

# „A *PhenoBox* in every lab“

Development of a flexible, economic, open source phenotyping solution



**2nd APPN meeting  
2018-04-17**

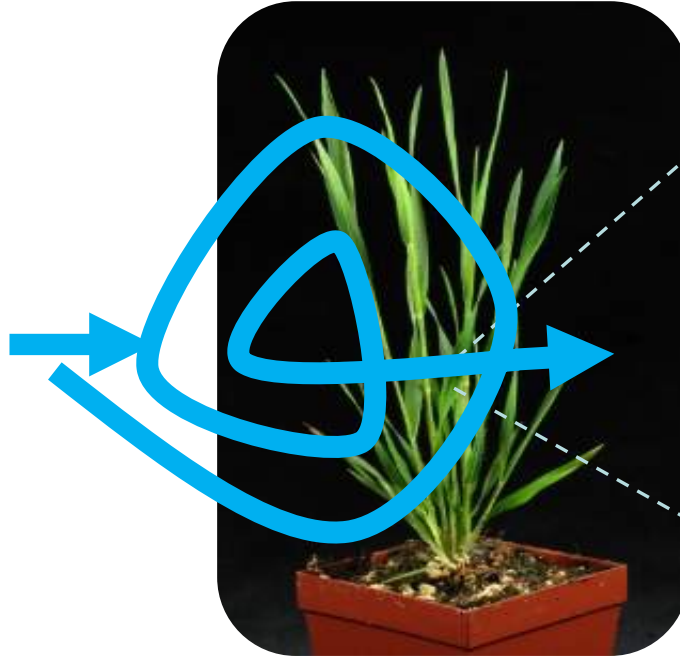
Angelika Czedik-Eysenberg  
Sebastian Seitner  
Djamei Group, GMI

# *Ustilago bromivora* is a headsmut

## Backgrounds

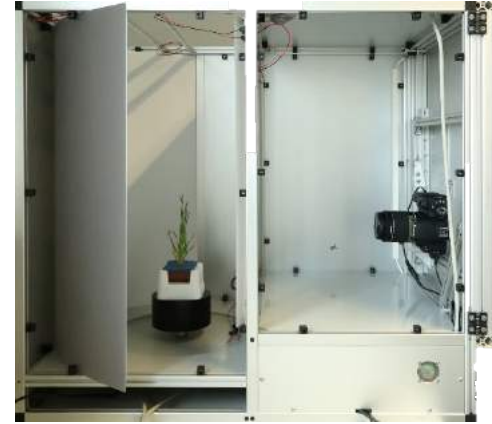
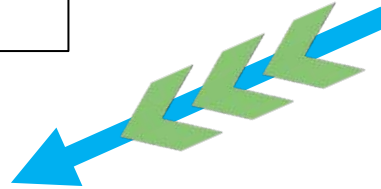


*Brachypodium* infected  
with *Ustilago bromivora*

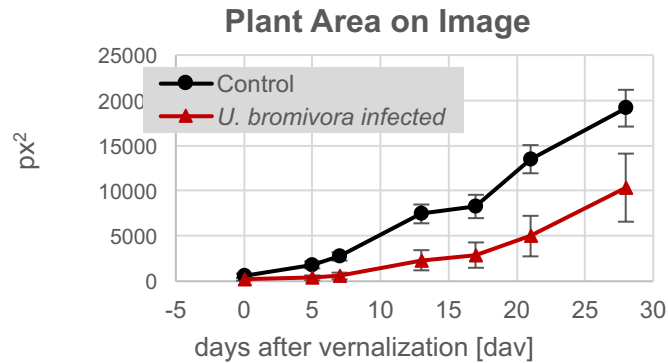


# Roadmap of this talk

## Backgrounds



PhenoBox & PhenoPipe



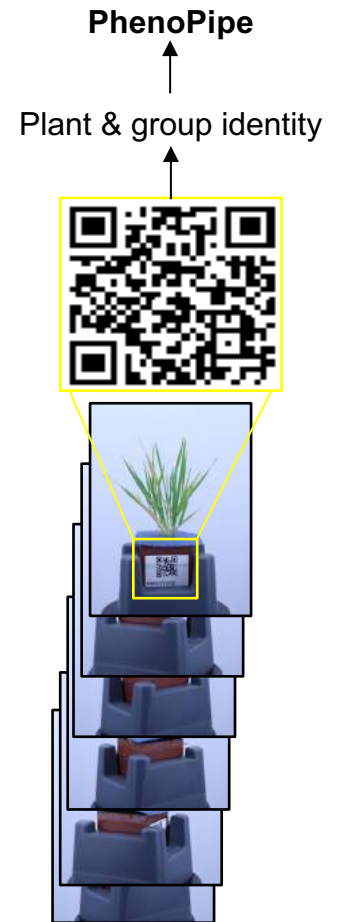
biology



technology

# The PhenoBox

Start with video?! Or is this animation enough?



