Automating Assessment of Scientific Reproducibility and Responsibility in the Health Sciences



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Co-Founder
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Reproducibility

Crisis

Billions spent on non-reproducible research.

Science is complicated. Trust in science is challenged.

Causes Solutions Selective reporting, publication pressure, poor statistics, unavailable methods/code/data, insufficient peer review

More robust research design, understanding of statistics, journals enforcing standards, **transparent reporting**

Publication



Methodological Workflow



Responsible Reporting





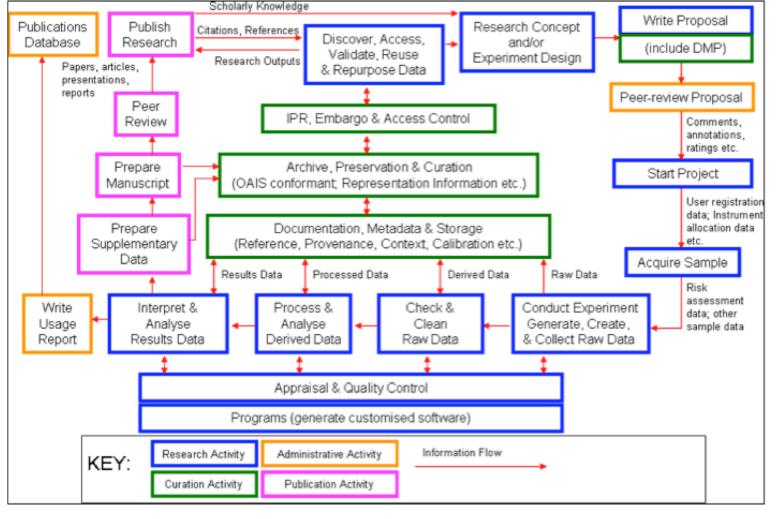


Image gathered from Ball, Alexander. "Review of data management lifecycle models." (2012).

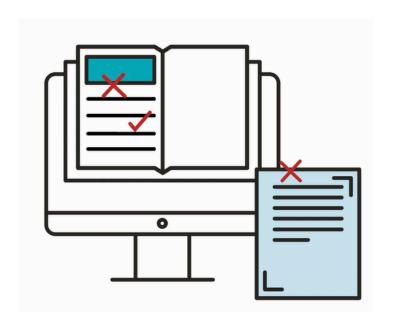
Guidelines for Reporting



400

different sets

Article Reviews



Peer review can take 6 months to over a year

Improving scientific reproducibility with minimal burden on scientists and those evaluating research



Measuring Reproducibility and Scientific Impact

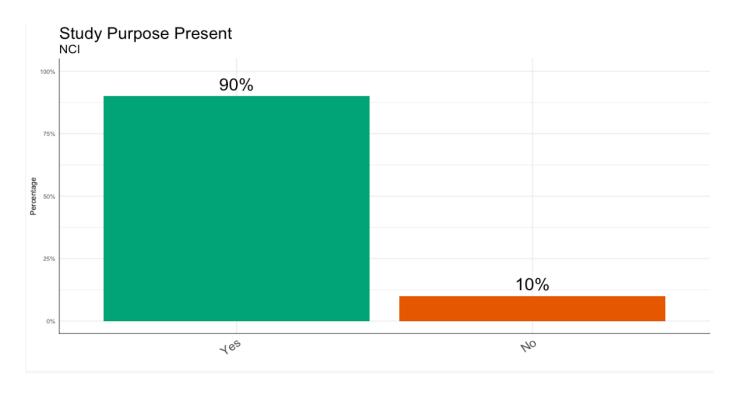
Detecting causes of non-reproducibilityDefining, measuring, and predicting the potential

reproducibility of a single publication.

Monitoring impacts of non-reproducibility

Tracking the scientific gain and impact of a publication as moderated by the science's reproducibility.

