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Selected example of small metagenomic project: Ciliates and their bacterial symbionts/consortia

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RECYCLES WORKSHOP
Metagenomics and metabarcoding
approaches to describe ecological
systems and infer their development

5th, 6th & 7th of July 2022

GA: 872053 — H2020 - MSCA - RISE-2019



European
Commission

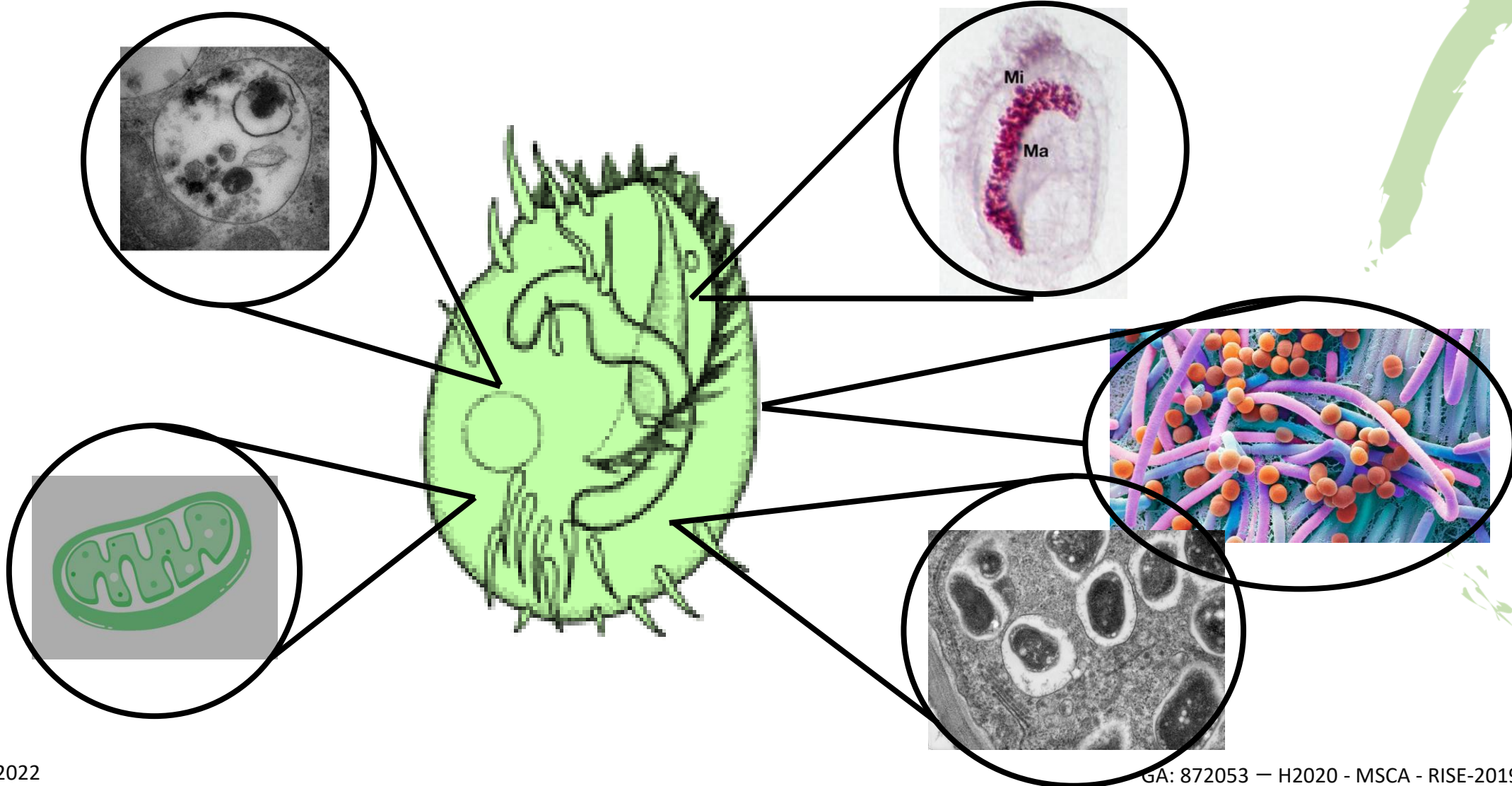


TALK STRUCTURE



- 1 - Why ciliates can be considered a small metagenome?
- 2 - How to deal with it. The Blobology method
- 3 - Some example of the Bolobology application

WHY A METAGENOME?



WHAT IS THE PROBLEM?

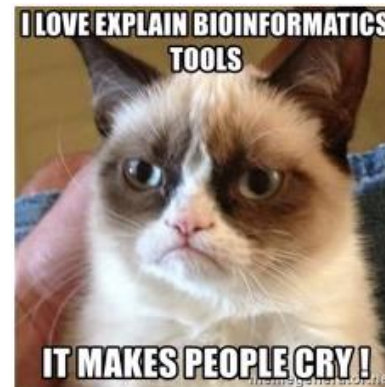


IT'S A QUITE COMPLEX SYSTEM!

