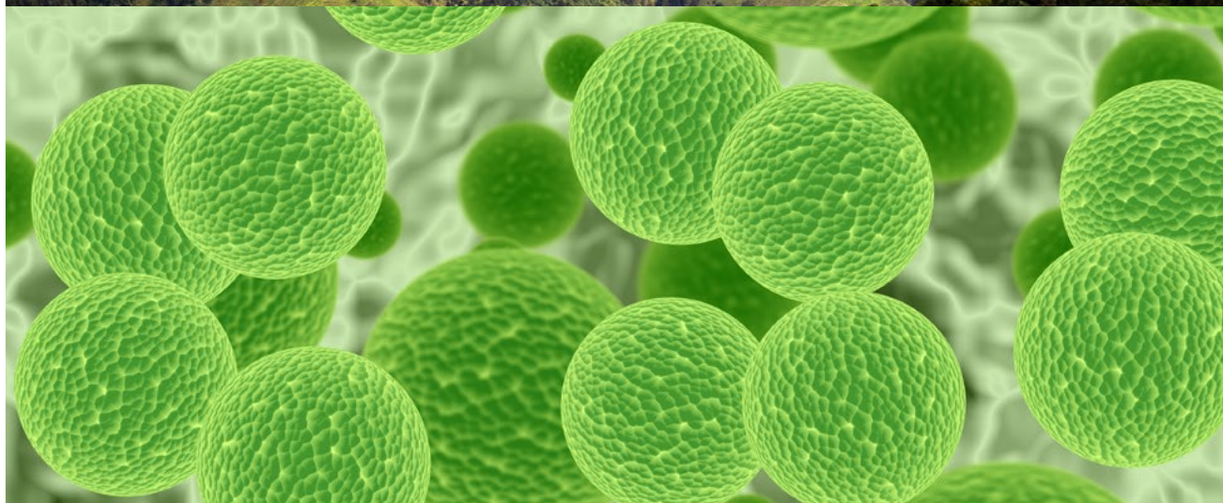
Innovate

17 - 19 November 2020



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Key themes

Fundamental research

Microbiomes and health

Conservation and Biodiversity

Agriculture and food security

Genomes and evolution

Genomics for precision medicine

Applications and tools

Sequencing tools, techniques and platforms

Bioinformatic software and tools

Data storage, visualisation and sharing

Automation platforms for molecular and synthetic biology

Scientific training

Digital Biology

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Clavijo Group

Complex crop genome assembly

The group specialises in complex genome assemblies, where the current state-of-the-art methods are still challenged to produce reliable references, for example to accurately reconstruct multiple copies of genomic regions with high similarity, such as repetitions or diverged haplotypes. The analytical methods and tools developed by the group enable concurrent analysis of information from different sequencing technologies, integration of genomic and genetic data from markers and genetic maps, comparative genomics and identification of genomic markers associated with specific traits of interest.

Interested in connecting with:

Academic groups and biotech companies interested in assembling complex genomes to identify genetic mechanisms of important agricultural traits.

Bernardo Clavijo
Bioinformatic Algorithms Group Leader

Specific expertise

Gonzalo Garcia Accinelli
Assembly methods development and assembly quality control

Jon Wright
Wheat genomics and methods testing

Ben Ward
Population genomics and genetic variability

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Davey Group

E-Infrastructure

The group specialises in developing bioinformatics servers and repository platforms for data and software distribution, publication and large-scale data visualisation. The Davey group focuses on building infrastructure to best manage, represent and integrate data for knowledge sharing. This includes exploring new hardware, algorithms and methodologies to develop tools for life science informatics.

Interested in connecting with:

Academic researchers and breeders interested in utilising wheat data in agriculture sector, and companies developing computer graphics and application processing.

Robert Davey
Head of Research e-Infrastructure

Specific expertise

Felix Shaw
Fish trait image recognition and machine learning

Xingdong Bian
Wheat data management for field trials, genomics and phenomics (Designing Future Wheat and Grassroots)

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Leggett Group

New methods for in-field and real-time sequencing

The group is focussed on developing methods (primarily software, but also wet lab) to take advantage of new sequencing advancements, particularly in the areas of in-field sequencing, real-time analysis and nanopore technology. Applications include species classification, antimicrobial resistance analysis and metagenome assembly in clinical and environmental samples. The group has analysed diverse samples from sources including the human gut, oceans, rivers, air and soil.

