PanicleVis: A Multidimensional and Multilevel Graph-Based Visualization System for Spatiotemporal Panicle Phenotyping Data

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***Abstract*—Phenotyping of crop panicles is crucial for identifying traits that influence yield and grain quality; however, the complexity and scale of modern phenotyping data pose significant analytical challenges. Modern phenotyping data are inherently multidimensional, combining spatial, genotypic, treatment, and temporal variations, making interpretation increasingly challenging and motivating scalable visualization approaches. Effective visualization is, therefore, critical for detecting patterns and guiding biological discovery. Existing approaches often treat all dimensions equally or rely on dimensionality reduction, which may obscure key relationships. Limited screen space further constrains effective analysis. To address these challenges, we propose a multidimensional and multilevel graph (MMG) model, where nodes represent hierarchical components of the panicle (panicle, branch, seed) and features are analyzed both within and across levels. Each node also supports exploration across genotype, treatment, and time. Building on this model, we introduce PanicleVis, a scalable visual analytics system that integrates relationships across dimensions and levels while optimizing screen space to maintain clarity. We evaluate PanicleVis with real-world rice datasets collected under diverse conditions. Expert feedback confirms both the interpretability of MMG and the system's effectiveness in handling large-scale, multidimensional data. Its flexible design also supports feature extensions, establishing PanicleVis as a scalable framework for complex phenotyping studies.**

***Index Terms*—Graph model, Multidimensional data, Multilevel data, Visual analytics, Scalable visualization, Plant phenotyping**

I. Introduction

Genotype-phenotype mapping captures the relationship between an organism's genetic composition (*genotypes*) and its observable traits (*phenotypes*), revealing insights into how genetic variations influence physical traits, behaviors, and physiological properties across different *environment* conditions. This mapping is critical for advancing fields such as medicine, agriculture, biotechnology, and so on [14], [22].

In agriculture, understanding how plant genotypes respond to environmental factors (such as temperature, water availability, and soil quality) is essential for enhancing crop yields and resilience, where phenotypic traits (such as panicle structure, grain size, number, and arrangement) significantly influence yield, quality, and adaptability. These efforts are crucial for maintaining stable and sustainable food production, especially when facing challenges like global population growth and climate change [1], [5].

Among staple crops, rice is of particular importance, supporting more than half the global population. The endosperm, the primary nutrient source in rice seeds, develops through the accumulation of photoassimilates during the grain-filling process. However, this process exhibits inherent variability within seed-bearing panicles and is highly sensitive to abiotic stresses [21], where the duration and severity of environmental stress significantly influence its rate and pattern. In addition, genetic diversity among rice germplasm accessions accentuates variability in seed size and quality under both normal and stress conditions.

To study genotype–phenotype–environment interplays, plant scientists analyze genotypes linked to specific traits and use phenotyping methods to assess responses under varying conditions. Conventional approaches [25], however, face difficulties with the scale and complexity of the data, which span multiple interacting dimensions such as genotypes, treatments, temporal dynamics, and spatial details across structural levels from entire panicles to individual branches and seeds. Systematically uncovering meaningful patterns and relationships across these dimensions in an intuitive way remains a major challenge. These challenges highlight the need for an integrated visual-analytics framework that unifies data modeling, analysis, and user interaction.

Visual analytic tools [4], [17] provide promising and practical ways to help domain scientists better understand the phenotyping data and discover relationships between genotype and phenotype. Existing works utilize visual elements (e.g., scatter plot, heatmap, or correlation matrix) to demonstrate 2D image-based phenotyping data, which, however, is not fully capable of handling emerging high-dimensional spatiotemporal phenotyping data, especially those involving multiple structural levels of the panicle. In addition, the limited space on a screen further constrains the visualization of complex data, making it difficult to maintain clarity and context. There is a growing need for more sophisticated and scalable visual analytics frameworks to tackle the increasing complexity of hierarchical spatiotemporal features in rich data generated by advanced panicle phenotyping platforms.

To address these analytical gaps, we propose *PanicleVis*, a multidimensional, multilevel graph-based visualization system specifically designed for spatiotemporal panicle phenotyping data. Although demonstrated on rice, PanicleVis is a scalable and generalizable framework capable of representing any hierarchical, multidimensional biological dataset, including other crops or cross-domain studies such as ecological or biomedical

systems. The system provides an intuitive and flexible platform that allows researchers to integrate and compare data across dimensions while simultaneously exploring fine-grained features at multiple levels of the panicle structure. To the best of our knowledge, this is the first visual analytics system specifically tailored to 3D spatiotemporal phenotyping, supporting the discovery of interactions among genotype, phenotype, and environment at scale. The key contributions of this work are as follows:

- Dimensional Integration: PanicleVis integrates features across user-selected dimensions (i.e., *genotype*, *treatment*, and *time*), enabling scalable and comprehensive analysis of their combined effects on panicle traits.
- Multilevel Analysis: The system supports hierarchical exploration of phenotypic features at the panicle, branch, and seed levels, providing a unified framework for holistic trait evaluation across scales.
- Interactive Visualization: PanicleVis introduces user-driven, interactive visualization tools that allow dynamic selection, filtering, and display of features, ensuring clarity even when handling large, complex datasets.

By leveraging these capabilities, PanicleVis offers a novel and scalable approach to visual analytics for rice panicle phenotyping, enabling researchers to better manage complexity, reveal genotype–phenotype–environment interactions, and advance understanding of factors driving crop yield and resilience.

II. Related Work

Visualizing and analyzing complex phenotype and genotype data often requires adapting and tailoring diverse techniques to address domain-specific needs. While many general-purpose visual analytics methods have been developed within individual perspectives, this section focuses on approaches specifically developed for or applied to phenotype and genotype data and their interrelationships from multidimensional, time-series, and relational perspectives.

A. Multidimensional Data Visualization

Glueck et al. introduce PhenoBlocks [11], PhenoStacks [10], and PhenoLines [12] to support the exploration of phenotype variation within and between cross-sectional patient cohorts and compare the differential hierarchy structure of the phenotyping data with multiple dimensions. Those methods use circular stacked bars to summarize scalar clinical phenotypes; however, they are not designed for hierarchical, 3D spatiotemporal plant phenotyping where features span panicle–branch–seed levels and evolve over time. Harnsomburana et al. provide a visual analytic framework [13] for plant phenotyping data; however, only the color phenotype in image space is provided. We target this gap by supporting spatial structure and temporal dynamics jointly, with consistent encodings across levels.

