

Plant Image Segmentation and Annotation with Ontologies in BisQue

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I. INTRODUCTION

The field of computer vision has experienced much progress in the last two decades. Image analysis of photography and video has moved out of computer science research labs and into a wide range of applications. One example of progress in image analysis concerns the segmentation of images on the basis of gray scale, color hue, texture, geometry, and other features. Such image segmentation allows for increasingly refined classification of images and their components. In a parallel development, semantic computing has pursued the creation of ontologies in hopes of capturing and defining what it is we “know” about the world, and presenting it in the form of a terminology network connected by defined relationships. This knowledge network is computable, and makes it possible to make logical inferences about facts and data annotated with ontology terms.

By combining these two innovations: image analysis and ontology annotation, we can imbue images with structured meaning and enable the inferential computability of image data. For example, it may be possible to segment an image of a plant leaf into diseased and undiseased tissue, and then to annotate these segments with ontology terms describing the disease state and associated phenotypes. Once a database of such images is developed, machine-learning algorithms can be applied to the data and predictive models can be developed. In this scenario, new images of plant leaves may be “tagged” with a disease state based on earlier examples.

We have already explored the segmentation and ontological annotation components in the desktop application AISO [1], but would like to see this functionality available in an online format that allows for better processing scalability, storage, security, and collaborative feature sharing. We also want to apply machine learning to a collection of segmented, annotated images, thereby automating future image processing.

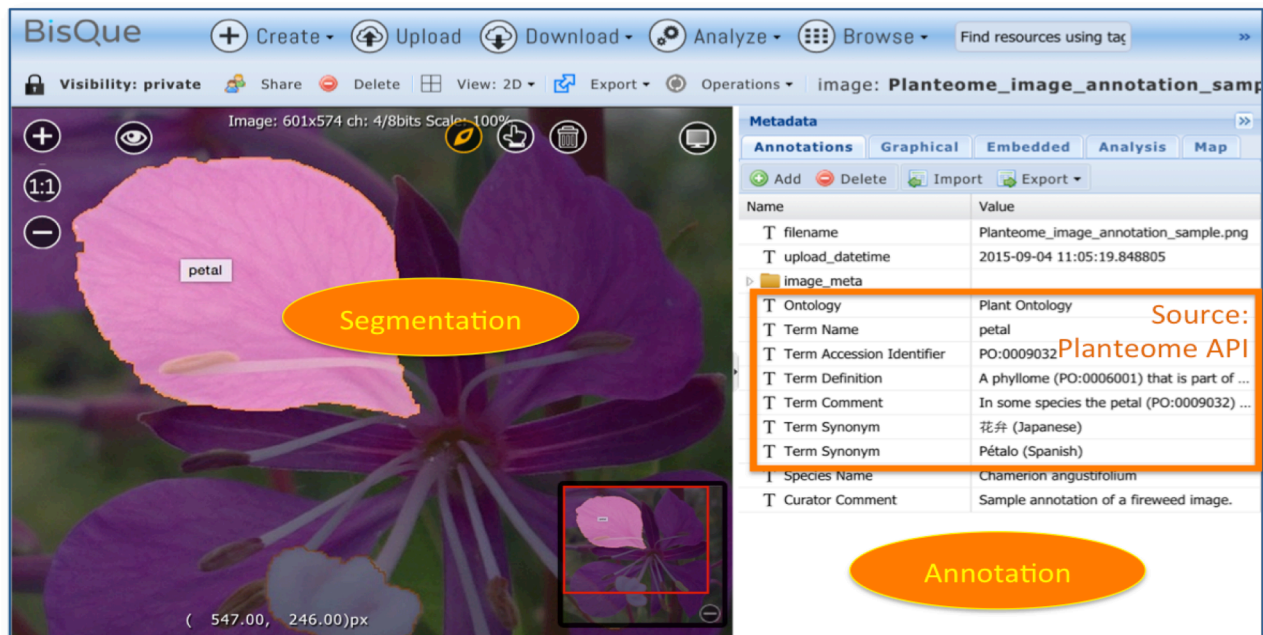
II. IMPLEMENTATION

The Planteome project [2] has partnered with BisQue and CyVerse to take advantage of their image analysis, storage and authentication features. BisQue (Bio-Image Semantic Query User Environment), a platform hosted at the UC-Santa Barbara Center for Bio-Image Informatics, is designed to store, visualize and analyze a wide range of multidimensional biological images [3]. CyVerse (formerly iPlant) provides a computational infrastructure for all manner of data-driven discovery projects in academic research [4]. BisQue is integrated specifically with the CyVerse authentication and storage systems.

The BisQue environment allows external development groups to build and contribute image analysis modules. Planteome is developing such a module to provide a segmentation feature utilizing a Dynamic Graph Cuts algorithm [5]. Planteome is working with BisQue to specify and develop service brokers and a user interface within BisQue that will give end-users the ability to label images and portions of images with ontology terms [Fig. 1].

III. RESULTS

We have established development servers hosting the BisQue engine, and have developed initial specifications for the module’s user interface and backend segmentation processing. Our server-side module consists of a MatLab package implementing the Dynamic Graph Cuts algorithm, and is heavily modeled on the preexisting Image Matting module [6], with notable modifications. User-guided segmentation requires lines (“markup”) drawn to indicate foreground and background elements relative to the desired segment. Our module user interface has been enhanced to allow multiple foreground and background markup lines. The Planteome project now has a running module in our development environment that successfully processes and returns a segmented image (<http://bisque-dev.planteome.org/>). (NOTE: This is an active development environment, and the module may not be available at all times). Our module source code is



(Image source: AISO & Bisque composite mock-up)

- [1] **Proposed interface for Planteome segmentation and ontology annotation in BisQue.** The image viewer on the left contains a mock-up design for displaying segmented image results labeled with an ontology term. The data panel on the right contains a hypothetical key-value pair listing for ontology term data associated with the segment on the left. Our project module is currently able to accept user-guided foreground and background markup, segment an image, and return that segment data to the viewer. Ontology APIs and annotation interface are still under development.

available on GitHub (<https://github.com/Planteome/planteome-image-annotator>).

With regard to ontology service development, the Planteome team has enabled an API from the AmiGO platform [7] that serves out multiple Planteome-developed ontologies in JSON. For example, API requests may be made for term details and autocomplete suggestions. Research is also underway on novel feature detection and prediction (*i.e.* leaf orientation and characterization) that may be incorporated into the machine-learning aspects of this project.

IV. DISCUSSION

We are currently in the process of defining specifications for ontology integration and annotation with the BisQue team. We believe it will be beneficial to allow multiple ontology terms to be applied to the same segment in the same image; that is a feature to be added at some point. Other key topics under discussion include whether to make the ontology annotation interface in BisQue configurable and extensible to external ontology services provided by multiple sources in different formats, and whether to allow user customization and localization of ontologies. These features will benefit the broader image analysis community, as all users of the BisQue platform will be able to take advantage of the ontology annotation functionality. Further user interface enhancements to the segmentation feature will include differential markup line coloring (red = foreground, blue = background); currently, all markup lines are colored red and may confuse the end-user.

V. CONCLUSIONS

The combination of a robust online image analysis platform, an efficient segmentation algorithm, ontology

services, and future machine learning can be a powerful tool in an era where high-throughput, high-quality digital images of biological phenotypes are readily available and ripe for computational analysis. The Planteome segmentation module and accompanying BisQue ontology annotation integration may point the way to an effective suite of auto-segmentation and auto-annotation tools built to meet this need.

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