

# Establishing a AU-NZ bioinformatics software accelerator program

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## ABSTRACT / INTRODUCTION

The creation of quality and performant bioinformatics software is a growing need as the field of data-driven omics continues to rapidly grow and expand. A proposed response to this challenge is the creation of a software accelerator program that supports the development, optimisation and sharing of software for bioinformatics, by providing the authors with expertise, best practice guidelines, and access to HPC and cloud facilities.

This idea arises from the existing Australian BioCommons Leadership Share (ABLeS) program, by providing environments on peak compute systems to test, scale, debug and enhance bioinformatics software (tools and workflows) in lock step with support and expertise in making software findable, understandable and citable (i.e. FAIR).

The ultimate vision is to accelerate the transition towards a culture of best practice bioinformatics at scale on peak infrastructures.

In this BoF we will collectively discuss and shape this proposed program, by exploring what the RSE community considers to be critical, and how we might share the outcomes of this effort across infrastructure partners in the region and beyond. These observations are broadly applicable to all domains, and we invite people of diverse domain backgrounds to the BoF.

This concept is being actively pursued as a collaborative effort by the Australian BioCommons, Pawsey Supercomputing Centre, New Zealand eScience Infrastructure and the National Computational Infrastructure.