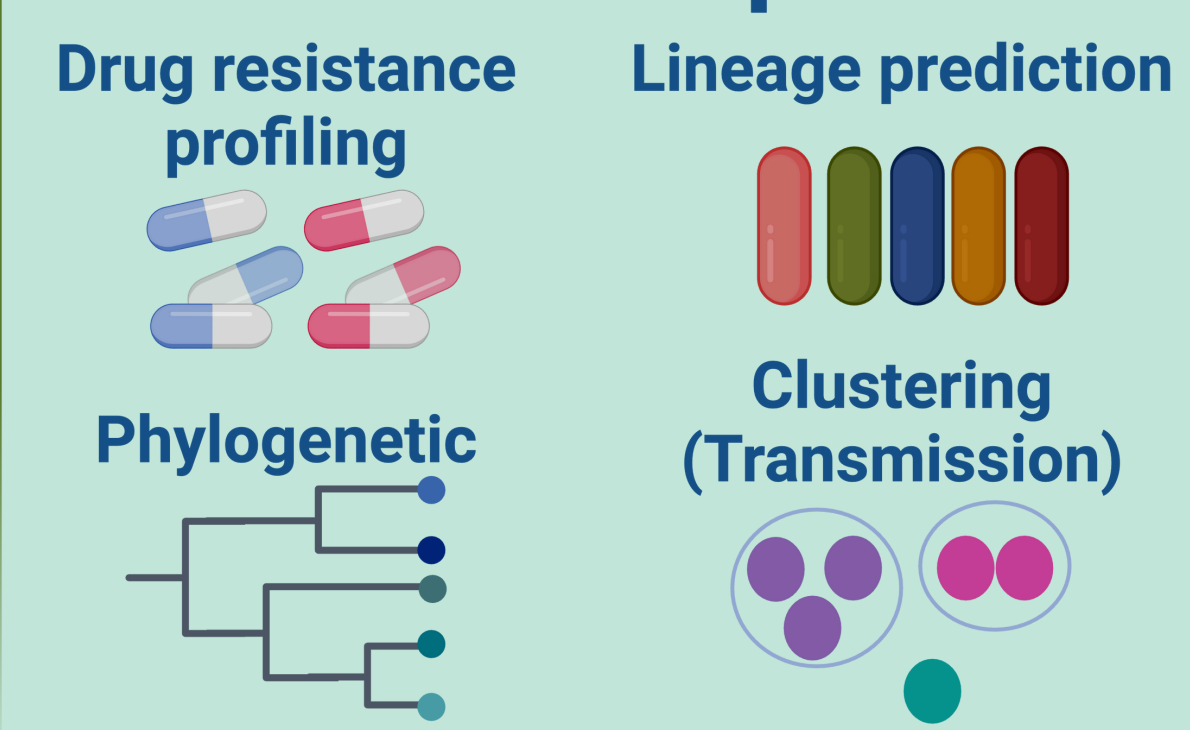
### 3. Bioinformatic

#### Analysis



#### Workflow

### 4. Interpretation



- The **workflow** details how the data was obtained and analyzed.
- Stellenbosch University's **server played a crucial role in the genome analysis.**

## Results and Discussion

- From **23 studies**, we obtained **2182 FASTQ** paired-end files, of which 65 failed quality control.
- Of the 2118 genomes analysed, 1340 were identified within 333 clusters using a 12 SNP cut-off, while **789 genomes clustered into 286 clusters with a 5 SNP cut-off.**
- Based on 12 SNPs, **21 clusters harboured strains from different states and regions:**
  - Southeast-Southeast (5)
  - Southeast-South (5)
  - South-Mideast (5)
  - Southeast-Mideast (4)
  - South-South (1)
  - Southeast-Southeast-Midwest (1)
- **This suggests transmission chains across these Brazilian regions.**

States: Pará (PA), Amazonas (AM), São Paulo (SP), Rio de Janeiro (RJ), Espírito Santo (ES), Mato Grosso do Sul (MS), Mato Grosso (MT), Santa Catarina (SC) and Rio Grande do Sul (RS).

**Brazilian Regions**

- "North (PA, AM)"
- "Southeast (SP, RJ, ES)"
- "Midwest (MS, MT)"
- "South (SC, RS)"

**Non-MDR vs. MDR**

- Non-MDR
- MDR

- **Lineage 4 (1994/94.15%) was the most frequent.**

- The drug-resistance prediction profile was:

- pan-susceptible (1364/64.40%)

- **multidrug-resistant (298/14.07%)**

- isoniazid monoresistant (149/7.03%)

- pre-extensively resistant (76/3.59%)

- rifampicin monoresistant (46/2.17%)

- others (185/8.73%)

- **No resistance was detected to para-aminosalicylic acid, clofazimine, linezolid, bedaquiline, or delamanid.**

