Symposium 2017 Programme

Sunday 12th March

10:00—First Session:
Sir Gregory Winter, Benjamin Jackson, Solène Rolland, Max Wilkinson, Dr Jason W. Chin
12:30—Lunch break
13:30—Second Session:
Laith Alexander, Ellese Cotterill, Guy Emerson, Dr Arthur Norman
15:15—Break (tea and biscuits will be served)
15:55—Third Session:
William Gao, Herschel Chawdhry, James D Manton, Maria T Codrean, Dr. Malte Grosche
18:00—Closing words

20:00—Annual Dinner

http://tcss.soc.srcf.net/

10:00—Sir Gregory Winter: Antibodies and Bicycles
Sir Gregory Winter, the Master of Trinity College is going to speak about his field of research—humanised and human antibodies and bicyclic peptides. Sir Gregory has founded several successful start-up companies, including Cambridge Antibody Technology in 1990 (acquired by Astra Zeneca in 2006), a Domantis in 2000 (acquired by GSK in 2006) and Bicycle Therapeutics in 2010, which is developing a peptide product for treatment of cancer

10:45—Benjamin Jackson: Functional roles of long non-coding RNAs in haematopoiesis
While the ability of protein-coding transcripts to be translated and affect cell fate decisions has been extensively studied, relatively little is known is known about the role of the non-coding genome in this process. An important component of the non-coding genome is long non-coding RNAs (lncRNAs), which have been shown to play critical roles in regulating transcription to affect cellular differentiation and development. One particular model of differentiation in which lncRNAs have been shown to play a role is haematopoiesis, in which all blood cellular components are developed from haematopoietic stem cells (HSC). My research is focused on identifying lncRNAs that are differentially expressed across normal haematopoietic development and characterizing their function using murine in vivo bone marrow reconstitution. Because the murine haematopoietic system has been extensively studied—with a well-characterized model of differentiation from HSCs—it represents a powerful system to study lncRNA dynamics across cell fate decisions and to begin to further elucidate lncRNA molecular mechanisms.

11:05—Solène Rolland: Development of a homogeneous TR-FRET assay for the characterisation of GPCR ligands binding kinetics
During lead optimisation, the pharmaceutical industry heavily relies on high-throughput assays in order to find potential drug candidates. These assays usually focus on two main compound characteristics: affinity for its disease target, and its ability to selectively modulate function. Understanding the binding kinetics of compounds can help explain or predict pharmacological phenomena such as the desired clinical effects or the side-effects. The main goal is to set up the optimum parameters for characterising the kinetic constants of ligands/compounds interacting with the receptor.

11:25—Max Wilkinson: Splicing snapshots: cryo-EM structures of spliceosomes
For a gene to be translated into protein it must first be transcribed to produce a messenger RNA (mRNA). However, all genes in higher organisms contain long non-coding (or "junk") sequences called introns that must be excised, or "spliced" from the mRNA before it is exported to the cytoplasm for protein synthesis by ribosomes. The two chemical reactions of splicing occur within a large molecular machine called the spliceosome, a complex that has defied structural biology for decades due to its low abundance and extreme flexibility. I made use of recent technological advances in cryo-electron microscopy (cryo-EM) to solve atomic resolution structures of the spliceosome carrying out each chemical step of splicing, revealing how introns are recognised and how their excision is catalysed.

11:45—Dr Jason W. Chin: Reprogramming the Genetic Code
The information for synthesizing the molecules that allow organisms to survive and replicate is encoded in genomic DNA. In the cell, DNA is copied to messenger RNA, and triplet codons (64) in the messenger RNA are decoded—in in the process of translation—to synthesize polymers of the natural 20 amino acids. This process (DNA-RNA-protein) describes the central dogma of molecular biology and is conserved in terrestrial life. We are interested in rewriting the central dogma to create organisms that synthesize proteins containing unnatural amino acids and polymers composed of monomer building blocks beyond the 20 natural amino acids. I will discuss our invention and synthetic evolution of new 'orthogonal' translational components (including ribosomes and aminoacyl-tRNA synthetases) to address the major challenges in re-writing the central dogma of biology. I will discuss the application of the approaches we have developed for incorporating unnatural amino acids into proteins and investigating and synthetically controlling diverse biological processes, with a particular emphasis on understanding the role of post-translational modifications.

13:30—Laith Alexander: Neurobiology of depression: insights from animal models
Depression is a major contributor to global disease burden, but its neurobiological basis remains unclear. Correlative human neuroimaging studies have shown that the subgenual anterior cingulate cortex (sgACC) is over-active in depression, but whether this over-activity is causally related to depressive symptoms or merely compensatory is unknown. Using marmoset monkeys, we have over-activated sgACC with intracerebral microinfusions of drugs to excite this brain region. By combining wireless cardiovascular monitoring and behavioural measurements, we have shown that over-activity in sgACC causally contributes to both anhedonia (reduced capacity to experience pleasure) and anxiety (intolerance of uncertainty) associated with depression. I am currently using chemogenetic techniques to further investigate the role of sgACC in endocrine and cardiovascular dysfunction related to depression.

13:50—Ellese Cotterill: Multi-view classification of neuronal cell types
Conducting a comprehensive census of cell types in the brain has recently been identified as a key priority of several major international neuroscience collaborations. Classification of neuronal cell types is essential for understanding the composition and functional properties of neuronal circuits, accessing and manipulating them experimentally, as well as differentiating the effect of neurological diseases on different cell types. Previous work in this area has generally been restricted to using one type of properties of neurons, such as anatomical, electrophysiological, molecular or positional features, to classify cell types. We have examined the potential benefits of using a combined feature set, consisting of both the electrophysiological and morphological properties of cells, to achieve a more comprehensive cell classification. Our results show that use of these dual data sets and multi-view clustering techniques adopted from a variety of fields of machine learning can provide a more robust and accurate classification of neuronal cell types, which we demonstrate on a number of experimental data sets.

