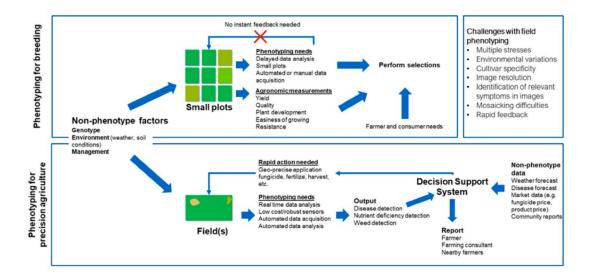


Detecting potato late blight in the field

Erik Alexandersson & Murilo Sandroni, Swedish University of Agricultural Sciences

Plant disease phenotyping for...

- Plant breeding
- Precisions agriculture





High-Throughput Field-Phenotyping Tools for Plant Breeding and Precision Agriculture

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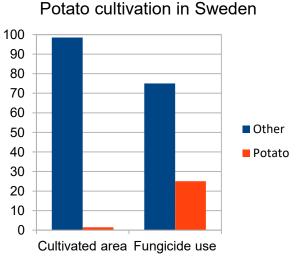
Abstract: High-throughput field phenotyping has garnered major attention in recent years leading to the development of several new protocols for recording various plant traits of interest. Phenotyping of plants for breeding and for precision agriculture have different requirements due to different sizes of the plots and fields, differing purposes and the urgency of the action required after phenotyping.



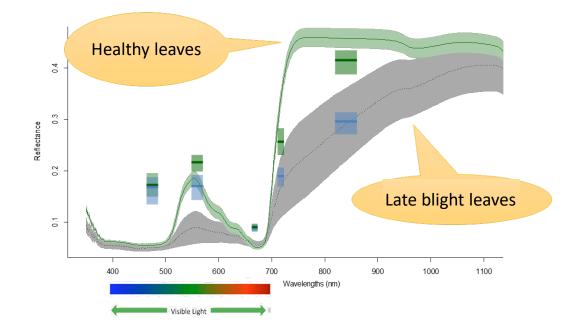
Relevance phenotyping Potato late blight

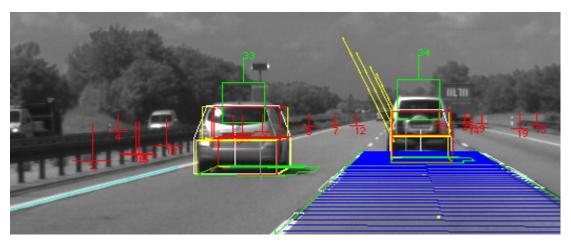
- Potato: high value crop and 3rd most important food crop
- P. infestans causing potato late blight costs 7 billion USD per year
- High fungicide use in Sweden pro-active spraying
- Early and accurate detection
- Resistant breeding material needed





Spectral analysis vs computer vision

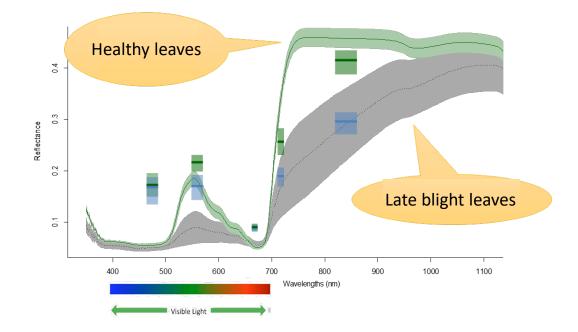




GitHub: Computer Vision



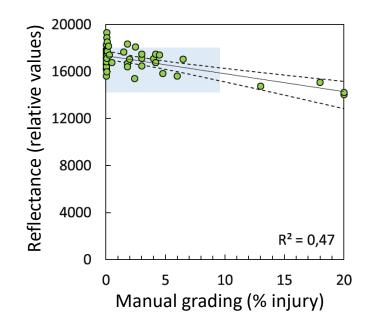
Spectral analysis vs computer vision

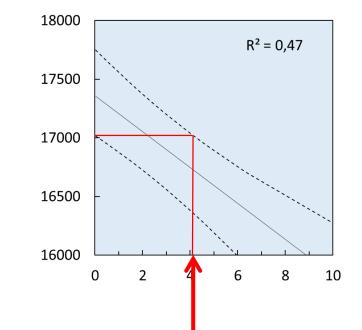




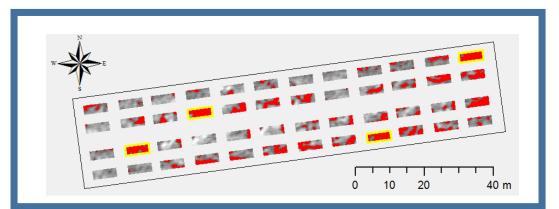


Late blight detection by spectral analysis





An infection of 5 % is associated with a significant decrease in mean reflectance in red-edge band





