microbetag: simplifying microbial network interpretation through annotation, enrichment and metabolic complementarity analysis

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Abstract

*

Up to 350 words.
The abstract must include the following separate sections:
Background: the context and purpose of the study
Results: the main findings
Conclusions: a brief summary and potential implications

*Looks liks Chris Quince is our editor.

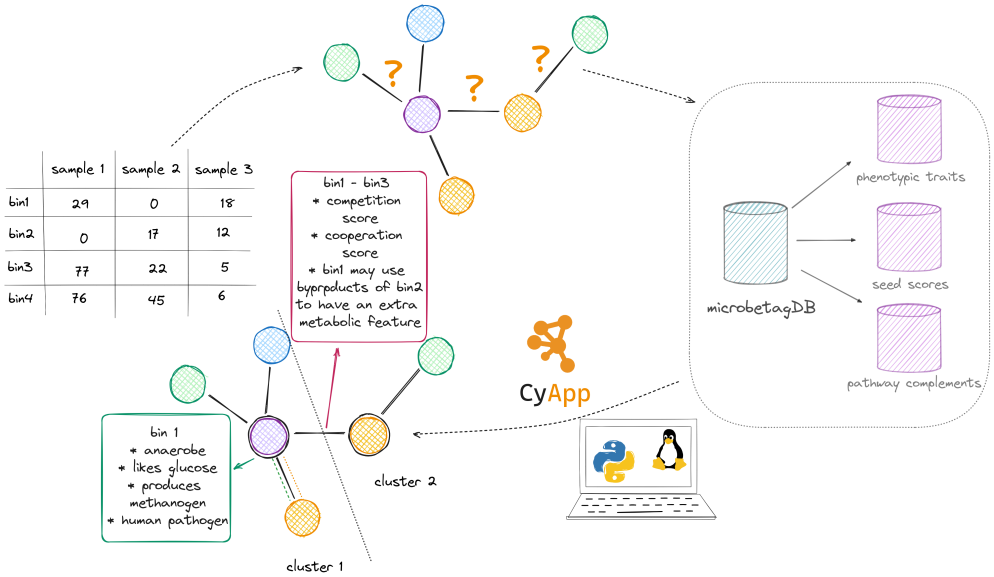

Figure abstract.

Keywords: microbial associations, enrichemnt analysis, data integration, pathway complementarity, seed set

Background [1] [2]

Microbial ecology plays a fundamental role in the stability and resilience of ecosystems and their processes; from soils, aquatic environments and biogeochemical cycles [1] to host-associated environments and the human health [2, 3]. Most microbial species live only in communities [4] and most natural microbial communities consist of hundreds or even thousands of species [5]. Each species exhibits a unique repertoire of metabolites and showcases adaptability across various metabolic niches, each with specific nutrient and environmental requirements. To unravel microbial ecology involves disentangling the principles that dictate the organization of a community, encompassing both its composition and metabolic activities. This, in turn, entails understanding the dynamics governing interactions among microbial species and their relationships with the surrounding environment [6].

In recent years, there has been a compelling suggestion proposing an elegant paradigm for microbial ecology: the correlation between community functional and taxonomic composition hinges on the relative importance of metabolic niche effects

[1] We are to submit in the Microbiome journal as a "Software" manuscript, thus we follow these rules
[2] The introduction should not include subheadings. The Background section should explain the relevant context and the specific issue that the software described is intended to address.

relative to the processes inducing variability within functional groups [7]. Comparable environments should foster similar microbial community functions, even though there may be taxonomic variations within individual functional groups, while in more heterogeneous environments functional β diversity would be strongly correlated with taxonomic β diversity. In the latter, the decoupling between community composition and metabolic functioning is concealed by robust metabolic niche effect [7]. Thus, an interaction between two taxa may vary in different environments. Microbial interactions can be the result of multiple phenomena, such as exchange of metabolic products [8], biofilm formation [9], gene transfering [10] and signaling [11].

