MAGMA

(Maximum Accessible Genome for Mtb Analysis)

Comprehensive Genomic Analysis of Clinical *Mycobacterium tuberculosis samples*

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NGS for Tuberculosis Control

Could revolutionise TB control and improve patient outcomes

- Determine drug resistance profile for individual patients
- Monitor the emergence of drug resistance
- Improve understanding of drug resistance mechanisms
- Identify transmission events

Challenges

- Clinical samples: complex bacterial communities and low *Mtb* burden
- *Mtb* enrichment through subculturing is a slow process (6+ weeks)
- Limited infrastructure and human expertise low-income countries

Key Features

gatk

Joint variant calling

Enhanced variant filtering

TB Profiler

Multiple Infection Detection

Drug Resistance Inference

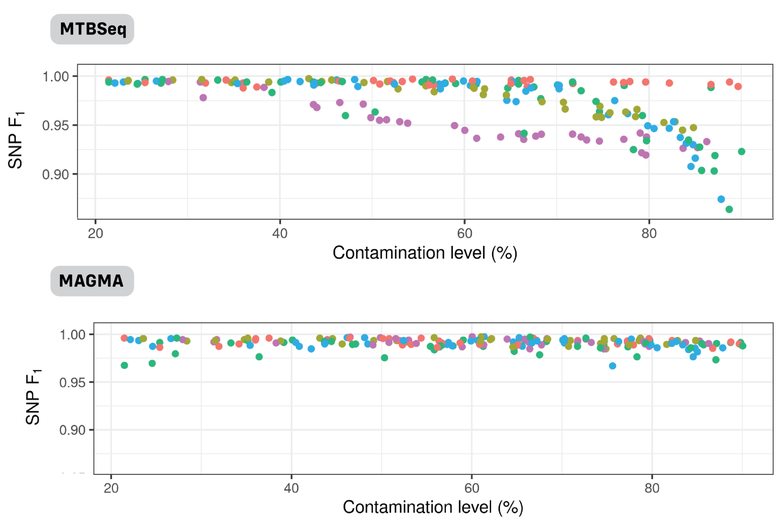
nextflow

Accessible | Reproducible

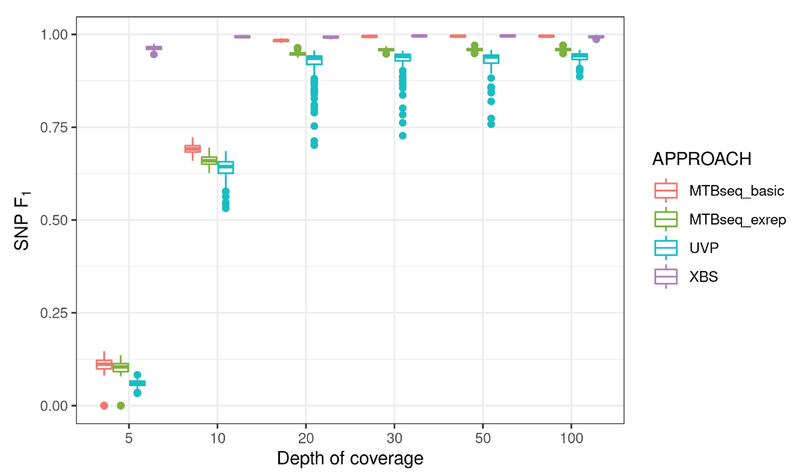
Scalable | Standardized

Comparative Performance of *Mtb* Pipelines

Accuracy in the Presence of High Levels of Contamination



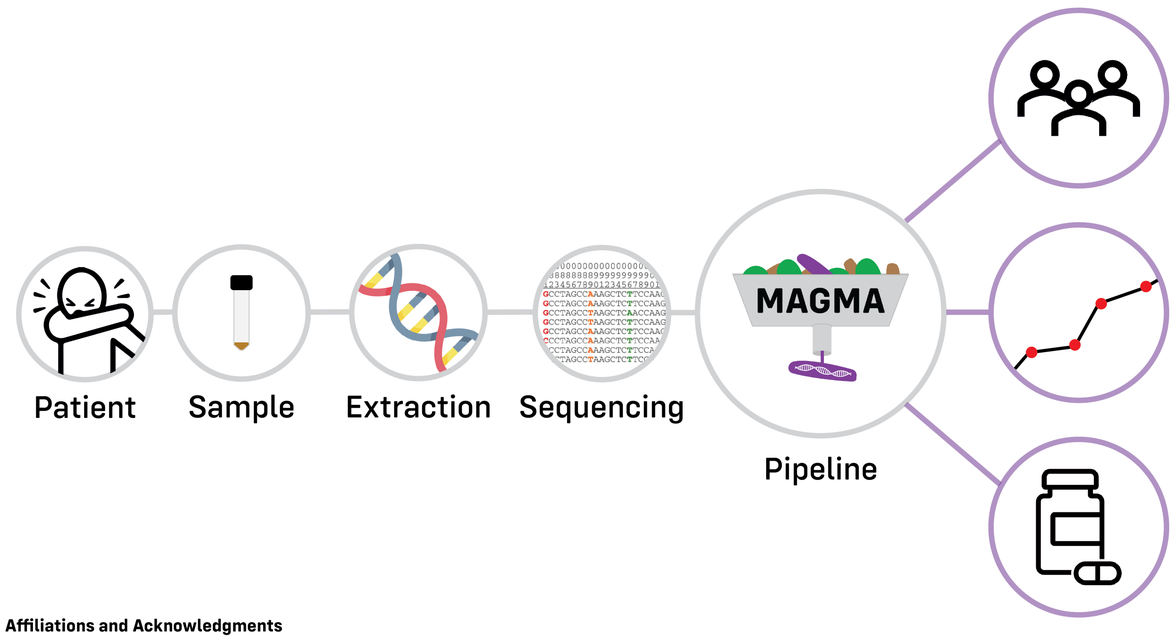
Accuracy in Sequenced Genomes with Low Coverage



Conclusion

- MAGMA outperforms other Mtb-specific pipelines in data with low coverage and high contamination
- Significant step up in the ongoing effort of implementing WGS analysis due to the ability to analyse *Mtb* early primary cultures

Future Development: From Pipeline to Action



- Precision public health to interrupt transmission
- Surveillance of emerging drug resistance
- Precision medicine for effective treatments

- Further address the gap between research and clinical use
- In the clinical context, data must be actionable
- Transformation from bioinformatics pipeline to user-friendly platform

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2. South African Medcial Research Council Centre for Tuberculosis and DST/NRF Centre of Excellence for Biomedical Tuberculosis Research, Division of Molecular Biology and Human Genetics, Stellenbosch University. Stellenbosch, South Africa

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