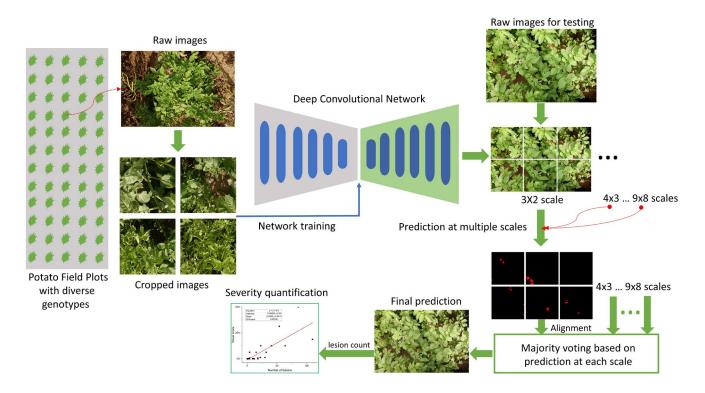




2014-08-06



"Automatic late blight lesion recognition and severity quantification based on field imagery of diverse potato genotypes by deep learning"



Junfeng Gao, Jesper Cairo Westergaard, Ea Høegh Riis Sundmark, Merethe Bagge, Erland Liljeroth, Erik Alexandersson

Under review

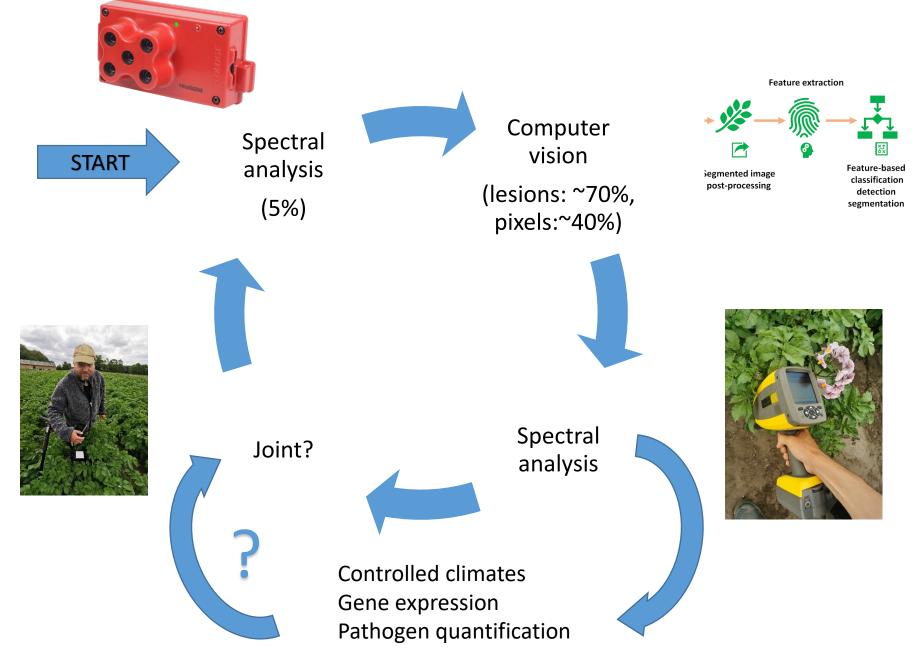
Book chapter "Computer vision and less complex image analyses to monitor potato traits in fields"

