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# Assessment of soil health for sustainable agriculture through metaphenomic approaches.

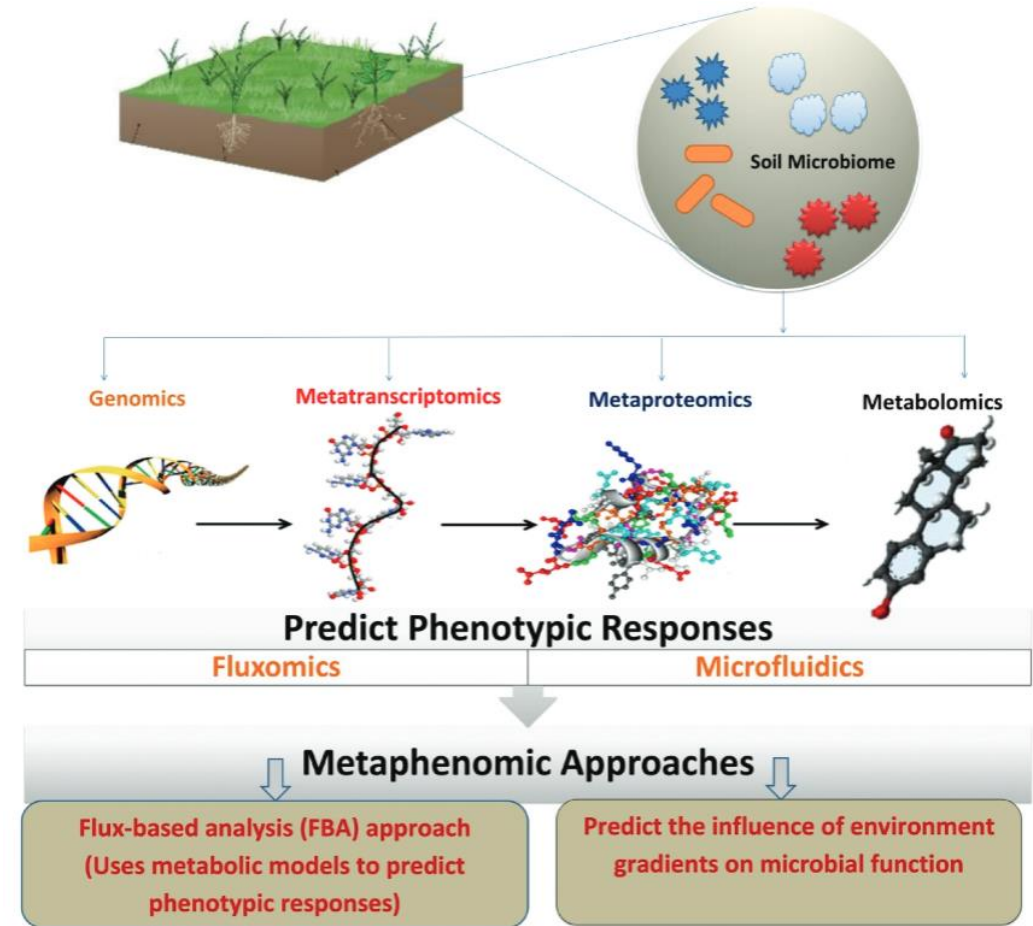
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# Can we assess and predict soil health through metaphenomic approaches?

- Soils as 'homes' for microbial communities
  - Can we identify specific microbial metagenomic and metabolomic characteristics for different soil types and histories (i.e., land use)?
- Linking microbiome to soil health
  - Can we establish clear pathways between microbial 'signatures' and environmental conditions (as well as anthropogenic pressures)?
  - Can we establish and predict whether a soil is healthy by looking at these relationships?



Source image: Azeem et al, 2022

# Project aims/approaches

- Extracting and sequence nucleic acids from soil samples and annotating functional genes
  - Skills learned:
    - Identification of soil types and characteristics (pedo-regions and pedo-climatic differences)
    - DNA and RNA isolation (Qubit fluorometer and Nanodrop 2000 - Thermo Fisher Scientific)
    - Taxonomic characterization of microbial communities present in the soil samples by 16S rRNA gene characterization
- Evaluating the physiological responses of the soil microbiome to external conditions and their pathways of interactions with plants and/or microbes
  - Skills learned:
    - Extraction of macromolecules for metabolomic and proteomic analyses
    - Identification of phenotypes, mapping metabolites and multiomics
- Developing an open-access bioinformatics tool that can be used to predict the environmental effects on soil microbe community
  - Skills learned:
    - Random Forest and machine learning algorithms
    - Bioinformatic and online tools (e.g., Kyoto Encyclopedia of Genes and Genomes Orthology)



