Accelerating Research Impact with Open Technologies
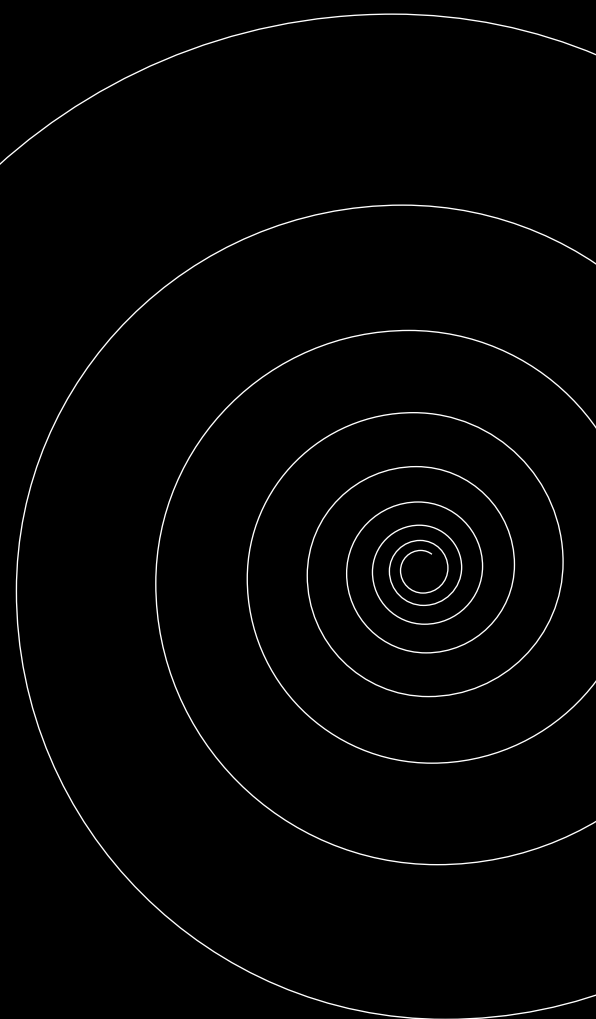
Stories from the University of Cambridge

UNIVERSITY OF CAMBRIDGE

EngBio IRC

Introduction

Open technology, data and knowledge is open for anyone to use, reuse, modify and commercialise. In particular, open technology has been fundamental to the growth of the digital economy. For example, research suggests that 97% of applications leverage some aspect of open-source code[1], and 90% of companies are applying or using open source software in some way. OpenUK estimates that open data, software and hardware deliver an economic boost of between £29.5 billion and £43.2 billion to the UK[2]. This points at the huge global community of contributors to open source software: GitHub alone had 413 million open-source software (OSS) contributions in 2022[3].

Open technologies therefore present us with an opportunity to democratise technology, promote collaboration and generate intellectual, societal and economic value. However, they often receive less attention than proprietary tools and technologies. In part this is because by their nature, their downstream use and impact is more challenging to track. We have worked with researchers and innovators to tell the stories of open technologies emerging from the University of Cambridge and the broader Cambridge tech ecosystem, explore their current use and applications, the challenges faced and lessons learned, and their future potential.

The University of Cambridge has been sharing world-leading knowledge and innovations for over 800 years, and the contribution it can make to society through the dissemination and application of knowledge is core to its mission and values[4]. Through the stories in this report, we see the role that collaborative development and open sharing of technology can play in forging innovative partnerships, growing inclusive innovation communities and accelerating the translation of research to impact. We hope that you find these technologies as inspiring, intriguing and impactful as the researchers who were motivated to both develop them and to share them with the world.

DR Jenny Molloy
EngBio IRC Co-chair

The Engineering Biology Interdisciplinary Research Centre has maintained a strategic focus on open technologies throughout its ten year history and particularly in advancing open technologies for science. It has only been possible to capture a small percentage of the projects taking place across the University, and we encourage others to get in touch, so we can maintain and update this record. We also encourage you to find out more about our work on open source technologies at https://www.engbio.cam.ac.uk

1. https://www.synopsys.com/software-integrity/resources/analyst-reports/open-source-security-risk-analysis.html?intcmp=sig-blog-ossra22
2. https://openuk.uk/press-releases-posts/open-source-software-contributed-an-estimated-46-5bn-to-uk-business-in-2020-according-to-openuk/
3. https://octoverse.github.com/
4. https://www.cam.ac.uk/about-the-university/how-the-university-and-colleges-work/the-universitys-mission-and-core-values

Contents

Biomedical Sciences

Agriculture and Sustainability

Biomedical Sciences

An open source automated PEG precipitation assay to measure the relative solubility of proteins with low material requirement

Area
Biomedical sciences

Launch year
2021

Authors and affiliations
Marc Oeller[1,2], Pietro Sormanni[1], Michele Vendruscolo[1]

1 Department of Chemistry, Centre of Misfolding Diseases, University of Cambridge, Cambridge, UK **2** Current Address: Proteomics and Signal Transduction, Max Planck Institute of Biochemistry, Martinsried, Germany

Contact
Marc Oeller: **oeller@biochem.mpg.de**
Pietro Sormanni: **ps589@cam.ac.uk**
Michele Vendruscolo: **mv245@cam.ac.uk**

Website
https://gitlab.developers.cam.ac.uk/ch/sormanni

ABOUT THE OPEN-RESOURCE

Background

High protein solubility is a key property for the development of protein-based products, such as chemical reagents and pharmacological medicines. A common method routinely applied in many laboratories is based on polyethylene glycol (PEG), a large molecule that induces protein precipitation. Even though this method has been used since the 1960s, it is still challenging, resource intensive, and low throughput. Marc Oeller was developing a software to predict protein solubility during his PhD in the Vendruscolo Lab, at the Yusuf Hamied Department of Chemistry, and he was planning to verify the predictions using the common PEG assay. "But what I found was that, first of all, the published methods were either very heavy on the material requirement or required very expensive pipetting robots. And even though they were published methods, I couldn't find clear protocols," says Marc. The Vendruscolo Lab decided to develop their own assay with a much cheaper robot, low material requirement, and with a medium to high throughput. The protocols are publicly available and open source, being a valuable resource for the scientific community.

Function

It is a fully automated PEG precipitation assay that uses a cost-effective open source pipetting robot, and low material consumption to assess relative solubility of proteins.

Development process

Although the principle idea of the PEG precipitation protocol assay has been known for many years, Marc explained that working with PEG is challenging as it is an extremely viscous substance, like honey, making it almost impossible to accurately pipette small volumes (<5 µL) manually. The development process started with a very simple assay requiring high PEG volume, and then gradually scaled down to reduced volumes. The protocol optimisation was reasonably straightforward, but the tricky step was to tweak the robot to pipette the PEG volumes correctly. "We went down to less than a microlitre and that took a long time for us to get correct with the PEG," says Marc.

Target user

Researchers working on protein developability, protein drugs and protein solubility in general.

Comparison to other technologies

The main advantages of this protocol compared to others available are the low amount of material required, its higher throughput, and the lower cost. But the most valuable point is actually that it is open source, making it very easy to be implemented in other laboratories. "We set the whole thing up as being as open as possible, and that's why we were happy with the robot that we used because the robot cost less than £10,000, which is still, of course, quite a jump, but several times cheaper than other robots," explains Marc.

Outline of the procedure for the measurement of protein relative solubility using an automated PEG assay. © 2021, Oeller et al., licensed under CC-BY 4.0. Reproduced from Scientific Reports 11, 21932, https://doi.org/10.1038/s41598-021-01126-4.

> "I think we always publish papers as open access, and we try to publish everything on bioRxiv first. And I think it's just the way science is going, as much open access as possible."
>
> Marc Oeller

Current use

The complete protocol is currently used in the Vendruscolo and Sormanni Labs, but there are other research groups definitely using part of the analysis tools published with the protocol.

Open source choice

"I think we always publish papers as open access, and we try to publish everything on bioRxiv first. And I think it's just the way science is going, as much open access as possible," says Marc.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

Marc and collaborators want to ensure that the protocol developed by the Vendruscolo Lab is widely disseminated, as they anticipate that this method will facilitate technology transfer to other labs due to its cost-effective open source approach, and easy implementation.

autohaem

Authors and affiliations
Samuel McDermott[1], Pietro Cicuta[1],
Catherine Mkindi[2], Richard Bowman[3]
1 Department of Physics, University of Cambridge,
Cambridge, UK **2** Ifakara Health Institute, Bagamoyo,
Tanzania **3** Department of Physics, University of Bath, Bath,
UK

Contact
Samuel McDermott: **sjm263@cam.ac.uk**
Pietro Cicuta: **pc245@cam.ac.uk**

Main publication
McDermott S, Kim J, Leledaki AA, Parry D, Lee L, Kabla A, Mkindi C, Bowman R, Cicuta P. 2022. autohaem: 3D printed devices for automated preparation of blood smears. *Rev Sci Instrum* **93**, 014104.

Website
https://autohaem.org

ABOUT THE OPEN-RESOURCE

Background

Blood smears are used for investigating a variety of haematological disorders and parasitic infections. The procedure consists of placing a drop of blood on a microscope glass slide and spreading it using a second microscope glass slide. The thin film of blood is then fixed, stained, and examined on an optical microscope. In large-scale blood testing centres, blood smearing is automated. However, this process is still frequently performed manually in many locations, which is a repetitive and time-consuming task. Samuel McDermott, a post-doctoral research associate in the Biological Physics group, at the Department of Physics, was working on how to automate the diagnosis of malaria using the OpenFlexure microscope (an open source optical microscope, additional information on https://openflexure.org/), when he realised that a lot of the slides sent to him from rural clinics in Tanzania were low quality. "It's a very hard technique to do manually. And so, I did a bit of research and spoke to some people in some other countries and they were all having the same problem with the manually prepared slides," says Samuel. He decided to take a step back and improve the blood-smearing stage before focusing on the automation of malaria diagnosis.

Function

autohaem are devices for automated blood smear preparation.

Development process

The devices are composed essentially of two parts: 3D printed ones and electronic components. The 3D parts were designed in a very easy way to print, and there is no need to use a particularly special 3D printer. The electronics can easily be purchased from electronic suppliers. Samuel managed to design a lot of prototypes quickly and then started working on improving them. "It was a very iterative process. In particular, we were looking at two main parameters, which were the speed and the angle that the device uses, and so we did a lot of experiments testing the different angles and speeds and compared it to human experts in the technique. We wanted to be as good as someone who does it every day." At the moment, Samuel is working with a team of manufacturers in Ethiopia and they have been going through the components to find alternatives that are available in their context.

Target user

Research laboratories especially in low-income countries, where it is more difficult to access equipment. But also, in research labs globally, as blood smear is usually done by hand.

Comparison to other technologies

Most commercial automated smearing devices on the market are expensive, and use single-use plastic blades as a spreader, generating a lot of plastic waste. The only open design, low cost devices available at the moment are autohaem. Samuel said that as his research goal was to study malaria, they would have used another available tool to make high quality blood smears. However, as there was not anything available, they decided to design it themselves.
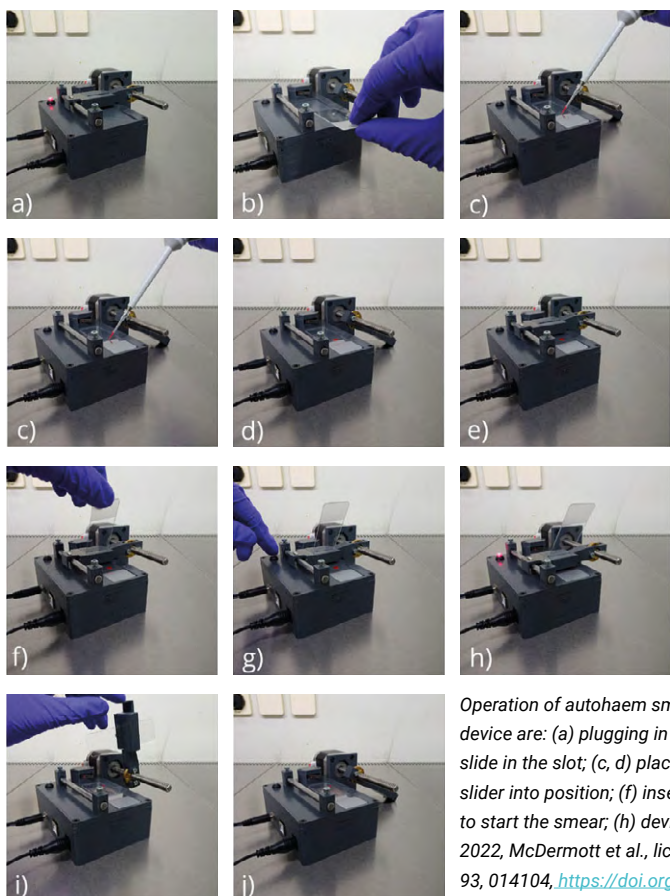
Operation of autohaem smear+. The key steps in the operation of the electro-mechanical device are: (a) plugging in the device; (b) rotating the slider and placing the microscope slide in the slot; (c, d) placing a drop of blood on the microscope slide; (e) rotating the slider into position; (f) inserting the spreader microscope slide; (g) pressing the button to start the smear; (h) device is producing the smear; (i) removing the spreader slide. © 2022, McDermott et al., licensed under CC-BY 4.0. Reproduced from Rev. Sci. Instrum. 93, 014104, https://doi.org/10.1063/5.0076901.