High-throughput sequencing (HTS) has provided great insight into the diversity and composition of microbial communities [12]. Uncultivated species can now be detected and their featues can be inferred through their genomic information [13]. Moreover, the composition of thousands of microbiome samples is now accessible allowing for the inference of patterns among sets of samples. A widely used approach to extraxt such patterns, is the creation of co-occurrence networks based on metagenomic read data (amplicon and/or shotgun) [14]. A great number of approaches is avaialble for co-occurrence network inference based on a range of statistical concepts such as: correlation (e.g., CoNet [15], SparCC [16]), linear regression (e.g., SpiecEasi [17]) and causal inference (FlashWeave [18]). Nevertheless, microbial co-occurrence networks continue to encounter various challenges [19], encompassing issues associated with data analysis and network construction, leading to tool-dependent analysis [4, 20, 21]. But also, challenges regarding the interpretation of the networks. Addressing the well-articulated question of *What can we learn from the hairballs* posed by Röttjers et *al.* [4] could provide essential insight on the mechanisms of the interactions.

The use of microbial network inference as a means for predicting interactions has underscored its limited accuracy, and the fact that the biological implications of network properties remain unclear [22]. Theoretical principles derived from network studies might provide indications of emergent biological characteristics [4, 23]. For example, modules (highly interconnected nodes) within microbial co-occurrence networks could serve as indicators of ecological processes that govern community structure, including niche filtering and habitat preference[24]. Data integration and clustering have been suggested to address this challenge [19]. Clusters identified in microbial association networks have demonstrated their ability to mirror key drivers of community composition [25] and sevaral algorithms and implementations are available [26]. However, data integration approaches in microbial co-occurrence networks are so-far limited. Here, we present `microbetag` , a microbial co-occurrence network annotator that exploits several channels of information to enhance/diminish the confidence of the associations suggested on the network and generate hypotheseses for further investigation both at the paired-interaction and the community level

`microbetag` serves as a comprehensive platform that consolidates information on taxa along with their potential metabolic interactions from multiple channels (see Implementation 3). Key concept on the presented approach is the exploitation of the *reverse ecology* approach [27]. Reverse ecology leverages genomics to explore community ecology with no *a priori* assumptions about the taxa involved. Making the most of advancements in systems biology and genomic metabolic modeling, as well as

system-level analysis of intricate biological networks, the reverse ecology framework enables the prediction of ecological traits for less-understood microorganisms, their interactions with others, and the overall ecology of microbial communities [28]. In this context, seed set analysis has been a major contribution in the study of both the species and the community ecology based on their genetic information.

A metabolic network's "seed set" is the set of compounds that, based on the network topology, need to be acquired exogenously [29] (see Figure 1). Such nodes might be independent, i.e. they cannot be activated by any other node in the network, or they can be interdependent forming groups of seed nodes. Seeds have been proven themeselves a successful proxy for the habitat of the organism and an essential tool in the frameowrk of reverse ecology [29, 30]. Based on the seed concept, several graph theory-based metrics (indices) have been described to predict species interactions directly from their networks' topologies [31–34]. Over the last years, the seed apprach has been implemented at the Genome-scale metabolic network reconstructions (GENREs) level. GENREs encapsulate mathematical representations capturing the biochemical reactions that could take place within an organism [35–37].

Metabolic complementarity among species, serving as a reflection of potential cooperation within communities, assesses the capacity for collaboration; cross-feeding or syntrophy interactions are typical examples of such a collaboration. Contary, metabolic competition refers to the metabolic overlap between two species leading to exploitative competition, e.g. for nutrient resources. Seed and non-seed sets can be used to compute such indices. Thorough examination of such complements can reveal metabolic interactions leading to patterns observed on the co-occurrence network.

Considering complementarity as a range of alternatives and paired-wise microbial interactions in the context of the community as a whole, microbial species may also exchange metabolic compounds that may be not seeds at a certain time but may allow them to perform functions that currently are not capable of [38, 39]. Such by-products may be even metabolites not even necessary for themeselves but for the community as a whole [40]. To explore the potenial of a species metabolism given they benefit from a partner of theirs, genome annotations combined with collections of functional units to highlight can provide a valid proxy. We present here a naive approach exporting all possible complements between a pair of species based on their KEGG ORTHOLOGY (KOs) annotations and the KEGG MODULES database [41].

