The FAIRification of pharmacoepidemiological research

A practical introduction to reproducible analytical workflows using git and R

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# Abstract

**Objective**

**Study Design and Settings**

**Results**

**Conclusions**

**Introduction**

Transparency and reproducibility in conducting healthcare database studies in pharmacoepidemiology is one of the most critical scientific requirements for meaningful research. While many advances have been made in the reporting and documentation of study protocols and results1–4, the transparency around the actual implementation and analytical steps is still significantly lacking, especially when analyses are implemented via line programming steps in statistical programming languages like R5 or Python. Although in other quantitative disciplines such as computational biology6–8 or health informatics9, the sharing of programming code is frequently observed, this practice is not as common in the (pharmaco-)epidemiological community.

Based on the principles of *FAIR* *data*10, this concept can be extended to the implementation of pharmacoepidemiological study workflows by making all components of a study **F**indable, **A**ccessible, **I**nteroperable, and **R**eproducible. Version control systems (VCS), such as *Git*, can thereby provide easy and powerfultools to keep track of the versioning of analytical code, tables, figures and other resources, track and resolve errors, collaborate with peers, and share resources instantaneously upon submission or publication of a manuscript. By design, VCS workflows automatically enable researchers to comment, track and compare major changes made to documents and hence, increase the ability to comprehend the evolution of a project while maintaining a complete audit trail of all documents.11 Without VCS, this is often naturally done by assigning uninformative file names such as “*final\_1\_rev\_more\_changes.R*” which is bad practice as changes are difficult to track and reconcile, it leads to avoidable errors and is untransparent for any outside personnel. Particularly in disciplines like pharmacoepidemiology, where analyses can have far reaching impact on healthcare decisions, analytical code needs to be accessible and reproducible by anyone, not only the analyst who originally carried out the analysis.

To increase the adoption of transparent workflows using VCS, this tutorial aims to give a practical and tailored introduction for pharmacoepidemiologists on how to set up, structure, and implement reproducible workflows using Git as the most frequently used VCS in the scientific community.12 We will additionally showcase examples using the R open-source programming language, although the basic principles can be applied to any major coding language.

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