Study Overview: NCI-funded* publications



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Study Overview: Sufficient

Our aim was to demonstrate that identification of dMMR with clinically available assays has limitations, and we hypothesized that a multipronged approach is necessary to adequately stratify mCRPC patients who could potentially benefit from immunotherapy with immune checkpoint—blocking drugs.

Article Title: Immunogenomic analyses associate immunological alterations with mismatch repair defects in prostate cancer

Article DOI: 10.1172/jci121924

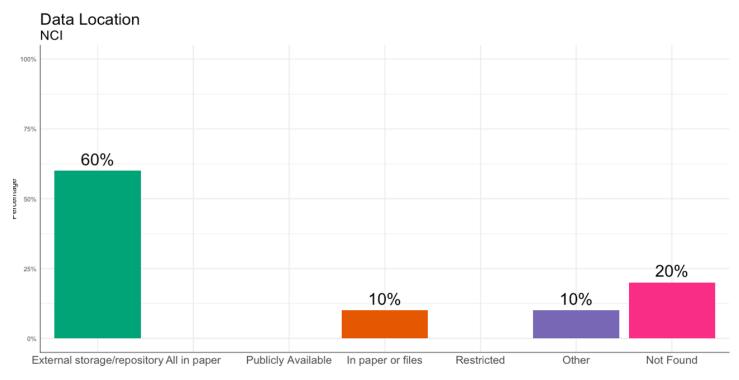
Study Overview: Needs Improvement

To this end, a number of bromodomain inhibitors, including JQ1 and I-BET, have been developed and have shown promising outcomes in early clinical trials. Although resistance to BET inhibitors has been documented in preclinical models13–15, the molecular mechanisms underlying acquired resistance are largely unknown. Here we report that cullin-3SPOP earmarks BET proteins, including BRD2, BRD3 and BRD4, for ubiquitination-mediated degradation.

Article Title: Prostate cancer–associated SPOP mutations confer resistance to BET inhibitors through stabilization of BRD4

Article DOI: 10.1038/nm.4378

Data Sharing: NCI-funded* publications



Data Sharing: External Repository

The RNA-seq and ERRBS data generated during the current study are available through **Gene Expression Omnibus (GEO) accession number**: GSE112830 with the following sub-series: https://www.ncbi.nlm.nih.gov/ geo/query/acc.cgi?acc=GSE112786, https://www.ncbi.nlm.nih.gov/geo/ query/acc.cgi?acc=GSE112829. The whole exome sequencing data related to this study are available through **Sequence Read Archive (SRA)** with accession number SRP138000. The published human data are available through dbGap:phs000909.v.p1 (http://www.cbioportal.org/study? id=nepc wcm 2016)6..

Article Title: Patient derived organoids to model rare prostate cancer phenotypes

Article DOI: 10.1038/s41467-018-04495-z

Data Sharing: In Paper or Files

"...supplemental material available online with this article...

Detailed methods are described in the Supplemental

Methods."

Article Title: COP1-DET1-ETS axis regulates ERK transcriptome and

sensitivity to MAPK inhibitors

Article DOI: 10.1172/jci94840

Data Sharing: Other

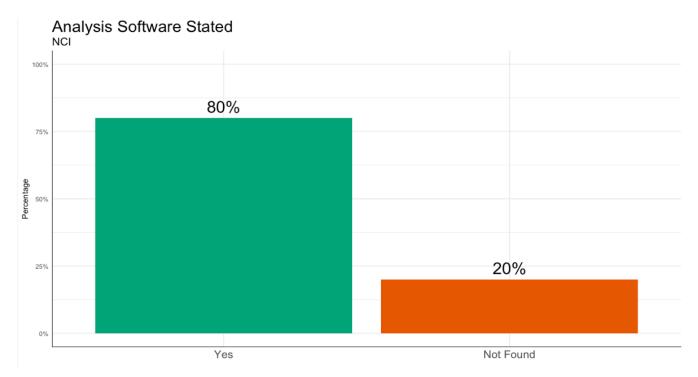
Uncropped images for immunoblots are available in Supplementary Figures 11–14. All other relevant data are available from the corresponding author upon reasonable request.