IMPACT

Current use

As autohaem are still in the prototype stage, currently they have only been used in the Biological Physics group at the University of Cambridge, and by their collaborators in Tanzania.

Open source choice

"I think the whole purpose of the project would be completely moot if it wasn't open source, because there's nothing that the community would gain if it was closed source," said Samuel. He emphasises how important the idea is of the community for open source development, as speaking to other people who have developed research tools as open source, plus the feedback from the community, helped him to speed up the learning process. However, after being in touch with users in Ethiopia, he is trying to identify what kind of business model will be the best to make the device available for who really needs it. Samuel points out that the open source model works well in Europe, America, and Asia, but that it does not seem to translate very well to lower- and middle-income countries where there is a huge barrier in terms of finding some of the components needed to build the device. "I would love for autohaem to be open source and always kept like that, but also we want to make sure that we can support local manufacturers to be able to make it and sell it in their communities as well. So, some bits of it would have to be commercialised, but it wouldn't be to make a profit, it would be a social enterprise."

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

Field trials are starting soon in Ethiopia, allowing the device to be tested by a range of users. Once Samuel has completed the field trials, the next step is to start to look for other sources of funding, to be able to turn autohaem into a commercialisable product especially in low- and middle-income countries. The long-term goal is to have the devices used for clinical purposes. However, Samuel is aware that this step will be more difficult to achieve, as the regulatory hurdles for the medical device manufacturing industry in some countries are a big step to overcome.

autohaem logo. © 2022, Samuel McDermott, licensed under CC-BY 4.0.

Open Enzyme Collection

Area
Biomedical sciences

Launch year
2019

Authors and affiliations

Jenny Molloy[1], Chiara Gandini[1], Felipe Buson[1], Fernán Federici[2], Tamara Matute[2], Isaac Núñez[2], Anibal Arce[3], Isaac Larkin[4], Scott Pownall[5]

1 Department of Chemical Engineering and Biotechnology, University of Cambridge, Cambridge, UK **2** Molecular Genetics and Microbiology Department, Pontifícia Universidad Católica de Chile, Santiago, Chile **3** Department of Chemical and Biological Engineering, Northwestern University, Evanston, USA **4** Free Genes Project, BioBricks Foundation, San Francisco, USA **5** Open Science Network Society, Vancouver, Canada

Contact

Jenny Molloy: **jmc80@cam.ac.uk**

Website

https://openbioeconomy.org/projects/open-enzyme-collections

ABOUT THE OPEN-RESOURCE

Background

Access to reagents and consumables in the biotechnology and synthetic biology fields can be a real challenge for some labs around the world. Enzymes in particular require cold-chain shipping and can take weeks to months to be delivered to parts of Africa, Latin America and Asia. Jenny Molloy, group leader of the Open Bioeconomy Lab in the Department of Chemical Engineering and Biotechnology, realised that this challenge came up repeatedly from colleagues at a number of events she attended on open hardware for science. "It was clear that the equipment was one part of the problem. But if you've got the equipment, you still need to keep stocking it with reagents and consumables." As a result, in 2018 Molloy started her Shuttleworth Foundation Fellowship to create an open source toolkit for reagent production, aiming to make biotechnology research more accessible in low- and middle-income countries.

Function

Open Enzyme Collection consists of DNA coding for essential enzymes commonly used in techniques involving reading and editing DNA constructs. The kit enables researchers who encounter challenges to access resources to have the tools to express their own enzymes.

Development process

The process started with brainstorming with a number of collaborators, around which enzymes and parts should be included in the collection. The next step was to identify which of those were already off-patent. The Open Enzyme team then made some changes to the digital DNA code to ensure successful expression in the lab workhorse bacteria *Escherichia coli*, and submitted the sequences to the project Free Genes at Stanford University where they were de novo synthesised. Open Enzyme is an ever-growing collection, Molloy said, "During the pandemic we designed the research in diagnostics collection to help groups developing new COVID tests, added different types of proteins and we're currently extending it again through an open consultation process."

Harry Akligoh, a member of the Open Bioeconomy Lab Ghana Node since 2018 using some of the tools developed by OpenEnzyme. © 2021, Open Bioeconomy Lab, licensed under CC-BY 4.0.

Target user

Researchers in the molecular biology field located in low- and middle-income countries. Also, whoever has challenges in accessing enzymes for their molecular biology research, education or innovation activities, for whom it would help to have the protein expression tools to produce their own enzymes.

Comparison to other technologies

The key factor that differentiates Open Enzyme Collection from available alternatives is the open source aspect, and curation of the "most useful" DNA in one single toolkit. Although there is a cost for the maintenance of the plasmids and delivery, recipients then have a lot of freedom. Open Enzyme Collection is distributed under an Open Material Transfer Agreement (OpenMTA, https://openmta.org), which means that the resources can be used commercially and also redistributed to other labs. Typically, when plasmids are purchased from commercial suppliers, most of them have non-commercial and non-redistribution clauses unless high fees are paid. "That's against what we're trying to do, which is to make sure that resources are more accessible, reduce transaction costs and shorten supply chains, making the waiting time for the material reduced" says Molloy. Molloy and colleagues also started the Reagent Collaboration Network (Reclone) to connect users of the toolkits. This has a forum and monthly meetings where users can present problems for troubleshooting.

Current use

Open Enzyme has reached more than 500 labs in around 50 countries. However, as Molloy pointed out, "There's a difference between people having the DNA and people actually producing enzymes, and we'd be interested to understand more about how to move from access to impact." Close partnerships show that the resources have been used in South America, including labs in Chile, Peru and Colombia. Thailand, Philippines, Ghana, Cameroon, South Africa, Kenya, and Ethiopia are other locations where labs are actively using some aspects of the collection. It has been distributed to 375 student teams worldwide through the international genetically engineered machines competition (iGEM).

Successful stories

With access to the enzymes, a Chilean research group led by Dr Fernan Federici has made a number of innovations for COVID-19 diagnostics, and locally produced potato virus diagnostics. Also, due to the fact that "homebrew" enzymes produced with the Open Enzyme Collection are much cheaper than the commercial alternatives, he was able to use these enzymes for educational purposes, running molecular biology practical courses with university students and even developing "take-home" kits during lockdowns.

In Cameroon, a start-up company using the Open Enzyme Collection developed 6 PCR products, which are now being sold for local researchers. This is important in the Cameroonian context because the students, who are often self-funded, struggle to afford the reagents for their projects. Also, reagents can take several months to be delivered because of supply chain issues, which is avoided when they can be sourced from local markets. From the perspective of the company, they have had a lot of recognition as they are the first company in Cameroon to express recombinant proteins commercially; leading to recognition and partnerships with numerous local research institutions and the Ministry of Science.

Open source choice

"The benefit of having the collection as an open source is that it ideally reduces not only any kind of concern about the intellectual property, but also the transaction costs of negotiating licences," says Molloy. However, this is just the bureaucratic side of the story. Molloy is concerned with making sure the whole manufacturing pipeline is more accessible. The Open Enzyme Collection team is constantly optimising protocols because they recognise that just because they have shipped someone some DNA that codes for the enzyme, the users still need different pieces of instrumentation and several reagents to manufacture enzymes, so Open Enzyme have to go further. In addition to its technological aspect, Molloy is always thinking about what type of troubleshooting and support the users might need. Having a community that can support each other and also improve the collection is Molloy's next goal. "We want to advance the researchers from users of the toolkit to contributors of new DNA parts and data, so they really benefit from open collaboration, not just open access."
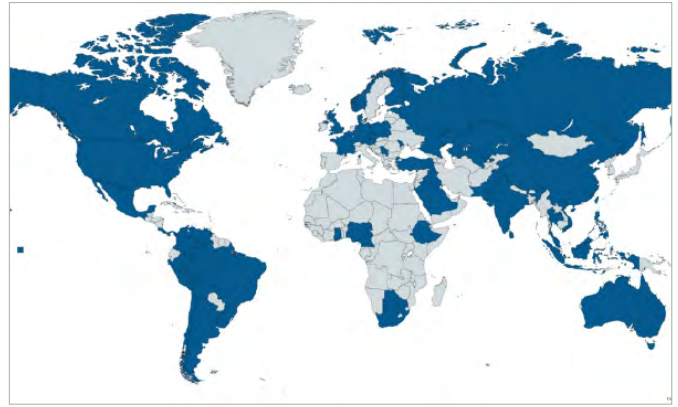
Map showing in dark blue the countries where Open Enzyme has been currently used. © 2023, Open Bioeconomy Lab, licensed under CC-BY 4.0.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

"Enzymes manufactured using the Open Enzyme Collection being used for products with real-world applications beyond research. We are looking for proactive partners who are willing to be regional hubs for distribution of the collection, but also for training and supporting the local research community."

"We want to advance the researchers from users of the toolkit to contributors of new DNA parts and data, so they really benefit from open collaboration, not just open access."

Jenny Molloy

Deployable 3D printer for soft materials

Area
Biomedical sciences

Launch year
2022

Authors and affiliations
Yan Yan Shery Huang[1,2], Corrado Mazzaglia[1,2], Yaqi Sheng[1,2], Leonor Nunes Rodrigues[3], Iek Man Lei[2], Jacqueline D. Shields[3,4], Chon Lok Lei[1,2], Cilian Leow[1,2]
1 The Nanoscience Centre, University of Cambridge, Cambridge, UK **2** Department of Engineering, University of Cambridge, Cambridge, UK **3** MRC Cancer Unit, University of Cambridge, Cambridge, UK **4** Comprehensive Cancer Centre, King's College London, London, UK

Contact
Shery Huang: **yysh2@cam.ac.uk**
Corrado Mazzaglia: **cm986@cam.ac.uk**
Yaqi Sheng: **ys549@cam.ac.uk**

Main publication
Mazzaglia C, Sheng Y, Rodrigues LN, Lei IM, Shields JD, Huang YYS. 2023. Deployable extrusion bioprinting of compartmental tumoroids with cancer associated fibroblasts for immune cell interactions. Biofabrication **15**, 025005.
Lei IM, Sheng Y, Lei CL, Leow C, Huang YYS. 2022. A hackable, multi-functional, and modular extrusion 3D printer for soft material. *Scientific Reports* **12**, 12294.

Website
https://github.com/iekmanlei/Printer.HM

ABOUT THE OPEN-RESOURCE

Background

Three-dimensional (3D) printing is a technology that has rapidly gained importance in different sectors in the last decades especially due to its versatility, allowing the users to customise product designs fully. Compared to the different 3D bioprinting methods, extrusion bioprinting is the most widely used as it has a lower material usage and waste, and it can accommodate a broad range of material. Even though a lot of innovations in extrusion 3D printing have been achieved in recent years, most of the available systems are expensive and difficult to be relocated due to its bulkiness. Corrado, Research Associate in the Biointerface group, at the Department of Engineering, was interested in applying 3D printing to biomedical sciences, and he explains that, "When you work with biological material, sometimes you need to be in a sterile environment, in a biosafety cabinet, but usually bioprinters are these kind of big units." Thinking about how to make extrusion 3D printers more accessible, the Biointerface group decided to develop a low-cost and easy to transport extrusion 3D printer.

Function

It is a deployable 3D extrusion printer for soft materials that can be folded, transported, and rapidly re-assembled, e.g., for switching between working spaces; or, for printing inside a biosafety cabinet when applying its use to biological materials that are non-transportable (due to a materials transfer agreement or ethical restrictions).

Development process

The portable 3D printer consists of a printhead controlled by Arduino (an open source electronic board with a simple microcontroller), and a robotic arm controlled by Python codes, all assembled into supporting metal frames. As the Biointerface group is highly-multidisciplinary, the deployable 3D printer was first developed for printing soft material in general. The next step was to translate the technique to biological materials, focused on cancer research. The robotic arm was then adapted to hold a Petri dish, enabling the user to generate 3D printed tumoroids. This generated tumour mass can be subsequently used for studies, with a huge potential for cancer drug testing in the near future. Yaqi, a PhD student in the Biointerface group was directly involved with the printer development and she explains that the biggest challenge for her was related to protocol optimisation, to try to achieve a satisfactory printing performance. For Corrado, on the other hand, as he was applying the technique to the biomedical field, the challenges that he encountered were more related to the communication between the engineering and biological fields, as different areas have different strengths and drawbacks.

Target user

Researchers, especially the ones focused on studying biological material, e.g., for drug testing, or for gaining mechanistic understanding on some specific organs or tissues.

