The Wellcome/ Cancer Research UK Gurdon Institute
Prospectus 2020/2021
Studying development to understand disease
Welcome to our new Prospectus, where we highlight our activities for - unusually - two years: 2019 and 2020. The COVID-19 pandemic has made it an extraordinary time for everyone. I want to express my pride and gratitude for the exceptional efforts of Institute members, who have kept our building safe and our research progressing; this applies especially to our core team, whose dedication has been key to our continued progress. As you will see, there is much to be excited about in our research and activities.

It was terrific to see Gurdon members receive recognition for their achievements. Steve Jackson received the Leopold Grifflue Award in Translational and Clinical Research, and the Royal Society Mullard Award. Hansong Ma was awarded a Philip Leverhulme Prize and selected as an EMBO Young Investigator, I received the Genetics Society of America’s George W. Beadle Award, and Office Manager Lynda Lockey was named the Unsung Heroine of Professional Services. We are also excited that a major component of the Wellcome-funded Human Developmental Biology Initiative is based in the Institute, led by Emma Rawlins, Ben Simons and Azim Surani.

I’m especially proud that our exceptional Public Engagement was recognised by a Silver Engage Watermark, the first such award in the University. Special thanks for this achievement go to Hélène Doerflinger, Phil Zegerman and Emma Rawlins. After incubating Steve Jackson’s company Adrestia in the Institute for two years, we wished them well as they moved to the Babraham Research Campus. We also sent our best wishes to Meri Huch and Rick Livesey and their labs, as they embarked on their new positions in Dresden and London, respectively.

I’m delighted that Emma Rawlins was promoted to Senior Group Leader and that two new Group Leaders joined us in Autumn 2020. Iva Tchasovnikarova studies epigenetic pathway mechanisms and how they are disrupted in disease, while David Fernandez-Antoran’s research is focused on cell competition and the impact of ionising radiation on selection.

Finally, I’m pleased to welcome two new Associate Group Leaders. John Perry (MRC Epidemiology Unit) uses human genetics to understand disease mechanisms, and Martin Howard (John Innes Centre) builds mathematical models of biological processes. We look forward to exciting and productive interactions with them.

Iva Tchasovnikarova, who was awarded a Philip Leverhulme Prize and selected as an EMBO Young Investigator, is pictured in the image.
About the Institute

The Wellcome/ Cancer Research UK Gurdon Institute is a world-leading centre for research at the interface between developmental biology and cancer biology.

Our research is focussed in four overlapping areas:

- Cell division, proliferation and genome maintenance
- Function and regulation of the genome and epigenome
- Mechanisms of cell fate determination, multipotency and plasticity
- Cell biological processes underlying organ development and function

We investigate these areas in both normal development and cancer using multiple model systems, from yeast to human organoids (pp. 20–50).

Since our formation in 1991, our research has led to major insights into the molecular and cellular defects that give rise to cancer and other diseases of ageing, and findings have been successfully translated to drug discovery through spinout companies.

The Gurdon Institute’s principal sponsors are Wellcome and Cancer Research UK, who support our excellent infrastructure through core grants, and our research through direct grants to group leaders. Our research is also funded by other sources including national and international governmental and charitable grants. Scientific progress and future plans are assessed at regular intervals by our International Scientific Advisory Board (p. 77).

The Institute is embedded within the University of Cambridge, providing unparalleled opportunities for collaborations and interactions across Cambridge’s vibrant research environment, including through department affiliations and teaching.

We benefit from:
- Core facilities with state-of-the-art equipment and support including super-resolution microscopy, next-generation sequencing and bioinformatics (pp. 56–57)
- Central services providing administration, computing and IT, stores, media preparation and glass-washing.
- A wealth of stimulating seminars and masterclasses, an annual Institute retreat, and Institute postdoc and PhD student groups (pp. 62–65)
- Award-winning public engagement between our scientists and the wider public (pp. 16–17)
- An on-site canteen, social events and sports groups, which enhance our welcoming and inclusive environment.
- An Athena SWAN Bronze Award for promoting equality and diversity across our workforce.

Join us

We have a thriving community of graduate students and postdocs who contribute to and benefit from our exciting research environment. We welcome enquiries from those interested in joining us, which can be done by writing to the relevant group leader.

Find out about the latest opportunities on our website.
What did we do during the coronavirus pandemic in 2020?

Along with institutions and businesses across England, the laboratory had to close from 20th March for Lockdown 1.0. Only minimal maintenance and technical staff remained, regularly checking the building and the fly stocks, while researchers could no longer access their benches and had to call a sudden halt to hundreds of experiments. Administrative staff took computers and files home. And that’s how it remained until 15th June when we re-opened at one quarter occupancy, slowly moving up to 50% occupancy by September. Many different staff, and especially researchers, were delighted to return once more to the building. Lockdown 2.0 in November sent some more staff back home again.

The core staff have done an incredible job to keep as much of the Institute open and functioning as possible (and legal) at all times, in terms of maintenance and safety in the building, supplying media, and enabling computing services for remote working. Meanwhile, other Institute members have contributed directly to fighting the pandemic:

Some of our scientists re-focused their research
Omer Ziv with Miska lab colleagues and collaborators at Justus Liebig University worked to produce a map and database of the short and long-range interactions of the SARS-CoV-2 RNA genome (details in ‘Research highlights 2020’). Ben Simons was involved in epidemiological modelling.

Others intermitted from research and returned to the clinic: Ben Fisher (Miska lab) says “I returned to full-time clinical work as a paediatrician at Addenbrooke’s Hospital from March to September. It was actually quite nice to have something to do during that first lockdown, although being coughed on by feverish children all day wasn’t ideal.”

Five researchers worked shifts as volunteers at the Cambridge Testing Centre that ran seven days a week from 6am to midnight to support the national effort to boost COVID-19 testing capacity.

The roles taken by Weronika Fic, Dmitry Nashchekin, Helen Zenner and Mihoko Tame (St Johnston lab) and Paolo Amaral (Kouzarides lab) were in sample preparation, RT-PCR tests and data analysis, the full team eventually processing over 8000 nasopharyngeal swab samples daily.

Paolo recalls: “Volunteering at the centre felt like a call of duty. As the number of samples to be processed quickly increased, with home tests arriving from all over the country, we were pushed to the limit and at one point caused a bottleneck of the whole pipeline. The solidarity and sense of responsibility of everyone in the team meant that we would ensure all the samples were processed each day, and we know we played an important part in helping contain the first COVID-19 wave.”

Core staff made Personal Protective Equipment: Alex Sossick and Charles Bradshaw of the Imaging and Bioinformatics teams each took home a 3D printer. The machines were set up to run 24-hours a day, making in total 500 visor headbands, which were distributed locally to key workers in GP surgeries, hospitals and care homes. “The Institute had given a lot of our own PPE, especially visors, to Addenbrookes,” says Alex.

“Then, of course, there was the wider shortage across the country, so Charles and I looked at what we could do.” Once our building opened again on 15th June under University guidance, the set up a no-touch log-in log-out system allowing the Institute to track numbers of people on site in real time, ensuring we stuck to the strict rules on numbers in different lab spaces.

