# Web-based Annotation tool for Image-based Phenotyping

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As Genome Wide Association Studies (GWAS) are now used extensively to identify genetic variants, effective and automatic phenotyping of complex traits has become an important limiting factor to GWAS discovery. We designed a web-based image annotation GUI (graphical user interface, Fig.1(b)), which eliminates the need for software installations and platform dependencies in the task of annotating objects and parts from an image at pixel-level accuracy. Our annotation GUI utilizes the state-of-the-art deep interactive object selection algorithm[2], where the user only needs to draw a few "scribbles" away from boundaries, and the system intelligently computes a boundary-accurate annotation of each object. Users have the capability of repeatedly refining those boundary annotations until satisfaction. The GUI development makes obtaining complex pixel-level annotations significantly easier and faster than traditional tools.

In a pilot analysis of the regeneration capacity in *Populus trichocarpa*, specific tissues of interest (callus, shoots, and stem (Fig.1)) are annotated by the user with the developed annotation GUI. These annotated images are then used to train a Deep Neural Network (DNN)[3] for semantic segmentation, which assigns each pixel to one type of the recognized tissues or background. Then, callus area and shoot area are computed as the traits of interest. Afterward, the GWAS method Sequence Kernel Association Test (SKAT)[1] is used to test the association between SNPs(Single-nucleotide polymorphisms) with the computed traits. And to control of non-normality of data, resampling was applied first(Fig.2). Results show that the automatic traits are substantially better in revealing links between genetic markers and regeneration related phenotypes, that shows the potential of the proposed approach for much greater genetic discovery.

## References

[1] Michael C Wu, Seunggeun Lee, and et al. Lin, Xihong. Rare-variant association testing for sequencing data with the sequence kernel association test. *AJHG*, 89(1):82–93, 2011. 1

[2] Ning Xu, Brian Price, Scott Cohen, Jimei Yang, and Thomas S Huang. Deep interactive object selection. In *cvpr*, 2016. 1
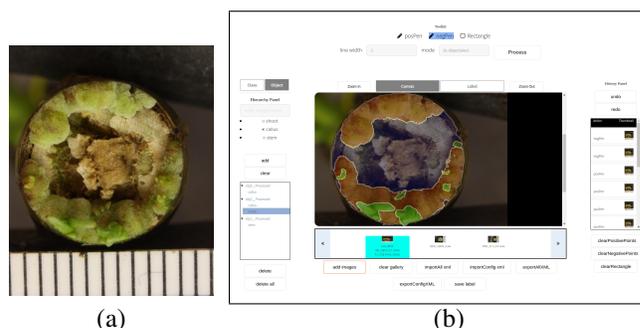
(a)        (b)

Figure 1. An example of annotating an image as callus, shoot, and stem. (a) input image (b) our GUI which contains: a hierarchy panel (left) for users to specify objects and the classes to annotate, a tool panel (top-center) to choose tool for annotation, an interactive canvas(center) with annotation result on the input image, the I/O management panel (bottom-center), and the history management panel(right)
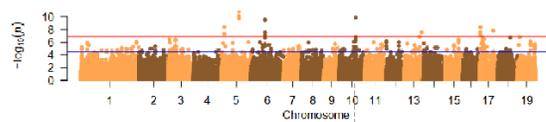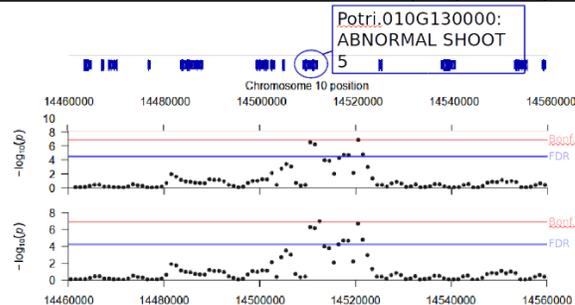


Figure 2. Manhattan plot and the zoomed-in plot on chromosome 10 subsection with 10 million permutations. It reveals a possible association of shoot area with a homolog of a known shoot regulator in *Arabidopsis*.

[3] Hengshuang Zhao, Jianping Shi, Xiaojuan Qi, Xiaogang Wang, and Jiaya Jia. Pyramid scene parsing network. In *cvpr*, 2017. 1