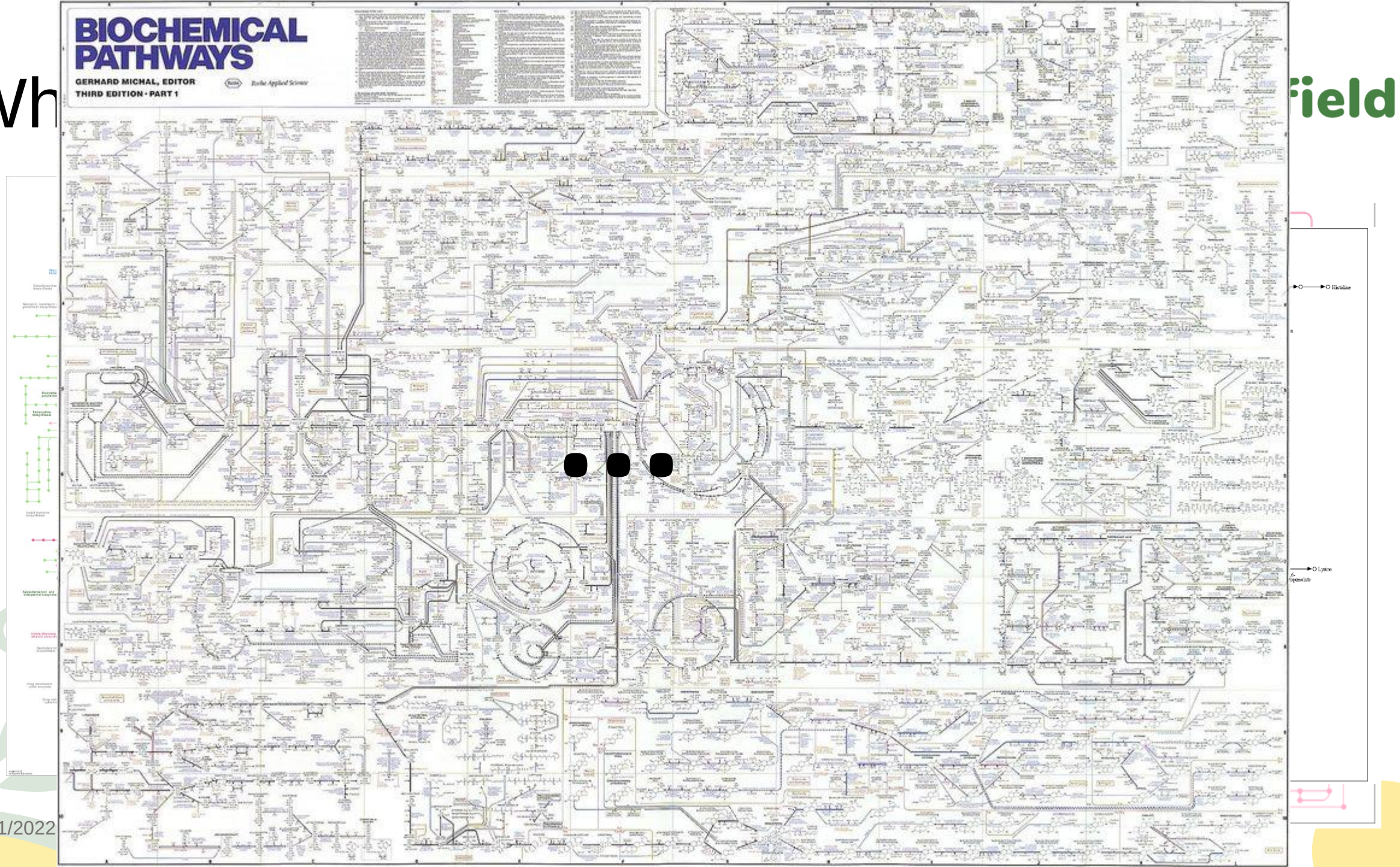
Digitizing the In-Field Agro-Ecological Reality - Goals, Achievements, Pitfalls

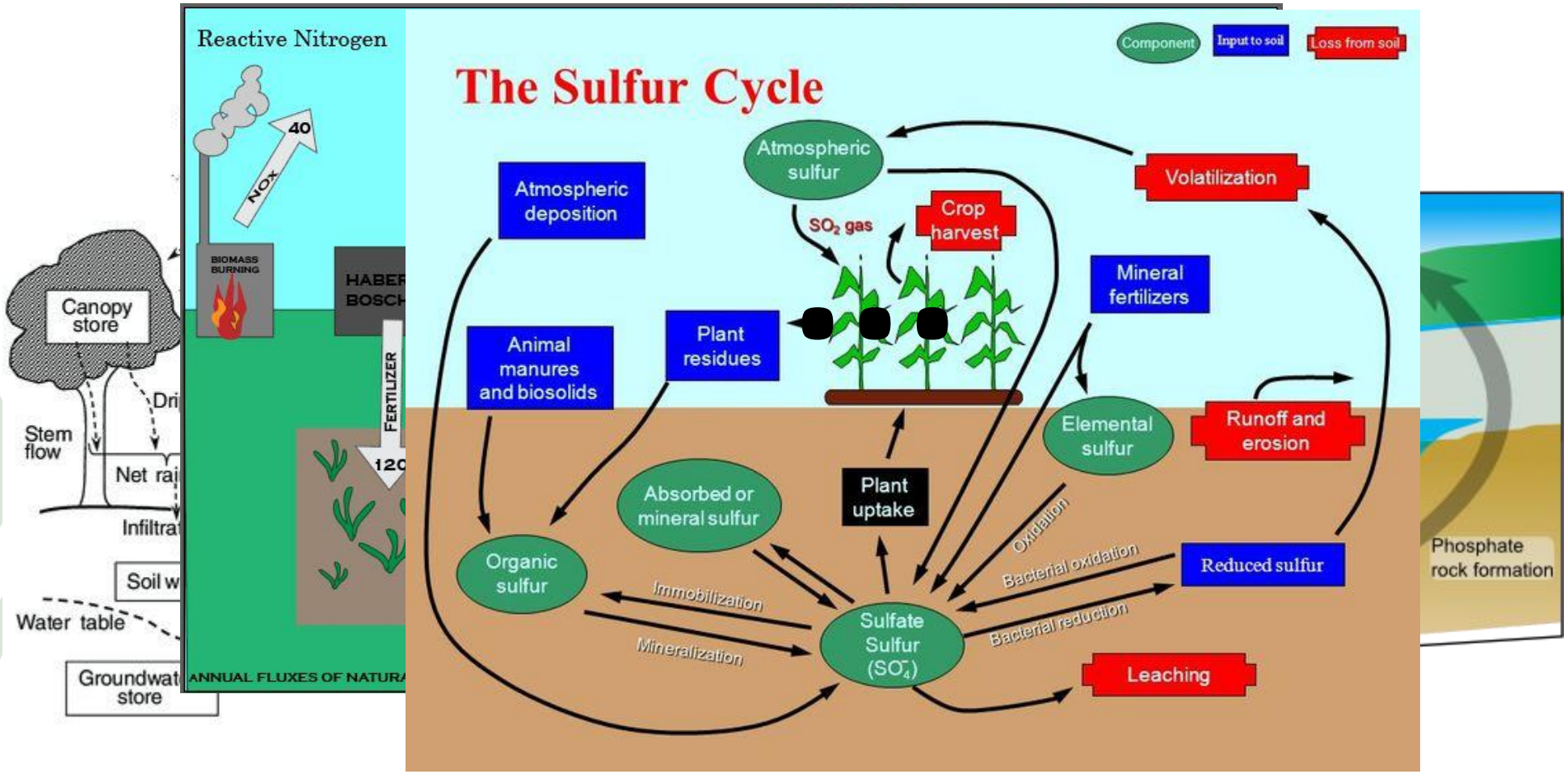
Vlatko Galić

The project "IoT-field: An Ecosystem of Networked Devices and Services for IoT Solutions Applied in Agriculture" is co-financed by the European Union from the European Regional Development Fund within the Operational programme Competitiveness and Cohesion 2014-2020 of the Republic of Croatia

