

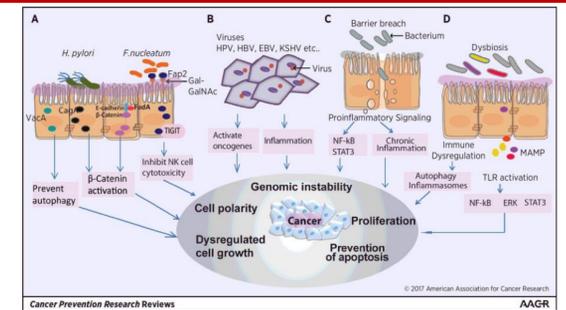
DEVELOPING MULTI-OMIC INFORMATICS WORKFLOWS WITHIN THE GALAXY PLATFORM TO UNCOVER CANCER-MICROBIOME INTERACTIONS

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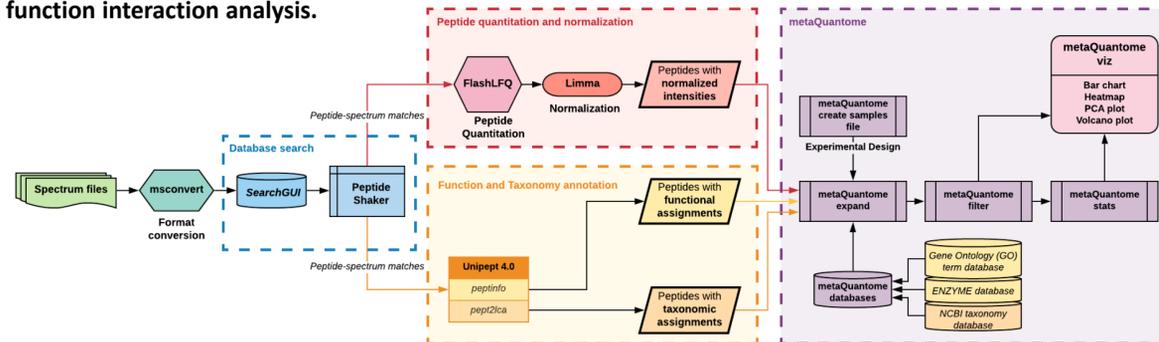
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- Microbiomes play a critical role in health and disease in human hosts and in environmental ecosystems. In cancer studies, although host microorganisms have been implicated for their role in cancer progression, challenges exist in understanding the mechanism of cancer host-microbiome interaction.
- We seek to use complementary microbiome -omics techniques to provide functional information by quantifying microbial RNA and protein expression levels. By using these functional microbiome analysis methods along with host expression data, we seek to unravel the microbiome dysbiosis linkage to cancer progression.



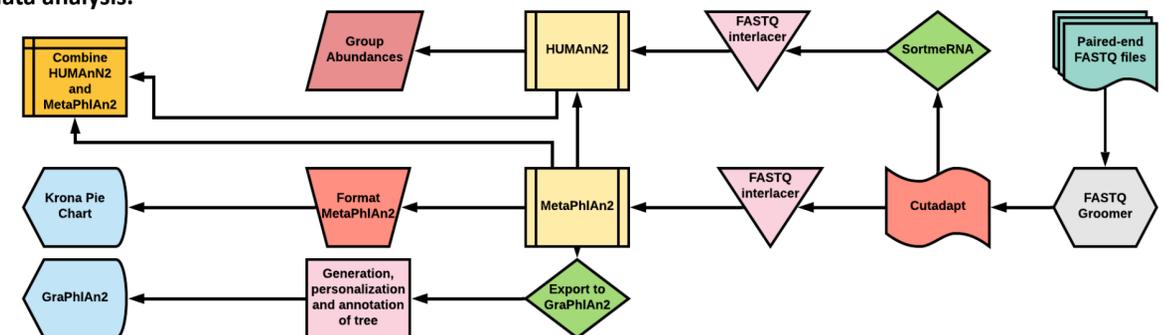
METAPROTEOMICS

The Galaxy-P team has developed contemporary metaproteomics workflows that analyzes microbial proteins to enable quantitative analysis of protein functional group expression, taxonomic abundance and taxonomy-function interaction analysis.

