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# SURESOFT: Towards Sustainable Research Software

Technische Universität Braunschweig



# Who are we?



**Dr. Jan Linxweiler**  
j.linxweiler@tu-braunschweig.de



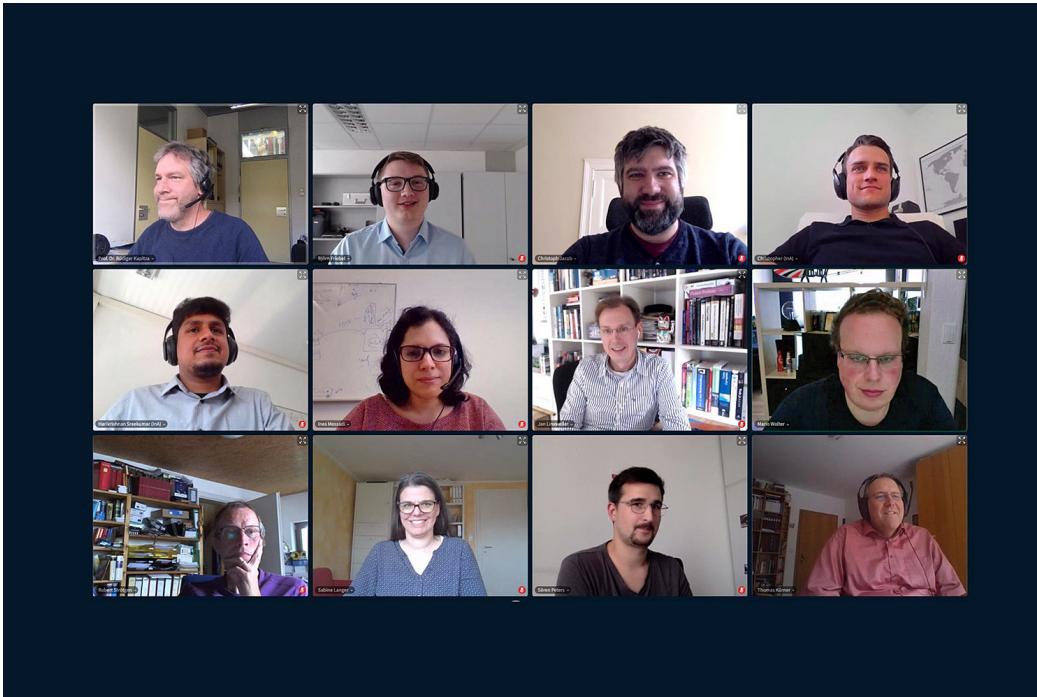
**Sören Peters**  
soe.peters@tu-braunschweig.de



**Sven Marcus**  
sven.marcus@tu-braunschweig.de

# Who are we?

18 People from 7 Institutes and Facilities



Institute of Operating Systems  
and Computer Networks



Institut für Nachrichtentechnik



Institut für Physikalische  
und Theoretische Chemie



University Library &  
Gauß-IT-Zentrum



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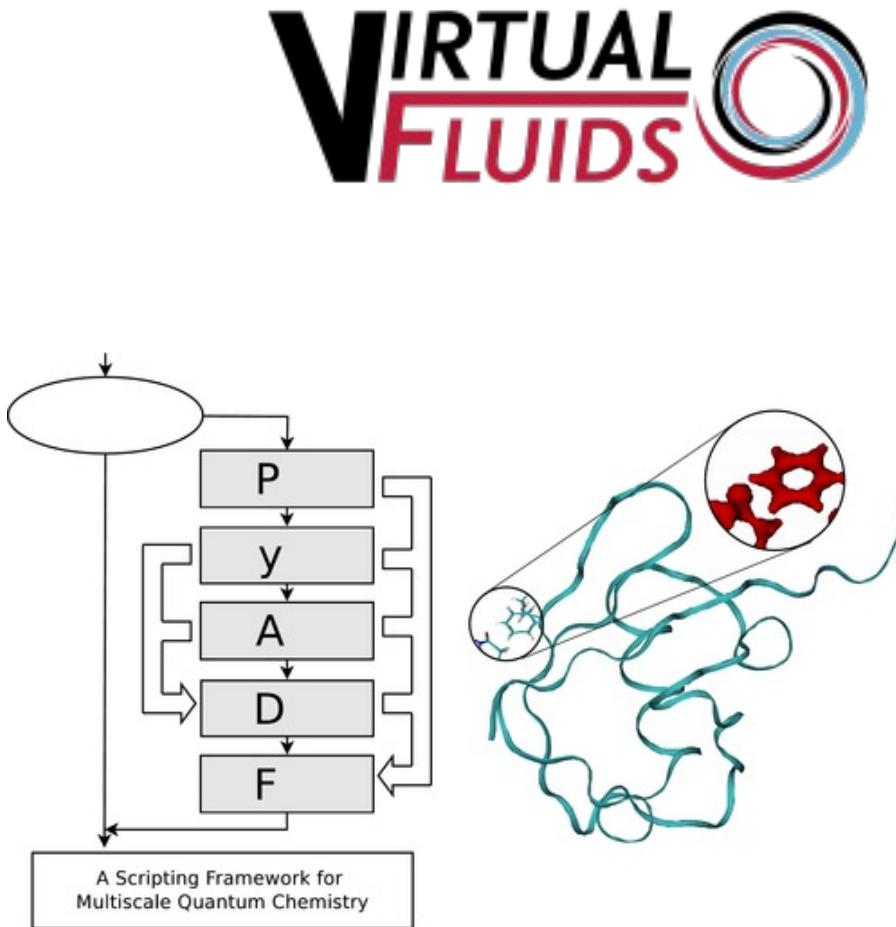
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<https://doi.org/10.5281/zenodo.10002995>