THE BLOBOLOGY METHOD



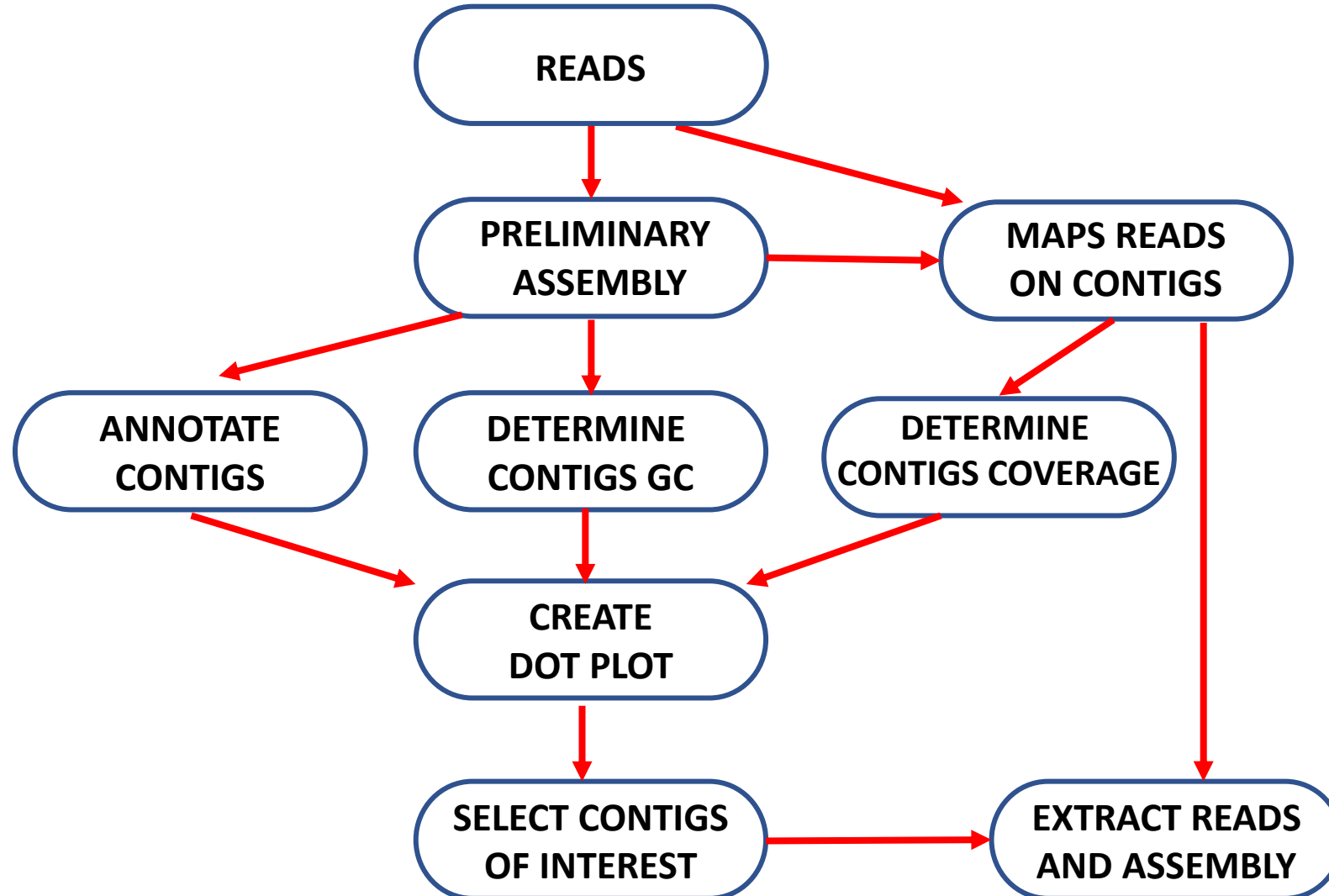
This approach is aimed to **reducing the complexity** of the investigated system. Dealing with a less complex system allows the assembler to obtain better results.



