MetaTree: an interactive web platform for hierarchical data visualization and multi-group comparison

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Abstract

Background

Hierarchical quantitative profiles are widely used in microbiome studies and other domains. However, comparing multiple samples and experimental groups while preserving hierarchical structure remains challenging. Many existing workflows require extensive manual figure assembly or do not support aligned comparisons across conditions on a shared hierarchy.

Results

We developed MetaTree, an open-source platform that runs in a web browser for interactive visualization and comparative analysis of hierarchical quantitative data. MetaTree anchors samples, groups, and contrasts between groups to a shared reference hierarchy, preserving one-to-one node correspondence so that the same clade is compared in the same position across views. In addition to visualization, MetaTree integrates statistical testing for comparisons between two groups with false discovery rate (FDR) control, enabling users to identify clades with consistent differences between conditions and interpret them in hierarchical context. MetaTree also provides user configurable controls for visual encoding, filtering thresholds, label density, and layout, allowing

figures to be adapted to different datasets and reporting needs. The interface remains usable for large hierarchies through interactive navigation, adaptive label handling, and branch collapsing.

Conclusions

MetaTree is an installation-free web platform (https://byemaxx.github.io/MetaTree) for topology-consistent visualization and comparison of hierarchical profiles, supporting coordinated multi-panel exploration and automated comparison matrices to enable rapid generation of publication-ready figures for microbiome and other hierarchical datasets.

Keywords: MetaTree, hierarchical visualization, heat-tree, topology-consistent comparison, web-based software

Background

Many biological datasets, including taxonomic hierarchies and functional classification systems [1-3], are organized across multiple levels. In microbiome workflows such as 16S rRNA sequencing [4], shotgun metagenomics [5] and metaproteomics [6], thousands of features are mapped onto these hierarchies. Interpreting how clades respond to perturbations therefore benefits from visualization methods that preserve hierarchical structure [7]. However, common approaches have significant limitations. Stacked bar charts typically require aggregation to coarse ranks and are constrained by the number of distinguishable colors, obscuring patterns at deeper and often biologically informative levels [8, 9]. Clustered heatmaps, even with dendrograms, separate the hierarchy from the quantitative matrix, requiring users to mentally reconcile the two and becoming difficult to read as feature counts increase [10].

Several tools support phylogenetic tree visualization, including PhyD3 [11], GraPhlAn [12], ETE Toolkit [13], Krona [14], and iTOL [15], but they primarily focus on rendering individual trees rather than systematic comparison across many samples or groups. Many require scripting or configuration files, and iTOL does not natively provide a topology-consistent multi-panel workflow, where all panels are rendered on a shared reference topology with one-to-one node correspondence [15]. Heat-tree visualizations partially address this gap by embedding quantitative values within the tree. Metacoder [9] introduced heat-tree displays for microbial community analysis, but its dependence on the R environment, static ggplot2 output [16], and limited label control make it challenging to scale to large or complex datasets. In practice, labels frequently overlap or become unreadable at deeper levels, and assembling multi-panel, multi-group figures often requires substantial manual editing of static plots [10].

To address these limitations, we developed MetaTree, a browser-based platform for interactive heat-tree visualization and comparison of hierarchical quantitative data. MetaTree provides an integrated workflow for data upload, exploration, and export of publication quality figures, without requiring programming. Implemented in JavaScript with D3.js [17], MetaTree constructs a shared reference topology from hierarchical items so that samples and groups can be displayed with consistent node alignment across views. Beyond visualization, it includes built-in two-group comparisons with FDR control, supports operational taxon–function (OTF) structures [18], and provides dedicated multi-group comparison modes to examine clade-level patterns across samples and experimental conditions within a single interactive framework.

Implementation

Visualization framework and interaction

MetaTree is implemented as a single-page web application and runs entirely in the user's browser. It first constructs a global reference tree by merging all hierarchical paths present in the input, ensuring that every panel shares an identical topology and differs only in the mapped quantitative attributes. This enables direct, side-by-side comparison of many samples or groups without re-rooting or re-ordering trees.

Quantitative information is encoded through multiple visual channels that can be adjusted interactively:

- **Tree color (nodes and branches)** encodes a user-selected variable such as abundance, intensity or log2 fold-change. MetaTree provides multiple built-in color palettes and allows users to adjust the value domain and the direction of the color scale. Transformations such as logarithmic or square-root scaling can be applied before mapping, making it possible to handle both highly skewed abundance distributions and centered contrast statistics.
- **Node size** reflects the magnitude of a quantity of interest, typically an aggregated abundance or intensity. Global size scaling controls allow users to emphasize or down-weight differences in node area for dense or sparse trees.
- **Branch width** can be used to enhance structural readability or to emphasize clades with higher overall signal, depending on the analysis goal.

MetaTree supports multiple layouts (radial, dendrogram, and circle packing) and provides panel-level controls for width/height, with optional synchronized resizing to facilitate figure assembly. Users can pan and zoom within panels; an optional synchronized zoom mode propagates navigation across panels, enabling aligned inspection of the same clade across many samples or contrasts.

To reduce clutter in deep hierarchies, MetaTree provides configurable label density (by depth and by abundance-driven thresholds) and a smart label-culling option that suppresses overlapping labels while preserving the underlying geometry. Targeted clade interrogation is supported through keyword search and an include/exclude filter list, as well as manual label-color overrides for highlighting specific taxa or functional categories.

For very large trees, readability and responsiveness are improved through interactive pruning. Users can collapse or expand branches by clicking internal nodes, reducing on-screen complexity while preserving global context; collapsed nodes are visually marked and can be restored via a dedicated control. Combined with include/exclude filtering and abundance-based thresholds, this enables progressive exploration from the full hierarchy to focused subtrees without changing the underlying reference topology.

