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## Ultra-fast drug resistance predictions from NGS sequence data using Cloud Computing

E Cullen<sup>b</sup>, M Mac Aogáin<sup>o,b</sup>, P Walsh<sup>b</sup>, B Kelly<sup>b</sup> and M Bekaert<sup>b,c</sup> <sup>o</sup>Trinity College Dublin, Ireland <sup>b</sup>NSilico Life Science, Ireland <sup>c</sup>University of Stirling, UK

Rapid and accurate prediction of drug resistance in pathogens is a growing need, affecting patient care and emerging personal medicine. Bacterial genome sequencing has been introduced in many hospitals as a cheaper alternative to gene targeted sequencing and PCR, but many handling issue remain to be overcome. Here, we address some of the challenges, by offering a cloud-based solution that while keeping security and privacy at the heart of the development allows remote management of large datasets, and ultra-fast drug resistance predictions without the need for local installation, maintenance or bioinformatics knowledge. Validated using literature references, we have implemented a profiler that reconstitutes (from raw sequences) the genes associated with resistance and produces an ultra-fast and accurate prediction of drug resistance. If raw sequences are available, regardless of the platform used, the profiler will generate a prediction within minutes, in contrast to other solutions which typically require hours of analysis time and interpretation. The profiler currently focuses on *Mycobacterium tuberculosis* and 9 key drugs, including Aminoglycosides (Kanamycin, Capreomycin, Amikacin, Viomycin), Ethambutol, Ethionamide, Fluoroquinolones, Isoniazid, Para-Aminosalisylic Acid, Pyrazinamide, Rifampicin, and Streptomycin.

## **Biography**

Ella Cullen is a graduate Trinity College Dublin's School of Genetics. She has worked on several projects relating to human disease, including psoriasis and neurodevelopmental disorders. She now works with NSilico Life Science. NSilico's focus is on the development of easy-to-use Ella Cullen clinical and bioinformatics software which can significantly accelerate the research process. Ella works with the company's research teams, which have a particular focus on infectious disease and cancer. She also works on forming collaborative projects with labs and companies around the world.

ella.cullen@nsilico.com

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