`microbetag` integrates user's co-occurrence network integrating phenotypic traits on the taxa present on the network (nodes) and potential metabolic interactions to their suggested associations (edges). A Graphical User Interface (GUI) is supported as a CytoscapeApp providing a user-friendly environment to investigate annotations in a straightforward way. All annotations present on microbetagDB are also available though an Application Programming Interface (API). `microbetag` 's source code is under a GNU GPL v3 license and available on GitHub. Documentation and further support on how to use `microbetag` is available at documentation web-site. To the best of our knowledge there is not a software with which `microbetag` could be compared with directly. To validate our annotations we used a recently published network with partially known interactions between some pairs of species found associated [42] (see Results section, paragraph 3). To demonstrate `microbetag` 's potential, we present

the main features of its interface and we discuss a real-world use-case (see Discussion section, paragraph 3).

Implementation [3]

Genomes included

Using the Genome Taxonomy Database (GTDB) v207 metadata files, we retrieved the NCBI genome accessions of the high quality representative genomes, i.e. completeness $\geq 95\%$ and contamination $\leq 5\%$. A set of $26,778$ genomes was obtained, representing $22,009$ unique NCBI Taxonomy Ids. Using these accession numbers, we were able to download their corresponding `.faa` files when available leading to a set of $16,900$ amino acid sequence files. The latter were annotated and used to obtain potential pathway complementarities beween pairs of genomes (see paragraph 3). Last, when available, their corresponding annotations on PATRIC database [43] were retrieved to reconstruct GENREs (see paragraph 3).

Taxonomy schemes

`microbetag` maps the taxonomy of each entry in the abundance table to their corresponding NCBI Taxonomy Id and, if available, their closest GTDB representative genome(s), since several GTDB representative genomes may map to the same NCBI Taxonomy Id. Two well established taxonomy schemes are supported: the GTDB [44] that is being broadly used for bins and/or MAGs taxonomical classification and the Silva database [45] that is widely used in amplicon studies. Both taxonomy schemes link their taxonomies to NCBI Taxonomy Ids [46]. In case none of those two taxonomies was used and the abundance table contains less than 1,000 taxa, `microbetag` maps the user provided taxonomies to NCBI Taxonomy. To this end, `microbetag` makes use of the `fuzzywuzzy` library that implements the Levenshtein Distance Metric to get the closest NCBI taxon name and thus its corresponding NCBI Taxonomy Id; a relatively high similarity score is used (90) to avoid false positives. Also, using the nodes dump file of NCBI Taxonomy, `microbetag` may retrieve the children taxa of a taxon in user's data, along with their corresponding NCBI Taxonomy Ids, if requested by the user. If the user provides their abundance table with taxonomies already mapped to the GTDB taxonomy, `microbetag` will report the best possible annotations in a time efficient manner.

Network inference

When a co-occurrence network is not provided by the user, `microbetag` exploits FlashWeave [18] to build one on the fly. Yet, `microbetag` supports the annotation of networks built from any algorithm/software, in any format Cytoscape can load.

[3] This should include a description of the overall architecture of the software implementation, along with details of any critical issues and how they were addressed.

`microbetag` pre-processing

In order to aid the user to map their sequences to the GTDB taxonomy, DADA2-formatted 16S rRNA gene sequences for both bacteria and archaea [47] were used to trained the TAXID classifier of the DECIPHER package [48] and are available through the microbetag preprocess Docker image. Likewise, when the abundance table consists of more than 1,000 taxa, providing a network as an input is mandatory. Again, in order to faciliate the user, `microbetag` preprocess Docker image supports the inference of a network using FlashWeave.

Literature based nodes annotation

Using a set of Tara Oceans samples [49] FAPROTAX [50] estimates the functional potential of the bacterial and archaeal communities, by classifying each taxonomic unit into functional group(s) based on current literature, announcements of cultured representatives and/or manuals of systematic microbiology. In this manually curated approach, a taxon is associated with a function if and only if all the cultured species within the taxon have been shown to exhibit that function. In its current version, FAPROTAX includes more than 80 functions based on 7600 functional annotations and covering more than 4600 taxa. Contrary to gene content based approaches, e.g. PICRUSt2 [51], FAPROTAX estimates metabolic phenotypes based on experimental evidence.