Export is supported directly from the interface via per-panel context actions, producing publication-ready SVG (vector) or PNG (raster) outputs. Because all mapping parameters (palette, domain, transforms, label rules and filters) are applied interactively, exported figures reflect the exact visual state used during exploration.

Data input and hierarchical model

MetaTree accepts two complementary table types to cover both raw hierarchical profiles and downstream statistical outputs:

- **Wide format**, rows represent hierarchical items and columns represent samples. Each row can be provided either as a delimited path (e.g. Kingdom; Phylum; Species) or as an explicit level-wise encoding, and MetaTree builds the tree by parsing the path into parent–child relationships.
- **Long format**, where each row encodes an item–sample or item–contrast pair with associated statistics, for example log2 fold-change, effect size and P-value obtained from statistical tools. This format enables direct visualization of statistical results (including significance-aware filtering) without requiring users to manually reshape outputs from external pipelines.

MetaTree provides an interactive import wizard that maps user columns to the required semantic fields (hierarchy/path, sample or group labels, and value/statistic columns) and supports flexible delimiters and missing-value handling. Internally, items are keyed by their full ancestor path to avoid collisions when identical labels occur under different parents. Optional sample metadata can be loaded to define groups (e.g. treatment, time, cohort). Groups can also be defined and re-ordered interactively.

Analysis modes

On top of the shared visualization framework, MetaTree implements four analysis modes:

- **Sample view (Individual samples):** multiple samples are shown simultaneously as separate heat-tree panels on the shared reference tree, with sample-specific values mapped directly to tree color and node size. This supports side-by-side inspection of sample-level heterogeneity and outlier detection.
- **Group view (Group samples):** samples are aggregated into user-defined groups based on metadata or interactive grouping, and group-level summaries (e.g. mean or median abundance) are visualized as one heat-tree per group. This mode facilitates comparison of overall hierarchical profiles across conditions.
- **Group comparison (Pairwise comparison):** two groups are selected for pairwise comparison. For each hierarchical item, MetaTree performs an exploratory between-group test using either the Wilcoxon rank-sum test [19] or Welch's t-test [20], and controls the false discovery rate using the Benjamini–Hochberg procedure [21]. MetaTree reports log2 fold-change, defined as log2(Group 2 / Group 1) using group-level summary abundances, together with FDR-adjusted *P*-values. To ensure numerical stability when group summaries contain zeros, fold-changes are computed using an additive pseudocount. These statistics are used primarily for interactive filtering: users can restrict the display to items exceeding an absolute log2 fold-change threshold and passing an FDR cutoff, thereby focusing the tree on clades with consistent between-group differences.
- **Comparison matrix (All-versus-all):** when more than two groups are present, MetaTree can automatically compute pairwise comparisons between all group pairs and arrange the results in a matrix of heat-tree panels. Any cell can be selected for detailed inspection using the same visualization and filtering controls as in group comparison mode, providing an overview of relationships between conditions while preserving access to individual contrasts.

Across all modes, additional filters allow users to subset the tree by metadata (e.g. selected groups), by item identity (e.g. specific clades or keyword matches) and by simple thresholds on abundance or other numeric variables. P-values and FDR can be used as filtering criteria to control which items are shown, thereby reducing visual clutter and highlighting the most relevant features.

Programmatic integration and deployment

Beyond the graphical interface, MetaTree exposes lightweight browser-side hooks for integration into analysis reports or dashboards. Data can be injected programmatically (e.g. via a JavaScript call that loads tabular text, or by embedding inline data in an HTML document), and a readiness event is emitted when the application has initialized. This design enables reproducible, shareable visualizations that remain fully functional when deployed as a static website (e.g. GitHub Pages) or run locally for offline, privacy-preserving analysis.

Results

Interface overview and workflow

MetaTree provides a browser-based interface for interactive visualization and comparison of hierarchical quantitative data (Fig. 1). Users begin by loading either a wide format abundance table that encodes hierarchical paths, optionally accompanied by sample metadata for grouping, or a long format table of statistical results such as log2FC with significance metrics. MetaTree constructs a shared reference tree from the input hierarchy and uses it as a fixed node set, preserving one-to-one node correspondence so that samples, groups, and contrasts are compared on the same topology across views. Quantitative values are encoded using three visual channels: node size, node color, and branch width. Users explore the data through four analysis modes: Sample View, Group View, Group Comparison, and Comparison Matrix. Interactive controls support synchronized zooming, adaptive label culling, filtering, and branch collapsing or expansion. The MetaTree home page is shown in Fig. 2. MetaTree provides extensive, user configurable controls for figure customization, including visual encoding, layout, label density, and filtering thresholds. It supports export of publication-ready figures and the associated statistics tables, and it can be accessed online or run locally without installation.