# Main Steps in Phenotyping Analysis

## Process

- Define experimental groups
- Labeling
- Imaging
- Data storage and management
- Image feature extraction
- Data analysis and visualization

# The PhenoPipe

## Overview

### Information



### Web Interface

[Create Project](#)  
[View Projects](#)

Tasks:

- [Analysis](#)
- [Postprocessing](#)
- [Modules](#)

Project Name: BenthamianaNaCl2

Project Description:  
second group of 200mM salt treated vs. control nicotiana benthamiana

Group Name: djamei

Scientist: angelika.czedik

Start Date: 2017-10-22

Start of Experimentation: 2017-10-22

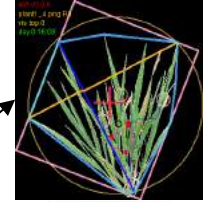
Created at: 2017-10-15 17:07

Updated at: 2018-01-12 13:05

Total # of plants: 22

[Print all Labels](#) [Edit](#)

### Feature Extraction



Klukas et al., 2014

### Postprocessing Stacks



### PhenoBox



# The PhenoPipe

Process

Information



Web Interface

PhenoBox



○ Create Project

○ View Projects

Tasks:


○ Analysis

○ Postprocessing

○ Modules

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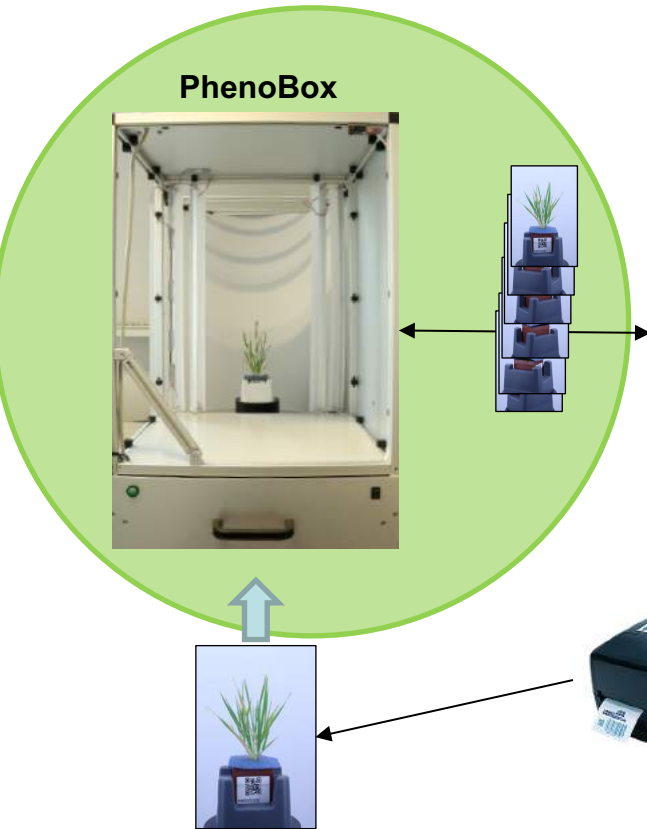
Print all Labels Edit