Family members sewed face coverings: The mother of a staff member sent about 600 of her hand-sewn, eco-friendly and washable face coverings all the way from her village in Italy, enough for everyone to have two each.
The Gurdon Institute

Awards

Feb ’19: Steve Jackson receives cancer research prize
The 47th ARC Foundation Léopold Griffuel Award in Translational and Clinical Research was presented to Steve Jackson at a ceremony in Paris on 10th April. The award was given “for his work on DNA damage repair and his role in the development of medicines such as PARP and 2 inhibitors used for cancer treatment.”

May ’19: Pisa Honorary Doctorate for John Gurdon
John Gurdon received a Doctorate Honoris Causa in Translational Medicine from the Scuola Superiore Sant’Anna of Pisa. He gave a lecture there and at Bologna University. While in Bologna he was interviewed by national newspaper ‘Il Resto del Carlino’.

Jul ’19: Gurdon researchers in Wellcome’s new £10M project on human development
The Human Developmental Biology Initiative aims to provide insights into how humans develop—from one cell to billions of different cells that make up our tissues and organs.

Three of the Institute’s labs are among more than a dozen across the UK working together to generate data, develop new tools and build a ‘family tree’ of cell divisions during development, starting at fertilisation. Azim Surani is a co-leader for “cell lineage in human epiblast specification and early differentiation”; Emma Rawlins is a co-leader for “human lineage analysis in a 3D spatial context: cardio-pulmonary system development”; and Ben Simons is a lead for one of three cross-cutting technology platforms — computational biology and data analysis.

Sep ‘19: Meri Huch wins BINDER Innovation Prize
The 2019 BINDER Innovation Prize was awarded to Group Leader Meri Huch for her research on liver organoids for the study of liver biology and disease. The award is given for “outstanding cell biological research with a focus on cell culture,” and awarded by the German Society for Cell Biology.

Nov ’19: Steve Jackson awarded ERC Synergy Grant
Recipients of the ERC Synergy Grants were announced in November and Steve Jackson is among them, awarded funding for a project on the DNA damage response in collaboration with partners in Switzerland and Austria. This was the first of the new Horizon 2020 grants to come to Cambridge.

Dec ’19: Song for the Unsung Heroine
The Institute’s Office Manager, Lynda Lockey, won the Unsung Heroine Award in the University of Cambridge Professional Services Recognition Scheme. Institute Director Julie Ahringer said “Lynda is a very deserving recipient of the award. Her dedicated and understated work makes things run smoothly, and positively impacts everyone”.

Jan ’20: Ahringer honoured by Genetics Society of America
Julie Ahringer was honoured with the Genetics Society of America’s George W. Beadle Award “for outstanding contributions to the community of genetics researchers…beyond an exemplary research career.”

Aug ’20: Award for research contributing to national prosperity
The Royal Society Mullard Award 2020 was awarded to Steve Jackson for his research that led to the discovery of the drug olaparib, which has reached blockbuster status for the treatment of ovarian and breast cancers.

Oct ’20: Philip Leverhulme Prize 2020 by the Leverhulme Trust. The prizes of £100,000 “recognise the achievement of outstanding researchers whose work has already attracted international recognition and whose future career is exceptionally promising”.

Dec ’20: Aztekin wins ELISIR scholarship at EPFL
PhD student in the Gurdon lab, Can Aztekin, moves directly to an independent principal researcher position at the Swiss Federal Institute of Technology in Lausanne (EPFL), as an EPFL Life Sciences Independent Research (ELISIR) scholar.

The awardees join a four-year programme that provides financial support, training and networking opportunities.

Dec ’20: Ahringer honours the next generation of leading life scientists
Institute Director Julie Ahringer said “Lynda is a very deserving recipient of the award...Her dedicated and understated work makes things run smoothly, and positively impacts everyone.”

Philosophy of the Gurdon Institute:
To understand how humans develop—from one cell to billions of different cells that make up our tissues and organs.

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Research in 2019

Fly gene provides clue to reversing mitochondrial disease

The Ma lab have identified a protein in fruit flies (Drosophila) that can be targeted to reverse the effects of disease-causing mutations in mitochondrial genes. The discovery could provide clues about how to counteract human mitochondrial diseases, for which there is currently no cure.


Alternative DNA repair pathway for MDC1

Salguero and colleagues in the Jackson lab applied next-generation DNA sequencing to over 4500 yeast strains in the Gene Knockout Collection. The resulting comprehensive resource identifies new genes responsible for maintaining the stability of DNA in cells, and whose absence or mutation leads to a variety of effects, from changes in short sequence repeats to the loss of whole chromosomes. These ‘mutational signatures’ can now also be studied in human cells.


New DNA stability genes uncovered in systematic study of Yeast Knockout Collection

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Don’t get your DNA in twist

The Zegerman lab’s new publication uncovered in systematic study of Yeast Knockout Collection. The Jackson lab applied next-generation DNA sequencing to over 4500 yeast strains in the Gene Knockout Collection. The resulting comprehensive resource identifies new genes responsible for maintaining the stability of DNA in cells, and whose absence or mutation leads to a variety of effects, from changes in short sequence repeats to the loss of whole chromosomes. These ‘mutational signatures’ can now also be studied in human cells.

Don’t get your DNA in twist

The Zegerman lab’s new publication shows that limiting the rate of DNA duplication - by limiting the number of DNA replication initiation events - is important to prevent interwining between the newly replicated chromosomes. This work may be relevant for the treatment of cancer cells, which are characterised by high rates of DNA duplication.


High regenerative potential, reside primarily in fruit fly ventral brain regions. G0 quiescent stem cells are more numerous in the dorsal brain. This is an important consideration in designing regenerative therapies.


New cell type in tail regeneration

Researchers in the Gurdon and Simons labs working under Jerome Julian identified a new cell type involved in regeneration of tadpole tails. They’ve named the ‘Regeneration-Organizing Cells’ for their role in promoting and coordinating new tissue growth after amputation and hope to find clues in these cells to inform new approaches to regeneration in mammals.


How to boost adult liver regeneration

A paper from the Huch lab - with collaborators in the Gurdon Institute, UK and Germany - describes the molecular mechanism triggered by TET1 that allows damaged adult liver cells to regenerate. This paves the way for design of drugs to boost regeneration in conditions such as cirrhosis or other chronic liver diseases where regeneration is impaired.


Brain location determines stem cell activation speed

Osulke and Brand revealed that stem cells activate rapidly or slowly depending on where they reside in the brain. G2 quiescent stem cells, which activate first and have high regenerative potential, reside primarily in fruit fly ventral brain regions. G0 quiescent stem cells are more numerous in the dorsal brain. This is an important consideration in designing regenerative therapies.


Nuclear membrane dysfunction underlying dementia

The Livesey and Jackson groups pooled expertise, studying patient-derived neurons in the lab to investigate how mutations in the tau gene cause frontotemporal dementia (FTD). They found that, in FTD neurons, microtubules deform the nuclear membrane and perturb nucleo-cytoplasmic transport, uncovering new links between different forms of dementia.


RNA modification pathway affects cancer cell migration

Researchers in the Kourtzidou lab and colleagues have characterised an ‘epitranscriptomic’ pathway with effects on lung cancer cell behaviour in vitro. They developed a technique to precisely locate which guanosine on a micro RNA called let-7 was modified with a methyl group, regulating its processing and downstream action to suppress cell migration.


