Postdoctoral Programme in Evolutionary and Epidemiological Dynamics
The Sanger Epidemiological and Evolutionary Dynamics (SEED) Postdoctoral Programme offers the chance to develop and implement innovative methods for analysis of large-scale genomic datasets to address fundamental problems concerning the evolution, transmission dynamics and control of major infectious diseases.

SEED Fellowships are based within the Parasite and Microbes Programme at the Wellcome Sanger Institute. Each project is co-supervised by an Associate Faculty member and a Sanger Group Leader, and where appropriate there can be more than two supervisors. By linking projects to both Associate and Core Faculty, we bring together a supervisory team comprising world leaders in genomics, infectious disease epidemiology and mathematical modelling.

This Postdoctoral Programme provides many opportunities for international collaboration. The Wellcome Genome Campus has a large critical mass of scientific expertise with well-equipped facilities and an active seminar programme.

Predefined projects
Listed below are a selection of projects and Faculty contact points that illustrate the research areas we envisage for the SEED Fellowships. However, we are keen to incorporate your own expertise and interests into these projects and so they provide a starting point only. If selected, we will work with you to develop a research projects which you will present in the final stage of the SEED recruitment process. Projects will be co-supervised by at least one member of our Associate Faculty members and a Sanger Group Leader in the Sanger Parasites and Microbes Programme. Please apply via our job site.

Transmission dynamics and control of major infectious diseases

- Mapping long range transmission across South and South East Asia
- Genomic epidemiology for SARS-CoV-2: sooner and later
- Genomic approaches to the evolutionary dynamics of malaria drug resistance
- Spatiotemporal Genomics in Anopheles mosquitoes

Fundamental questions concerning evolution and/or disease

- Biodiversity and Functions of Gut Phages Impacting Human Health and Disease

Innovative methods for analysis of large-scale genomic datasets

- Respiratory microbiome analytics
- Enabling latest machine learning tools for calibrating large-scale transmission simulator models to estimate parameters of epidemiological/evolutionary interest, and to test intervention policies in silico under uncertainty

A detailed outline of these projects can be found across the following pages.

Self-proposed projects
You are welcome to propose a project of your own. This would need to be co-supervised by at least one member of our Associate Faculty members and a Sanger Group Leader in the Sanger Parasites and Microbes Programme. Please submit a brief outline proposal (approximately 500-1000 words) to the Group Leader and Associate Faculty member who you would like to work with via SEEDfellowship@sanger.ac.uk. Your proposal will need to be approved before you submit the application. Once approved, please apply via our job site.
TRANSMISSION DYNAMICS AND CONTROL OF MAJOR INFECTIOUS DISEASES

Mapping long range transmission across South and South East Asia

Point of contact: Nick Thomson

Through successful collaborations with partners in Bangladesh and across South and South East Asia and by partnering with the major mobile phone operators we aim to understand the human population dynamics that leads to the dissemination of outbreaks. Over the next few years we will extend our collaborative networks to conduct detailed surveillance of important pathogens linked to diseases such as Cholera, Pneumonia and Covid19. Since surveillance for infectious diseases, like cholera, is virtually nonexistent in countries like Bangladesh outside of the capital cities Dhaka, we will maximise impact by combining the high throughput large scale sequencing capacity of the Sanger with a distributed genomic sequencing network using MinION nanopore sequencing approaches. These low-cost highly effective ‘lab in a suitcase’ have been successfully deployed by us and our partners in South Asia to analyze SARS-COV-2 genomes over the last year and a half.

By combining genomics, detailed epidemiology and mobility data streams we aim to discover environmental reservoirs, hotspots and transmission pathways to other parts of the country and region as well as building a distributed capacity for the reliable collection, generation and reporting of genomic epidemiological data in rural areas that are most vulnerable to disease.