**Suresoft**  
SUSTAINABLE RESEARCH SOFTWARE

# SURESOFT Projects



Themis



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## HERMES

Helmholtz Rich Metadata  
Software Publication



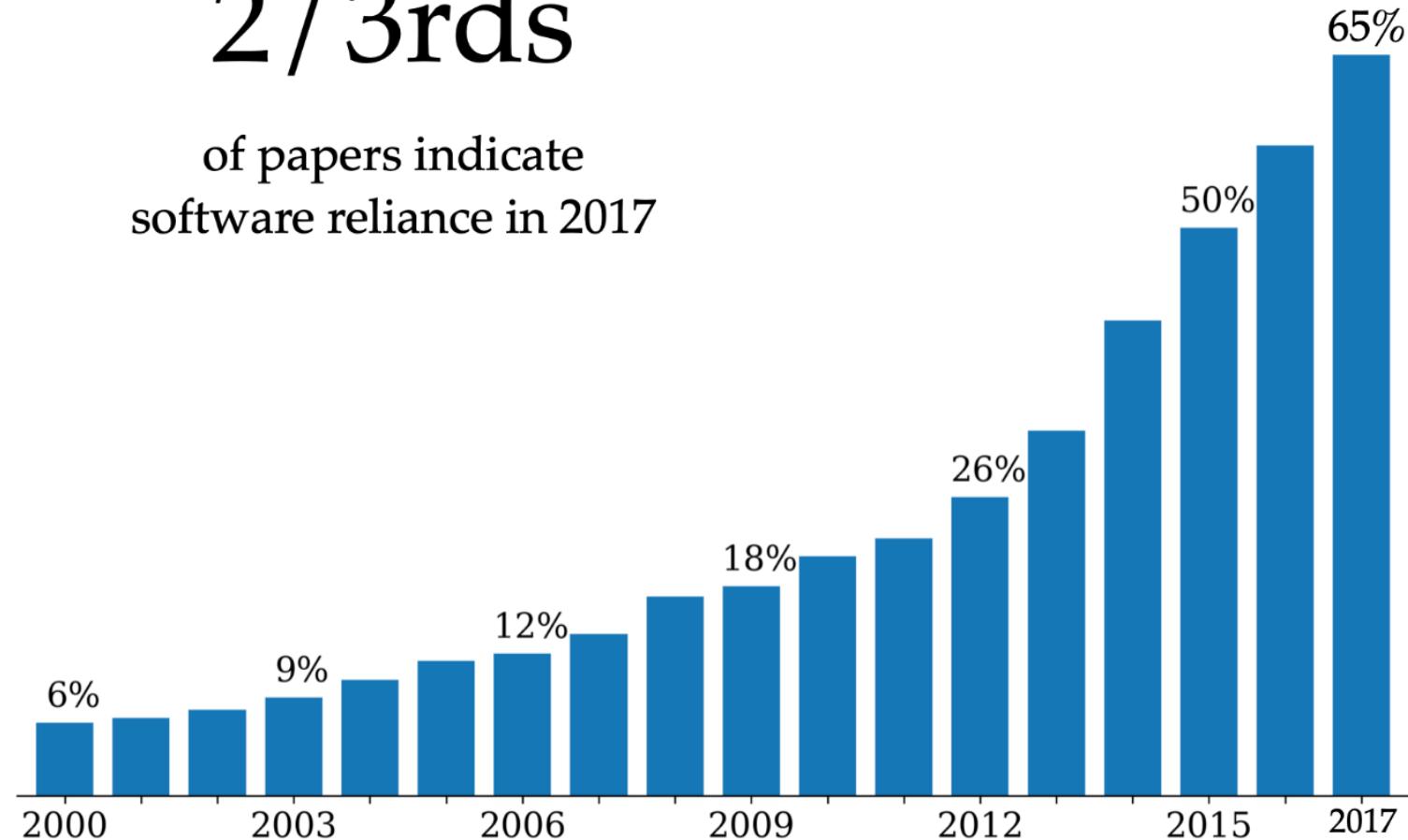
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# Publications relying on software

2 / 3rds

of papers indicate  
software reliance in 2017

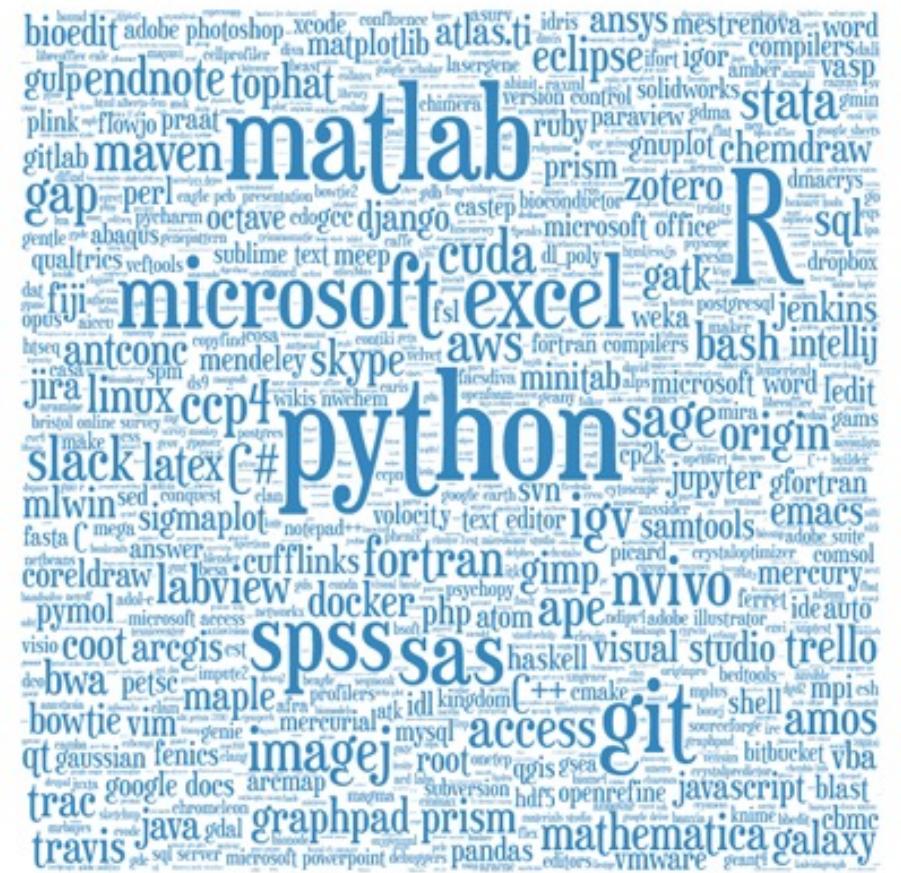


<https://bit.ly/37XEJ2u>

# Use of research software

- 92% of academics use research software
- 69% say that their research would not be practical without it
- 56% develop their own software