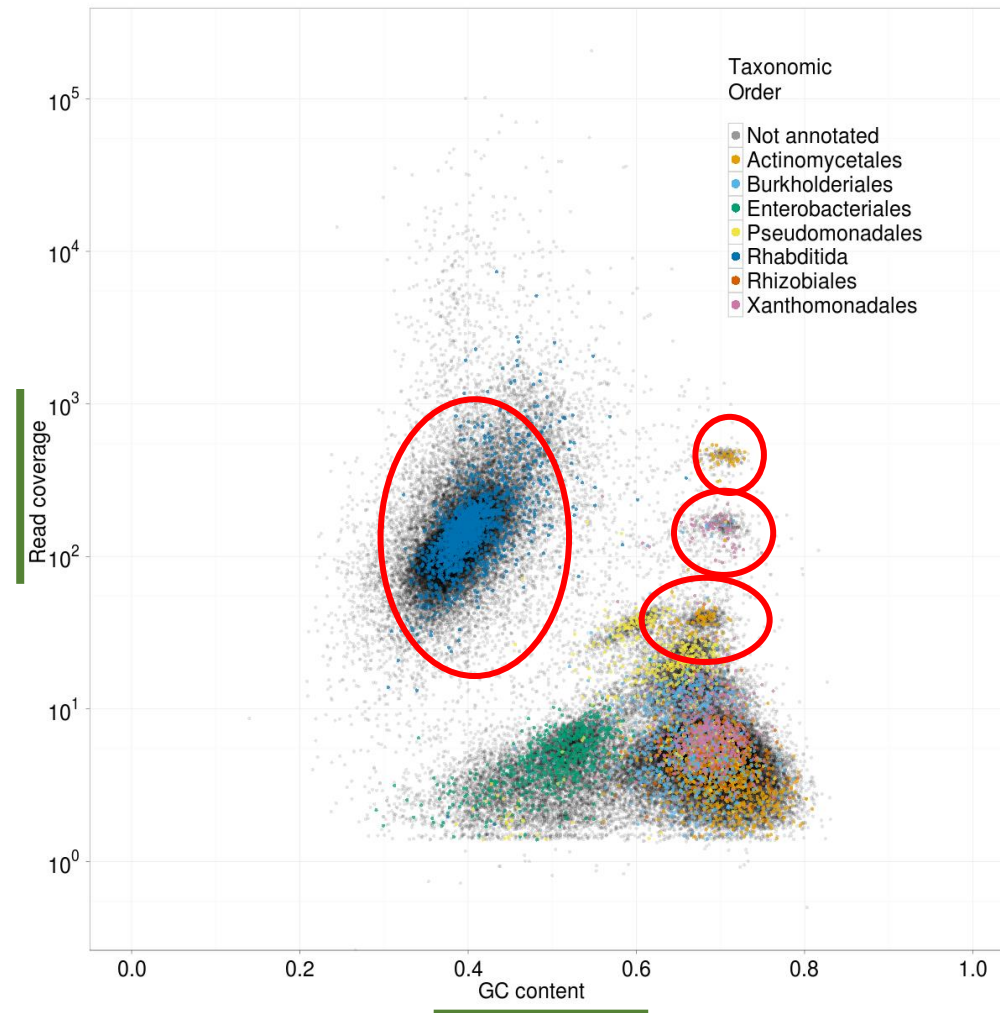
Three main steps involved:

- Contigs (i.e. assembled sequences) classification
- Contigs selection (based on experimenter criteria)
- Reads extraction and assembly