Here we propose to build

We propose to hire a talented SEED fellow to work on methods to integrate these two analytical approaches, since currently genomic surveillance and models parameterized using mobility data usually use separate analytic tools. In previous work (with collaborators including Prof Kwiatkowski) we have started to develop integrated models of this kind for malaria, but environmental samples represent a different challenge because they monitor complex environmental reservoirs for potentially outbreak-causing pathogens, rather than clinical samples. Spatial epidemiological models also tend to rely on one or other type of data, and in both cases these methods are relatively new, rather than leveraging both sources of information. The integration of this kind will require a researcher who is comfortable with dynamical modeling, bioinformatic and genomic analysis, and handling large data sets such as those from mobile phones.

This project will benefit from the expertise of other Associate Faculty members, since these analytical tools are generally applicable to other pathogens. In fact, the longer-term goal for this project is the integration of genomic data from multiple pathogens and mobility data, since - depending on the transmission route - these surveillance platforms should be relevant across infectious disease causing organisms. Bangladesh is an ideal place to start because it encompasses so many of the challenges facing LMICs globally, and we have long-standing collaborative networks across different pathogen systems, in industry, and in academia.
Transmission dynamics and control of major infectious diseases

Genomic epidemiology for SARS-CoV-2: sooner and later

Point of contact: Caroline Colijn

We propose an AF project to establish the immediate-term genomic epidemiology for SARS-CoV-2, including its use in real time, and the longer-term integrated modelling and genomic surveillance to detect increased transmission, monitor for emerging potential vaccine escape strains and to monitor for impacts of selection.

In the immediate future we would establish robust and flexible clustering methods to identify sets of cases that are plausibly linked by transmission; cluster-specific epidemiologic parameters and high-resolution (in time and across clusters) transmission dynamics. These include age- and/or location-specific contributions to the force of infection through time.

Clustering is challenging because both rapid bursts of transmission and longer-term partially-observed transmission chains contribute to epidemiologically-linked transmission, and because SC2 accrues limited genetic diversity on the time scale of an outbreak. The combination of genomic and epidemiologically-defined clusters can help to determine likely routes of transmission and to identify settings with a high risk of onward transmission, particularly if this can be done in collaboration with public health teams. We will establish a warning system to detect emerging clusters with a higher-than-expected rate of growth, and will develop the appropriate baselines for comparison.

We will establish methods to estimate population dynamics and epidemiological parameters in resolved clusters, using genomes and Ct values, age and demographic information where available, together with state of the art inference methods. Using and adapting insights from the PANGEA2 consortium we will elucidate genomic signatures of transmission sources and sinks over time, answering questions such as “what was the force of infection from university students in the autumn of 2020”. We will extend these to real-time analyses and estimates as the data flows become established. Together, these high-resolution cluster-specific inferences will allow us to model cluster-specific transmission dynamics and to determine which interventions might have the most impact on curbing transmission at which place and time. We anticipate that this will have direct application as vaccines become available, as age-specific forces of infection over time (together with knowledge of the timing of control measures) will help to inform models to simulate vaccination programmes.

In the second phase of the project we will establish real-time genomic surveillance capable of monitoring for sharp increases in transmission, building on the estimation and detection methodology in the first phase. In particular we would seek to detect any potential vaccine escape strains as early as possible, using a combination of the cluster-specific dynamics and knowledge of plausible determinants of vaccine escape, in the context of strong real-time sequencing. We will also establish real-time monitoring of impacts of other forms of selection acting on the virus. The aspect of the project should link to work in international genomic surveillance of zoonotic viruses and their evolution, including evolution in animal hosts.
Transmission dynamics and control of major infectious diseases

Genomic approaches to the evolutionary dynamics of malaria drug resistance

Point of contact: Dominic Kwiatkowski

The goal of this SEED fellowship project is to gain novel insights into the evolutionary, epidemiological and demographic processes that determine the emergence and spread of antimalarial drug resistance, using a large resource of genomic variation data that we have generated with our MalariaGEN partners around the world (www.malariagen.net). Over the next five years we plan to enlarge this dataset by sequencing over 50,000 samples collected longitudinally at approximately 100 locations around the world, along with data on malaria control interventions and key epidemiological variables at each sampling location. Each sample will have high quality genotype calls on over 3 million polymorphisms including SNPs, indels and copy number variations, thus enabling detailed analyses of population structure, drug resistance, gene flow, migration and natural selection at both the local and the global level.

