How to use this document

This is a 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 running, changing, saving, or even applying them to your own data. Specifically, we include the two datasets and entire workflow found below. If you are interested in these datasets, click on their links to download them. You can also import these datasets into your Galaxy workspace and start using them, either directly or via import as text. To import worklist, you must create a Galaxy account (if you don’t already have one) - a hassle-free procedure where you are only asked for a username and password.

This is the Galaxy history showing the generic analysis of metagenomic data. This corresponds to the “a complete metagenomic pipeline” section of the manuscript and Figure 3A.

Supplemental Analysis

Comparison between Galaxy pipeline and Megan