MAGMA – A novel bioinformatics pipeline developed for integration of WGS in clinical care and tuberculosis control

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NGS for Tuberculosis Control

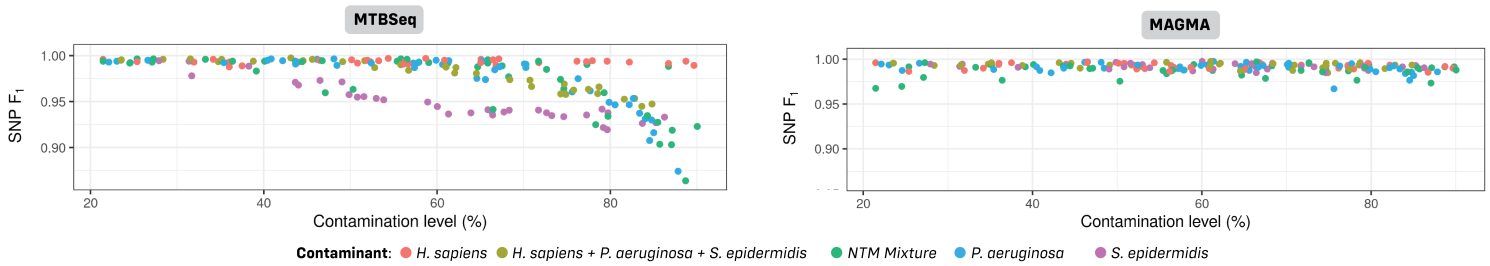
Could revolutionise TB control and improve patient outcomes

- 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 in low-income countries
- Detection of mixed infection and heteroresistance

Clinical *Mtb* Samples with High Contamination Loads



UVP

Cannot analyse samples with contamination load >10%

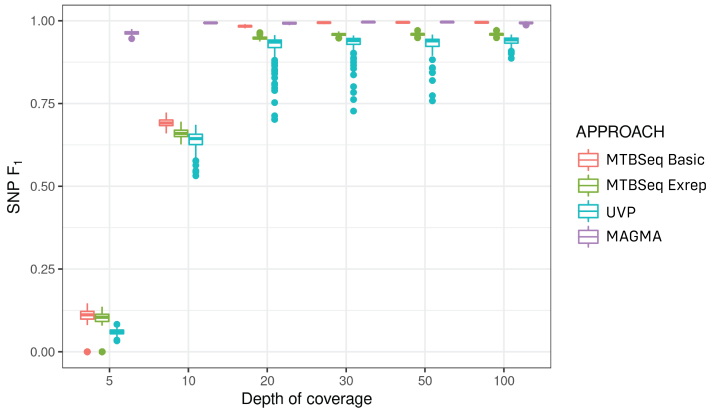
MTBSeq

Struggles to analyse samples with contamination load >60%

MAGMA

Can call variants with high accuracy regardless of contamination load

Samples with Low *Mtb* Burden



UVP

Variable accuracy regardless of coverage

MTBSeq

High accuracy at coverage >20x

MAGMA

High accuracy at coverage <5x

Heteroresistance | Mixed Infection

Pipeline's ability to detect:

	Minor Variants	Mixed Infection
UVP	✗	✗
MTBSeq	✗	✗
MAGMA	✓	✓

Note: See Comparison with Deeplex (Poster P71)

Conclusion

- All three pipelines perform similarly for standard analysis of WGS on high-quality *Mtb* DNA samples
- MAGMA outperforms other *Mtb*-specific pipelines in data with low coverage and high contamination
- MAGMA facilitates the 'real-time' WGS in routine care as it can analyse data from *Mtb* early primary liquid cultures
- Future prospects include development of user-friendly MAGMA platform, see oral presentation (OR10)

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