One of the most intriguing features of antimalarial drug resistance is that it often evolves in several stages, typically starting with a soft selective sweep of multiple independent origins of resistance. Some resistant lineages rise to a much higher frequency and spread over a much wider geographic range than others and, as they expand, they can acquire additional mutations and recombinant forms that increase their biological fitness. This raises a variety of fascinating evolutionary questions. Is it true, as is often postulated, that drug resistance mutations carry a fitness cost that is mitigated by compensatory mutation? Do major increases in fitness advantage result from epistatic interactions with other loci? What is the role of within host competition versus transmission fitness in selecting for dominant lineages? To what extent is drug resistance spread by local dispersal as opposed to long-range human migration?

This project will provide the opportunity to combine human migration data with longitudinal genomic data collected at high spatiotemporal resolution, developing new methods for integrating genetic data into epidemiological models, and for combining genetic data with mobile phone data to estimate patterns of human migration (Wesolowski et al., 2018). It could also include new methods for inference of evolutionary processes from longitudinal genomic data, such as phylodynamic analysis of specific drug resistance loci as well as computational approaches for constructing genealogies at all loci across the genome (Speidel et al., 2019, Kelleher et al., 2019).

The supervisors are open to other suggestions about how to utilise this major data resource to get at fundamental problems in parasite evolution and transmission dynamics. There are many different ways to approach this problem and it offers a great opportunity to explore this very rich biological dataset while also building new analytical and computational tools that will drive the field forward.
Spatiotemporal Genomics in Anopheles mosquitoes

Point of contact: Mara Lawniczak

Over the next five years, will generate whole genome sequence data on 50,000 mosquitoes from the species that account for most malaria transmission in Africa. These specimens will be collected in systematic spatiotemporal sampling frameworks to study evolutionary responses to malaria control. Additionally, for some sites and species (subject to museum collections) we will sequence genomes from historic specimens collected over the past century to understand longer term evolutionary changes, including when the first molecular signatures of insecticide resistance arose in different locations and longer term evaluation of population structure stability.

We are looking for a postdoc interested in examining demographic and evolutionary patterns across the entire genome, although insecticide resistance will be a major focus of our analysis both for its practical importance and because it provides a remarkable opportunity to study the evolution of an animal species under intense selective pressure and in near real time. A suite of new vector control tools will be deployed over the next decade including next generation bednets, novel insecticide formulations for indoor residual spraying, attractive toxic sugar baits to combat outdoor-biting mosquitoes, and possibly field testing of gene drive. We seek a postdoc interested in developing mathematical and statistical approaches to detect early warning signs of emerging resistance. Advances we make in this area will allow vector control programmes to take action, e.g. by rotating to a different insecticide formulation, while allowing us to gain unprecedented insights into the evolutionary process.

Furthermore, the spatial and temporal dimensions of this dataset will make it particularly valuable for analysis of vector population size, dispersal and long-range migration, which are of central importance for planning gene drive strategies and for monitoring vector control interventions in general. Depending on interests, the successful applicant can also lead or contribute to efforts to use haplotype sharing methods to estimate recent migration and population size (Al-Asadi et al., 2019) and to construct genome wide genealogies to estimate longer term fluctuations in population size, population structure and rates of gene flow between species (Speidel et al., 2019, Kelleher et al., 2019).

We are also keen to develop new tree based methods for identifying non neutral processes and this might also be an area a successful applicant is interested in pursuing. There is growing recognition that the process of speciation is far more reticulate than previously thought, i.e. the Tree of Life has many intertwining branches. These longitudinal Anopheles data will be an excellent system to investigate the evolutionary process because of the porous species boundaries and the extremely strong selective pressure that is exerted by insecticides on the whole genus.
Biodiversity and Functions of Gut Phages Impacting Human Health and Disease

Point of contact: Trevor Lawley

Bacterial phages are key drivers of bacterial evolution with wide-reaching influences on ecosystem compositions and functions. A number of human pathogens, such as Vibrio cholerae, Escherichia coli, and Clostridium botulinum, have evolved significant virulence through the acquisition of phage that carrying toxins. Phage have evolved a variety of mechanisms to maintain complex life cycles, such as lysogenic or lytic cycles, or sophisticated defence systems, such as CRISPR, which have been exploited to develop transformational new genomic technologies. Thus, phage genomics represents an untapped treasure trove of unexplored biology and a massive opportunity for biological discovery using data-driven analytics.