Transmissible RNA pathway in honey bees

The Miska lab’s Eyal Maori along with colleagues in UK, Israel and the USA have discovered a pathway by which honey bees share RNA, through secretion and ingestion of worker and royal jellies, offering a promising route for administering bee ‘vaccines’. In addition, the researchers identified a specific protein in royal jelly that binds and protects the RNA in granules while outside the body.


RNA uptake to the hemolymph

These RNA signatures are now being studied in a systematic way to understand how RNA is taken up to the hemolymph (the fluid similar to blood in insects) and identify its many downstream effects.


RNA ingestion in royal jelly

The RNA is packaged in small RNA granules that are passed from worker to queen bees through the feeding glands, and are progressively tf4transmitted to pupae for cell regeneration. This RNA is then taken up by hemolymph, the insect’s ‘blood’.

Research in 2020

How inflammation affects regeneration

Why can regeneration-incompetent tadpoles not regenerate their tails? The Gurdon lab show that immune cells behave differently on chromatin to direct gene expression. While previous studies suggest that residency times are only seconds or minutes, this experiment showed a long-term association of hours or days, which could explain the stability of cell fate commitment.


Is TF residency time the key to cell fate commitment?
The Gurdon lab used a competition assay to test how long the transcription factor Ascl1, which is a determinant for nerve, resides on chromatin to direct gene expression. While previous studies suggest that residency times are only seconds or minutes, this experiment showed a long-term association of hours or days, which could explain the stability of cell fate commitment.


Tailless/TLX directs cell fate change in tumourigenesis

Hakas and Brand uncover the cell fate changes that occur during brain tumour initiation. They show that high levels of Tailless/TLX, known to be associated with aggressive glioblastomas, revert intermediate progenitors to neural stem cells as a first step to tumourigenesis. Their findings also support enforced differentiation as a determinant for nerve, resides transcription factor Ascl1, which is a key feature of the mouse skin epidermis, during stretch-mediated expansion of epidermal stem cells, while a transient bias in the renewal activity of epidermal stem cells, while a second subpopulation of basal progenitors remains committed to differentiating into keratinocytes.


Pancreas organoids to model disease

Pancreas organoids can be successfully generated from single cells, or fresh and frozen tissue, then expanded and maintained long-term in culture, say the Huch lab colleagues.


How does stretching skin make it grow?
By tracing the dynamics of cells during stretch-mediated expansion of the mouse skin epidermis, collaborative studies by the Simons lab have shown, at single-cell resolution - how stem cells react to regenerate tissue and restore homeostasis. Stretching induces skin expansion by creating a transient bias in the renewal activity of epidermal stem cells, while a second subpopulation of basal progenitors remains committed to differentiating into keratinocytes.

Berquez, Gadsby, Festa and Gallop lab colleagues discovered that stretching skin makes epidermal stem cells more sensitive to epidermal growth factor, thereby promoting their division and increasing the number of stem cells.


Embryo polarisation link to cell cycle

The Zegerman lab, with Gurdon Institute colleagues, provided the first direct molecular mechanism through which polarisation of the embryo is coordinated with DNA replication initiation factors, linking developmental cues with changes in the cell cycle, in the nematode C. elegans.

Gaggioli V et al. (2020) Genetics 16 (12): e1008948.

Gene regulatory architectures in germline and somatic tissues

Jacques Serizay and Ahringer lab colleagues profiled and compared transcriptional and regulatory element activities across five tissues of the adult nematode worm, C. elegans. The results demonstrate fundamental differences in regulatory architectures of germline and somatic tissue-specific genes, and provide a tissue-specific resource for future studies.


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Cancer drug hope for genetic disease

Beroukh, Gadsby, Festa and Gallop lab colleagues discovered that adjusting membrane composition with the PI3K inhibitor alpelisib rebalances actin cytoskeletal organisation in cell culture and alleviates absorption defects in an in vivo mouse model of Lowe syndrome/Dent disease. Their findings also support enforced differentiation as a determinant for nerve, resides transcription factor Ascl1, which is a key feature of the mouse skin epidermis, during stretch-mediated expansion of epidermal stem cells, while a second subpopulation of basal progenitors remains committed to differentiating into keratinocytes.


Sperm populations show homogeneous epigenetic marks

Gurdon lab and colleagues, led by Jerome Julien, examined histones in sperm to uncover a conserved mechanism for transmission of epigenetic information to the embryo. As sperm develop they lose a large proportion of the histones found in somatic cells, but the remainder are retained in the same position across the sperm population, indicating the potential for the embryo to prime transcription for embryonic development.


Long-range interactions in SARS-CoV-2 RNA

Omer Ziv from the Miska lab, in collaboration with Justus-Liebig University colleagues, has revealed precise details of the base-pairing patterns formed by the long RNA genome of the SARS-CoV-2 virus, responsible for the COVID-19 pandemic. Ziv devised the method that takes a snapshot of both short- and long-range interactions in the RNA, which are essential for viral function and therefore present potential therapeutic targets.

Mission: to make our fundamental biological research accessible and responsive to the public for the mutual benefits of inspiration, knowledge-exchange and trust.

Generate increased trust in fundamental research and ensure our research remains relevant to society.

Empower and inspire the next generation.

Embed public engagement in research culture.

Our projects in 2019 to support the public engagement strategy included:

Scientists’ Collaborative Project with Educators (SCoPE)
We aim to bring contemporary research into GCSE and A-level classrooms with support for teachers and students to deepen their knowledge of fundamental biology and current research. Teachers and our scientists co-created four innovative teaching ‘toolkits’, free to use in classrooms across the UK. The Cell Explorer (online interactive 3D cell model), Explore Epigenetics (an online game about epigenetics), a kit for Fruit Fly Larvae Dissection (teaching about the size and scale of cells, tissues and organs) and Unlocking Genetic Editing (a hands-on problem-solving game). The project was funded by Wellcome and evaluated by the University of Cambridge Faculty of Education. SCoPE website: https://scopegurdoninstitute.co.uk

Tattoo My Science
Our scientists created designs based on their biology research, and we turned these into fun, temporary tattoos. Visitors to festivals and events could choose a tattoo from our collection of designs and then have a chance to discuss the research with the scientist applying their tattoo. Afterwards, they could show off their new tattoo to friends and share their new science knowledge. Thank you to the Wellcome Centre for Cell Biology in Edinburgh for sharing their idea!

Aspiring Scientists Training Programme
Providing an inspiring, immersive experience to encourage groups that are underrepresented in science, we welcomed 11 Sixth-form students for a week at the Institute. Students attended morning workshops about scientific topics or presentation skills. Then they spent the rest of the day in a lab to talk with lab members about their research and science careers. The project was funded by the University of Cambridge Widening Participation Project. The Gurdon Institute provided accommodation, travel expenses and food to all participants. Students told us “It gave me an experience hard to find elsewhere” and “I learned that I can become a scientist.”