Article Title: Prostate cancer—associated SPOP mutations confer resistance to

BET inhibitors through stabilization of BRD4

Article DOI: 10.1038/nm.4378

Analyses: NCI-funded* publications



Data Analyses: Sufficient

For Cox regression analyses, the primary aim was to determine whether tumor CNA burden is associated with cancer specific survival (CSS). First, we assessed whether there was an association between tumor CNA burden and CSS by utilizing a univariate Cox model, censoring patients who did not die at the date of their last follow-up and patients who died of other causes at their death date. Secondly, in order to assess whether there is information from tumor CNA burden over and above biopsy Gleason score, we utilized a multivariable Cox model, adjusting for biopsy Gleason sum categorized as ≤6, 7, and ≥8. Finally, to assess whether there is an association between tumor CNA burden and CSS after accounting for the preoperative predictors of CSS, we utilized a multivariable Cox model...

Article Title: Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death

Article DOI: 10.7554/elife.372941

Note: The article provided both the how the data were collected as well as analyzed.

Data Analyses: Needs Improvement

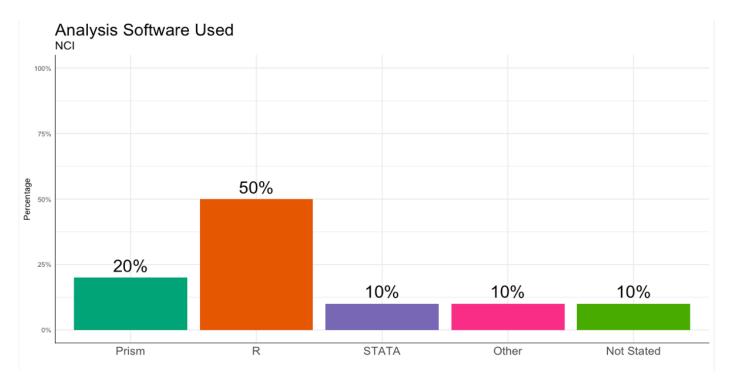
All statistical comparisons between two groups were performed by GraphPad Prism software 6.0 using a two-tailed unpaired t-test. The variance between the statistically compared groups was similar.

Article Title: Aberrant Activation of a Gastrointestinal Transcriptional

Circuit in Prostate Cancer Mediates Castration Resistance

Article DOI: 10.1016/j.ccell.2017.10.008

Software: NCI-funded* publications



Software: Sufficient

Graphs were generated by using <u>Graphpad Prism 5 project</u> (Graphpad Software Inc, CA, USA) or Microsoft Office Excel 2010... Differences between groups were compared by unpaired <u>t-tests or Wilcoxon rank sum test</u> with continuity correction by <u>R software version 2.15.0</u> (http://www.r-project.org).

Article Title: Dual inhibition of AKT-mTOR and AR signaling by targeting HDAC3 in PTEN- or SPOP-mutated prostate cancer

*based of an inverse of 105 or tick the have been final endow the NCI Moonshot project

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Code: Needs Improvement

No code was provided.

Article Title: Challenges in validating candidate therapeutic targets in

cancer

Article DOI: 10.7554/elife.32402





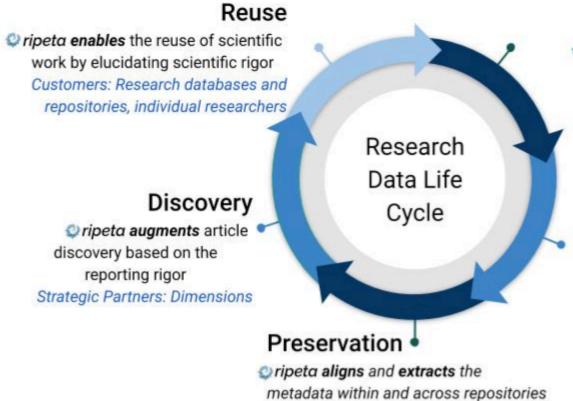
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Evaluate your portfolio for robust scientific reporting by checking publications on your projects