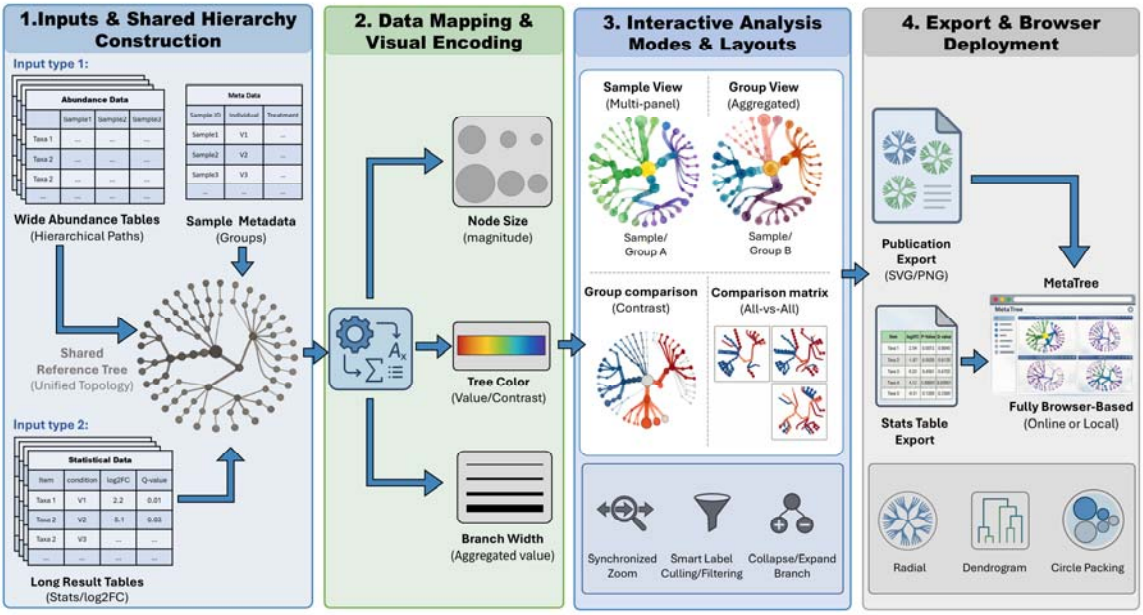

Figure 1. MetaTree interface overview and end-to-end workflow for hierarchical visualization and comparison. MetaTree visualizes hierarchical profiles on a shared reference topology for topology-consistent comparison. Node size/color and branch width encode abundance or contrasts.

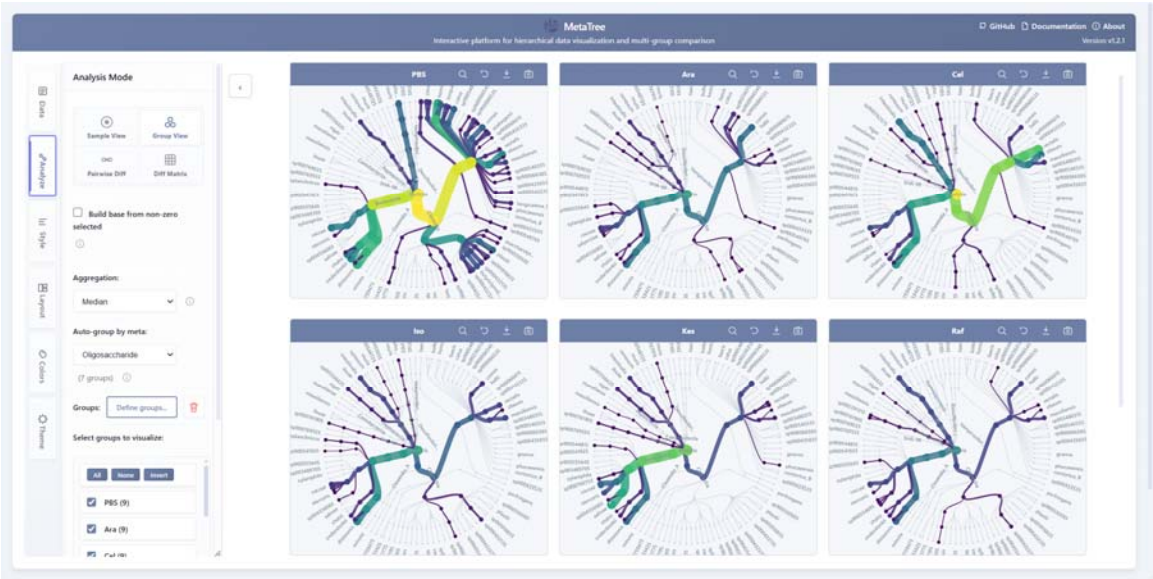

Figure 2. MetaTree graphical user interface (GUI). MetaTree provides a browser-based interface for coordinated multi-panel exploration of hierarchical profiles. Interactive navigation and export support figure generation.

Exploration and comparison on a shared reference tree

To demonstrate MetaTree's capabilities, we applied it to a previously published human gut microbiome metaproteomics dataset generated from stool-derived communities of three donors cultured in vitro with several structurally distinct oligosaccharides [22]. Taxonomic and operational taxon–function (OTF) intensity tables were generated using MetaX, a peptide-centric metaproteomics workflow [18], and used as input to MetaTree. In this dataset, donor identity is denoted as V1–V3, and we use these donor labels as example groups for illustrating group-level summaries and contrasts.

MetaTree provides four analysis modes on a shared reference tree, allowing hierarchical profiles and contrasts to be interpreted on a consistent topology: Sample View and Group View for profile exploration, Group comparison for two-group contrasts, and Comparison matrix for systematic multi-group screening. Sample View renders one heat-tree per sample as a panel set, whereas Group View aggregates replicates within user-defined groups and renders one heat-tree per group. Figure 3 highlights the comparison-oriented modes. Group View summarizes group-level patterns for V1 and V2 on the same topology with a shared color scale (Fig. 3a). Group comparison visualizes a selected contrast between two groups and can restrict the display to nodes passing user-defined significant thresholds (Fig. 3b). In this mode, MetaTree provides built-in per-node hypothesis testing using either a Wilcoxon rank-sum test or Welch's t-test and applies Benjamini–Hochberg correction to control FDR. For studies with more than two groups,

Comparison matrix computes all pairwise contrasts and arranges them as a matrix of differential heat-trees for rapid screening; each cell can be opened for focused inspection (Fig. 3c).