Stitching Science
The Public Engagement Seed Fund Project for 2019 was devised and led by Stephanie Norwood, a former PhD student. The project aims to create an informal environment for scientists to interact with local communities and learn a new craft, disseminate information about research projects, and increase public trust in fundamental research. The project engaged crafters through a series of knitting workshops, craft fairs and other events. Participants create a detailed crochet cell containing various organelles (mitochondria, cytoplasm and membrane) and discuss the different parts of the cell with scientists as they knit. Website: https://bitly.com/StitchingSci

Sixth-form workshops
Our Sixth-form workshops aim to inspire A-level biology students. State schools from across the country can bring groups of Year 12 biology students to the Institute to learn about our research. The visit includes a tour of our facilities, a seminar about the history of science and the future of cancer research, a hands-on workshop where students can test their skills at identifying cancerous tissue with microscopes, and a Q&A with our PhD students.

Silver Engage Watermark
The Gurdon Institute was awarded a Silver Engage Watermark in December 2020, the first such award at the University of Cambridge. The Silver Engage Watermark, awarded by the National Co-ordinating Centre for Public Engagement, recognises the Institute’s “robust and committed approach to public engagement”.

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Activities and impacts in 2019

The Gurdon Institute

Focus on research
How is chromatin regulated to direct correct gene expression programmes? Animal development is a remarkable process during which a single-celled totipotent zygote produces a myriad of different cell types. A driving force is the differential control of chromatin activity, which establishes gene expression programmes that drive cellular identity. Deciphering this control is necessary for understanding how the genome directs development and the diseases that result from chromatin dysregulation.

We study how cell-type specific gene expression and chromatin organisation are achieved using the simple C. elegans model, focusing on controls and interactions at regulatory elements, the formation and function of euchromatin and heterochromatin, and the regulation of 3D nuclear organization. Taking advantage of the experimental amenability and defined lineage of C. elegans, we apply high-throughput genomics, super-resolution microscopy, single-cell analyses, and computational approaches to understand core mechanisms of gene expression regulation in development.

Selected publications:

JULIE AHRINGER
Developmental regulation of chromatin structure and function

Heterochromatin in early development in C. elegans
Embryonic nuclei imaged using STED super-resolution microscopy reveals that H3K9me2 is found in distinct foci.
Stem cell populations in tissues as varied as blood, gut and brain spend much of their time in a mitotically dormant, quiescent, state. A key point of regulation is the decision between quiescence and proliferation. The ability to reactivate neural stem cells in situ raises the prospect of potential future therapies for brain repair after damage or neurodegenerative disease. Understanding the molecular basis for stem cell reactivation is an essential first step in this quest.

In Drosophila, quiescent neural stem cells are easily identifiable and amenable to genetic manipulation, making them a powerful model with which to study the transition between quiescence and proliferation. These stem cells exit quiescence in response to a nutrition-dependent signal from the fat body, a tissue that plays a key role in the regulation of metabolism and growth. My lab combines cutting-edge genetic and molecular approaches with advanced imaging techniques to study the reactivation of Drosophila neural stem cells in vivo. This enables us to deduce the sequence of events from the level of the organism, to the tissue, the cell, and finally the genome.

Selected publications:
How does ionising radiation affect tissue homeostasis? Healthy adult epithelial tissues progressively accumulate clones of cells carrying mutations implicated in cancer. Expansion of the clones follows Darwinian evolution rules, where some mutations can increase cell fitness and promote the growth of clones at the expense of the non-mutated normal adjacent cells, in a process of clonal competition.

Ionising radiation has long been studied as one of the most common environmental mutagenic agents that promotes tumour formation by damaging DNA and creating new oncogenic mutations. However, little is known about its effects on clonal evolution and tissue dynamics. We have recently shown that radiation can act as an environmental selective pressure, affecting cell competition mechanisms and promoting expansion of pre-existing oncogenic mutations, which might increase the risk of cancer development.

We use long-term human and mouse 3D primary epithelial cultures, in vivo cell lineage tracing, mathematical modelling, next generation sequencing methods and state-of-the-art confocal microscopy techniques to unravel the molecular responses and the cellular interactions that control normal and mutant cell behaviours after exposure to ionising radiation.

Our final aim is to set the basis for designing external interventions that can modulate cell competition outcomes during radiation exposure, eliminate oncogenic mutations and reduce the risk of cancer initiation and progression.

Selected publications:

The fight for space during ionising radiation exposure
This rendered image shows an irradiated mouse oesophageal epithelium populated by fitter oncogenic mutant clones (green) that are expanding at the expense of non-mutated normal adjacent cells. Proliferation markers are shown in white and red; cell nuclei in blue.
How do cells control their movement? Cells move during embryonic development and throughout the life of an organism. When they move, cells reorganise a system of filaments - the actin cytoskeleton - that gives them their shape and exerts force on the surrounding tissues. When regulation of the actin cytoskeleton is disrupted it can lead to cancer metastasis, intellectual disability, kidney dysfunction and other problems.

We study how the actin cytoskeleton is assembled in different ways. The cell membrane is an important site of control of actin rearrangements because it is the boundary between the outside and inside of the cell and is responsible for initiating communication between and within cells, which is called signalling.

We have developed cell-free systems using phospholipid bilayers and frog egg extracts that allow us to find out how signalling lipids in the cell membrane precisely control the molecular events of actin assembly. We use combine these cell-free systems with the use of fruit flies, frog embryos and cultured human cells to test and generate hypotheses about the molecular events underlying actin regulation during development and disease.

Selected publications:

Watching filopodia grow
Three-dimensional reconstruction of filopodia-like structures growing from a supported lipid bilayer. The structures were segmented based on fluorescent actin intensity in a stack of microscopy images of size 76.13 x 76.13 x 30 microns.

Colours were randomly assigned as a guide for the eye. The segmentation was performed using a custom image-analysis pipeline.
Can we make cell reprogramming more efficient? Our group focuses on somatic cell nuclear transfer to amphibian eggs and oocytes from two complementary points of view. One aims to identify the molecules and mechanisms by which the cytoplasm of an egg or oocyte can reprogramme the nucleus of a differentiating somatic cell to behave like that of an embryo. From this state, many different kinds of cells for replacement can be generated.

The other aim is to identify the molecules and mechanisms that stabilise the differentiated state of somatic cells, as a result of which they resist reprogramming procedures. For these purposes we use single nuclear transfer to unfertilised eggs or multiple nuclear transfer to ovarian oocytes.

We make use of the special properties of an amphibian oocyte to inject messenger RNA that codes for a transcription factor protein. When this has been synthesised, it concentrates in the oocyte nucleus. The next day we inject plasmid DNA directly into the oocyte nucleus, where the factor causes transcription, and later expression, of a reporter gene in the plasmid.

Selected publications:
DNA is constantly damaged by environmental and endogenously arising agents. Cell survival and genome integrity are promoted by the DNA-damage response (DDR), which detects, signals the presence of and repairs DNA damage. DDR defects are associated with developmental disorders, immunodeficiencies, infertility, premature ageing and cancer. Our research aims to characterise the cell biology and mechanisms of established and new DDR pathways and components, and to apply this knowledge to better understand and treat human diseases.

We have taken the global approach of cataloguing the >4,500 knockout genes of the diploid yeast knockout collection, using next-generation sequencing to identify those genes that have an impact on genome stability. Analysing this dataset revealed genes affecting repetitive element maintenance, and nuclear and mitochondrial genome stability, and showed how strains adapt to loss of non-essential genes. At the other end of the scale spectrum, we determined what structural features of the DDR factors PALB2 and MDC1 associate with chromatin in ways that are crucial for effective DDR in the absence of BRCA1 and H2AX, respectively.