<https://bit.ly/2zZPhSa>

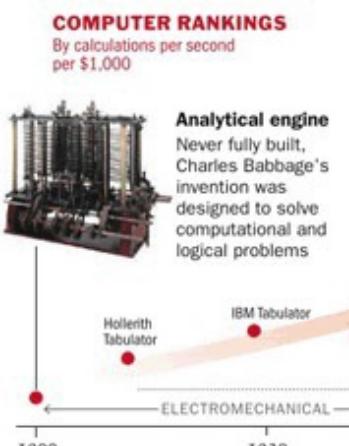
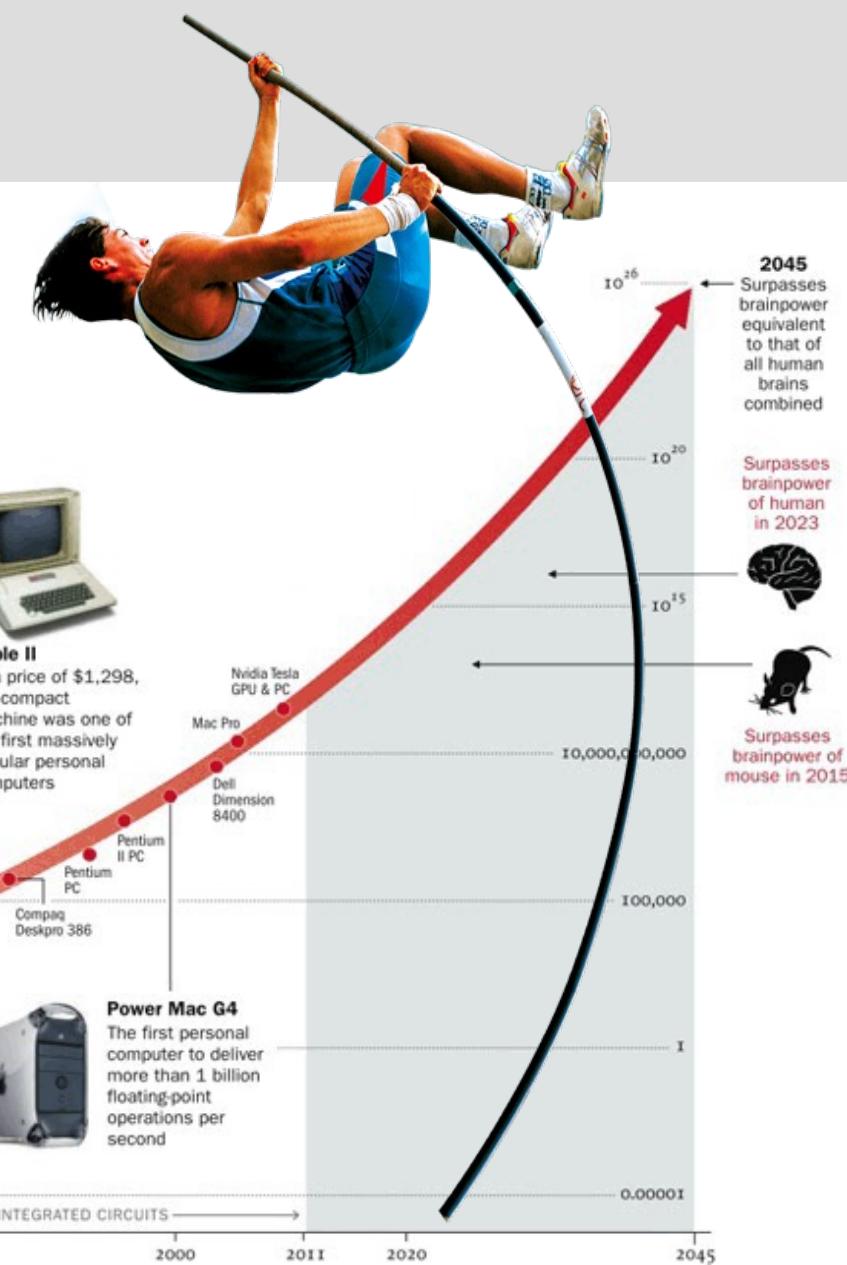


<https://bit.ly/2BAvzwQ>



# Growing demands on scientific software

- Increasing Complexity (e.g. multi physics, multiple groups)
- Longer Life Span (base your work on the work of others)
- Reproducible and Verifiable Results



# Motivation

## Researchers

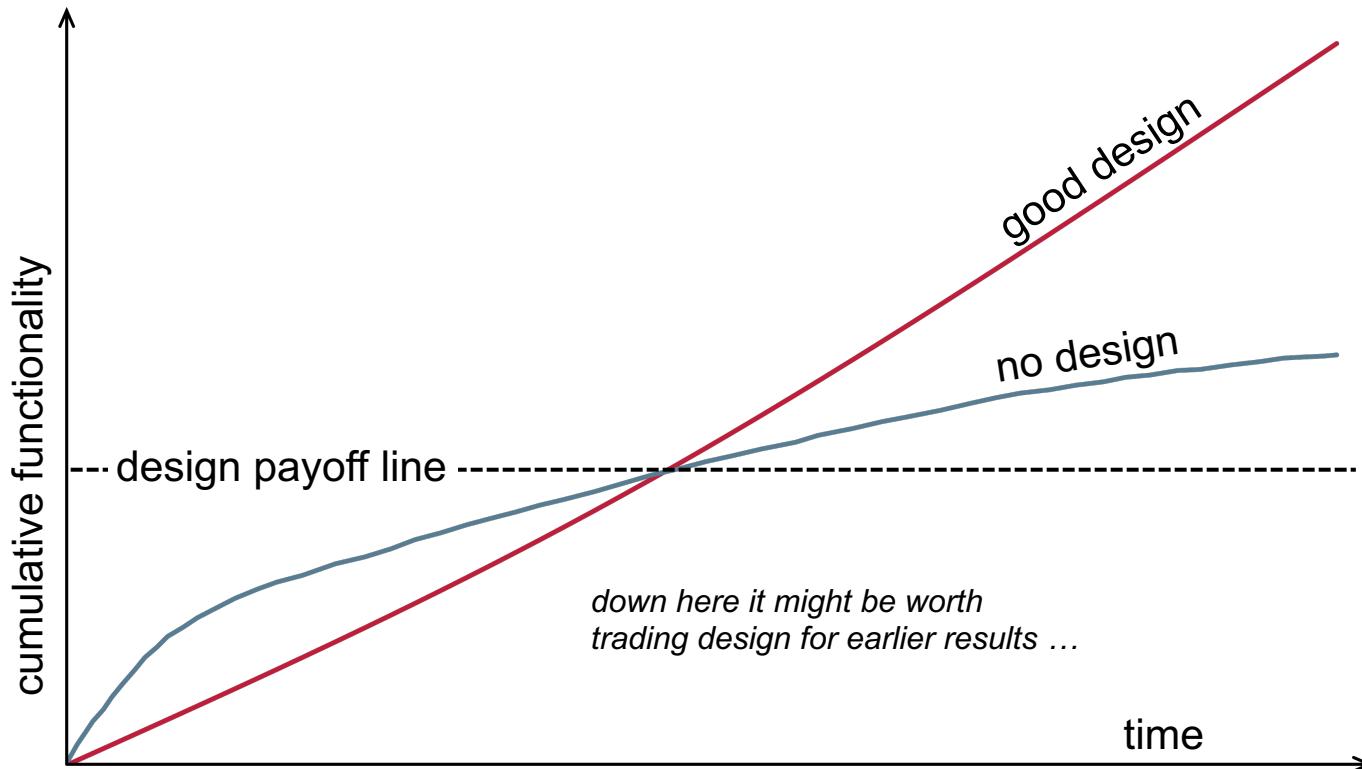
- often lack knowledge about the principles and practices of the software engineering discipline [5, 4]
- don't gain a reputation for developing software
- are pressed to publish results as fast as possible [2]



# Productivity Crisis

- floating point performance is constantly rising
- time-to-solution is increasing
- scientists spend 50% of the time finding bugs