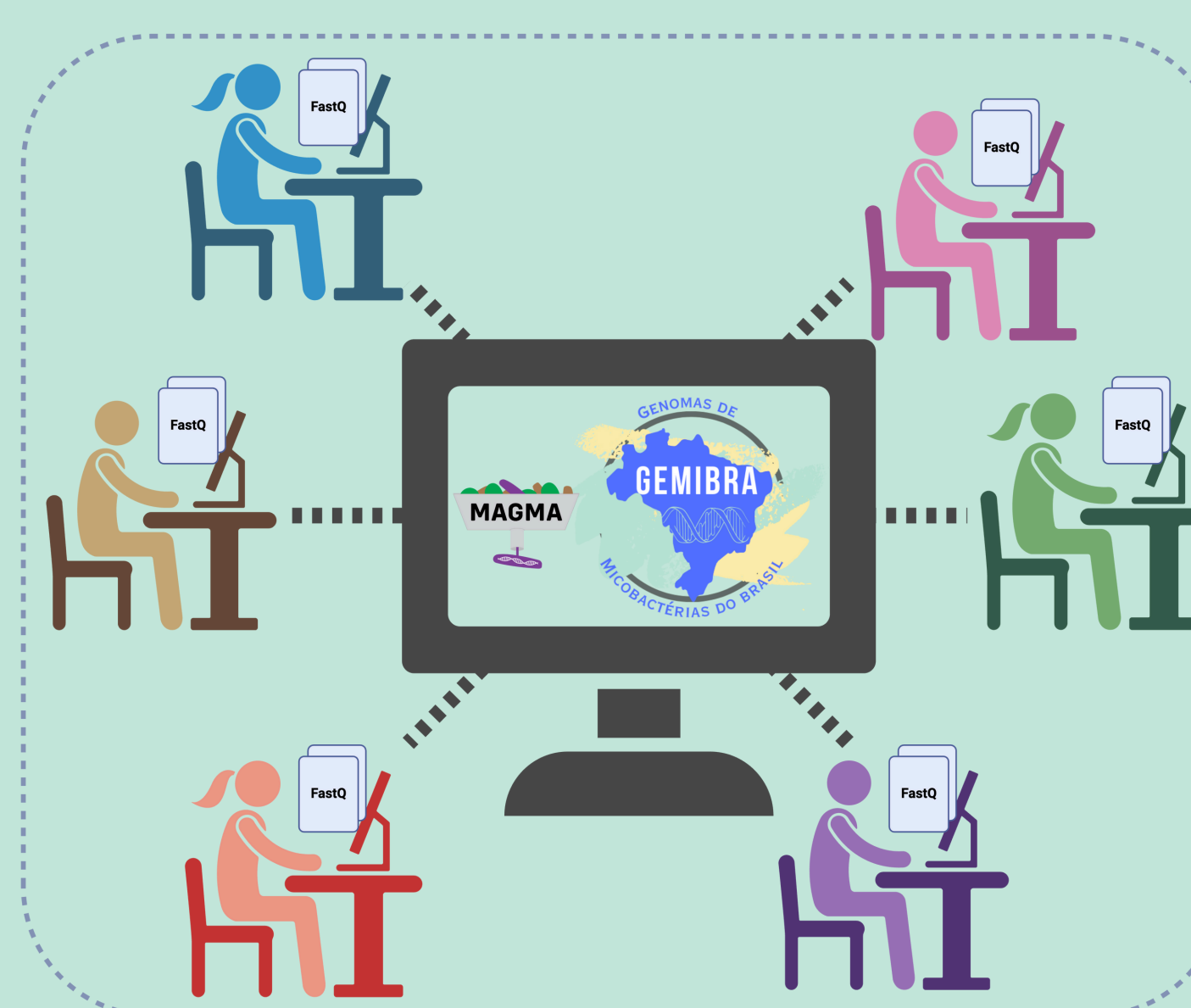
- **It was not observe TB transmission between humans and animals, or zoonotic TB.**

**Phylogenetic tree using IQ-tree on 2118 rooted in *M. canettii* and coloured according to the Brazilian regions and MDR comparison.**

## Conclusion

- Analysis of 2118 publically available *M. tuberculosis* genomes originally from Brazil using the MAGMA pipeline shows:
  - **Transmission chains across these Brazilian regions;**
  - **No resistance detected to new drugs (CFZ, LZD, BDQ, or DLM).**
- Data obtained before the introduction of new drugs in the country in 2021!
- This study was the basis (phase 1) for the GEMIBRA database manual curation and the first data analysis.

## Perspectives

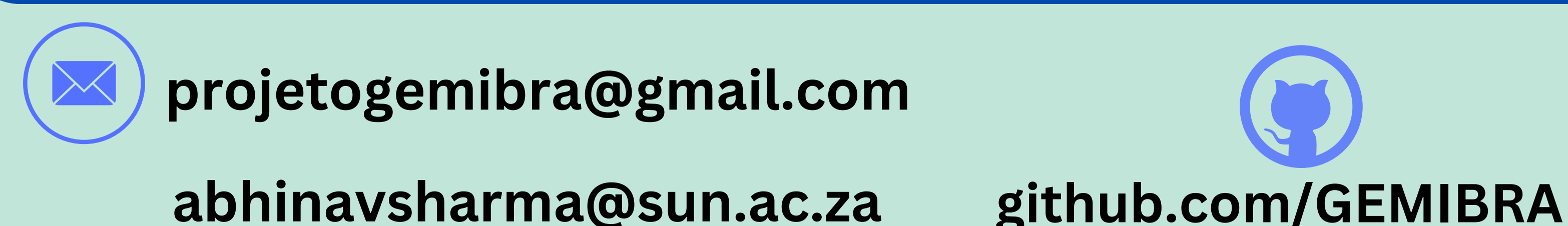


With this dataset as a foundation, we plan **to develop GEMIBRA phase 2: a digital platform (dashboard) for WGS analysis using MAGMA pipeline written in Nextflow.**

## Funding and Acknowledgment



## Contact us!



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