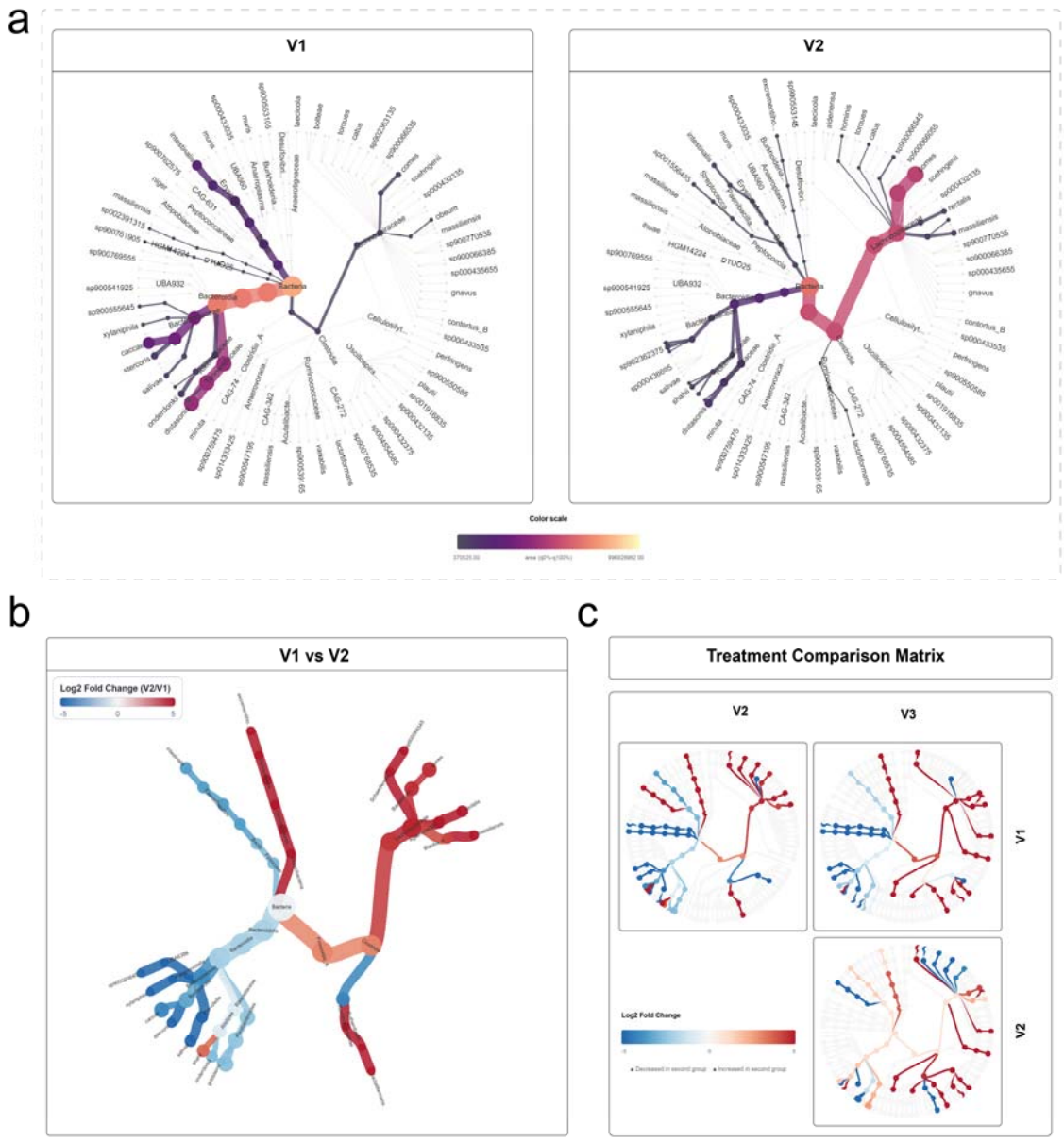

Figure 3. Group-level summaries and differential comparisons in MetaTree. (a) Group View: aggregated profiles for V1 and V2 on a shared topology. **(b)** Group comparison: V1, V2 contrast. **(c)** Comparison matrix: all pairwise contrasts among V1–V3.

Interactive controls for comparative visualization and multi-layout rendering

MetaTree provides GUI panels to configure data input, visual encoding, and figure layout (Fig. 4a). Hierarchical abundance tables and optional sample metadata can be loaded with automatic input parsing, including detection of common table delimiters and hierarchy separators, reducing manual preprocessing. Users can filter samples by metadata and restrict displayed features by name to focus on specific conditions or clades.

Visual encoding is configurable via sequential and diverging palettes, optional palette reversal, and user-defined color domains to enforce consistent scaling across panels. Label presentation can be tuned through font and length limits, hierarchy-level selection, and automatic overlap culling for dense trees. In addition, label colors can be assigned automatically or customized to match user-defined groupings, improving interpretability without changing the underlying hierarchy.

MetaTree supports multiple layouts for the same hierarchy, including radial trees, dendrogram trees, and circle packing (Fig. 4b). Layout parameters and panel dimensions can be adjusted interactively. For comparative exploration, MetaTree enables coordinated multi-panel interaction with synchronized navigation (linked zoom, pan), and hover tooltips provide node-level details without adding persistent visual clutter.

