

Analysis of SGB4964

Computational Microbial Genomics
project

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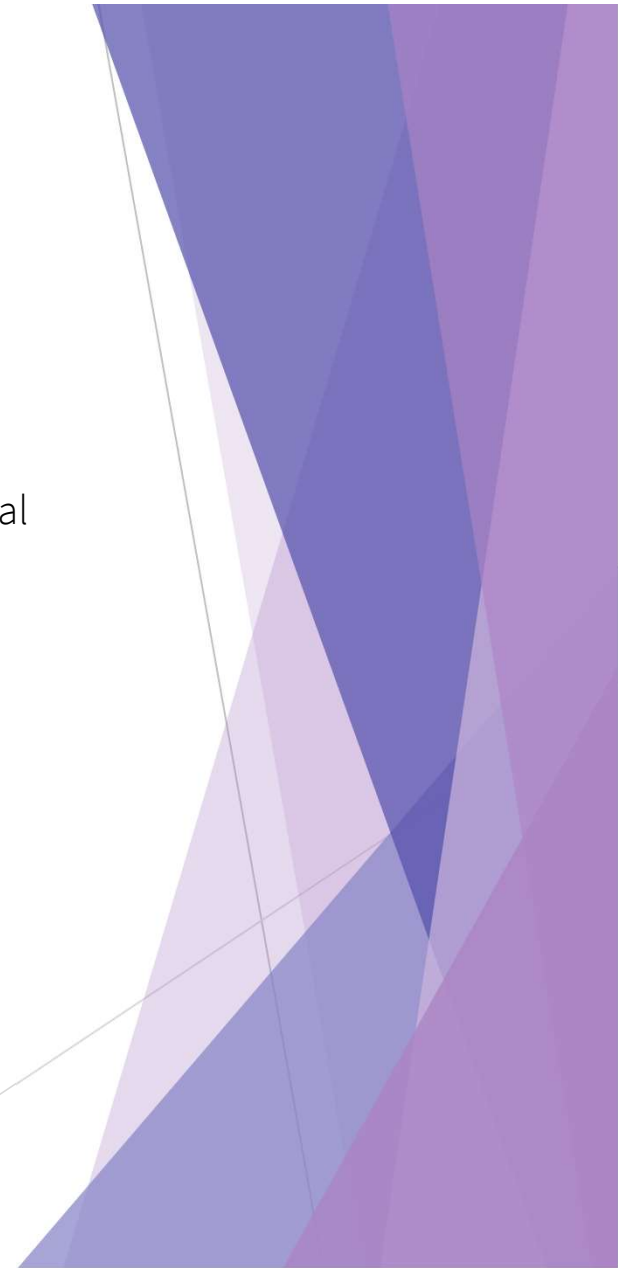
Introduction

Gut samples as most studied human microbiome

Difficulties of growing all bacteria in the lab, probably we just have not yet found the ideal conditions for this to happen