B. Time-series Data Analytics

Plant phenotyping inherently involves time-series data reflecting the growth dynamics of crops. Fulcher et al. propose hctsa [8] to automatically identify interpretable quantitative phenotypes from time-series data for high-throughput phenotyping. Zapata et al. provide a self-supervised feature extraction [18] from image time series in plant phenotyping through transfer learning, which learns information-rich representations without using any phenotype labels. Choudhury provides another deep-learning-based method [6] utilizing long short-term memory (LSTM) and autoregressive neural networks to perform phenotypic prediction. Choi et al. [3] develop DXplorer, an all-in-one platform that integrates essential image processing and data analysis functionalities to support the interactive analysis of dynamic dendritic spines. Existing works mostly process 2D image-based time-series data for phenotypes, which limits 3D structural and temporal correlation analysis. Our method is capable of visualizing 3D time-series data (e.g., volume, aspect ratio, and spreading) to reveal the spatial changes of the phenotype over time, which is crucial for summarizing plant growth patterns and insights.

C. Relation Visual Analytics

Several tools have been developed to visualize genotype–phenotype–treatment relationships. Phenostat [23] supports rapid distribution and correlation analysis, while Phenoview [24] enables comparative visualization of genotype–phenotype patterns. PhenoTree [2] applies sparse PCA to visualize health records and reveal patient groupings. Facetto [15] integrates unsupervised and supervised learning for hierarchical analysis of multichannel tissue images, and DU map [19] provides reasoning about diversity in genotype–phenotype mapping. Most of these tools rely on static visualizations such as scatter plots (Phenostat), hierarchical trees (PhenoTree, Facetto), box plots (Phenoview), or heatmaps (DU map), which mainly capture one-to-one mappings. In contrast, panicle phenotyping requires joint evaluation of multiple spatial and temporal features. Existing approaches also lack flexible interaction for exploring the relationship between specific genotypes and their phenotypic variations. Our proposed multidimensional and multilevel graph (MMG) provides an interactive framework where dimensions can be mapped to multiple 3D spatial phenotyping features, enabling more effective phenotypic screening and interpretation.

III. Background

A. Panicle Phenotyping

Panicle phenotyping is a branch of plant phenotyping focused on observable traits such as height, leaf size, growth patterns, and yield. These analyses help assess the effects of genotypes and treatments. In this work, we target rice, a representative crop with a compound inflorescence of branches and seeds. Agricultural scientists provided samples spanning multiple genotypes and treatments, with phenotyping data collected at different growth stages (see Section VI). For clarity, a *sample* denotes a unique combination of genotype, treatment, and time, while a *panicle* refers to genotype and treatment only. Data construction involves three steps: multi-view imaging, 3D reconstruction, and feature extraction.

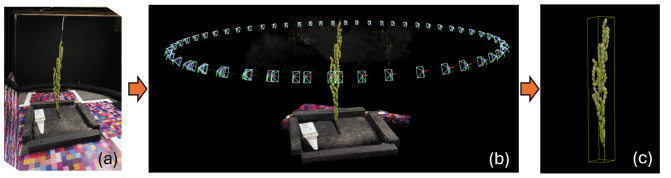


Fig. 1: An overview of the panicle phenotyping process.

Multiview Image Capture: We use a high-accuracy, high-throughput multiview imaging system for plants [9] to capture panicle images. Images are taken at multiple angles (approximately 60 views) for full 3D coverage. The system provides full side-view coverage at 6000×4000 resolution (Figure 1 (a)). Original images are cropped to retain key elements such as plant structures and the color checkerboard, then downsampled to 1600×1400 pixels to balance reconstruction quality and computational efficiency.

3D Reconstruction: Traditional phenotyping methods, such as those based on Structure from Motion (SfM) [26], involve substantial computational effort due to the complexity of processing large-scale imaging datasets. To improve efficiency, we adopt Neural Radiance Field (NeRF)-based techniques, specifically the Instant Neural Graphics Primitives method [20], to reconstruct the 3D geometry of panicles with high accuracy. This method achieves fast convergence with multiresolution hash encoding. The resulting voxel models (Figure 1 (b)) are further denoised by removing dark cloud artifacts, ensuring faithful visualization consistent with the ground truth.

Feature Extraction: To correct deviations in the imaging system, sample coordinates are optimized to keep the base consistently horizontal. The voxel size is also adjusted to uniformly rescale samples for valid comparisons. The resulting optimized 3D voxel models are designated as final models (Figure 1 (c)), from which features such as height, volume, and spreading are extracted across multiple phenotyping levels, including panicle, branch, and seed.

B. Feature Characterization Across Levels

Guided by the study objectives of agronomy experts, features are derived at the panicle, branch, and seed levels. A subset of these features is shown in Figure 2.

Panicle Level: The horizontal line through the panicle neck node (Figure 2 (a)) is defined as the panicle baseline, while an upright line through the same node is the growth line. Panicle height is measured as the distance from the baseline to the top, and spread as the distance from the outermost seed to the growth line. Stems extending from the panicle axis are identified as branches, and their counts are recorded.

Branch Level: Branch-level features are shown in Figure 2 (b). Branch height is the distance from the baseline to the top seed, and branch spread is the distance from the outermost seed to the growth line. For a segmented branch, the endpoint attached to the panicle axis is the inner point, and the opposite endpoint is the outer point. Branch length is the Euclidean distance between these points, and the branch angle is the angle between the growth line and the line connecting them. The branch index is determined by the smallest z-position value, with lower values indicating lower indices.

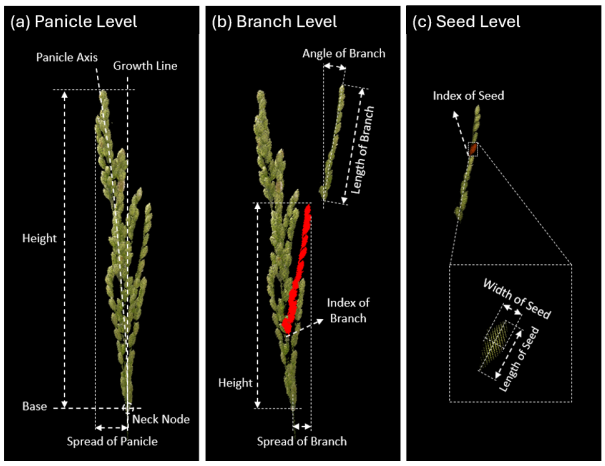


Fig. 2: Features at panicle (a), branch (b), and seed (c) levels.