Selected publications:


Do enzymes that modify chromatin and RNA offer therapeutic targets? DNA exists in the cell nucleus wrapped around histone proteins to form chromatin. The DNA and histones are decorated with many types of covalent chemical modifications, which can affect transcription and other cellular processes. In addition, non-coding RNAs that regulate chromatin function can be similarly chemically modified. Our lab is involved in characterising the pathways that mediate and control DNA, RNA and histone modifications. We try to understand the cellular processes they regulate, their mechanism of action and their involvement in cancer.

Our focus at the moment is modifications of messenger RNA (mRNA) and non-coding RNA. There are very few modifications identified on these low-abundance RNAs, unlike on transfer RNA and ribosomal RNA, where there are many. We have been developing sensitive technologies to detect modifications, such as specific antibodies, chemical reactivity assays and mass spectrometry. Using these, we have been able to detect a number of novel modifications on mRNA and microRNA (short-length non-coding RNAs) and have shown that these function to regulate mRNA translation and microRNA processing. Furthermore, we have shown that the enzymes that mediate these modifications are implicated in cancer. We are developing small-molecule inhibitors against some of these enzymes in collaboration with STORM Therapeutics.

Selected publications:
How mitochondrial genomes are transmitted and maintained. In addition to the nuclear genome, all animals have another genome packed inside the mitochondrion called mtDNA. This maternally inherited genome encodes important proteins for energy production. During development and ageing, as mtDNA continues to replicate and turnover, mutations can occur to some of the copies. The subsequent prevalence of these mutants, which determines the progression and inheritance of the clinical abnormalities of mitochondrial disorders, depends on how they compete with the co-existing wild-type genomes for transmission. To date, over 50 mtDNA-linked disorders have been described in humans.

We have developed genetic systems in Drosophila to study the rules governing the transmission of mtDNA mutations. By creating fruit flies carrying both functional and pathogenic mitochondrial genomes, we reveal nuclear factors and mtDNA sequence polymorphisms that bias the transmission of one genome over the other. We also study repair mechanisms that safeguard the integrity of mtDNA during development and ageing.

Selected publications:

The maternally transmitted mitochondrial DNA (mtDNA) is a multi-copy genome that shows complex transmission patterns during developing and aging, and between generations due to relaxed replication, random segregation, and selection that favours the transmission of one genome over another in the pool. In addition to mitochondrial diseases caused by accumulation of a particular mutant, random mtDNA mutations have been shown to increase with age, contributing to mitochondrial dysfunction and various age-related conditions.
What does non-coding RNA do in development and disease?

Most of the RNA transcribed from the DNA in our genome is not translated into protein but instead has direct functions in regulating biological processes. This paradigm shift in nucleic acid biology has been supported by technical advances in high-throughput sequencing, molecular genetics and computational biology, which can be combined with more traditional biochemical analyses.

Many species and roles of non-coding RNA have been identified. Our goal is to understand how non-coding RNAs regulate development, physiology and disease. We are exploring microRNA in the pathology of cancer and other diseases, RNA interference in viral immunity, Piwi-interacting RNA in germline development and genome integrity, and endogenous small interfering RNA in epigenetic inheritance – where we predict a big impact in understanding human health. Our model organisms are the nematode worm, the cichlid fishes of the Rift Lakes of East Africa, mouse, and human cell culture. More recently we have developed a technology to assess RNA structure and RNA–RNA interactions in living systems. We used this to uncover unexpected biology for the Zika virus, and key regulatory mechanisms for SARS-CoV-2.

Selected publications:


The Zika virus genomic structure inside human cells

The Zika virus genome adopts alternating structures as the 5’ cyclization sequence (CS) participates in interaction with host microRNA miR-21 (top), capsid translation (right), and genome cyclization (left).
How do stem cells build and maintain the lung? The complicated three-dimensional structure of our lungs is essential for respiration and host defence. Building this structure relies on the correct sequence of division and differentiation events by lung progenitor cells, which also maintain the slowly turning-over airway epithelium in the adult. How is the production of different cell types controlled in embryonic development and adult maintenance? We apply mouse genetics, live imaging, single-cell molecular analysis and mathematical modelling to understand lung stem cells, with a longer-term aim of directing endogenous lung cells to repair, or regenerate, diseased tissue.

In the adult lung we focus on the cellular mechanisms that maintain stem cell quiescence at steady-state, but allow a rapid repair response when needed. In the embryonic lung we study a population of multipotent progenitors that undergo steroid-induced changes in competence during development. In the embryo, we have recently switched our focus to normal human lung development, primarily using an organoid system that we developed. We combine the analysis of fresh human embryonic tissue with gene-targeting in the organoids, to determine the molecular and cellular mechanisms of normal human lung development. This will provide insights into conditions related to premature birth and into the possibility of therapeutic lung regeneration.

Selected publications:
Nikolić M et al. (2017) Human embryonic lung epithelial tips are multipotent progenitors that can be expanded in vitro as long-term self-renewing organoids. Elife 6: e26575.
How do cells know ‘up’ from ‘down’? Most cells in the body perform different functions at opposite sides of the cell. This cell polarity is essential in development, for example: in determining the head-to-tail axis of many animals, for cell migration and for asymmetric stem-cell divisions. Furthermore, loss of polarity is a hallmark of tumour cells and is thought to contribute to tissue invasion and metastasis. Our work focuses on epithelia, the sheets of polarised cells that form barriers between compartments and make up most of our organs and tissues. We study the factors that mark different sides of epithelial cells and how these organise the internal cell architecture, using the Drosophila intestine and the follicle cell epithelium as models.

We have recently discovered that the gut epithelium polarises by a fundamentally different mechanism from other fly epithelia, and is much more similar to mammalian epithelia. We are now identifying new polarity factors in the fly gut and are testing whether these play similar roles in mouse intestinal organoids. We are also using live microscopy to visualise polarised secretion in epithelial cells, and quantitative super-resolution microscopy to examine the clustering and co-localisation of polarity proteins.

Selected publications:
Fic W et al. (2019) Drosophila IMP regulates Kuzbanian to control the timing of Notch signalling in the follicle cells. Development 146: dev168963.
How do stem and progenitor cells regulate their fate behaviour to specify and maintain tissues? During development, cell proliferation and differentiation must be coordinated with collective cell movements to specify organs of the correct size, pattern and composition. In the adult, stem cells must regulate a precise balance between proliferation and differentiation to maintain tissue homeostasis.

To address the mechanisms that regulate stem and progenitor cell fate, we combine cell lineage-tracing approaches and single-cell gene expression profiling with concepts and methods from statistical physics and mathematics. Applied to epithelial tissues, we have shown how common principles of self-organisation and emergence provide predictive insights into the cellular mechanisms that regulate tissue development, maintenance and repair. As well as questioning the nature of stem cell identity and function, these studies emphasize the role of cell fate stochasticity and state flexibility, and establish a quantitative platform to investigate pathways leading to cancer initiation and progression.