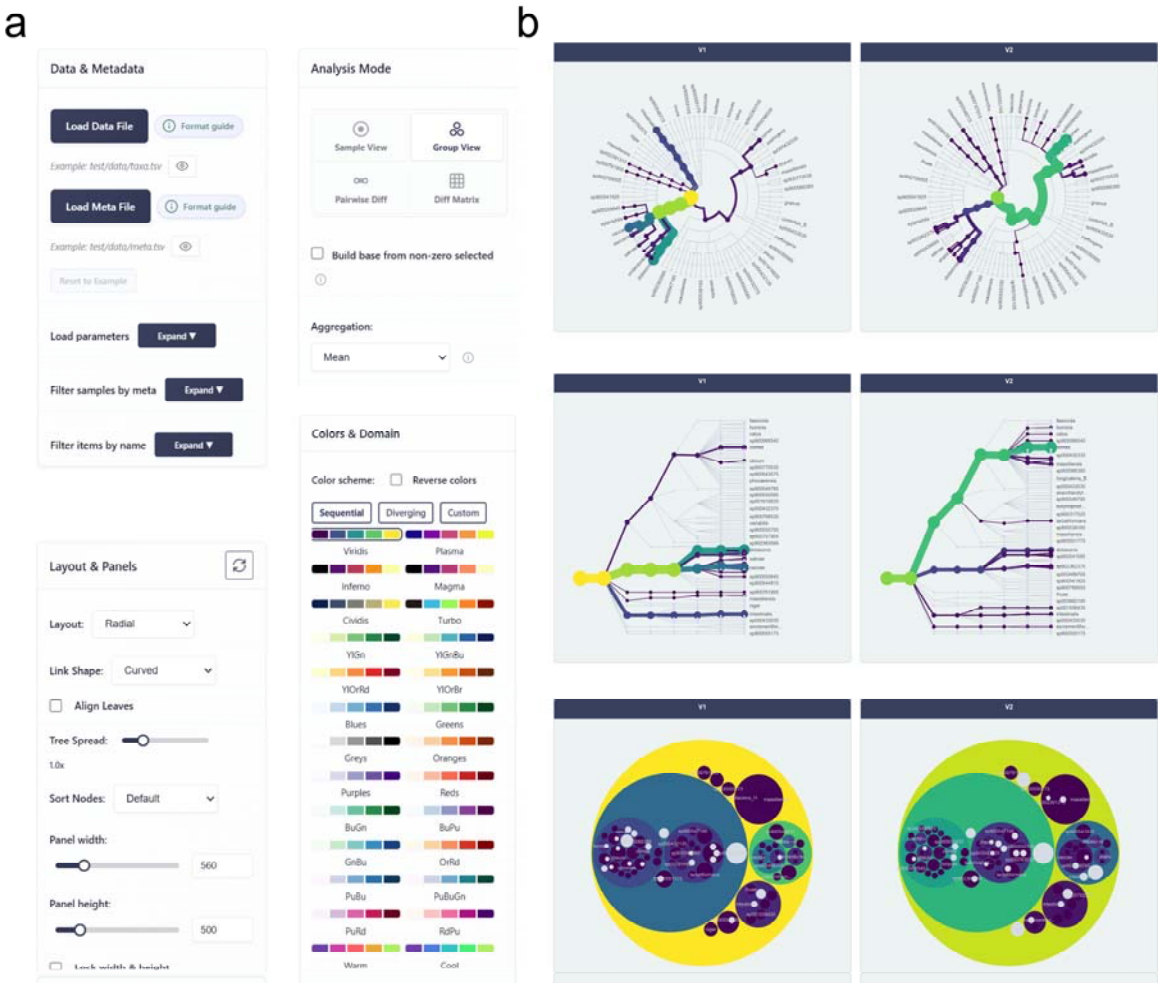

Figure 4. Interactive configuration panels and multi-layout rendering in MetaTree. **(a)** Control panels for data loading, filtering, label settings, and layout configuration. **(b)** The same dataset rendered with different layouts (radial tree, dendrogram tree, and circle packing).

Discussion

MetaTree is designed for systematic comparison and reporting of hierarchical profiles through a browser-based interface optimized for multi-panel inspection and figure production. It supports common input formats for quantitative tables and statistical results, and optionally uses metadata for grouping and sample selection. By anchoring all views to a shared reference hierarchy, MetaTree preserves a one-to-one correspondence of nodes across panels and contrasts, so differences between conditions are expressed solely through visual encodings on a consistent topology. MetaTree also exposes a programmatic API for embedding the viewer in external applications and integrating it into custom analysis workflows.

In addition to visualizing externally computed results, MetaTree integrates statistical testing for rapid exploratory screening. Users can perform two group comparisons, project effect sizes and adjusted P values onto the hierarchy, filter results using user defined thresholds, and export publication-ready figures and associated tables. For confirmatory inference in complex designs, users can fit appropriate models externally and import the resulting statistics into MetaTree for hierarchical interpretation and reporting.

We compared MetaTree with iTOL [15], Krona [14], and Metacoder [9] as representative tools for hierarchical visualization (Table 1). MetaTree prioritizes coordinated comparison workflows. iTOL [15] provides rich annotation and styling for user supplied trees, and Krona supports interactive drill down of hierarchical profiles, but neither provides a native workflow for topology-consistent multi-panel comparison with synchronized navigation and an all-versus-all comparison matrix. Metacoder enables heat tree visualization in R, but it is primarily code driven and focuses on static figure generation; for large hierarchies, maintaining label readability may require substantial manual tuning. MetaTree addresses these gaps through integrated rendering across multiple layouts, adaptive label management (label culling and branch collapsing), and linked navigation to keep dense hierarchies interpretable during exploration. MetaTree also provides built in two group testing with multiple testing correction, filtering by effect size and adjusted P values, systematic screening via a pairwise comparison matrix, and direct export of publication-ready figures and statistics tables.

Table 1. Comparison of MetaTree with representative hierarchical visualization tools.