Interested in connecting with:

Academic and industry researchers, and government bodies interested in developing computational tools and pipelines for applications in agritech, biotech, and pharma sectors.

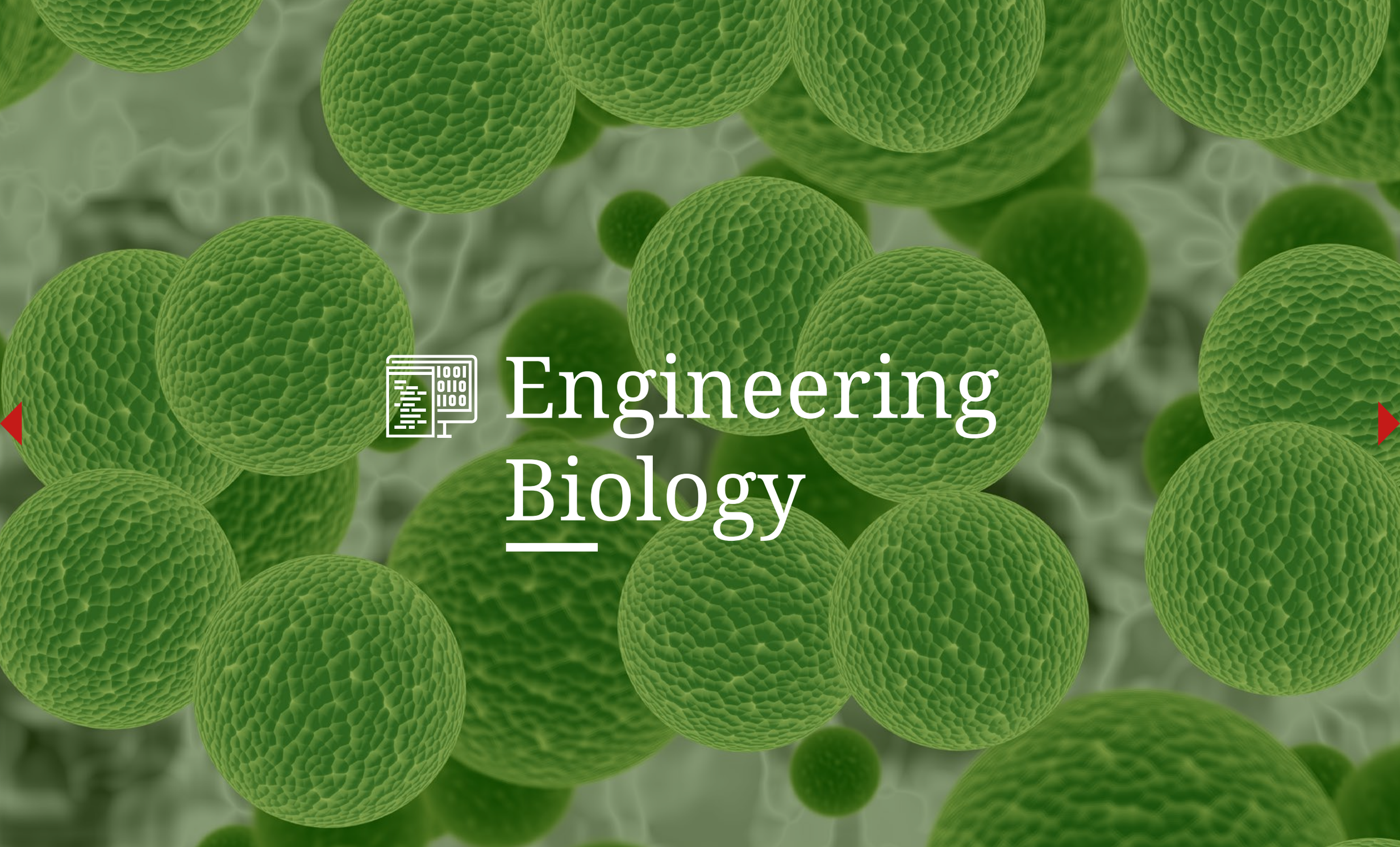
Richard Leggett
Technology Algorithms Group Leader

Specific expertise

Mark Alston
Computational biology with expertise in metagenomics

Samuel Martin
Bioinformatics, mathematics and software engineering

Darren Heavens
Molecular biology, DNA extraction and sequencing technology


Engineering
Biology

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Macaulay Group

Multi-omic approaches for single cell analysis

The group specialises in the development and application of high-throughput single cell sequencing and approaches, in particular in the development of novel “multi-omics” approaches - in which both the genome (or epigenome) and the transcriptome of a single cell can be assayed in parallel. These methods can provide key insights into biological heterogeneity at the single cell level, and address a diverse range of biological questions in both basic and translational science. The group routinely apply single-cell approaches to microbial, plant, animal and human cells.

