

Conclusions

- Information you get about the metagenome will be determined by database quality
- Database quality is a determinant of what we think is in the microbiome
- We can identify genomes already in publicly available databases that improve our mapping of dark matter, but in order to fully understand strain-level diversity, we need to culture and sequence.

Acknowledgements

Segre Group

Julie Segre

Sean Conlan

Clay Deming

Diana Proctor

Payal Joglekar

Xin Huang

Catriona Harkins

Qiong Chen

Michael Chambers

Choon Kiat Sim

Shih-Queen Lee-Lin

Kong Group