Shotgun metagenomic DNA sequencing

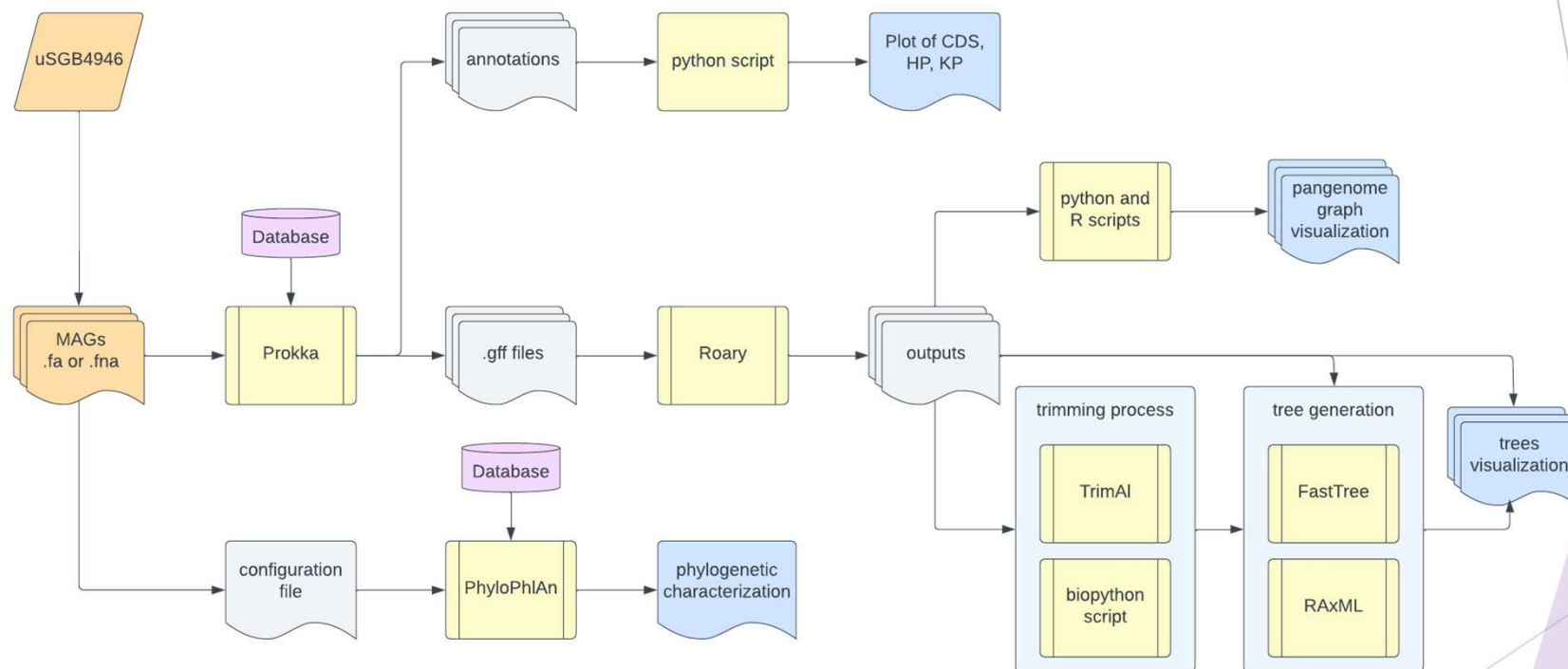
- **SGB4964**: up to now uncharacterized species-level genome bin
- consists of **31** metagenomic assembled genomes (**MAGs**)



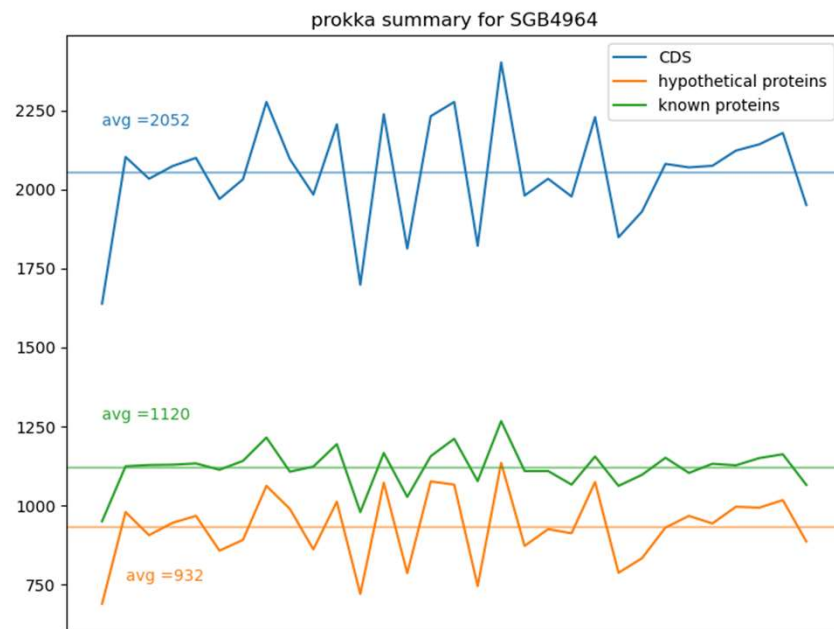
Methods

- Prokka* — gene annotations
- Roary* — pangenome analysis
- PhyloPhlAn* — taxonomic annotation
- TrimAl/biopython* — trimming of alignment
- Raxml/FastTree* — phylogenetic tree construction