Comparison to other technologies

Compared to the commercial options, the deployable 3D printer is much more affordable, smaller, and lighter. Moreover, it is foldable, and easy to assemble, making it easy to store and transport. As the printer is open source and was built from simple components, its parts can be readily sourced and fabricated. Another advantage is that the deployable 3D printer operates with smaller volume when compared to the commercial options, making it compatible with many biological materials. Yaqi points out that portable printers have a lower mechanical resolution than commercial systems. However, the one described here is the most precise when compared to other 3D portable printers available.
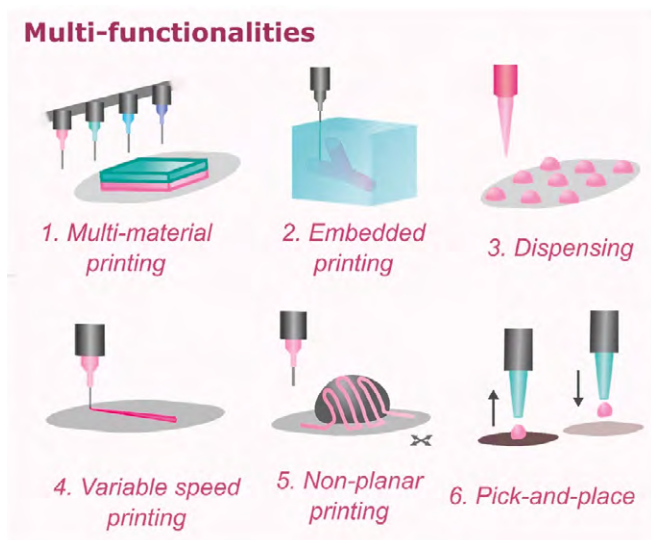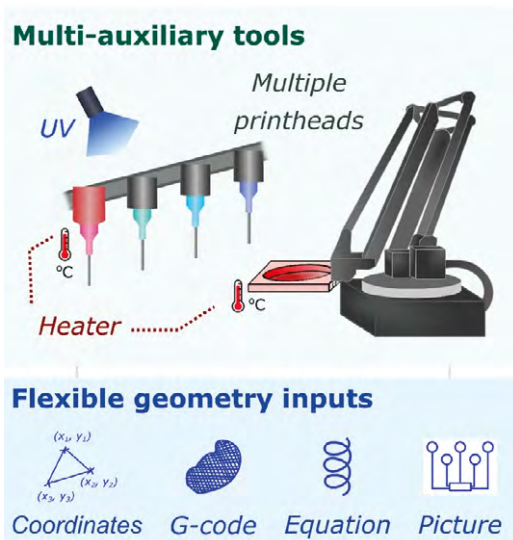
Features of the deployable printer showing its multi-functionalities in one-platform. © 2022, Lei et al., licensed under CC-BY 4.0. Reproduced from Scientific Reports 12, 12294, doi: https://doi.org/10.1038/s41598-022-16008-6.

The deployable printer can be folded, transported, and easily re-assembled. © 2023, Mazzaglia et al., licensed under CC-BY 4.0. Reproduced from Biofabrication 15, 025005, https://doi.org/10.1088/1758-5090/acb1db.

IMPACT

Current use

At the moment, the deployable 3D printer has been used just by the Biointerface group and collaborators, but due to its portability and versatility, more researchers are becoming interested in it.

Successful stories

Corrado's study in Biofabrication (additional information can be found here) is one of the examples of the potential that the 3D printer has for developing strategies in cancer drug testing. Another successful application of the system has been published in Nature Communication by Lei and collaborators (additional information can be found here), where 3D printed cochleae were used to replicate patient cochlear profiles for implant testing.

Open source choice

The main reason why the Biofabrication group decided to release the deployable 3D printer as open source was to make it more accessible, as in their field commercial equipment can be cost-prohibitive. "Since the beginning it wasn't to commercialise something, it was more to make something new and have it available for everyone," says Yaqi.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

The Biofabrication group is always open to collaboration, especially in projects with potential application to the biological field.

"Since the beginning it wasn't to commercialise something, it was more to make something new and have it available for everyone."

Yaqi Sheng

CellphoneDB

Area
Biomedical sciences

Launch year
2018

Authors and affiliations

Roser Vento-Tormo[1], Mirjana Efremova[1], Miquel Vento-Tormo[2], Sarah A. Teichmann[1,3,4]

1 Wellcome Sanger Institute, Cambridge, UK **2** YDEVS software development, Valencia, Spain **3** Theory of Condensed Matter Group, The Cavendish Laboratory, University of Cambridge, Cambridge, UK **4** European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Cambridge, UK

Contact

Sarah Teichman: **st9@sanger.ac.uk**
Roser Vento-Tormo: **rv4@sanger.ac.uk**
Nicholas England: **ne6@sanger.ac.uk**

Website

https://www.cellphonedb.org/index.html

ABOUT THE OPEN-RESOURCE

Background

Understanding cell-to-cell communication mediated by ligand-receptor complexes is crucial for comprehending biological processes like development, differentiation, and inflammation. Investigating the crosstalk between different cell types provides insights into how physiological processes are facilitated. The scalability of single-cell genomics technologies has allowed for parallel analysis of multiple cells from the same tissue, providing a unique opportunity to study cell communication. However, existing tools for estimating ligand-receptor interactions faced two major issues: (i) the majority of ligands and receptors stored were not curated, leading to a lot of false positives (i.e. interactions stored in a database that do not exist in the reality); (ii) the existing methods did not account for the multimer nature of the majority of the ligand-receptor interactions, meaning each receptor (or ligand) consist by more than one subunit. The latter is important to make accurate predictions as it is the combination of subunits what gives specificity to the ligand/receptor interactions. To address these challenges, Dr Roser Vento-Tormo, group leader in the VenTo Lab, at Wellcome Sanger Institute, and collaborators developed CellphoneDB.

Function

CellphoneDB is a suite to study cell-to-cell communication from single-cell transcriptomics data. Identifying ligand−receptor interactions from single-cell RNA sequencing (scRNA-seq) requires both the annotation of complex ligand−receptor relationships from the literature (i.e. database) and a statistical method that integrates the resource with scRNA-seq data and selects relevant interactions from the dataset (ie. tool). CellphoneDB is composed of two units, a database and a tool. CellphoneDB database is a publicly available repository of curated receptors, ligands and their interactions. The database can be used to search for a particular ligand/receptor or in combination with the tool to interrogate your own single-cell transcriptomics data.
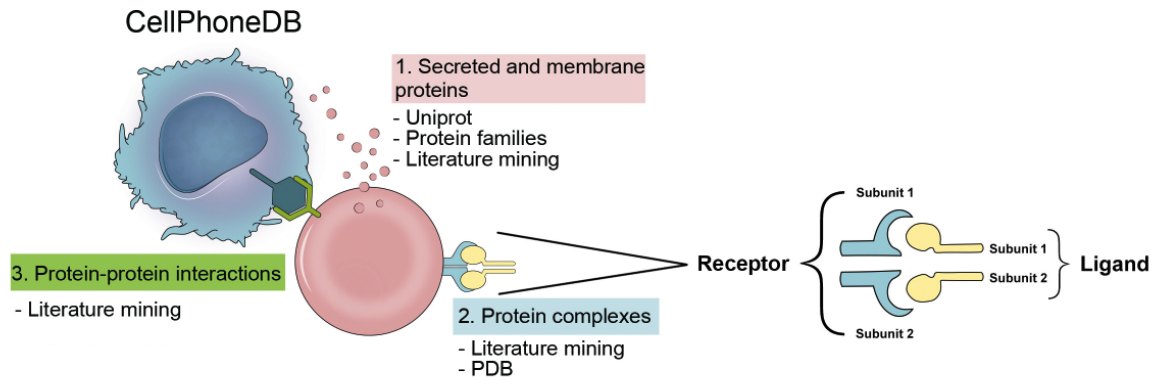
Overview of the database: (1) secreted and membrane proteins stored in protein_input; (2) protein complexes stored in complex_input; and (3) protein−protein interactions stored in interaction_input. © 2018, Wellcome Sanger Institute, licensed under CCC-BY-NC-ND 2.5 (https://creativecommons.org/licenses/by-nc-nd/2.5/). Reproduced from https://www.cellphonedb.org/index.html.

Development process

The development process was a highly collaborative and multidisciplinary work, that started in the Teichmann lab (additional information can be found here). "The computational approach was discussed multiple times in the lab meetings where multiple members from the Teichmann lab contributed to choose the best statistical approach used to infer ligand-receptor interactions.", said Dr Vento-Tormo. The team also worked closely with experts in the field to ensure that receptor and ligand interactions stored in their database were correct. That included Gerry Graham, Professor at the University of Glasgow (additional information can be found here), an expert on cell-cell communication through chemokines. In addition, the group established collaborations with software developers that enabled to build the structure of the database, make the code scalable and have a webpage to query the ligand/receptor interactions present in the database.

One of the most challenging part in the development process was the scalability, explains Dr Vento-Tormo. "Since 2016, when we started the method, the amount of single cell generated has increased significantly and we had to account for this. Also, it was surprising how little we know about protein complexes (i.e. multimers) which are essential to understand receptors."

Target user

In the first instance researchers. Also, anyone who wants to make their own synthetic sitting pathways, try some new combinations or expressing these new cell types, or using it for some new technology. CellphoneDB has a lot of translational potential and non-academic researchers are becoming more interested in it because the receptors are surface proteins that can be targeted with biologics.

Comparison to other technologies

The first differential of CellphoneDB database is that it only includes curated data, meaning that only interactions linked to a manuscript are included. Secondly, the database considers that the majority of receptors are multimers: in other words, that multiple subunits are required in order for the receptor to be functional. Thirdly, in later versions CellphoneDB also includes information about: a) non-protein ligands (e.g. steroid hormones), by taking into account the last enzyme involved in the production of the non-protein ligand; b) transcription factor and receptors that are part of the same signalling pathway. The link with downstream transcription factors, could be used as a sensor of the ligand-receptor interaction. Finally, the database and tool are continuously updated and made compatible with other tools to analyse single-cell genomics data.

CellPhoneDB logo. © 2018, Wellcome Sanger Institute, licensed under CC-BY-NC-ND 2.5 (https://creativecommons.org/licenses/by-nc-nd/2.5/). Reproduced from https://www.cellphonedb.org/index.html.

Current use

On the GitHub CellphoneDB has been forked 103 times, and its publication has been cited more than 1300 times. Some examples of how to use it include: a) inferring function of a cell by quantifying the signals that is receiving or sending to other cells in the environment; b) comparing ligand/receptor interactions between two conditions (e.g. healthy vs disease); and c) informing specific *in vitro* protocol by knowing the signals that a specific cell is receiving from its surroundings (i.e. other cells).

Successful stories

The study published in Nature (2018) by Vento-Tormo and collaborators is one of the examples of the potential that CellphoneDB database has in inferring the communication between cells. The study resolves the maternal uterus-fetal placental communication during human pregnancy, and found that maternal uterine immune cells play a key role in placentation by downregulating inflammation (to avoid rejection) and promoting migration of the fetal placental cells into the uterus, an event crucial for pregnancy success. Another successful application of the database can be found in the publication by Garcia-Alonso and co-authors in Nature (2022), exploring the formation of follicle formation in the developing human ovaries. During development, the female eggs (carrying the genetic information) are surrounded by a specific cell type named "granulosa cells" forming the ovarian follicle. These structures are required for the future maturation of the egg. Using CellphoneDB, the authors could gain insights into the cell-cell communication events between the eggs and granulosa cells that are required to form these follicles.

Open source choice

"For us, it was essential for people to use CellphoneDB in their own research and for this, we had to opt for open source", said Dr Vento-Tormo.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

VenTo Lab would like their method to be integrated with other data modalities and statistical methods available. For this, they are continuously developing the tool and making it compatible with other formats required in other complementary single-cell genomics tools.

"For us, it was essential for people to use CellphoneDB in their own research and for this, we had to opt for open source."

Roser Vento-Tormo

COVID-19 Sounds App

Area
Biomedical sciences

Launch year
2020

Authors and affiliations
Cecilia Mascolo[1], Pietro Cicuta[2],
Andres Floto[3], Chloë Brown[1],
Jagmohan Chauhan[1,4], Jing Han[1],
Andreas Grammenos[1], Apinan
Hasthanasombat[1], Dimitris Spathis[1],
Tong Xia[1], Ting Dang[1], Erika Bondareva[1]
1 Department of Computer Science and Technology,
University of Cambridge, Cambridge, UK **2** Department
of Physics, University of Cambridge, Cambridge, UK
3 Department of Medicine, University of Cambridge,
Cambridge, UK **4** ECS, University of Southampton,
Southampton, UK

Contact
Cecilia Mascolo: **cm542@cam.ac.uk**
Tong Xia: **tx229@cam.ac.uk**

Main publication
**Han J, Xia T, Spathis D, Bondareva E,
Brown C, Chauhan J, Dang T, Grammenos
A, Hasthanasombat A, Floto A, Cicuta P,
Mascolo C.** 2022. Sound of COVID-19:
exploring realistic performance of audio-
based digital testing. *npj Digital Medicine*
5, 16.