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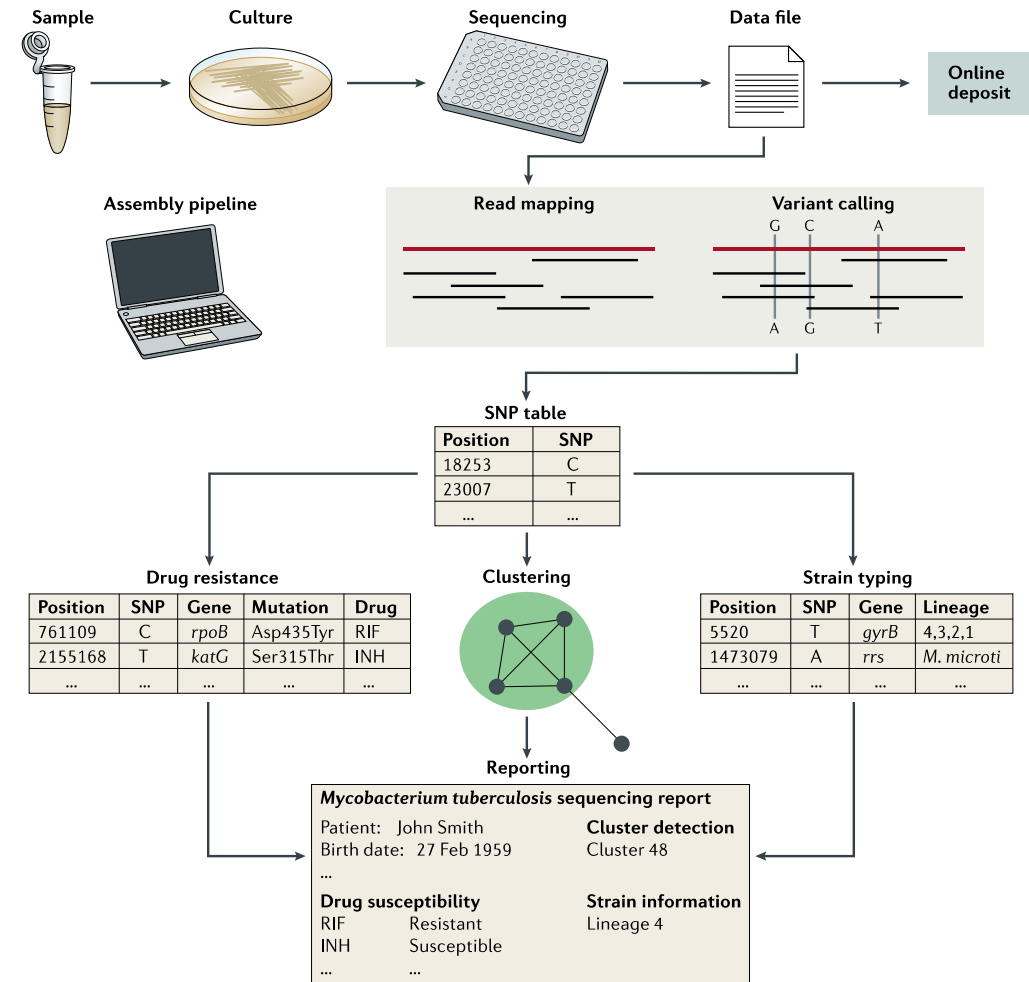
# Developing genomic epidemiology frameworks for pathogenic mycobacteria in animals.

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# How do we track transmission of mycobacteria?

- Most frameworks are developed for *Mycobacterium tuberculosis* variants infect humans
  - Specific genome similarity cut-offs
  - Known lineage assignments
- Need to expand this to other mycobacteria
  - How do we track mycobacterial infections in animals?
  - What kind of pathogen population structure do we see in different wildlife and agricultural species?



# Project aims/approaches

- Extend and validate the frameworks made for human-associated tuberculosis to animal-associated variants and non-tuberculosis mycobacterial infections
  - Skills learned:
    - UNIX pipeline creation
    - Python script writing
    - Comparative genomics
    - Bayesian and maximum likelihood phylogenetics
- Create new within-lineage population structure markers to help identify circulating strains
  - Skills learned:
    - Population genetics
    - Rscript
- Explore genomic datasets for new insights into the epidemiology of animal-associated mycobacteria
  - Skills learned:
    - Molecular epidemiology
    - Genome assembly
    - 'Omics processing

