# Improving software quality in bioinformatics through teamwork

Katalin Ferenc<sup>1</sup>, Ieva Rauluseviciute<sup>1</sup>, Ladislav Hovan<sup>1</sup>, Vipin Kumar<sup>1</sup>, Mariekie Kuijjer<sup>1</sup>, and Anthony Mathelier<sup>1,2, $\boxtimes$ </sup>

- Centre for Molecular Medicine Norway (NCMM), Nordic EMBL
  Partnership, University of Oslo, 0318 Oslo, Norway
  Department of Medical Genetics, Institute of Clinical Medicine,
- <sup>2</sup> Department of Medical Genetics, Institute of Clinical Medicine, University of Oslo and Oslo University Hospital, Oslo, Norway
- <sup>™</sup> Correspondence: <u>Anthony Mathelier</u> <anthony.mathelier@ncmm.uio.no>

## 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**

TODO: code examples

## **SUPPLEMENTARY TABLES**

TODO: SQ attributes description TODO: software seminar topics - corresponding to themes in table  $\boldsymbol{1}$