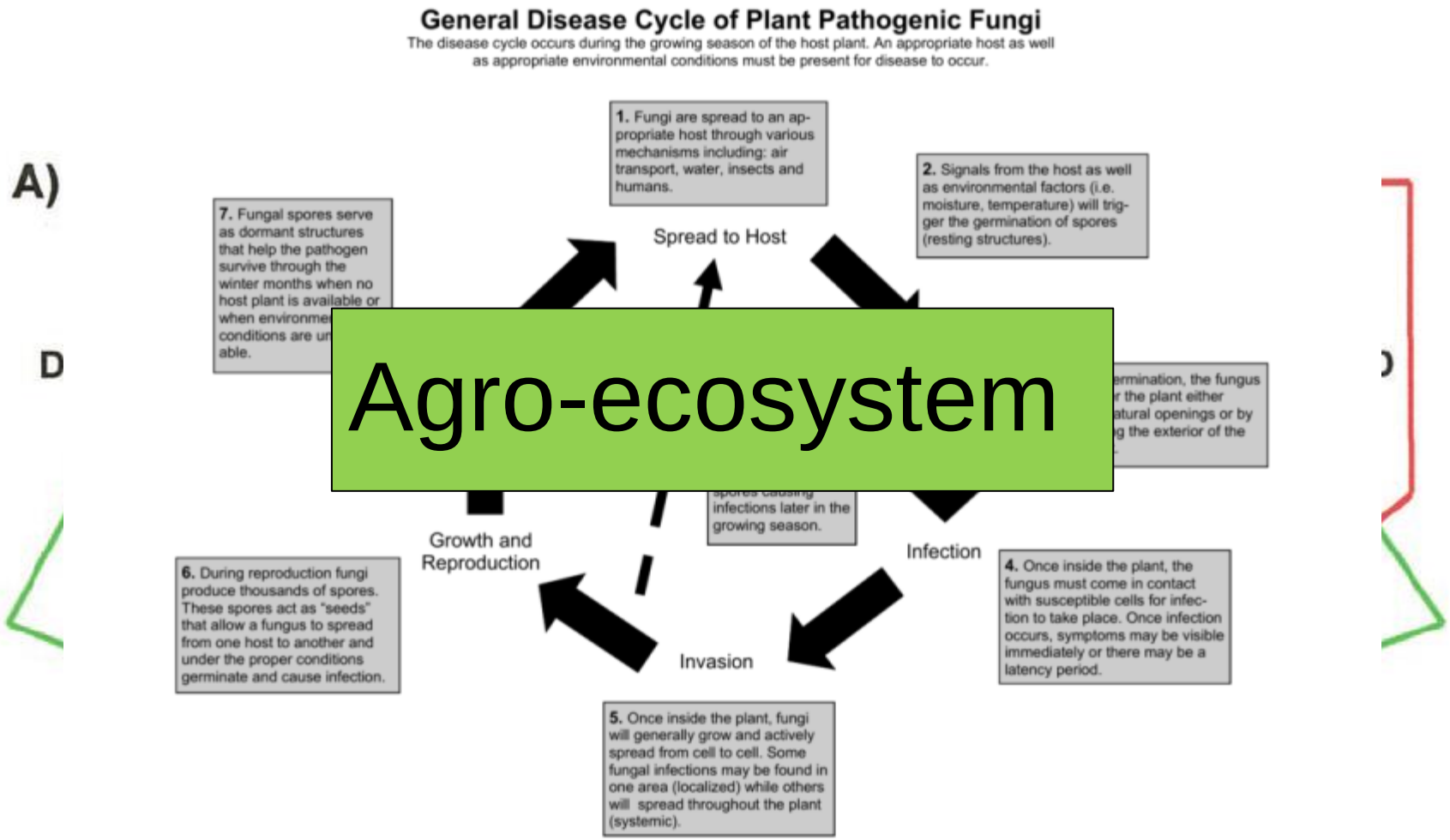
Wh ield


BIOCHEMICAL PATHWAYS
GERHARD MICHAL, EDITOR
THIRD EDITION · PART 1
Wiley Applied Science
Histidine
Lysine

Biological reality – integrated into higher level cycles (hydrological, chemical. etc.)



Cycles of climate, pests and disease



Single yeast cell wiring diagram

RESEARCH ARTICLE SUMMARY

YEAST GENETICS

A global genetic interaction network maps a wiring diagram of cellular function

Michael Costanzo,* Benjamin VanderSluis,* Elizabeth N. Koch,* Anastasia Baryshnikova,* Carles Pons,* Guihong Tan,* Wen Wang, Matej Usaj, Julia Hanchard, Susan D. Lee, Vicent Pelechano, Erin B. Styles, Maximilian Billmann, Jolanda van Leeuwen, Nydia van Dyk, Zhen-Yuan Lin, Elena Kuzmin, Justin Nelson, Jeff S. Piotrowski, Tharan Srikumar, Sondra Bahr, Yiqun Chen, Raamesh Deshpande, Christoph F. Kurat, Sheena C. Li, Zhijian Li, Mojca Mattiazzi Usaj, Hiroki Okada, Natasha Pascoe, Bryan-Joseph San Luis, Sara Sharifpoor, Emira Shuteriqi, Scott W. Simpkins, Jamie Snider, Harsha Garadi Suresh, Yizhao Tan, Hongwei Zhu, Noel Malod-Dognin, Vuk Janjic, Natasa Przulj, Olga G. Troyanskaya, Igor Stagljar, Tian Xia, Yoshikazu Ohya, Anne-Claude Gingras, Brian Raught, Michael Boutros, Lars M. Steinmetz, Claire L. Moore, Adam P. Rosebrock, Amy A. Caudy, Chad L. Myers,† Brenda Andrews,† Charles Boone†

INTRODUCTION: Genetic interactions occur when mutations in two or more genes combine to generate an unexpected phenotype. An extreme negative or synthetic lethal genetic interaction occurs when two mutations, neither lethal individually, combine to cause cell death. Conversely, positive genetic interactions occur when two mutations produce a phenotype that is less severe than expected. Genetic interactions identify functional relationships between genes and can be harnessed for biological discovery and therapeutic target identification. They may also explain a considerable component of the undiscovered genetics associated with human diseases. Here, we describe construction and analysis of a comprehensive genetic interaction network for a eukaryotic cell.

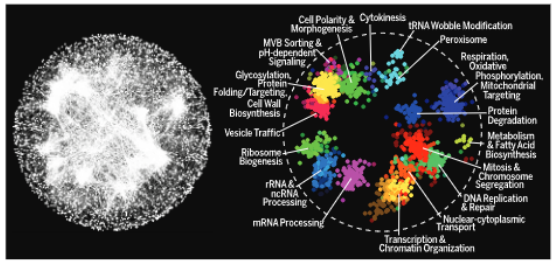
RATIONALE: Genome sequencing projects are providing an unprecedented view of genetic variation. However, our ability to interpret genetic information to predict inherited phenotypes remains limited, in large part due to the extensive buffering of genomes, making most individual eukaryotic genes dispensable for life. To explore the extent to which genetic interactions reveal cellular function and contribute to complex phenotypes, and to discover the general principles of genetic networks, we used automated yeast genetics to construct a global genetic interaction network.

RESULTS: We tested most of the ~6000 genes in the yeast *Saccharomyces cerevisiae* for all possible pairwise genetic interactions, identifying nearly 1 million interactions, including ~550,000 negative and ~350,000 positive interactions, spanning ~90% of all yeast genes. Essential genes were network hubs, displaying five times as many interactions as nonessential genes. The set of genetic interactions or the genetic interaction profile for a gene provides a quantitative measure of function, and a global network based on genetic interaction profile similarity revealed a hierarchy of modules reflecting the functional architecture of a cell. Negative interactions connected functionally related genes, mapped core bioprocesses, and identified pleiotropic genes, whereas positive interactions often mapped general regulatory connections associated with defects in cell cycle progression or cellular proteostasis. Importantly, the global network illustrates how coherent sets of negative or positive genetic interactions connect protein complex and pathways to map a functional wiring diagram of the cell.