# The PhenoPipe

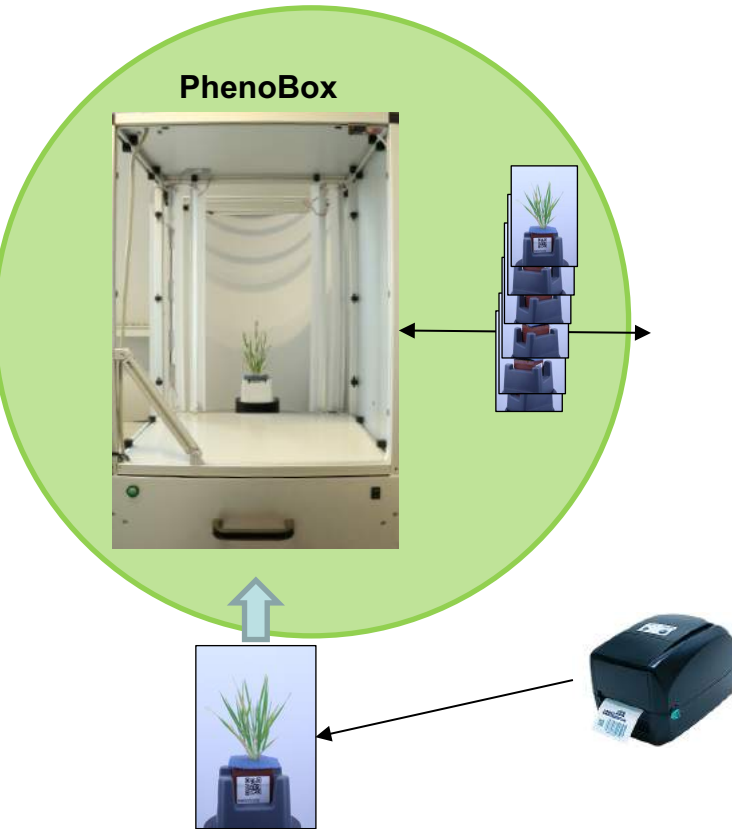
Labeling/Imaging





# The PhenoPipe

## Labeling/Imaging



- Print Labels directly from Web Interface
- Plant identification based on QR-Code
- Automated naming and grouping of images
- Automatic creation of Timestamps

# The PhenoPipe

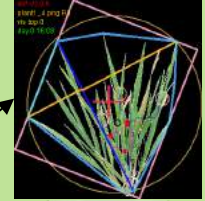
Process

Information



Web Interface

Feature Extraction



Klukas et al., 2014

Postprocessing Stacks



PhenoBox



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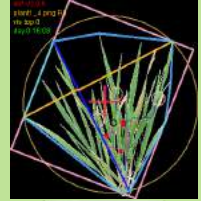
Total # of plants: 22

[Print all Labels](#) [Edit](#)



- Open Source high-throughput Image Analysis
- Customized to be used in PhenoPipe
- Works by defining 'Pipelines' to analyze images
- Users can upload their own pipelines

