JAMES RENNIE BEQUEST

REPORT ON EXPEDITION / PROJECT / CONFERENCE

Expedition/Project/ Conference Title:	
-	Synthetic Biology: Engineering, Evolution and Design Conference 2019
Travel Dates:	
-	22/06/2019 to 27/06/2019
Location:	USA
Group member(s):	
Aims:	Present my work, learn about latest developments in the field,
	Network with other members in the field and explore future job opportunities
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OUTCOME (a minimum of 500 words):-

The Synthetic Biology: Engineering, Evolution and Design Conference 2019 (SEED 2019) conference offered a great opportunity to interact with some of the leaders within the field of synthetic biology. We heard of some of the latest breakthroughs in protocell development for exploring the origin of life, with alterations of salt concentration proving instrumental in successful protocell formation in the presentation given by the keynote speaker, Prof. Jack Szostack. In the talk by Prof. Mikhail Shapiro, we saw the capacity to generate gas vesicles within *E.coli*, with the creative application of sound waves enabling the selective bursting of E.coli containing molecules for delivery. Finally we were also able to see the Cas13 based 'SHERLOCK' platform could enable highly sensitive, rapid detection of the zika virus in patient samples in the talk by Dr. Cameron Myhrvold from the Sabeti lab.

The conference also featured the latest work by the synthetic yeast genome project (Sc2.0) consortium as well as current work as part of the GP-write project. These talks featured ongoing work on chromosome design in both yeast and mammalian cells, discussing some of the limitations of the chromosomes and how they may be overcome. Some of this work ties in with my current PhD project and helped inform me in some difficulties experienced in my pathway design and assembly.

Alongside the reinforcement of existing collaborations and improving knowledge of the tools I have been working with, I was able to connect with several researchers at Newcastle University and learn about the application of Design of Experiments (DoE) for optimising experiments with multiple confounding variables. Not only can this be used to optimise a protocol, but it has also been used to understand fundamental biological processes (such as the how a promoter, RBS, and a terminator interact and play in gene expression). Developments in DNA synthesis

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and assembly technologies have made the generation of different combinations/modifications relatively easy however the means of analysing these interactions lag behind. Therefore, current research has been limited to exploring the role of single factors at a time or simply utilising a fraction of the data gathered. In several talks given by members of the Howard group at Newcastle, they have demonstrated the use of DoE in optimising cell free protein synthesis (by Dr. Alice Banks) and cell free protein synthesis in hydrogels (Dr. Colette Whitfield). DoE is an approach that cannot be ignored in an age of big data, where multiple variables are in play and researchers want to effectively explore the 'space' (relationships between different variables and outcomes). With my interest in learning more about this tool for protocol optimisation, they have mentioned a workshop that they will have in Newcastle in a few months which I hope to attend.

The conference also included talks from biotechnology companies such as Gingko bioworks, featuring their work on searching the enzyme space to mining for variants with improved activity. This involved the utilisation of computational design tools along with large scale DNA synthesis provided by the company, Twist. They have also discussed multiple different collaborations with companies such as synlogic, Genomatica, impossible burger and Joinbio for the optimisation of pathways for different purposes (ie. Improve bacteria for agriculture, engineering yeast to produce cannabinoids and engineering therapeutic organisms). During the conference, I was able to meet a few representatives and engineers from the laboratory automation start-up company, Opentrons. Their company aimed to build relatively cheap benchtop automation platform that can be easily utilised and accessible by most researchers. Their automation platform utilises python for script development and many protocols are open source. Following the conference, I had the opportunity to visit their headquarters in Brooklyn to meet other members of the company and discuss developments and ways to improve the user experience.

This conference also provided a brilliant opportunity for me to present my work to the several hundred attendees from the field, showcasing published tools that the community would have interest in as well as precipitating conversations with group leaders about potential future work.



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