We recently discovered 140K phage clades present in the human gut (Camarillo-Guerrero et al Cell 2021) and generated high-quality phage reference genomes allowing us to map their global epidemiology. We are currently at the beginning of a rapid expansion of publicly available human metagenomes (currently 70K publicly available gut metagenomes), from healthy humans and individuals with variety of diseases (IBD, cancer, infections, etc). Coupling this with high-quality, long-read reference genomes of bacteria isolated from the human microbiome provides opportunities to study phage-bacteria dynamics at unprecedented scales and precision. In addition, incorporating available human metadata, we can begin to identify phage functions linked to human health status. By integrating large-scale, high-quality genomic data of gut phages, gut microbiomes and bacterial isolates, the study dataset is ideal for the development and application of innovative statistical and machine-learning approaches. To advance this area, new methods and tools are needed to integrate and analyse heterogenous datasets into robust biological signatures.

We are seeking a data-driven scientist to analyse large-scale genomic datasets using novel machine learning and advanced statistical approaches to explore the biology of the human gut phage to focus on topics such as:

1. Phage-bacteria interactions to identify keystone phage that drive bacteria towards beneficial or pathogenic lifestyles.

2. Mining genomic datasets for phage and phage genes with novel biotechnological applications (i.e. DNA enzymes or therapeutic bioactives).


4. Phage associated with the human disease through analysis of large global metagenome datasets.

5. Tracking strain-level, vertical acquisition and horizontal transmission of gut phages from mother to infants at birth, and between twins and family members.
**Innovative methods for analysis of large-scale genomic datasets**

**Respiratory microbiome analytics**

Point of contact: Stephen Bentley

All respiratory pathogens must encounter the respiratory microbiome through continuous carriage in healthy individuals and during primary or secondary infection. As such, the respiratory microbiome plays a key role in the survival and evolution of respiratory pathogens and the pathways towards disease. Furthermore, the microbiome acts as a barrier to pathogen infection and plays a key role in modulation of immune responses. As already demonstrated for intestinal infections, understanding the composition and dynamics of healthy and diseased respiratory microbiomes has the potential to bring new understanding of these processes. However, respiratory infectious diseases are behind the curve of microbiome research due to the problem of low biomass samples which presents challenges in both sample processing and data analysis.

Building on our successes in gut microbiome and respiratory pathogen research, our aim is to develop a world-class platform for studying the respiratory microbiome. We will exploit access to rare high-value samples to test and validate the application of current technologies and to inform design of potential new approaches. Larger scale studies will then be conducted in collaboration with partners in LMICs to study cohorts of healthy and diseased individuals to allow for statistically rigorous interpretations.

We propose to hire a postdoc who will be dedicated to development of analytics for these future studies. The work will exploit data from large gut microbiome studies (and pilot respiratory microbiome studies) to inform the development of simulations representing equivalent scenarios in the respiratory microbiome that will be used to test potential analytical approaches. Parallel work will focus on the processing and analysis of real respiratory microbiome data. To understand the complex nature of longitudinal microbiome data and its connections to disease and health of the individuals, it is necessary to amend advanced bioinformatics, which process the raw data into analyzable formats, with a range of statistical and computational techniques that include network analysis, supervised machine learning with high-dimensional predictors and unsupervised machine learning to structure data and to identify outliers.

