Multispectral Analysis of Spinach Seeds

Results of master thesis by

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ABSTRACT

The **goal** of the thesis is to determine if a spinach seed is fungus infected and if so with which fungi it infected, and to what degree it is infected.

The **main approach** used is spectral unmixing which decomposes the image into a number of endmembers, each corresponding to clean seed or the fungi. 5 different fungi were chosen for this study. With the decomposition specific fungus infection on the seed may be determined and each pixel can be a mix of different fungi infections. The image data are extended with morphological closing and Laplace filtering with the aim of getting better results. Statistical classification is also used to identify the fungi in order to compare spectral unmixing with a simple method.

Results: When applying spectral unmixing on the seed data, it is possible to find out if a seed is infected or not. Using an extension based on morphological closing, it is also possible to clearly identify 3 of the 5 fungi studied. This makes it possible to determine which fungus a whole seed is infected with if it only has one infection, but the result was not good enough to determine the fungi at a pixel level. Classification was able to identify all fungi, but once more, not at a pixel level. With spectral unmixing it is possible to determine the degree of infection, while this is not possible with classification.

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Master thesis download: orbit.dtu.dk
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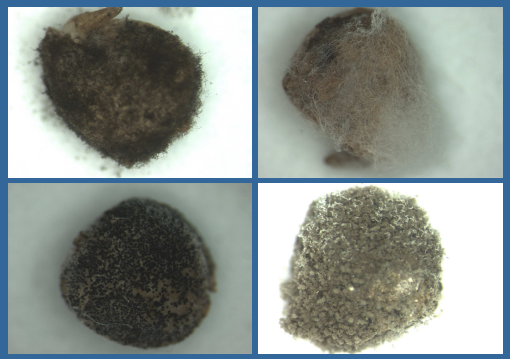
INTRODUCTION

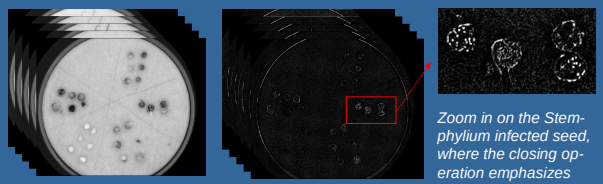
The quality of spinach seeds depends on which fungi they are infected with. To be able to determine the infection degree of a batch, a sample with hundreds of seeds must be examined. Today the process is done manually by microscope. This poster present the results of a master thesis which deals with automating the examination by using multispectral imaging.

Fungi infection as seen in microscope



Microscope images of fungi infected spinach seeds. From top left: Alternaria, Fusarium, Verticillium and Cladosporium.

Multispectral image data



Original multispectral image data and the result of a closing operation on the images. The closing operation is used to bring neighbor pixel information into the pixels. This is done because the mixing model works on a single pixel.

Zoom in on the Stemphylium infected seed, where the closing operation emphasizes the spatial structure. There is high response (white) for areas with dot like structure.

Spectral unmixing

Spectral unmixing is a decomposition of an image into endmember spectra and abundances. Using unmixing each pixel will be a combination of the distinctive material spectra that make up the pixel. This means that a single pixel can be 'classified' as consisting of uninfected seed and multiple different fungi. This makes spectral unmixing superior to traditional statistical classification.

The most frequently used model for the decomposition is a linear model which is as follows:

$$\mathbf{x} = \sum_i p_i \cdot \mathbf{E}_i$$

where **x** is a pixel, p_i the abundance of the i'th endmember and E_i the endmember spectrum of the i'th endmember. The model is illustrated bellow. To the left are the endmember spectra and to the right the endmember spectra are mixed with 3 different abundances, representing data for 3 pixels.

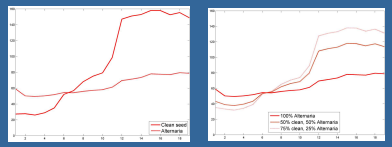


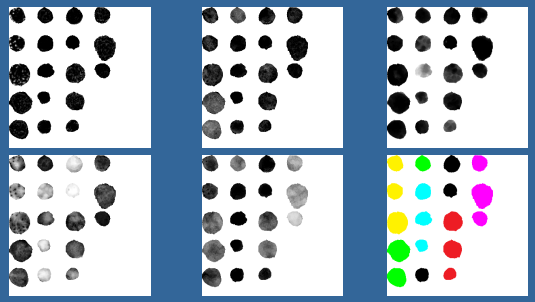
Illustration of mixing model

Methods

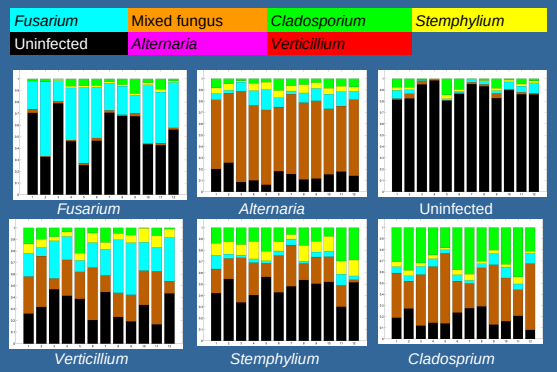
Estimates of the endmember spectra are needed to make the decomposition. A wide variety of methods exists for obtaining the estimates. In the thesis, a selection of methods was tested. Among those ICE gave good results. This algorithm relies on a geometric interpretation of the pixel intensities when viewed in a coordinate system. It iteratively updates endmember and abundance estimates. Although it is designed to work on spectral data it was able to use the closing extended data to better identify the fungi.

Results

The analysis showed that it is possible to use spectral unmixing to distinguish between a number of the fungi for a whole seed. Endmembers for uninfected seed, *Fusarium*, *Cladosporium* and *Stemphylium* were found. However, almost every pixel has some abundance for all endmembers. Therefore more work is required for the model to work at pixel level. Abundance images and summarizing bar plots are shown below.



Abundance images for segmented seeds. Each image shows abundance for one endmember. White is 100% and black is 0%. The lower right image shows the infection type (see below for key)



Bar plots showing mean abundances. Each column is a seed with a given infection type and shows the mean abundance distributed over the different endmembers. The correct endmembers are dominating for Fusarium and Cladosporium infected seeds and uninfected seeds. The Stemphylium endmember only applies to some part of the infection and is therefore not dominating. It is also seen that fungi endmembers are found on uninfected seeds.