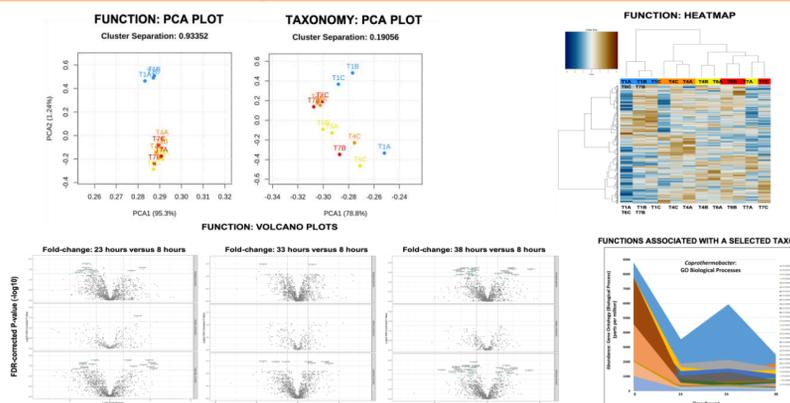


METATRANSCRIPTOMICS

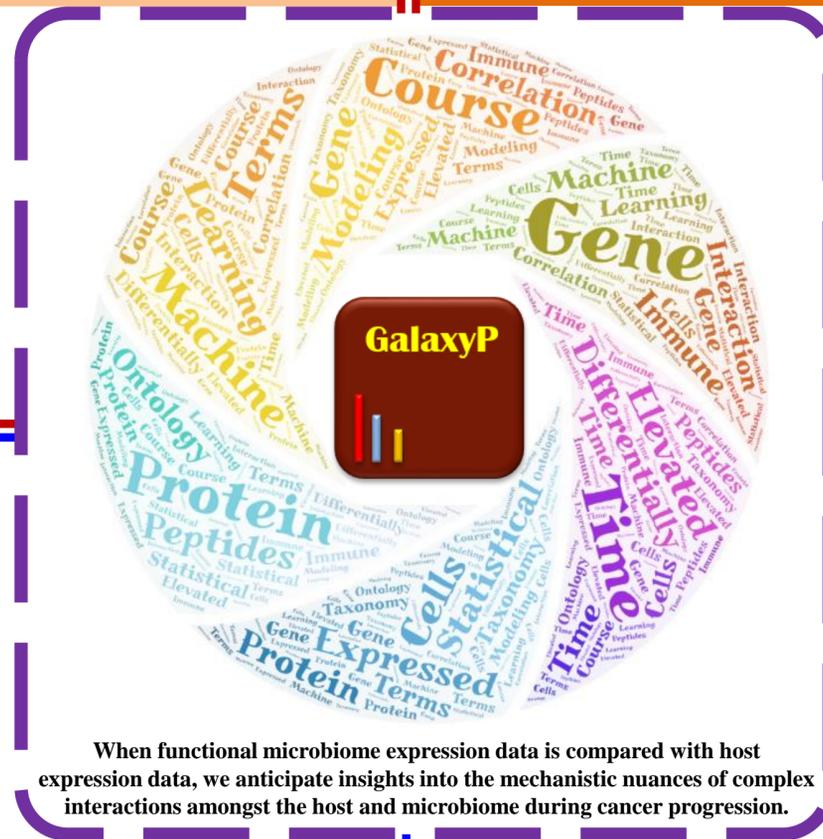
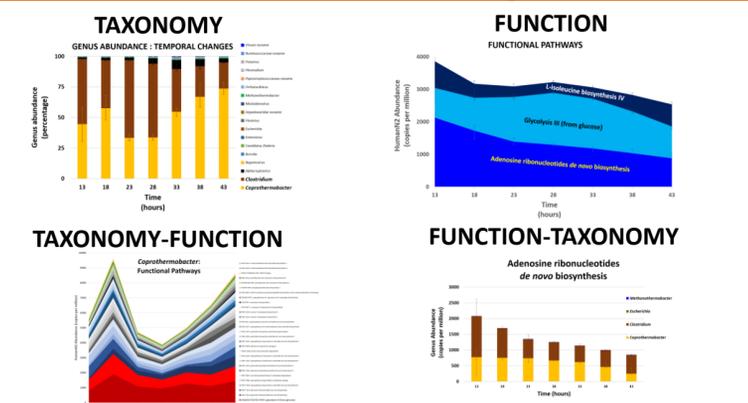
For metatranscriptomics data, the ASaiM workflow (<https://doi.org/10.1093/gigascience/giy057>) was modified to enable assembly, extraction, functional and taxonomy visualization, and taxonomy-functional interaction data analysis.



EXAMPLE OUTPUTS

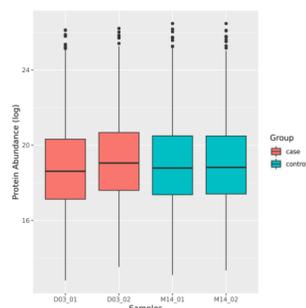


EXAMPLE OUTPUTS

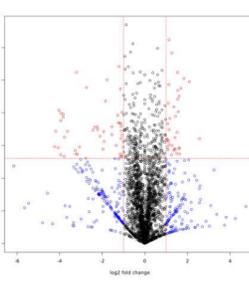


When functional microbiome expression data is compared with host expression data, we anticipate insights into the mechanistic nuances of complex interactions amongst the host and microbiome during cancer progression.