### Feature Extraction



Klukas et al., 2014

# The PhenoPipe

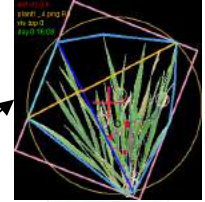
Process

Information



Web Interface

Feature Extraction



Klukas et al., 2014

Postprocessing Stacks



PhenoBox



○ Create Project

○ View Projects

Tasks:

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Print all Labels Edit



## Postprocessing

- Modular approach
  - Multiple scripts form so called 'Postprocessing Stacks'
  - Each script can pass information on to the next
  - Multiple Stacks can be applied/executed simultaneously
  - Tied into the web interface
    - Status Messages
    - Progress indication
- }Customizable

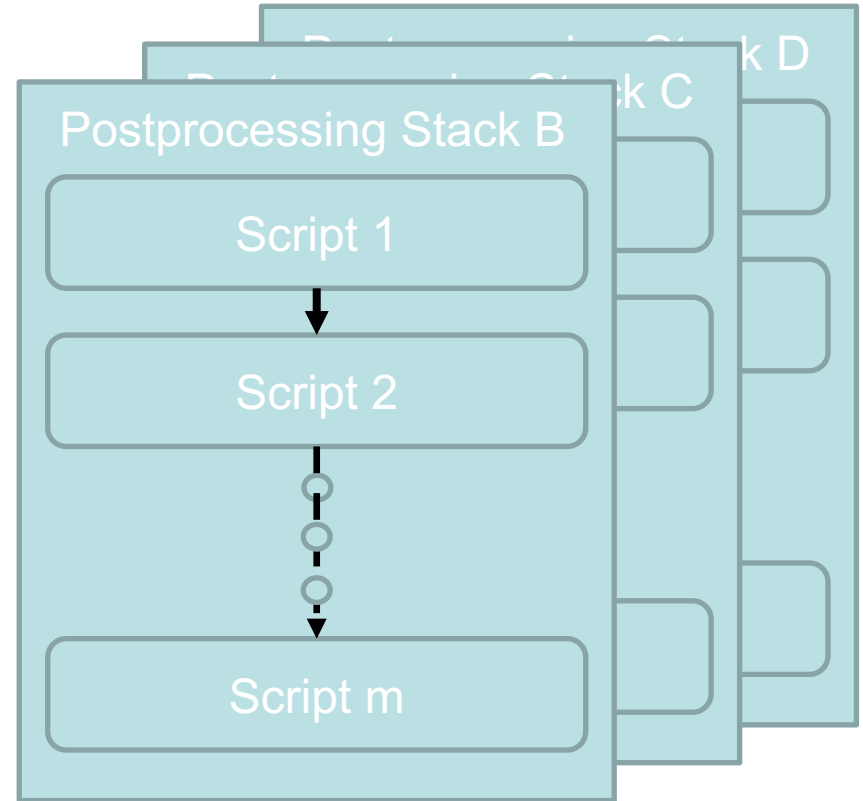
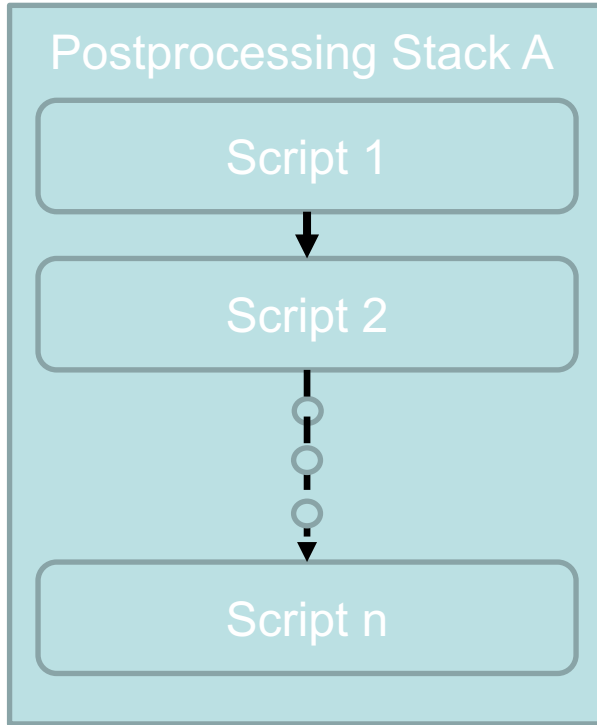
**Postprocessing Stacks**



