

Opening the cellular black box of melanoma

Malignant melanoma represents only 15% of skin cancers but it accounts for almost all skin-cancer deaths, and Australia has the highest mortality rate from malignant melanoma worldwide.

That's one of the reasons why Australian researchers involved in the Melanoma Genome Project (MGP) have analysed genome sequences from primary tumours and metastases to identify common genetic mutations that cause this deadly cancer.

Matthew Field, in Professor Chris Goodnow's group at The Australian National University, used the NCI's HPC resources to analyse 150 whole genome samples. Mr Field says the project wouldn't have been successful without access to NCI facilities.

"Each melanoma sample requires 5000 hours of compute time and 1TB (1000GB) of storage.

"NCI was instrumental in allowing this large sequencing project to succeed. Not only were they capable of meeting the large compute and storage needs of the project, NCI staff were involved from the beginning and able to effectively facilitate in the integration of our large pipeline with their HPC resources," he said.

The data is expected to provide insights into the progression of melanoma.

The researchers hope the project will lead to more personalised and better treatment options for patients.

"The project aims to characterise the melanoma genome with the ultimate goal of developing new targeted treatments for individuals suffering from the disease," says Mr Field.

The MGP is one of Australia's largest and most complex biomedical research projects and the researchers intend for data from the project to be made publically available, in the International Cancer Genome Consortium.