

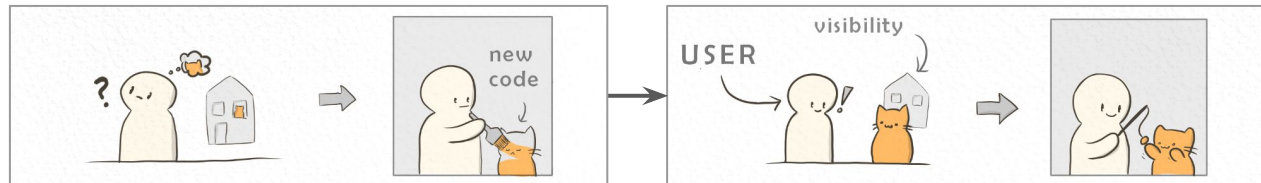
Supporting community-driven open-access simulation software with **MDAnalysis** toolkits



# Scientific code is increasingly shared

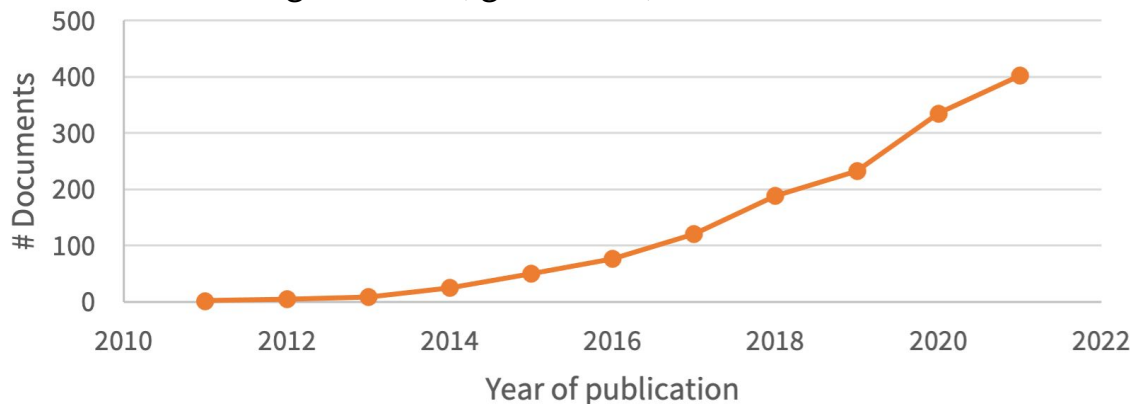


- MD community has made effort to share more and more code



- Lets you replicate methodology
- Lets you re-use code
- Reduces duplication of effort
- Reduces risk of implementation error

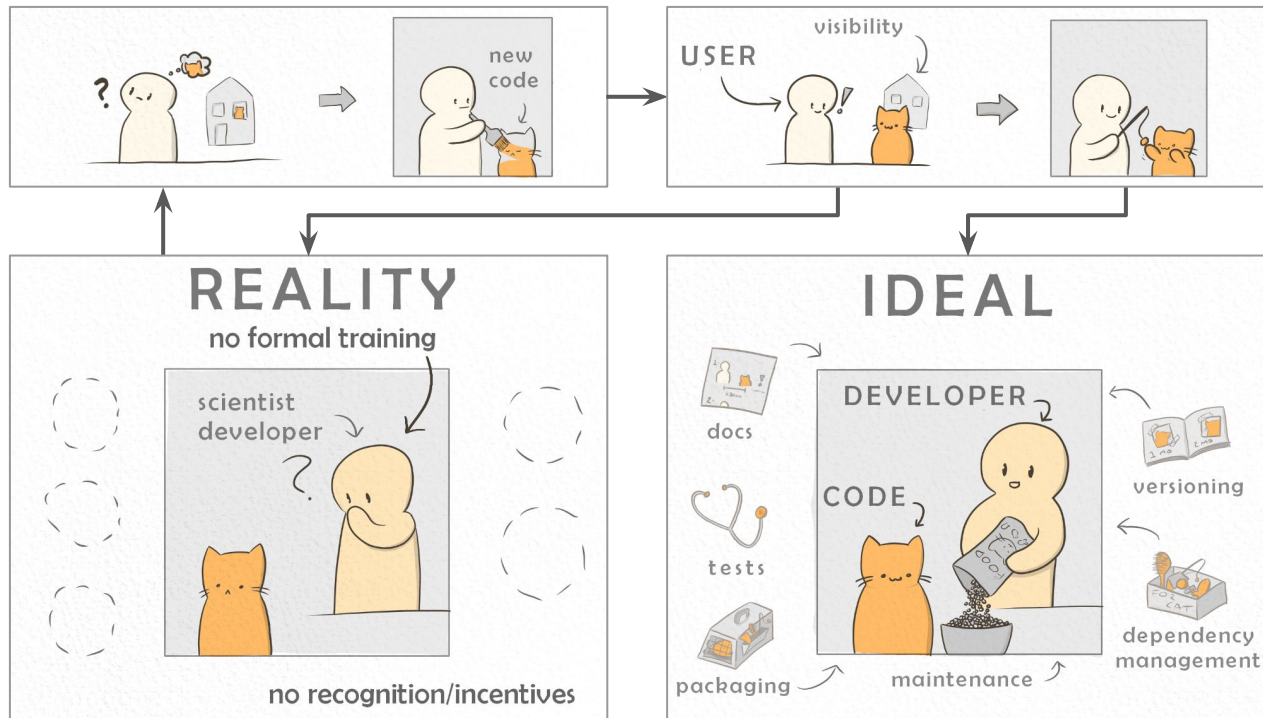
Documents in Scopus with “molecular dynamics” and github.com, gitlab.com, or bitbucket.com



