COMBAT TB Explorer,
a TB data exploration workbench.

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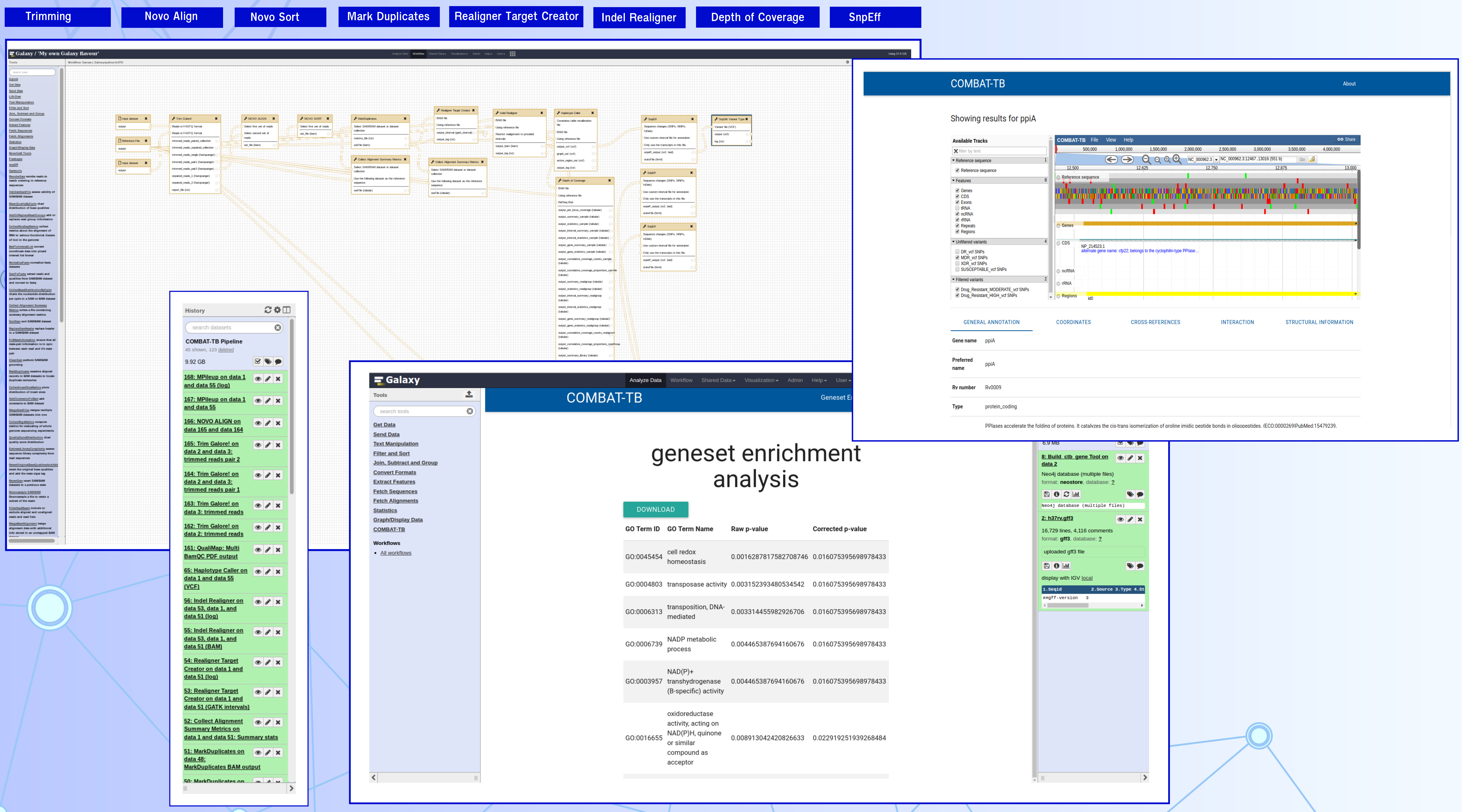
Introduction

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 million 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 *M. 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 and 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* and a downstream tool that combines variant calls with a reference database of *M. tuberculosis* genome annotation and a JBrowse based genome browser to produce a new Galaxy datatype (ctb_report). To visualise the resulting datasets we implemented COMBAT TB Explorer, a Galaxy Interactive Environment. The result is that variants gleaned from novel sequence data can be explored in the context of known annotation, both from genome-centric and annotation-centric perspectives. The COMBAT TB Explorer also contains a module for geneset enrichment analysis (GSEA).



168: MPileup on data 1 and data 55 (log)
167: MPileup on data 1 and data 55
166: NOVO ALIGN on data 165 and data 164
165: Trim Galore! on data 2 and data 3: trimmed reads pair 2
164: Trim Galore! on data 2 and data 3: trimmed reads pair 1
163: Trim Galore! on data 3: trimmed reads
162: Trim Galore! on data 2: trimmed reads
161: QualiMap: Multi BamQC PDF output
65: Haplotype Caller on data 1 and data 55 (VCF)
56: Indel Realigner on data 53, data 1, and data 51 (log)
55: Indel Realigner on data 53, data 1, and data 51 (BAM)
54: Realigner Target Creator on data 1 and data 51 (log)
53: Realigner Target Creator on data 1 and data 51 (GATK intervals)
52: Collect Alignment Summary Metrics on data 1 and data 51: Summary stats
51: MarkDuplicates on data 48: MarkDuplicates BAM output

Showing results for ppiA

Gene name	ppiA
Preferred name	ppiA
Rv number	Rv0009
Type	protein_coding

PPlases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides. {ECO:0000269|PubMed:15479239.

geneset enrichment analysis

GO Term ID	GO Term Name	Raw p-value	Corrected p-value
GO:0045454	cell redox homeostasis	0.0016287817582708746	0.016075395698978433
GO:0004803	transposase activity	0.003152393480534542	0.016075395698978433
GO:0006313	transposition, DNA-mediated	0.003314455982926706	0.016075395698978433
GO:0006739	NADP metabolic process	0.004465387694160676	0.016075395698978433
GO:0003957	NAD(P)+ transhydrogenase (B-specific) activity	0.004465387694160676	0.016075395698978433
GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	0.008913042420826633	0.022919251939268484

8: Build_ctb_gene Tool on data 2
Neo4j database (multiple files)
format: neostore, database: ?

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Neo4j database (multiple files)
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2: h37rv.gff3
16,729 lines, 4,116 comments
format: gff3, database: ?
uploaded gff3 file
display with IGV local

Conclusions and acknowledgements

- Integrating novel sequencing results with existing annotation will be key to researching M. tuberculosis and ultimately fighting tuberculosis.
- Our data exploration environment allows biomedical researchers to analyse, visualise and explore their own data in the context of existing annotation.
- We intend to build on the foundation we have created by extending the COMBAT TB Explorer with additional analysis modules for interrogation molecular pathway relationships, human - pathogen and drug interaction data.

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