This project fits very naturally with the experience and ambitions of the Parasites and Microbes programme and will greatly benefit from the engagement to the Associate Faculty. While the initial focus is on human respiratory tract samples/studies, in the long term this work will develop a platform that will be valuable to any microbiome research, particularly studies that are restricted to working with complex and low biomass samples.
SEED Projects for 2021

INNOVATIVE METHODS FOR ANALYSIS OF LARGE-SCALE GENOMIC DATASETS

Enabling latest machine learning tools for calibrating largescale transmission simulator models to estimate parameters of epidemiological/evolutionary interest, and to test intervention policies in silico under uncertainty

Point of contact: Jukka Corander

We seek excellent candidates who are interested in operating simultaneously at the frontiers of machine learning and genomic epidemiology. Many recent models in biology describe nature to a high degree of accuracy but are not amenable to analytical treatment. Such models can, however, be simulated on computers to study complex phenomena, such as transmission of pathogens, vectors and genes, and natural selection acting on them. Approximate Bayesian Computation (ABC) and Synthetic Likelihood (SL) are generic likelihood-free inference (LFI) techniques that offer a principled way of fitting such models to data and to quantify uncertainty about model parameters (say $R_0$, strength of selection, effective population size, etc). For a recent example of using such techniques to calibrate a Covid-19 transmission model aimed at assessing the effect of travel restrictions during an earlier phase of the pandemic, see Chinazzi et al. (2020). Recent advances in LFI have accelerated inference by several orders of magnitude to make it a more practically applicable tool. ELFI software by Lintusaari et al. (2018) makes these tools available on an open-source software platform that is under continuous further development. Several new algorithms and features are currently being added by the development team to expand the applicability of ELFI and our near future aim is to bring neural network enabling computational architecture into ELFI via GPyTorch and BoTorch.

The project aims to lay the ground for future ELFI and for calibrating large-scale simulator models to estimate parameters of epidemiological or evolutionary interest. This further allows testing of possible intervention policies in silico while accounting for uncertainty about model parameters. An example of a large-scale spatio-temporal transmission model is provided by Di Ruscio et al. (2019), who considered transmission dynamics of MRSA simultaneously in the healthcare and community settings using a nation-wide simulator model of Norway with millions of geo-located individuals with realistic population densities and mobility patterns. Another example of a large-scale transmission model is the PopART HIV individual-based simulator by Pickles et al. (2020).
Role Profile

Current job title: Postdoctoral Fellow

Reports to: Associate Faculty/Sanger group leader

Role purpose and primary objective: To carry out original research within a defined scientific area appropriate to the team and publish it, while receiving training in research skills from a variety of sources.

Core Accountabilities [in approximate order of importance to role purpose]:

1. To plan a programme of research that is original but fits within the general research area of the team, taking into account the relevant literature, own experience, and advice from the team leader and other appropriate scientists.
2. To carry out the research, developing the practical skills required for successful completion.
3. To analyse data and write up results for publication, and to deal with all aspects of the publication process.
4. To communicate the results through other relevant means, such as talking or presenting posters at scientific meetings.
5. To seek appropriate training, including taking an active part in any training programmes organised for postdoctoral training fellows. This will include transferable skills training.
6. To take a full part in the general duties of the team, and to pass on skills and knowledge to other team members and visitors. To take part in wider Sanger Institute activities as appropriate.
7. To complete training period in a timely manner, publish the research and document any unpublished data and materials before moving on to a new position.

Interacts with Purpose of the interaction

Own team and others Transfer of knowledge, skills, in both directions

Collaborators and other scientists worldwide as appropriate to project Seeking and passing on knowledge, reagents

Describe the most complex/challenging aspects of the role

Planning and carrying out research, and striking an appropriate balance between fitting in with the goals of the team and developing their own independent research projects.
Knowledge, skills and experience required:  

Knowledge, skills and experience required:  E = Essential  D = Desirable

- PhD in a relevant subject area (E)
- Knowledge of a range of research techniques and methodologies in experimental/computational areas (E)
- Research expertise in an area that will complement and enhance the Institute’s research strategy and goals (E)
- Ability to develop research objectives, projects and proposals for own and joint research, with the assistance of a mentor if required (E)
- Experience of carrying out both independent and collaborative research (E)
- Ability to plan and prioritise own work in order to meet deadlines, including using initiative to plan research programmes (E)
- Highly developed communication skills to engage effectively with a wide-ranging audience, both orally and in writing, using a range of media (E)
- Interest in and enthusiasm for the subject matter of the project (E)
- Commitment to personal development and updating of knowledge and skills (E)
- Working collaboratively with others and building working relationships with stakeholders at all levels (E)
- Demonstrates inclusivity and respect for all (E)
- Respects and demonstrates our core competencies outlined in our Behavioural Competency Framework (E)
- Experience working with international collaborators (D)
- Experience of handling and analysing computationally intensive datasets (D)
Application Process

Application process

Pre-defined projects
Please apply via jobs.sanger.ac.uk.