Pipeline



Description of the set and genomic annotations

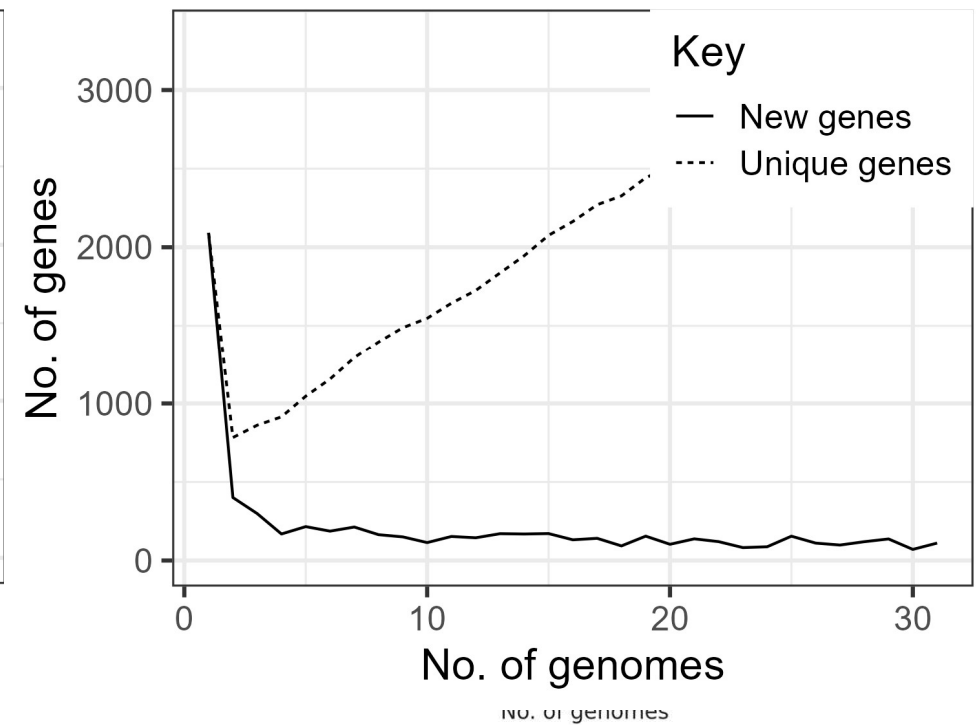
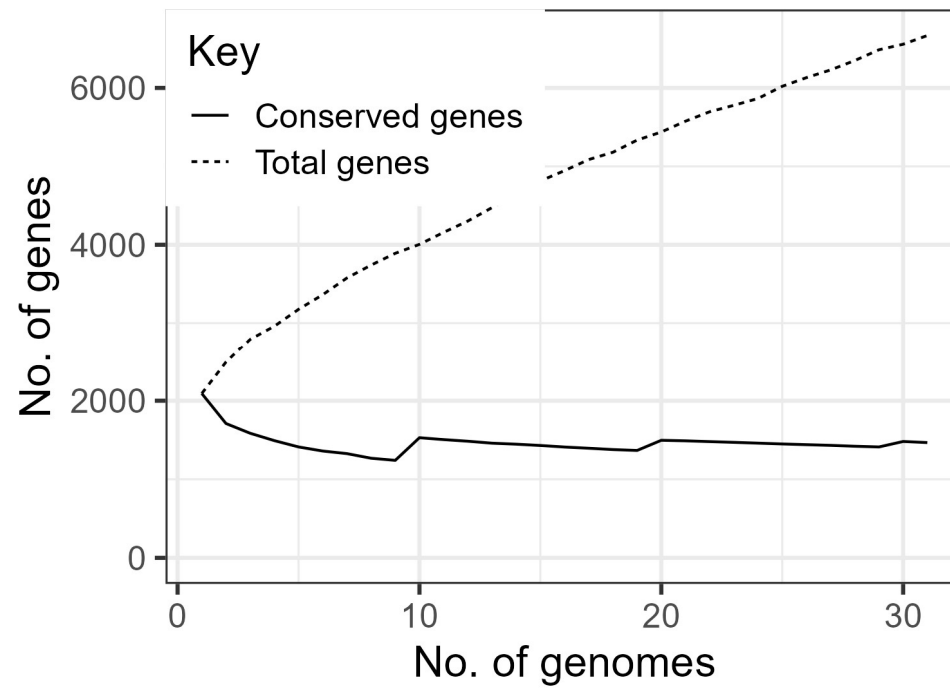