Junfeng Gao, Jesper Cairo Westergaard and Erik Alexandersson Under review

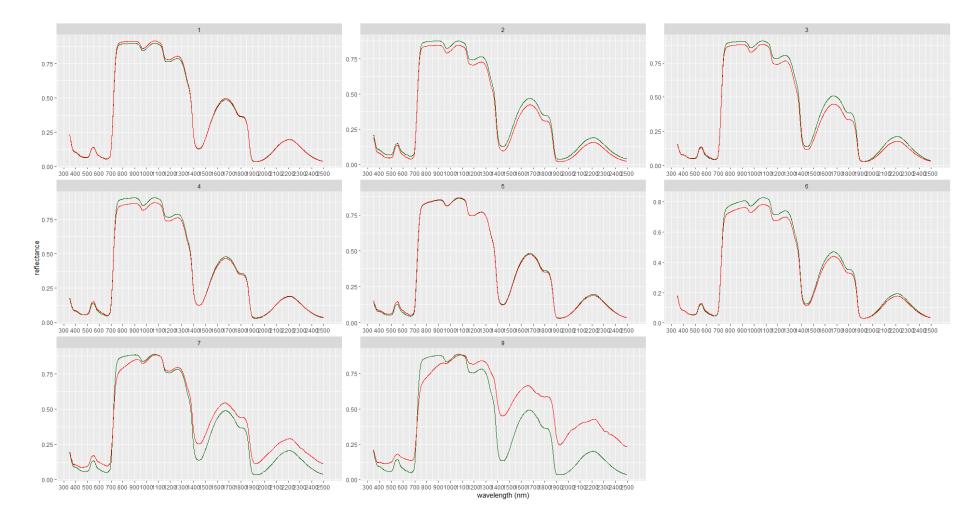




Detecting late blight in the field

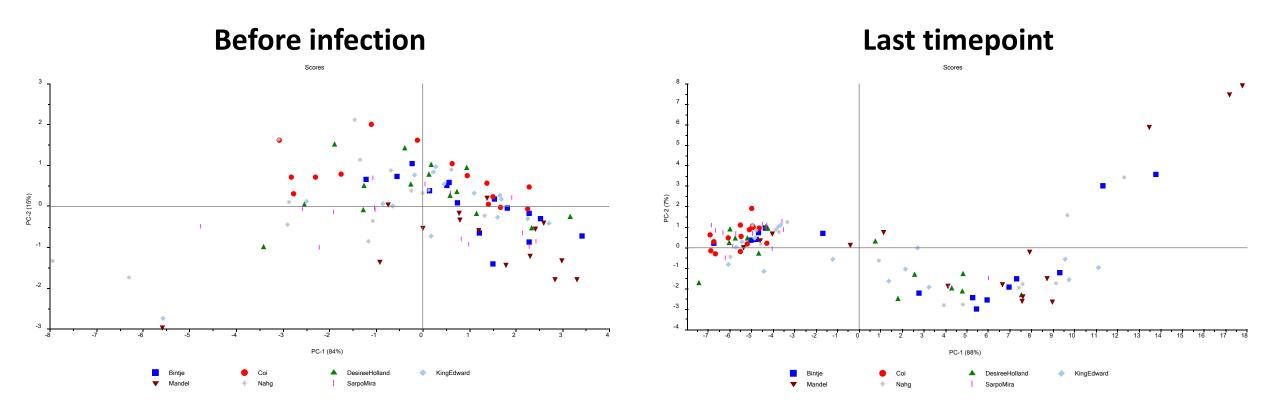


Controlled environment (Biotron), 2019

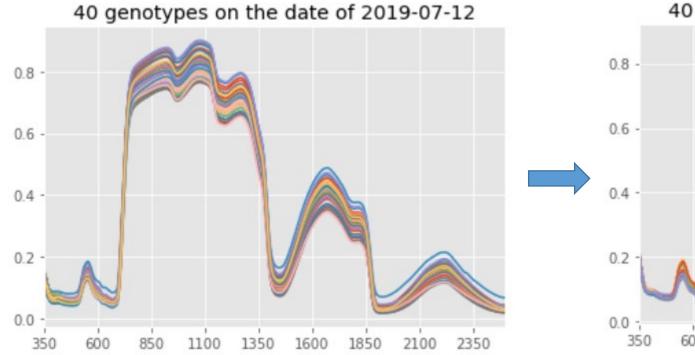


Average reflectance from control (in green) and infected (in red) potato plants (cv. Bintje) on different dates.