# Scientific code often falls short of FAIR tenets



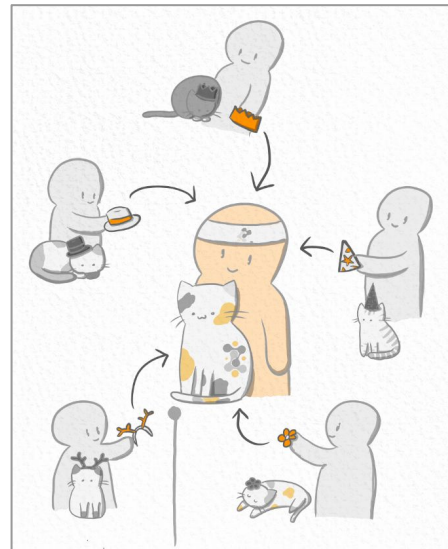
- **F**: findable
- **A**: accessible
- **I**: interoperable
- **R**: reusable



# Centralising in MDAnalysis is a limited solution



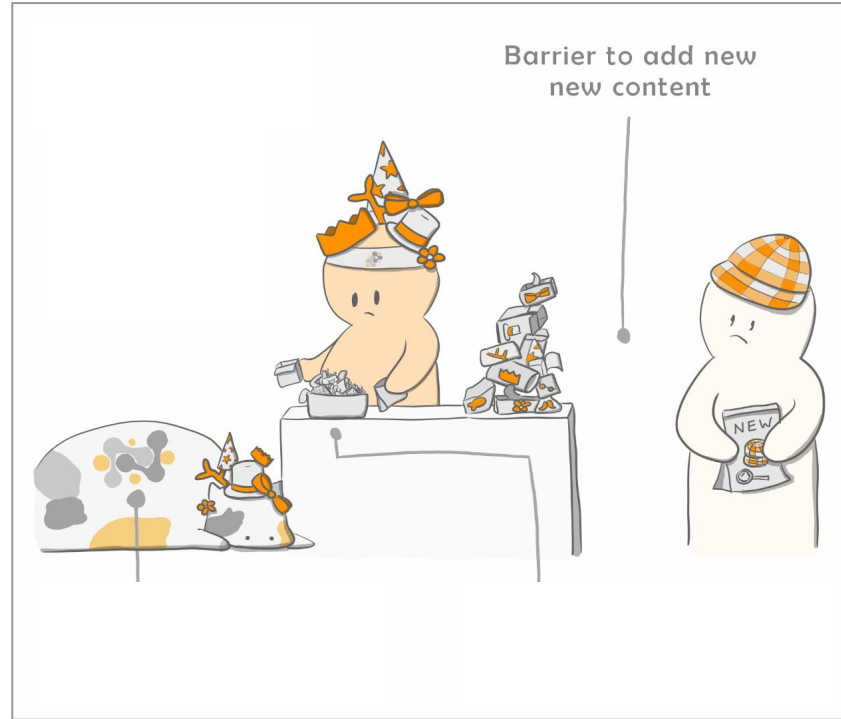
- Asking for contributions to MDAnalysis has many advantages
  - Setting up documentation, packaging, automatic tests, etc already taken care of
  - Experienced developers ensure code follows best practices
  - Code automatically accessible to user base – even promoted
  - MDAnalysis developer team can maintain code, so original developers can move on



