Introduction

Beyond growth inhibition, fungicides can also trigger specific morphological modifications visualized under transmitted light microscopy. These morphological changes result from the activity of a given compound via the inhibition of a molecular target, commonly named as its mode of action (MoA). We are hence able to classify different molecules into their respective MoA by observing their phenotypic signature, and even to detect new MoA with unknown phenotypic effect for further deconvolution. The aim of the presented work is to develop a robust method for automated recognition and classification of these phenotypic signatures in order to lead to a Mode of Action hypothesis. We compare two machine-learning methods (Random forest and Convolutional Neural Network) for direct processing of images generated on the grey mold Botrytis cinerea subjected to different antifungal molecules.

Strategy

From morphology recognition to Mode of Action prediction: the power of artificial intelligence to automatize fungal precision phenotyping.

Method 1: Morphometric parameters extraction and Random Forest-based classification (1)

1. Object detection and individualization
2. Skeletonization and graph generation
3. Morphometric parameters computation
4. Random Forest for phenotypes clustering

In summary:
Precise analysis and classification of cellular objects within images. Access to known and defined morphometric features values. Limited number of morphometric features. Run time: few minutes/image

Method 2: Application of a pre-trained image recognition Convolutional Neural Network (CNN) for phenotype classification (2)

1. Image pre-processing
2. CNN for phenotypes clustering
3. Test & classifier efficiency evaluation: comparison A prediction vs. human expertise

In summary:
Global analysis and object classification of the entire image. Access to unknown features (morphometric or others?) High number of features (~million) Run time: few seconds/image

Results & Conclusions

Cross-validation

Evaluation on 4 different phenotypes
Morphometric parameters: Nbr of molecules with correct prediction
Sensitivity (%) Precission (%)
RF: 77 / 79
CNN: 92 / 95

Method 1: Random Forest (RF)

RF n = 500 trees
Training set: 14 / 22
2/3 training population: 1/4 test population

Method 2: Deep Learning (DL)

CNN for phenotypes clustering

In summary:
Robustness intra-experiments

Evaluation on 4 different phenotypes, Nbr of images / experiments
Morphometric parameters: Nbr of molecules with correct prediction
Sensitivity (%) Precission (%)
RF: 15 / 35
CNN: 31 / 35

To date, CNN provides better phenotype classification than Random-Forest based method.

We are going to further investigate respective approaches in order to evaluate which one, or a combination, will permit to ensure a robust automation of phenotyping recognition in a larger number of phenotype.