`microbetag` invokes the accompanying script of FAPROTAX and converts the taxonomic microbial community profile of the samples included in the user's abundance table or of the taxa present in the provided network, into putative functional profiles. Then, it parses FAPROTAX's subtables to annotate each taxonomic unit present on the user's data with all the functions for which they had a hit. FAPROTAX annotations are not part of the microbetagDB but are computed on the fly.

Genomic based nodes annotation

phenDB [52] is a publicly available resource that supports the analysis of bacterial (meta)genomes to identify 47 distinct functional traits, e.g. whether a species is producing butanol or it has an halophilic lifestyle. It relies on support vector machines (SVM) trained with manually curated datasets based on gene presence/absence patterns for trait prediction. More specifically, the model for a particular trait is trained using a collection of EggNOG annotated genomes where the knowledge of whether that trait is present or absent among its members is available. These models (classifiers) are used to predict presence/absence of their corresponding traits in non-studied species.

In the frameowrk of microbetagDB, classifiers were re-trained using the genomes provided by phenDB for each trait to sync with the latest version of eggNOG [53] and the `phenotrex` [52] software tool. Genomes were downloaded from NCBI using the Batch Entrez program. Then, *genotype* files were produced for all the high quality GTDB representative genomes. Each model was then used against all the GTDB *genotype* files to annotate each with the presence or the absence of the trait. A list of all

the phenotypic traits available for the genomes present on microbetagDB is available on `microbetag` 's documentation site. The updated models are also available

Pathway complementarity

To infer potential pathway complementarities we consider the modules described in KEGG MODULES database [41]. A KEGG module is defined as a functional unit within the KEGG framework, that represents a set of enzymes and reactions involved in a specific biological process or pathway [54]. Such a unit consists of several *steps*, each of which may have more than one molecular ways to occur (Figure 1). A module's definition is a logical expression and consists of KOs that may be coupled with one another as: a. connected steps of the pathway b. parts of a molecular complex, c. alternatives of the same step, and d. optional entities of a complex. Both (a) and (b) cases should be considered as the `AND` logical operator, while (c) would be the `OR` (Figure 1). Given a module's definition, we will consider as an *alternative* any subset of the KO terms mentioned in the definition, that has exactly one way to perform each step, provided that all the steps of the module are covered. We define a genome as having a *complete* module, if and only if all of the KOs of at least one alternative are present on the genome.

Within this framework, `kofamscan` [55] was used to annotate with KEGG ORTHOLOGY terms (KOs) the 16,900 high quality GTDB representative genomes for which a `.faa` was available [56]. The KOs of each genome were then mapped to their corresponding KEGG modules; a KO may map to more than one modules ($1 : n$).

All modules definitions were retrieved using the KEGG API and parsed. A dictionary was built with all the alternatives of each module. Each pair of the KEGG annotated genomes was then investigated for potential pathway complementarities, i.e. whether a genome lacking a number of KOs ($genome_A$) to have a complete module ($module_x$) could benefit from another's species genome(s) ($genome_B$). In that case, $genome_B$ does not necessarily have a complete alternative of $module_x$; as long as it has the missing KOs that $genome_A$ needs to complete an alternative of it, $genome_B$ potentially complements $genome_A$ with respect to $module_x$. In total, 341,568 unique complementarities were exported.

Thanks to the graphical user interface (GUI) of the KEGG pathway map viewer [57, 58], each complementarity can be visualised as part of the closest KEGG metabolic map; where the KOs coming from the donor are shown with a blue-green colour, while those from the beneficiary's genome itself with rose.

`microbetag` annotates the edges of a co-occurrence network by isolating pairs where both taxa map to an annotated genome present on microbetagDB. Since co-occurrence networks are undirected, both nodes of a suggested association are considered as potential donors and beneficiary species. When more than one GTDB representative genomes map to the same NCBI Taxonomy Id all the possible genomes' combinations are considered. Finally, two edges are added in such pairs of taxa in the annotated network: one considering $species_A$ as the potential beneficiary and $species_B$ as the potenial donor species, and one vice-versa.

