**How to make a sharable code workflow for reproducible and efficient science: Learnings from {galah} and ALA Labs**

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Skills in coding – i.e. the use of scripting languages such as R or Python for data wrangling, analysis and visualisation – are increasingly seen as fundamental to quantitative ecology. Further, sharing the code for others to repeat your work is now an accepted tenet of open scientific principles. However, sharing code does not, by itself, equate to an analysis being reproducible. Many pieces make up a fully reproducible workflow that if partially complete can decrease or prevent another person (including your future self) from interpreting an analysis or reproducing an output. Using learnings from managing the Atlas of Living Australia’s R package {galah} and ALA Labs (labs.ala.org.au), we discuss the pieces that make up a whole reproducible workflow, and show how commitment to a complete workflow improves collaboration and, perhaps unexpectedly,efficiency. We’ve found that setting out with the intention to share a complete workflow – i.e. making code readable, independently packaging parts of long analyses, and creating a final rendered output – not only improves reproducibility but also creates an effective environment for scientific output. We hope to make a case that everyone can work reproducibly and offer tips of where to start and how to refine your workflow.