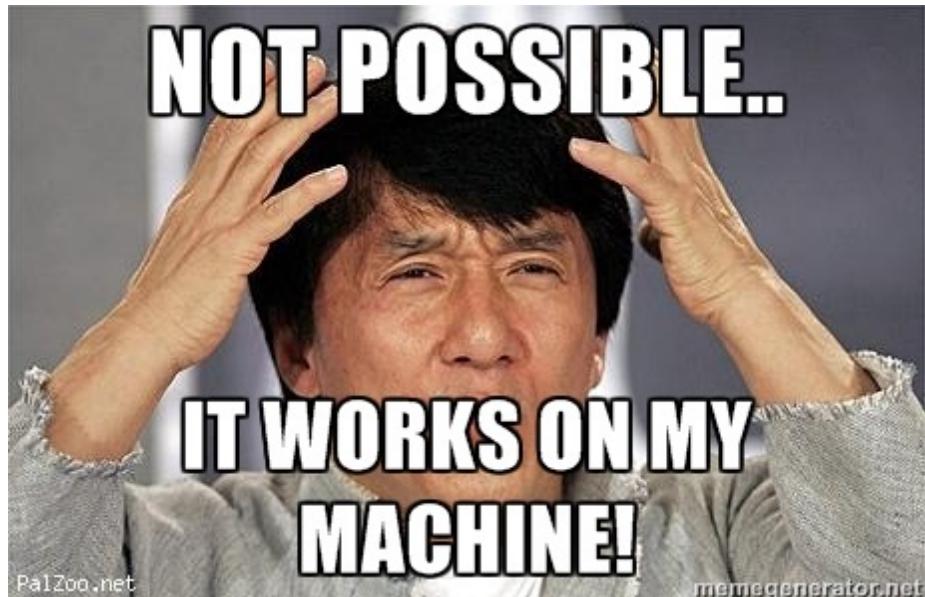
[P. Prabhu, A Survey of the Practice of Computational Science, 2011]



Design Stamina Hypothesis  
<https://bit.ly/2A64CAR>



# Consequences



Common problems of research software

- low code quality
- neither published nor documented
- depends on a specific runtime environment (e.g third party libraries), which may not be available to other researchers

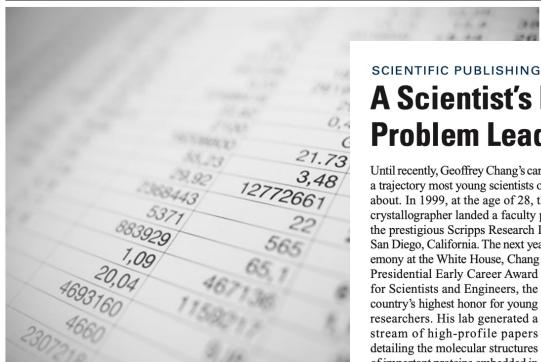
# Credibility Crisis

Questionable reliability, accuracy, reproducibility and verifiability of the results ...

■ 18 April 2013, 12:31 CEST

## FAQ: Reinhart, Rogoff, and the Excel Error That Changed History

By Peter Coy



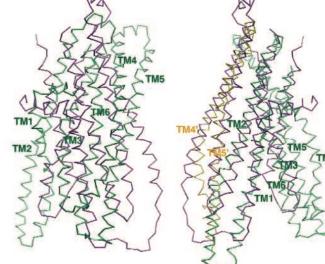
PHOTOGRAPH BY GREGOR SCHUSTER

### SCIENTIFIC PUBLISHING A Scientist's Nightmare: Software Problem Leads to Five Retractions

Until recently, Geoffrey Chang's career was on a trajectory most young scientists only dream about. In 1999, at the age of 28, the protein crystallographer landed a faculty position at the prestigious Scripps Research Institute in San Diego, California. The next year, in a ceremony at the White House, Chang received a Presidential Early Career Award for Scientists and Engineers, the country's highest honor for young researchers. His lab generated a stream of high-profile papers detailing the molecular structures of important proteins embedded in cell membranes.

Then the dream turned into a nightmare. In September, Swiss researchers published a paper in *Nature* that cast serious doubt on a protein structure Chang's group had described in a 2001 *Science* paper. When he investigated, Chang was horrified to discover that a homemade data-analysis program had flipped two columns of data, inverting the electron-density map from which his team had derived the final protein structure. Unfortunately, his group had used the program to analyze data for

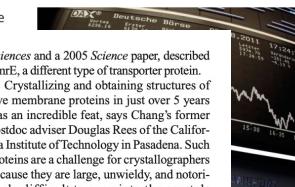
2001 *Science* paper, which described the structure of a protein called MsbA, isolated from the bacterium *Escherichia coli*. MsbA belongs to a huge and ancient family of molecules that use energy from adenosine triphosphate to transport molecules across cell membranes. These so-called ABC transporters perform many



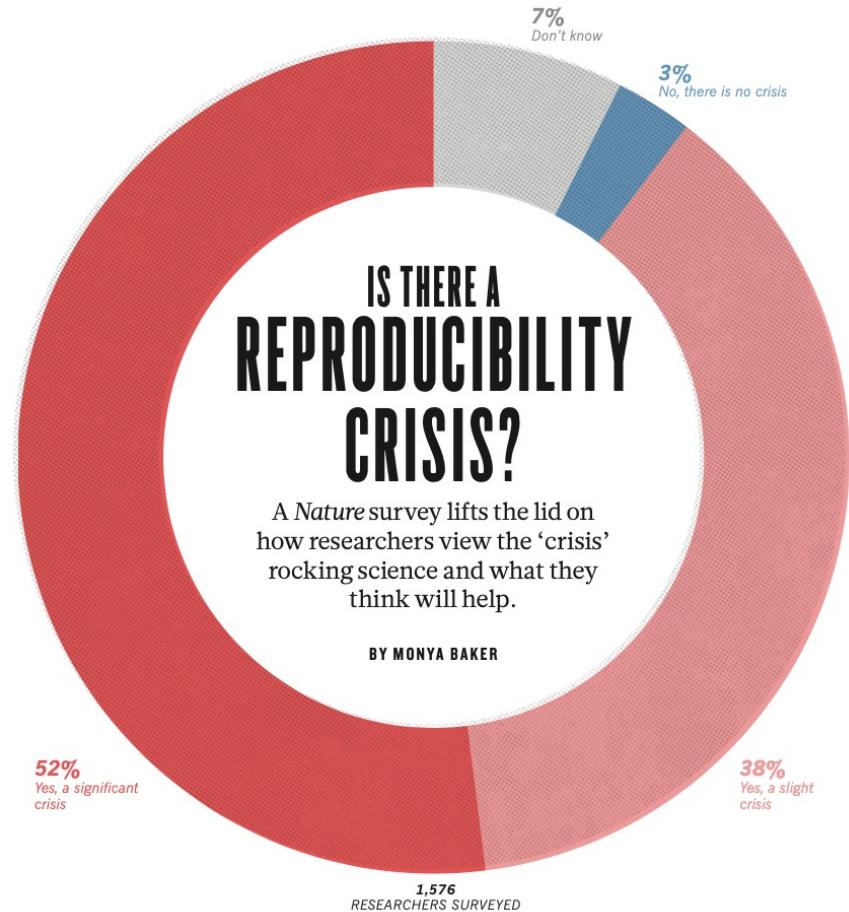
Flipping fiasco. The structures of MsbA (purple) and Sav1866 (green) overlap little (left) until MsbA is inverted (right).

