Texture Analysis of Fungi using Gabor-Filters

**Problem Description**
The most frequently occurring spoilage fungi on cheese is called *Penicillium commune*, and results in discolouring of the cheese surface and production of off-flavours.

In order to map the contamination routs of the fungi a study of isolated *Penicillium commune* has been sampled from cheese and production environments in two factories. By DNA fingerprints the *Penicillium commune* were classified into groups according to their genotype. Each class could be processed as clones and related to have a common origin in the factory. This way the contamination point could be determined.

**Finding Features – Colour and Texture**
The features extracted from the colour information in the fungi images were found by calculating the average intensity in three rings from the centre of each fungus - this was done in all three RGB layers.

Gabor filters were then introduced to disclose the texture of the fungi. A Gabor filter is essentially a band pass filter which ‘measures’ the pictorial energies in different directions. In advance it was known that the fungi had some radial and circular texture, therefore the images were processed with filters which were able to emphasize these specific patterns.

**Classification**
The classification of the fungi was carried out by a hierarchical clustering algorithm known as the group-average agglomerative method. From a feature vector consisting of 9 elements of colour information and 6 elements of texture information a dendogram of the fungi family was made.

**Results of a Gabor filtered fungus image**

**Conclusion**
First the classification results were tested subjectively. The fungi which were coherent according to our dendogram showed good similarities when compared visually.

The principal component analysis of the features revealed that most variation was given by the colors and that scaling of the Gabor filters did not give any additional valuable information and for that reason a single scale factor was used.

When the dendogram was compared with the DNA classification it showed out that the method only worked to some extend. It was clear to see that there was some sort of right classification, but there was also a lot of misclassifications – especially because the dataset contains many single member classes.

**References:**


**Informatics and Mathematical Modelling**

Thomas Stoltz and Dorthe Hofman-Bang
Work performed as part of the IMM course Advanced Image Analysis under supervision of Hans Henrik Thodberg