Seed Level: Figure 2 (c) illustrates the features at the seed level. The length of a seed is defined as its longest dimension, while the width is determined as the widest dimension along the direction of its length. The seed index along a branch is assigned based on the smallest z-value within the seed, with smaller z-values corresponding to lower indices.

In addition to these features, four vegetation indices derived from combinations of the red (R), green (G), and blue (B) color channels of the images are also included. At each level, these indices are calculated by averaging the corresponding values across all elements of that level.

IV. Tasks and Requirements

In this section, we outline the key analysis tasks and system requirements as identified in consultation with domain experts in panicle phenotyping. As noted in Section III-B, each sample point contains features at three levels (panicle, branch, and seed), and the tasks are grouped accordingly. The corresponding requirements highlight the needs of a visualization system to effectively support these tasks.

Panicle Level: Features provide an overview of panicle characteristics. **R1:** Visualize core traits for each sample, including height, volume, spread, branch count, and four user-defined vegetation indices. **R2:** Examine how genotype, treatment, and temporal sequences affect panicle traits and growth dynamics. **R3:** Visualize relationships among selected traits in the context of genotype, treatment, and time.

Branch Level: Features capture structural and temporal characteristics of branches. **R4:** Analyze temporal trends in branch height and spread. **R5:** Graph-based representation of branch architecture. **R6:** Visualize individual branches with traits such as volume, length, angle, and seed count.

Seed Level: Features emphasize the growth of the primary seed on each branch. **R7:** Analyze positional changes of top seeds across growth stages. **R8:** Support branch segmentation and visualization of selected seed traits, including volume, width, and length.

In addition to the feature levels, three dimensions are incorporated: genotype (**G**), treatment (**T**), and time (**S**). Combining these dimensions with feature-level tasks enables expanded analyses. For example, **GR1:** examine genotype effects on height for panicles with the same treatment on the same day (R1 with G); **TR5:** assess treatment effects on branch architecture for panicles under different treatments (R5 with T); **SR7:** trace the growth trajectory of the top seed on each branch over time (R7 with S). Overall, 28 tasks are defined: 7 base tasks focused on individual panicle properties and 21 extended tasks (7 each for genotype, treatment, and time).

V. Multidimensional and Multilevel Graph Representation

As discussed in Section IV, panicle phenotyping data poses challenges due to its multidimensionality (genotype, treatment, time) and hierarchical feature levels (panicle, branch, seed), which demand analyses both within and across levels. To address this, we introduce the *Multidimensional and Multilevel Graph (MMG)*, a structured representation that formalizes these complexities, unifies categorical dimensions with hierarchical levels, and enables scalable, flexible visual exploration.

Formally, let Γ, Θ, and Σ denote the sets of genotypes, treatments, and time points, respectively, and let $\mathscr{L} = \{P, B, S\}$ represent the hierarchical levels of panicle, branch, and seed. The MMG is defined as

$$\mathscr{M} = (V, E, \Phi, w),$$

where $V = \Gamma \times \Theta \times \Sigma$ is the set of nodes, with each node $v = (\gamma, \theta, \sigma)$ representing a sample point; $E \subseteq V \times V \times \mathscr{L} \times \mathscr{D}$ is the set of typed edges, where $\mathscr{D} = \{\Gamma, \Theta, \Sigma\}$ denotes the comparison dimensions of genotype, treatment, and time; $\Phi = \{\phi_\ell\}_{\ell \in \mathscr{L}}$ is the collection of feature labeling functions, with each $\phi_\ell : V \to \mathbb{R}^{d_\ell}$ assigning feature vectors to nodes at level ℓ (e.g., at the panicle level: height, volume, spread; at the branch level: length, angle, seed count; at the seed level: length, width, volume); and $w : E \to \mathbb{R}_{\geq 0}$ is a weighting function that quantifies similarity or difference between nodes for a given level and dimension.

The MMG supports both intra-node and inter-node exploration. Intra-node analysis links features across levels within a single sample, while inter-node analysis compares samples along one dimension while holding others fixed. In summary, the MMG formulation is domain-independent and linearly scalable with the number of nodes and edges, making it applicable not only to plant phenotyping but to any multidimensional and multilevel datasets such as biomedical, ecological, or neuroscience studies.

User interactions are formalized by a selection operator $\mathrm{Sel} : \mathscr{Q} \to 2^V$, where $\mathscr{Q}$ denotes the space of queries. Let $V(q) := \mathrm{Sel}(q) \subseteq V$ denote the set of nodes selected by query $q \in \mathscr{Q}$. Given a query q, the induced subgraph $\mathscr{M}[V(q)]$ contains all relevant nodes and edges, enabling focused analysis. Typical tasks such as panicle-level inspection (R1–R3), branch-level exploration (R4–R6), seed-level evaluation (R7–R8), and combined dimension-level comparisons (GR*, TR*, SR*) can thus be expressed as subgraph operations.

The MMG representation provides a precise basis for modeling panicle phenotyping data, ensuring that both hierarchical and multidimensional relationships are explicitly represented. It enables domain experts to explore genotype–phenotype–environment interactions at scale and supports the design of flexible visualization strategies tailored to complex phenotyping studies.

VI. PanicleVis

Building on the MMG representation, we introduce *PanicleVis*, a visualization system for analyzing complex multidimensional and multilevel phenotyping data. As illustrated in Figure 3, the system combines four coordinated views: (A) Model Description View, (B) Panicle View, (C) Branch View, and (D) Seed View. Together, these views provide an integrated environment for configuring analyses, visualizing panicle traits, exploring branch structures, and inspecting seed-level details. The design of PanicleVis is directly guided by the MMG: nodes V are visualized as sample points, categorical dimensions (Γ, Θ, Σ) are encoded through shape and color, edges E appear as bundled connections across feature levels, and feature functions Φ are expressed through visualizations such as scatter plots, radar charts, and temporal trajectories. This mapping ensures that both the multidimensional and hierarchical aspects of phenotyping data are explicitly preserved in the interface design.