Improve the reproducibility of articles during the peer-review process with an automated tool that supports evidence-based science



Strategic Partners: RGD, figshare

Creation and Planning

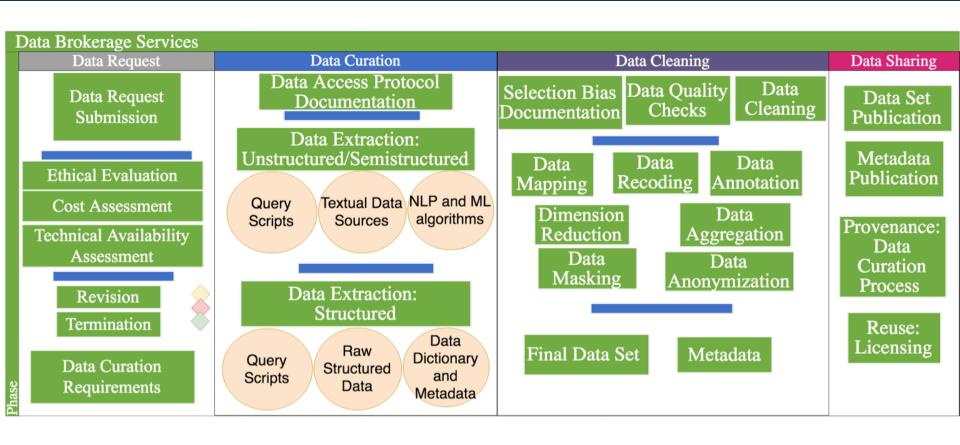
pripeta informs research design and grant proposal evaluation Customers: Granting agencies, academic institutions, individual researchers

Evaluation

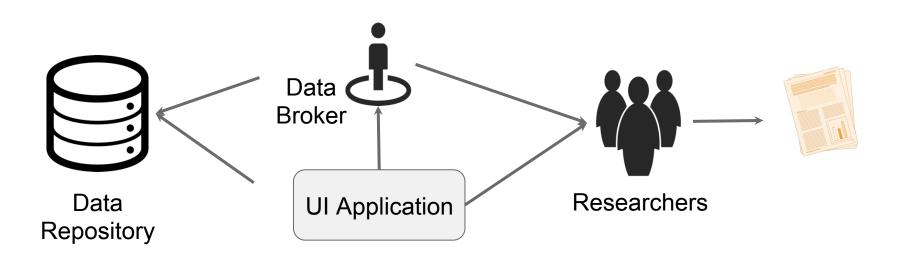
Pripeta automates the evaluation of scientific rigor of manuscripts

Customers: Publishers such as Springer-Nature, Wiley, Elsevier, and PLOS

Reproducible Health Data Workflows

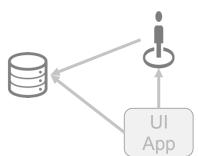


Research Data as a Service



Publications as a Product







Reproducible Scientific Workflows

"Reproducibility implies repetition and thus a

requirement to also move back – to retrace

one's steps, **Question** or **change** assumptions, and move forward again."

Millman, K. J., & Perez, F. (2014). Developing Open-Source Scientific Practice (V. Stodden, F. Leisch, & R. D. Peng, Eds.). In Implementing Reproducible Research (CRC the R series, pp. 149-183). Boca Raton, FL: Taylor & Francis Group, LLC.



The Grand Why

"The construction of a

scientific heritage

where anyone can validate the work of others and build upon it."1

Millman, K. J., & Perez, F. (2014). Developing Open-Source Scientific Practice (V. Stodden, F. Leisch, & R. D. Peng, Eds.). In Implementing Reproducible Research (CRC the R series, pp. 149-183). Boca Raton, FL: Taylor & Francis Group, LLC.



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Chris Westling
Data Integration Engineer



Leah Haynes Data Scientist, Intern



Sasha Mothershead Data Scientist, Intern



Josh Sumner Data Scientist