Selected publications:

Cell lineage tracing in the stomach corpus
Genetic lineage tracing using a multicolour confetti reporter system reveals the compartmentalisation of the mouse stomach corpus gland. (Credit: Juergen Fink and Seungmin Han.)
What makes a germline cell? We study primordial germ cells (PGCs), precursors to eggs and sperm, in the early embryo. We have established principles of early human development with a focus on human PGC (hPGC) specification. A unique epigenetic resetting follows in the germline after hPGC specification. Our work shows that SOX17 is the key regulator of human, but not mouse, germ cell fate. By developing in vitro models, and with authentic hPGCs from human embryos, we have also established how pluripotent stem cells gain competence for germ cell and somatic fates in human. These findings are important for studies on human pluripotent stem cells and regenerative medicine. The inheritance of genetic and epigenetic information from the germline through the totipotent state affects human development and disease for generations.

Whereas SOX17–BLIMP1 apparently initiate the epigenetic programme in early human germline, BLIMP1–PRDM14 play a similar role in mouse germline, resulting in the comprehensive erasure of DNA methylation (except for some resistant loci), X-reactivation and imprints erasure, followed by re-establishment of sperm- and oocyte-specific imprints. Defects in these gamete-specific imprints lead to a variety of human disease syndromes. We have also examined mitochondrial DNA (mtDNA) in PGCs, showing evidence for selection against mitochondria that harbour mutations. This mechanism is imperfect and can account for inherited mtDNA disorders.

**Selected publications:**


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**What we know about primordial germ cell development**

Primordial germ cells are the first cell type to be specified in vivo in early human development. We have developed a protocol using specific signalling molecules to generate primordial germ cell-like cells in vitro from human pluripotent stem cells. We found that SOX17 is a critical determinant of human germ cell fate.
The overarching goal of our research is to use novel genetic approaches to study epigenetic pathways and the mechanisms through which these processes are corrupted by disease-associated mutations in chromatin regulators. We aim to (1) understand the molecular mechanisms used by chromatin regulators to exert their function in healthy human cells, and (2) examine how these mechanisms are altered in cancer.

We leverage high-throughput genetic technologies, such as CRISPR/Cas9 genetic screens, to discover novel factors involved in chromatin pathways. This approach has led to the identification of HUSH, a previously uncharacterised chromatin-modifying complex. In addition to mediating position-effect variegation in human cells, the HUSH complex also plays key roles in the silencing of retro-elements and unintegrated retroviral DNA, and as a restriction factor for Human Immunodeficiency Virus. Therefore, a major focus of our research is achieving a mechanistic understanding of HUSH-mediated repression. In parallel, we are developing novel genetic approaches that would allow us to interrogate other epigenetic pathways in an analogous manner.

Selected publications:


What forces drive tissue morphogenesis? Embryos are made of soft materials consisting of cells with limited mechanical capacities, yet they develop in a robust and coordinated manner and produce large-scale deformations (morphogenesis). We are interested in the ways in which developing tissues produce and respond to mechanical forces in order to achieve the correct shape and pattern. This knowledge is useful for understanding complex birth defects and engineering stem or reprogrammed cells into tissues, as well as interpreting the changes in diseased tissues such as tumours.

We use early avian embryos as a model system. The large size and accessibility of these embryos allow us to image cell and tissue dynamics, perform molecular genetic perturbations, and deploy novel mechanical tools such as soft gels and cantilevers to measure and apply forces. By integrating cell and tissue dynamics, we found that the paraxial mesoderm and axial tissues coordinate their elongation through mechanical feedback. We are currently investigating if the identified forces are also important for the straightness (bilateral symmetry) of the tissues and the folding of the neural tube.

Selected publications:

Naturally occurring twin chick embryo
Bright-field image of a rare pair of well-formed separate embryos sharing one egg. The embryos show a head-to-head alignment. Body axis and somites are visible. (Credit: Daniele Kunz)
How is DNA replication controlled? A fundamental requirement for all life on earth is that an exact copy of the entire genome must be made before cell division. DNA replication is therefore tightly regulated because failures in this process cause genomic instability, which is a hallmark of many diseases, most notably cancers. In addition, inhibition of DNA replication is the primary mode of action of many anti-tumour therapies. Therefore, investigating DNA replication control is important for finding new ways to diagnose and treat cancers. The evolutionary conservation of DNA replication mechanisms allows us to study this process in multiple systems, facilitating the translation of findings to humans.

We have shown that the levels of several key replication factors are critical to control the rate of genome duplication, not only in the single-celled organism, budding yeast, but also during vertebrate development in frog embryos. Our studies demonstrate that regulation of the levels of these factors is vital not only for normal cell division, but also for regulating the rate of cell proliferation in animal tissue. This has important implications for the deregulation of cell proliferation, which occurs in cancers.

Selected publications:
How are cellular memory states switched and maintained? Our group combines simple, predictive mathematical modelling with long-lasting experimental collaborations, to dissect biological mechanisms too complex to unravel by experiments alone. In many cases we are able to rationalise complex biological dynamics into simple underlying mechanisms, with few components and interactions. Our approach is highly interdisciplinary and relies heavily on the techniques of statistical physics and applied mathematics, as well as on close collaboration with experimental groups. This truly interdisciplinary approach allows us to get to the heart of biological mechanisms more speedily.

At present the main focus of the group is epigenetic dynamics, probing how epigenetic memory states are set up and then stably maintained. In this context, we work with histone modification memory systems, as well as on DNA methylation, collaborating with experimentalists in systems ranging from plants to mammalian stem cells. A particular focus has been the Polycomb epigenetic system, where we have proposed an all-or-nothing epigenetic switching mechanism, with epigenetic gene silencing directly antagonised by transcription. Overall, as epigenetic systems are central to health, understanding how they work at a fundamental level is of vital importance.

Selected publications:

Modelling Polycomb epigenetic dynamics
Top: schematic of chromatin state in active (upper) and repressed (lower) state. KDM: histone demethylase; Pol II: RNA Polymerase II; PRC2: Polycomb Repressive Complex 2; orange hexagons: histone H3K27 di- and trimethylation. Middle: key ingredients of a mathematical model for Polycomb dynamics; me0/1/2/3: methylation state of H3K27. Bottom: simulation of repressed state (high H3K27me3) (left) and of repressed state switching to an active state (right), both periodically perturbed by DNA replication. (Image credit: Dr Scott Berry).
What are the biological mechanisms that link patterns of growth and reproductive ageing to later life disease? Epidemiological studies have long linked patterns of early-life growth and reproductive ageing to later life diseases, yet the biological mechanisms underpinning these associations remain unclear. For example, what are the pathways that link variation in onset of puberty to risk of type 2 diabetes and cancer decades later? To explore this, we use large-scale human population studies to identify genetic variants that influence risk of disease or contribute to variation in quantitative traits. Through integration with transcriptomic and proteomic datasets we can then prioritise genes and pathways for evaluation with experimental collaborators using animal and cellular models.

My research is primarily based at the MRC Epidemiology Unit where I co-lead an MRC-funded programme with Professor Ken Ong. My Associate position at the Gurdon Institute focuses on one of the key biological mechanisms emerging from our population-based research: DNA damage response (DDR). Although often considered in the context of cancer susceptibility, it is now clear that DDR processes influence other complex diseases and traits. For example, our human genetics work has highlighted DDR as the major pathway governing reproductive ageing and fertility in women. We aim to better understand these processes, when they act over the life-course and how they might be modified to preserve fertility and prevent disease.

