sourmash taxonomy: LCA summarization of genome-resolved taxonomic profiling

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✉ — Correspondence possible via GitHub Issues

Abstract

Background

Taxonomic profiling intro...

Sourmash gather is a method to use combinatorial observations of k-mers to find the minimum set of reference genomes that contain all k-mers of the query dataset. Sourmash gather results are non-overlapping: each k-mer is assigned to one and only one genome match. Gather results are to specific genomes, but many biological applications work at the species-level, rather than strain level. This is especially important as these strain matches may not be the best/ideal results. In many cases, the specific strain in your dataset may not be available in the database, meaning the results end up matching to a few suboptimal reference genomes. Sourmash taxonomy is a sourmash module designed to ingest sourmash gather results, integrate taxonomic information, and optionally aggregate the results using a lowest-common-ancestor approach.

Implementation

Sourmash taxonomy conducts LCA-style taxonomic summarization of the genomic profiling results from sourmash gather. It was introduced in sourmash v4.2.

LCA-Style Lineage summarization

Sourmash gather uses a minimum set cover approach to identify the smallest set of reference genomes that contain all query information (k-mers) [1]. These matches are non-overlapping; that is, the sum of the query fraction assigned to each genome will be at most 100% (entire query matched to reference genomes).

Sourmash taxonomy LCA approaches apply the taxonomic information from these reference genomes to their assigned query fraction and sum matches that correspond to the same taxonomic rank. For example, if the `sourmash gather` results for a metagenome include matches to 10 different strains of a given species, `sourmash tax` LCA can sum the fraction uniquely matched to each strain to obtain the total fraction uniquely matched to this species.

Because this approach relies upon non-overlapping reference assignments, separate `sourmash gather` results for the same query cannot be combined. However, `sourmash gather` can be run with any number of desired reference databases at once to produce a single set of non-overlapping assignments.

Two `sourmash tax` commands use this LCA-Style summarization: `metagenome` and `genome`.

sourmash tax metagenome

"sourmash tax metagenome" is designed to conduct LCA aggregation for metagenomes to build a taxonomic profile. `tax metagenome` ingests sourmash gather results from one or more metagenome queries and summarize the results for each metagenome at each taxonomic rank. `tax metagenome` provides several output formats, including some that are designed to facilitate input into downstream analysis tools.

krona

lineage_summary

kreport

csv_summary

sourmash tax genome

`sourmash tax genome` is designed to aggregate sourmash gather results run on genome assemblies. Rather than summarizing at each taxonomic rank, sourmash `tax genome` summarizes gather results starting from the lowest rank (species) and will classify the genome as soon as a user-modifiable criterion is reached. There are two classification strategies: classify the query once a match threshold is reached (e.g. 10% containment or 95% cANI), or classify the query once a rank is reached, regardless of percent match. The first strategy is recommended for more robust classification; the second strategy is required for downstream tools requiring all inputs at the same rank.

Outputs for downstream visualization

Note we also offer krona output from metagenome or rank-classified genome results, as well as a lineage_summary output for tax metagenome that may be useful for external multi-sample visualization tools.

Utility commands

sourmash tax annotate

tax annotate annotates gather results with taxonomic information, without doing any LCA summarization.

sourmash tax prepare

tax prepare is a method for converting a csv of taxonomic lineage information into an sqlite database to enable faster loading and lineage assignment. It can also be used to combine lineage information for more that one database (e.g. GTDB, NCBI).

sourmash tax summarize

Summarize the lineage information in a human-reaedable summary

sourmash tax grep

select genomes entries by lineage; most useful for selecting subsets of results or reference genomes for sourmash analyses.

Results

Tax Metagenome

Reads

Contigs

Tax Genome

Discussion

- Database recommendations
- gather thresholding discussion/recommendations
- Limitations
    - K-mer size – > specificity/ sensitivity
    - K21 will give you species assignments, but you might not want to use them…
- Improvements:
    - Tax db inside of zip database?
    - Additional plotting?
    - CAMI output (need taxid)
    - genbank vs gtdb taxonomy translation?

References

1. **Lightweight compositional analysis of metagenomes with FracMinHash and minimum metagenome covers**
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