*Sciences* and a 2005 *Science* paper, described EmrE, a different type of transporter protein. Crystallizing and obtaining structures of five membrane proteins in just over 5 years was an incredible feat, says Chang's former postdoc adviser Douglas Rees of the California Institute of Technology in Pasadena. Such proteins are a challenge for crystallographers because they are large, unwieldy, and notoriously difficult to coax into the crystals needed for x-ray crystallography. Rees says determination was at the root of Chang's success: "He has an incredible drive and work ethic. He really pushed the field in the sense of getting things to crystallize that no one else had been able to do."

Chang's data are good, Rees says, but the faulty software threw everything off. Ironically, another former postdoc in Rees's lab, Kaspar Locher, exposed the mistake. In the 14 September issue of *Nature*, Locher, now at the Swiss Federal Institute of Technology in Zurich, described the structure of an ABC transporter called Sav1866 from *Saprophytoccus aureus*. The structure was dramatically—and unexpectedly—different from that of MsbA. After pulling up Sav1866 and Chang's MsbA from *S. typhimurium* on a computer screen, Locher says he realized in minutes that the MsbA structure was inverted. Interpreting the "hand" of a molecule is always a challenge for crystallographers,



t. includes.



<https://go.nature.com/2DgtDKR>



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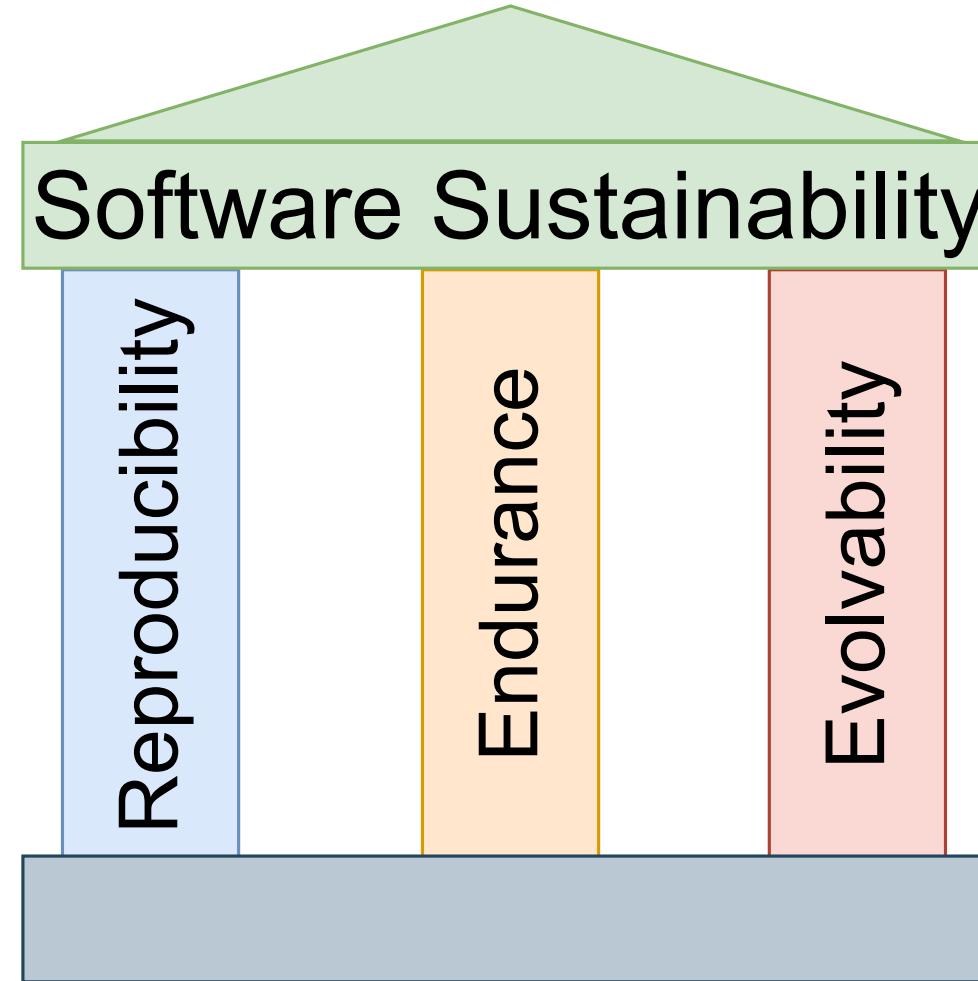
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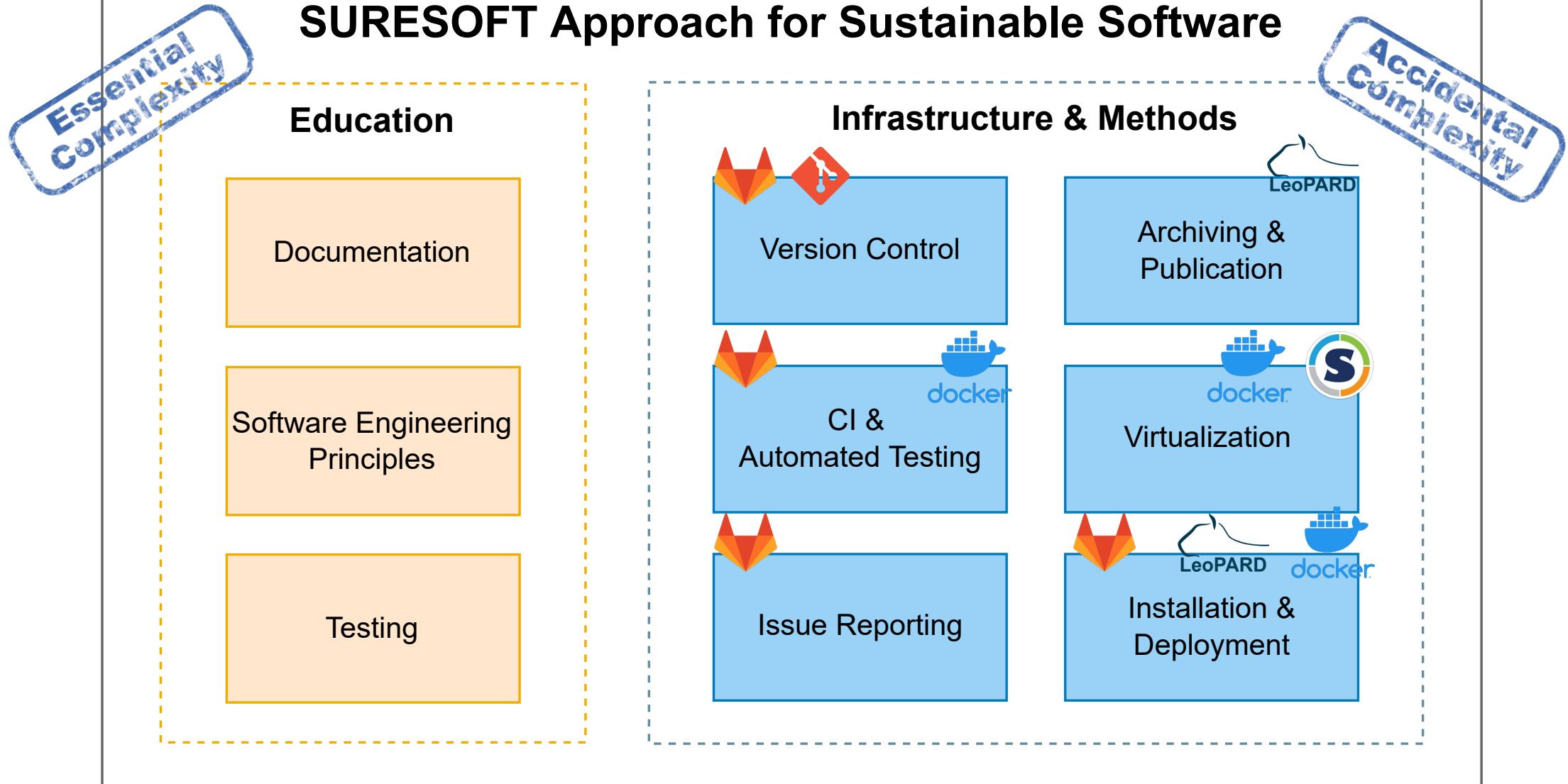
# Approach