14:10—Guy Emerson: Machine Learning and Linguistics: A Tale of Love and Heartbreak
Machine learning and linguistics have had a complicated relationship, full of excitement and passion, but also full of mutual distrust. The field of natural language processing is being rapidly taken over by neural network models, pushing forward the state of the art, while eschewing much of traditional linguistics. Could this be the end of their relationship? Not so, I say! In this talk, I will present work hoping to open a new chapter in their relationship - where probabilistic graphical models can be interpreted as logical forms, where big data can be used to learn truth-conditional semantics, and where machine learning and linguistics can embrace one another.

14:30—Dr Arthur Norman: Developing and supporting long lasting scientific software
The system “Reduce” does Symbolic Computer Algebra—that means it can expand and simplify formulae, integrate and differentiate and address a large range of specialised mathematical transformations. Work on it was started by Tony Hearn in 1963 when he was working in quantum electrodynamics and wanted to automate some of the messy non-commutative algebra involved. Over the years it grew to become more than just a system for high energy physics, and an international group of collaborators joined in working on it - including some here in Cambridge. Today it is available under an Open Source License on SourceForge, free to everybody. There have been at least four sorts of motivation for computer algebra. Scientists with particular problems have worked on code to help them in their work (e.g. in celestial mechanics and general relativity as well as high energy physics). Educators have wanted general algebra systems to support maths teaching down to a school level. Automating what mathematicians do was seen as a branch of artificial intelligence, while constructivist pure mathematicians could be motivated to seek not just methods to solve basic mathematical problems, but efficient ones. All these challenges remain—along with that of looking after one or two million lines of code and supporting a rather random mix of users. I will comment on the history, issues and future direction to illustrate what can happen to a software project when it ends up as a 50+ year success.

15:55—William Gao: The Expansion Dynamics of the 1D Bose-Hubbard Model
Unlike the quantum physics we're normally interested in, i.e. the ground state properties, one growing theme in many-body physics concerns with the excited states higher up in the energy spectrum and the time evolution of the quantum states. In this talk, I will present a study on the expansion dynamics of interacting bosons in a deep, 1D square lattice potential. One model for such a system is the Bose-Hubbard model (BHM), which gained lots of attention following advancements of techniques in cold-atom experiments. Like most models for interacting quantum systems, BHM cannot be solved analytically. However, in a low dimension (1D, that is) numerical calculations can be done on a 'reasonable' numbers of lattice sites and bosons before the size of the Hilbert space catches up with our computational powers.

16:15—Herschel Chawdhry: The biggest microscopes in the world—a crash course in particle physics
What are the fundamental laws of Nature? How does the Universe work? What is matter made of? Particle physics seeks to answer these most fundamental of questions; progress in this field during the last 50 years has led to the most precisely-tested predictions in the history of science. In this talk, I will discuss the history of the field, the current state of research and my own work on predicting results from experiments at the Large Hadron Collider—the biggest machine in the world.

16:35—James D Manton: ASTROTIRF: total internal reflection fluorescence microscopy away from the coverslip
Fluorescence microscopy is a powerful tool for the investigation of the structure and dynamics of biological and material samples, but is limited in its resolving power by the effects of the diffraction of light. While 2D resolutions of ~200 nm can be achieved, the 3D resolution of conventional techniques such as confocal microscopy or multiphoton microscopy is much worse, at around 600 nm. Total internal reflection fluorescence microscopy (TIRF) circumvents this limitation by using evanescent fields to create a thin, 100 nm sheet of illumination at the interface between the glass and the sample, but this can only be used to image the near surface of a cell. In this talk, I will describe our work on Axial Section TRanslation of TIRF (ASTROTIRF), a new method that circumvents this limitation and allows the creation of thin sheets of illumination at depth, allowing 3D imaging with a resolution of 200 nm in samples up to 1 micron thick.

16:55—Maria T Codrean: Artificial Chemotaxis of Phoretic Swimmers
This talk will provide a brief insight into the mathematics and physics behind phoretic nano-swimmers and their mechanism for chemotaxis. It may also explain the connection between Poké Balls, Roman gods, and drug carriers.

17:15—Dr. Malte Grosche: The quantum dance of electrons in solids
In an age of coal and steel, in late 19th-century Cambridge, the experiments undertaken by J. J. Thomson on the nature of the electron may have seemed exotic and entirely without application. A generation later, when an entire industry had grown around the use of vacuum tubes, few people again would have seriously considered replicating these devices in solids. But because in high purity crystals electrons can travel over long distances without scattering—replicating properties of the vacuum in the solid state—electrons can be controlled and manipulated to a previously unimagined degree. Our present electronics and computer industries are based on this unprecedented control over matter in semiconductor devices. Whereas in semiconductors the mobile electrons are strongly diluted, electrons in metals form a dense, interacting quantum liquid, which can host entirely new cooperative phenomena, such as superconductivity or certain types of topological order. This talk will review research in this area and consider where it may lead.

We will also be holding our **AGM** at 18:15 on Tuesday 14th March, in the Blue Boar Common Room (next to the Winstanley Lecture Theatre). We are looking for any Trinity students who would like to help run our society to **join our committee** next year. You can find more information about the roles via the listing on our website (tcss.soc.srcf.net). If you would like to enquire about or run for a position, contact Adam Přáda (ap837@cam.ac.uk).