

COMBAT TB Explorer, a TB data exploration workbench.

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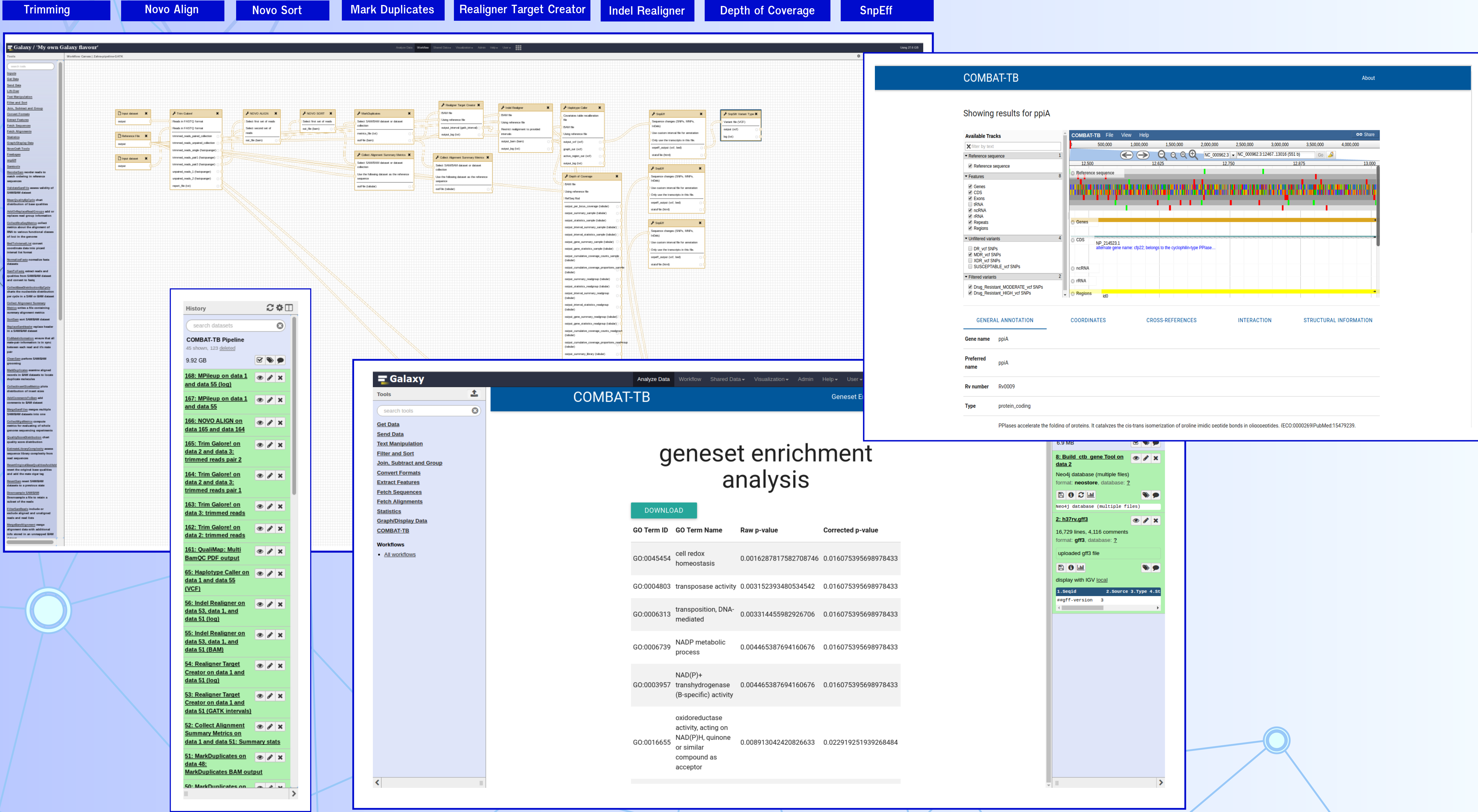


Introduction

Tuberculosis (TB), an infectious disease caused by the *Mycobacterium tuberculosis*, ranks as one of the leading causes of death worldwide, with WHO recording 9.6 people falling ill with 1.5 million deaths in 2014. This disease burden has arguably been matched with continued increase in genomic, transcriptomic and proteomic data for *Mycobacterium tuberculosis* as a result of NGS technologies. This continued expansion of data is exemplified by the growth of data repositories such as the tuberculosis database (TBDB) and the pathosystems resource integrated center (PATRICBRC). Unfortunately, these resources 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 *M. tuberculosis* sequence data.

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*.
- Combined variant calls with a reference database of *M. tuberculosis* genome annotation to produce a new Galaxy datatype (ctb_report).
- Implemented COMBAT TB Explorer, a Galaxy Interactive Environment that allows novel data to be explored in the context of the *M. tuberculosis* genome (visualised in the JBrowse genome browser) and with reference to known annotation.



Conclusions and acknowledgements

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