# Postprocessing

## Stacks

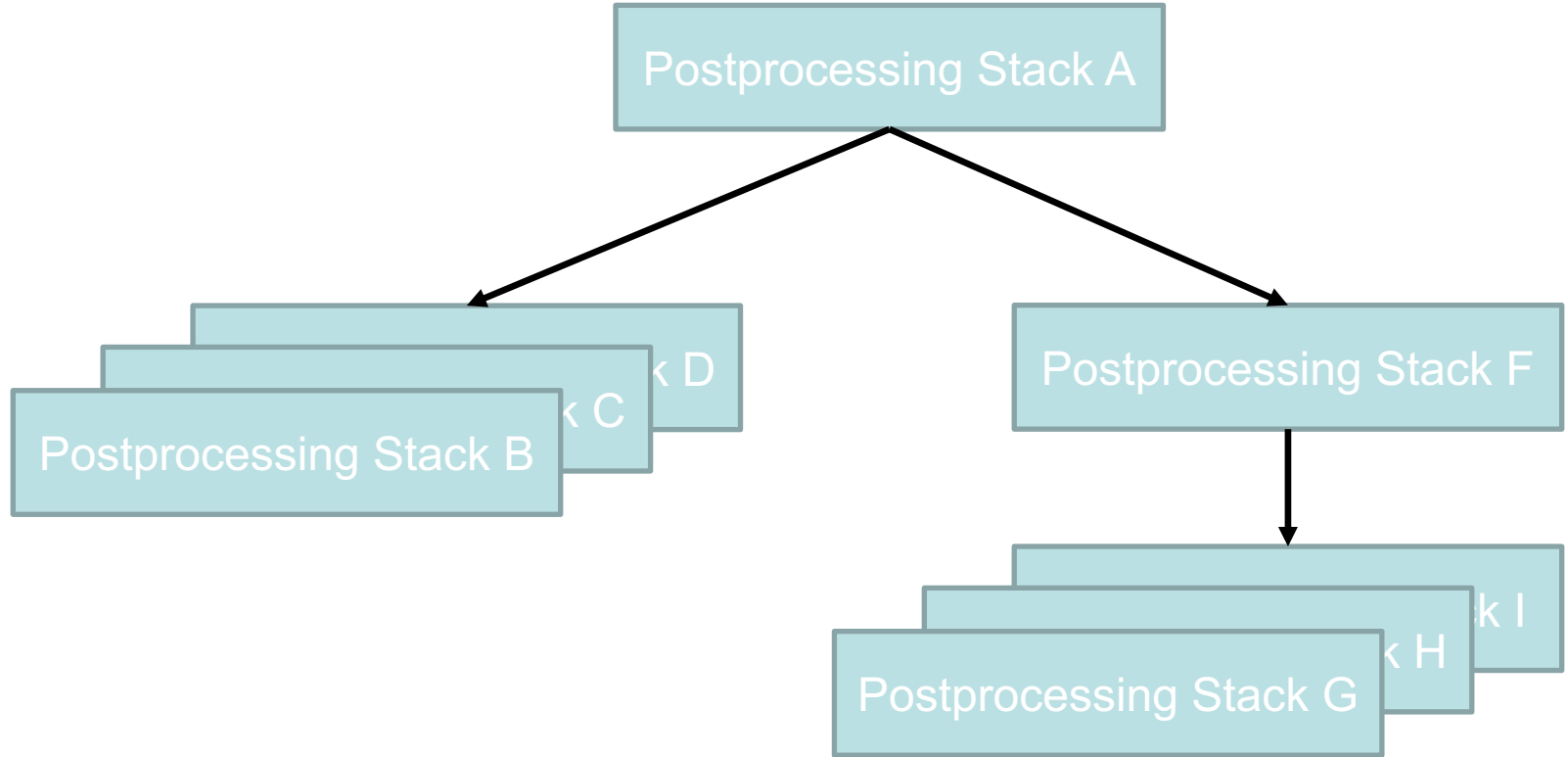
Execution Flow



# Postprocessing Future

Plans

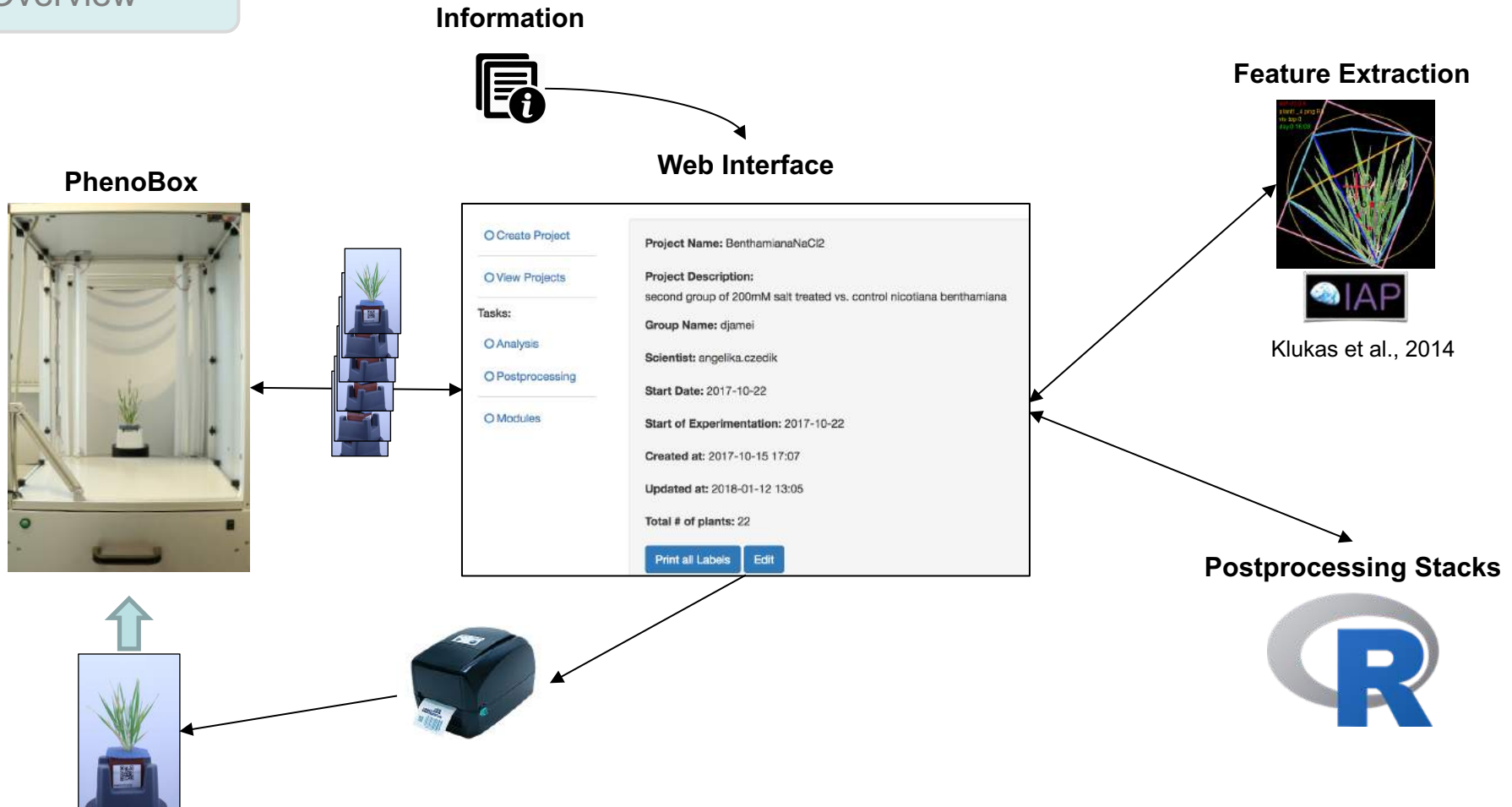
Execution Flow





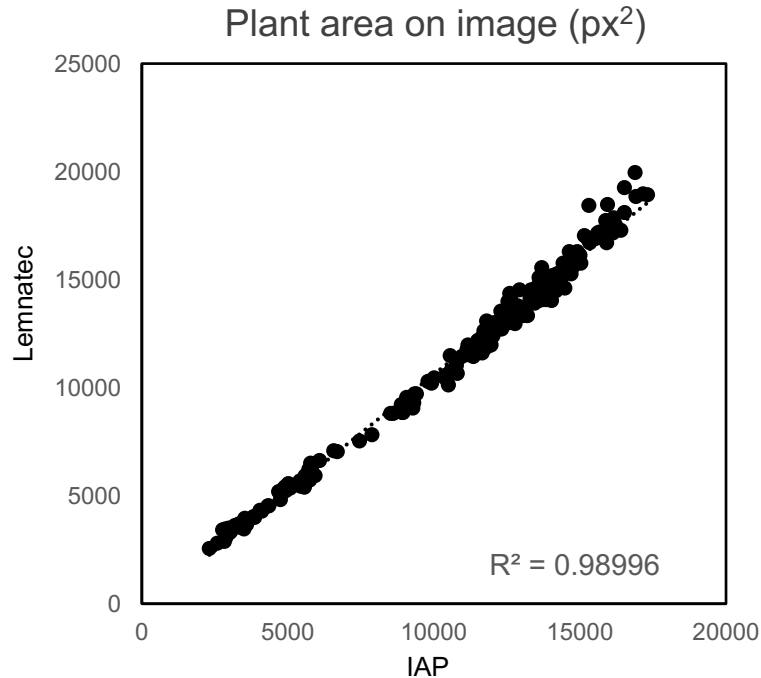