To demonstrate the design and functionality of PanicleVis, we use our target panicle phenotyping dataset as a running example. It defines five genotypes (KIT, HO1, HO2, HC2, HC5), two treatments (High Day and Night Temperature (HDNT) and Control), and three time points (Day 4, Day 7, Day 10). Using this dataset, we describe the main components of PanicleVis and show how the system supports exploration and analysis across dimensions and hierarchical levels.

Different visualization elements are employed across views, but the radar chart serves as a central component for representing multidimensional traits. The design is consistent across levels, with each chart featuring eight axes. However, the meaning of the axes depends on the level of analysis: panicle-level charts capture traits such as volume, height, spread, and maximum spread; branch-level charts encode volume, length, angle, and branch index; and seed-level charts depict volume, length, width, and seed index. In all cases, four additional axes represent user-defined vegetation indices. An overview of the radar chart design is shown in Figure 4.

A. Model Description View

To accommodate the multidimensional nature of panicle phenotyping data, the Model Description View (Figure 3 (A)) provides an overview of the data configuration in PanicleVis corresponding to the MMG's node set $V = \Gamma \times \Theta \times \Sigma$ and allowing users to define and explore analysis settings across spatial and categorical dimensions. The view includes two

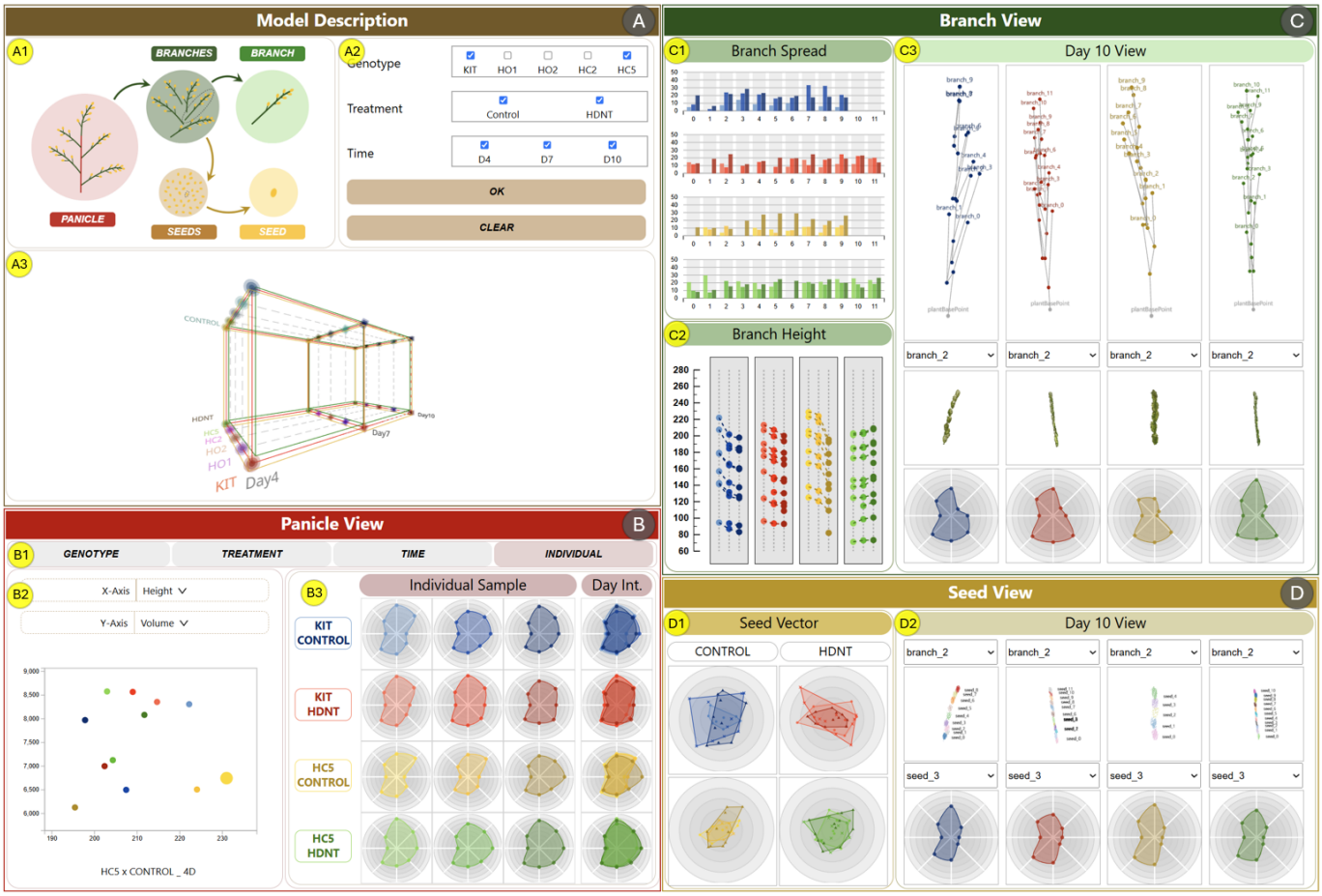


Fig. 3: PanicleVis interface overview: (A) Model Description View configures spatial and categorical dimensions; (B) Panicle View visualizes panicle traits across genotypes, treatments, and time; (C) Branch View highlights structural and temporal branch characteristics; and (D) Seed View tracks seed growth and inspects individual traits. Built on the MMG data model, PanicleVis provides scalable and flexible exploration of complex phenotyping data.

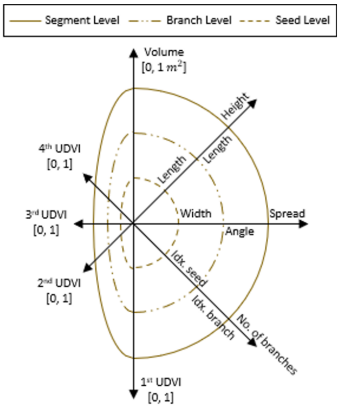


Fig. 4: Radar chart design in PanicleVis. Each chart has eight axes: four for level-specific traits (panicle, branch, or seed) and four for user-defined vegetation indices.

selection panels: (A1) a spatial panel and (A2) a dimension panel. The spatial selection panel enables users to focus on any combination of spatial components of the panicle, including overall traits, individual branches, temporal comparisons within a panicle, and seed-level features. The dimension selection panel allows users to choose categories from the Genotype, Treatment, and Time dimensions, supporting flexible comparisons or integrated analyses. In this panel, selecting multiple genotypes, treatments, and time points generates a set of distinct samples that can be explored interactively. Users can confirm selections with the OK button or reset them with the CLEAR button.

