

E Innovate

17 - 18 November
2021



Contents

2. Contents and Key themes

3. Digital Biology

- 4. Complex Genome Assembly
- 5. E-Infrastructure for Data Sharing
- 6. In-field Sequencing
- 7. High Resolution Microbiomics

8. Engineering Biology

- 9. Single Cell Sequencing
- 10. Engineering Plant Biology

11. Organisms and Ecosystems

- 12. Crop Genomic Diversity
- 13. Biodiversity and Resilience
- 14. Functional Traits and Disease Targets
- 15. Biocontrol and Bioprospecting
- 16. Metagenomic Strain Tracking
- 17. Precision Medicine Tools
- 18. Single Molecule Analysis

19. Projects

- 20. Darwin Tree of Life
- 21. ELIXIR-UK
- 22. GROW Colombia

23. Services

- 24. Advanced Training
- 25. Earlham Biofoundry
- 26. Genomics Services
- 27. Core Bioinformatics Services
- 28. High Performance Computing
- 29. Contact

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



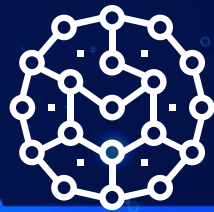
Data storage, visualisation and sharing



Automation platforms for molecular and synthetic biology



Scientific training



Digital Biology



Microbiomes
and health



Conservation and
Biodiversity



Agriculture and
food security



Genomes and
evolution



Genomics for
precision medicine



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platforms



Bioinformatic
software and tools



Data storage,
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Automation platforms
for molecular and
synthetic biology



Scientific training

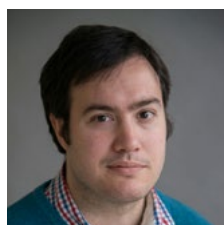
Clavijo Group

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:

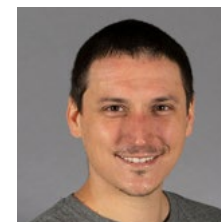
Academic groups and biotech companies interested in assembling complex genomes to identify genetic mechanisms of important agricultural traits.



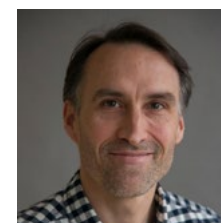
Bernardo Clavijo
Bioinformatic Algorithms Group Leader



Specific expertise



Gonzalo Garcia Accinelli
Assembly methods development and assembly quality control



Jon Wright
Wheat genomics and methods testing



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and health



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Scientific training

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



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



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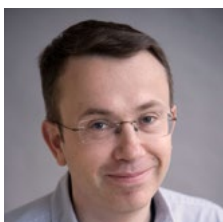
Leggett Group

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:

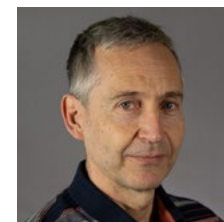
Academic and industry researchers, and government bodies interested in developing computational tools and pipelines for applications in agritech, biotech, and pharma sectors.



Richard Leggett

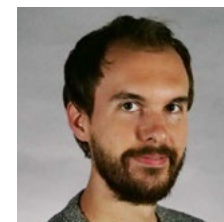
Technology Algorithms Group Leader

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





Microbiomes
and health



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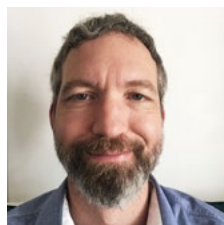
Quince Group

Developing Improved Methods to Understand the Complexity of Microbial Communities

Applied to the gut microbiome, the Quince group pioneered metagenomic analysis techniques that accurately capture the diversity in microbial communities. These approaches have been applied to urgent clinical conditions; to identify transmission, for targeted intervention, of non-viral gastroenteritis. Advance treatment of paediatric Crohn's disease & understanding the evolution antimicrobial resistance (AMR). The Quince group continually develop novel analytical approaches to a range of systems.

Interested in connecting with:

Academic researchers, biotechnology companies, microbiome therapeutics industry and the wider microbiology community interested in the improved genome resolved metagenomics for analysing large data sets from environmental & human associated environments.