# Software sustainability

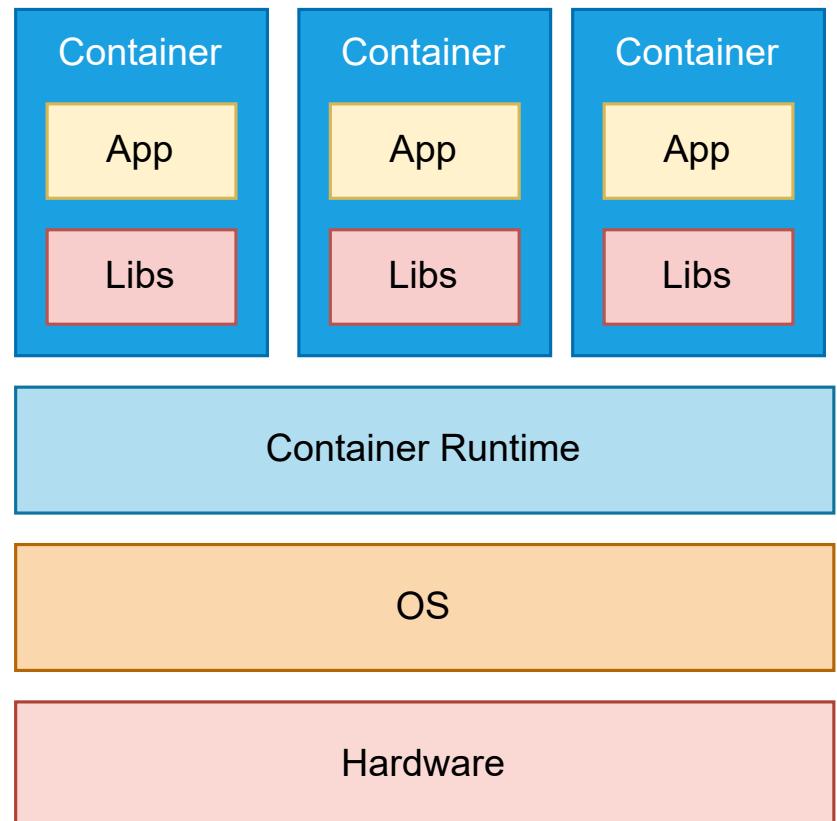


# SURESOFT Approach for Sustainable Software



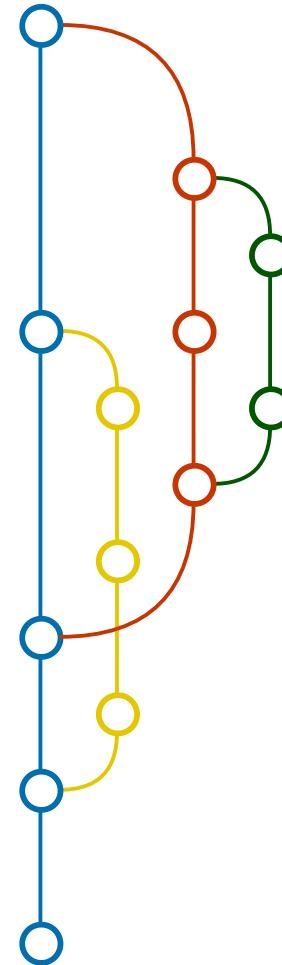
# Container technologies

- Docker in CI, Singularity in HPC
- Encapsulate entire runtime environment, including dependencies
- Easy to share and use Ensures reproducibility
- Scripted environment provides basic documentation

