
Supplementary information

**Reproducible, scalable, and shareable
analysis pipelines with bioinformatics
workflow managers**

In the format provided by the
authors and unedited

Supplementary Information

Supplementary Table 1: details for each entry in table 1 (sheet 1) and a list of supported infrastructure for scalability (sheet 2).

Supplementary Note: To illustrate the different workflow managers, we provide a minimal proof-of-concept implementation of a simplified RNA-Seq analysis workflow as shown in Figure 1 for a graphical workflow manager, DSL workflow managers, and a workflow specification (<https://github.com/Goekelab/bioinformatics-workflows>). For workflow implementations that make full use of all the features outlined in this review we highly recommend exploring official documentation and pipeline initiatives.