# The PhenoPipe

## Overview

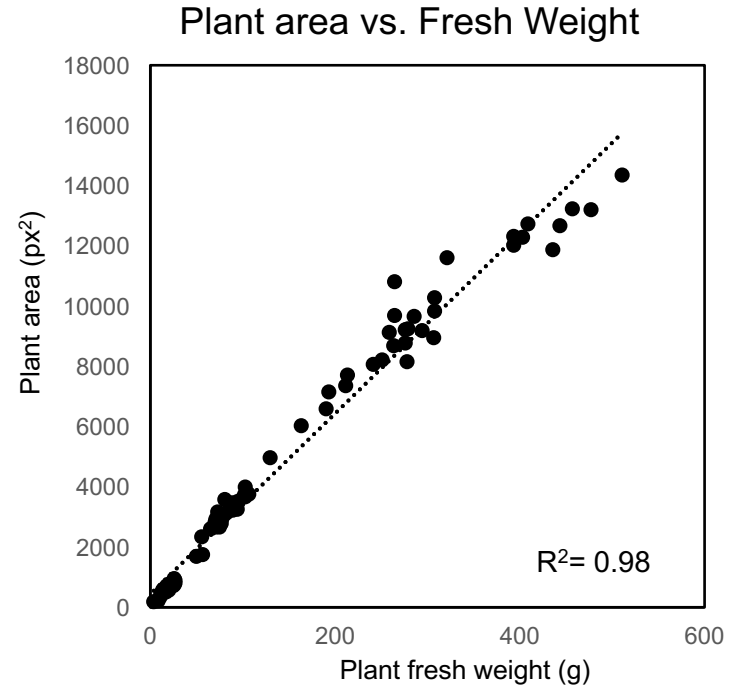


# How reliable is the PhenoBox-PhenoPipe system?

## Benchmarking



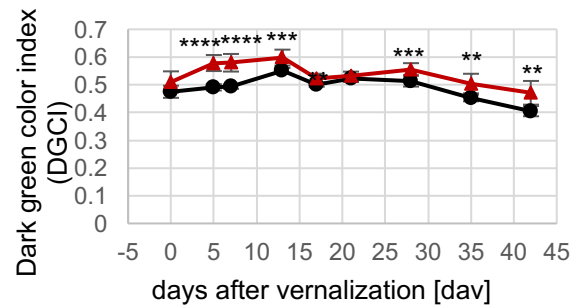
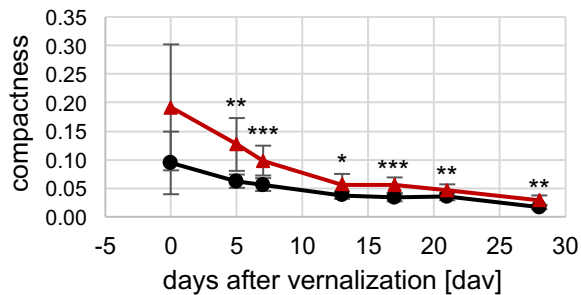