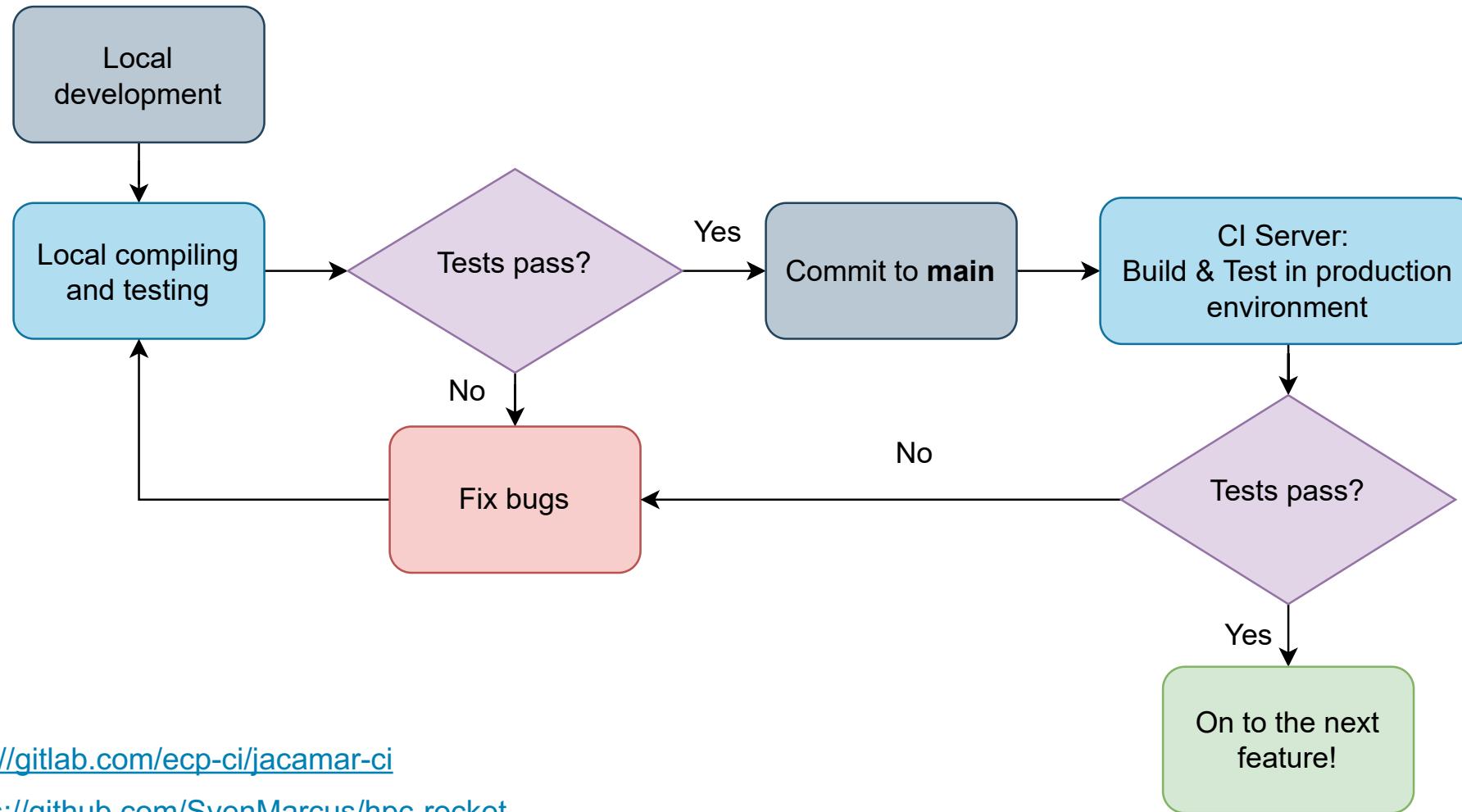


# Version Control

- Track and manage changes of source code
- Commits create versions with unique identifier, documenting changes over time
- Enable collaboration through centralized repository hosting platforms (e.g. GitLab)