Website
https://covid-19-sounds.org/en/

ABOUT THE OPEN-RESOURCE

Background

Affordable, easily accessible, and accurate screening tools to detect human physiological signals (such as cardiac or respiratory signals) is an ultimate goal in medical care. Prof Cecilia Mascolo, head of the Mobile Systems Research Laboratory, at the Department of Computer Sciences and Technology, has been demonstrating how audio collected by portable devices widely used by most parts of the world population can aid the diagnostics of some diseases. Prof Mascolo's research group was applying these concepts especially on heart disease diagnostics, when the COVID-19 pandemic happened. They took it as an opportunity to explore if it would be possible to use cough, breathing and voice to detect Coronavirus disease. COVID-19 Sounds App was then developed for audio-based digital testing of COVID-19.

Function

COVID-19 Sounds App is used to collect the sounds of voice, breathing and cough from the participants, to inform the diagnosis and disease stage of COVID-19 by developing algorithms; and to understand the difference between the sounds of COVID-19 and other respiratory illnesses.
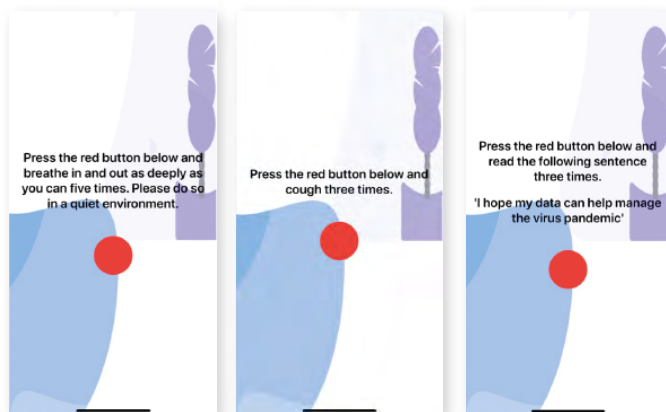
COVID-19 Sounds App sound collection page. © 2020, Mobile Systems Research Laboratory, licensed under CC-BY 4.0. Reproduced from https://www.covid-19-sounds.org/en/.

Development process

The app development started during lockdown in 2020. Prof Mascolo points out that the app development per se was not too complicated as her group had backbone apps to work with. The difficulty was to release an app with COVID-19 in its title during a pandemic, where Apple and Google were very careful on what they allowed to be released. "It took us weeks or months to go through the approval of Google and Apple for the app. Some colleagues inside the University of Cambridge and the Department of Public Health helped with letters, supporting our research initiative," says Prof Mascolo.

Target user

The data collected by the COVID-19 Sounds App is constrained to academic research only, because of data privacy policies.

Comparison to other technologies

COVID-19 Sounds is the largest multi-modal dataset of COVID-19 respiratory sounds. Even though there are other large datasets related to respiratory diseases, Prof Mascolo said that they carefully thought about how to release audio data openly and in a safe way, a differential compared to most of the other technologies available.

IMPACT

Current use

Although the code of the COVID-19 Sounds App is shared, the metadata related to the collection is the most successful point about it. The data collected through the COVID-19 Sounds App has already been shared with more than 300 institutions. Data analysis shows the potential of machine learning for respiratory disease detection as well and its progression and evolution within individuals.

Successful stories

The numbers that COVID-19 Sounds App has already generated are impressive. It is a dataset crowd-sourced from 36,116 participants, consisting of 53,449 audio samples (over 552 hours in total). This dataset is comprehensive in terms of demographics and spectrum of health conditions and also provides participants' self-reported COVID-19 testing status with 2,106 samples tested positive.

Open source choice

"We are a university and I think that open source should be our model, and in particular for COVID-19, as it was an international endeavour. It was almost a no brainer that it had to be done in an open way," says Prof Mascolo.

COVID-19 Sounds App homepage. © 2020, Mobile Systems Research Laboratory, licensed under CC-BY 4.0. Reproduced from https://www.covid-19-sounds.org/en/ .

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

At the moment, the Mobile Systems Research group is working towards a data collection for disease progression. Some of the app users are providing more than one sound sample, so it is possible to understand how they are getting out of COVID-19 infection. Also, there are other institutions using the dataset to work on different diseases.

CamCOPS

Area
Biomedical sciences

Launch year
2021

Authors and affiliations
Rudolf N. Cardinal, Martin Burchell
Department of Psychiatry, University of Cambridge, Cambridge, UK

Contact
Rudolf Cardinal: **rnc1001@cam.ac.uk**
Martin Burchell: **mb2353@cam.ac.uk**

Website
https://camcops.readthedocs.io/

ABOUT THE OPEN-RESOURCE

Background

In psychiatry and related fields, quantitative data on symptoms and cognitive function is an important tool, and can improve the implementation of appropriate treatment strategies. Old-fashioned ways of capturing information via pen and paper are very labour intensive and prone to error, and not useful for data analysis. Data entry by an NHS healthcare professional in electronic health records, or by a researcher into spreadsheets, can also be cumbersome. In an attempt to address this problem, Dr Rudolf Cardinal, associate professor at the Department of Psychiatry, developed CamCOPS, the Cambridge Cognitive and Psychiatric Assessment Kit. This is a software system that allows clinicians (or researchers), patients (or research subjects), or both together, to capture information relevant to research or clinical care in an easy way.

Function

CamCOPS is an open source cross-platform system that enables quick, simple, and accurate structured data capture in the domain of psychiatry, psychology, and clinical neurosciences. It can be used on touchscreen tablet devices or computers. It offers simple questionnaires and more complex tasks, such as animated tests of specific aspects of brain function, and sends information securely to a server within the host institution.

CamCOPS logo. Reproduced from https://camcops.readthedocs.io/en/latest/.

Development process

The CamCOPS "app" is written in the programming language C++, using the Qt framework to create its user interface. "When you're writing an application, you need to deal with the challenge that people use lots of operating systems, including Android, iOS, and Windows," explains Cardinal. The server software is written in Python, another programming language. The next step was to obtain the various information governance and security approvals required for NHS use. The final step was a professional security test of the software. "To become approved for NHS use, you've got to be crystal clear about the security aspects of data storage, where the data goes and what kind of data." CamCOPS development continues, as Cardinal and Martin Burchell, software developer at the Department of Psychiatry, are working on adding more tasks to the application, and on improving the integration with clinical record systems.

Target user

CamCOPS has two modes of operation: a "clinician" mode and a "single patient" mode. In "clinician mode", the target users are health professionals or researchers working with one or multiple patients. In this case, clinicians have access to a range of tasks that they can conduct or ask the patients to perform. In the patient mode, the target users are the patients using their own device to register their experiences of symptoms.

Comparison to other technologies

CamCOPS is free and open source software, which eliminates direct software costs and allows anyone to inspect the code. And it can operate offline, allowing its use in areas with poor internet connectivity, whether on home visits in places with poor mobile phone signal or deep within hospitals without good Wi-Fi. The difficulty with offline operation is that it excludes the simpler software model where all testing is performed online via a web site, and it brings some complexities in development, and data security management.

IMPACT

Current use

CamCOPS is used by a number of clinical services within Cambridgeshire and Peterborough NHS Foundation Trust (CPFT), which provides mental health and community services, in Cambridge University Hospitals NHS Foundation Trust (Addenbrooke's and the Rosie Hospitals), and in the University of Cambridge for research. For example, it was used in a study examining the impact of "long COVID" on mental health. It is also used for research in Denmark and Singapore. No data is collected centrally: Cardinal explained that as the app can collect highly sensitive mental health data, they deliberately decided to have a very clear use policy that no additional data will be collected or shared, and the user's data will only be sent to their chosen server (e.g. their hospital or research team).

Open source choice

"I'm philosophically strongly inclined towards free and open source work and fortunately we're encouraged to do it with public research funding," says Cardinal. Another advantage is that because the code is public, anyone can look at it and spot errors, if there are any. Cardinal also hopes that the free open source model will encourage wider NHS adoption.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

At the moment the challenge that Cardinal and Burchell are trying to overcome is how to integrate the collected data easily into clinical record systems. "We care because we want information that's clinically relevant to go into the main clinical record immediately, within seconds of receipt. It's easy for authorised users to see the data on the CamCOPS server, and easy for CamCOPS to send data like that, but the clinical record system needs to be able to receive it too." Once they have cracked that nut, they would like expand the use of CamCOPS.

OSAIRIS

Area
Biomedical sciences

Launch year
2011

Authors and affiliations

Rajesh Jena[1], Alex Constantinou[1], Andrew Hoole[1], Abigail Bushi[1], Terry Parlett[2], Dafne Chirivino[2]

1 Department of Oncology, Cambridge University Hospitals NHS Foundation Trust, Cambridge, UK **2** Cambridge Enterprise, University of Cambridge, Cambridge, UK

Contact
Rajesh Jena: **rjena@nhs.net**

Main publication

Oktay O, Nanavati J, Schwaighofer A, Carter D, Bristow M, Tanno R, Jena R, Barnett G, Noble D, Rimmer Y, Glocker B, O'Hara K, Bishop C, Alvarez-Valle J, Nori A. 2020. Evaluation of deep learning to augment image-guided radiotherapy for head and neck and prostate cancers. *JAMA Network Open* **3**, e2027426.

Website
http://www.camradiotherapy.org.uk/rdst/index.html

Funding

Additional information about OSAIRIS can be found at
https://youtu.be/AHchuDX0nn4

ABOUT THE OPEN-RESOURCE

Background

Radiotherapy is an essential component of cancer treatment, used every year in more than half a million patients diagnosed with cancer. Planning radiotherapy treatment is an extremely time-consuming task, where the patient's scans are manually marked up by an oncologist, to select precisely the area to direct the radiation to the target. Thinking about how to speed up this laborious task, Dr Rajesh Jena and his team in the Department of Oncology, at the University of Cambridge; and Addenbrooke's Hospital, in collaboration with Microsoft Research, used artificial intelligence and machine learning to train computers to annotate the scans automatically. The project OSAIRIS (Open-Source Artificial Intelligence Radiotherapy Imaging System) has shown how the computers can perform the preparation around 2.5 times faster than a human, saving time for busy clinicians, and allowing patients to receive more effective and faster treatment.

Function

It is a machine learning tool to analyse patient scans and speed up preparation for radiotherapy treatment.
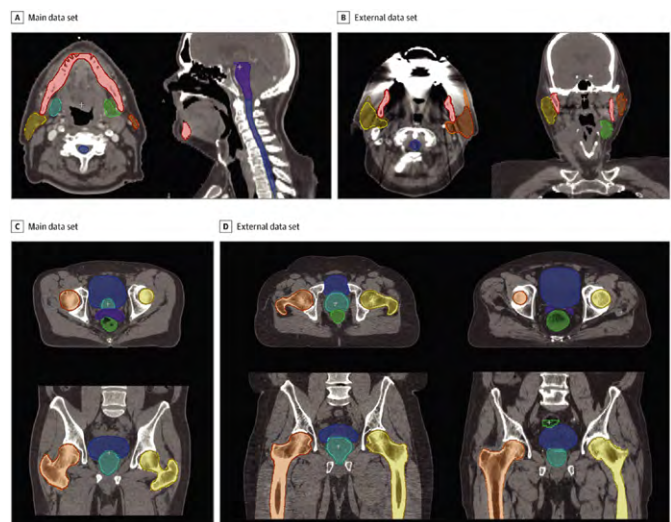
Qualitative evaluation of expert and autogenerated contours on head and neck computed tomography scans. © 2020, Oktay et al., licensed under CC-BY 4.0. Reproduced from JAMA Netw Open. 3, e2027426, https://doi.org/10.1001/jamanetworkopen.2020.27426.

Development process

The project was initially developed in 2012 to commercial standards but subsequently released as an open source repository in 2019. "The key thing that we learned was the difference between software risk, which tends to be the focus of people who do software development engineering, and clinical risk of a piece of software that is open source," says Dr Jena. Even though the original repository from which OSAIRIS was forked had software engineering principles rights, it took more than 18 months of work around the clinical risk in order to turn it into an open source medical device.

Target user

Hospitals that perform radiotherapy treatment.

Comparison to other technologies

"We believe OSAIRIS is one of the first open source software as a medical device deployment," says Dr Jena. Even though there are other software development kits available for a wide set of medical images, none of those are yet ready for a clinical implementation. With OSAIRIS the user gets both the code repository, and also the documentation for a technical file that can be used for medical purposes.

IMPACT

Current use

OSAIRIS has been used in the University Hospitals in Cambridge and in Birmingham. The University College London Hospitals (UCLH) are also implementing OSAIRIS.

Successful stories

OSAIRIS has been running in Addenbrooke's Hospital since October 2020, and at the moment is the standard system used for radiotherapy preparation for two different types of cancers. Every month, around 120 patients benefit from this technology. Dr Jena explains that this preparation stage, which used to take the oncologist about 90 minutes, now takes around 35 minutes.