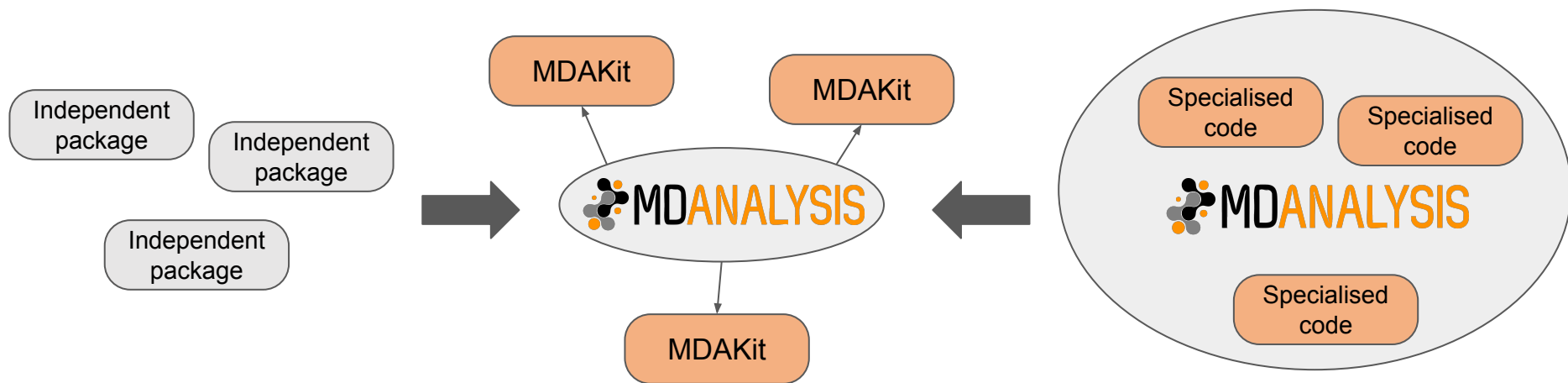
# Centralising in MDAnalysis is a limited solution



- But many disadvantages make this unsustainable for us

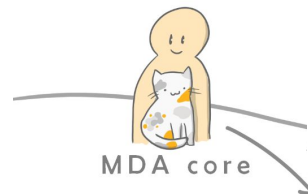


# MDAKits (MDAnalysis toolkits)





- Researchers supported in developing software and being FAIR-compliant
- Cookiecutter template provided
- Toolkits that meet standards are promoted to the community on an MDAKit registry
- Users can check here for analysis packages
- Developers can find users and collaborate with each other

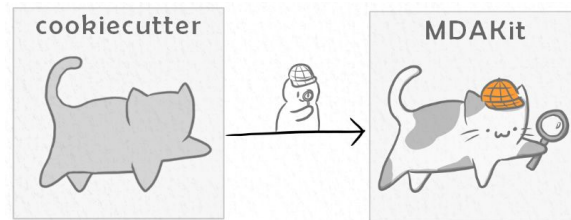


# Cookiecutter template (cookiecutter-mdakit)



```
$ cookiecutter gh:MAnalysis/cookiecutter-mdakit

project_name [ProjectName]: My Project Name
repo_name [my_project_name]: example-repository
package_name [example_repository]: package_name
description [A short description of the project.]: A package to do MD analysis
github_username [Your personal GitHub username]: my-github-username
github_host_account [GitHub account for hosting example-repository (e.g.
my-github-username or an organization account). Press Enter to use
my-github-username]:
author_name [Your name (or your organization/company/team)]: My Name
author_email [Your email (or your organization/company/team)]:
my_example_email@gmail.com
Select dependency_source:
1 - Prefer conda-forge over the default anaconda channel with pip fallback
2 - Prefer default anaconda channel with pip fallback
3 - Dependencies from pip only (no conda)
Choose from 1, 2, 3 [1]: 1
Select include_ReadTheDocs:
1 - y
2 - n
Choose from 1, 2 [1]: 1
template_analysis_class [Class name to template (e.g. MyProjectName )].
Press Enter to skip including analysis templates]: MyAnalysisClass
```



First step in MDAKit framework

\*Based off MolSSI's  
cookiecutter-cms!