THE BLOBOLOGY METHOD

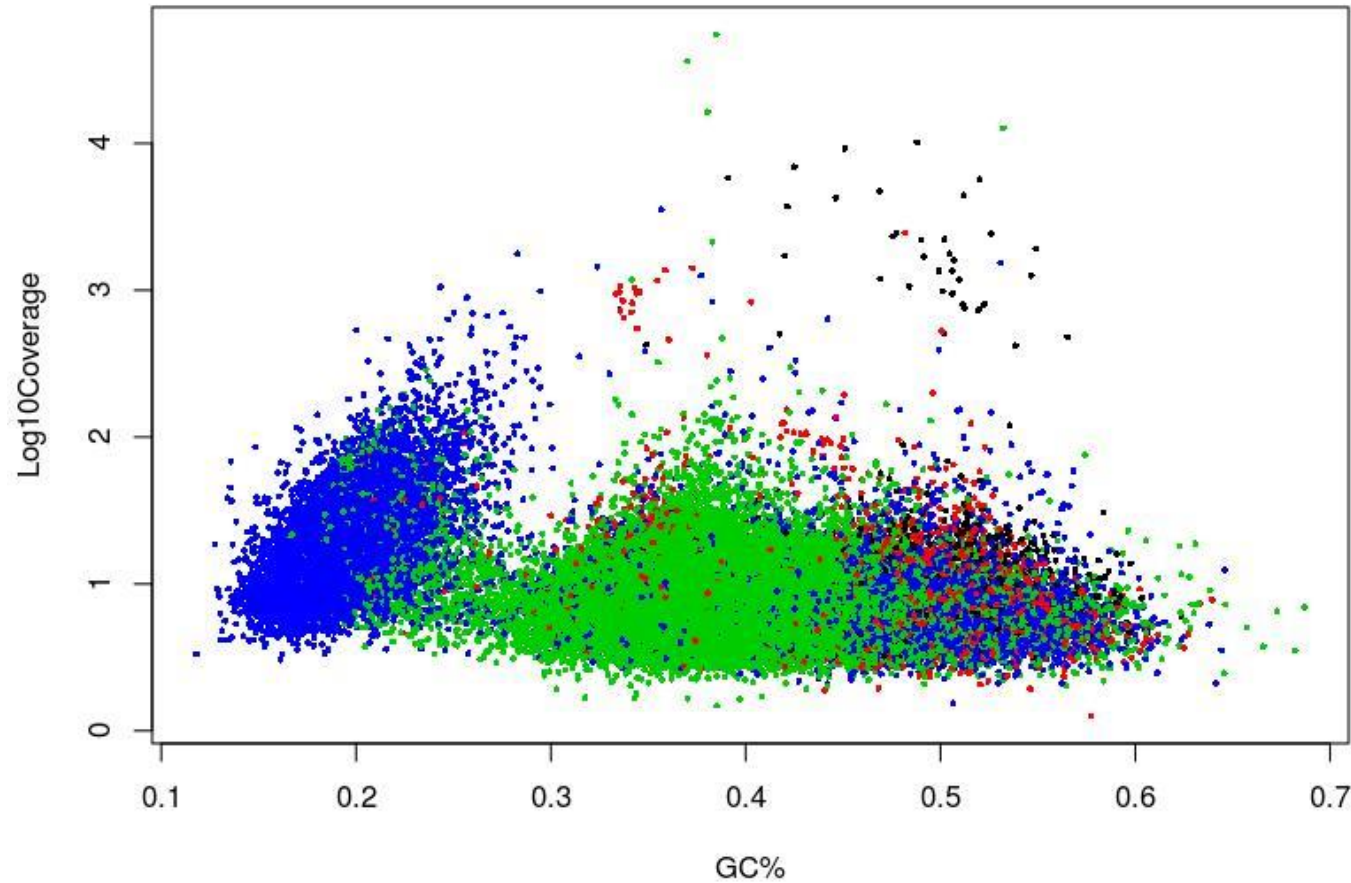


THE BLOB-PLOT



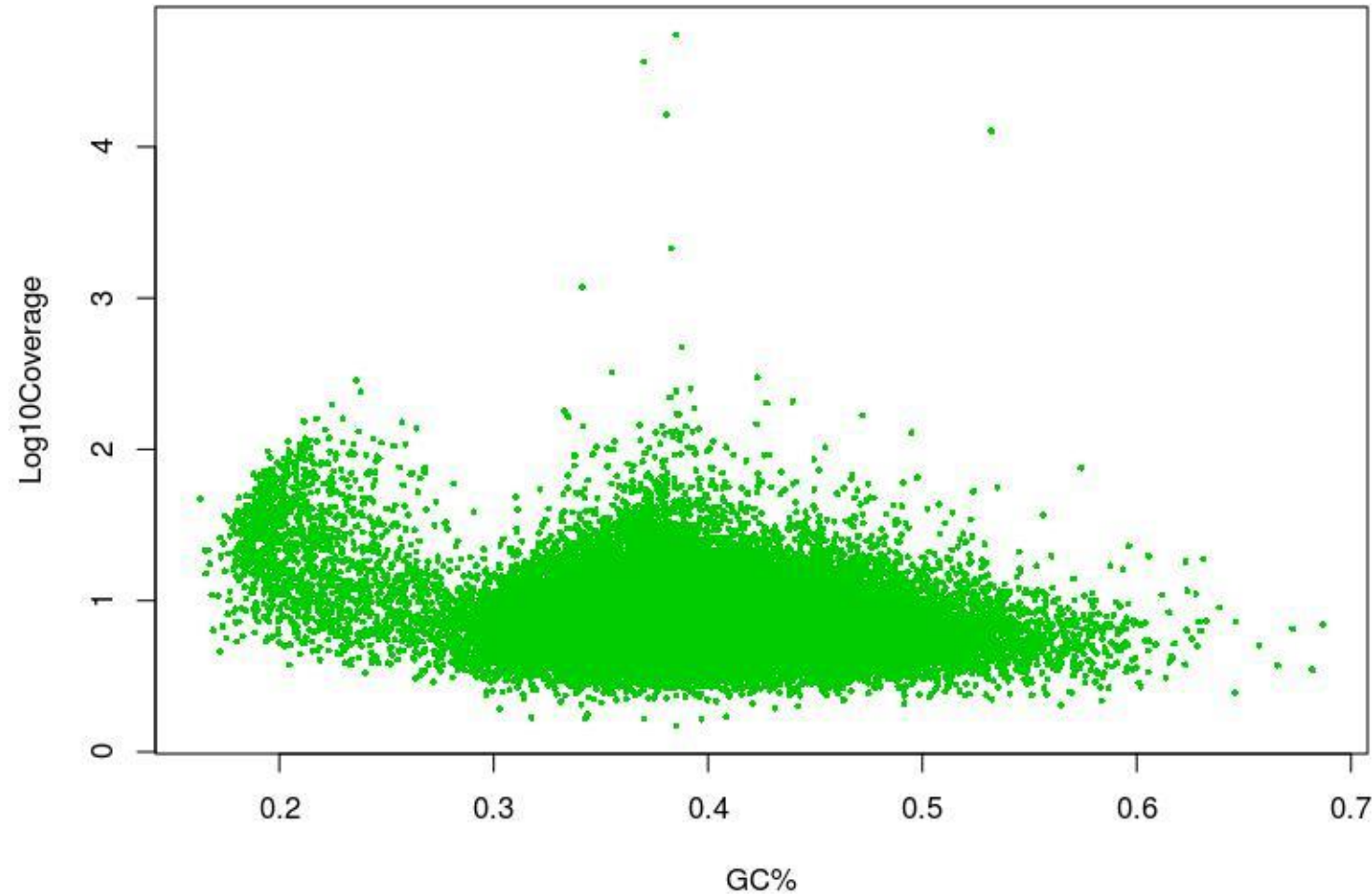
Kumar et al. 2003

A FIRST EXAMPLE

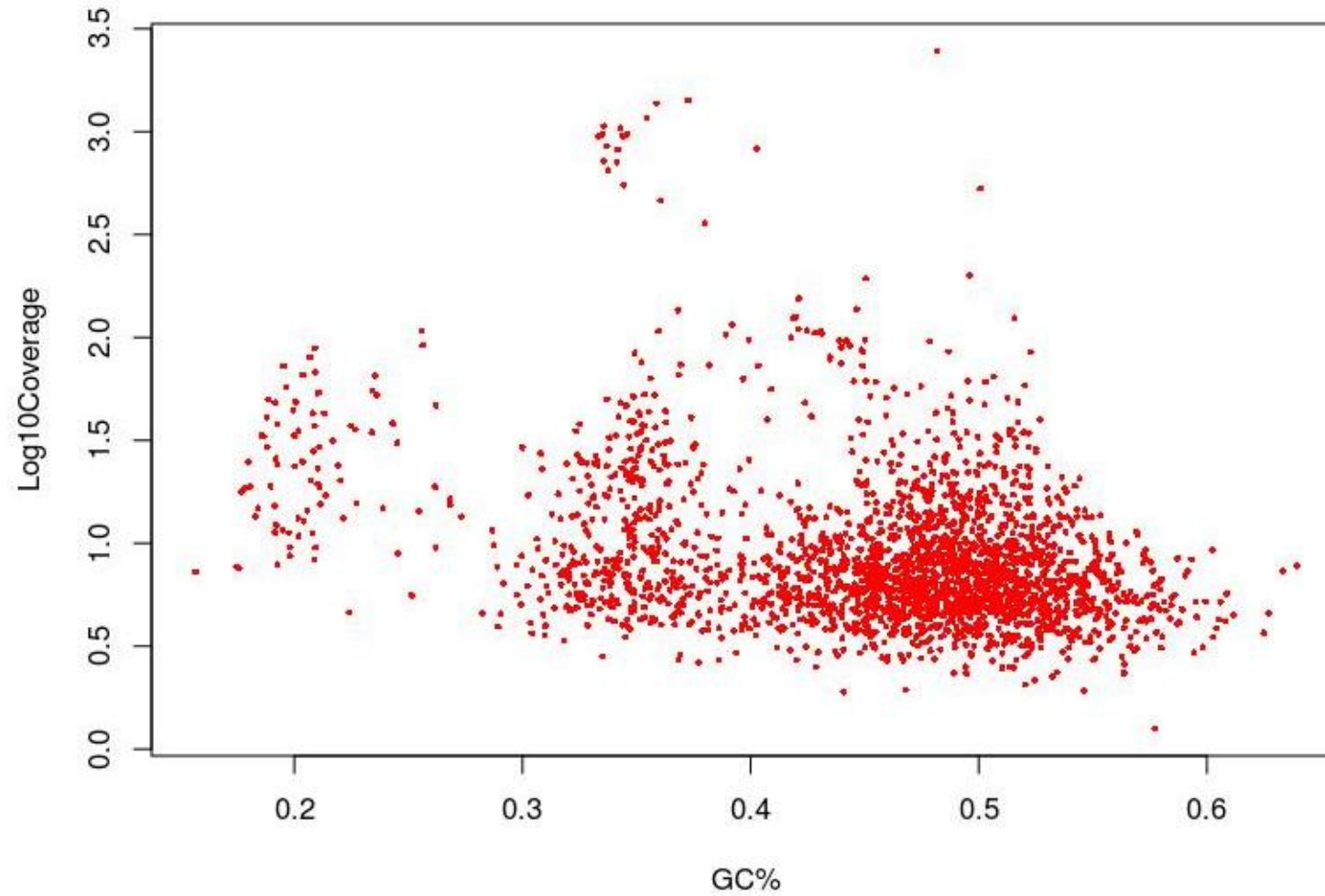


- Bacteria
- Eukariota