ON OUR WEBSITE

Read the full article at http://dx.doi.org/10.1126/science.aaf1420

CONCLUSION: A global genetic interaction network highlights the functional organization of a cell and provides a resource for predicting gene and pathway function. This network emphasizes the prevalence of genetic interactions and their potential to compound phenotypes associated with single mutations. Negative genetic interactions tend to connect functionally related genes and thus may be predicted using alternative functional information. Although less functionally informative, positive interactions may provide insights into general mechanisms of genetic suppression or resiliency. We anticipate that the ordered topology of the global genetic network, in which genetic interactions connect coherently within and between protein complexes and pathways, may be exploited to decipher genotype-to-phenotype relationships. ■



A global network of genetic interaction profile similarities. (Left) Genes with similar genetic interaction profiles are connected in a global network, such that genes exhibiting more similar profiles are located closer to each other, whereas genes with less similar profiles are positioned farther apart. **(Right)** Spatial analysis of functional enrichment was used to identify and color network regions enriched for similar Gene Ontology bioprocess terms.

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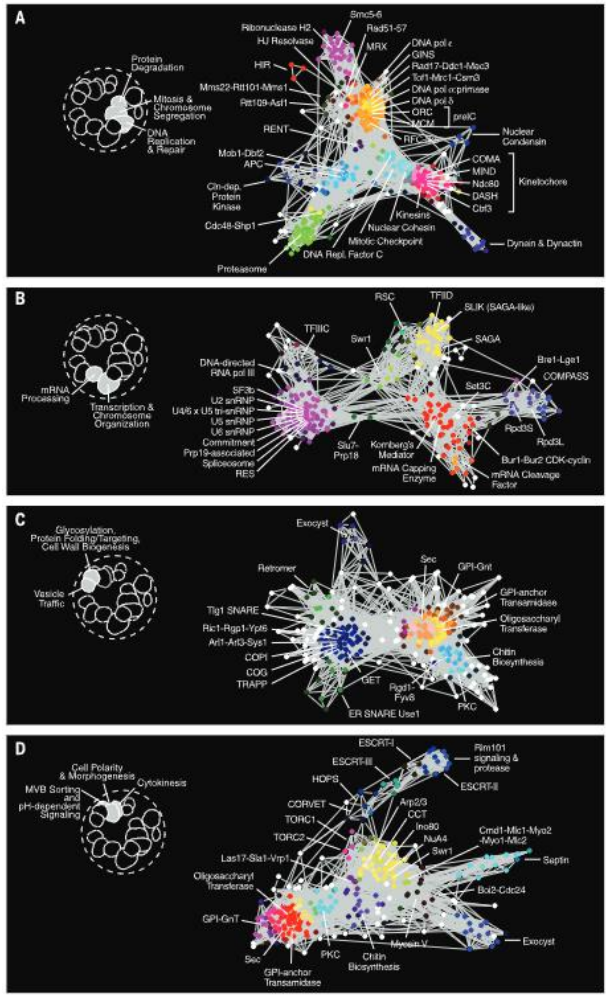

Biological reality

in silico Plants
OXFORD UNIVERSITY PRESS

Opinion

Biological reality and parsimony in crop models—why we need both in crop improvement!

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Abstract. The potential to add significant value to the rapid advances in plant breeding technologies associated with statistical whole-genome prediction methods is a new frontier for crop physiology and modelling. Yield advance by genetic improvement continues to require prediction of phenotype based on genotype, and this remains challenging for complex traits despite recent advances in genotyping and phenotyping. Crop models that capture physiological knowledge and can robustly predict phenotypic consequences of genotype-by-environment-by-management (G×E×M) interactions have demonstrated potential as an integrating tool. But does this biological reality come with a degree of complexity that restricts applicability in crop improvement? Simple, high-speed, parsimonious models are required for dealing with the thousands of genotypes and environment combinations in modern breeding programs utilizing genomic prediction technologies. In contrast, it is often considered that greater model complexity is needed to evaluate potential of putative variation in specific traits in target environments as knowledge on their underpinning biology advances. Is this a contradiction leading to divergent futures? Here it is argued that biological reality and parsimony do not need to be independent and perhaps should not be. Models structured to readily allow variation in the biological level of process algorithms, while using coding and computational advances to facilitate high-speed simulation, could well provide the structure needed for the next generation of crop models needed to support and enhance advances in crop improvement technologies. Beyond that, the trans-scale and transdisciplinary dialogue among scientists that will be required to construct such models effectively is considered to be at least as important as the models.

Keywords: Crop improvement; crop model; genomic prediction; phenotypic prediction; plant breeding.

Introduction

Based on current rates of yield improvement for major crops, comprehensive analyses have shown that by 2050, there will be a significant shortfall in global food production capacity (Mueller *et al.* 2012; Ray *et al.* 2013; Fischer *et al.* 2014). It is imperative that we hasten yield advance. The world population can no longer take for granted an ability to feed itself in 2050 and beyond. This will necessarily involve the sustainable intensification of production systems requiring combinations of agronomic and breeding interventions.

Dynamic crop growth and development models (CGMs) have the capacity to explore consequences of potential agronomic and breeding interventions in

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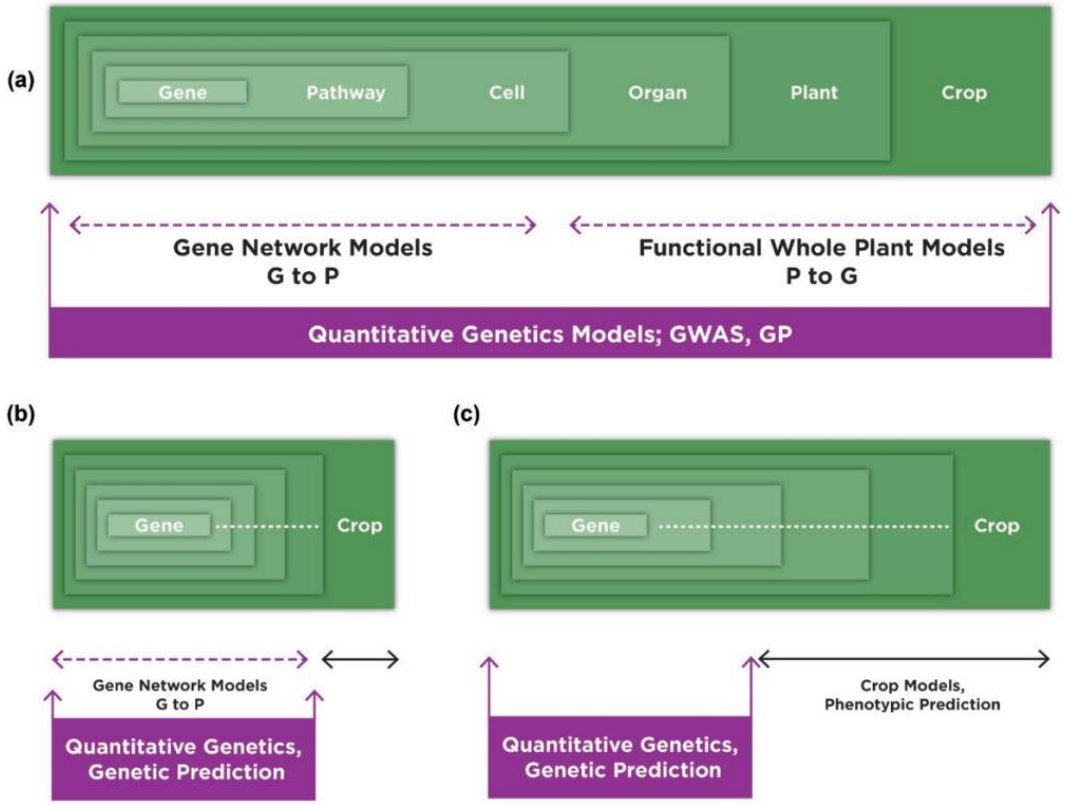

Biological reality

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REVIEW

"Essentially, all models are wrong, but some are useful"—a cross-disciplinary agenda for building useful models in cell biology and biophysics

Julien Berro [1,2,3]

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Abstract
Intuition alone often fails to decipher the mechanisms underlying the experimental data in Cell Biology and Biophysics, and mathematical modeling has become a critical tool in these fields. However, mathematical modeling is not as widespread as it could be, because experimentalists and modelers often have difficulties communicating with each other, and are not always on the same page about what a model can or should achieve. Here, we present a framework to develop models that increase the understanding of the mechanisms underlying one's favorite biological system. Development of the most insightful models starts with identifying a good biological question in light of what is known and unknown in the field, and determining the proper level of details that are sufficient to address this question. The model should aim not only to explain already available data, but also to make predictions that can be experimentally tested. We hope that both experimentalists and modelers who are driven by mechanistic questions will find these guidelines useful to develop models with maximum impact in their field.