# Cookiecutter example



README.md

## TestMDAKit\_with\_condaforge-deps\_and\_ReadTheDocs

Latest release	release no releases github no releases or repo not found docs unknown
Status	GH Actions CI passing codecov unknown lgtm project not found
Community	License GPLv3 powered by MDAAnalysis

Test MDAKit Project with dependencies using condaforge and ReadTheDocs

TestMDAKit\_with\_condaforge-deps\_and\_ReadTheDocs is bound by a [Code of Conduct](#).

### Installation

To build TestMDAKit\_with\_condaforge-deps\_and\_ReadTheDocs from source, we highly recommend using virtual environments. If possible, we strongly recommend that you use [Anaconda](#) as your package manager. Below we provide instructions both for `conda` and for `pip`.

#### With conda

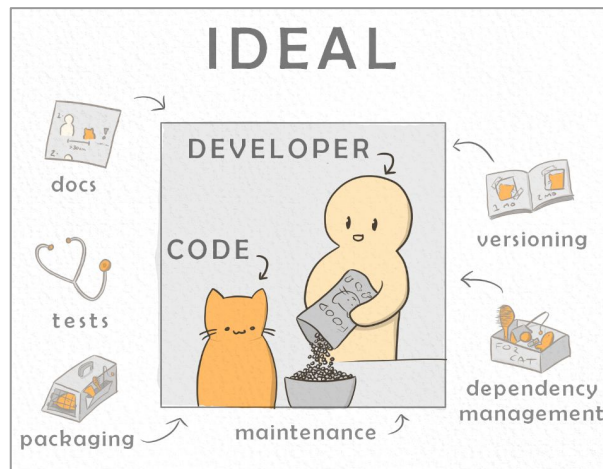
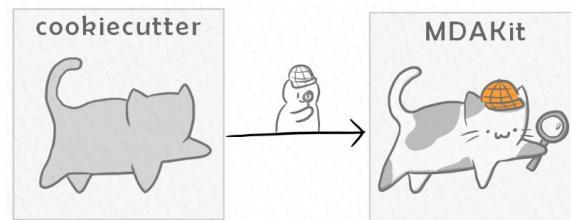
Ensure that you have `conda` installed.

Create a virtual environment and activate it:

```
conda create --name mdakit-cookie
conda activate mdakit-cookie
```

Install the development and documentation dependencies:

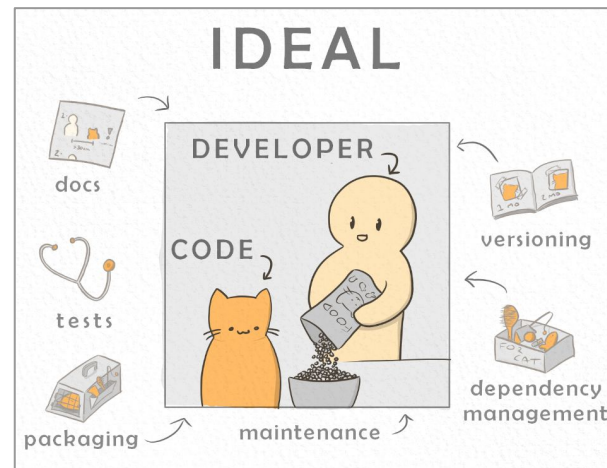
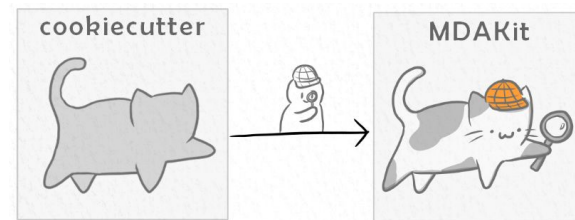
```
conda env update --name mdakit-cookie --file devtools/conda-envs/test_env.yaml
conda env update --name mdakit-cookie --file docs/requirements.yaml
```