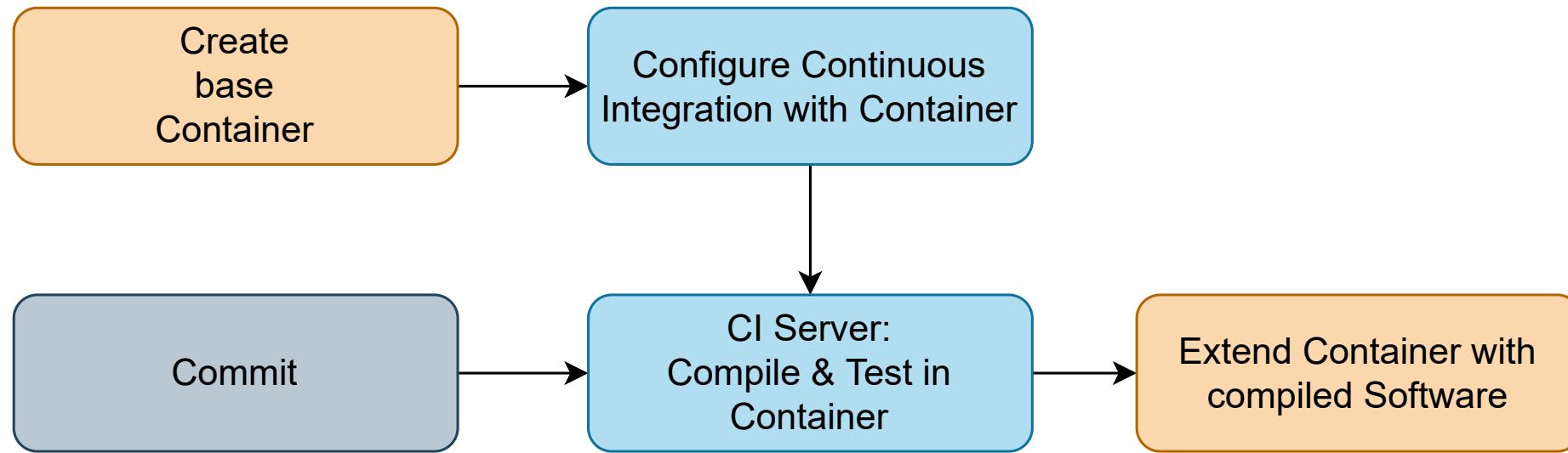
# Continuous integration



Jacamar CI: <https://gitlab.com/ecp-ci/jacamar-ci>

HPC-Rocket: <https://github.com/SvenMarcus/hpc-rocket>

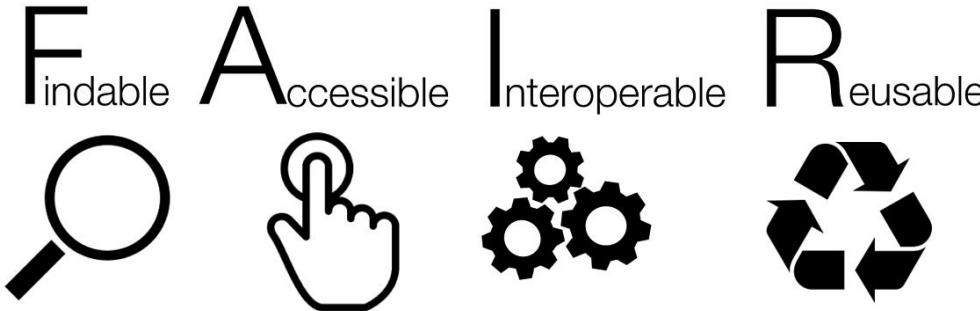
# Continuous analysis



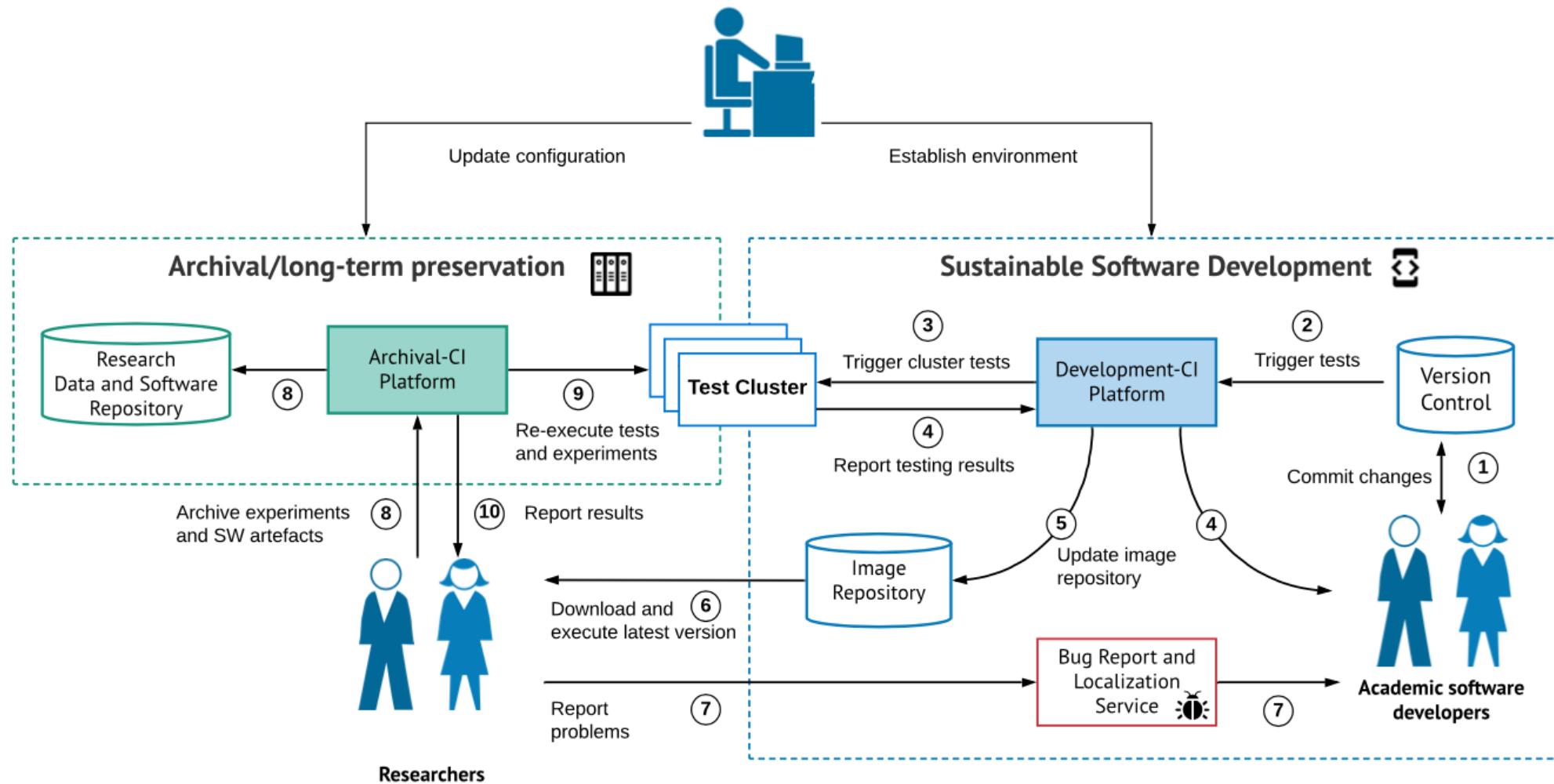
<https://doi.org/10.1038/nbt.3780>

# Publication & Archiving

- publish & archive the source code and the compiled executable together with a complete runtime environment in an accessible repository
- provide meaningful metadata including a unique identifier (DOI) to ensure citability, findability and reusability according the FAIR principles.

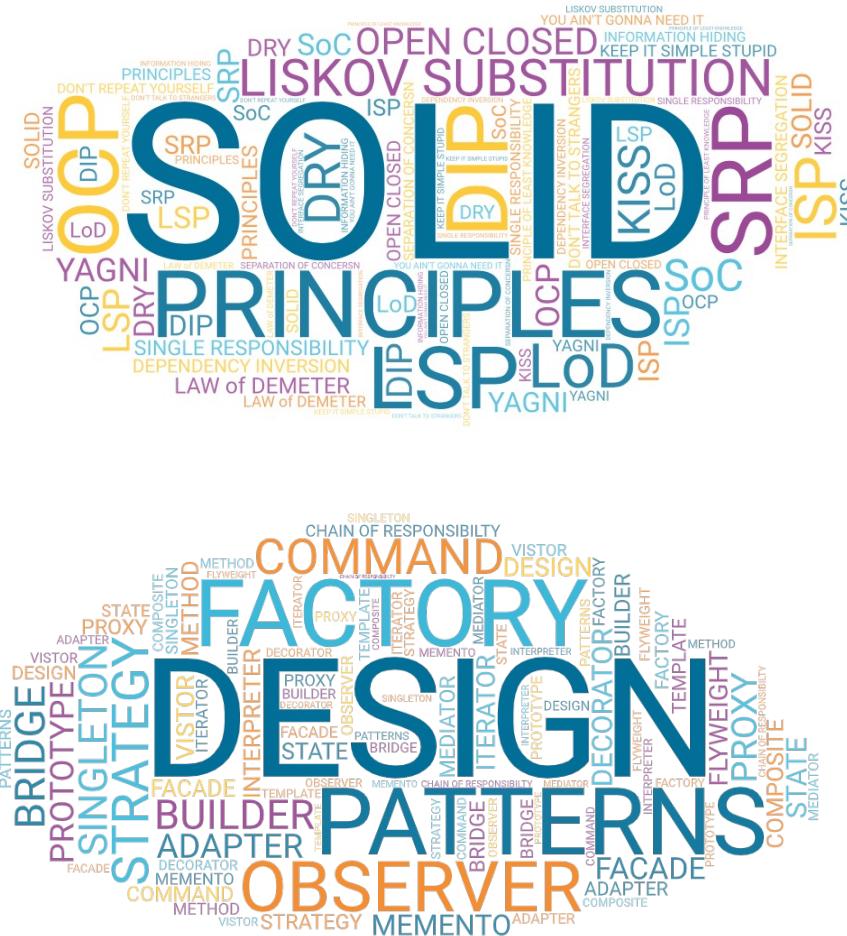


# SURESOFT workflow



# **Education & Support**

- Documentation
  - Software Engineering Principles:
    - SOLID
    - Design Patterns
  - Testing, TDD
  - Version Control & CI
  - Containerization
  - Research Data Management & Long-term archiving
  - Software Licensing



# Workshop Series

- SURESOFT Workshop Series 2022: 9 Workshops
- deRSE 2023
- RSE UK 2023
- HefDi Summer School 2023: 4 Workshops
- <https://suresoft.dev>

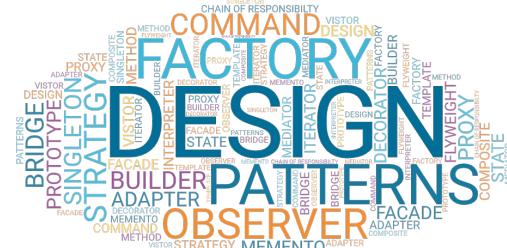


<https://zenodo.org/communities/suresoft>

# New Workshop-Series



HeFDI Code School 'Sustainable Research Software'



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4 half-day workshops from 9 am – 1 pm

- 27 October 2023
- 10 November 2023
- 24 November 2023
- 8 December 2023

<https://lnk.tu-bs.de/8oyp07>



# Get in touch!

website online

<https://suresoft.dev>

chat 19 user

<https://matrix.to/#/#suresoft-general:matrix.org>

Zenodo Community

<https://zenodo.org/communities/suresoft>

Mailinglist

<https://lists.tu-braunschweig.de/sympa/info/musen-rse>



<https://git.rz.tu-bs.de/suresoft>



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<https://doi.org/10.5281/zenodo.10002995>

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# Bibliography

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- [6] Mark D Wilkinson u. a. "The FAIR Guiding Principles for scientific data management and stewardship". In: *Scientific data* 3.1 (2016), S. 1–9.