Capability	MetaTree	iTOL	Krona	Metacoder
Topology-consistent comparison across groups	✓	—	—	✓
Coordinated multi-panel interaction	✓	—	—	—
No installation (web-based)	✓	✓	△	—
Multiple layouts	✓	✓	—	—
Interactive visual encoding controls	✓	✓	✓	—
Built in two group testing	✓	—	—	—
Pairwise comparison matrix (all-versus-all)	✓	—	—	—
Publication-ready export (vector and raster)	✓	✓	△	✓

✓ supported; △ possible but not a native workflow; — not supported.

Although we demonstrate MetaTree using phylogeny-based profiles, the design is not limited to phylogenetic trees or biological data. MetaTree can be applied to any rooted hierarchy in which quantitative values are associated with nodes and edges, including taxonomies, functional hierarchies, ontologies, and user defined category trees.

MetaTree is intended to remain lightweight and installation-free while supporting large hierarchies through progressive disclosure and adaptive label management. Future work will focus on improving reproducibility through provenance capture for exported figures and expanding comparison options.

Conclusion

MetaTree is an installation-free web platform for topology-consistent visualization, exploration, and comparison of hierarchical profiles. It supports coordinated multi-panel exploration, automated comparison matrices, and integration of statistical results with interactive filtering and thresholding. These capabilities enable rapid generation of publication-ready figures for microbiome and other hierarchical datasets.

Availability and requirements

Project name: MetaTree

Project home page: https://github.com/byemaxx/MetaTree

Operating system(s): Platform independent

Programming language: JavaScript

Other requirements: A modern web browser

License: MIT

Any restrictions to use by non-academics: No

List of abbreviations

D3.js: Data-Driven Documents (JavaScript library)

FDR: false discovery rate

GUI: graphical user interface

HTML: HyperText Markup Language

iTOL: Interactive Tree Of Life

log2FC: log2 fold change

OTF: operational taxon–function

PNG: Portable Network Graphics

rRNA: ribosomal RNA

SVG: Scalable Vector Graphics

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Availability of data and materials

MetaTree is available as a hosted web application (https://byemaxx.github.io/MetaTree). The source code, documentation, and example datasets are available on GitHub (https://github.com/byemaxx/MetaTree). For convenience, the web interface provides a Load Example option that loads example datasets for rapid exploration without manual data preparation. Optional local deployment for offline analysis is described in the GitHub documentation.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

Q.W. designed the method, developed the software, and drafted the manuscript. A.Z. provided key insights, tested the software, and reviewed the manuscript. Z.N. contributed to methodological enhancements and reviewed the manuscript. D.F. reviewed and provided feedback on the manuscript.