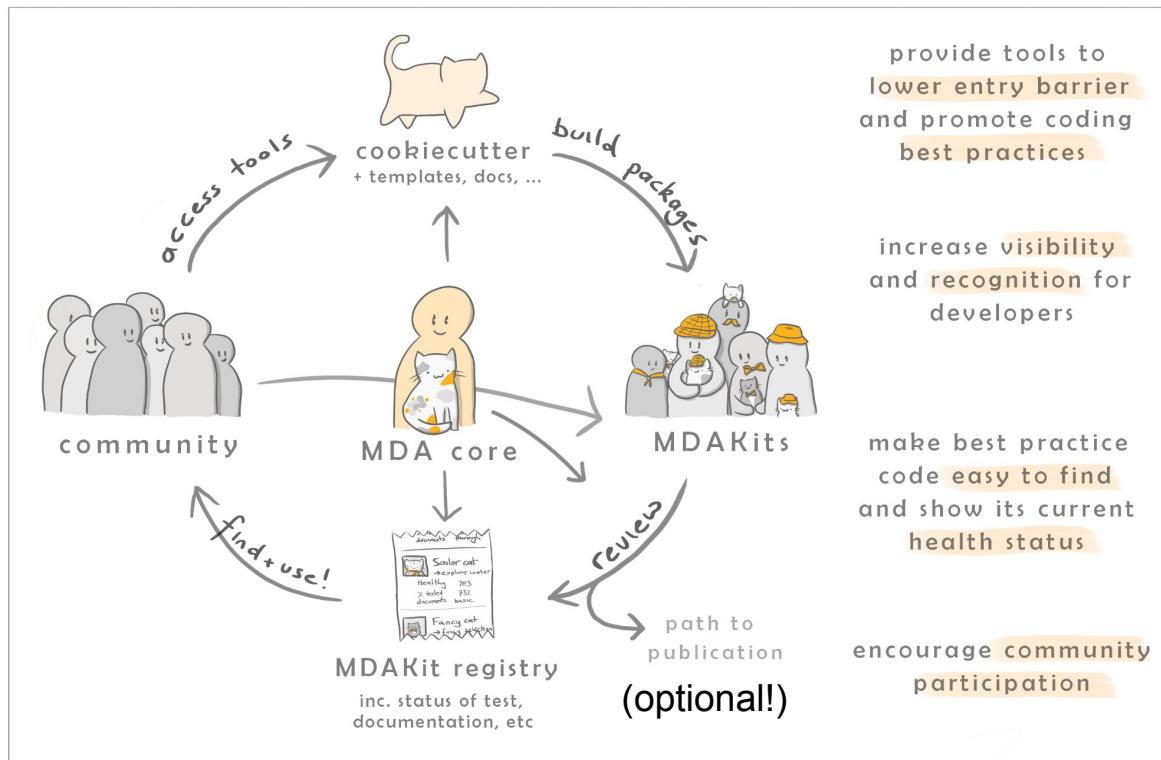
# Cookiecutter template (cookiecutter-mdakit)



- Builds skeleton repository with:
  - **Continuous integration** for GitHub Actions with a matrix of OS, Python, MDAnalysis versions
  - Basic example **test** structure with PyTest
  - Instructions for creating development environments
  - Choice of **dependency management** from conda-forge, anaconda, or PyPI
  - Initial basic **documentation** configured
  - Modern best-practice Python **packaging**
  - Automatic **version control**
  - Configuration for helpful hooks for code coverage, Python code quality, online documentation, etc
  - Community infrastructure e.g. code of conduct, author list, change log
  - Template code for a custom Analysis class



