

Galaxy

Annotation, sharing, publishing

www.galaxyproject.org

Tagging and annotation

Nearly all Galaxy entities can be tagged or annotated

Tag:

Short, structured metadata associated

Annotation:

Completely free-form text used to describe or contextualize

Sharing and Publishing

Share:

Make something available to someone else

Publish:

Make something available to everyone

Galaxy Page:

Analysis documentation within Galaxy; easy to embed any Galaxy object

Sharing & Publishing enables **Reproducibility**

Galaxy aims to push the goal of reproducibility from the bench to the bioinformatics realm

All analysis in Galaxy is recorded without any extra effort from the user.

Histories, workflows, visualizations and *pages* can be shared with others or published to the world.

Sharing & Publishing enables **Reproducibility**





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Windshield splatter analysis with the Galaxy metagenomic pipeline

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Footnotes

[Supplemental material is available online at <http://www.genome.org>. All data and tools described in this manuscript can be downloaded or used directly at <http://galaxyproject.org>. Exact analyses and workflows used in this paper are available at <http://usegalaxy.org/u/aun1/p/windshield-splatter>.]

Windshield splatter analysis with the Galaxy metagenomic pipeline: A live supplement



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How to use this document



This document is a live copy of supplementary materials for [the manuscript](#). It provides access to the **exact** analyses and workflows discussed in the paper, so you can play with them by re-running, changing parameters, or even applying them to your own data. Specifically, we provide the two histories and one workflow found below. You can view these items by clicking on their name to expand them. You can also import these items into your Galaxy workspace and start using them; click on the green plus to import an item. To import workflows you must [create a Galaxy account](#) (unless you already have one) – a hassle-free procedure where you are only asked for a username and password.

This is the Galaxy history detailing the comparison of our pipeline to MEGAN:




[Galaxy History | Galaxy vs MEGAN](#)


Comparison of Galaxy vs. MEGAN pipeline.

This is the Galaxy history showing a generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3A**):


[Galaxy History | metagenomic analysis](#)


This is the Galaxy workflow for generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3B**):


[Galaxy Workflow | metagenomic analysis](#)


Generic workflow for performing a metagenomic analysis on NGS data.

Accessing the Data

Windshield Splatter datasets analyzed in this manuscript can be accessed through this [Galaxy Library](#). From there, they can be analyzed through Galaxy using the shown workflows or downloaded.

About this Page



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Sharing for Galaxy Administrators Too

Data Libraries

Make data easy to find

Galaxy Tool Shed

Wrapping tools and datatypes

Summary

Everything you do in Galaxy can be shared and published for others to access

Tagging and annotations allow you to provide more information about the steps of your analysis, workflow, etc.

Galaxy pages provide a way for a way to describe multiple entities that make up an entire analysis in a way that readers can easily access all of the details