Interested in connecting with:

Academic and industrial researchers interested in using single cell sequencing approaches for a diverse range of applications; biotech and instrumentation companies developing equipment and consumables for single cell sequencing.

Iain Macaulay
Technical Development Group Leader

Specific expertise

Iain Macaulay
Cell isolation platforms

Ashleigh Lister
Single cell analysis protocols

Laura Mincarelli
Applications of short- and long-read sequencing in single cell analysis

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Patron Group

Engineering plant biology

The group specialises in applying engineering approaches to investigate plant biology and advance plant biotechnology. The Patron group investigate and engineer gene regulatory networks that underpin complex traits such as responses to nitrate; identify novel bioactive molecules for health and agriculture; and engineer plants as photosynthetic biomanufacturing platforms for small molecules, including insect pheromones.

Interested in connecting with:

Researchers at SMEs or large companies interested in the use of biotechnology in agriculture and industrial biotechnology including genome editing, natural product discovery and biomanufacturing.

Nicola Patron
Group Leader

Specific expertise

Yaomin Cai
Plant gene regulation

Tufan Oz
Plant genome engineering

Melissa Salmon
Genetics and biomanufacturing of natural products

Organisms and Ecosystems

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Anthony Hall Group

Computational tools to leverage genomic diversity in crops

The group is interested in mechanisms of genome evolution within large complex genomes. The group deploys next generation genetic tools to explore evolution and genetic variation with a focus on wheat. From this fundamental interest the group have developed genome re-sequencing genotyping approaches and tools/methods for exploring macro/micro genetic variation. In addition, these tools have been used to identify genes underpinning key traits involved in recombination, biological timing, heat, drought and yield robustness.

Interested in connecting with:

Academic researchers, breeding companies, biotech companies and wider agrochemical sector developing new genotyping platforms, and interested in new targets for improving key agricultural traits.

Anthony Hall
Head of Plant Genomics

Specific expertise

Anthony Hall
Genetic diversity in wheat, increasing recombination

Joshua Colmer
Machine learning techniques to analyse gene expression

Ben White
Bioinformatics tools for variant calling and gene expression

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De Vega Group

Diversity of crops and soils to build resilience to climate change

The group specialises in agricultural biodiversity and genomics, soil quality health and climate adaption. The group are exploring the natural diversity in crop collections for advantageous adaptation that could be used to improve crop tolerance. The De Vega group also conduct metagenomic analysis to assess soil health and pests that impact arable fields.

Interested in connecting with:

The agricultural community including plant breeders, researchers and gene banks that are interested in enhancing crop resilience as well as preserving and enhancing biodiversity.

Jose De Vega
Group Leader

Specific expertise

Janet Higgins
Crop diversity and collections

Nasmille Larke-Mejía
Soil metagenomics

Jose De Vega
Building the BIO economy

Haerty Group

Exploring functional non-coding sequence for desirable traits and disease targets

The group are experts in functional genomic and population and comparative genomics. The Haerty group specialises in characterising sequence variation within coding and noncoding sequences critical to gene expression regulation through the integration of genomic, epigenomic, and transcriptomic (short and long read) data. Industrial projects include identifying disease drug targets in humans.

Interested in connecting with:

Pharmaceutical industry, oncology clinicians and academic researchers.

Wilfried Haerty
Evolutionary Genomics Group Leader

Specific expertise

Tarang Mehta
Tilapia genomic resources and population genetics

Adam Ciezarek
Eukaryotic genomes and population genomics

Will Nash
Non-coding RNA/sequences evolution, gene family evolution and splicing variation

Graham Etherington
Single cell sequencing analyses

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Hall Group

Evolutionary and population genomics

The group are experts in applying genomic methods developed from microbial species to more complex genomes. The Hall group focuses on evolution, population genomics and microbial single cell analysis, to understand how microbes evolve and adapt to different hosts. They work on bacteria, including Salmonella and eukaryotes - for example, fungi and protists - and study their contribution to plant and animal disease, infection and resistance.