Open source choice

Dr Jena is passionate about open source tools and he points out that all the research tools developed by his group are submitted as open source. To the best of his knowledge, OSAIRIS is the first open source artificial intelligence in imaging to be created within the NHS. Furthermore, because OSAIRIS is a data-driven AI technology, it learns from patient data.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

Right now, Dr Jena and his team are working in collaboration with Cambridge Enterprise to understand the bureaucracies behind how OSAIRIS can be offered as an open source software. In simple words, although OSAIRIS is open source and technically anyone can implement it, in practice to have it as a medical device, it requires a level of support that is more than would be achieved just by downloading the code.

"We believe OSAIRIS is one of the first open source software as a medical device deployment."

Rajesh Jena

Agriculture and Sustainability
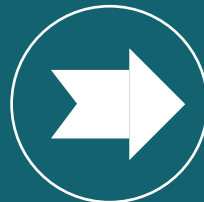
OpenPlant kit

Authors and affiliations
Eftychios Frangedakis, Susanna Sauret-Gueto, Jim Haseloff
Department of Plant Sciences, University of Cambridge, Cambridge, UK

Contact
Eftychios Frangedakis: **e391@cam.ac.uk**
Jim Haseloff: **jh295@cam.ac.uk**

Main publication
Frangedakis E, Guzman-Chaves F, Rebmann M, Markel K, Yu Y, Perraki A, Tse SW, Liu Y, Rever J, Sauret-Gueto S, Goffinet B, Schneider H, Haseloff J. 2021. Construction of DNA tools for hyperexpression in Marchantia chloroplasts. *ACS Synthetic Biology* **10**, 1651−1666.

Sauret-Gueto S, Frangedakis E, Silvestri L, Rebmann M, Tomaselli M, Markel K, Delmans M, West A, Patron N, Haseloff J. 2020. Systematic tools for reprogramming plant gene expression in a simple model, Marchantia polymorpha. *ACS Synthetic Biology* **9**, 864−882.

Website
https://www.openplant.org/

ABOUT THE OPEN-RESOURCE

Background

Plant synthetic biology is a field where engineering principles are applied to design plants with new or enhanced characteristics. Plants are attractive organisms for synthetic biology for many reasons: they can "make their own food" through the photosynthetic process; can be cultivated in large scale at low cost; and have substantial secondary metabolism, that can be exploited to produce a wide range of bioproducts. Plants also have chloroplasts, the organelles where photosynthesis occur, that have the potential to support high levels of transgene expression. OpenPlant, a research initiative part of the UK Synthetic Biology for Growth Programme (additional information can be found here), brought together researchers from the University of Cambridge, John Innes Centre, and the Earlham Institute with the main goals of developing new tools and methods for plant synthetic biology. OpenPlant toolkit is one of the outcomes of the OpenPlant initiative. Eftychios Frangedakis, Research Associate in the Haseloff Lab and developer of OpenPlant toolkit explains that, "*Marchantia polymorpha* was selected as the liverwort testbed thanks to its simplicity as an experimental system."

Function

OpenPlant toolkit consists of a series of resources and techniques that allow both nuclear and/or chloroplast engineering applications primarily in *Marchantia*, but potentially in other plant systems. The toolkit enables the establishment of common standards and the use of this simple plant as a testbed for synthetic biology.

Marchantia polymorpha with gemmae, used for asexual propagation © 2017, Prof Jim Haseloff, licensed under CC-BY 4.0. Reproduced from https://www.openplant. org/marchantia.

Development process

As usual in science, there was a lot of trial and error during the development of OpenPlant toolkit. However, Eftychios points out that thanks to the simplicity of *Marchantia* as an experimental system, trouble-shooting was relatively straightforward.

Target user

Research groups around the world that work with plant systems, but also companies that focus on plant synthetic biology application.

Comparison to other technologies

The main difference of the developed tool is that it is open source, standardised, simple and efficient.
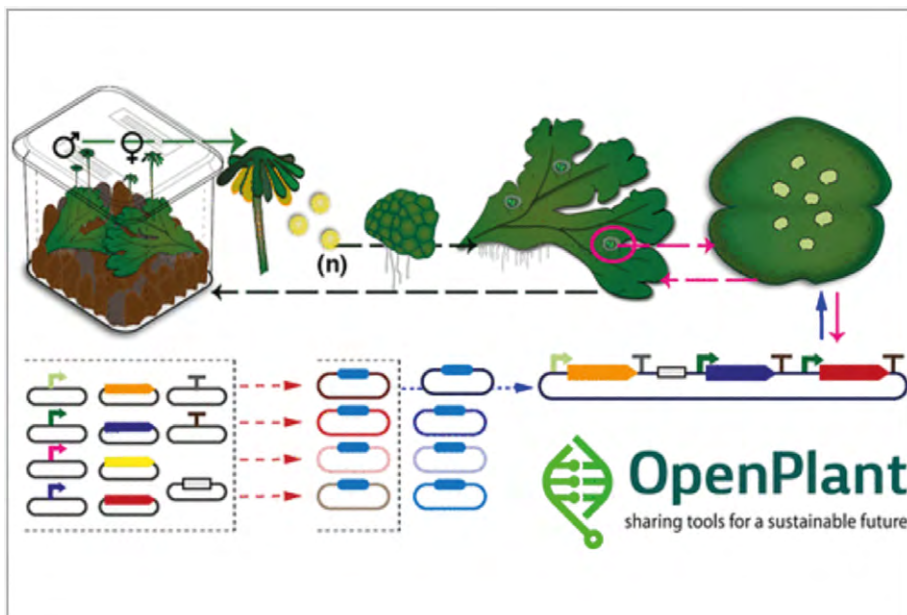
Marchantia life cycle for propagation in the laboratory (sexually through spores and asexually through gemmae). The OpenPlant toolkit contains the Loop assembly vector systems for nuclear and chloroplast transformation and genome editing in Marchantia. Reprinted with permission from ACS Synth. Biol. 2020, 9, 864–882. Copyright 2020 American Chemical Society.

IMPACT

Current use

The OpenPlant toolkit has been adopted mainly by research groups in Europe, USA and Japan, as well as by a UK-based private company. Distribution of the toolkit was initially delayed due to the COVID-19 pandemic, however, more than 20 research groups are currently using the OpenPlant kit, and/or parts of the resource.

Open source choice

"We are strong advocates of open source because it makes science more accessible, reliable and it facilitates and enhances collaboration," said Eftychios. He also explains that due to its open source approach, the distribution of OpenPlant toolkit has been much simpler and users are more willing to adopt the system.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

"We hope that the tools we developed will stimulate research in plant synthetic biology, promote standardisation practices and open science in general."

Eftychios Frangedakis

lowRISC

Area
Agriculture sciences

Launch year
2014

Authors and affiliations
William Drewry[1], Prof Dr Claudia Eckert[2], Dr Gavin Ferris[3], Prof Sir Andy Hopper, CBE FRS FIET FREng[4], Prof Robert Mullins[5], Cyrus Stoller[1]
1 Google, **2** Chair for IT Security, Technical University of Munich, **3** Co-founder and CEO, **4** Independent chair, **5** University of Cambridge

Contact
Robert Mullins:
Robert.Mullins@cl.cam.ac.uk
lowRISC: **info@lowrisc.org**

Website
https://lowrisc.org/
https://opentitan.org

ABOUT THE OPEN-RESOURCE

Background

Continuing advances in semiconductor technology support the construction of ever more capable silicon chips. This has driven many of the recent advances in computer science, artificial intelligence and the growing importance of digital technologies. The lowRISC project started within the Department of Computer Science and Technology in 2014 and was subsequently spun out as a not-for-profit community interest company (C.I.C). It has grown from 3 people and currently employs 30 people in the UK, Switzerland, Canada, Portugal and the U.S. Its goal is to help make open source silicon a reality and ultimately become as ubiquitous as open source software. lowRISC explores how best to develop open hardware designs and they have been refining a collaborative development framework called the "Silicon Commons". This innovative workflow merges open source software development best practices with an industrial-strength, chip-design methodology, and it enables the creation of reusable, high-quality silicon IP by a diverse coalition of corporate and academic partners.

lowRISC's flagship project OpenTitan, chartered in 2018, is the world's first open source silicon root-of-trust (RoT) design and most active collaborative silicon design project. A RoT anchors security at the lowest level in a computer system. It has both logical and physical security protections and it is designed to counter attempts to extract secret information. It stores secret keys, provides accelerated and secure cryptographic functions and maintains the integrity of the system below the operating system level.

Function

lowRISC offers a home for multi-partner projects that produce verified, high-quality hardware designs, documentation, and tools. lowRISC is also a full-stack engineering company and makes significant contributions to the projects it helps to deliver.

Target user

Industry and the broader open source community in need of high-quality hardware designs and tools. It also provides academia access to industrial-quality designs for research and aids the transfer of ideas between academia and industry. It has already been the basis of numerous papers that evaluate new security tools and defenses from a range of different academic groups.

Comparison to other technologies

lowRISC supports and maintains projects as an independent not-for-profit organization. It maintains a strictly enforced governance framework, exhaustive documentation, shared test and development infrastructure and a collaborative development workflow. Companies support lowRISC in order to help deliver complex open source projects. They benefit by sharing costs, a framework for collaboration and ongoing maintenance and support.

Delivering open source hardware is challenging and historically has not been undertaken at the scale, or had the impact, of open source software projects. This has partly been due to the resources needed to fund complex multi-year development and produce high-quality designs. lowRISC has worked hard to develop a viable business model in order to work at the necessary scale. In addition, there has been a very clear focus on delivery, governance structures and process, high-quality documentation and training, industrial-quality design verification (DV) and ensuring the existence of a fully-open repository. These have all proved to be key in ensuring the project is capable of delivering complex projects while maintaining the highest standards in terms of quality and correctness. Designs are also carefully designed to be modular and can be reconfigured as required for discrete designs or on-chip (integrated) uses or completely different applications.

IMPACT

Current use

The OpenTitan (additional information can be found here) standalone chip top-level design is now complete and engineering sample chips are expected by the end of 2023. This is the culmination of a large coordinated effort from a community of commercial and academic partners - including Google, G+D Mobile Security, ETH Zurich, Nuvoton, Winbond, Seagate, Western Digital, Rivos, and zeroRISC, plus a number of independent contributors. The design consists of 1.5M+ lines of code including 500k lines describing the hardware itself. OpenTitan's broad community has been critical to its success with more than 140 contributors to the code base.

In addition to OpenTitan, lowRISC hosted designs and processors have also been extended and incorporated into many other projects and products. This includes the very popular Ibex (additional information can be found here) microcontroller which has been adopted by Microsoft and extended with CHERI, a joint research project of SRI International and the University of Cambridge, to create cheriot-ibex.

Open source choice

lowRISC has found that the open source approach works particularly well for designing high-quality, complex and secure systems. It naturally encourages transparency and permits auditable designs. The development process and history is also public and can be explored. Open source also supports the goal of raising the bar for security by offering a permissively licensed (Apache2) implementation freely available to all of industry, this reduces barriers to the adoption of state-of-the-art hardware security practices and encourages further innovation in this space.

More broadly, lowRISC hopes that its approach will serve as a template to help others develop similar initiatives in other disciplines to help populate a larger technology commons. Knowledge and adaptable building blocks can then be used from this pool to help produce solutions to some of our most challenging problems as quickly and efficiently as possible.

In vivo sensing of pH in tomato plants using a low-cost and open source device for precision agriculture

Area
Agriculture sciences

Launch year
2021

Authors and affiliations
Antonio Ruiz-Gonzales, Harriet Kempson, Jim Haseloff
Department of Plant Sciences, University of Cambridge, Cambridge, UK

Contact
Antonio Ruiz-Gonzalez:
a.gonzalez.16@alumni.ucl.ac.uk
Harriet Kempson: **hljk2@cantab.ac.uk**
Jim Haseloff: **jh295@cam.ac.uk**

Website
https://www.hackster.io/antonio-ruiz

ABOUT THE OPEN-RESOURCE

Background

Precision agriculture can provide farmers with valuable information on a range of aspects of their crops, such as nutrient levels, presence of pests and diseases, and abiotic stress. This data allows them to apply appropriate management strategies, helping to enhance crop yield. Although in the past few years remote sensing technologies have been advancing and becoming widespread, current methods for monitoring plant biomarkers directly are still very scarce. Thinking about the potential of these methods, Antonio Ruiz, Research Associate in the Haseloff Lab, at the Department of Plant Sciences, developed a low-cost electrochemical sensor to monitor pH of xylem sap in plants. "We focused on pH as it is quite a well reported biomarker, especially for abiotic stress. Sensors that measure moisture in soil are widely available, but it might not necessarily reflect on the plant status. The plant might have the ability to endure a bit longer in the soil that is dry, and you might be able to save some water, which is in high need in some places," said Antonio.

Function

It is an electrochemical sensor designed to monitor the pH in xylem sap continuously.