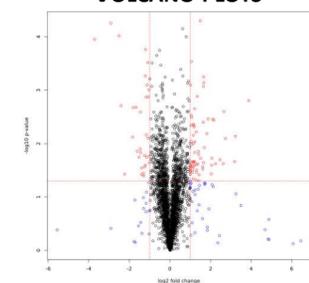
PROTEIN BOXPLOTS



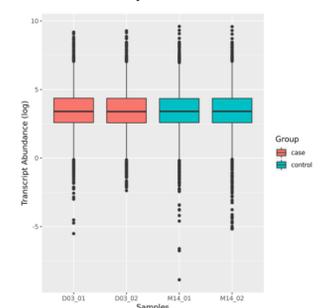
PROTEIN ABUNDANCE VOLCANO PLOTS



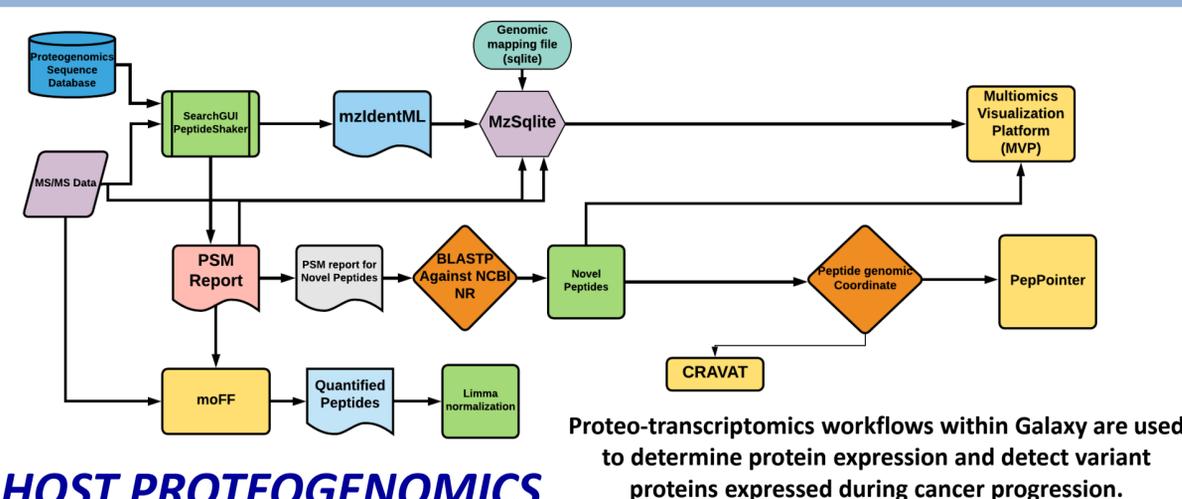
TRANSCRIPT ABUNDANCE VOLCANO PLOTS



RNASEQ BOXPLOTS



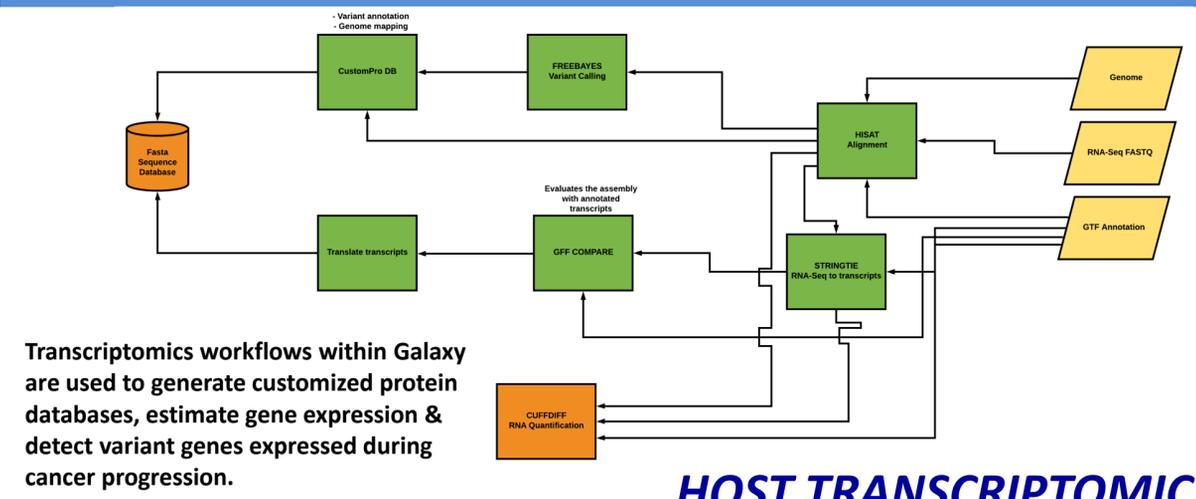
EXAMPLE OUTPUTS



Proteo-transcriptomics workflows within Galaxy are used to determine protein expression and detect variant proteins expressed during cancer progression.

HOST PROTEOGENOMICS

EXAMPLE OUTPUTS



Transcriptomics workflows within Galaxy are used to generate customized protein databases, estimate gene expression & detect variant genes expressed during cancer progression.

HOST TRANSCRIPTOMICS