**Will your code run again? Tips for making code reproducible in R**

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Many biologists and ecologists choose to use R for running robust analyses. But no matter how statistically robust an analysis may be, if the code can’t be re-run by others (or even yourself in the future), the value of a great analysis can be wasted or lost entirely. At the Atlas of Living Australia (ALA)—Australia’s largest biodiversity data infrastructure—we value reproducibility but recognise how hard it can be to know where to start, what tools are available, and what steps are most important. In this talk, we’ll walk through how to turn a common-but-difficult-to-reproduce code example into a reproducible one using tips learned from creating [the galah package](https://galah.ala.org.au/), [ALA Labs](https://labs.ala.org.au/), and [*Cleaning Biodiversity Data in R*](https://cleaning-data-r.ala.org.au/). We’ll demonstrate how simple changes add up to become more than the sum of their parts, making code far easier to share, re-run, and reproduce results, preserving the value of your analyses into the future.