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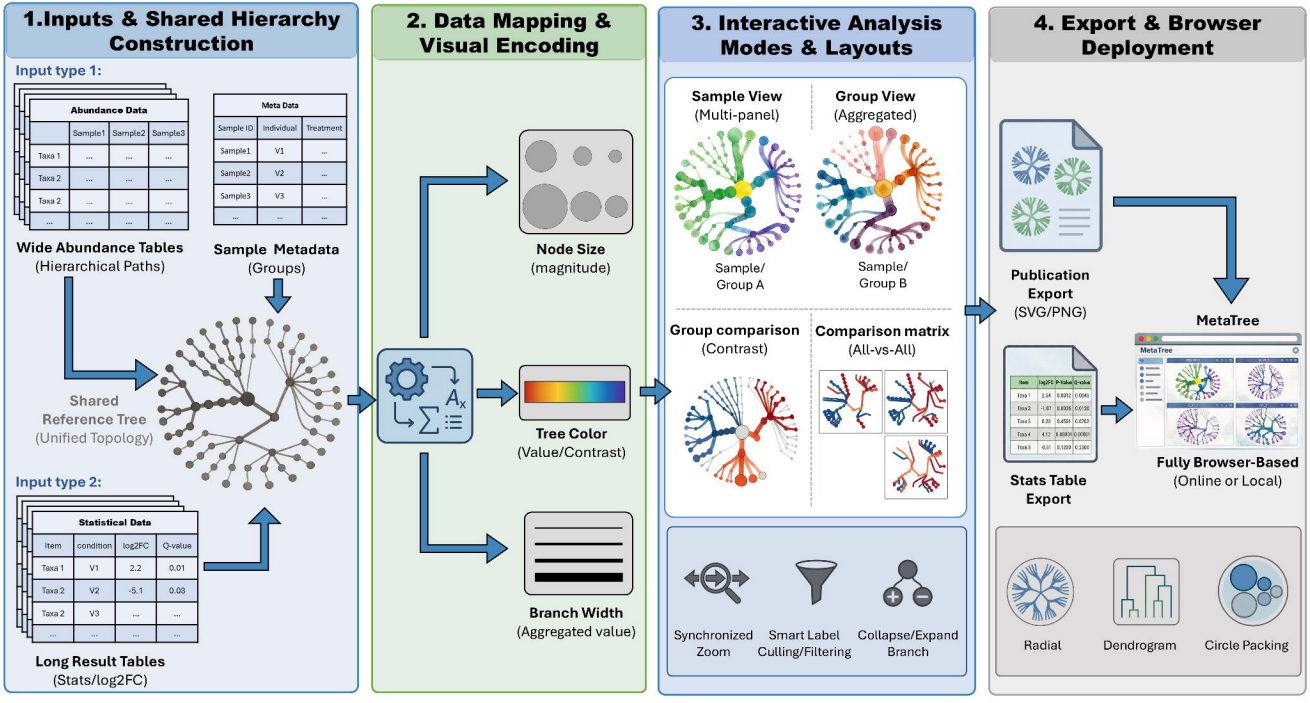
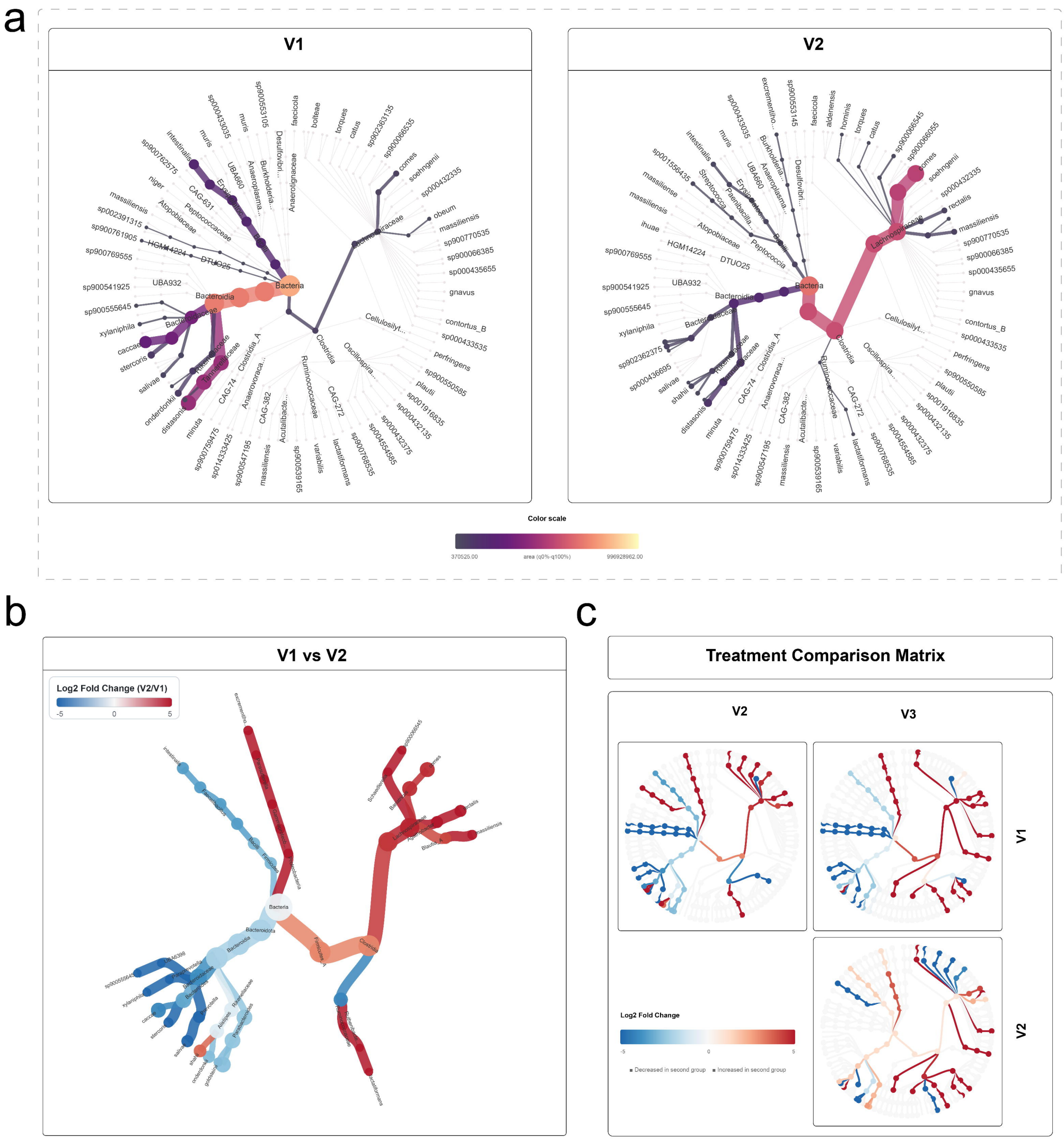

1.Inputs & Shared Hierarchy Construction
Input type 1:
Abundance Data
Sample1 Sample2 Sample3
Taxa 1 ... ...
Taxa 2 ... ...
Taxa 2 ... ...
... ...
Wide Abundance Tables
(Hierarchical Paths)
Meta Data
Sample ID Individual Treatment
Sample1 V1 ...
Sample2 V2 ...
Sample3 V3 ...
... ...
Sample Metadata
(Groups)
Shared
Reference Tree
(Unified Topology)
Input type 2:
Statistical Data
Item condition log2FC Q-value
Taxa 1 V1 2.2 0.01
Taxa 2 V2 -5.1 0.03
Taxa 2 V3 ... ...
... ...
Long Result Tables
(Stats/log2FC)
2. Data Mapping & Visual Encoding
Node Size
(magnitude)
Tree Color
(Value/Contrast)
Branch Width
(Aggregated value)
3. Interactive Analysis Modes & Layouts
Sample View
(Multi-panel)
Sample/
Group A
Group View
(Aggregated)
Sample/
Group B
Group comparison
(Contrast)
Comparison matrix
(All-vs-All)
Synchronized
Zoom
Smart Label
Culling/Filtering
Collapse/Expand
Branch
4. Export & Browser Deployment
Publication
Export
(SVG/PNG)
MetaTree
Stats Table
Export
Fully Browser-Based
(Online or Local)
Radial
Dendrogram
Circle Packing