Interested in connecting with:

Academic researchers, agriculture sector, biotech/pharmaceutical industry interested in biocontrol and bioprospecting.

Neil Hall
Director

Specific expertise

Mark McMullan
Plant fungal pathogen, ash dieback, host-microbe

Matt Bawn
Antimicrobial resistance and bacterial evolution

Ross Low
Salmonella genomes and protist genome evolution

Sally Warring
Protist diversity

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Hildebrand Group

Unravelling disease aetiology via bacterial evolution, metagenomics and population genetics

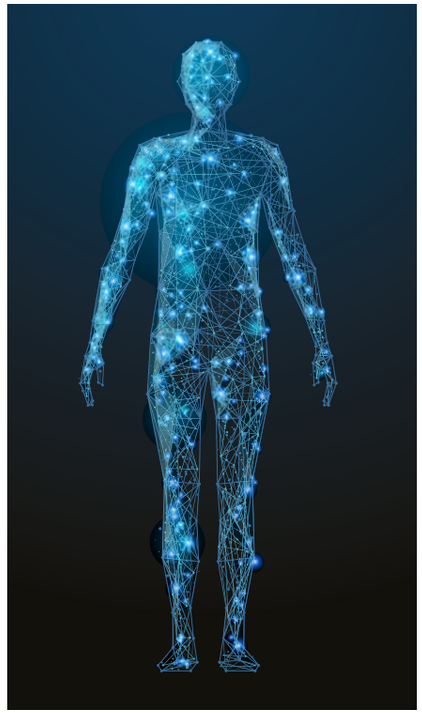
The group has expertise in combining microbial ecosystems, bacterial evolution and gene transmissions. The Hildebrand group developed microbiome analysis pipelines for metagenomic strain tracking, and to identify taxonomic signature and pathogenicity at the population level. These could be applied to both animal and human gut as a personalised treatment strategy, for example IBD and Parkinson's diseases.

Interested in connecting with:

Industry and academics interested in microbiome in health and disease, strain tracking and bacterial evolution.

Falk Hildebrand
Group Leader

Specific expertise



Understanding complex human diseases

Metagenomics strain tracking

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Korcsmáros Group

Multi-scale analysis of human intestinal diseases

Combining diverse experimental model systems with in-house developed computational pipelines, the Korcsmáros group carries out analysis using big multi-omics data for precision medicine applications. These systems-based analytical tools can advance understanding of diseases such as infections, inflammatory bowel disease (IBD) and cancer, providing a valuable resource for researchers, clinicians and healthcare, pharma and AI industry.

Interested in connecting with:

Academics, industry and clinicians interested in exploring more representative model systems for IBD. Industry and clinicians with multi-omics data on patients for stratification and biomarker discovery.

Tamás Korcsmáros
Tenure-track Group Leader

Specific expertise

Isabelle Hautefort
Intestinal models (including organoids) to study host-microbe interaction

Dezso Modos
Precision medicine and network pharmacology

Agatha Treveil
Computational pipelines to analyse multi-omics and single cell datasets

Projects

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Darwin Tree of Life
Investigating British biodiversity

Darwin Tree of Life (DToL) aims to sequence the genomes of all 60,000 eukaryotic species in Britain and Ireland, with the hope of transforming the way we do biology, conservation and biotechnology. Within this ambitious project, The Earlham Institute is developing novel methods to read the genomes of single-celled organisms. Complementing the DToL ambition, EI is investigating the genomes of endangered pollinators and mining plants genomes and metabolomes.

Interested in connecting with:

Wildlife trusts and conservationists for analysis of specimens and application of data. Sequencing centres and assemblers interested in advances in sequencing pipelines and methods. Biotechnology based companies looking for custom sequencing and pipeline development.

Seanna McTaggart
Programme Manager

Robert Davey
Metadata management and data brokering

Specific expertise

Karim Gharbi
Sequencing, automation

Wilfried Haerty
Pollinator genomes

Neil Hall
Genome evolution

Iain Macaulay
Single cell extraction and library preparation protocols

Nicola Patron
Plant metabolites

David Swarbreck
Novel assembly and annotation methods

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GROW COLOMBIA
growcolombia.org

GCRF
Global Challenges Research Fund

Preserving, restoring and managing Colombian biodiversity through responsible innovation

GROW Colombia combines biological sciences, computational biology, and socio-economics to preserve, restore and manage the extensive biodiversity of Colombia. Its agricultural diversity programme includes the economically important crops coffee, banana, sugar cane and cacao. The natural diversity programme helps conservation efforts to save the spectacled bear and the unique Andean Paramos.

