

Improving software quality in bioinformatics through teamwork

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SUPPLEMENTARY FILE

SUPPLEMENTARY METHODS

Following the standard methods of literature review, here we list the phrases and platforms of search. The literature search was performed in multiple iterations using Google (to include grey literature), PubMed and Google Scholar based on phrases “guidelines for bioinformatics software”, “rules for biologists learning bioinformatics”, “scientific software development”, “software engineering bioinformatics” and “bioinformatics software recommendations” throughout 2023. Additionally, relevant articles were selected based on the snowball effect from the references of the initial publications.

SUPPLEMENTARY FIGURES

Modularization

old design

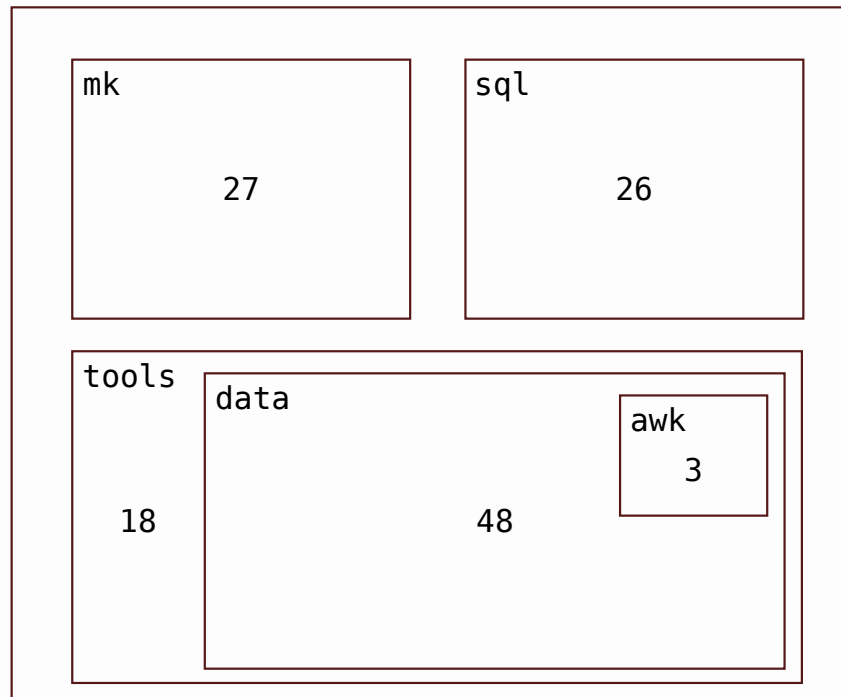


Figure 6: Improving the modularization of a large codebase: previous In the previous design the files were arranged by on their type. The numbers denote the number of files in each directory represented by the rectangle. mk: makefile

new design

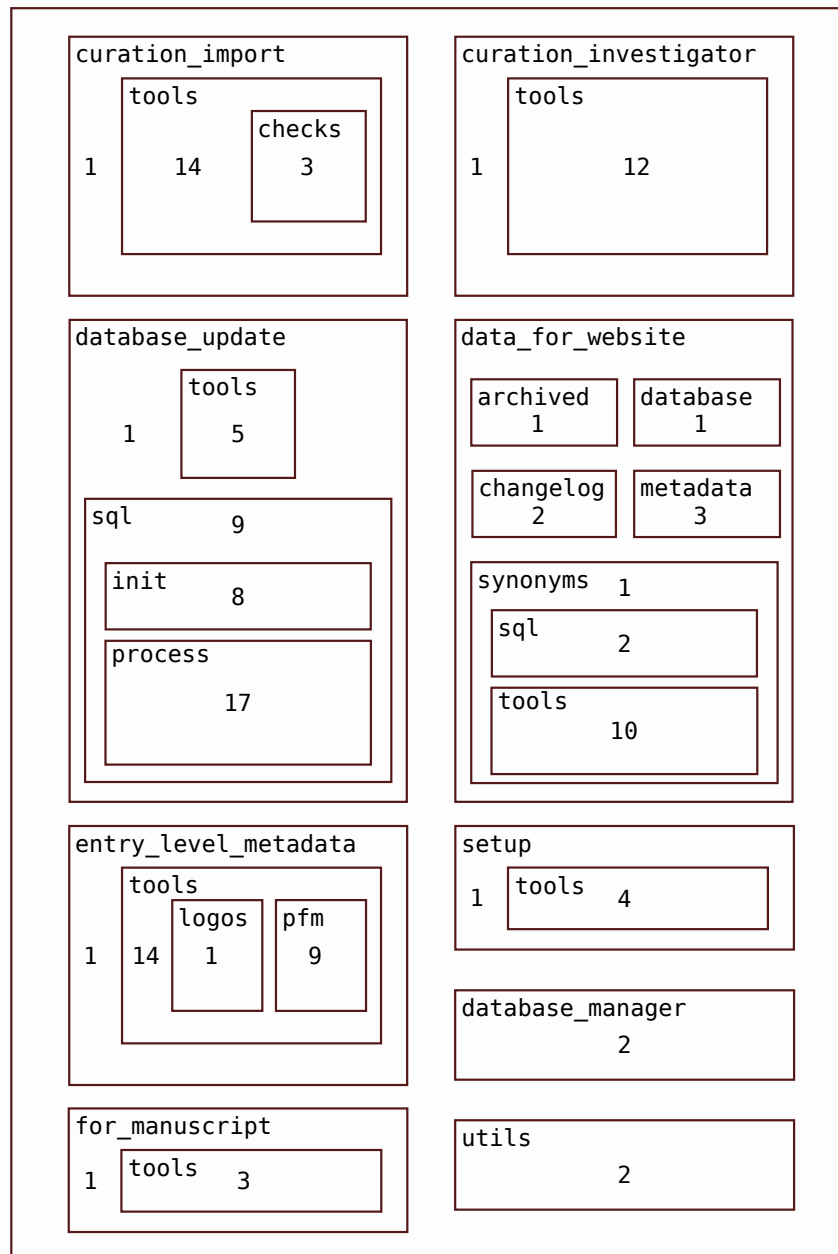


Figure 7: Improving the modularization of a large codebase: current In the current design the files are arranged by their function. The numbers denote the number of files in each directory represented by the rectangle. pfm: position frequency matrix

SUPPLEMENTARY TABLES

TODO: SQ attributes description

Supplementary Table 2: Examples of software quality meeting topics This table contains examples of the topics of past

software quality meetings. It has been organised to follow the same categories as **Table 1**.

Category	Title	Description
Software development 101	To be identified	To be filled
Advanced software development	Design patterns	To be filled
Software development process	Code review	To be filled
Testing and validation	Why testing?	To be filled
Reproducibility	Dependency management	To be filled
Documentation	On Pages and Reports	To be filled
Community effort	To be identified / we never covered it probably	To be filled