Digital Imaging of Root Traits (DIRT) – An online high-throughput phenotyping platform for analysis of root images

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Introduction

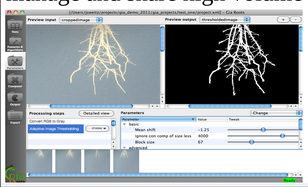
Imaging technologies allow rapid acquisition of high-resolution images of the spatial organizations in plant networks such as leaf venation networks, root networks and tree crowns. As a result the volume of data increases and scientific discoveries are rather limited by the availability of analysis platforms than data. The challenges in big data analysis of plant networks include:(i) reconstruction and representation of the network from the imaging data;(ii)translation of network analysis to the problem domain of plant networks; (iii) distribution and visualization of network features along with its metadata to not so-technical audiences. Existing plant network data[5] analysis platforms lack in integrating data management, analysis and interpretation. We present **DIRT** as the first **fully automated web platform** to store, manage and analyze plant networks from **field grown crop root images**.

Objectives

1. Design a platform to store and manage large collections of crop root networks along with experimental metadata
2. Execute the computation of algorithms to extract root traits as input for large scale gene discovery in plants
3. Enable open-source community science by seamlessly sharing and combining field experimental data

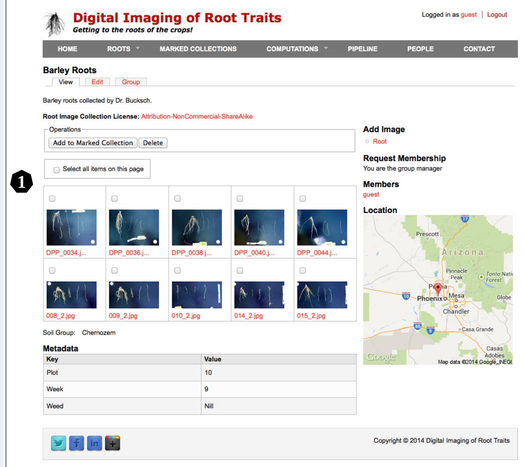
Background

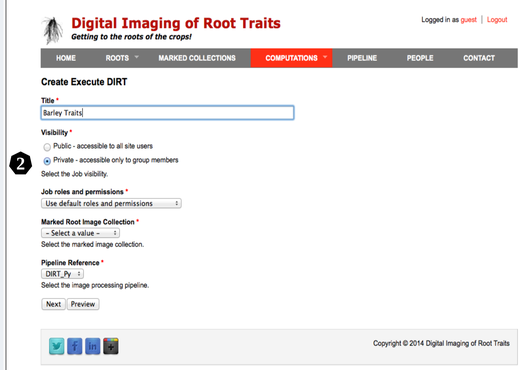
Discovering the relation between plant network morphology and related genes relies on measurement of geometric and topological traits. For significant results, measurement needs to be repeated multiple times per genotype. A number of software tools have been developed [1-4] to estimate traits from images, especially from crop roots grown in laboratory environments such as gellan gum and transparent soil replacements, limiting the observation to just few weeks of growth. However, mature root systems from real soil conditions pose greater challenge because of network size and excavation process. The application of algorithms to images from fields with large variations, faces two main bottlenecks: 1) complex root networks need more computation time demanding the use of super computers 2) wide morphological variation requires large number of images to be collected per genotype, in turn demanding an efficient system to store, manage and share high volume of heterogeneous data.

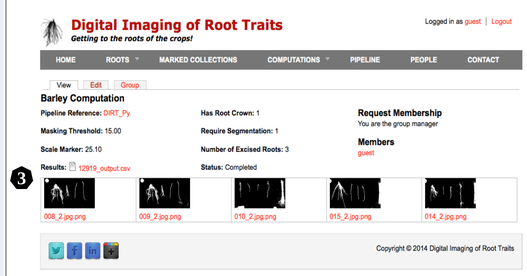


This is an image of a 15 days old rice root grown in gellan gum medium within the limits of the growth container

Important features of the platform







1. Create root image collection: Enables user to create private or public root image collection with metadata information. Users have option to add their own metadata information in key-value format

2. Bulk upload root images and its metadata

3. Manage root image collections: Update existing collection's metadata, share private collections with specific users/members of the community.

4. Marked Collections: User have option to maintain multiple marked collections by selecting images from different root image collections.

5. Run existing image processing pipeline on **high-throughput grid computing environment** to compute traits of choice

6. Provide values for predefined set of parameters of the pipeline that automates computation of traits

7. Existing pipeline computes 70 different traits from root images. Users have option to select and compute traits of choice

8. Manage computation to be either private or public and share with specific member of the community

9. View the computed masked images and its traits. Download computed traits in the form of a csv file for further analysis

Results

1. Results enabled by the DIRT platform were recently published in Plant Physiology [6].

A Six examples from the cowpea diversity panel. Different root architectures in mature cowpea with the genotype denoted in each image are illustrated.

B Overall phenotype differentiation of the cowpea diversity panel. Black crosses show the trait values of the whole dataset, the lines are three selected examples with error bars denoting the standard error of the mean. The 3 example genotypes distinguish by at least one D- and DS-value and by the second dominant angle. The D-values demonstrate, that UCR 779 differentiates from Petite'n'Green at higher depth levels and from Early Scarlet a deeper depth levels. UCR 779 differentiates additionally in central path diameters from Petite and Green and Early Scarlet. The connection between points supports the reader visually to identify the 3 genotypes shown in Figure A. (STA= soil tissue angle, RTA= root tissue angle, TD = tip diameter, DD90max = maximum diameter at 90% - 100% depth, RTP = Root Tip Path, dia. = diameter)

2. Currently we are running a beta-version of our platform at Georgia Tech (**http://dirt.biology.gatech.edu**). The server is coupled to the Georgia Tech's high performance **grid computing** environment PACE.

3. The system is being tested and used at field sites around the world such as **Italy, Germany, South Africa, Thailand and the USA** by researchers from PennState, Duke University, University of Georgia, Forschungszentrum Jülich (Germany), University of Bologna (Italy), University of Limpopo (South Africa).

Future Work

1. Release of DIRT to the whole root research community through the iPlant cyber-infrastructure including the coupling of heterogeneous high performance computing platform
2. Integration of advanced statistical analysis such as trait heritability and GWAS
3. Design of a flexible system API to allow extensions for 3D data and their respective algorithms.

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