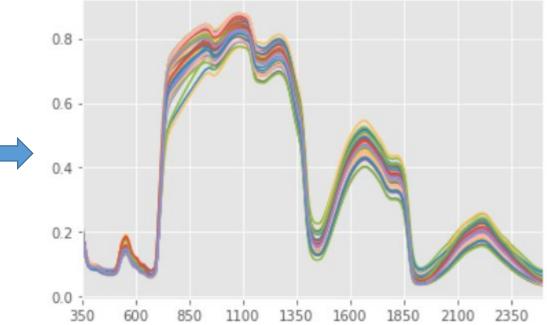
Controlled environment (Biotron), 2019



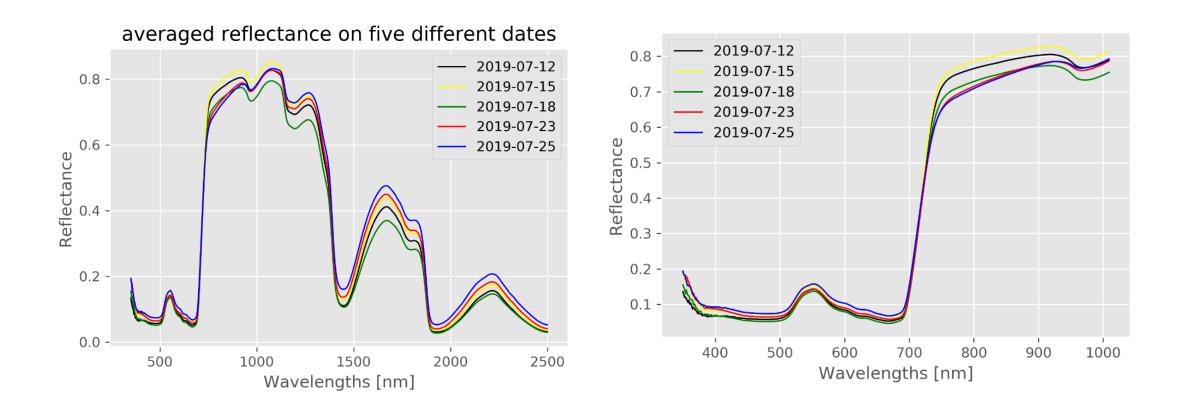
Field, 2019



40 genotypes on the date of 2019-07-25

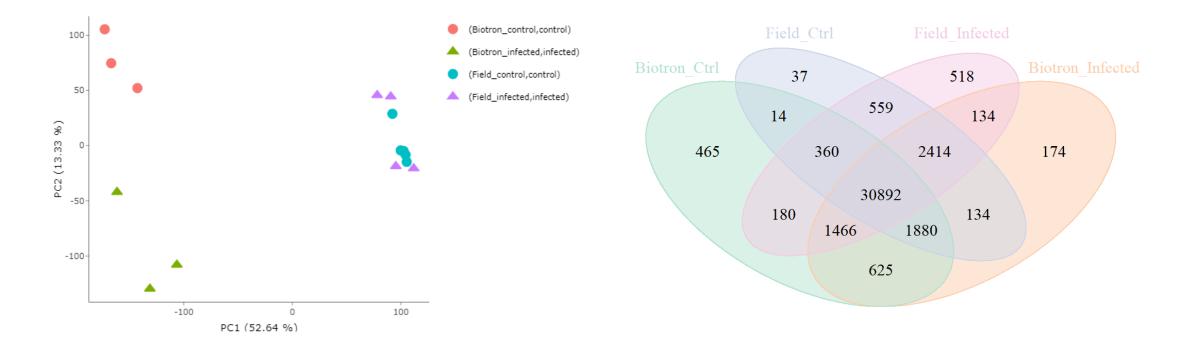


Field, 2019



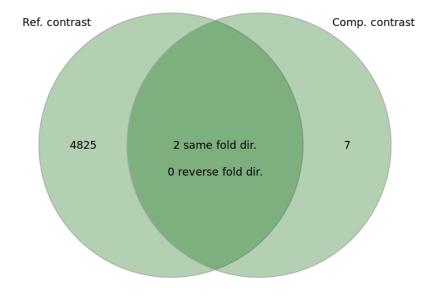
RNAseq from both Biotron and field

Global expression

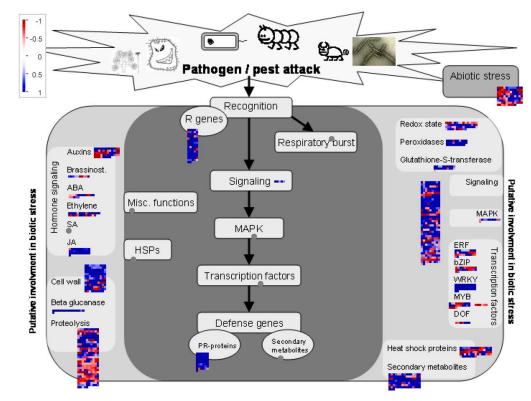


RNAseq from both Biotron and field

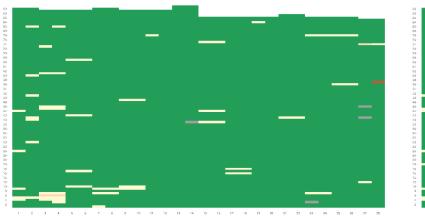
B.Inf-B.Ctrl x F.Inf-F.Ctrl

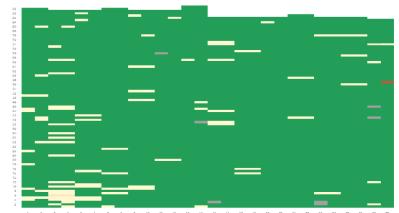


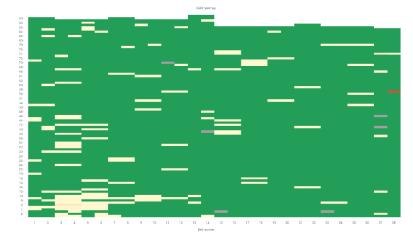
Metabolic pathways involved



2020



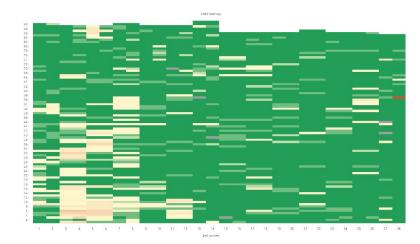




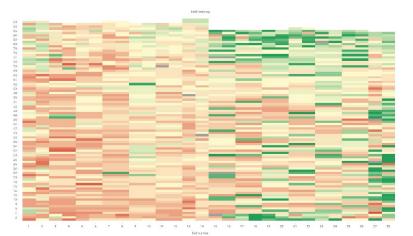
13-Jul-2020

15-Jul-2020

17-Jul-2020







20-Jul-2020