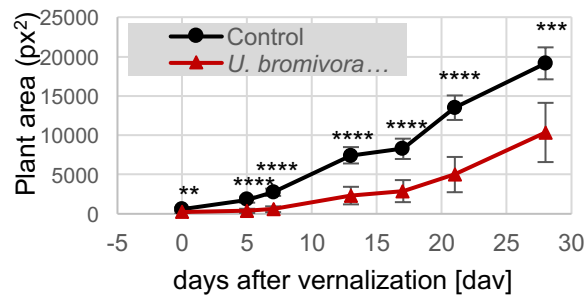
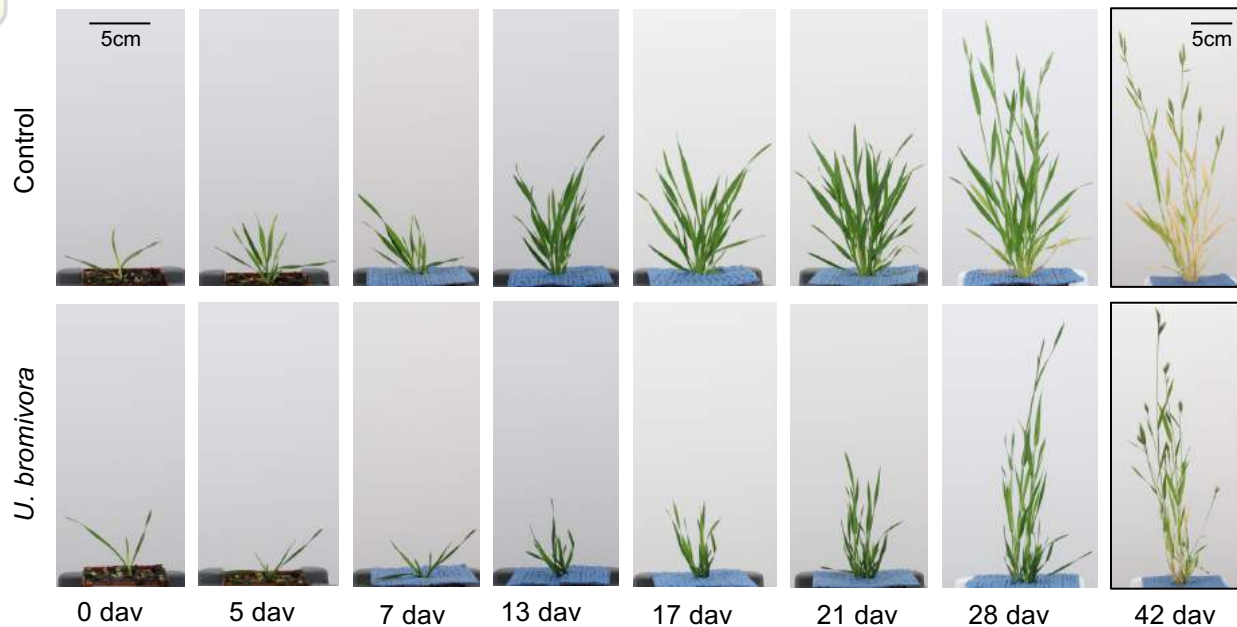
Lemnatec results reproducible by IAP  
IAP covers additional traits



Plant area is an effective proxy for fresh weight over a wide range of plant sizes.