Chris Quince
High-Resolution Microbiomics Group Leader



Specific expertise



Sébastien Raguideau
AMR genetic analysis of environmental microorganisms



Odin Manuel Moron Garcia
Alan Turing Fellow, Metagenomic data interpretation through phenotypic ML



Engineering Biology



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Scientific training

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:

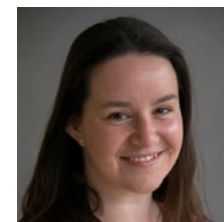
Academic and industrial researchers interested in using single cell sequencing approaches for a diverse range of applications; biotech and instrumentation companies developing equipment and consumables for single cell sequencing.



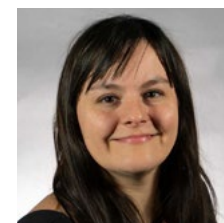
Iain Macaulay
Technical Development Group Leader



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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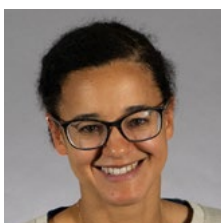
Patron Group

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:

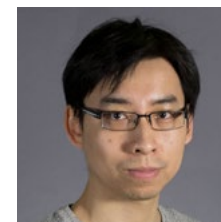
Researchers in academia, biotech companies or breeding companies interested in natural products, biomanufacturing, plant genome editing and engineering biology.



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



Microbiomes
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Scientific training

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.



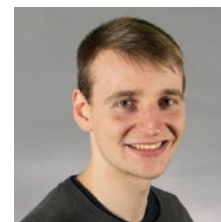
Anthony Hall
Head of Plant Genomics



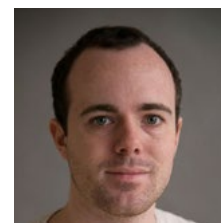
Specific expertise



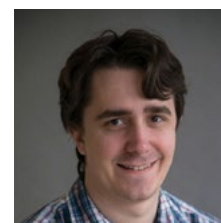
Anthony Hall
Genetic diversity in wheat, increasing recombination



Joshua Colmer
Machine learning techniques to analyse gene expression



Ben White
Bioinformatics tools for variant calling and gene expression



Ben Ward
Computation biology and bioinformatics



Microbiomes
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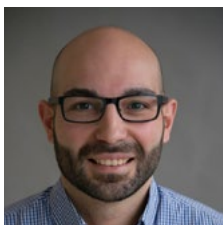
De Vega Group

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:

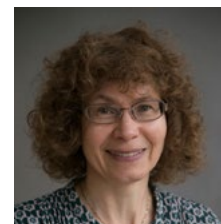
The agricultural community including plant breeders, researchers and gene banks that are interested in enhancing crop resilience as well as preserving and enhancing biodiversity.



Jose De Vega
Group Leader



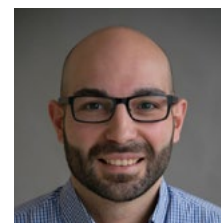
Specific expertise



Janet Higgins
Crop diversity and collections



Nasmylle Larke-Mejia
Soil metagenomics



Jose De Vega
Building the BIO economy



Microbiomes
and health



Conservation and
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Scientific training

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:

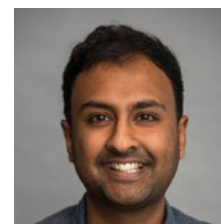
Pharmaceutical industry, oncology clinicians and academic researchers.



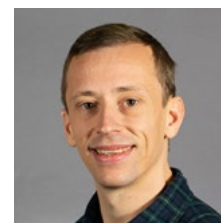
Wilfried Haerty
Evolutionary Genomics Group Leader



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



Microbiomes
and health



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food security



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Scientific training

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.



