

June 20th, 2015

Re. SFI Investigators Programme proposal

TO WHOM IT MAY CONCERN

I am writing to confirm my support for Prof. Cathal Seoighe's application to the SFI Investigators Programme, entitled "**Deconvolution and analysis of the human epigenome**".

The proposal involves the development of models and software for the analysis of samples consisting of multiple distinct types of cells. Using DNA methylation and gene expression data these tools can provide estimates of cell type proportions and the characteristics of the cell types present in the samples. In my own field of cancer genomics, tumour samples typically consist of mixtures of normal cells with clonal populations of cancer cells and, therefore there is much scope for the application of computational deconvolution techniques. Internationally, the generation of large datasets that include DNA methylation and gene expression from multiple tumour samples by projects such as The Cancer Genome Atlas has become increasingly common. Such projects should prove a rich resource for applications of the proposed models.

Being able to deconvolute the signature of different cell types in mixed samples would be critical to help fully exploiting the large wealth of data that is currently being generated in cancer, but that is often hard to make sense of from a clinical perspective.

I am enthusiastic about collaborating with Prof. Seoighe on this project and happy to offer advice on the development of models that would be relevant to the cancer genomics community.

Yours sincerely,

Andrea Sottoriva, PhD
Group Leader, Evolutionary Genomics & Modeling
Centre for Evolution and Cancer
The Institute of Cancer Research

A handwritten signature in black ink, reading 'Andrea Sottoriva', written in a cursive style.

The Institute of
Cancer Research

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