Development process

The first step in the sensor development was the material choice to ensure that the sensor could be used for long-term measurements and would be compatible with the plant organism. Antonio and his colleagues decided to deposit ruthenium oxide-based nanoparticles on top of the copper electrodes, as this material has been shown to be more stable and biocompatible than other options available. Also, the presence of ruthenium oxide is responsible for the H+ sensitivity, the ion measured to determine pH. When the first tests were performed with the sensor, the data generated had high noise rates, resulting in inaccuracies on the measured pH. To improve the stability and reduce the noise, the developers applied a cellulose-based coating to the electrodes. The final device was able to monitor pH in the xylem sap of tomato plants for at least 5 hours, with low noise.

Target user

Researchers and farmers aiming to assess plant abiotic stress *in vivo* directly.

Comparison to other technologies

Lab-bench pH meters with the reference probe suspended in a solution are common and well tested pieces of equipment. However, there are not many studies reporting devices to measure pH directly in the plant xylem. Antonio explains that most of the publications available use very destructive processes, extracting the sap, and then measuring the pH afterwards with a common pH meter. "We took the precision process of the sensors, which is normally done with benchmark equipment, to an easy setting that I managed to assemble at home, during lockdown. I don't think it's reported elsewhere of any other low-cost devices which are similar to ours," explains Antonio. Another new aspect that this work has highlighted was the healing process that takes place between the sensor and the plant tissue, a response that is not well reported in the literature, and it is one of the major challenges in the field of implanted biosensors.
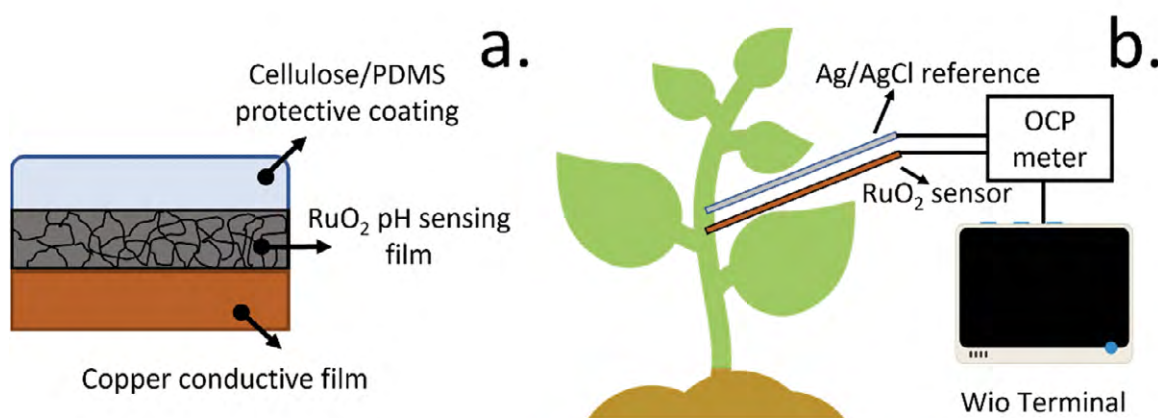
(a) Schematic representation of sensor structure, and (b) its implantation inside a tomato plant. The open circuit potential was measured using a Wio terminal device (a microcontroller with Wi-Fi support). © 2022, Ruiz-Gonzales et al., licensed under CC-BY 4.0. Reproduced from Biosensors 12, 447, https://doi.org/10.3390/bios12070447?.

Current use

At the moment the device has been used only by the Haseloff Lab, but Antonio said that there have been a lot of comments and views on his hackster webpage (additional information can be found [here](#)), where the project was made openly available.

Open source choice

"Open source is the quickest way to make an impact in this field. From my point of view, you can see how people benefit a lot more when things are open and transparent to the community," says Antonio. He points out the fact that the project has been published as a scientific paper and in hackster (a large hardware developer community) as it was very important to reach out to a broader audience. "We did get a lot of views from people that are not necessarily academics or researchers and you wouldn't get that otherwise. You'd be surprised to see how immense the world of developers is outside the research paper."

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

Antonio's goal is to make the pH device more applied, trying to translate the fundamental science on sensors to an applied approach in precision agriculture.

"Open source is the quickest way to make an impact in this field. From my point of view, you can see how people benefit a lot more when things are open and transparent to the community."

Antonio Ruiz-Gonzales

A low-cost and open source solution to automate imaging and analysis of cyst nematode infection assays for *Arabidopsis thaliana*

Authors and affiliations
Olaf Prosper Kranse[1], Itsuhiro Ko[1,2], Roberta Healey[1], Unnati Sonawala[1], Siyuan Wei[1], Beatrice Senatori[1], Francesco De Batté[1], Ji Zhou[3,4], Lawrence Percival-Alwyn[4], Sebastian Eves-van den Akker[1]

[1] Department of Plant Sciences, The Crop Science Centre, University of Cambridge, Cambridge, UK [2] Plant Pathology Department, Washington State University, Pullman, WA, USA [3] Jiangsu Collaborative Innovation Center for Modern Crop Production Co-Sponsored By Province and Ministry, Academy for Advanced Interdisciplinary Studies, Nanjing Agricultural University, Nanjing, China [4] Cambridge Crop Research, National Institute of Agricultural Botany (NIAB), Cambridge, UK

Contact
Olaf Kranse: **ok297@cam.ac.uk**
Sebastian Eves-van den Akker: **se389@cam.ac.uk**

Website
https://github.com/OlafKranse/A_low_cost_imaging_tower

ABOUT THE OPEN-RESOURCE

Background

Plant-parasitic nematodes are responsible for considerable losses in crop yield. However, the current screening methods used to phenotype nematode infections are slow, limiting the knowledge that can be generated in the plant pathology field. "It all started off as a side project, but then when we realised the potential output of the machinery, it has become my main focus," says Olaf Kranse, a postgraduate student in the Plant-Parasite/Pathogen Interactions group, at the Crop Science Centre. To study nematode parasitism, the group utilises the ability of *Heterodera schachtii* (the beet cyst nematode) to infect the model plant *Arabidopsis thaliana*. Olaf's focus is to determine the frequency of infection for various host genotypes. While analysing some *Arabidopsis* mutant lines as part of his PhD project, Olaf realised that some of the plants had reduced root area, which could be an important factor for infection. The challenge would be to normalise infection to the root surface areas in a quick way, as manual measurement of the root surface area is extremely time consuming. While Olaf was playing with some of the root images, he noticed that it was possible to see the nematodes clearly on these plates. "And if you could also automatically count the nematodes? Problem solved," says Olaf. The outcome is a system that allows the user to access root surface area, and nematode numbers and sizes. Previously the nematodes were counted manually using a microscope, which is a very low throughput technique. In Olaf's opinion, he was lucky that nobody else developed a similar tool before, as it has probably been doable for a long time.

Function

This open source project is by design a low-cost easy-to-build and -use image analysis system to measure root area and phenotype nematode infection. But it does more: essentially, it can be used to image anything that fits in a 5 cm Petri dish, i.e., it could potentially be used for measuring plant growth over time, or any other system that fits in the tool.

Development process

In the initial development stages, the imaging system was a desk lamp with a camera taped to it, to assess the possibility of capturing a photo of a plate. As Olaf and the research group saw potential in the rudimentary system, the next step was to design a more complex imaging system, consisting of a lens mounted to a camera, which is connected to a Raspberry Pi (a small, affordable computer). These imaging components are then assembled onto a custom 3D-printed "tower". Even though Olaf had some experience with 3D printing before, designing pieces that slot into each other perfectly showed to be challenging as the printing system has imperfections. Another challenge faced by the developers was related to the knowledge needed in the engineering field. A good lesson learned by Olaf was to get more people involved in the development process, as an extra person looking into it with a different perspective can save a lot of time and bring new ideas.

Target user

As this imaging system is optimised for small plants (i.e. *Arabidopsis*), it potentially limits its application to researchers working on other plant systems. The target user is anyone who needs consistent images of tissue culture in 5 cm petri dishes.

Comparison to other technologies

The use of imaging analysis systems is becoming more popular in the biological sciences field. Yet, for plant parasitic nematode studies, this is the only one available at the moment. Olaf presented this tool in 2021 at a nematology conference and the feedback was very positive "people said, finally, we don't have to count nematodes under the microscope anymore, because it takes a lot of time to do this."
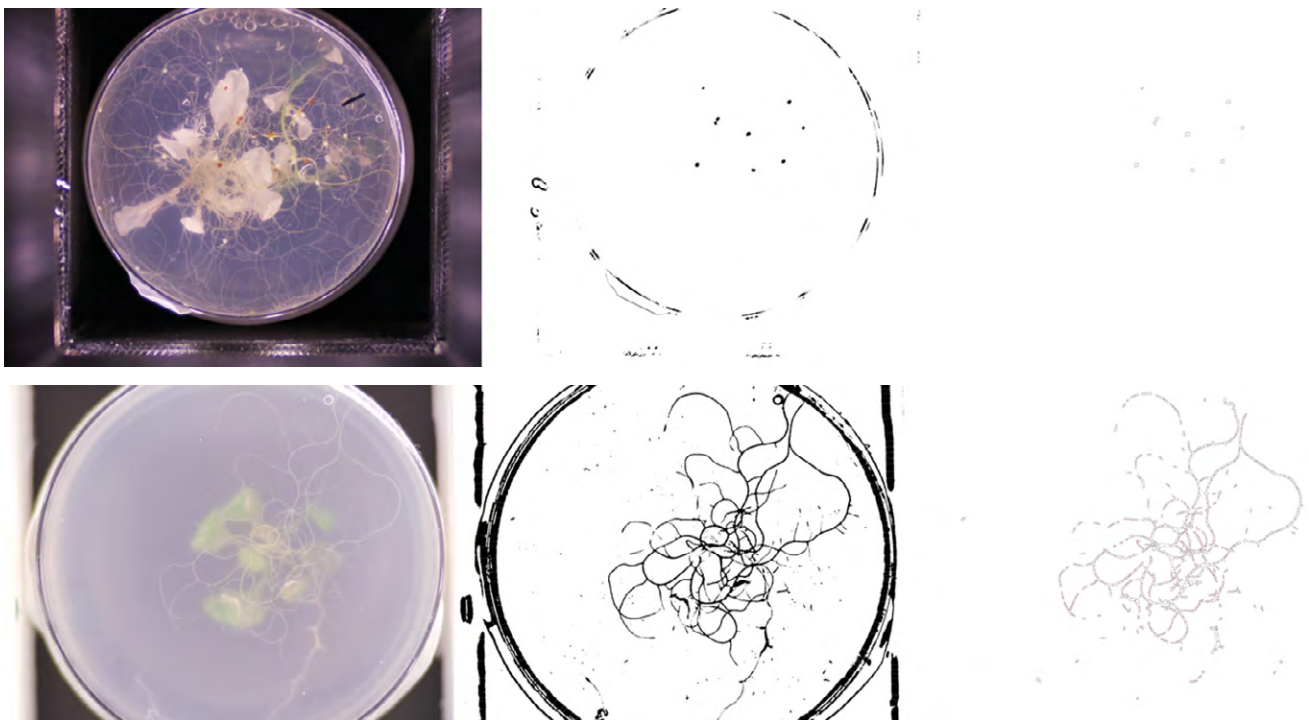
Example of an image taken by the imaging system, evidencing the nematodes (top) and the plant roots (bottom).
© 2022, The Plant-Parasite/Pathogen Interactions group, licensed under CC-BY 4.0 (individual, open license).

Current use

As pointed out before, the imaging system is optimised for Arabidopsis. Currently, just the Plant-Parasite/Pathogen Interactions group at the University of Cambridge is using it, but more researchers in the area are getting interested in it. Olaf and his colleagues are thinking about future versions of the machine that could be used in crops, opening its use to crop research too.

Open source choice

There were different reasons why Olaf and his colleagues decided to make the imaging system open source. "The entire idea behind this was to make it affordable because in my opinion it's important that any member of the academic community has access to these tools." On the other hand, Olaf points out that there is the argument that if a technology is commercialised, the throughput and outreach are potentially higher.

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

Now that the Plant-Parasite/Pathogen Interactions group found an efficient way to take images of roots and nematodes, the next, bigger bottleneck is analysing the images, as some manual verification is required. Machine learning approaches may be the next step to increase screening speed. Furthermore, the group strives to expand the use of the imaging system to crop systems, allowing those studying crop parasitism to be able to use the platform.

"In my opinion it's important that any member of the academic community has access to these tools."

Olaf Prosper Kranse

Large-scale plant phenotyping and trait analysis toolkits

Area
Agriculture sciences

Contact
Ji Zhou:
ji.zhou@niab.com, Ji.Zhou@NJAU.edu.cn

GENERAL OVERVIEW

Background

Plant phenotyping is the process of characterising visible traits in plants such as height, leaf colour, vegetation indices, and canopy surface area. It can assist researchers to understand the relationship between genes and these observable characteristics, valuable information to accelerate plant breeding programmes. However, plant phenotyping under field conditions is commonly a bottleneck in genotype–phenotype studies as it is costly, labour-intensive and prone to error. Large-scale phenotyping and trait analysis solutions can contribute to alleviate this bottleneck. Prof Ji Zhou, Head of Data Sciences Department at Cambridge Crop Research NIAB, focuses on developing large-scale phenotypic analytic solutions using computer vision and artificial intelligence techniques. Below, three of these phenotyping and analytic tools are described: SeedGerm, AirMeasurer, and CropQuant-3D. Prof Zhou's labs in the UK and China (Nanjing Agricultural University) are always looking for partners who are passionate about sharing, or collaborators that could benefit from the research-based toolkits developed by his groups.