The selected setup is summarized in the model configuration view (A3). Each node $v = (\gamma, \theta, \sigma)$ of MMG corresponds to a sample point, with categorical dimensions visually encoded by shape for time (spheres, tilted cubes, and cubes), fill color for genotype, and color shade for treatment. Nodes also encapsulate features across hierarchical levels of panicle, branch, and seed, supporting both intra-level and cross-level exploration. MMG edges E are displayed as bundled sub-edges, colored red for panicle, green for branch, and orange for seed, thereby encoding relationships across levels defined in $\mathscr{L}$. When users select subsets of nodes, the relevant edges are highlighted to reveal comparisons such as temporal growth, genotype

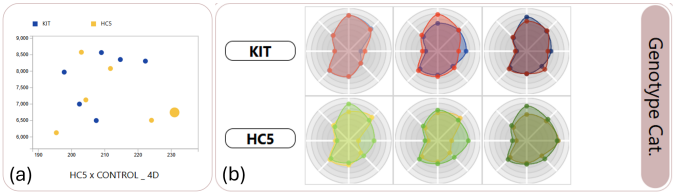


Fig. 5: Panicle View example: (a) Scatter plot showing relationships between selected features across categories, and (b) integrated radar charts comparing temporal and categorical differences based on user-selected dimensions.

effects, or treatment effects. Selecting a single node expands its detailed features across all levels, including panicle (R1–R3), branch (R4–R6), and seed (R7–R8), offering a precise and flexible view of phenotypic traits that is further elaborated in the following sections.

B. Panicle View

The Panicle View (Figure 3 B) focuses on panicle-level features, corresponding to the panicle feature function $\phi_P \in \Phi$. It provides an overview of panicle traits and supports flexible exploration across categorical dimensions or individual samples. The dimensions (Γ, Θ, Σ) are reflected in grouping and color encodings, enabling inter-node comparisons by genotype, treatment, or time. In this way, the view directly implements ϕ_P while leveraging MMG dimensions to structure comparisons.

Specifically, the selection panel (B1) offers four display modes. Choosing Genotype, Treatment, or Time groups samples for comparison across categories, while the Individual option shows each sample separately. For example, selecting Genotype enables direct comparison between KIT and HC5.

The scatter plot panel (B2) visualizes relationships between two user-selected features, such as height, volume, spread, number of branches, or growth rate. Axis selectors are provided at the top, the plot itself occupies the center, and the hovered sample name appears at the bottom. Distinct colors encode categories within the chosen dimension, enabling intuitive comparisons. Hovering over a point enlarges it and displays the sample name in real-time.

The radar chart panel (B3) complements the scatter plot, using the radar chart design described in Figure 4 to represent multidimensional panicle traits. For our target dataset, charts are arranged in three columns for Days 4, 7, and 10. Rows represent categories, and overlapping radar plots highlight contrasts across treatments or genotypes.

Another example is shown in Figure 5. The user selects genotypes KIT and HC5, treatments Control and HDNT, and all three time points. With height on the x-axis and volume on the y-axis, the scatter plot (Figure 5 (a)) separates KIT (blue) and HC5 (yellow). Hovering over a point enlarges it and shows its label (e.g., "HC5 × Control_4D"). The radar charts (Figure 5 (b)) arrange KIT in the first row and HC5 in the second, with columns for Days 4, 7, and 10. Overlaid plots compare Control and HDNT, revealing treatment effects across genotypes and time.

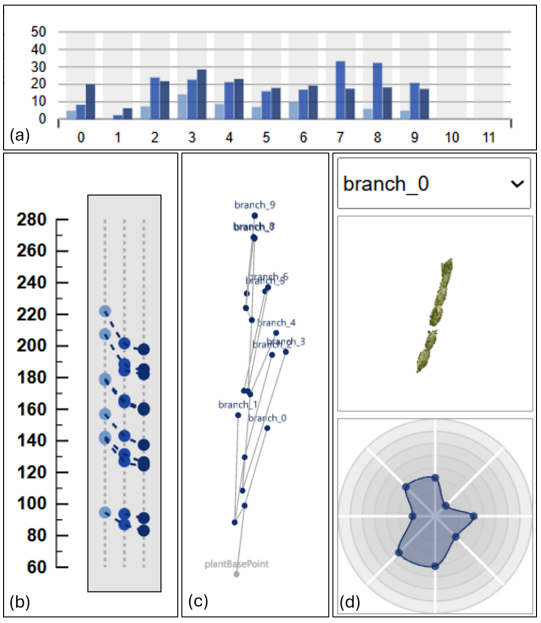


Fig. 6: Branch View example: (a) Histogram of branch spreads; (b) UpSet plot of branch heights across time points; (c) 3D interactive tree graph of branch structures; (d) Selected branch with point cloud rendering and radar chart of features.

C. Branch View

The Branch View (Figure 3 C) enables users to examine panicle structure at the branch level, corresponding to $\phi_B \in \Phi$. Temporal comparisons (Figure 3 C1, C2) use inter-node edges across Σ (time), while individual-day inspections (Figure 3 C3) emphasize intra-node structure by visualizing a single sample's branches. Thus, the view provides both an overview of temporal development and a detailed inspection of individual branches and helps capture how branches emerge, grow, and contribute to the overall panicle structure.

Branch Features across Time Series: Two primary features, branch spread and branch height (defined in Section III-B), are tracked across time (i.e., Days 4, 7, and 10 in our target dataset). Spreads of different branches are shown with bar charts (Figure 3 C1), where the x-axis encodes branch index and the y-axis spread values. Three bars per index represent the three time points, using light, medium, and dark tones. Missing bars indicate branches that emerge later in development, allowing users to detect when new branches appear between time points. Heights are visualized with a modified UpSet plot [16] (Figure 3 C2). Each column corresponds to a time point, and points represent branch heights ordered by the top seed's position. Dashed lines connect the same branch across days, enabling users to trace growth trajectories. Figures 6 (a) and (b) show another example where branch heights decrease as the panicle grows while spreads expand outward. Missing values, such as those for the second and eighth branches on Day 4, reflect branches that emerged later.