25-Jul-2020

31-Jul-2020

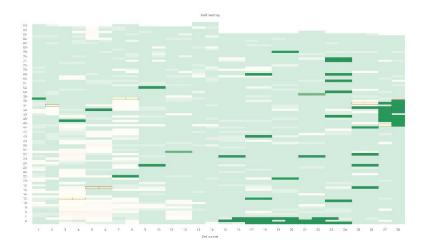
2020



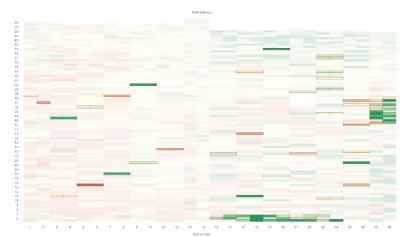
13-Jul-2020

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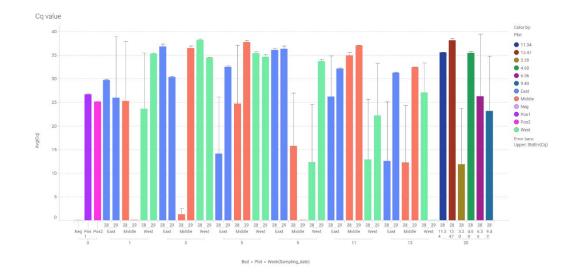
20-Jul-2020

25-Jul-2020

31-Jul-2020

2020

DNA quantification



Next steps:

- Spectral data 2019+2020
- Correction/normalization
- PLSR



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Murilo Sandroni, SLU Jesper Cairo, UCPH Junfeng Gao, SLU Mathieu Gremillet, SupAgro Hanne Grethe Kirk, Danespo Mia Mogren, SLU Svante Resjö, SLU Joost van Ham, LU Kristin Piikki, SLU Mats Söderström, SLU Erland Liljeroth, SLU Ea Riis, Danespo Merethe Bagge, Danespo

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