- Archaea
- Not annotated

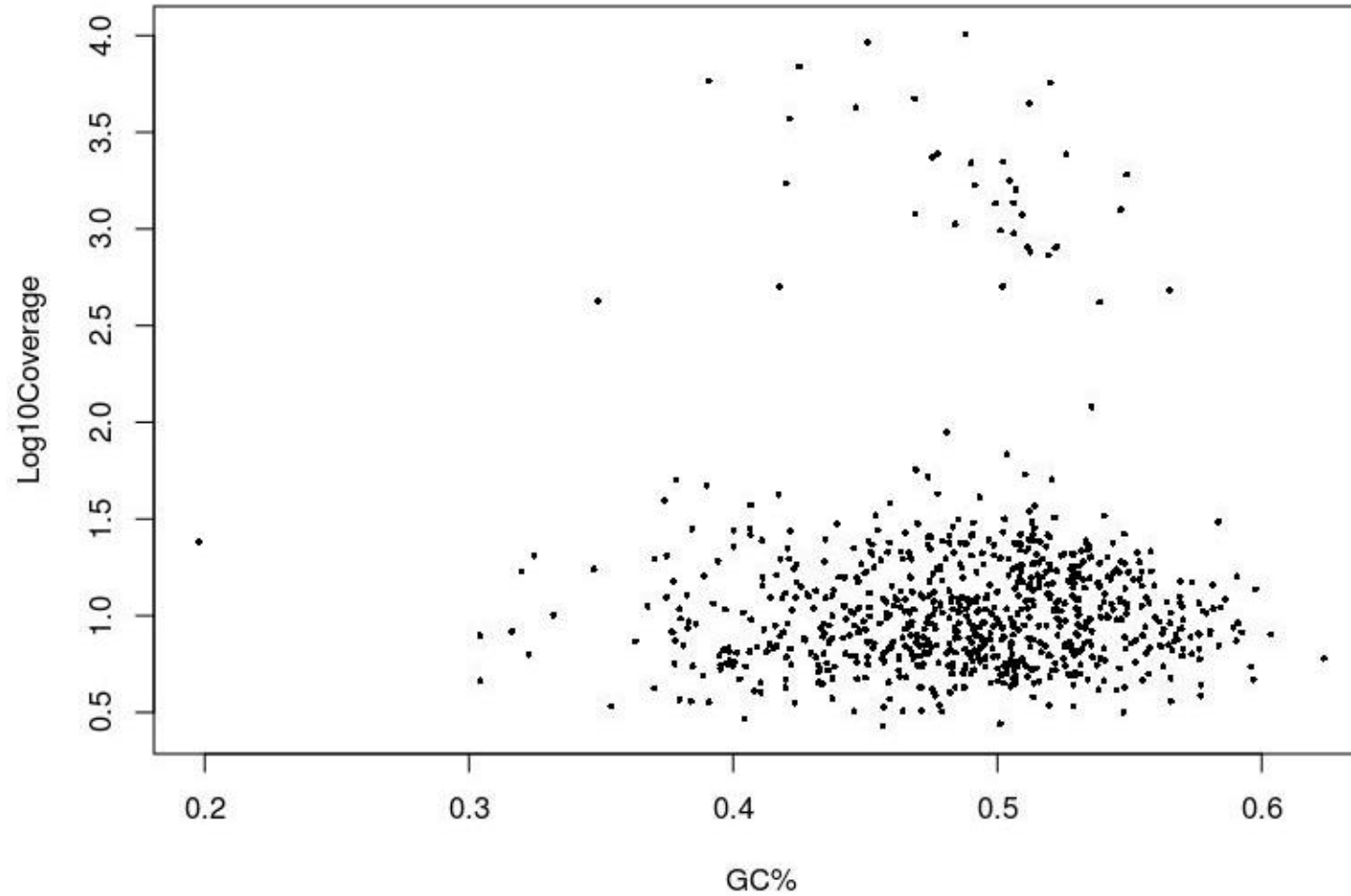
ONLY EUKARYOTS

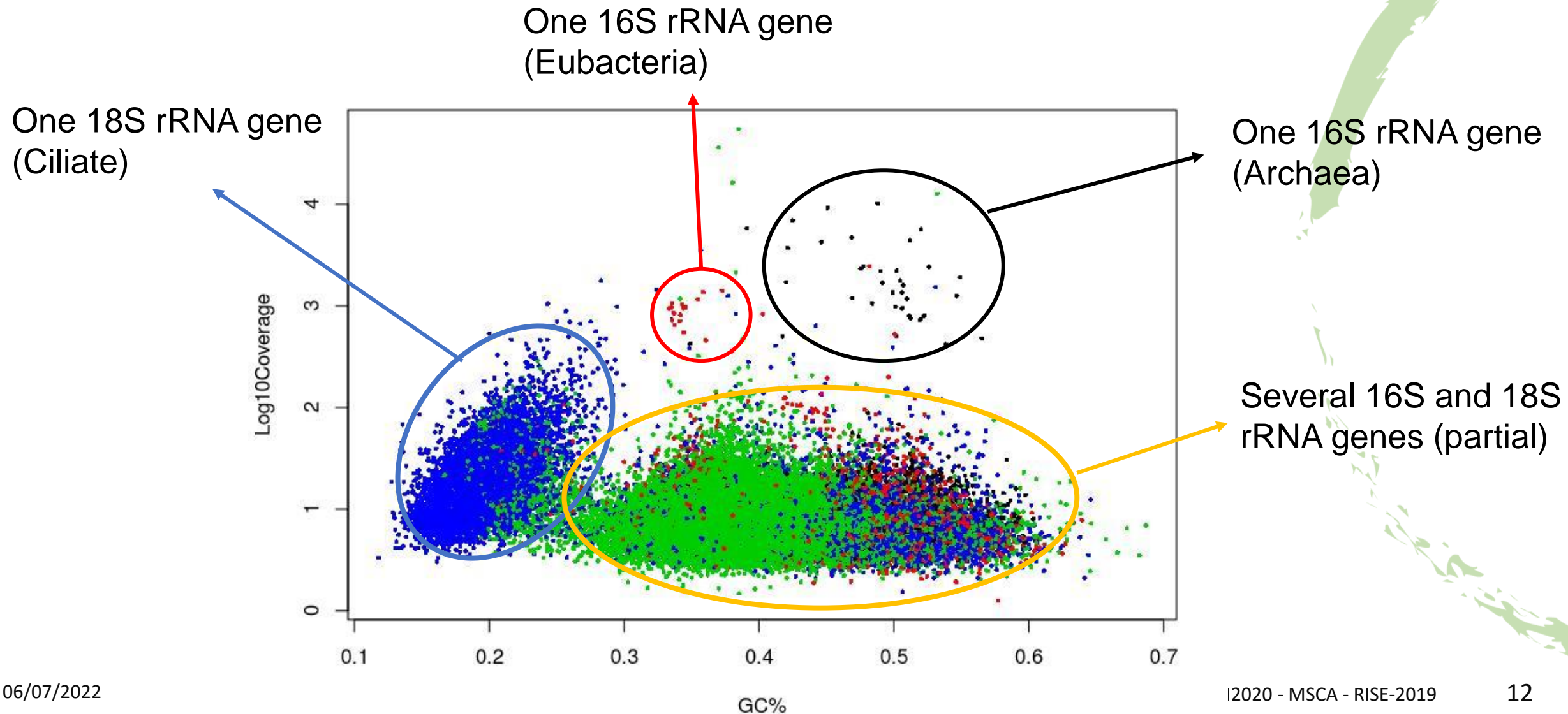


ONLY EUBACTERIA



ONLY ARCHAEA



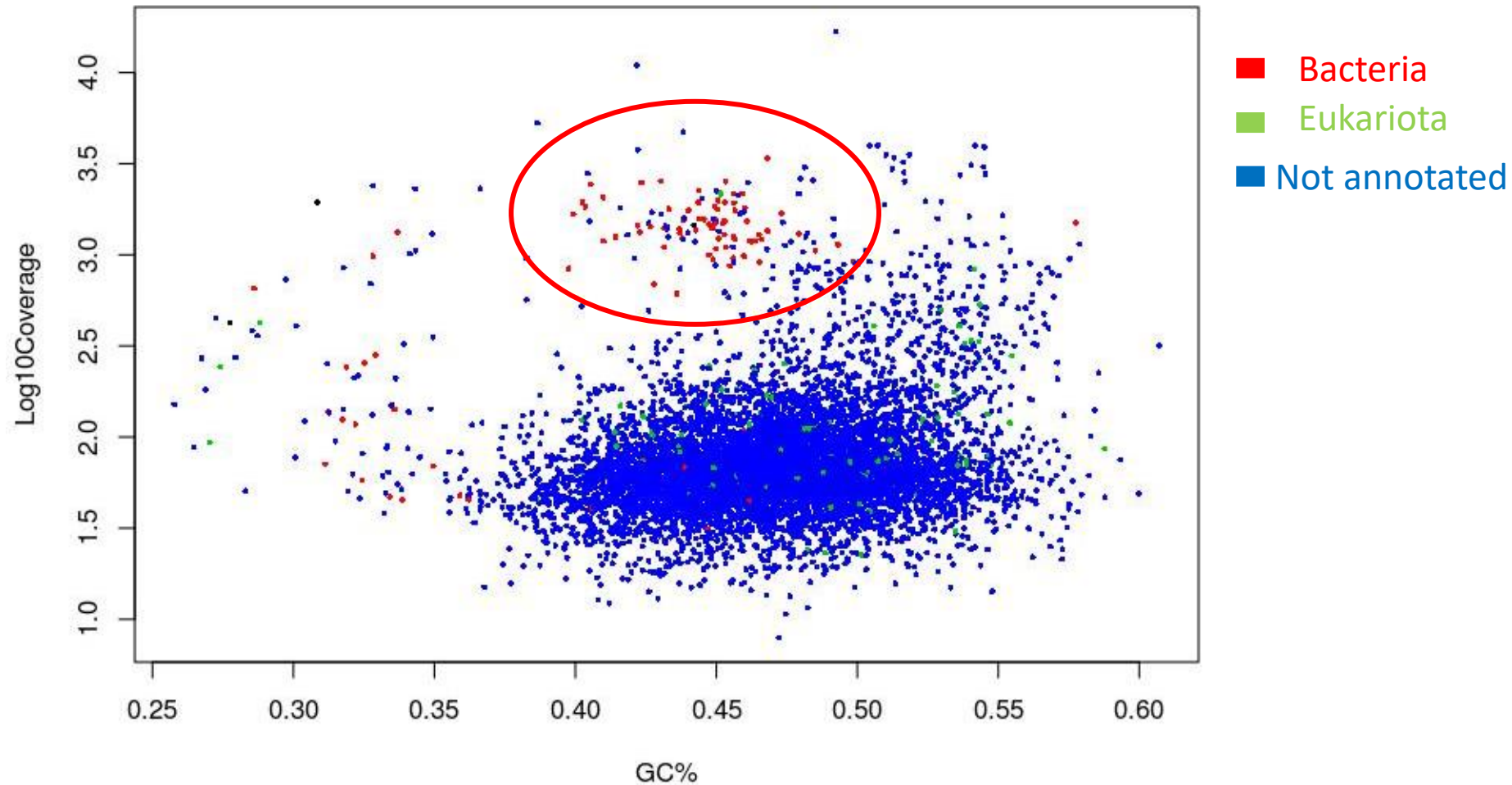


THE BIG QUESTION