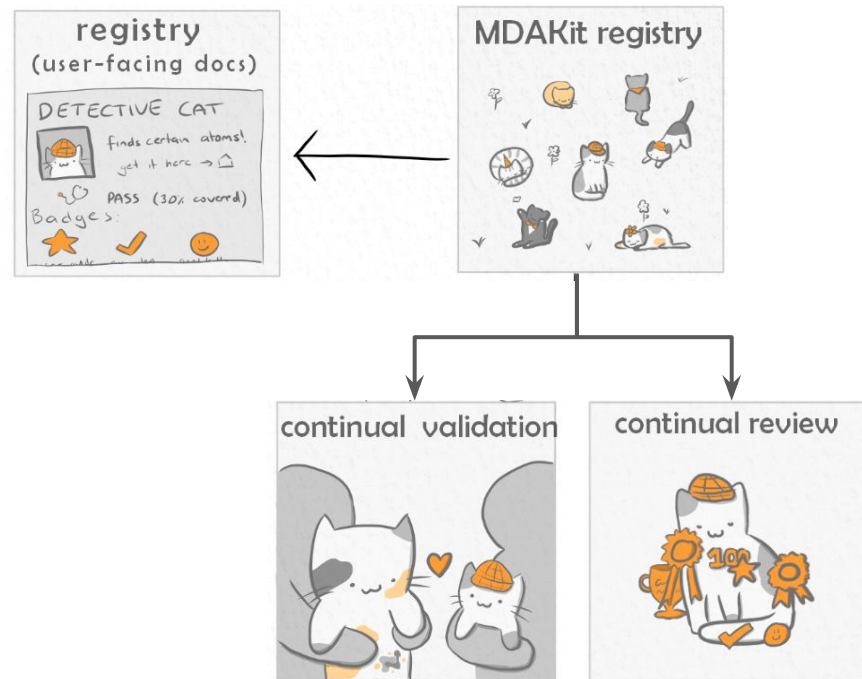
# MDAKits - beyond just packages



# MDAKit Registry



- List of MDAKits that fulfil quality standards
- Each MDAKit gets its own page with badges and recent validation data
- Badges include information about test coverage, presence of a user guide, etc
- Validation data lists versions of Python and MDAAnalysis that pass tests
- The Registry runs continual checks to validate the health of each registered package





## Registry of MDAnalysis Toolkits (MDAKits)

The MDAKit registry contains a list of all MDAKits which have been added to this repository. The aim of this registry is to:

1. Inform members of the community about existing MDAKits
2. Provide sufficient details to allow others to use and potentially participate in the development of the MDAKits
3. Provide information about the current state of the MDAKits and how they interact with the latest versions of MDAnalysis

Each of the MDAKits in the following table links to a page with more details about what the MDAKits do, how they can be installed and how to participate in their development.

Show  entries

Search:

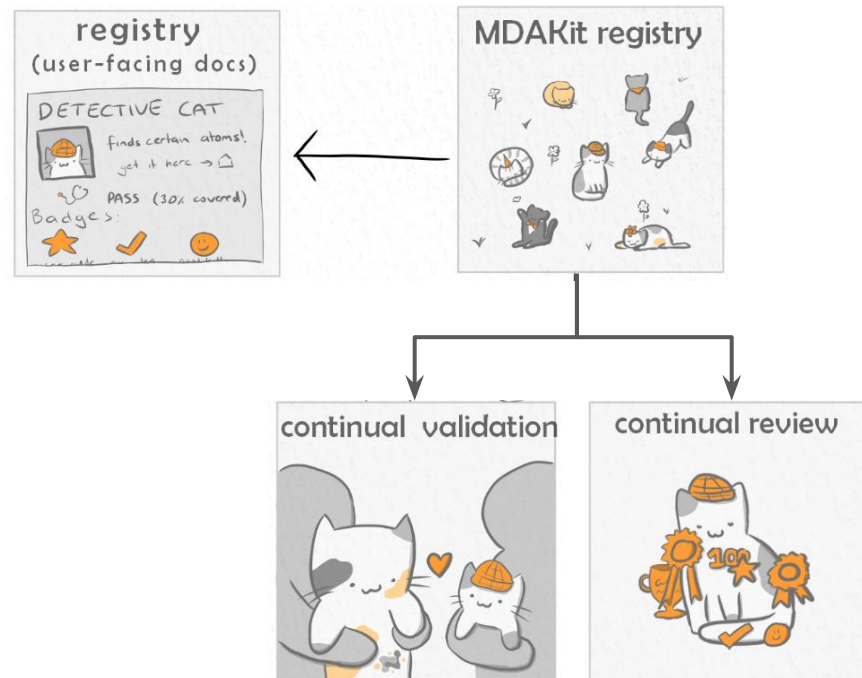
*List of registered MDAKits*

MDAKit	Keywords	Authors	CI badges
<a href="#">lipyds</a>	lipids, membranes	lilyminium	<div>latest unavailable</div> <div>develop failed</div>
<a href="#">maicos</a>	Molecular Dynamics, Confined Systems	<a href="#">maicos authors</a>	<div>latest passed</div> <div>develop passed</div>
<a href="#">mda-tui</a>	transformations, TUI	<a href="#">mda-tui authors</a>	<div>latest passed</div> <div>develop passed</div>
<a href="#">mdachecker</a>	structure analysis, conformation checks	IAIibay	<div>latest passed</div> <div>develop passed</div>

# MDAKit Registry - responsibility



- Registry maintainers
  - Keeping the registry components working
  - Adding new components as needs arise
  - Helping with addition of new mdakits
  - Helping with advice on continual improvement
  - Note: packages will *not be removed* if they fail continuous validation
- MDAKits maintainers
  - Ensuring registry for their mdakits remain green
  - Ensuring the information in the registry is up to date