Applications should include:

• A cover letter specifying the project you are applying for (pre-defined by the applicant)
• Your Curriculum Vitae
• Two recent letters of references

Self-defined projects
Before applying via jobs.sanger.ac.uk, you must submit a brief outline proposal (approximately 500-1000 words) to the Group Leader and Associate Faculty member who you would like to work with via SEEDfellowship@sanger.ac.uk. Once approved, please apply on our website, including:

• A cover letter specifying your approved self-defined project
• Your Curriculum Vitae
• Two recent letters of references

Deadline

There will be no specific closing date. Applications will be considered and reviewed on an on-going basis and therefore the post may be filled.

Applicants will be shortlisted and successful candidates will be asked to work with the supervisory team to further develop the project proposal. This is an opportunity for you to incorporate your own ideas and interests into the project plan. The shortlisted candidates will present these extended project outlines at the interview.

Reasonable adjustments

We are committed to creating an environment where everyone can fulfill their potential and thrive. We welcome and encourage applications from all parts of the community. If you require reasonable adjustments during the recruitment process, please contact the recruitment team via recruit@sanger.ac.uk.
It's an exciting time to join us as we continue to build an international centre for scientific, business, cultural and educational activities emanating from Genomes and BioData. With a significant expansion of our Wellcome Genome Campus on the horizon, we are now able to shift our horizons to ask and answer even bolder questions.

Our mission is “to maximise the societal benefit of knowledge obtained from genome sequences”. The ambition of Genome Reserach Limited, with our Campus partners, is to progressively strengthen its well-established foundations in scientific research and discovery, and to build on them, developing the Wellcome Genome Campus over the forthcoming 25 years.

Genomic research is still in the foothills of extracting and using the knowledge buried in the 6 billion letters of code in the human genome. The ever increasing numbers of human genomes sequenced for research or clinical diagnosis will reveal patterns and motifs that will shape health and disease research for decades to come. When we also consider the rest of the genomes on Earth the potential is vast and the Wellcome Sanger Institute will be in the vanguard of this revolution in science and society.

Professor Sir Mike Stratton, FMedSci FRS

Director of the Wellcome Sanger Institute and Chief Executive Office of the Wellcome Genome Campus
Wellcome Sanger Institute

Our mission is to maximise the societal benefit of knowledge obtained from genome sequences.

The Wellcome Sanger Institute is a world leading genomics research centre. We undertake large-scale research that forms the foundations of knowledge in biology and medicine. We are open and collaborative; we share our data, results, tools and technologies across the world to advance science. Our findings are used to improve health and to understand life on Earth.

Our science is large-scale and organised into Programmes, led by our Faculty who conceive and deliver our science, and supported by our Scientific Operations and IT teams responsible for all data production pipelines, compute and storage facilities at the Institute.

With secured funding from Wellcome Trust, we are able to strategically focus our work in five key research fields:

- **Cancer, Ageing and Somatic Mutation**
  Provides leadership in data aggregation and informatics innovation, develops high-throughput cellular models of cancer for genome-wide functional screens and drug testing, and explores somatic mutation’s role in clonal evolution, ageing and development.

- **Cellular Genetics**
  The Programme is focused on cell-atlasing and cellular genetics. It uses these approaches to map cells in the human body combining cutting-edge methodologies and computational approaches. This enables us to understand what the identity of cells are, how they are regulated, relationships between them and importantly how this can change during development, health disease and ageing.

- **Human Genetics**
  Applies genomics to population-scale studies to identify the causal variants and pathways involved in human disease and their effects on cell biology. It also models developmental disorders to explore which physical aspects might be reversible.

- **Parasites and Microbes**
  Investigates the common underpinning mechanisms of evolution, infection and resistance to therapy in bacteria and parasites. It also explores the genetics of host response to infection and the role of the microbiota in health and disease.