Keywords Model · Theory · Cross-disciplinary research

Introduction

A popular joke about modeling goes as follows: A group of farmers desperately trying to increase their cows' milk production calls a theorist to help them find a solution. After a few months of hard work, the theorist calls back: "I found the optimal solution. Consider a spherical cow in a vacuum …"

The trove of quantitative data produced by modern biology has highlighted that the complex behaviors of biological systems, even the simplest ones, are difficult to comprehend with our intuition alone (Mogilner et al. 2006; Pollard 2010; Pollard and De La Cruz 2013; Howard 2014; Marshall 2017). An increasing number of experimentalists appreciate the need for mathematical modeling to explain their data and uncover the underlying molecular mechanisms for their favorite biological systems (Pollard 2013; O'Shaughnessy and Pollard 2016). However, mathematical modeling is not as widespread as it could be. We believe one of the main reasons for the limited use of modeling by experimentalists in the cell biology and biophysics communities is a common misunderstanding of what mathematical modeling can achieve. As the spherical cow joke demonstrates, another common reason is that mathematicians and physicists who model biological processes sometimes make simplistic assumptions, or do not explain or justify the simplifications clearly enough when they are legitimate. Last, good communication between fields is important to develop models, and produce outputs that can be translated by experimentalists into testable predictions.

Joke aside, what would be the best way to model a cow if a sphere is not a good model? Should we include its limbs, head, and tail? Its digestive system? The different cell types involved in digestion? The dynamics of actin filaments in each cell? The atomic interactions between the actin subunits? One could enumerate infinite details but it is clear that not all details are meaningful or relevant for the problem at hand.

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The problem of data sparsity

- Variability in field conditions:
  - **Plant based** factors (genotypes, morphology, adaptness)
  - **Environmental** factors (soil status, high/low temperatures, precipitation, etc...)

- **The data collected by farmers underrepresents true field conditions**

- Usually a **single datapoint** on plant side is collected once the plant is already a **dead tissue -> harvest**

Stress states -> modelling what counts

- Empirical optima of plant states -> often **violated** by **deviations** of environmental conditions
- **Deviations** from **optimum** affecting the plant status -> PLANT **STRESS STATES**

Stress intensity:

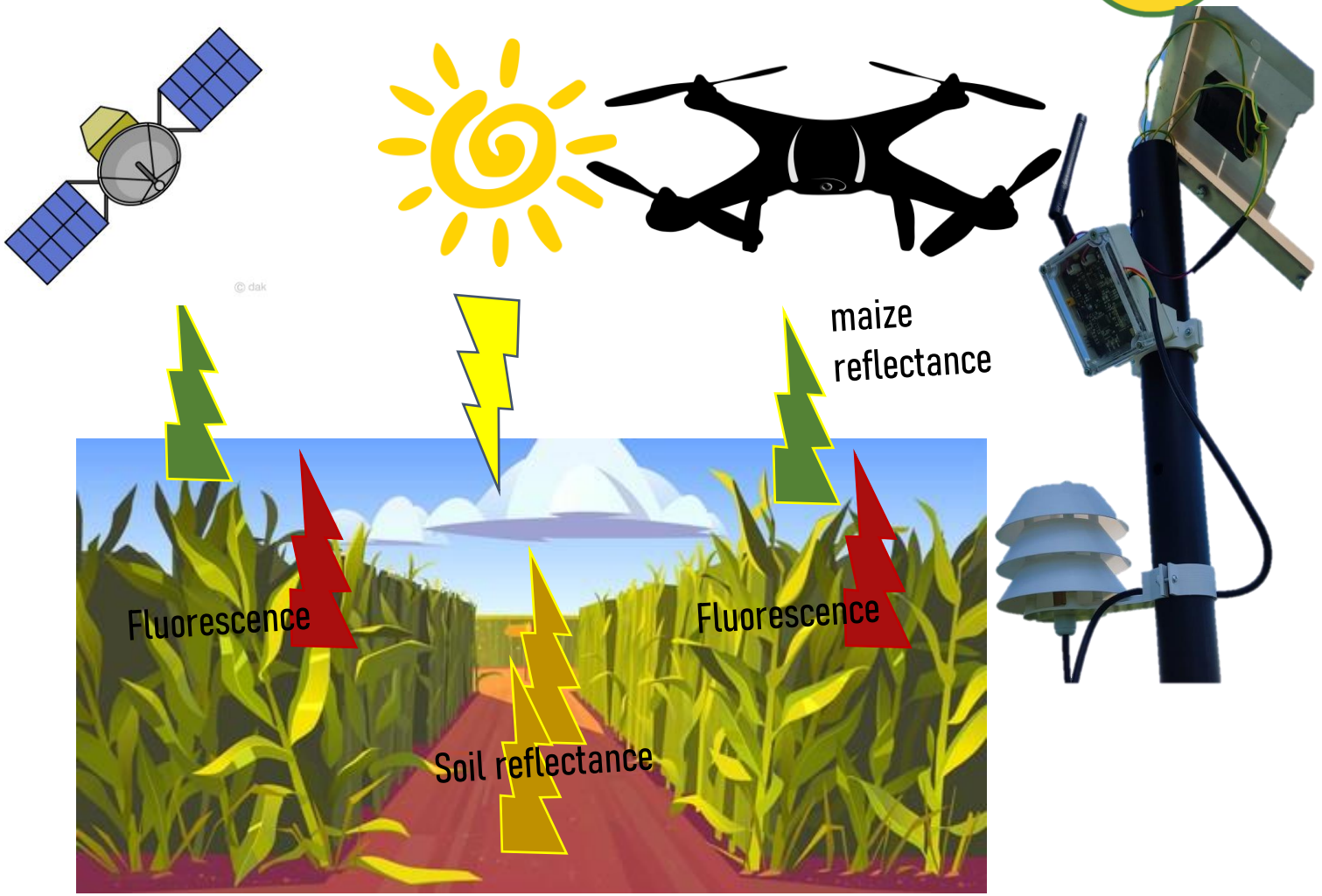
1. **No stress -> no measures need to be applied (no detectable stress)**
2. **Mild stress -> good time for application of measures (if detectable)**
3. **Moderate stress -> last call for measures (easily detectable, moderately detrimental)**
4. **Severe stress -> critical measures and remedies can be applied (detrimental effects, sometimes lethal)**
5. **Plant death**

Major goal – lead transition to **data-driven decisions in agriculture**

- Identification of **critical moments** in **crop vegetation** to mitigate effects of climate change
- **Timely** application of **agrotechnical measures** for stable development of plants
- **Prediction** of **crop yield** to plan storage and drying capacity and costs