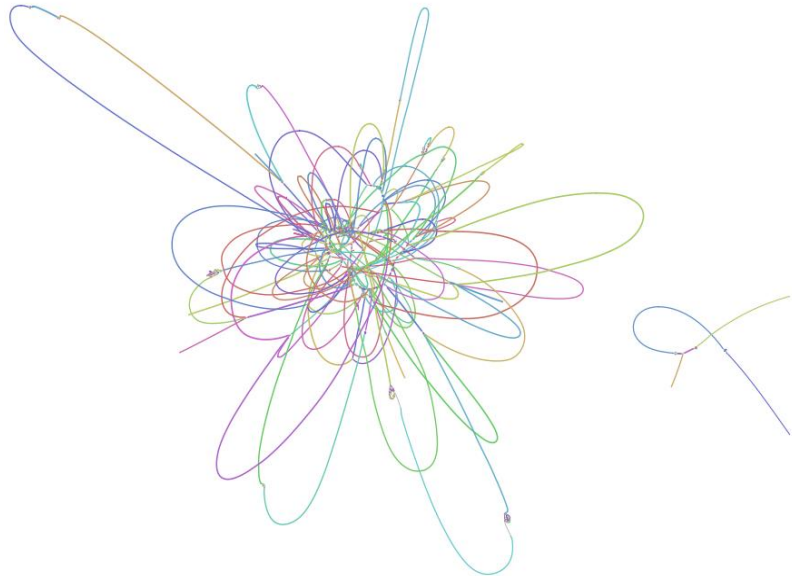


YES, BUT DOES IT WORKS?

Outline

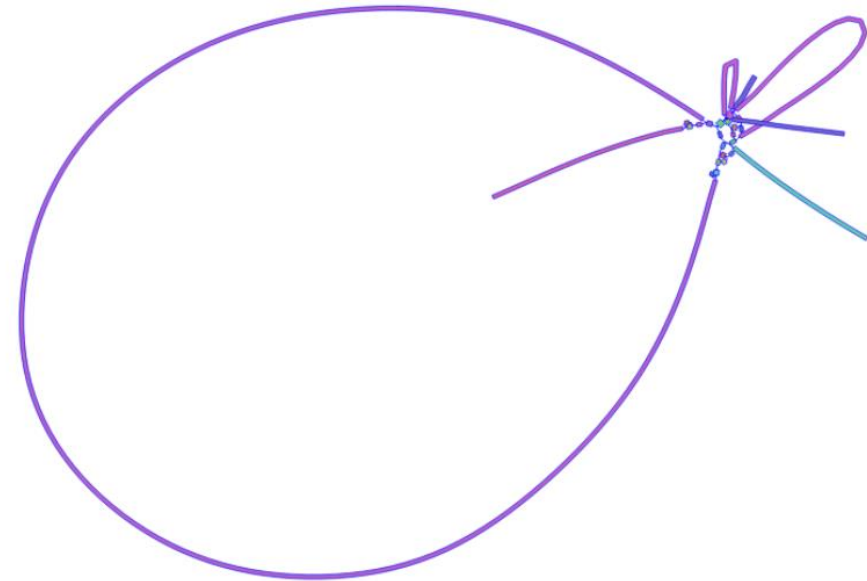


After the first preliminary assembly



203 contigs
2.530.225 total bp

After three rounds of re-assembling



27 contigs
2.582.098 total bp

TAKE HOME MESSAGE



- Obtaining good quality assemblies from metagenomic data can be quite challenging
- The Blobology method allow you to reduce the amount of data analyzed in order to help the assembly programs
- It can be applied to more complex systems. The less the elements of the system can be “spatially” separated the less this method can be applied

THAT'A ALL FOLK



THANK YOU FOR
YOUR ATTENTION