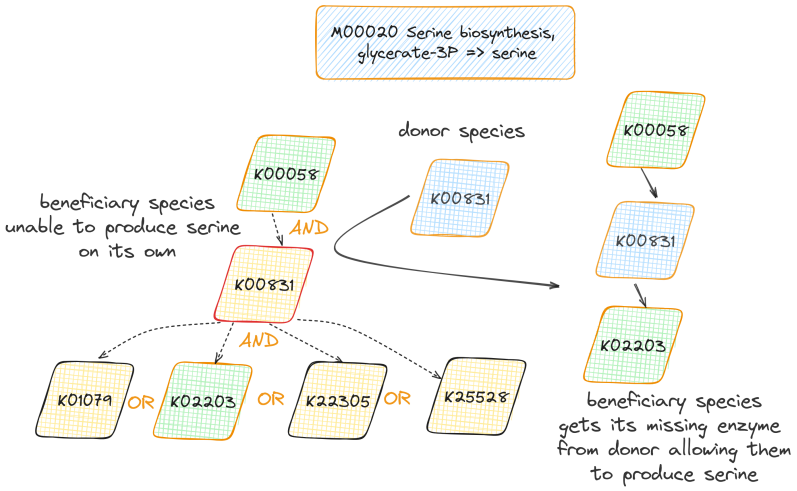

Fig. 1: Pathway complementarity approach. The high quality GTDB genomes were annotated with KEGG ORTHOLOGY (KO) terms. The various ways of getting a KEGG module complete were enumerated and all the possible ways a donor species could "fill" a beneficiary's non-complete module were calculated. In this case, there are 4 unique ways for having the serine biosynthesis module complete; in all of them K00831 is required. However, it is missing from the beneficiary species that supports the 2 out of the 3 steps of the module's definition. A donor species having and potentially sharing the corresponding enzyme of K00831 may enable the beneficiary species to produce serine.

Seed scores using genome scale metabolic reconstructions

The Metabolic Complementarity Index ($MI_{Complementarity}$) measures the degree to which two microbial species can mutually assist each other by complementing each other's biosynthetic capabilities. As described in [59], it is defined as the proportion of seed compounds of a species that can be synthesized by the metabolic network of another, but are not included in the seed set of the latter. $MI_{Complementarity}$ offers an upper bound assessment of the potential for syntrophic interactions between two species. Further, the Metabolic Competition Index ($MI_{Competition}$) represents the similarity in two species' nutritional profiles. This index establishes an upper limit on the level of competition that one species may face from another. Those indices have been thoroughly described and implemented in the NetCooperate [31] and NetCompt [32] tools correspondingly. We will be referring to those two indices as "seed scores".

Recently, the `PhyloMint`tool [59] was released supporting the calculation of the seed scores of GENREs in SBML format.

In the framework of microbetag, seed scores were computed using `PhyloMint` and draft GENREs for all pairwise combinations of GTDB representative genomes that have been RAST annotated in the framework of the PATRIC database [43]. GENREs were reconstructed using the Model SEED pipeline [60] through its Python interface ModelSEEDpy.

Moreover, the computed seed and the non-seed (i.e., set of metabolic compounds a genome can build on its own) sets of each genome were used to get their overlap among all the pair-wised combinations of those genomes. More specifically, the overlap of *seed* $set_{species_A}$ with the *non seed* $set_{species_B}$ was retrieved. `microbetag` then annotates again the edges of the co-occurrence network where both taxa have been mapped to a at least one GTDB genome, mentioning all the KEGG maps for which there is at least one seed compound of the potentially beneficiary species

Clustering network

manta is a heuristic network clustering algorithm that clusters nodes within weighted networks effectively, leveraging the presence of negative edges and discerning between weak and microbetag invokes manta [26] to infer clusters from the microbial network. A taxonomically-informed layout is

strong cluster assignments. ++ taxonomy layout

Groups of annotations

Biologically meaningful groups were built using the micrO ontology [61].

