COMBAT TB Explorer, a TB data exploration

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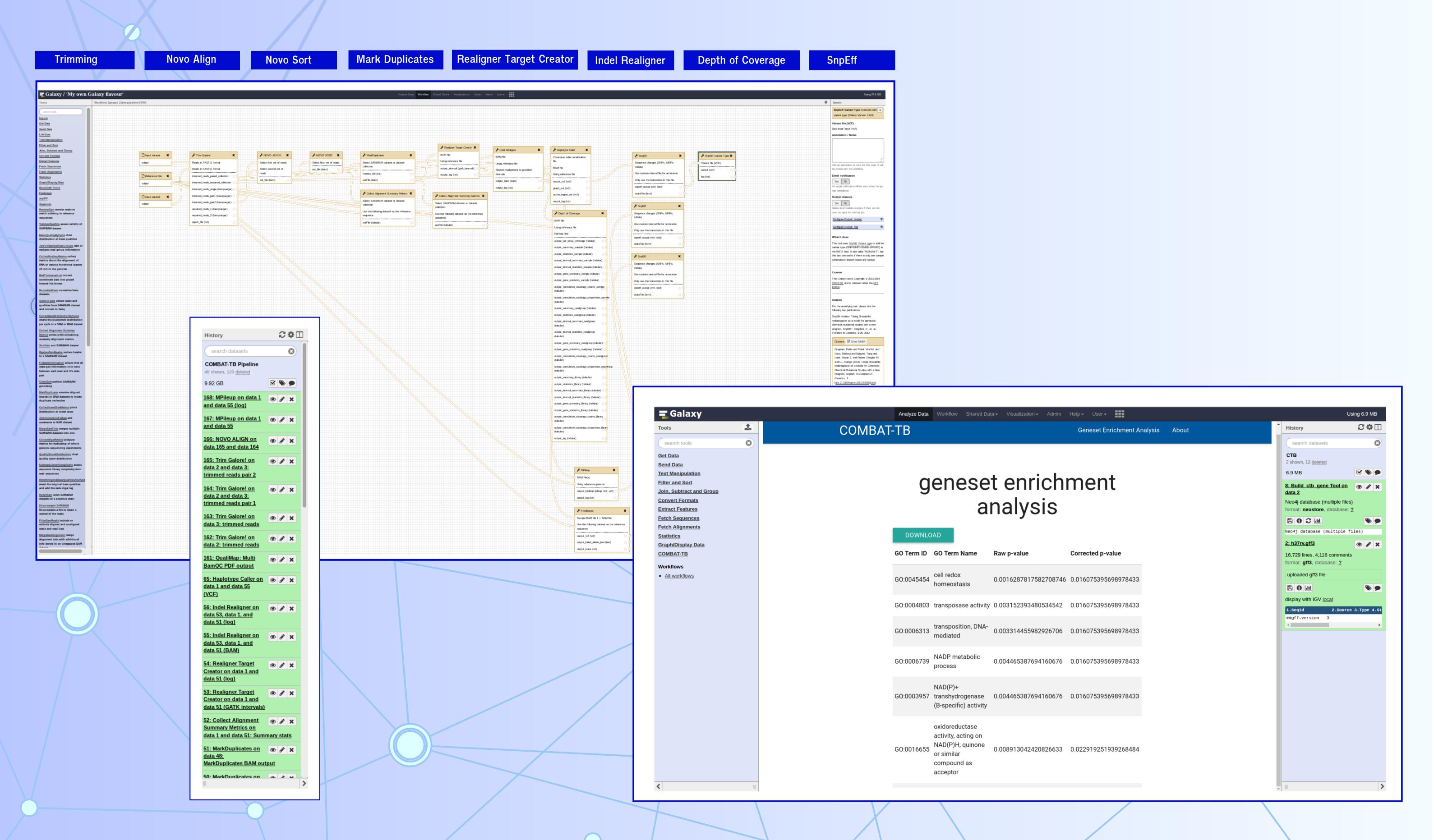
Introduction

Current data repositories only present pre-computed data and do not provide the computational toolkit for biomedical researchers to analyze their own data. We have created the COMBAT TB Explorer, a Galaxy-based environment for annotating and exploring Mycobacterium tuberculosis sequence data. COMBAT TB Explorer currently combines a genomic variant calling pipeline with a web based tool for exploring the relationship between variants and known annotation and allows the user to perform geneset enrichment analysis.

Methods & Results

• We implemented a bacterial genomic variant calling workflow in Galaxy, based on previous SANBI work on analysing mutations in drug resistance strains of M. tuberculosis.

• Variant calls were combined with a reference database of M. tuberculosis genome annotation to produce a new Galaxy datatype.

• z_mplemented a COMBAT TB Explorer, a Galaxy Interactive Environment. This allows novel data to be explored both in the context of the M. tuberculosis genome (visualised in the JBrowse genome browser) and with reference to known annotation.

| Trimming | Novo Align | Novo Sort | Mark Duplicates | Realigner Target Creator | Indel Realigner | Depth of Coverage | SnpEff |

Conclusions

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