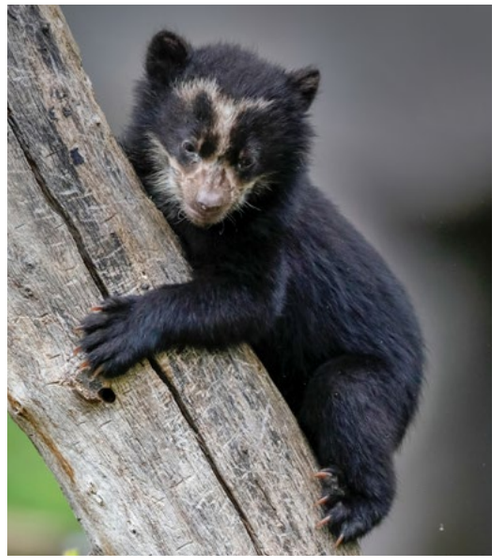
Interested in connecting with:

Academics, start-ups and SMEs interested in sustainable breeding practices and identification of favorable crop traits to improve market value. Government bodies and the tourism industry requiring evidence based conservation recommendations aspiring to achieve sustainable bioeconomies.

Wilfried Haerty
Natural diversity and conservation of indigenous species

Jose De Vega
Agricultural diversity and soil health

Horizon 2020 Innovate



Services

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ADVANCED TRAINING

Advanced Training

Our training programme is aimed at life scientists, who are increasingly engaging in data-driven research projects relating to -omics techniques.

Addressing skills in genomics and bioinformatics, our programme of events engages with researchers in this fast-paced research space through a multitude of formats: project-based courses with an underpinning biological question; resource-based courses and workshops including best practice; networking and discovery events.

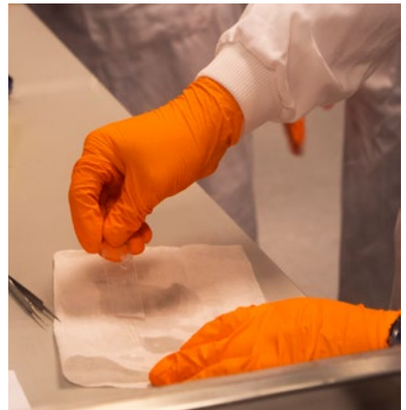
Interested in connecting with:

Academic researchers and companies interested in developing skills or using EI's in-house developed tools and resources for their research or commercial projects.

Emily Angiolini
Scientific Training and Education Team Manager

Roanne Epithite
Events Manager

EI Innovate 2020



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BIO FOUNDRY

Earlham BIO Foundry

The BIOFoundry hosts a suite of automated platforms for molecular and microbiological workflows. It specialises in the rapid design, construction, and testing of genetically reprogrammed organisms. Our automated workflows include DNA assembly, genome engineering, cell-free protein synthesis, library screening and micro fermentation. The expertise can also be applied to automate numerous laboratory workflows, increasing experimental throughput, while reducing reaction volumes and human error. Access to the BIOFoundry can be provided as a service or in collaborative projects, including hosting and training research staff.

Interested in connecting with:

Academic researchers and companies interested in using laboratory automation for their bespoke research or commercial projects.

Jose A. Carrasco Lopez
Earlham BIO Foundry Manager

Lesley Ives
Automation Senior Research Assistant

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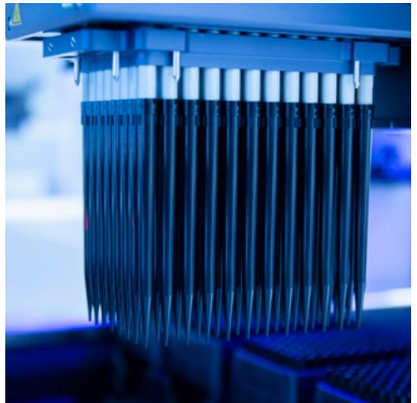