Branch Features on a Single Day: For detailed inspection, branches on a selected time point (e.g., Day 10) are shown as 3D tree graphs (Figure 3 C3). Each branch is defined

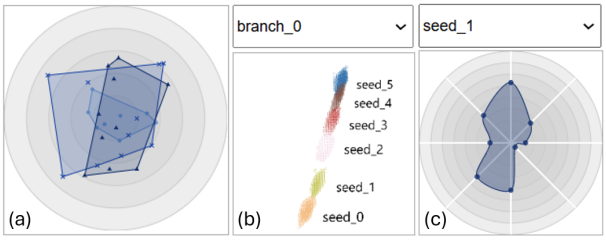


Fig. 7: Seed View example: (a) Polygon plots illustrating minimum areas on the x-y plane; (b) Segmented branch showing individual seeds; (c) Radar chart of features for the selected seed.

by two endpoints, with gray edges representing branch skeletons and green edges forming the panicle stem. The graph is fully interactive, allowing rotation, zooming, and tilting. Users can also select a branch by index to display its point cloud with original colors, as shown at the bottom of C3. Figure 6 (c) illustrates a 3D tree graph of branches, while (d) shows branch 0 selected and rendered in light green. A radar chart summarizes its features, including volume, length, angle, seed count, and four vegetation indices. Together, these tools provide both a structural and quantitative understanding of branch development and its role within the panicle.

D. Seed View

The Seed View (Figure 3 D) supports detailed inspection of seed-level features $\phi_S \in \Phi$. Temporal trajectories (Figure 3 D1) realize inter-node exploration across Σ (time), while individual seed inspection (Figure 3 D2) emphasizes intra-node features such as seed length, width, and volume.

Seed Features Across Time Series: Seed growth is explored by projecting positions onto the x-y plane and computing minimum polygons for each sample (Figure 3 D1). Each node represents a seed position, and polygons summarize spatial spread. Users can highlight polygons interactively and use vectors to track growth direction across time. By visualizing temporal polygons and radar charts as encodings of $\phi_S(v)$, this view preserves the MMG's explicit seed-level representation, enabling comparisons both within branches and across treatments or genotypes. Figure 7 (a) illustrates overlapping polygons for one seed: light blue for Day 4, medium blue for Day 7, and dark blue for Day 10. This visualization allows users to trace how seeds move across the plane and compare spreading rates among samples.

Seed Features on a Single Day: At the individual level, users can explore detailed seed traits within a selected branch (Figure 3 D2). After choosing a branch by index, seeds are segmented with distinct colors and labels. Selecting a seed reveals its radar chart, which summarizes volume, length, width, branch index, and four vegetation indices. Figure 7 (b) shows branch 0 segmented into six seeds; selecting seed 1 produces the radar chart in Figure 7 (c). This functionality supports comparisons across seeds within a branch as well as across different samples.

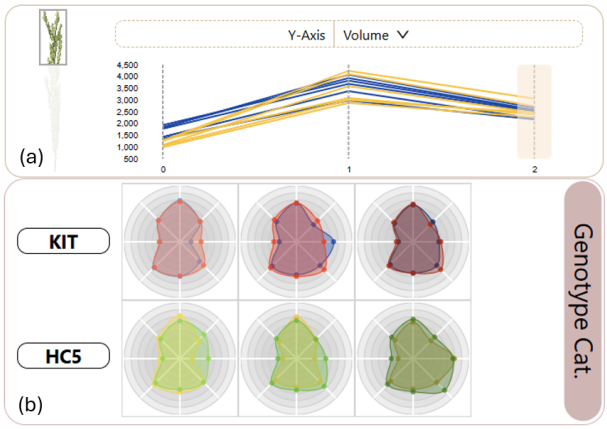


Fig. 8: Extended features for evenly segmented panicle analysis: (a) Segment selection and parallel coordinates showing a chosen feature across segments; (b) Radar charts grouped by dimension categories for the selected segment.

E. Extended Features

PanicleVis enables augmentation of Φ based on specific research needs, further enhancing its applicability in visual analytics of complex phenotyping datasets. We illustrate this with two examples.

User-defined Vegetation Index Specification: Each phenotyping sample contains intrinsic color information represented by R, G, and B values. Users can define custom vegetation indices using R, G, and B channel combinations for plant health, growth, and environmental conditions. These indices are then calculated and added as axes in the radar charts, supporting tailored analysis across different hierarchical levels.

Evenly Segmented Panicle Analysis: For detailed exploration, the panicle can be divided into three segments: upper, middle, and lower. Users select a segment interactively (Figure 8 (a)), after which the system displays parallel coordinates with segment index on the x-axis and a user-specified feature on the y-axis. Data points are color-coded by genotype, and the selected segment is highlighted for clarity. The y-axis feature type can also be changed dynamically through a feature selection button. Segments are further grouped by categories within the chosen dimension, and radar charts are generated to provide an integrated view of features across categories (Figure 8 (b)). For example, selecting the upper panicle segment with Volume as the chosen feature separates samples into KIT (blue) and HC5 (yellow), following the color scheme in Figure 5. The rightmost coordinate highlights the volume for the top segment, while radar charts compare KIT in the first row with HC5 in the second, enabling genotype-specific feature analysis.

VII. Example Usage Scenarios

The MMG representation and the PanicleVis system together provide a foundation for analyzing complex phenotyping data. We demonstrate the practical use of the design and functionality of PanicleVis as described in Section VI. It is often challenging for conventional phenotyping methods

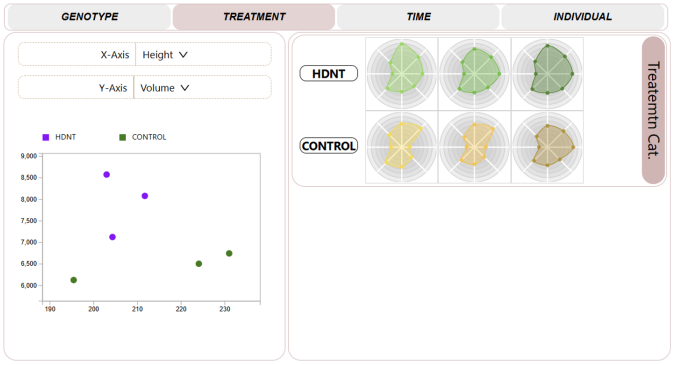


Fig. 9: Use case 1: Treatment effect on whole-panicle traits. The scatter plot shows Height vs. Volume for HC5 panicles under Control and HDNT treatments.

