Towards fully automated root phenotyping in the field: from Minirhizotron image acquisition to data analysis

Kaining Zhou[1], Adam Soffer[2], Jhonathan E. Ephrath[1], Ofer Hadar[2], and Naftali Lazarovitch[1]

[1]French Associates Institute for Agriculture and Biotechnology of Drylands, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Sede Boqer Campus, 8499000, Israel (zhoy@post.bgu.ac.il)

[2]School of Electrical and Computer Engineering, Ben-Gurion University of the Negev, 8410501 Beer Sheva, Israel

Root phenotyping in the field remains challenging from root imaging to data analysis since each part of this process is time-consuming and labor-intensive. Extensive efforts have been taken to explore the possibility to automate parts of this process. However, few studies have provided an integrated solution to make the whole process in a manner of low cost, automated, and customizable for different tasks. In this study, we have worked towards this goal. A newly designed root imaging system called RootCam addresses the above-mentioned limitations. RootCam moves a small camera with fully automated operations for long-term *in-situ* monitoring. It captures high-resolution root images (2592 x 1944 pixels). These images are saved to a "Raspberry Pi" device which is accessible by a network cable allowing users to control the system remotely. Users can also control time intervals between runs and set image capturing either overlapped or non-overlapped. This camera was tested in a net house by imaging bell pepper roots which shows superior performance over commercial minirhizotron systems. A deep convolutional neural networks (CNN) model was developed to detect plant roots and calculate root length. This model was trained and calibrated with a dataset of ~18,000 tomato root images and has been used for calculating bell pepper root length on 832 images. The high correlation coefficient (R^2 = 0.854) between the measurements from the automated and manual methods proved that our model is able to generalize well over different crop roots. However, the model underestimates root length when there are many roots in an individual image. In summary, the platform we developed to automatize minirhizotron image acquisition and analysis has the promising potential to benefit both the root research community via accelerating high throughput root phenotyping in the field for root studies and farmers via making real-time root development information available for decision making.