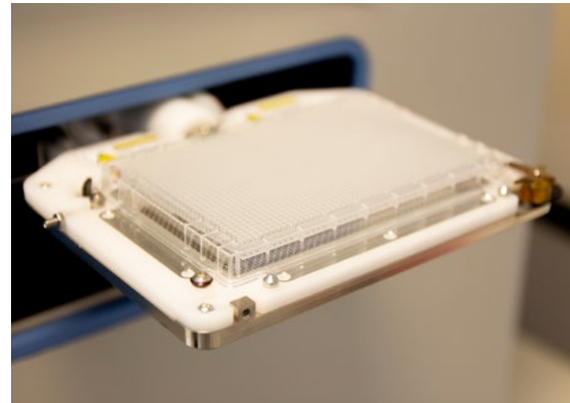

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ELIXIR UNITED KINGDOM

Coordinating bioinformatics infrastructure in the UK, for Europe and beyond

Coordinating life science resources across Europe under a single infrastructure, ELIXIR — an intergovernmental organisation — brings together services central to many industrial researchers, particularly in pharmaceutical, medical, and biotechnology sectors.

As the lead institute of the ELIXIR-UK Node with 18 member organisations, Earlham Institute provides coordination, data brokering, biological databases, cloud resources, and training for current data challenges.

Interested in connecting with:

Industry e.g. pharmaceutical, agritech etc, who would like to engage and influence the consortium on FAIR (findable, accessible, interoperable, reuseable) implementation for efficient and effective digital transformation.

Neil Hall
Joint Head of Node

Innovate 2020

How to access services from ELIXIR-UK

Catherine Hunter
Project Manager

Hannah Norman
Community Engagement Officer

Nicola Soranzo
Technical Co-ordinator, ELIXIR-UK

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GENOMICS PIPELINES

Genomics services

The Genomics Pipelines group provides a high-throughput genomics and single-cell analysis facility to support UK research communities. EI hosts a number of sequencing platforms and liquid handling automation. The group's expertise includes sample processing and preparation, laboratory automation pipelines, data generation, software, algorithms and bioinformatics pipelines for data analysis. This group specialises in testing new technologies and matching them to applications, as well as translating new protocols developed within EI into high throughput pipelines that can then be offered as a service.

Interested in connecting with:

External academic researchers, who would benefit from the expertise of this group; businesses, government departments and NGOs wishing to develop bespoke sequencing and bioinformatics platforms; companies developing new sequencing and automation technologies, equipment, and consumables.

Karim Gharbi
Head of Genomics Pipelines

Specific expertise

Chris Watkins
Project management team

Leah Catchpole
Bespoke sample preparation and laboratory automation

Iain Macaulay
Single cell sequencing

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GENOMICS PIPELINES

Core bioinformatic services

The Core Bioinformatics group provides bioinformatic services, as well as developing software/pipelines to enable large scale data analysis for both industrial and academic projects. Our expertise can be applied across plant, microbial and animal genomes, with analyses including genome assembly and annotation, metagenomics, single cell multi-omics analysis to assess genetic, epigenetic and transcriptomic heterogeneity. We also support consortia in large scale genomics projects, for example International Wheat Genome Sequencing Consortium. Access to the core bioinformatics group can be provided as a service or through collaborative contracts and we welcome enquiries to tailor the bioinformatic analysis to your aims and needs.

Interested in connecting with:

Academic and industrial researchers interested in bioinformatics services or requiring large scale data analysis to develop applications and tools in agritech, biotech and pharma sectors.

David Swarbreck
Head of Core Bioinformatics

Specific expertise

Gareth Linsmith
Genome assembly

Vladimir Uzun
Single cell analysis

Luca Venturini
Eukaryotic transcriptomics

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RESEARCH E-INFRASTRUCTURE

High performance computing

Our high performance computing provides state-of-the-art computing and storage technology to accelerate computational tasks for the processing of large and complex data. This enables research widely applicable to genomics and bioscience. Users can store huge amounts of data and complete complex computational tasks in matter of hours that would have otherwise taken months on standard desktop computing resources.

Interested in connecting with:

Scientific community who are interested in enquiring or accessing high performance computing resources.

Robert Davey
Head of Research e-Infrastructure

Specific expertise

Nicola Soranzo
Bioinformatic analysis platforms (Galaxy)

Alice Minotto
Data brokerage and publishing (Collaborative Open Plant Omics)

Earlham Institute

Decoding Living Systems

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