**GALAXY-P: RECENT DEVELOPMENTS AND EMERGING APPLICATIONS**


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**Introduction.** The Galaxy for Proteomics (Galaxy-P) project was launched several years ago, with the objective of extending the genomics-centric Galaxy bioinformatics framework (*Genome Biol.* 11: R86) to employ proteomics informatics tools. Since its inception, the Galaxy-P project has moved its focus from proteomics tools to integrative analysis across different ‘omic domains (i.e. multi-omics). The Galaxy software framework offers numerous advantages as a platform for multi-omics data analysis and informatics (*Nat Biotechnol* 33: 137). These include the flexibility to implement and integrate disparate software programs that cross ‘omic domains, scalability for large data volumes and compute-intensive operations, and easy sharing of tools and complete workflows, even those comprised of complicated, multiple step processes.

**Results.** Here we outline the current state of the Galaxy-P project, summarizing recent developments and emerging future plans in multi-omic data analysis and informatics. Areas of active development described include:

- Results visualization and interpretation
- MS-based metabolomics data analysis and informatics
- Integrative genomic-proteomic data analysis and informatics
- Collaborations and outreach activities

**Conclusions.** Galaxy-P has enabled numerous research studies in multi-omics. Emerging and future developments will focus on enhancing its capabilities, especially in the realm of visualization and interpretation of results, and dissemination of the high-value workflows and tools to the community.

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**Emerging and future work.** MVP has been developed with an eye toward extensibility, enabling not only visualization of data and results, but also connectivity to informatics resources to aid in interpretation. Future extensions will include:

- Enhanced functionalities for filtering peptide sequence matches and post-translational modifications
- Added functionalities for viewing and interpreting MS-based metabolomics data
- Connectivity to web-based informatics resources to enable results interpretation (e.g. CBioPortal for cancer informatics, NDEX for pathway analysis)

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**Collaborations, outreach and training**

**Current status.** From the outset, Galaxy-P development has been based on collaborations with biology and biomedical researchers with challenging project, such as those employing proteogenomics and metaproteomics. Numerous joint studies have been published through these collaborations (see z.umn.edu/galaxypreferences). We have also engaged in numerous collaborations with software developers (e.g. the Compomics team). We have also presented a number of workshops at national conferences, such as ASMS and ABRF, seeking to promote and train others in the use of Galaxy for multi-omic applications. Our Galaxy-based tools are made publically available through the Galaxy Tool Shed.

**Emerging and future work.** A main focus going forward is making the Galaxy-based multi-omics tools accessible by more researchers. Two main avenues for these dissemination include:

- We are actively working with Globus Genomics to implement our Galaxy-P instance in cloud infrastructure backed by Amazon Web Services. The Globus instance will be used for training purposes and as a scalable option for collaborative, large-scale studies
- We are leveraging the Docker technology, to create Galaxy-P “Flavours”, which are customized instances that can be downloaded and easily installed on local infrastructure or implemented in cloud-based infrastructure

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