Building the CytoscapeApp

The `microbetag` CytoscapeApp was build based on the source code of the scVizNet [62]. Java @Ermis to add

Enrichment analysis is supported. Hypergeometric distribution FDR +++

Dependencies, Web server and API

The `microbetag` web service is container - based and consists of three Docker [63] (v24.0.2) images: a. the MySQL database b. an nginx [64] web server and c. the app itself. The latter uses Gunicorn (20.1.0) to build an application server which communicates with the web server using the Web Server Gateway Interface (WSGI) protocol and handles incoming HTTP requests. `microbetag` is implemented as a Flask application (v2.3.2); Flask is a micro web framework for developing Python web applications and RESTful APIs. A thorough description of `microbetag` 's API is available at the ReadTheDocs web site. The source code of the `microbetag` web service is available on GitHub.

python 3.11 slim docker image julia 1.7.1 for flashweave mysql.connector 8.0.27 python library pandas 2.1.1. numpy 1.26.0 multiprocessing

text processing using awk

KEGG API

Results [4]

`microbetag` and microbetagDB

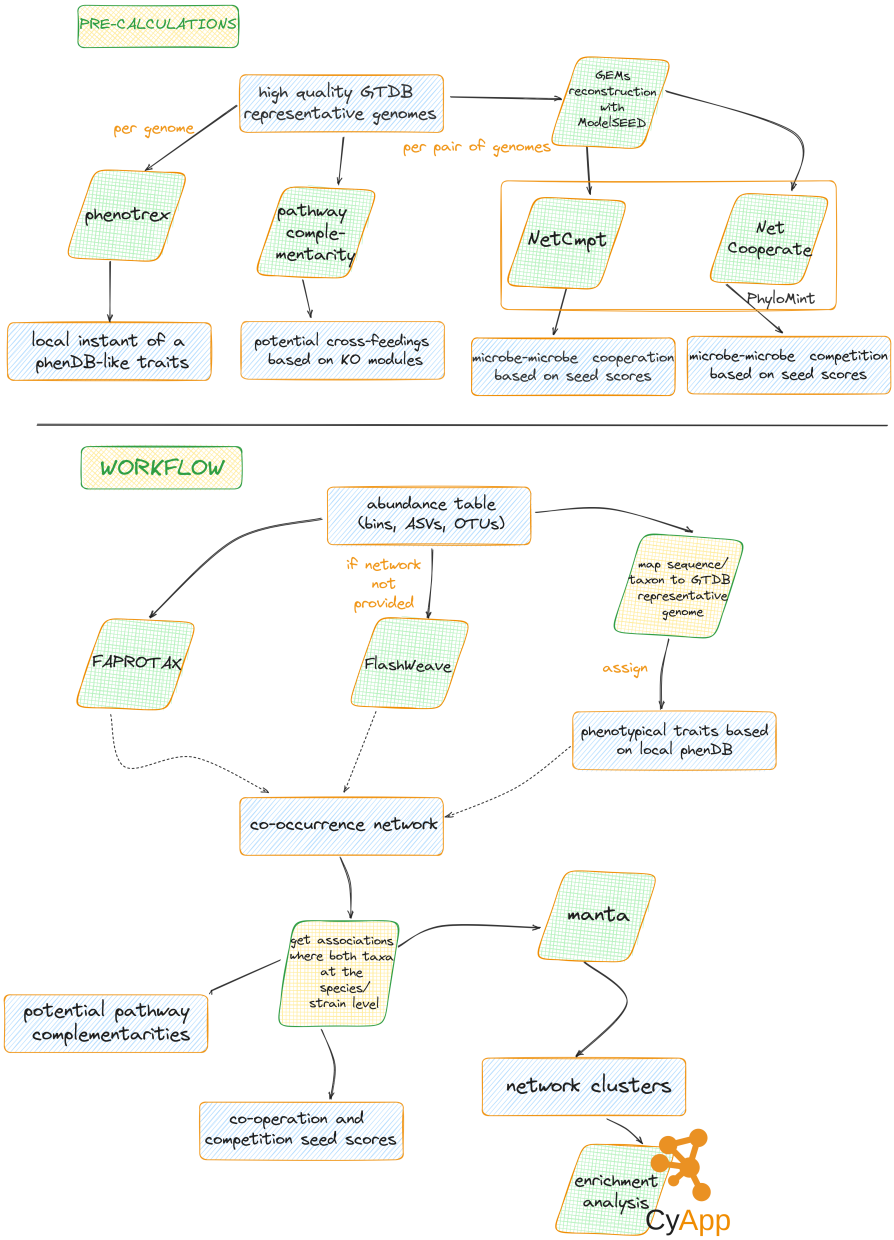

Fig. 2: Diagram of the `microbetag` pre - calculations and the on the fly workflow. GTDB v207 representative genomes were filtered and for those of high-quality 33 phenotypic traits were predicted using `phenotrex`. To this end, models were re-trained to sync with recent version of eggNOG.

