# Hyperspectral image segmentation of plants grown under real world conditions – sub plant level segmentation to deal with variability in illumination


Dominic Williams
James Hutton Limited

Ali Karley
James Hutton Institute

Hamlyn Jones
University of Dundee

Christine Hackett
Biomathematics and Statistics Scotland

Matt Aitkenhead
James Hutton Institute

Susan McCallum
James Hutton Institute

Kenneth Loades
James Hutton Institute

Julie Graham
James Hutton Institute


## Abstract


Hyperspectral imaging is being increasingly used as part of high throughput phenotyping platforms. This technique measures the spectral reflectance of plants. The spectrum received at the sensor is a function of incident light, plant reflectance, plant fluorescence, angle of leaf relative to light source and angle of leaf relative to sensors. Although many of these factors can be controlled in the laboratory, many applications to high throughput plant phenotyping require measurements in the complex radiation environments of glasshouses and the field. In this study we investigated the differing spectra received from the brightest and the darkest (shaded) pixels and the potential implications for the extraction of key biophysical variables relating to plant performance.


Figure 1. Example rgb representation of hyperspectral images

We are currently developing an imaging platform for glasshouse and field use with two hyperspectral sensors; a visible and near infrared (VNIR) hyperspectral camera covering the region between 400-950nm with 398 wavelength bands and, a shortwave infrared (SWIR) hyperspectral camera covering the region 1000-2500nm with 278 bands.

The data used here were obtained in a glasshouse with the platform mounted on a trolley that is pushed manually along the plant rows. The trial included 96 raspberry plants with three different plant genotypes (Glen Moy, Latham and an unreleased variety) and four different treatments (low water, high water, root rot infection and vine weevil infestation) arranged in a randomised block design. The plants were imaged weekly for a period of 14 weeks. Segmentation of the plant material from background was carried out by applying a threshold to values of normalised difference vegetation index (NDVI). This was able to accurately identify the plant material from the background. The binary mask generated was used to split the image into individual plants and a mean spectrum for each plant generated. Due to the structure of the plant different leaves will have received different amounts and qualities of incoming light, with both spectrum and intensity varying. In order to investigate whether the separation of treatments was most effective for the brighter or darker pixels, the pixels were ranked by brightness and ANOVA was used to calculate the significance of differences between treatments and genotypes for different brightness ranges. The mean spectrum for each plant using only a subsection of pixels according to their brightness was calculated and subjected to ANOVA.

Although no significant genotype x treatment interactions were found, significant differences were found for both treatment and genotype effects. For the VNIR data increasing significance across all wavelengths was found when using only brighter pixels. Normalising the image to remove the brightness effect on an individual pixel basis reduced the ability to detect a genotypic difference. For the SWIR data different trends were found at different wavelengths.

These results show that differing illumination of different parts of the plant affects the ability of spectral information to determine biologically relevant features, and that better discrimination could be achieved by use of only a limited range of brightness values, rather than using data from all pixels. The best results were obtained using a subset of the brightness range concentrating on the brighter pixels. More advanced leaf level segmentation techniques may further improve results.