**Selected publications:**
Media/glasswashing service
The media team provide quality-controlled buffers, growth media, worm plates, bacterial plates, fly vials and bottles, and standard and custom solutions. They collect and wash used glassware and provide sterile supplies.

Typical annual production of media includes 400,000 vials and bottles of fly food, 300,000 nematode worm plates; and over 100 different recipes for buffers, media and solutions.

Find out more about the media team in the video for our YouTube series: ‘A Year in Institute Life’.

Microscopy and image analysis
The team run the technical support for a wide range of the latest imaging technologies, as well as providing training, research contributions and custom software development.

Researchers have access to confocal, light-sheet and super-resolution (STORM, PALM, STED, SIM) microscopes. We also have a cell-sorting core.

The duo building our new super-resolution microscopes describe their work in a video in our YouTube series: ‘A Year in Institute Life’.

Next-generation sequencing and bioinformatics
On-site sequencing allows researchers to access results with a quick turnaround. Bioinformatics expertise is provided by core posts as well as by research-group-based posts. A High Performance Computer cluster offers researchers the capability to process sequencing data in-house. These services are backed up by locally available courses in a variety of programming and analysis tools.

The sequencing service is featured in a video in our YouTube series: ‘A Year in Institute Life’.

IT/computing
The computing team provides flexible and high-quality IT infrastructure, services and support for all research and administrative computing activities within the Institute. We maintain high performance, high capacity and high bandwidth systems that are secure, resilient and highly available, ensuring the efficient movement, secure storage, and future accessibility and re-use of a very large volume of research data. We also strive to provide the very best levels of user support and engagement, responding rapidly to both problems and opportunities for new services.
Support staff

Administration
Bruce Daniels LLB DipLP BTh
Administration and Operations Manager
Jane Course
Finance Manager
Jayne Fisher
Finance/ Accounts Assistant
Diane Foster
Deputy Administration and Operations Manager, Principal Technician
Emma Gant BA PGCert
Research Grants/ HR Coordinator
Iolanda Guerra
Health and Safety Adviser
Lynda Lockey
Office Manager

Sylviane Moss PhD
Safety and Compliance Manager
Dermot Nolan
Receptionist
Samantha Wilson BSc
Receptionist
Daniel Sargent
HR Administrator
Victoria Stubbs PhD
Shared Facilities Manager

Natalie Walls BSc
Public Engagement Coordinator

Computing/ IT
Alastair Downie
Computer Systems Manager
Nigel Smith
Computer Associate
Peter Williamson BSc
Computer Associate

Communications/ Public engagement
Hélène Doerflinger PhD
Public Engagement Manager
Claire O’Brien PhD
Information and Communications Officer

Bioinformatics
Charles Bradshaw PhD
Bioinformatician

Sequencing
Kevin (Kay) Harnish MSc
Wellcome Research Assistant (Sequencing Facility)

Imaging
Alexander Sossick BSc
Head of Microscopy and Scientific Facilities Co-ordinator, Laser Safety Officer
Richard Butler PhD
Research Associate (Imaging)
Nicola Lawrence PhD
Microscopy Associate/ Deputy Head of Imaging, Laser Safety Officer

Accounts/ Purchasing/ Stores
Ian Fleming
Stores/ Purchasing Manager
Simon Aldis
Purchasing/ Accounts Assistant
David Cooper
Stores Technician
Andrew Vincent
Senior Stores Technician

Media/ Glasswashing
Juanita Baker-Hay
Media/ Glasswashing Manager
Lisa Baker
Laura Carlton
Vincent Dams
Sandra Human

Media/ Glasswashing
Miguel Leon Salvador
Tracy Mitchell
Nathy Villalobos Martinez MA

Imaging

Combined building & services group
Alan Rix
Building Services Manager
Clive Bennett
Custodian
Katharine Bennett
Custodian
Paul Turrell
Custodian
Regimantas Vysniauskas
Senior Building Services Technician

Technical facilities
Polly Attlessey RAnTech MIAT
Facilities Manager
Therese Jones-Green BSc
Manager of Aquatic Services

Zest catering
Amanda Harris
Melissa Plowden Roberts
The Gurdon Institute

Seminars, events and publications in 2019/2020
Seminars

The Gurdon Institute Seminar Series brings high-profile international scientists in front of an audience drawn from across the University, biological sciences departments. Our speakers were:

5 March 2019
Yunsun Nam, The University of Texas Southwest Medical Center, USA. Chemical regulation of functional RNAs of Texas Southwestern Medical Center, USA.

29 October 2019
Arturo Londoño-Vallejo, Institut Pasteur, Paris, France. Human Regulator of TEomere Length (TELcase 1 (TEL1)) couples nuclear envelopping and functions to genome replication.

31 October 2019
Hiten Madhani, University of California, San Francisco, USA. Epigenetic memory over geological timescales.

26 November 2019
Lori Passmore, MRC Laboratory of Molecular Biology, Cambridge, UK. Mechanistic insights into the miRNA poly(A) tail machinery and DNA repair.

28 January 2020
Elaine Fuchs, Rockefeller University, New York, USA. Stem Cells; It’s All About the Poly(A) tail machinery and DNA repair.

28 January 2020
Eduardo Moreno, Champalimaud Centre for the Unknown, Lisbon, Portugal. Cell competition during development and disease.

04 February 2020
Naama Barkai, Weizmann Institute of Science, Rehovot, Israel. The de novo generation of complex traits.

22 Aug and 20 Sept ‘19: East of England MEPs Catherine Rowett (UK Green Party) and Barbara Gibson (Liberal Democrat) visited the Institute to learn about who we are and what we do. Each was on a fact-finding mission to hear from group leaders and young researchers about the impact of the Brexit vote and continuing uncertainty about the future, on people’s lives, career decisions and the UK science base.

14 Oct ’19: Artist Caroline Walker was commissioned by Cambridge University Library to capture images of women working in the lab at the Gurdon Institute. After shadowing researchers in the Rawlin lab and taking photographs, Caroline created a huge oil painting for the library’s entrance hall, on view to the public as part of the exhibition ‘The Rising Tide: Women at Cambridge’. [You can see details from the preparatory oil sketches throughout this prospectus.]

20 Sept ’19: Over 2000 cyclists from 184 organisations across Greater Cambridge took part in the Global Bike Challenge and clocked up 290,466 miles during Cycle September – and many of those were logged by Gurdon Institute staff. The Institute bagged 2nd place in the league tables for companies in our size range. Cycle September is run by cycling organisation Love to Ride.

Jan ’20: The newly launched Cambridge Centre for Physical Biology aims to support and facilitate multidisciplinary collaborations across the University of Cambridge. Gurdon Institute Group Leader Professor Ben Simons is one of the main leaders of the project.

External events

Seminars for the local academic community
Beyond the Gurdon Institute seminars, our members organise, host and support several other series: Developmental Biology Seminars, Cambridge 3Rs (replication, repair and recombination), Life Science Masterclasses and Worm Club.