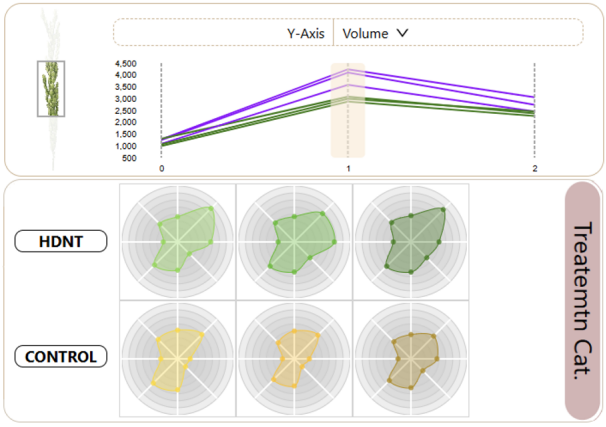


Fig. 10: Use case 1: Treatment effect on panicle segments. Parallel coordinates and radar charts highlight differences across top, middle, and bottom panicle segments.

to capture the phenotypic impacts of environmental and genetic perturbations, such as high temperature stress or natural variation in grain filling, across diverse rice genotypes. These limitations make it difficult to analyze variations in growth dynamics, yield potential, and seed quality at multiple structural levels. PanicleVis addresses this challenge by enabling exploration of hierarchical features (panicle, branch, seed) across categorical dimensions (genotype, treatment, time), thus directly supporting the tasks and requirements defined in Section IV. To illustrate this capability, we present four usage scenarios that show how PanicleVis helps domain experts move from high-level overviews to fine-grained comparisons, revealing relationships that would be difficult to detect with conventional methods.

A. Exploring Treatment Effects Across Panicle Segments

Temperature plays a significant role in rice crop production. A high-temperature environment negatively impacts yield formation, including reducing tiller/panicle number, decreasing grain number per plant, and lowering grain weight. Therefore, studying how high stress affects the growth of panicles is important. We use panicle volume to approximate yield formation and explore the effect of HDNT treatment on the rice panicle with genotype HC5, echoing panicle-level tasks (R1–R3) and their treatment dimension extensions (TR1–TR3).

Figure 9 shows the Panicle View interface. The scatter plot illustrates the relationship between Height and Volume for HC5 panicles under Control and HDNT treatments. The results indicate that high temperature produces larger panicle volume compared to the control, while height is relatively unaffected. Users can hover over the radar chart axes to obtain exact values for each sample over time. To further explore treatment effects at finer granularity, PanicleVis also supports analysis by panicle segments (Figure 10). The parallel coordinates highlight that the middle segment of the panicle exhibits a significant volume increase under HDNT, which is further validated by the radar chart comparison. This demonstrates PanicleVis' ability to support both top-down and bottom-up analysis, aligning with extended tasks (TR1–TR3).

B. Classifying Panicle Growth Trends Over Time

Genotype and treatment can strongly influence panicle growth dynamics, with some panicles ripening earlier than others. PanicleVis supports branch-level temporal analysis (R4) and time-based comparisons (SR4). Figure 11 (a) compares branch height trends across Days 4, 7, and 10 for KIT_CONTROL (blue) and HO1_CONTROL (cyan). KIT_CONTROL begins ripening earlier (Day 4), indicated by decreasing branch heights from heavier seeds, while HO1_CONTROL ripens later (Day 7) with a delayed saddle point. This enables classification of genotype-specific ripening trends at the branch level.

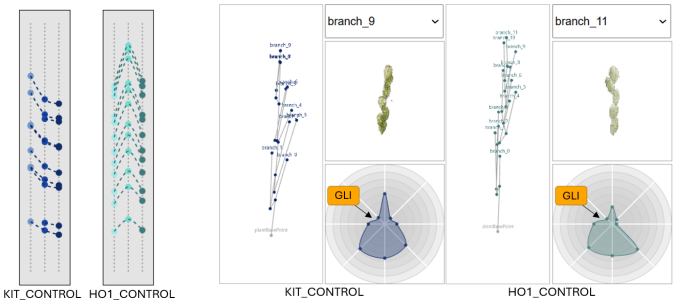
C. Comparing Branch-level Vegetation Index Across Genotypes

RGB-based vegetation indices are commonly used to assess crop health and maturity. The Green Leaf Index (GLI) [7], defined as $\mathrm{GLI} = (2G - R - B)/(2G + R + B)$, yields high values for early-stage panicles retaining chlorophyll and low values for maturing or senescing panicles.

From the interactive 3D graph model, users can learn the number of branches in the panicle on Day 10 and the branch indexes are assigned based on the height orders of the top end of each branch from end to the top. In this example, users use the GLI of the top branch from each sample and detect the crop maturity for the sample KIT_CONTROL (Blue) and HO1_CONTROL (Cyan). After choosing the top branch and hovering over the feature axis for GLI, KIT_CONTROL, and HO1_CONTROL exhibit GLI values of 0.15 and 0.13 in Figure 11 (b). It indicates that both samples contain low chlorophyll content and are in the ripening stage. Compared to KIT_CONTROL, the HO1 panicle ripens more readily.

D. Analyzing Seed Shape Under Treatments

Seed shape, defined as the ratio of width to length, is a critical indicator of yield potential and grain quality. A higher ratio corresponds to plumper seeds with greater weight, while a smaller ratio indicates slender seeds with reduced



(a) (b)

Fig. 11: Use cases 2 and 3: (a) Temporal classification of branch growth trends across genotypes; (b) Comparison of a user-defined vegetation index (GLI) across genotypes.