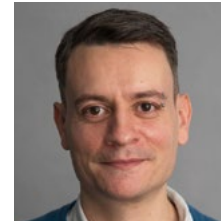
Neil Hall
Director



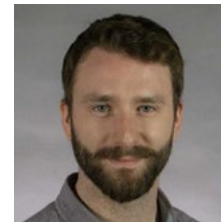
Specific expertise



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



Matt Bawn
Antimicrobial resistance and bacterial evolution



Ross Low
Salmonella genomes and protist genome evolution



Microbiomes
and health



Conservation and
Biodiversity



Agriculture and
food security



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Scientific training

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



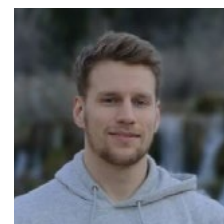
Specific expertise



Ezgi Ozkurt
Defined biases in metagenomic sequencing experiments



Rebecca Ansorge
Bacterial strains and their pan genomes



Joachim Fritscher
High-resolution metagenomics, algorithm development



Microbiomes
and health



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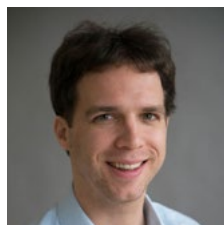
Korcsmáros Group

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:

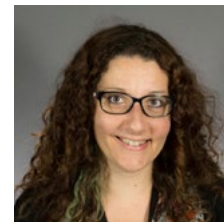
Academics, industry and clinicians interested in exploring more representative model systems for IBD. Industry and clinicians with multi-omics data on patients for stratification and biomarker discovery.



Tamás Korcsmáros
Tenure-track Group Leader



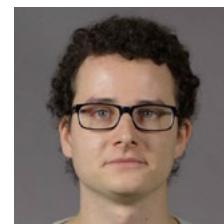
Specific expertise



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



Dezso Modos
Precision medicine and network pharmacology



Marton Olbei
Computational pipelines to analyse multi-omics and single cell datasets



Microbiomes
and health



Conservation and
Biodiversity



Agriculture and
food security



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Scientific training

Nieduszynski Group

Exploring the impact of DNA replication on the stability of natural and synthetic genomes

Combining single molecular genome analysis, population genomics and mathematical modelling, the Nieduszynski Group specialises in DNA replication and genome stability underlying health and disease. These novel insights are applicable to human, bacteria, eukaryotes and synthetic genomes, and could be used to identify source of drug resistance, applied to patient diagnosis, or develop synthetic biology resource to maintain stable replication of DNA.

Interested in connecting with:

Sequencing technology and genomic reagents providers, as well as academics interested in developing single molecule advances and pipelines for DNA replication stability.



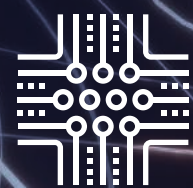
Conrad Nieduszynski
Group Leader



Specific expertise



Sathish Thiyagarajan
Computational biology, machine learning, algorithm development



Projects



Microbiomes
and health



Conservation and
Biodiversity



Agriculture and
food security



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Scientific training



Darwin Tree of Life Investigating British biodiversity

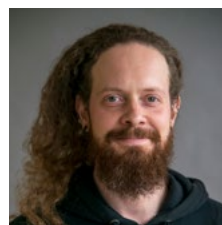
Darwin Tree of Life (DToL) aims to sequence the genomes of all 60,000 eukaryotic species in Britain and Ireland, with the hope of transforming the way we do biology, conservation and biotechnology. Within this ambitious project, the Earlham Institute is developing novel methods to read the genomes of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



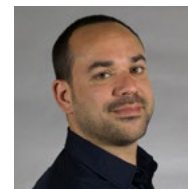
Seanna McTaggart
Programme Manager



Robert Davey
**Metadata management
and data brokering**



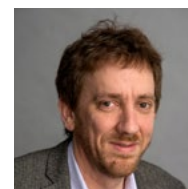
Specific expertise



Karim Gharbi
Sequencing, automation



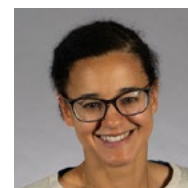
Wilfried Haerty
Pollinator genomes



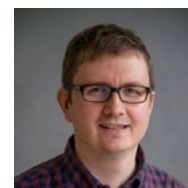
Neil Hall
Genome evolution



Iain Macaulay
Single cell extraction and library preparation protocols



Nicola Patron
Plant metabolites



David Swarbreck
Novel assembly and annotation methods



Microbiomes
and health



Conservation and
Biodiversity



Agriculture and
food security



Genomes and
evolution



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visualisation and
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synthetic biology



