Jody Emile Phelan

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Qualifications and skills

- Research fellow at London School of hygiene and Tropical Medicine (LSHTM)
- Extensive computational biology experience – Processing of extremely large datasets to provide biological insights
- Multilingual – English (native fluency), Dutch (advanced)

Employment

2017- present   ***Research Fellow – LSTHM***
Investigating the use of next generation sequencing data in the context of *Mycobacterium tuberculosis* (Mtb). Design and implementation of data analysis pipelines to process and collate terabytes of data from various structured and unstructured sources to provide biological insights such as population structure, transmission and drug resistance. Routing use of scripting languages such as python, perl, bash and R to process and visualise large quantities of data efficiently. Application of various regression techniques to detect unique patterns in raw sequencing data affecting Mtb drug resistance and host-susceptibility. These findings were then integrated into a publically available pipeline to predict drug-resistance from new data (github.com/jodyphelan/TBProfiler)

Education

2013 – 2017   ***PhD Student – LSHTM***
A bioinformatics analysis of tuberculosis and host genomic data. Analysis of Mtb next generation sequencing data, aiming to explain the genotype-phenotype relationship for drug-resistance, transmission and host susceptibility.

2010 – 2013   ***BSc in Biochemistry – University College London (UCL)***
Overall Grade: 2.1 (Honours)

2006 – 2010   ***A-Levels – British International School of Wrocław, Poland***
Chemistry (A*), Human Biology (A*), Physics (B), Maths (B)

Expertise and Achievements

- Unix, Python, Javascript, R, Perl, SQL, D3. Use of specialist bioinformatic programs involved in the analysis of next generation sequencing data
- Teaching and demonstrating experience in multiple internal and international workshops
- Awarded British Council travel grant to speak at GEID2016 and GEID2017
- Baseball player in the UK national league: Most valued player (2014, 2015), Golden Glove holder (2015)

Work Experience

March 2017	***World TB Day – UCT, Cape Town, South Africa*** Organised and taught in a workshop on analysis of next generation sequencing data in the context of infectious disease at University of Cape town to coincide with World TB Day. Invited speaker at University of Stellenbosch, Division of Molecular Biology & Human Genetics.
Aug-Nov 2016	***BBSRC DTP secondment – Barclays, Canary Wharf, UK*** As part of my PhD program I went on secondment to Barclays bank. I worked in the division of physical and cyber security and performed rapid prototyping of a real-time threat dashboard. I created a front end based on D3 to visualise graph structures stored in Orient DB and elasticsearch.
2013 – Present	***Pathogen genomics workshops – UK, Brazil, Thailand, Philippines*** Regular lecturing at and organisation of short courses teaching next generation sequencing analysis techniques. Responsibilities include lecturing, setting up IT infrastructure and demonstrating at practical sessions. These courses have been held internally (at UCL and LSHTM) and overseas (USP - Brazil, UCT - South Africa, UP – Philippines and Mahidol – Thailand).
2012 – 2013	**Research Assistant -** *Institute of Neurology, UCL* Involved in the creation of a synteny map between mouse and human and a web interface to query and visualise. This requires whole genome alignment and the subsequent creation of a dynamic relational database and synteny viewing platform. This data will be used by groups in the Institute of Neurology (ION) and the National Institute of Medical Research (NIMR).

Selected Publications

Phelan J, Maitra A, McNerney R, Nair M, Gupta A, et al. 2015. The draft genome of Mycobacterium aurum, a potential model organism for investigating drugs against Mycobacterium tuberculosis and Mycobacterium leprae. *Int. J. Mycobacteriology*. 4(3):207–16

Phelan JE, Coll F, Bergval I, Anthony RM, Warren R, et al. 2016. Recombination in pe/ppe genes contributes to genetic variation in Mycobacterium tuberculosis lineages. *BMC Genomics*. 17(1):151

Phelan J, Coll F, McNerney R, Ascher DB, Pires DE V, et al. 2016. Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. *BMC Med.* 14(1):31

Phelan J, O'Sullivan DM, Machado D, Ramos J, Whale AS, O'Grady J, et al. The reliability of whole genome sequencing technology for detecting resistance to anti-tuberculous drugs. *Genome Med* 2016

Interests and Hobbies

I enjoy travelling, cooking and experiencing new cultures. I also enjoy outdoor activities such as swimming, weight training, snowboarding, basketball, baseball and ice skating.

References

PhD Supervisor: Prof Taane Clark
At: London School of Hygiene and Tropical Medicine
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