Sept. 20: Adrestia Therapeutics, the latest biotech company to spin out from the Jackson lab, moved out of the Institute’s temporary incubation space and into new premises on the Babraham Research Campus. The company’s Disease Rebalancing Platform uses synthetic viability to identify phenotypic and molecular imbalances of disease as the basis of novel drug discovery. In Dec ’20 GlaxoSmithKline and Ahren Innovation Capital co-led a substantial Series A investment in Adrestia.

2020:
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- Seminars for the local academic community
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The Gurdon Institute

Events

We hold regular social and sports activities, celebrations and specific events organised by our postdoc and PhD student associations. Here is a selection:

17 Jan ‘19: A Fizz & Food party to celebrate Daniel St Johnston’s 10 years as Director. Several past Group Leaders and our previous Institute Administrator attended. Speeches were followed by an inspired song specially written and sung by Andrew Plygawko (St Johnston lab PhD student).

Feb ’19: Launch of Climbing Club, organised by Miguel Leon Salvador from the Media team. Club sessions run on two evenings per week at the local sports hall.

June ‘19: Launch of the Gurdon Institute PhD Society. Vanessa Sokleva (Rawlins lab), the new President, says: “We want it to be a friendly and safe space for PhD students to talk to each other, ask any questions, and raise concerns - basically get to know each other. We plan to hold events throughout the year.”

7 July ‘19: ‘Our First Family Day’, on a Sunday, featuring a walk, games and a picnic in Grantchester Meadows. Organised by Gurdon Institute Postdoc Association (GIPA) and the Wellbeing, Equality and Diversity (WED) Committee.

12 July ‘19: Our Gratitude Festival was the perfect moment to say Goodbye and a big Thank You to Suzanne (retiring long-serving HR & Grants Manager) and to the Huch and Livesey labs (moving to Dresden and London, respectively). Activities included face painting, tie-dyeing, a bouncy castle and science tattoos.

3 & 4 Oct ‘19: Institute Retreat at Dunston Hall in Norfolk (see p. 76). The schedule had all the usual activities. Talks from all our group leaders, guest speaker Prof Anna Philpott (Stem Cell Institute and Head of School of the Biological Sciences), ‘treasure hunt’ games, poster session and plenty of fun on the dance floor after dinner.

Prizes announced at the Retreat: Three best posters (Rue Jones-Green, Leis Judge & Israel Salguero); Image competition (Chufan Xu); Video competition (Chufan Xu); Public Engagement Champion (Bernhard Strauss for many years running workshops for sixth formers, supporting work experience students, and taking part in numerous external events); Kathy Hilton Energy and Environment Champion (Kate Dry, for crisp packet recycling scheme); Ann Cartwright Good Citizen Award (the Maintenance Team for their unfailing brilliant work); Martin Evans Award for the greatest contribution to Institute social life (Miguel Salvador, for organising Climbing Club).

25 Oct ‘19: Halloween Happy Hour by the Jackson lab. The undisputed winner of the pumpkin carving competition was David Jordan (Miska lab).

22 Nov ‘19: GIPA Pub Quiz Happy Hour.

10 and 13 Dec ’19: Children’s and Adults’ Christmas parties (the latter with Cartoon Character fancy dress).

6 Mar ‘20: GIPA Carnival evening July ’20: The PE team supported one session of the Secret School for Curious Children. ‘Invisible Nature’ took place in the sunny outdoors with social distancing, and featured the popular Zoom boxes that create a microscope out of a mobile phone. Children scavenged for specimens and learnt about magnification.

1 & 2 Oct ’20: virtual Institute Retreat. We had two half days to hear the talks from researchers and core teams, and an evening session for the ‘treasure hunt/ quiz’. Awards went to those making exceptional contributions to the Institute during the pandemic. For enabling lockdown and reopening: Fabian Braukmann, Chris Camia, Andrea Frappoti and Rsopali Pradhan. For handmade masks: Carmen Calabrese. For bringing us through lockdown 1.0 and safely back to work: Dr Foster, Sylviane Mosi, Katherine Wallington and Arianna Pezzuolo.

The Public Engagement Champion Award 2020 goes to Edward Allgeyer, for creating a workshop enabling students to build simple microscopes for the CAST microscopy challenge, run in collaboration with our Imaging team and Zeiss.
Publications in 2019


Publications in 2019


Publications in 2020


- DOI: 10.1038/s41467-020-15555-8.

- Nat Commun 11:1741. doi: 10.1038/s41467-020-18276-1

- RNA likely independent of nutritional dsRNA uptake.

- EA 10.7554/eLife.55325.


- DOI: 10.1038/s41593-020-00759-4.


- DOI: 10.1371/journal.pgen.1008948.


- DOI: 10.1073/pnas.2000467117.


- DOI: 10.1101/2020.08.13.249698.

- (2020) Visualization of individual cell division and cell cycle in C. elegans Samples Using Nanofluidic Technology.

- DOI: 10.1371/journal.pbio.2008470.

- Cell Populations as Self-Renewing Many-Particle Systems.


- The Gurdon Institute


Full staff lists for 2019 and 2020 can be found in the online supplement at www.gurdon.cam.ac.uk/about/prospectus

International Scientific Advisory Board 2019 and 2020

Professor Sir Adrian Bird (Chair)
Wellcome Trust Centre for Cell Biology, University of Edinburgh

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The Francis Crick Institute, London

Dr Pierre Léopold
Institut Curie, Paris

Acknowledgements

Photo and image credits

Front cover image: By Andy Li (Ma lab), who says: “This image shows the testis of Drosophila melanogaster expressing centrosomin-GFP (green) and tubulin-RFP (red) and stained to show cell nuclei (DAPI; blue), captured on the Leica SP8 confocal microscope at 630X magnification. The image has been processed to resemble a projection of the world map, to symbolise the international scientific community at the Gurdon Institute.”

Back cover image: By Oné Livia Batlle (Brand lab). Drosophila melanogaster salivary glands, captured with an SP8 confocal microscope at 10X magnification, visualised by staining cell nuclei (DAPI; cyan) and actin (Phalloidin; magenta).

Portait groups: Group leaders by Chris Green, except: pp 3. 28 & 30 by James Smith; p 28 by Lisa Himmelseder; p 48 by brandAnonymous; pp 22, 24, 46, 48, 52 & 54 unknown.

Research group and support staff photos by Chris Green except pp 24 & 54.

Other photos: P 5 (l) and p 63 (MEP) James Smith; p 5 (mid and r) Natalie Glasberg; p 17 (l) Naum Glencross-Bird; (r) Stephanie Norwood; p 56 Sylivane Mosis; p 57 (l) Al Downie; p 64 Miguel Salvador; pp 65 labcoats & 76 by Peter Williamson; p 65 family day by Jelle van den Ameele, party costumes by Florence Leroy.

Other images: Research illustrations pp 4, 16 (l), 29, 31, 33, 35, 37, 41, 45, 47, 51 & 53 by Claudie Randolfi; pp 6-7 coronavirus by Onisha Patel; p 16 (l) Danila Sarac; p 64 Claudie Stochler.

Section-headers pp 8-9, 18-19 & 60-61: details from oil sketches by Caroline Walker.

Production: Edited and produced by Claire O’Brien, thanks to Emma Sans, Daniel Sergent, Helene Dowerfinger and Kathy Oswald.