[4]Significant advance over previously published software (usually demonstrated by direct comparison with available related software) This should include the findings of the study including, if appropriate, results of statistical analysis which must be included either in the text or as tables and figures. This section may be combined with the Discussion section for Software articles.

`microbetag` in numbers: 34,608 GTDB representative genomes 32 phen-model-oriented metabolic functions 92 FAPROTAX functions 341,568 unique complements involved in > 184 million beneficiary - donor pairs' complementarities 30,755 GENREs leading to 1 billion competition and complementarity scores

annotated network returned in `.cyjs` format

For a computationally efficient way to annotate large networks, a Docker image is provided so the user runs a taxonomy assignment using the IDTAXA algorithm [48] of the DECIPHER R package [65]. A co-occurrence network is also built using FlashWeave [18], as `microbetag` also does.

`microbetag` CytoscapeApp

Overall comment, the CytoscapeApp returns averages and s.d. for example in seed scores. If you want the exact values, go through the API.

A. GTDB-tk: 480 bins

Step	Time(sec)	Notes
Taxonomy mapping	Cell 1,2	on the fly
Network inference	Cell 2,2	on the fly
microbetag annotations	Cell 3,2	on the fly
manta clustering	Cell 4,2	on the fly

B. GTDB 16S: 3000 ASVs

Step	Time(sec)	Notes
Taxonomy assignment		Docker image on HP[5]
Taxonomy mapping	Cell 1,2	Cell 1,3
Network inference	Cell 2,2	Cell 2,3
microbetag annotations	Cell 3,2	Cell 3,3
manta clustering	Cell 4,2	Cell 4,3

C. Silva:

Step	Time(sec)	Notes
Taxonomy mapping	Cell 1,2	Cell 1,3
Network inference	Cell 2,2	Cell 2,3
microbetag annotations	Cell 3,2	Cell 3,3
manta clustering	Cell 4,2	Cell 4,3

D. fuzzywuzzy:

Step	Time(sec)	Notes
Taxonomy mapping	Cell 1,2	Cell 1,3
Network inference	Cell 2,2	Cell 2,3
microbetag annotations	Cell 3,2	Cell 3,3
manta clustering	Cell 4,2	Cell 4,3

Table 1: Computating times per step using an abundance table of 400 taxa with taxonomy: A. taxonomy scheme B. C. D. [5] specs of the laptop used.

The app was based on the StringApp and supported by the NRNB group.

Validation of `microbetag` potential

vitamin dataset [42]

Metagenomic or metabarcoding data are often used to predict microbial interactions in complex communities, but these predictions are rarely explored experimentally. Here, we use an organism abundance correlation network to investigate factors that control community organization in mine tailings-derived laboratory microbial consortia grown under dozens of conditions.

The network is overlaid with metagenomic information about functional capacities to generate testable hypotheses.

Thiamine alternative pathway [66, 67]

Study those 2 to understand our findings

Discussion [6]

Interpreting a real-world network with `microbetag`

Annelies' dataset.

`microbetag` as a resource

Limitations

As shown in [68] (see Figure 6b), the original version of CheckM [69] that is still used on GTDB returns lower completeness scores to genomes that correspond to phyla known for having shorter genomes in general, e.g. Patescibacteria representative genomes on GTDB have an average completeness $\tilde{6}5\%$. `microbetag` inherits this in the filtering process for getting only high quality genomes and thus, only few representatives from these taxonomic groups are present on microbetagDB.

It is well known that higher-order interactions, i.e. interactions involving more than two species [33] Pairwise relationships do not capture more complex forms of ecological interactions, in which one species depends on (or is influenced by) multiple other species. [3]

Future work

Further indices using the seed concept have been also presented such as the metabolic interaction potential (MIP) and the metabolic resource overlap (MRO). MIP is defined as the difference between the minimal number of components required for the growth of all members in a noninteracting community and an interacting community, i.e. the maximum number of essential nutritional components that a community can provide for itself through interspecies metabolic exchanges [33]. Similarly, MRO is defined as the maximum possible overlap between the minimal nutritional requirements of all member species [33]. Regression and association rule mining [70] can be applied to address this challenge.