Scientific training



Coordinating bioinformatics infrastructure in the UK, for Europe and beyond

Coordinating life science data 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 20 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



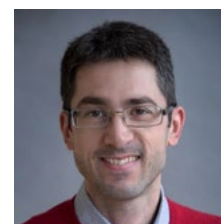
Specific expertise



Catherine Hunter
Project Manager



Hannah Norman
Community Engagement Officer



Nicola Soranzo
Technical Co-ordinator, ELIXIR-UK



Microbiomes
and health



Conservation and
Biodiversity



Agriculture and
food security



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evolution



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techniques and
platforms



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Scientific training



Preserving, restoring and managing Colombian biodiversity through responsible innovation

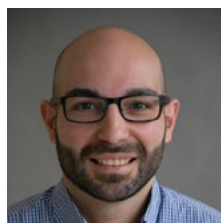
GROW Colombia combines biological sciences, computational biology, and socio-economics to preserve, restore and manage the extensive biodiversity of Colombia. Its agricultural diversity programme includes the economically important crops coffee, banana, sugar cane and cacao. The natural diversity programme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

Interested in connecting with:

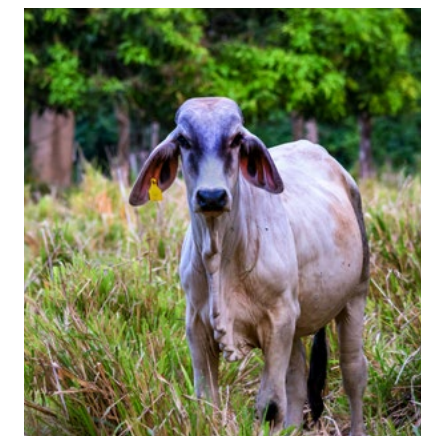
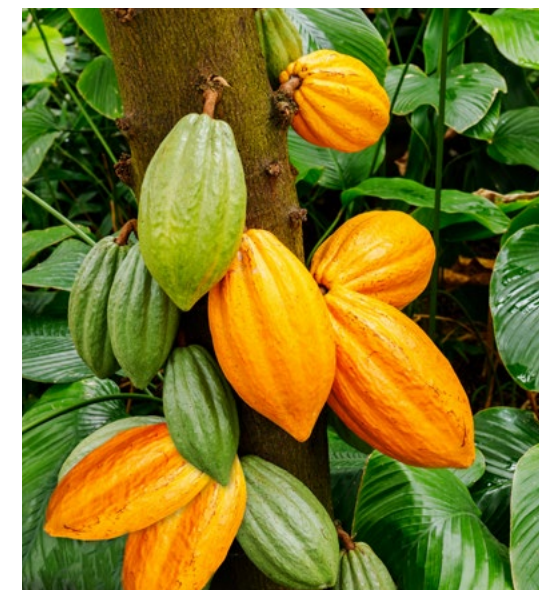
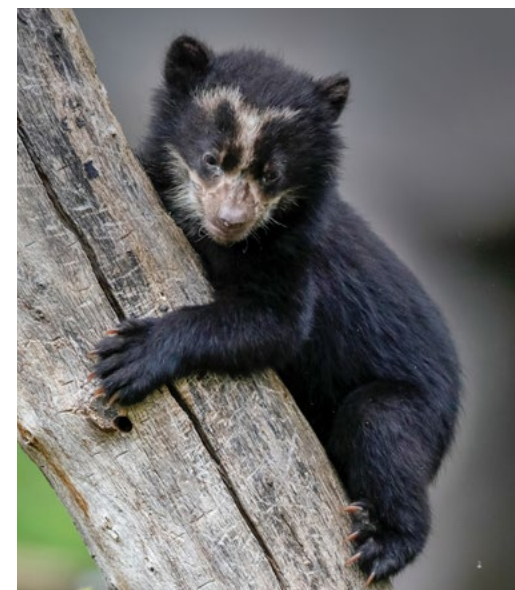
Academics, start-ups and SMEs interested in sustainable breeding practices and identification of favorable crop traits to improve market value. Government bodies and the tourism industry requiring evidence based conservation recommendations aspiring to achieve sustainable bioeconomies.