# Phenotypic effects of *U. bromivora* infection

## Phenotyping



# Phenotyping to predict *U. bromivora* infection outcome

## Analysis



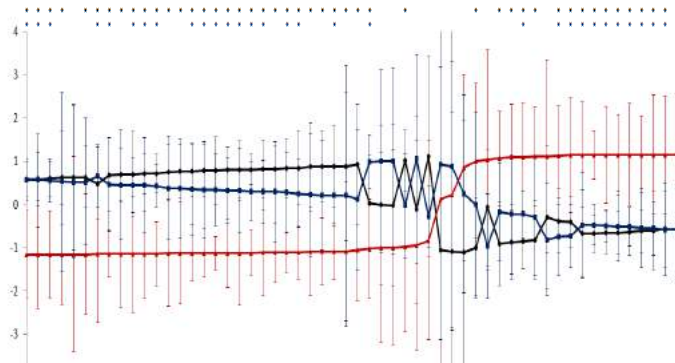
Control



Infected

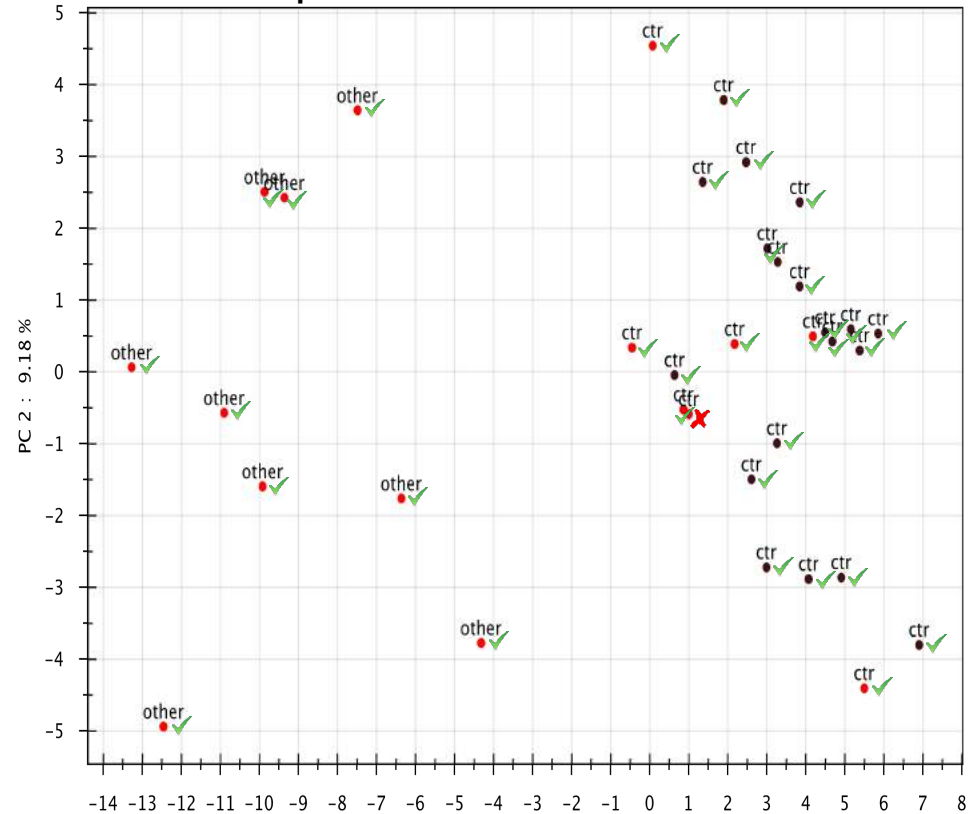


Failed Infection



Average values of image traits **control**, **infected**, **failed**  
(z-score transformed)

## 5 dav - prediction of infection outcome



● Control plants

● Infection treated plants

PC 1 : 56.7% ✓ Infection outcome correctly predicted

✗ Infection outcome wrongly predicted

## Summary

- Define experimental groups
- Labeling
- Imaging
- Data storage and management
- Image feature extraction
- Data analysis and visualization



Affordable



Customizable by User

**All Open Source**

<https://github.com/Gregor-Mendel-Institute/PhenoBox-System>

## Outlook

- Easier Installation
- Faster QR-Code decoding
- Image Previews and Data Visualization in the Web Interface
- More powerful postprocessing options
  - Stack dependencies
  - Parameterization
- Postprocessing Stack and IAP Pipeline sharing options
  - Make them available to certain people or groups
- Option to set PhenoBox/Camera parameters up front
  - Read via QR-Code

# Acknowledgements

Thank you!

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Erich Birngruber,  
MENDEL



A. Czedik-Eysenberg, S. Seitner, U. Guldener, S. Koemeda, J. Jez, M. Colombini and A. Djamei (2018). "The 'PhenoBox', a flexible, automated, open-source plant phenotyping solution." New Phytol., doi: 10.1111/nph.15129.