- pathway and seed complementarities for higher-order interactions
- spatial dimension
- transcriptomics data integration: compare potential complementarities with what is going on
-

Conclusions

[7]

Data integration

[6] The user interface should be described and a discussion of the intended uses of the software, and the benefits that are envisioned, should be included, together with data on how its performance and functionality compare with, and improve, on functionally similar existing software. A case study of the use of the software may be presented. The planned future development of new features, if any, should be mentioned.

[7] This should state clearly the main conclusions and provide an explanation of the importance and relevance of the case, data, opinion, database or software reported.

Supplementary information. [8]

Declarations

- **Availability of data and materials**
  - Raw sequences for the use case:
  - Raw data for the validations case:
- **Funding**
  This work was initiated thanks to an EMBO Scientific Exchange Grant to HZ. It was then supported by the 3D'omics Horizon project (101000309). We would also like to thank the National Resource for Network Biology (NRNB) and the Google Summer of Code 2023 for the support of E.I.M.D.
- **Conflict of interest/Competing interests**
  The authors declare that they have no other competing interests.
- **Authors' contributions** [9]
  Conceptualization: K.F. Methodology: K.F. and H.Z. Software: H.Z., E.I.M.D. and J.M Validation: H.Z. and K.F. Formal analysis: H.Z. and K.F. Investigation: H.Z. Resources: K.F., A.E. and A.G. Data Curation: H.Z. Writing - Original Draft: H.Z. and K.F. Writing - Review & Editing: all Visualization: H.Z. Supervision: K.F., H.Z. and S.M. Project administration: K.F. Funding acquisition: K.F., H.Z.
- **Acknowledgements**
  We would like to thank Dr Christina Pavloudi and ++ for the insight on how to organise the trait groups.
- **Ethics approval**
  Not applicable
- **Consent to participate**
  Not applicable.
- **Code availability:**
  - microbetagDB related scripts: https://github.com/hariszaf/microbetag
  - microbetagApp and webserver: https://github.com/msysbio/microbetagApp.
  - CytoscapeApp: https://github.com/ermismd/MGG/
  - Validation and use case: ¡think of having that under the 3D'omics organization¿
  - Documentation web-site: https://hariszaf.github.io/microbetag/

Appendix A Mappings

$n : 1$ $n : n$ etc

[8] If your article has accompanying supplementary file(s) please state so here. E.g. supplementary figures and tables captions.

[9] Based on the CRediT system. Current list is indicative.

Appendix B Background on seed scores and complementarities

B.1 Background on seed scores

In that case, once a seed is assured, it activates all the rest of that group. Therefore, a confidence level (C) ranging from 0 to 1, has been previously described to quantify the relevance of each seed:

$$C_i = 1/seed's\ group\ with\ i\ size \tag{B1}$$

$C = 0$ corresponds to a non-seed node, while $C = 1$ represents an independent node.

$$MI_{Complementarity} = \frac{|SeedSet_A \cap \neg SeedSet_B|}{|SeedSet_A \cap (SeedSet_B \cup \neg SeedSet_B)|} \tag{B2}$$

As also described in [59], it is calculated as the proportion of compounds in a species' seed set that coincide with those in an other's, while also factoring in the confidence scores associated with seed compounds.

$$MI_{Competition} = \frac{\sum C(SeedSet_A \cap SeedSet_B)}{\sum C(SeedSet_A)} \tag{B3}$$

B.2 Background on pathway complementarity

For example, the definition of the D-Galacturonate degradation in Bacteria (M00631) is:

K01812 K00041 (K01685,K16849+K16850) K00874 (K01625,K17463)
that once breaking down, it leads to 4 alternative sets of KOs (pathways):

K01812 K00041 K01685 K00874 K01625

K01812 K00041 K16849+K16850 K00874 K01625

K01812 K00041 K01685 K00874 K17463

K01812 K00041 K16849+K16850 K00874 K17463

B.3 Complementarities

KEGG compound ModelSEED compounds ModelSEED compounds mapped to KEGG compounds and kept only those related to KEGG modules.

References

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