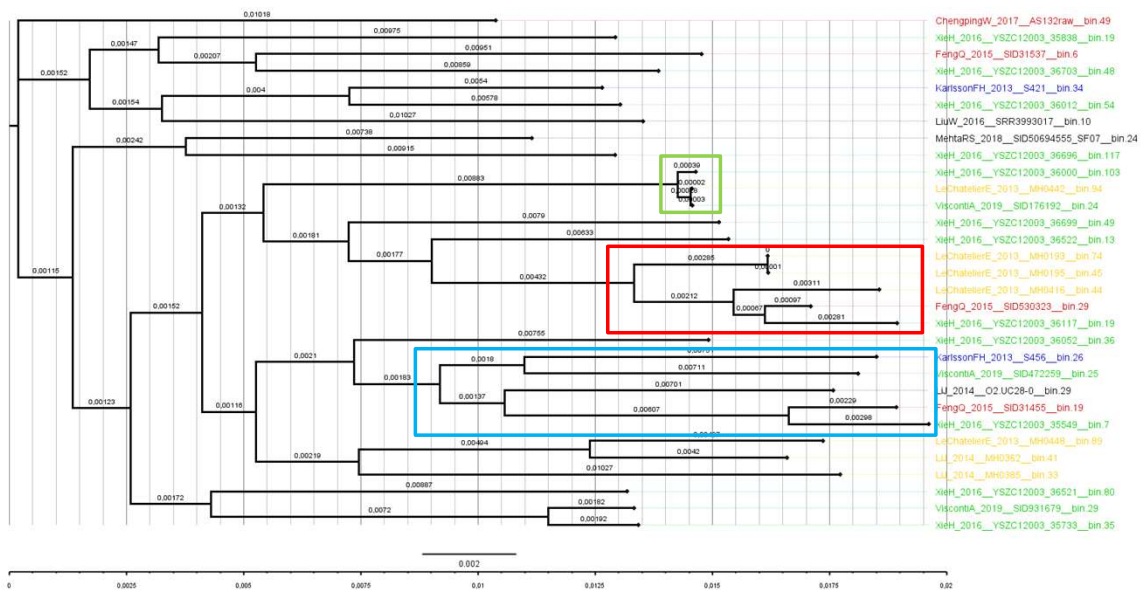
31 high quality MAGs (>90% completeness, <5% redundancy)

Mainly from westernized healthy individuals, lot of N/As fields

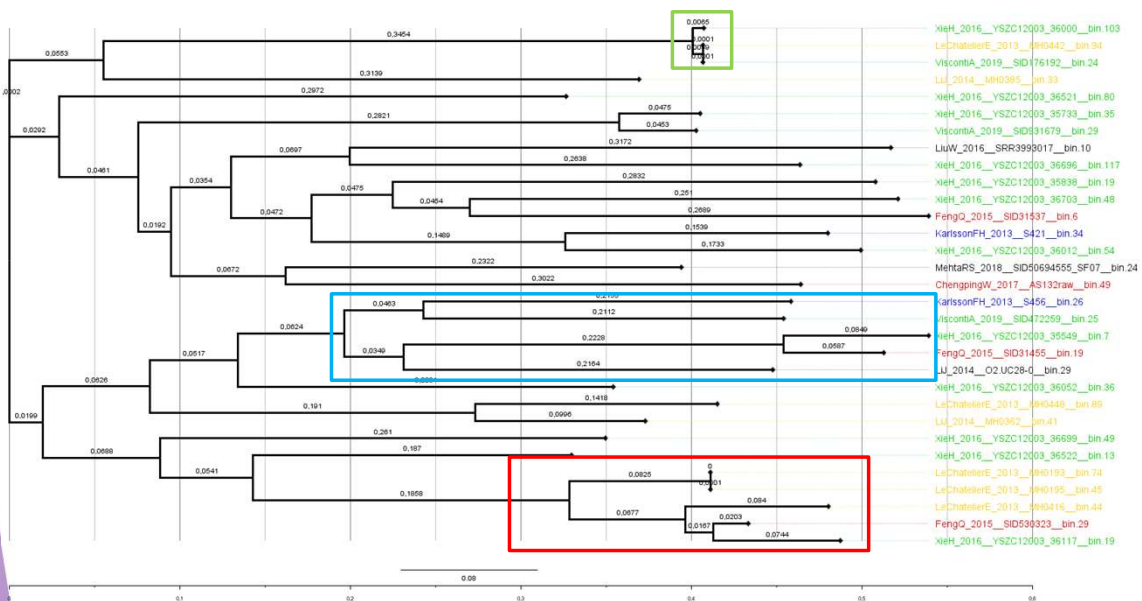
From prokka analysis we get more annotations of **known proteins** rather than hypothetical ones