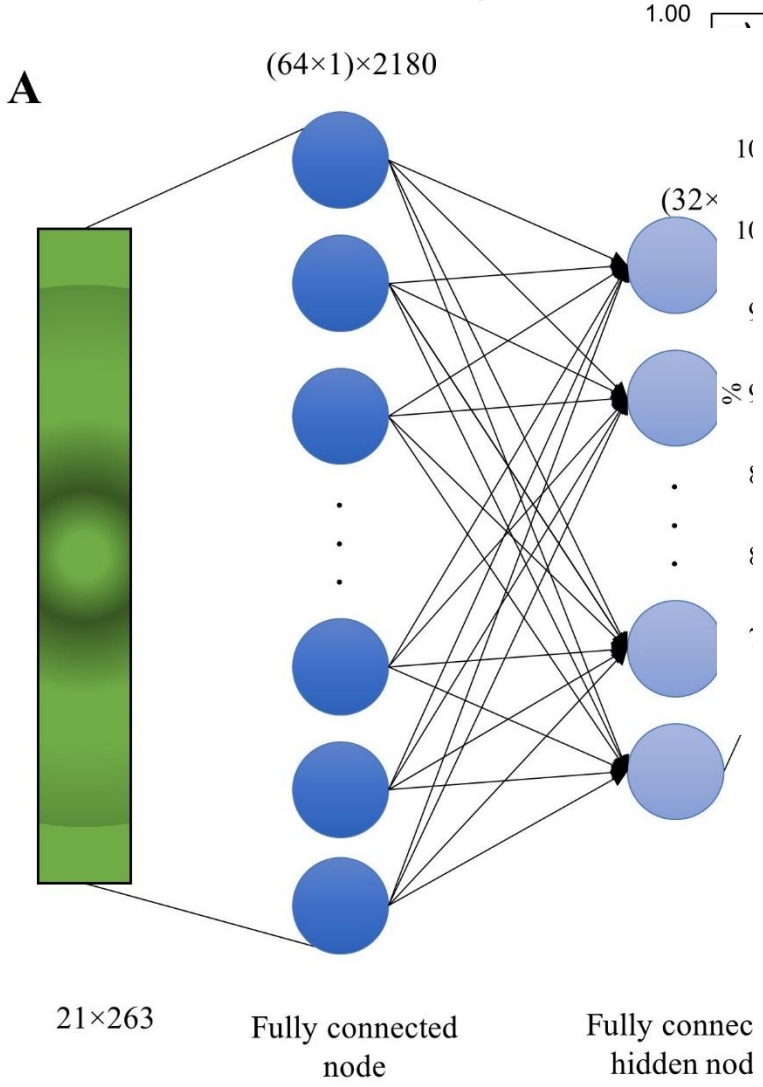
Strategy of choice: Remote and proximal monitoring of crop fluorescence / reflectance and micro-climate

IoT-field


maize
reflectance
Fluorescence
Fluorescence
Soil reflectance

In support to objectives: domain knowledge and neat engineering

IoT-field



IoT Based Network Model And Sensor Node Prototype For Precision Agriculture Application

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Abstract *— The recent advancement of the Internet of Things (IoT) enabled the development of precision agriculture by using high technology sensors and analysis tools for improving crop yields and assisting management decisions. Due to its highly interoperable, scalable, widespread, and open nature, the IoT approach is an ideal match for precision agriculture. We built our model in response to the above benefits and potentials of IoT in precision agriculture. In this paper we propose a low cost IoT based network model using the developed IoT sensor node for precision agriculture applications consisting of a near-infrared sensor and general purpose microcontroller for gathering data from agricultural fields. Our model architecture is extremely flexible, and it provides a machine learning data analytics solution that enables small size data processing at the edge of the network (sensor nodes) and large-scale data processing on real-time observation streams of data from a number nodes in the cloud. We employ LoRaWAN™, a wide area networking protocol as a transmission protocol in our solution, which has a low power consumption, long-range capability, it's affordable and requires little maintenance, making it perfect for large fields and variable number of sensor nodes. According to the first results of device testing presented in this report, our device might provide affordable means of field-based spatio-temporal sensing.*

Keywords *— IoT, LPWAN, near-infrared spectroscopy, precision agriculture, sensor*

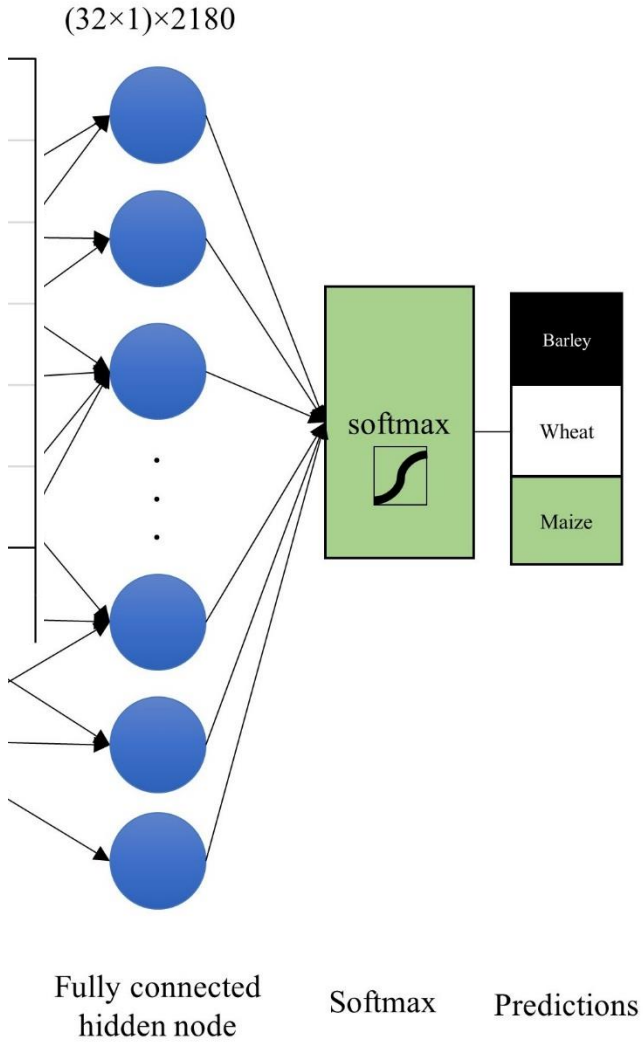
I. Introduction

In the last few years, due to the advancement in technology and applications, various Internet of Things (IoT) applications have become globally available for various purposes such as for Smart Cities and Homes, eHealth, Environmental monitoring, Smart Agriculture, Transportation, Energy management, Manufacturing, etc. Several Non-3GPP and 3GPP technologies, including LoraWAN™, NB-IoT, Sigfox and LTE-M, were created particularly to meet the needs for achieving satisfying data rates with reduced bandwidth [1]. Since these networks are limited, supporting a standard, interoperable network stack,

In the last decades, population growth has dramatically increased the pressure on agriculture [4] and it will continue to grow since it is estimated that by 2050 the global population growth will by 31% [5], which will result in 72% increase for natural resources and food [6]. This decade has seen a shift from traditional methods to the most advanced with the advent of technology. The IoT is changing the quality and quantity of agriculture departments. Species hybridization and real-time monitoring of farms pave the way for resource optimization. Scientists, research institutes, academics, and most of the world are relocating their research and practice and developing community projects to explore the horizons of this field of service. The technology industry is working hard to provide more optimized solutions. Combining IoT with the cloud computing, big data analytics, and wireless sensor networks can provide enough scope to predict, process, and analyze the situation and improve the activity in the real-time agriculture scene [7], [8], [9].

Agriculture and development of hardware and software systems make public and private industry projects, and startups worldwide begin delivering precise, innovative, and sustainable solutions. The Internet of Things (IoT) paradigm introduces features to these applications that span from sporadic transmissions of small packets to high-data-rate streams, including low-latency and critical traffic. Some of them, such as, smart agriculture, telemetering, environment monitoring and intelligent tracking, also require extended coverage and long battery life [10], [11], [12].