- **Tree of Life**
  Tree of Life investigates the diversity of complex organisms - animals, plants, fungi and protists - through genomic sequencing and analysis to understand their evolution, and provide resources for species conservation, ecosystem monitoring and future biotechnologies.
Our Mission
To maximise the societal benefit of knowledge obtained from genome sequences.

Delivery of this mission will have three elements:
• Research: advancing understanding of biology using genome sequences and other types of large-scale biological data.
• Innovation: applying genome science for human health and other societal benefits.
• Learning and Engagement: fostering knowledge exchange and discussion of the scientific, medical and wider implications of genomes.

Our Structure
The high-throughput, large-scale biological research undertaken at the Wellcome Sanger Institute is a central defining characteristic distinguishing our science from that of most research institutes and universities. Our science is organised into Programmes, led by our Faculty who conceive and deliver our science, and is supported by our Scientific Operations teams responsible for all data production pipelines at the Institute.

The data production platforms are organised into a single management structure. This ensures that we have refined processes and ensures that we have appropriate levels of investment and manning, with robust forward-planning and realistic targets.

Our Campus
Set over 130 acres, the stunning and dynamic Wellcome Genome Campus is the biggest aggregate concentration of people in the world working on the common theme of Genomes and BioData.

It brings together a diverse and exceptional scientific community, committed to delivering life-changing science with the reach, scale and imagination to pursue some of humanity’s greatest challenges. Find out more about our Genome Wellcome Campus.

Our Benefits
Our employees have access to a comprehensive range of benefits and facilities including:
• 25 days annual leave (extra 1 day to a maximum of 30 days for every year you work)
• Auto-enrolment into a generous Group Defined Contribution Pension Scheme, with enhanced company contribution
• Up to 2 days annual paid volunteering leave
• Up to 10 days paid Emergency Carers Leave per year
• Family friendly environment including options for flexible and part-time working, an on-site Workplace Nursery Salary Sacrifice Schemes for pre-school children and Summer holiday club
• Life Assurance – six times your pensionable pay if you are a member of our pension scheme
• Group Income Protection Scheme (if on a contract exceeding 12 months)
• Enhanced maternity, and parental leave
• Access to a substantial number of courses and training events onsite
• Private Healthcare Scheme
• Eyecare and Dental payment plans
• Concessions and discounts from our corporate perks site
• Flexible working, with a mixture of on-site and home-working available

Our open approach
The Wellcome Sanger Institute is an Equal Opportunity employer. We aim to attract, recruit, retain and develop talent from the widest possible talent pool, thereby gaining insight and access to different markets to generate a greater impact on the world.

We positively encourage applications from suitably qualified and eligible candidates regardless of sex, race, disability, age, sexual orientation, gender reassignment, religion or belief, marital status, or pregnancy and maternity status.

We are open to a range of UK-based flexible working options including part-time or full-time employment as well as flexible hours due to caring or other commitments.
Equality, Diversity and Inclusion

In April 2020 we were awarded the Athena SWAN Silver award, having been one of the first research institutes to achieve the Bronze award in April 2014.

The organisation values the diversity of its employees, students, visiting scientists and collaborators and is committed to providing equal opportunities. The diversity of our workforce is of critical importance in drawing together the talent, skills and experience on which we depend to conduct world-class science and support biomedical discovery.

Our strategy is to foster an inclusive culture where everyone can thrive and diversity is celebrated. For more information about EDI at GRL see our Equality in Science Programme: https://www.sanger.ac.uk/about/equality-science

Behavioural Competency Framework

We strive to create opportunities that spark conversations and inspire new thinking as we pursue our common goal of scientific research to maximise the benefits of knowledge obtained through genome sequences.

To guide us, we have recently defined a set of core behaviours that we value and lay out our expectations for everyone. By demonstrating these attitudes and behaviours throughout GRL we will build and support an inclusive culture where every member of our community is respected, heard and supported.

We have identified the following six core competencies:

- Collaboration
- Communication
- Leadership
- Results-Driven
- Innovation
- Integrity