Target user

Researcher communities and commercial use.

Open source choice

"We are computational biologists, and open software is more secure and stable than proprietary software as we could view and modify the source code to tailor analytic solutions for trait analysis. Also, we could correct errors based on the original source code," says Prof Zhou. Another advantage of being open source is the modular design approach, and hence researchers can use just part of the modules for their own research needs.

SeedGerm

Area
Agriculture sciences

Launch year
2022

Authors and affiliations

Joshua Colmer[1], Carmel M. O'Neill[2], Rachel Wells[2], Aaron Bostrom[1], Daniel Reynolds[1], Danny Websdale[1], Gagan Shiralagi[2], Wei Lu[3], Qiaojun Lou[4], Thomas Le Cornu[1], Joshua Ball[1], Jim Renema[5], Gema Flores Andaluz[5], Rene Benjamins[5], Steven Penfield[2], Ji Zhou[6,7]

1 Engineering biology, Earlham Institute, Norwich Research Park, Norwich, UK **2** Crop Genetics, John Innes Centre, Norwich Research Park, Norwich, UK **3** College of Engineering, Nanjing Agricultural University, Nanjing, China **4** Shanghai Agrobiological Gene Center, Shanghai Academy of Agricultural Sciences, Shanghai, China **5** Syngenta Seeds BV, Enkhuizen, the Netherlands **6** State Key Laboratory of Crop Genetics and Germplasm Enhancement, Plant Phenomics Research Center, Jiangsu Collaborative Innovation Center for Modern Crop Production co-sponsored by Province and Ministry, Nanjing Agricultural University, Nanjing, China **7** Cambridge Crop Research, National Institute of Agricultural Botany, Cambridge, UK

Main publication

Colmer J, O'Neill CM, Wells R, Bostrom A, Reynolds D, Websdale D, Shiralagi G, Lu W, Lou Q, Le Cornu T, Ball J, Renema J, Andaluz GF, Benjamins R, Penfield S, Zhou J. 2020. SeedGerm: a cost-effective phenotyping platform for automated seed imaging and machine-learning based phenotypic analysis of crop seed germination. *New Phytologist* **228**, 778-793.

Website

https://github.com/Crop-Phenomics-Group/SeedGerm/releases

Funding

ABOUT THE OPEN-RESOURCE

Background

Effective seed germination and establishment are crucial characteristics for plant research and agricultural production. Routine germination scoring is still frequently based on visual inspection, but in large-scale experiments this task is time-consuming and prone to mistakes. Thinking about how to speed up and reduce errors in seed phenotyping methods, Prof Ji Zhou and collaborators developed the SeedGerm system, an imaging tool that could have wide ranging applications in both research and industrial contexts.

Function

SeedGerm is a platform designed for automating seed imaging and high throughput germination analysis, and it works in a variety of crop seeds. It combines cost-effective hardware and open source software for seed germination experiments, automated seed imaging, and machine-learning based phenotypic analysis. The software can process multiple image series simultaneously and produce reliable analysis of germination- and establishment-related traits, in both comma-separated values (CSV) and processed images (PNG) formats.

Development process

Prof Zhou explains that SeedGerm development was an iterative approach for hardware and software development. To make SeedGerm results reliable and reproducible, a lot of steps needed to be optimised during the development process. A software calibration has been added to the system to improve accuracy for low-quality images. Also, a number of tests using different sowing distances have been performed, and the results found that a distance of at least 1 cm between seeds improves the accuracy of the analysis. As expected when working with imaging processing, the task can be highly demanding on computing resources. Therefore, the developers do not recommend processing multiple image series simultaneously on an average computer.

Comparison to other technologies

SeedGerm is the first open scientific platform that combined imaging hardware (powered by Raspberry Pi, a computer and tailored control software) and automated trait analysis software (using a range of machine learning and computer vision techniques) to analyse germination-related traits that are key to seed science research and the assessment of seed vigour.
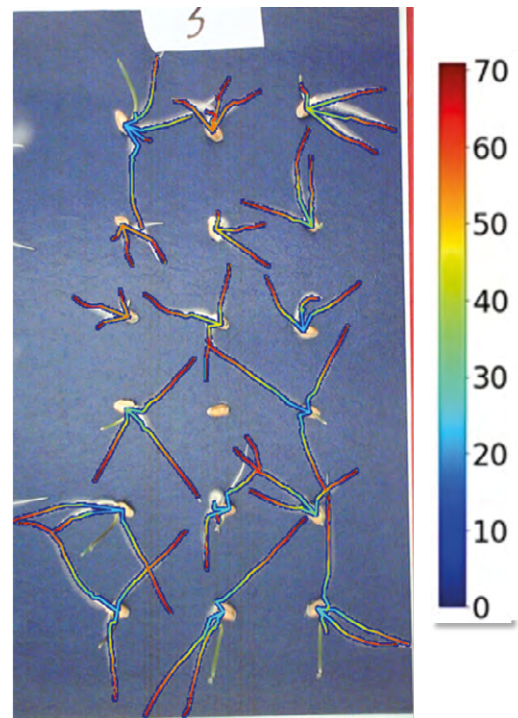
The pseudo colour indicated germination time, which enabled to assess seed germination related traits with temporal information. © 2023, Ji Zhou, licensed under CC-BY 4.0.

IMPACT

Current use

The system has been applied to a range of germination experiments for five important crop species: tomato, pepper, barley, and maize, and it was able to match seed specialists' observations for the scoring of germination. Also, SeedGerm was successfully used to characterise morphological traits, such as seed size, width and length, providing insights into the physiological process by which seeds germinate. As far as the developers know, there are many academic and industrial research groups using the system, including John Innes Centre (UK), Nanjing Agricultural University (China), NIAB (UK),

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

As the morphology of different crop seeds vary greatly, it can be difficult to transfer some morphological measurements from one species to another. Therefore, the application of online learning or transfer learning tools may be advantageous for future developments of SeedGerm.

The application of online learning or transfer learning tools may be advantageous for future developments of SeedGerm.

CropQuant-3D

Area	Launch year
Agriculture sciences	2021

Authors and affiliations

Yulei Zhu[1], Gang Sun[1], Guohui Ding[1], Jie Zhou[1], Mingxing Wen[1,2], Shichao Jin[1], Qiang Zhao[3], Joshua Colmer[4], Yanfeng Ding[1], Eric S. Ober[5], Ji Zhou[1,5]

1 State Key Laboratory of Crop Genetics and Germplasm Enhancement, College of Engineering, College of Agriculture, Plant Phenomics Research Center, Academy for Advanced Interdisciplinary Studies, Jiangsu Collaborative Innovation Center for Modern Crop Production co-sponsored by Province and Ministry, Nanjing Agricultural University, Nanjing, China **2** Zhenjiang Institute of Agricultural Science in Hill Area of Jiangsu Province, Jurong, China **3** National Center for Gene Research, CAS Center for Excellence in Molecular Plant Sciences, Chinese Academy of Sciences, Shanghai, China **4** Earlham Institute, Norwich Research Park, Norwich, UK **5** Cambridge Crop Research, National Institute of Agricultural Botany (NIAB), Cambridge, UK

Main publication

Zhu Y, Sun G, Ding G, Zhou J, Wen M, Jin S, Zhao Q, Colmer J, Ding Y, Ober ES, Zhou J. 2021. Large-scale field phenotyping using backpack LiDAR and CropQuant-3D to measure structural variation in wheat. *Plant Physiology* **187**, 716-738.

Website

https://github.com/The-Zhou-Lab/LiDAR/releases

ABOUT THE OPEN-RESOURCE

Background

Light detection and ranging (LiDAR) is a remote sensing technique that sends out laser pulses and then measures the time it takes for the laser pulses to return. Using this technique, LiDAR collects 3D point clouds (the collections of 3D points) that capture the spatial information of objects or surfaces. In plant phenotyping, this technology can provide information on plant morphological and structural traits. Mobile, or backpack LiDAR, is advantageous for large-scale field experiments phenotyping as it is easy to transport and use. However, the widespread use of LiDAR-based phenotyping has been limited by the capacity to process and evaluate the massive datasets generated by this technique, especially in average computing powers. Prof Zhou and collaborators addressed this issue by developing CropQuant-3D, which processes large LiDAR-acquired 3D point cloud data and consists of original algorithms packaged into user-friendly graphical user interface (GUI) software (a user interface that uses mouse, icons, and menus) to output multiple 3D canopy traits.

Function

It is a large-scale phenotyping solution that combines a commercial backpack LiDAR device and the analytic CropQuant-3D software. The use of LiDAR can acquire millions of 3D points to represent spatial features of crops, and CropQuant-3D can extract meaningful canopy-level performance traits from large, complex point clouds.

Development process

CropQuant-3D was developed through a collaboration between NIAB, the Chinese Academy of Sciences (CAS), and Nanjing Agricultural University. Some 3D point clouds analysis algorithms were jointly developed and implemented in the UK and China, followed by in-field testing and improvement back in the two countries.

Comparison to other technologies

The CropQuant-3D open source solution shares its source code with the community, including not only access to the software, but also the data analysis approach that Zhou's lab established for processing large-scale 3D point cloud datasets.

Although mobile LiDAR is more affordable than other large-scale phenotyping systems, Prof Zhou points out that the equipment is still relatively expensive.
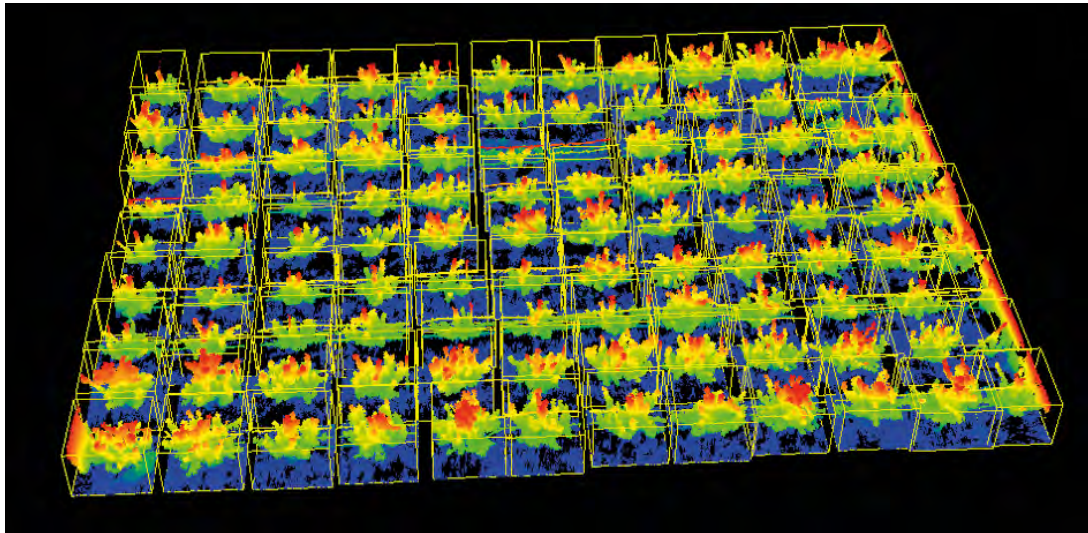
3D segmentation of apple trees using CropQuant-3D, pseudo colour applied to 3D points according to a height scale bar (0−250+ cm), indicating trees' spatial features. © 2023, The Zhou Laboratory, licensed under CC-BY 4.0 (individual, open license).

IMPACT

Current use

The technology has been employed to screen the effect of a range of nitrogen treatments on crop growth and structural variation in wheat varieties, for breeding and agronomic purposes studies. The studies were performed both at NIAB (UK), and Nanjing Agricultural University (China). Recently, CropQuant has been licenced and commercialised by a leading Agri-Tech company in Far East Asia. Several academic and industrial research groups are using the platform, including Nebraska-Lincoln University (UK), Nanjing Agricultural University (China), NIAB (UK), and ZealQuest Ltd. (Shanghai; additional information can be found here).

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

Some colour- or spectral-related features in plants (e.g., senescence of the lower canopy or water deficit), were not intended to be addressed by CropQuant-3D software when it was created. Therefore, adjustments to how LiDAR is used are required to capture such traits. The next steps of the research will also further broaden the use of CropQuant-3D, enabling the algorithms created for wheat to be applied to dealing with biological issues in other crop species.

Prof Zhou is looking for technology developers and academic partners who are interested in 3D trait analysis (from plant level to population level), as well as interested in sharing and jointly benefiting the plant research community.