Pangenome analysis





ChengpingW_2017_AS132raw_bin 49
 xieH_2016_YSCZ12003_35898_bin 19
 FengQ_2015_SID31537_bin 6
 xieH_2016_YSCZ12003_36703_bin 48
 KarlssonFH_2013_S421_bin 34
 xieH_2016_YSCZ12003_36012_bin 54
 LuW_2016_SRR3993017_bin 10
 MehtaRS_2018_SID50694555_SF07_bin 24
 xieH_2016_YSCZ12003_36696_bin 117
 xieH_2016_YSCZ12003_36000_bin 103
 LeChabotierE_2013_MH0442_bin 54
 ViscontA_2019_SID176192_bin 24
 xieH_2016_YSCZ12003_36699_bin 49
 xieH_2016_YSCZ12003_36522_bin 13
 LeChabotierE_2013_MH0193_bin 74
 LeChabotierE_2013_MH0195_bin 45
 LeChabotierE_2013_MH0416_bin 44
 FengQ_2015_SID330323_bin 29
 xieH_2016_YSCZ12003_36117_bin 19
 xieH_2016_YSCZ12003_36052_bin 36
 KarlssonFH_2013_S456_bin 26
 ViscontA_2019_SID472259_bin 25
 LU_2014_O2UC28-0_bin 29
 FengQ_2015_SID31455_bin 19
 xieH_2016_YSCZ12003_35549_bin 7
 LeChabotierE_2013_MH0448_bin 85
 LU_2014_MH0362_bin 41
 LU_2014_MH0362_bin 33
 xieH_2016_YSCZ12003_36521_bin 80
 ViscontA_2019_SID931679_bin 29
 xieH_2016_YSCZ12003_35733_bin 35



xieH_2016_YSCZ12003_36000_bin 103
 LeChabotierE_2013_MH0442_bin 54
 ViscontA_2019_SID176192_bin 24
 LU_2014_MH0362_bin 33
 xieH_2016_YSCZ12003_36521_bin 80
 xieH_2016_YSCZ12003_35733_bin 35
 ViscontA_2019_SID931679_bin 29
 LuW_2016_SRR3993017_bin 10
 xieH_2016_YSCZ12003_36696_bin 117
 xieH_2016_YSCZ12003_35898_bin 19
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 LeChabotierE_2013_MH0193_bin 74
 LeChabotierE_2013_MH0195_bin 45
 LeChabotierE_2013_MH0416_bin 44
 FengQ_2015_SID330323_bin 29
 xieH_2016_YSCZ12003_36117_bin 19

Phylogenetic analysis

Conclusions

- ▶ association with the phylogenetic family of Lachnospiraceae
- ▶ common gut associated microbe
- ▶ In literature it is generally linked with an inflammatory response
- ▶ starting point for further analysis on the identification of this possible new species.

The background of the slide is a repeating pattern of various microorganisms, including bacteria, viruses, and fungi, rendered in shades of purple and blue. The pattern is dense and covers the entire slide area. The text "Thanks for your attention!" is centered in the middle of the slide, overlaid on a lighter, semi-transparent rectangular area.

Thanks for
your attention!