

COMMUNITY-BASED DEVELOPMENT AND EVALUATION OF BIOLOGICAL MASS SPECTROMETRY SOFTWARE VIA THE GALAXY TOOL SHED

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INTRODUCTION

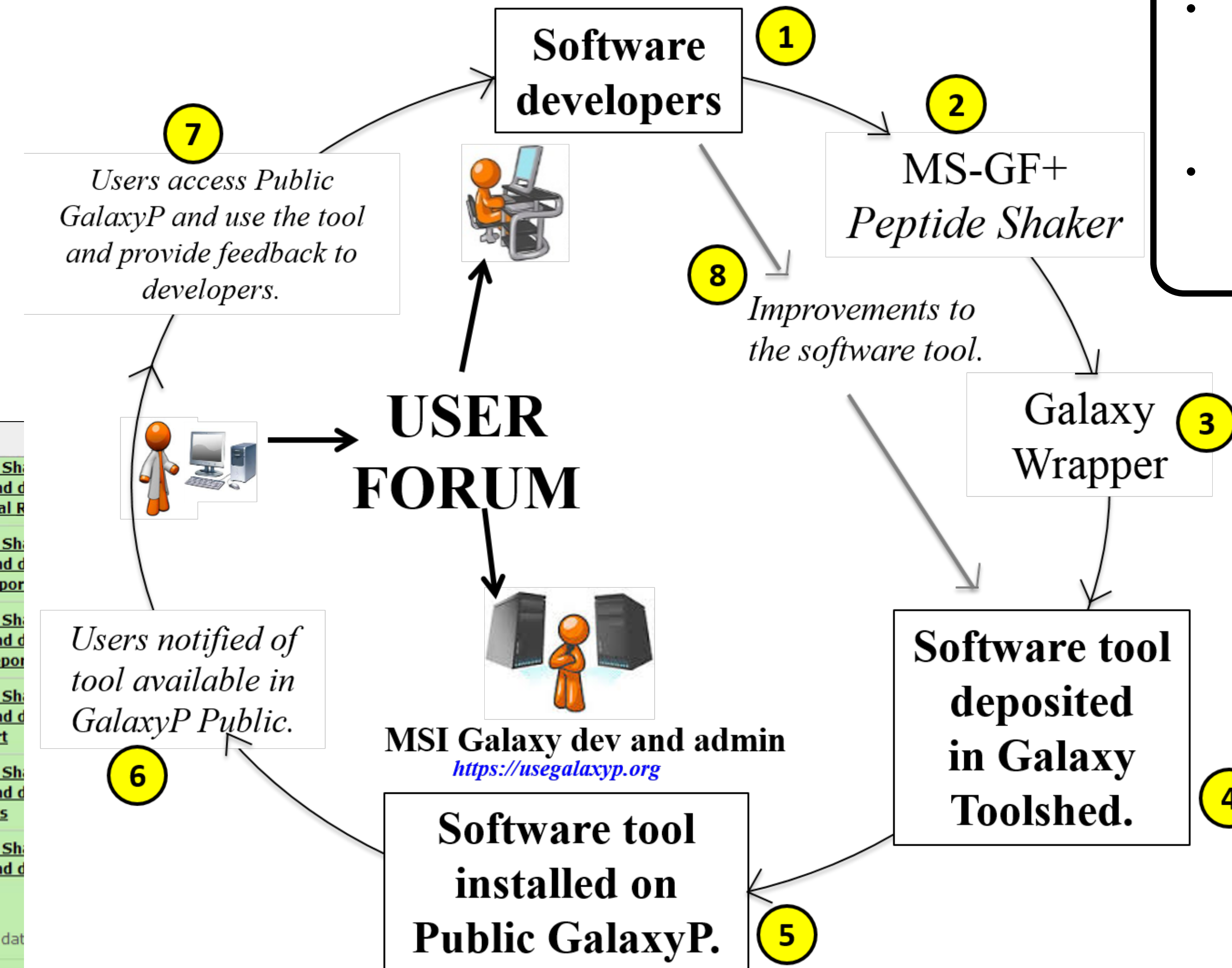
- The GalaxyP workbench is an extension of the widely used genomics Galaxy platform and is designed to support proteomics analytical workflow needs.
- Data and software sharing is at the core of Galaxy and contributions from the Galaxy community in maintaining the high quality of the tools being shared.
- To effectively engage the larger community of users and their communication with developers and ensure tool quality, the GalaxyP team has implemented a standard process for external developers interested in developing GalaxyP tools.

METHODS

- SearchGUI for search algorithms such as MS-GF+, X!Tandem and OMSSA along with PeptideShaker were chosen as software tools that would be developed, wrapped and deposited in Galaxy toolshed before installing it on public GalaxyP site.
- Galaxy Toolshed is designed to allow individuals or groups to share tools that have been prepared for installation and execution within Galaxy.
- GalaxyP Google Group User forum was used for coordination of tool wrapping, depositing into the Tool Shed, installation on Public GalaxyP, tool testing, and feedback to the tool developer. Developers and users in nine institutes across five countries communicated using this forum. The User Forum is available for other users to browse, comment and reference.
- The methodology accounts for the necessity of an iterative process which results in a tool that has been tested and verified to work in a standard Galaxy installation.

REFERENCES.

PeptideShaker: <http://peptide-shaker.googlecode.com>
SearchGUI: <http://searchgui.googlecode.com>
MS-GF+: <http://omics.pnl.gov/software/ms-gf>
Galaxy Tool Shed: <http://toolshed.g2.bx.psu.edu>
Galaxy Test Tool Shed: - <http://testtoolshed.g2.bx.psu.edu>
GalaxyP Google Group User Forum: <https://groups.google.com/a/umn.edu/forum/#forum/galaxy>
Public GalaxyP: <https://usegalaxy.org>
Public Galaxy: <http://usegalaxy.org>



CONCLUSION

- The use of the Galaxy framework promotes publication and wider use of established biological MS software.
- Galaxy promotes collaboration between software developers, Galaxy developers and end-users.
- As a result of this work, we now offer the many functionalities of PeptideShaker in Galaxy, along with opportunities for integration with other software tools via use of workflows.
- Our community-based model should prove effective for future implementation, testing and continued improvement of command-line driven software tools.

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GalaxyP