AirMeasurer

Area
Agriculture sciences

Launch year
2022

Authors and affiliations
Gang Sun[1], Hengyun Lu[2], Yan Zhao[2], Jie Zhou[1], Robert Jackson[3], Yongchun Wang[2], Ling-xiang Xu[1], Ahong Wang[2], Joshua Colmer[4], Eric Ober[3], Qiang Zhao[2], Bin Han[2], Ji Zhou[1,3]

1 State Key Laboratory of Crop Genetics and Germplasm Enhancement, Academy for Advanced Interdisciplinary Studies, Jiangsu Collaborative Innovation Center for Modern Crop Production co-sponsored by Province and Ministry, Nanjing Agricultural University, Nanjing, China **2** National Center for Gene Research, CAS Center for Excellence in Molecular Plant Sciences, Chinese Academy of Sciences, Shanghai, China **3** Cambridge Crop Research, National Institute of Agricultural Botany (NIAB), Cambridge, UK **4** Earlham Institute, Norwich Research Park, Norwich, UK

Main publication
Sun G, Lu H, Zhao Y, Zhou J, Jackson R, Wang Y, Xu L-x, Wang A, Colmer J, Ober E, Zhao Q, Han B, Zhou J. 2022. AirMeasurer: open source software to quantify static and dynamic traits derived from multiseason aerial phenotyping to empower genic mapping studies in rice. *New Phytologist* **236**, 1584-1604.

Website
https://github.com/The-Zhou-Lab/UAV/releases/

ABOUT THE OPEN-RESOURCE

Background

Unmanned aerial vehicles (UAV) such as drones, have become more popular for field-based plant phenotyping in the last few years due to their portability, adaptability, and lower cost compared to other phenotyping approaches. Most of the studies using UAV focus on collecting data at a specific time, often miss the dynamic nature of plant growth and development. Another limitation in most of the studies is related to how to extract meaningful information from the images collected with UAV. Thinking about how to acquire high-quality data at key plant growth stages, Prof Ji Zhou and collaborators developed AirMeasurer.

Function

AirMeasurer is an open source and expandable platform that combines automated image analysis, machine learning and dynamic phenotyping algorithms to perform trait analysis using 2D/3D aerial imagery acquired by low-cost drones. It generates a range of static and dynamic traits, including crop height, canopy coverage, vegetative indices, and their growth rates, which can be used to screen varieties, identify genetic variants associated with target traits using genetic mapping, and explore new candidate genes that are key to crop improvement.

Development process

Similar to CropQuant-3D, AirMeasurer was developed through a collaboration between NIAB, the Chinese Academy of Sciences (CAS), and Nanjing Agricultural University. The researchers performed a range of field experiments in different locations in China and in the UK, to make sure that the results obtained were reproducible in different environments. During the tests, the group was able to access possible limitations in the platform, including the fact that UAVs cannot be operated in unstable weather (such as high or gusty wind, rainfall, or heavy fog); and how to try to mitigate image colour variation due to changes in light conditions.

Comparison to other technologies

The main advantage that AirMeasurer brings compared to other technologies available is the dynamic phenotypic analysis, producing static and dynamic traits using fitted-growth-profiles that were previously difficult to generate under complex field conditions.
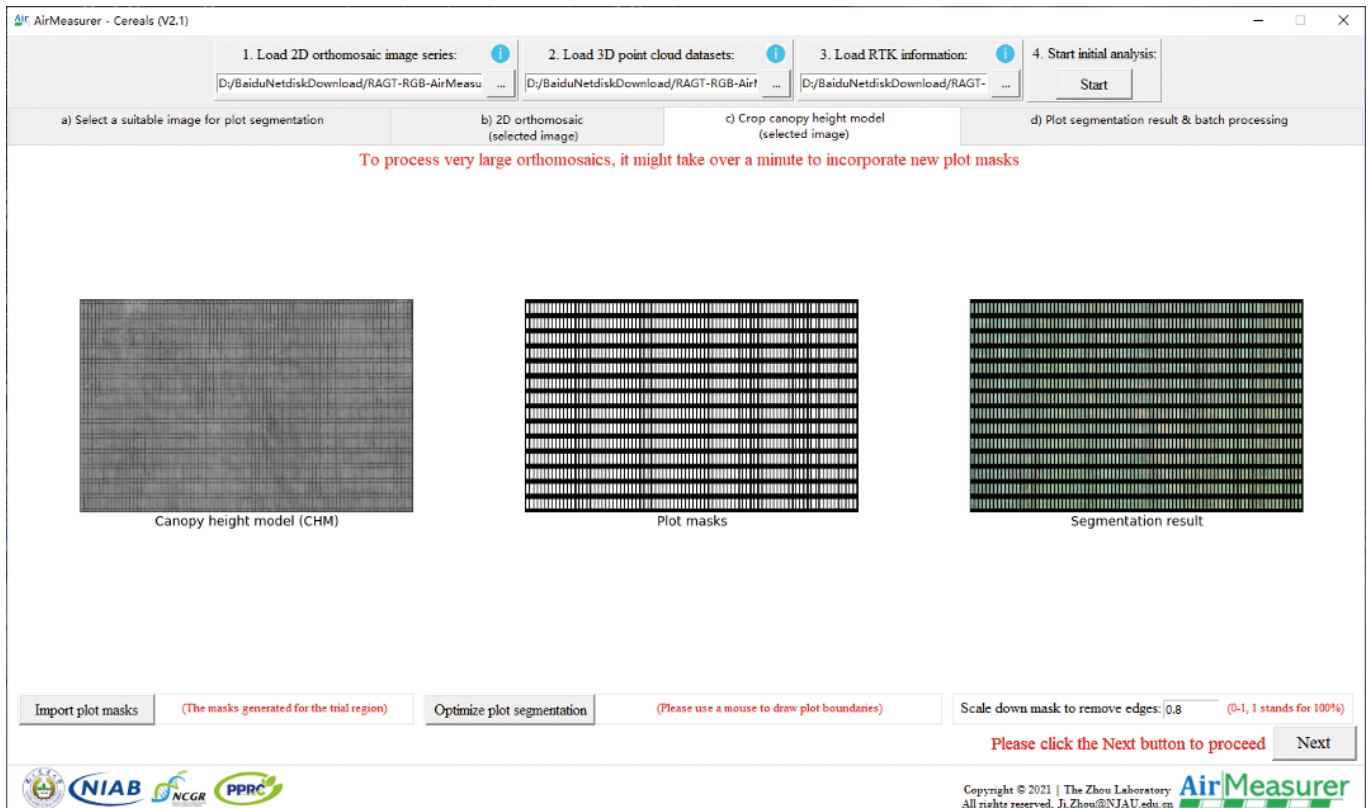
AirMeasurer used to generate a field-level plant canopy height model (CHM) and plot masks for thousands of 12-m yield plots at RAGT's UK field trial centre, with small changing-seeds plots removed. © 2022, The Zhou Laboratory, licensed under CC-BY 4.0 (individual, open license).

IMPACT

Current use

The platform has been applied to studies in sites located in both China and in the UK, covering over 5,000 rice/wheat genotypes from 2018 to present. Recently, it has been employed in Bayer Crop Sciences' (US) global G4T programme (additional information can be found here), and the UK based company RAGT seeds (additional information can be found here) started to use the AirMeasurer platform to process thousands of wheat yield plots to quantify performance traits that were highly correlated with yield production and hence, the yield prediction in the field. CGIAR (additional information can be found here), a leader in global research partnership for food-security, will trial the platform in their programmes too.

Graphic user interface (GUI) of AirMeasurer when batch processing a series of 2D orthomosaics and 3D point clouds for 2D/3D trait analysis of thousands of 12-m yield plots at the RAGT field trial in the UK. © 2023, The Zhou Laboratory, licensed under CC-BY 4.0 (individual, open license).

GOING FORWARD - WHERE TO IN THE NEXT 3-5 YEARS?

Even though AirMeasurer has already shown its valuable advance in dynamic aerial phenotyping, Prof Zhou explains that there is potential to explore further applications of dynamic phenotyping (e.g., timing and duration of phenotypic changes) in genetic mapping and molecular marker identification. Therefore, it will help scientists to gain insights into the genetic makeup of the studied crops, to understand the inheritance of traits, and potentially to discover genes responsible for certain desirable traits. Further developments that could be included in AirMeasurer are the analysis of more specific traits, difficult to analyse by conventional phenotyping approaches. For example, it could be applied for selecting specific flowering characteristics, and grain-filling timing. The developers also see a big potential to use AirMeasurer not just in rice, but in other crops such as wheat.

The main advantage that AirMeasurer brings, compared to other technologies available, is the dynamic phenotypic analysis.
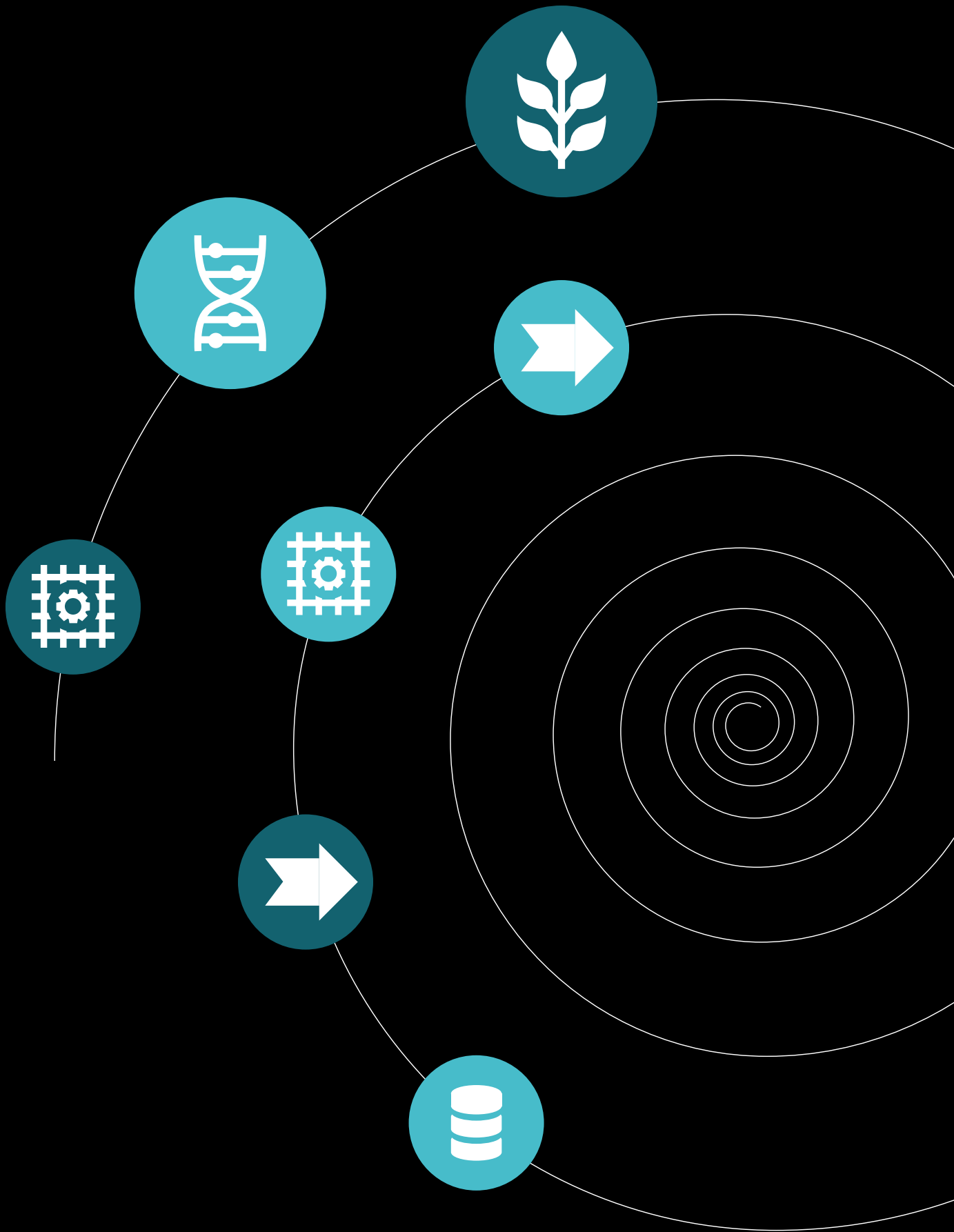
The Engineering Biology Interdisciplinary Research Centre (EngBio IRC) is a centralised hub for Engineering Biology research at the University of Cambridge. It brings together researchers, commercial partners and external collaborators. It supports researchers working across disciplines - at the intersections of biology, engineering, computer sciences, design and bioethics. The EngBio IRC was established in 2013 to advance the University of Cambridge as a nationally and internationally recognised centre of excellence in engineering biology.

Contact

Engineering Biology Interdisciplinary Research Centre

Department of Biochemistry
Sanger Building
Tennis Court Road
Cambridge
CB2 1GA

www.engbio.cam.ac.uk

coordinator@engbio.cam.ac.uk