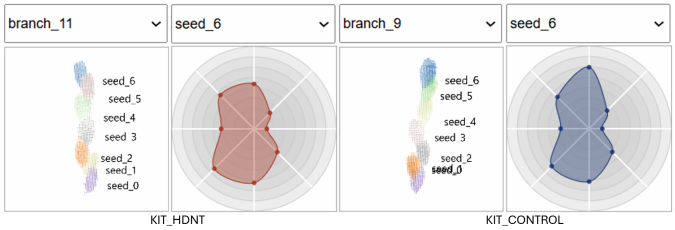


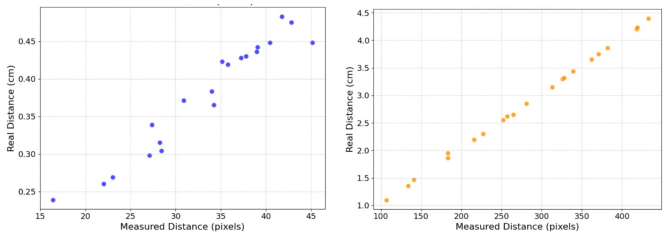
Fig. 12: Use case 4: Treatment effect on seed shape. Radar chart comparison shows differences in seed length, width, and ratios between treatments.

biomass. This relates to seed-level tasks (R7, R8, TR7, TR8). Using PanicleVis, users compare the top seed on the top branch of KIT under Control and HDNT treatments. Figure 12 shows radar charts for seed length and width (see Figure 4 for axis definitions at the seed level). KIT_HDNT produces seeds with length 8.23 mm and width 4.69 mm (ratio 0.57), compared to KIT_CONTROL seeds with length 9.29 mm and width 4.84 mm (ratio 0.52). These results indicate that HDNT produces plumper seeds with higher yield potential, demonstrating the ability of PanicleVis to support fine-grained, seed-level comparisons.

E. Validation Against Traditional Measurements

To ensure reliability, we validated PanicleVis traits against traditional manual measurements. Two representative features were compared: seed width as an intra-seed trait and inter-seed distance as an inter-seed trait. As shown in Figure 13, both exhibit strong linear correlations with manual ground truth, confirming that phenotyping traits derived from PanicleVis are accurate. In addition to accuracy, PanicleVis offers substantial efficiency gains: while manual measurement of a panicle can take several minutes to hours depending on complexity [25], PanicleVis produces results interactively through user operations, making it more scalable for large datasets.

Beyond providing these traits interactively, PanicleVis also supports visual exploration and analysis of complex multidimensional, multilevel data, as described in the previous sections, providing insights into relationships and patterns that conventional manual methods cannot easily reveal.



(a) (b)

Fig. 13: Validation of PanicleVis traits against manual measurements: (a) seed width (intra-seed trait) and (b) inter-seed distance. Both show strong correlations with ground truth, confirming accuracy and demonstrating PanicleVis's efficiency and scalability over traditional methods.

F. Discussion

These use cases and validation experiments demonstrate how PanicleVis supports the full set of analysis tasks and requirements defined in Section IV. At the panicle level, the system enables visualization of core traits and their relationships (R1–R3); at the branch level, it captures both temporal patterns and structural details (R4–R6); and at the seed level, it supports positional analysis and detailed trait evaluation (R7–R8). By incorporating genotype, treatment, and time dimensions, PanicleVis further enables extended GR, TR, and SR analyses. These tasks correspond directly to subgraph operations on the MMG $\mathscr{M}$, ensuring that both multidimensional and hierarchical relationships are consistently preserved across analysis and visualization. The validation against manual measurements further confirms its accuracy, while its scalability and efficiency make it a practical tool for high-throughput phenotyping studies.

VIII. Expert Feedback

Feedback from five agronomy experts (mean usability rating = 4.7/5 and $\approx$ 40% faster task completion than manual plots) highlights PanicleVis as effective for addressing key challenges in rice phenotyping. Its intuitive interface lowers the barrier to exploring complex multidimensional and multilevel traits, enabling rapid, flexible analysis of grain-filling patterns and panicle development across diverse genotypes.

In particular, the ability to assess seed development by panicle position, combined with RGB pixel distributions and user-defined vegetation indices, was highlighted as a powerful, adaptable feature for studying environmental stress. Segmentation and branch-level analysis were also valued for revealing structural traits such as panicle volume, branch length and angle, and seed distribution, offering deeper insight into branching architecture and yield characteristics. For example, use cases 3 and 4 (Sections VII-C and VII-D) demonstrate how PanicleVis helps experts detect subtle ripening dynamics and branch-level chlorophyll differences that are difficult to capture with conventional phenotyping methods, enabling more precise characterization of genotype–environment interactions.

Experts further recognized that these features enhance the identification of stress-tolerant genotypes and support func-

tional genomic studies by linking phenotypic patterns to underlying genetic and environmental factors. Overall, PanicleVis was acknowledged as a valuable resource for advancing phenotyping research, providing both precision and scalability while addressing limitations of traditional manual methods.

IX. Conclusions and Future Work

This work introduces a graph-based framework for panicle phenotyping and its implementation in PanicleVis, a scalable visualization system for multidimensional and multilevel analysis. By formalizing phenotyping data as a Multidimensional and Multilevel Graph (MMG), we capture intra- and cross-level relationships, integrating spatial hierarchy with genotypic, treatment, and temporal dimensions. PanicleVis leverages this model to provide intuitive yet rigorous exploration of panicle, branch, and seed traits, supporting tasks from overview to detailed inspection. Through interactive views, users can visualize structural and temporal patterns, examine treatment and genotype effects, and extend the system with custom indices or segmentation strategies. Expert feedback confirms the system improves the interpretability of complex phenotyping datasets and supports biological discovery.

Future work will extend the MMG to cross-domain datasets (e.g., tumor progression, neural connectivity, or ecological monitoring) and integrate automated graph clustering, temporal modeling, and machine learning for predictive analysis. One direction is extending analysis from top seeds to all seeds within a panicle, including partially occluded ones, enabling finer-grained insights into grain filling, seed development, and yield potential. Linking PanicleVis with high-throughput phenotyping pipelines will also support large-scale breeding programs. Addressing challenges in computational efficiency, data resolution, and usability will be essential. With these advances, PanicleVis will continue evolving as a comprehensive and adaptable framework for phenotyping research, bridging complex datasets with new biological understanding.

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