# MDAKit minimal requirements



1. Must use **MDAnalysis**! Powered by **MDAnalysis**
2. **Open source** under an OSI approved license
3. Code is **versioned** and provided in a version-controlled repository
4. Clearly designated **authors** and maintainers
5. At least minimal **documentation**
6. Minimal regression **tests** and **CI**

## Requirements for MDAKit registration



uses MDA



open source



versioning



authors  
+ contact details



(basic) docs  
what it does + example



(basic) tests



packaging



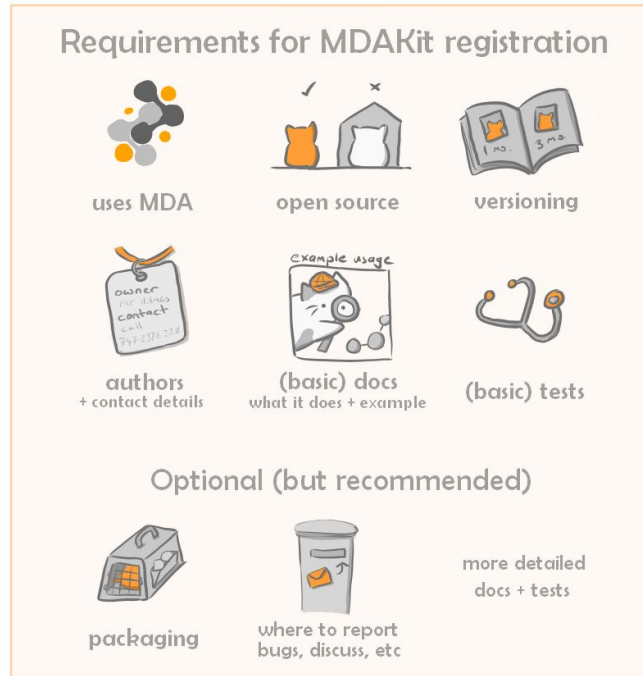
where to report  
bugs, discuss, etc

more detailed  
docs + tests

# MDAKit ideal standards



1. Must use **MDAnalysis**!
2. **Open source** under an OSI approved license
3. Code is **versioned** and provided in a version-controlled repository
4. Clearly designated **authors** and maintainers
5. API **documentation** and **user guide**
6. Unit **tests** with >80% code coverage
7. **Packaging** for easy installation
8. **Community** infrastructure  
(e.g. code of conduct, discussion channels)





# Towards publication (future)



- Our best practices are similar to criteria in software journals (e.g. Journal of Open Source Software)
- MDAKits are encouraged to consider publication
- We are working with journal editors at JOSS to streamline the publication process





## MDAKits: A Framework for FAIR-Compliant Molecular Simulation Analysis

Irfan Alibay<sup>‡†\*</sup>, Lily Wang<sup>‡†</sup>, Fiona Naughton<sup>§†</sup>, Ian Kenney<sup>¶†</sup>, Jonathan Barnoud<sup>||</sup>, Richard J Gowers<sup>‡</sup>, Oliver Beckstein<sup>||</sup>

**Abstract**—The reproducibility and transparency of scientific findings are widely recognized as crucial for promoting scientific progress. However, when it comes to scientific software, researchers face many barriers and few incentives to ensure that their software is open to the community, thoroughly tested, and easily accessible. To address this issue, the MDAKits framework has been developed, which simplifies the process of creating toolkits for the MDA analysis simulation analysis package (<https://www.mdanalysis.org>) that follow the basic principles of FAIR (findability, accessibility, interoperability, and reusability). The MDAKit framework provides a cookiecutter template, best practices documentation, and a continually validated registry. Registered kits are continually tested against the latest release and development version of the MDA analysis

Consequently, scientific code frequently fails to meet the basic tenets of FAIR: findability, accessibility, interoperability, and reusability [1], [2]. With the publication of “The FAIR Guiding Principles for scientific data management and stewardship” in 2016 and the follow-up “FAIR Principles for Research Software (FAIR4RS Principles)” in 2022, it has become increasingly acknowledged that abiding by the principles of FAIR is crucial to promoting robust, reproducible, and efficient scientific discovery and innovation [1], [2]. We believe that extending FAIR principles to include open-source software not only significantly advances

### The MDAKit framework