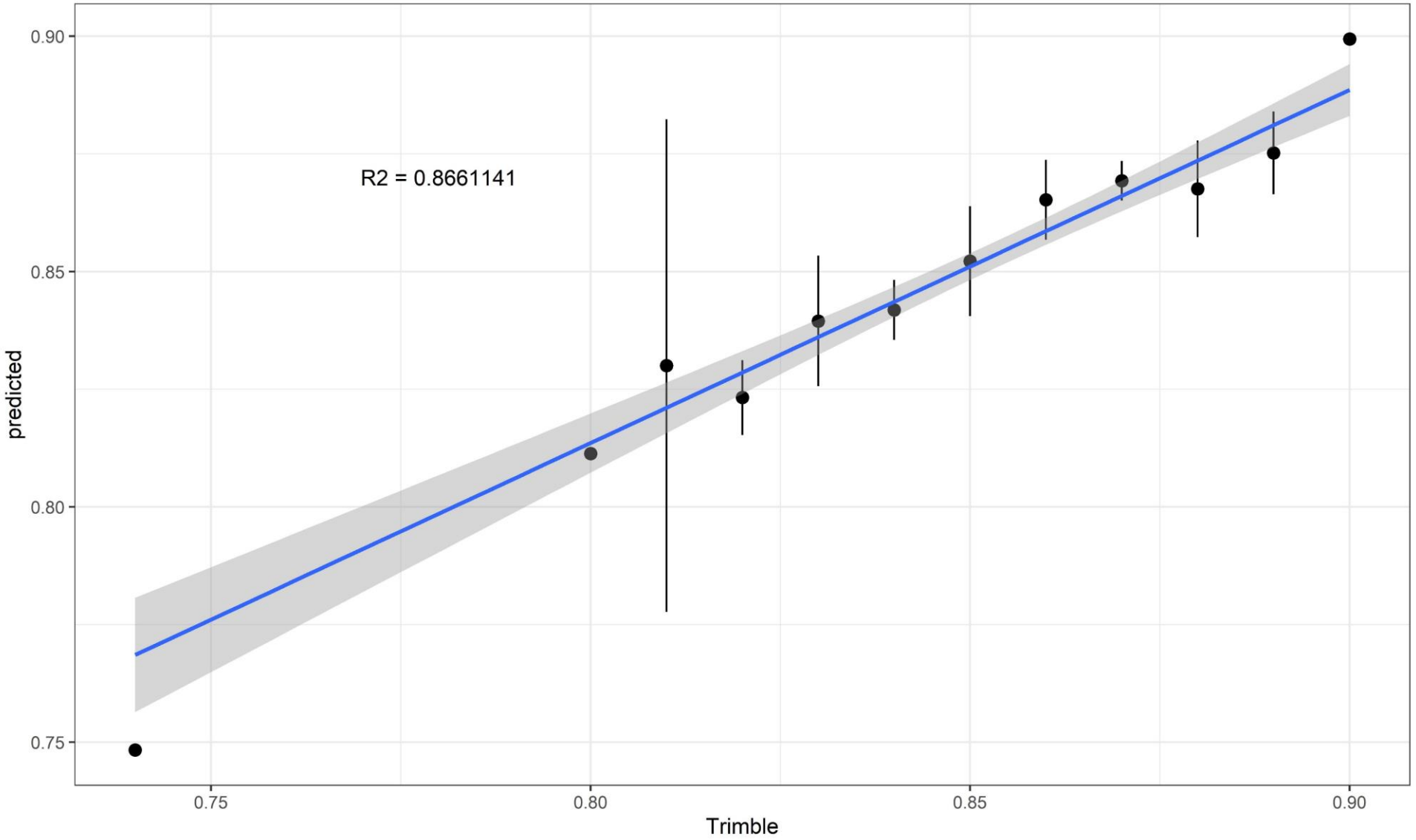
By its very nature, agriculture is a complex scientific field involving a wide range of expertise, skills, methods, and processes that computer systems can effectively support. Numerous efforts have been made to create an automated farming framework capable of controlling measured data. Recent advances in LPWAN communication technology have enabled the ability to collect, process, and analyze data from various sources and remote fields while supporting the concept of agricultural intelligence. A thriving environment



layer

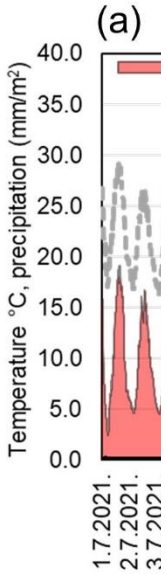
In support to objectives: domain knowledge and neat engineering

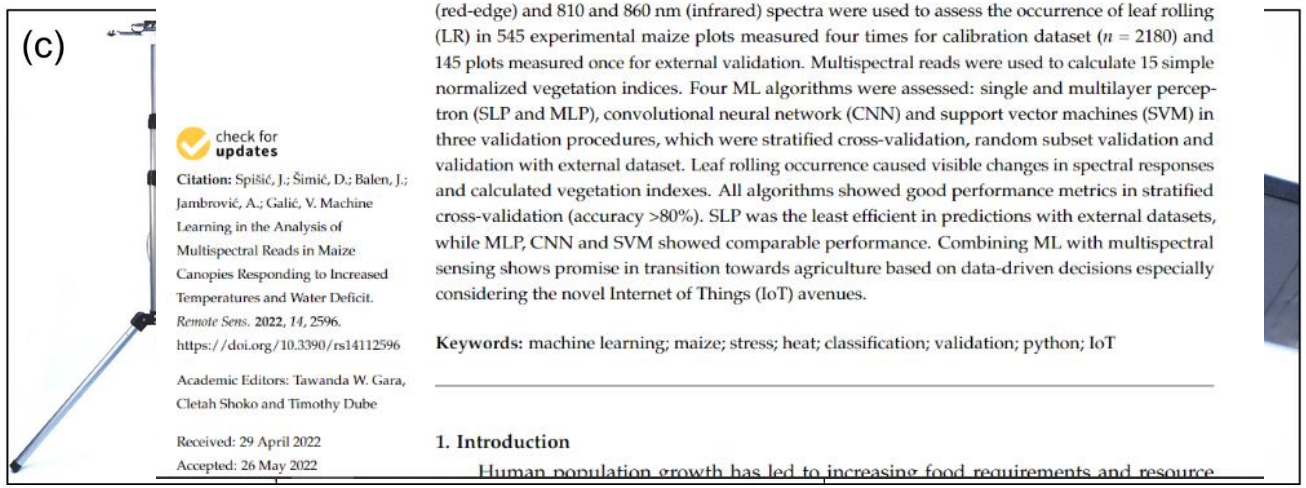
- despite the flawless design of beta 0.01
- device version beta 0.02 was constructed – June 14th 2021
- compared to commercial sensors in maize, wheat and barley



In support to objectives: domain knowledge and neat engineering

- device version beta 0.021 also included LCD display and 3d printed mount – July 2021
- Tested in maize





remote sensing MDPI

Article

Machine Learning in the Analysis of Multispectral Reads in Maize Canopies Responding to Increased Temperatures and Water Deficit

Josip Spišić [1], Domagoj Šimić [2], Josip Balen [1], Antun Jambrović [2] and Vlatko Galić [2,*]

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* Correspondence: vlatko.galic@poljinos.hr

Abstract: Real-time monitoring of crop responses to environmental deviations represents a new avenue for applications of remote and proximal sensing. Combining the high-throughput devices with novel machine learning (ML) approaches shows promise in the monitoring of agricultural production. The 3 × 2 multispectral arrays with responses at 610 and 680 nm (red), 730 and 760 nm (red-edge) and 810 and 860 nm (infrared) spectra were used to assess the occurrence of leaf rolling (LR) in 545 experimental maize plots measured four times for calibration dataset (n = 2180) and 145 plots measured once for external validation. Multispectral reads were used to calculate 15 simple normalized vegetation indices. Four ML algorithms were assessed: single and multilayer perceptron (SLP and MLP), convolutional neural network (CNN) and support vector machines (SVM) in three validation procedures, which were stratified cross-validation, random subset validation and validation with external dataset. Leaf rolling occurrence caused visible changes in spectral responses and calculated vegetation indexes. All algorithms showed good performance metrics in stratified cross-validation (accuracy >80%). SLP was the least efficient in predictions with external datasets, while MLP, CNN and SVM showed comparable performance. Combining ML with multispectral sensing shows promise in transition towards agriculture based on data-driven decisions especially considering the novel Internet of Things (IoT) avenues.