Wilfried Haerty
**Natural diversity
and conservation of
indigenous species**



Jose De Vega
**Agricultural diversity
and soil health**



Services





Microbiomes
and health



Conservation and
Biodiversity



Agriculture and
food security



Genomes and
evolution



Genomics for
precision medicine



Sequencing tools,
techniques and
platforms



Bioinformatic
software and tools



Data storage,
visualisation and
sharing



Automation platforms
for molecular and
synthetic biology



Scientific training



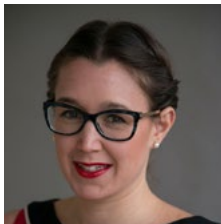
Advanced Training

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
**Head of Advanced
Training**



Roanne Ephithite
Events Manager





Microbiomes
and health



Conservation and
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Scientific training



Earlham Biofoundry

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:

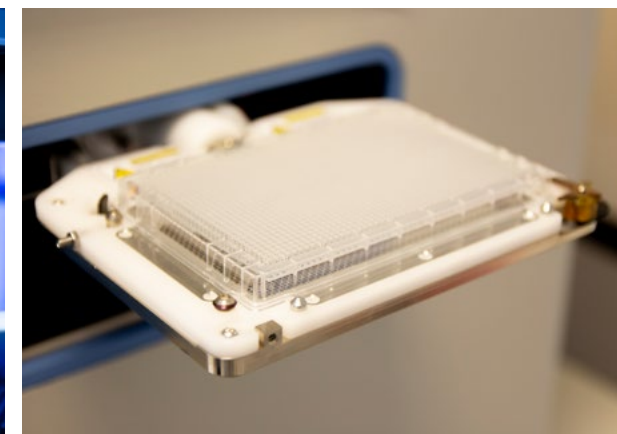
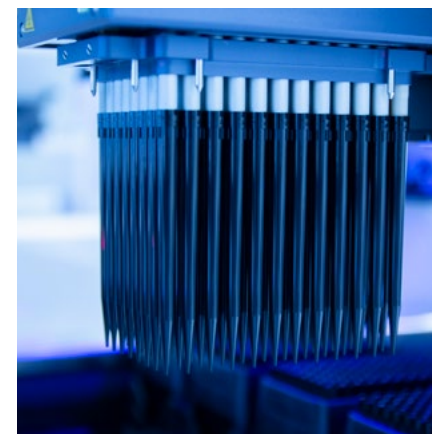
Academic researchers and companies interested in using laboratory automation for their bespoke research or commercial projects.



Jose A. Carrasco Lopez
**Earlham Biofoundry
Manager**



Lesley Ives
**Automation Senior
Research Assistant**





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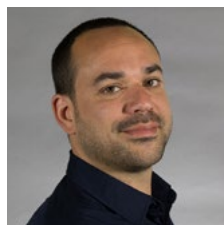


Genomics services

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.



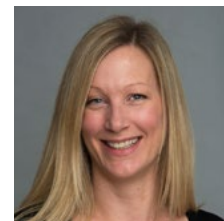
Karim Gharbi
Head of Genomics Pipelines



Specific expertise



Chris Watkins
Project management team



Leah Catchpole
Bespoke sample preparation and laboratory automation



Iain Macaulay
Single cell sequencing



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Scientific training



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



Gemy Kaithakottil
Eukaryotic transcriptomics



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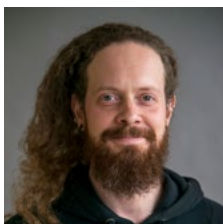


High performance computing

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)



Krister-Jazz Urog
Cloud computing infrastructure (CyVerse)





Contact:

Earlham Institute
Norwich Research Park
Norwich
NR4 7UZ

Email: business.development@earlham.ac.uk

Telephone: +44 1603 450 001

Website: earlham.ac.uk