MetaTree
Interactive platform for hierarchical data visualization and multi group comparison
GitHub
Documentation
About
Version v1.2.1
Data
Analyze
Style
Layout
Colors
Theme
Analysis Mode
Sample View
Group View
Pairwise Diff
Diff Matrix
Build base from non-zero selected
Aggregation:
Median
Auto-group by meta:
Oligosaccharide
(7 groups)
Groups:
Define groups...
Select groups to visualize:
All
None
Invert
PBS (9)
Ara (9)
PBS
Ara
Cel
Iso
Kes
Raf


a
V1
V2
Color scale
370525.00
area (q0%-q100%)
996928962.00
b
V1 vs V2
Log2 Fold Change (V2/V1)
-5
0
5
c
Treatment Comparison Matrix
V2
V3
V1
V2
Log2 Fold Change
-5
0
5
Decreased in second group
Increased in second group

a

Data & Metadata

Load Data File | Format guide

Example: test/data/taxa.tsv

Load Meta File | Format guide

Example: test/data/meta.tsv

Reset to Example

Load parameters — Expand ▼

Filter samples by meta — Expand ▼

Filter items by name — Expand ▼

Layout & Panels

Layout: Radial

Link Shape: Curved

☐ Align Leaves

Tree Spread: 1.0x

Sort Nodes: Default

Panel width: 560

Panel height: 500

☐ Lock width & height

Analysis Mode

Sample View | Group View

Pairwise Diff | Diff Matrix

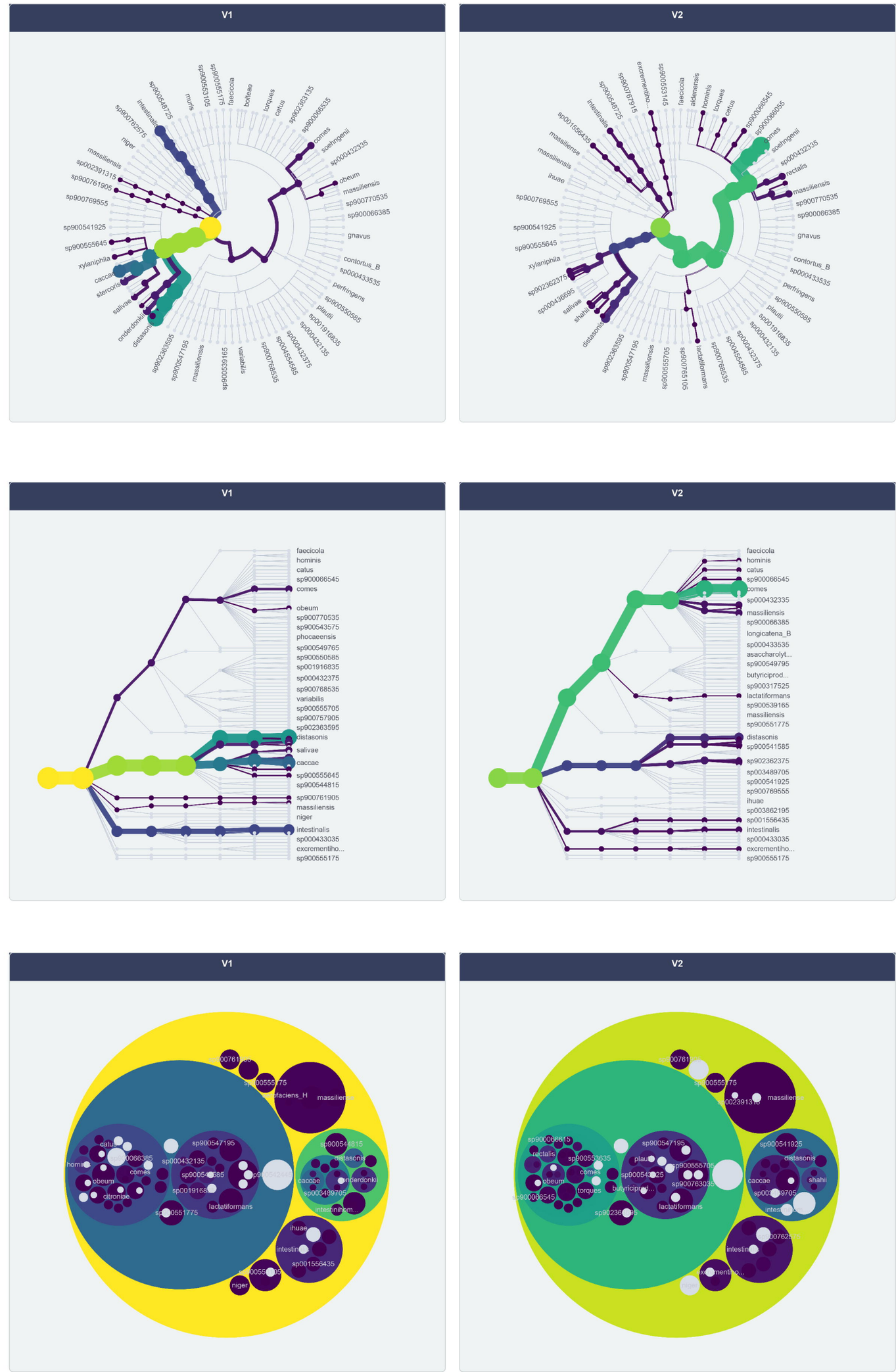
☐ Build base from non-zero selected

Aggregation: Mean

Colors & Domain

Color scheme: ☐ Reverse colors

Sequential | Diverging | Custom

Viridis, Plasma, Inferno, Magma, Cividis, Turbo, YIGn, YIGnBu, YIOrRd, YIOrBr, Blues, Greens, Greys, Oranges, Purples, Reds, BuGn, BuPu, GnBu, OrRd, PuBu, PuBuGn, PuRd, RdPu, Warm, Cool

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