Keywords: machine learning; maize; stress; heat; classification; validation; python; IoT

check for updates

Citation: Spišić, J.; Šimić, D.; Balen, J.; Jambrović, A.; Galić, V. Machine Learning in the Analysis of Multispectral Reads in Maize Canopies Responding to Increased Temperatures and Water Deficit. *Remote Sens.* **2022**, *14*, 2596. https://doi.org/10.3390/rs14112596

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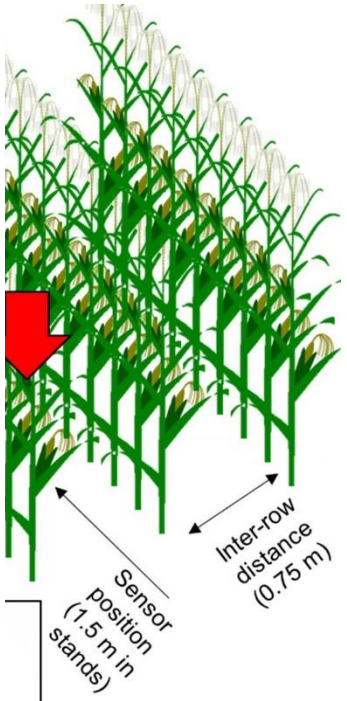
1. Introduction

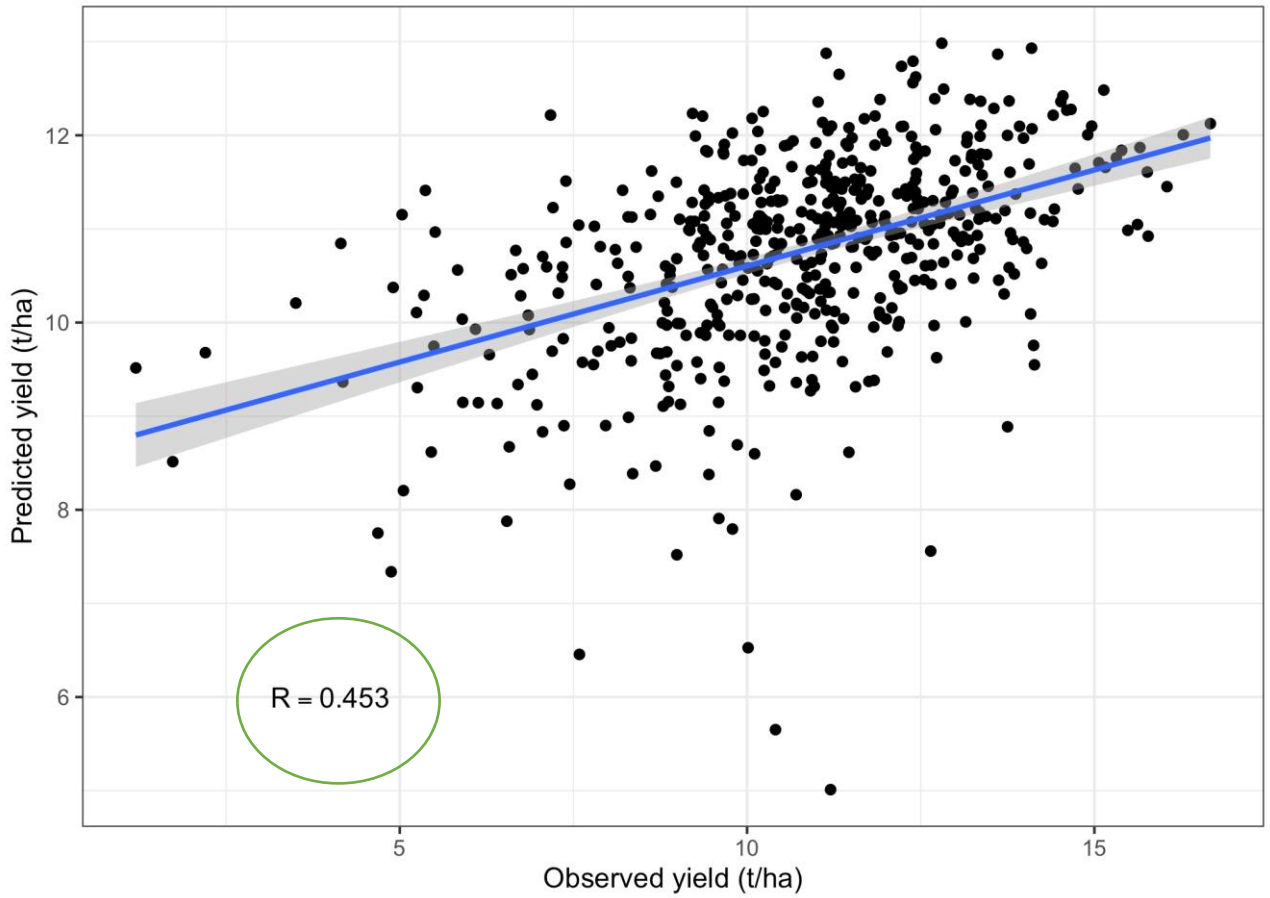
Human population growth has led to increasing food requirements and resource



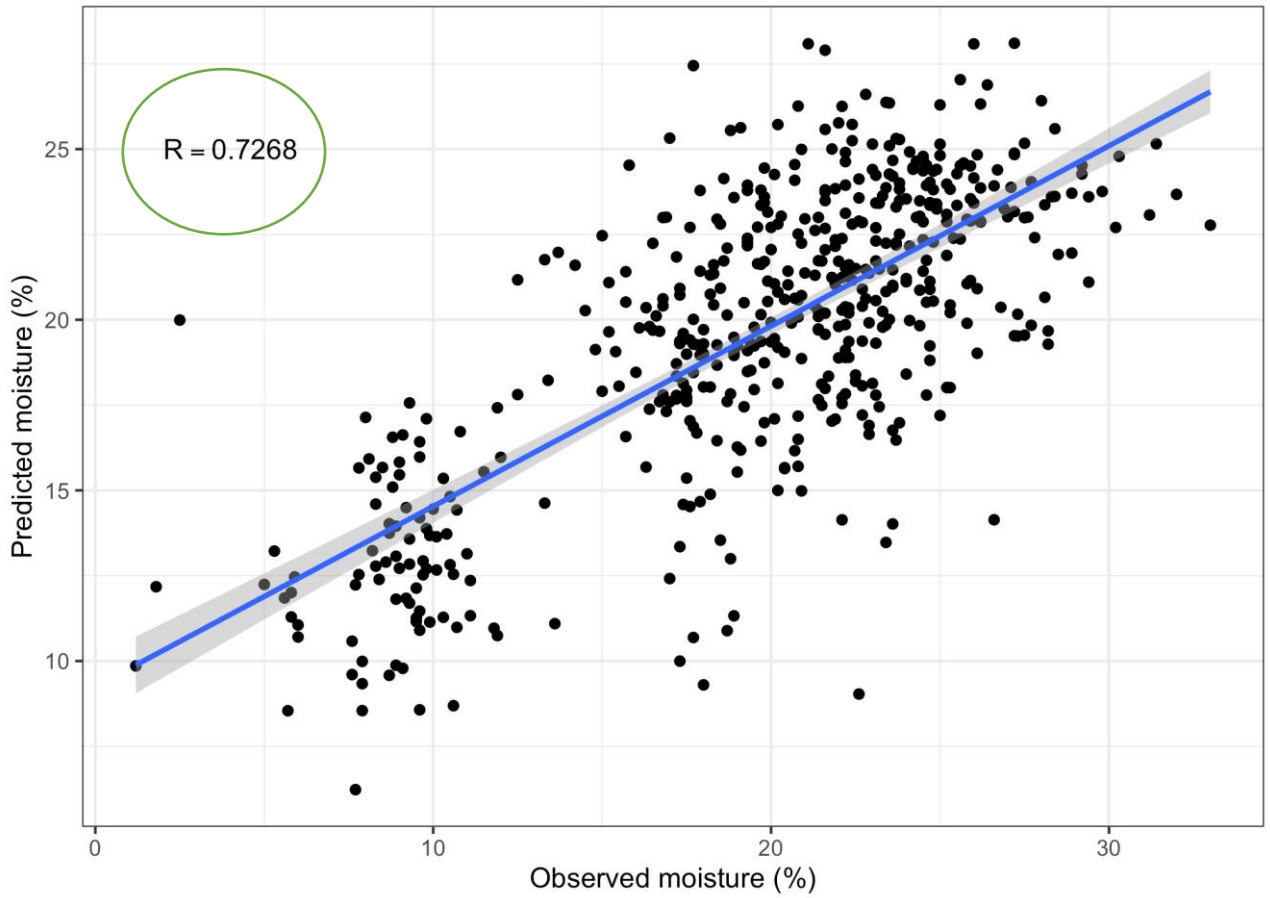
In support to objectives: domain knowledge and neat engineering

