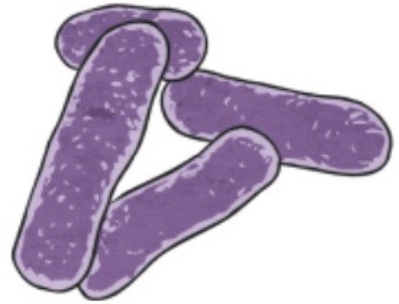
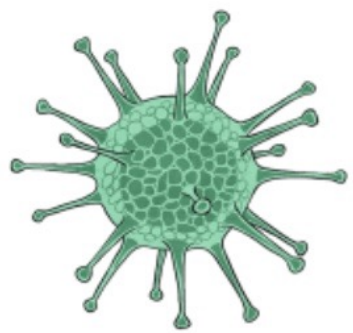
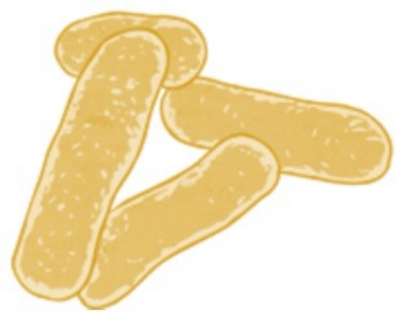




Microbial community genomics block course
Student projects

[TECHNICAL]

Project 1: Exploration of the effect of MAG quality on metabolic reconstruction

- **Rationale:** GEMs are ideally built with complete genomes from a single organism. However MAGs are rarely complete and may represent to some extent a consensus genome of closely-related organisms.
- **Goal:** Explore the effect of completeness and contamination on the reconstructed GEMs.
- **Notes:**
  - A good approach would be to identify species clusters with many MAGs of varying completeness/contamination, run GEMs for all genomes and compare them.

[TECHNICAL]

Project 2: Exploration of the effect of *carveme* stochastic component on GEM reconstruction

- **Rationale:** One feature of *carveme* is that different GEMs may result if *carveme* is run several times for the same genome.
- **Goal:** Explore the effect of this stochastic component on the resulting GEMs at different levels (reaction/metabolite/uptake/secretion).

- **Notes:**
  - A good approach would be to pick up the ~10 most relevant genomes (most abundant?) and build 10 independent GEMs for each.

[METABOLISM]

Project 3: Description of the metabolic potential of a global collection of marine microbes

- **Rationale:** Translating genomic information into metabolic capacities and potential of organisms is far from being a straightforward exercise. However, understanding the metabolic potential of marine microbes and its relation to genome features is very relevant.
- **Goal:** Extract simple but informative metrics from GEMs which describe the metabolic potential of organisms (such as the total number of genes, reactions or metabolites) and describe how these are related to each other, how these relate to genomic features and how these are distributed across taxonomic groups.

- **Notes:**

[METABOLISM]

Project 4: Description of the metabolic capacities of a global collection of marine microbes

- **Rationale:** Translating genomic information into metabolic capacities of organisms is far from being a straightforward exercise. GEMs is one way of doing that.
- **Goal:** Describe the metabolic capacities of all GEMs built from a global collection of marine genomes. Describe if coherent cluster of genomes can be found and what metabolisms they represent.

- **Notes:**
  - Data available. Can be done for different layers of info (reaction/metabolite/uptake/secretion)
  - Comparison of different layers might inform on metabolic redundancy
  - Will require some skills in multivariate statistics (PCA or similar, clustering, etc.)

[METABOLISM]

Project 5: Describe the phylogenetic conservation of metabolic capacities

- **Rationale:** Understanding how metabolic capacities are distributed across phylogenetic groups is key to understand the evolution of metabolism.
- **Goal:** Describe the “core” and “accessory” reactions at different taxonomic levels to understand the relationship between taxonomy and metabolism.

- **Notes:**
  - Data available. Conceptually complex. Might need some reading on pangenomes to get inspiration.

[METABOLISM]

Project 6: Describe the variation in the metabolic capacities of the key lineages in the ocean

- **Rationale:** Closely related organisms may highly differ in their genomic content and this might be the result of adaptation to different environments. This has been previously described for several marine lineages based on genomic data but has never been addressed based on GEMs.
- **Goal:** Describe the differences in the metabolic capacities for closely related genomes of the key lineages in the ocean and how these relate to the environment.

- **Notes:**
  - Data available.
  - Potential clades: Prochlorococcus, Synechococcus, Alteromonas, etc.
  - Results would need to be contrasted to existing literature.

[METABOLIC INTERACTIONS]

Project 7: Describe amino acid auxotrophy

- **Rationale:** Many microorganisms in nature are auxotrophic, that is, they are unable to synthesize all of the vital nutrients. Access to these nutrients is therefore essential, and the lack of these nutrients inhibits cell division and growth. Describing how auxotrophies are distributed across the marine microbiomes is an essential first step to understand how and why auxotrophy is maintanined.
- **Goal:** Describe the distribution of aa auxotrophies.

- **Notes:**
  - Can be combined with SMETANA to infer potential prototrophs

[METABOLIC INTERACTIONS]

Project 8: Metabolic interaction analysis of marine communities across a spatial gradient

- **Rationale:** Species interactions are thought to be one of the factor shaping community composition. Information derived from GEMs allow to infer potential metabolic interactions between species. However this has never applied to actual marine microbial communities.
- **Goal:** Reconstruct metabolic interactions based on GEMs from the members composing real marine communities and explore these along latitude and/or depth.

- **Notes:**
  - Choose the ~10 most abundant members of real communities along a spatial gradient (latitude and/or depth)
  - Run SMETANA for such communities and analyze the results

[METABOLIC INTERACTIONS]

Project 9: Metabolic interaction analysis of marine communities across a seasons

- **Rationale:** Species interactions are thought to be one of the factor shaping community composition. Information derived from GEMs allow to infer potential metabolic interactions between species. However this has never applied to actual marine microbial communities.
- **Goal:** Reconstruct metabolic interactions based on GEMs from the members composing real marine communities and explore these along seasons.

- **Notes:**
  - Choose the ~10 most abundant members of real communities along an entire year using time series (e.g. 1 sample/month from HOT or SPOTS)
  - Run SMETANA for such communities and analyze the results

[METABOLIC INTERACTIONS]

Project 10: Reproduction of known metabolic dependencies using Species Metabolic Interaction Analysis

- **Rationale:** Information derived from GEMs allow to infer potential metabolic interactions between species. However SMETANA has not been thoroughly validated. However, well-known metabolic interactions exists in the marine environment that can be used as benchmarking examples.
- **Goal:** Use well-known cases of metabolic dependencies in the marine environment and test if these are reproduced when SMETANA is applied to the corresponding genomes.

- **Notes:**
  - Require some reading and finding known cases. Some might be:
    - Nitrification (NH3 -> NO2 -> NO3)
    - Prochlorococcus + SAR11
    - Prochlorococcus + Alteromonas