- device version beta 0.03 February 1st 2022
- Fully functional communication (LoRa)
- Fully functional meteorological station in Stevenson screen
- Retrieving data on 15-minute basis
- Tested in several environments in various setups

Grain yield



Grain moisture



Pitfalls

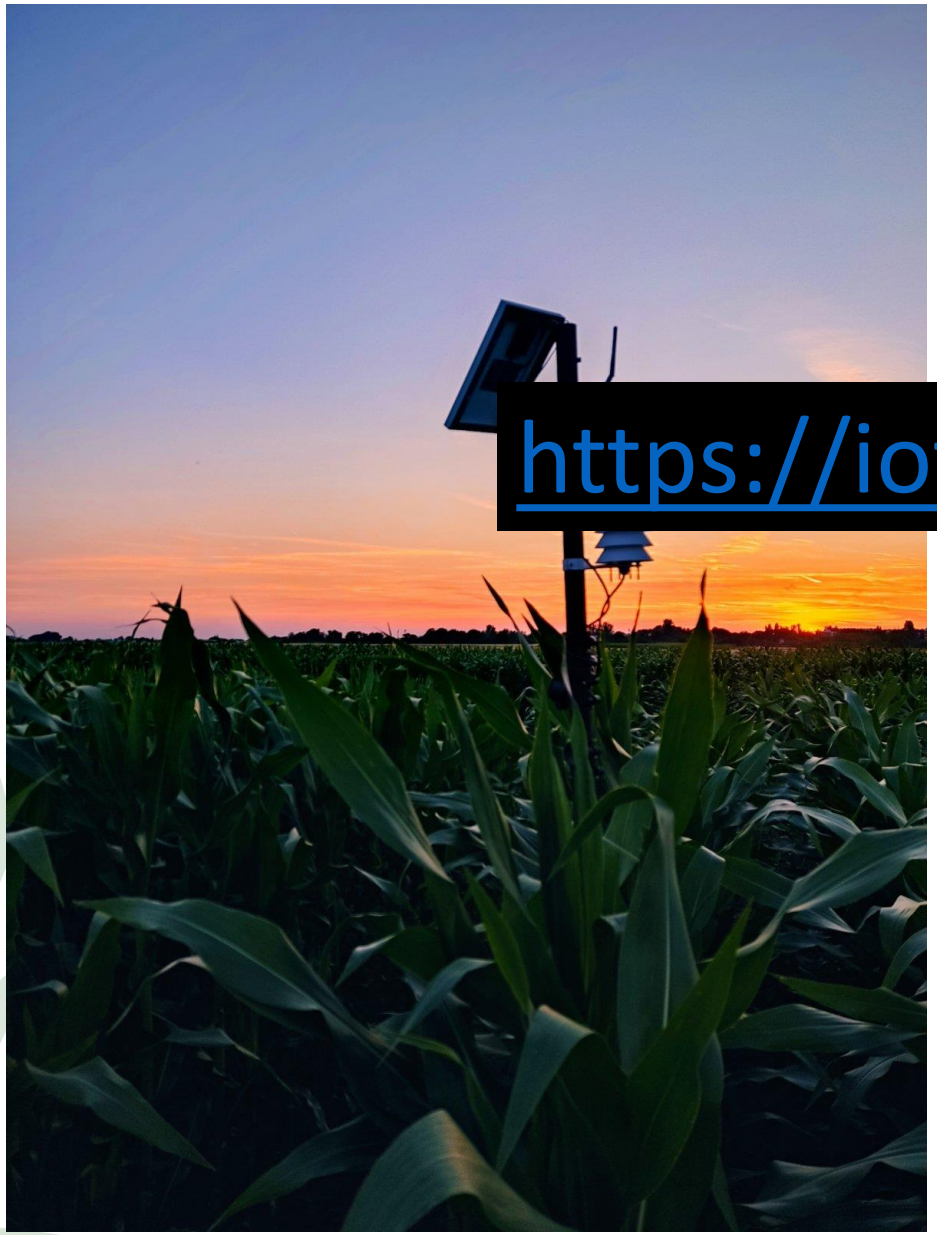
- p>n type of problems – temporally collected data in field – used to model a single outcome -> grain yield
- design flaws -> wear and tear problems with housing – material deterioration in the outdoor environment
- season based recalibration of the models

- **Did the sensor increase the information density as expected?**

Perspectives

- **Application for another grant to increase the TRL of the technology**
- **Work on software solutions to make the important data as accessible as possible**
- **Improve model performance and interpretability**

- **MAKE THE TECHNOLOGY ACCESSIBLE AND AVAILABLE TO FARMERS**



https://iot-polje.fer.hr/iot-polje

O PROJEKTU NOVOSTI ISTRAŽIVAČKI TIM PUBLIKACIJE RADIONICE KONTA

Naslovnica / O projektu

EN

- O projektu
- Novosti
- Istraživački tim
- Publikacije
- Radionice

Ekosustav umreženih uređaja i usluga za Internet stvari s primjenom u poljoprivredi

Internet stvari (*Internet of Things*, IoT) ima značajan potencijal za **primjenu u poljoprivredi** jer omogućuje kontinuirano prikupljanje i obradu mikroklimatskih i agronomskih podataka radi optimizacije i

IoT-polje

najčešći uzrok nerentabilnih prinosa najvažnijih k
entni procesi klimatskih promjena značajno utjec
održivost proizvodnje poljoprivrednih kultura od strateške važnosti za RH.

Projekt *Ekosustav umreženih uređaja i usluga za Internet stvari s primjenom u poljoprivredi* (skr. ***IoT-polje***) će pota primjenu IoT rješenja u poljoprivredi u RH kroz interdisciplinarna istraživanja **Fakulteta elektrotehnike i računa** (FER), **Fakulteta elektrotehnike, računarstva i informacijskih tehnologija** (FERIT) i **Poljoprivrednog instituta** (PIO) radi **smanjenja utjecaja klimatskih promjena na poljoprivredne prinose** u RH korištenjem naprednih tehnologija i dostupnih izvora podataka o stanju usjeva i okoliša. Projektne aktivnosti su usmjerene na istraživ razvoj interoperabilnih i sigurnih tehničkih rješenja ekosustava za prikupljanje i naprednu obradu stvarnovreme mikroklimatskih i agronomskih podataka, radi unaprjeđenja biljne proizvodnje u RH. Ekosustav će integrirati post dostupnu infrastrukturu i izvore podataka te uvesti inovativna tehnička rješenja za cjelovitu slika o stanju usje omogućuje

1. primjenu statističkih metoda nad sasvim novim skupovima podataka i
2. uvođenje novih praktičnih aplikacija za različite dionike u poljoprivredi.

Posebna će se pozornost posvetiti istraživanju **utjecaja suše** na biljnu proizvodnju radi primjene pravovre agrotehničkih mjera i procjene fiziološkog stanja usjeva na temelju fluorescencije klorofila. Predviđa se dizajn i **inovativnog umreženog uređaja za mjerenje fluorescencije klorofila u stvarnom vremenu** te odgovarajuće be senzorske mreže. Potom se planira primjena blok-lanca za praćenje

1. stanja usjeva,
2. provedenih agrotehničkih i fitomedicinskih mjera i
3. poštivanja zakonskih direktiva vezano za primjenu pesticida.

Cilj projekta je povećati tržišno orijentirane IRI aktivnosti u područjima Interneta stvari i biljnih znanosti za uspo ekosustava umreženih uređaja i inovativnih usluga s primjenom u poljoprivredi. Važnost projekta se ogleda u znač

Partneri:

FERIT

POLJOPRIVREDNI INSTITUT OSIJEK