Open Science in all its Facets with a Focus on Research Software

Konrad U. Förstner

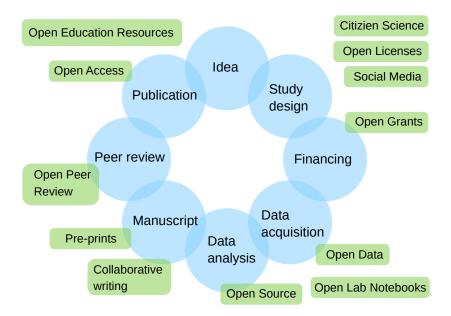
ZB MED – Information Center Life Sciences, Cologne, Germany & TH Köln, Cologne Germany

Novel approaches in Open Science University Library, University of Mannheim Oct. 22nd 2018









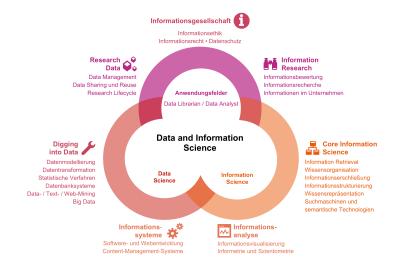




Shifting to Data Savvy: The Future of Data Science In Libraries

Burton, Matt and Lyon, Liz and Erdmann, Chris and Tijerina, Bonnie (2018) Shifting to Data Sawy: The Future of Data Science In Libraries. Project Report. University of Pittsburgh, Pittsburgh, PA; https://d-scholarship.pittedu/id/eprint/33891

New Bachelor at TH Köln: Data and Information Science



Currently under contruction at the ZBIW of the TH Köln:

Certificate course Data Librarian











https://librarycarpentry.org/



Data intro for librarians

An introduction to data structures, regular expressions, and computing terms



Unix Shell An introduction to command line interfaces and task automation using the Unix shell



OpenRefine An introduction to cleaning up and enhancing a dataset using OpenRefine



Git Intro for Librarians An introduction to version control using Git and GitHub for collaboration



SQL for Librarians An introduction to relational database management using the SQLite tool



Webscraping An introduction to extracting structured data from websites using a range of tools



Tidy data for librarians

An introduction to good data organisation, which is the foundation of much of our day-to-day work in libraries.



Introduction to Python

An introduction to Python, a general purpose programming language



Data Intro for Archivists An introduction to data structures, regular expressions, and computing terms for archivists

https://librarycarpentry.org/

Science \rightleftharpoons Technology

https://librarycarpentry.org/



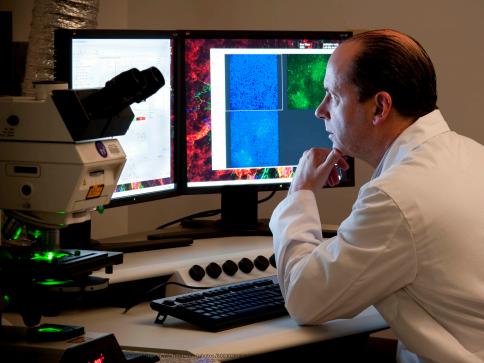






Software - an ubiquitous research tool







It is unquestionable that there is a strong and growing dependence of research on software.

Software is also a result of the scientific work.

Quality, accessibility, citability, etc. have to be ensured.

The importance of software for research is widely ignored.

[HTML] A Statistical Analysis of Peptide Electron Transfer Dissociation Fragmentation Mass Spectrometry

RJ Chalkley, KF Medzihradszky, AL Lym., ² Analytical ..., 2010 - ncbi.hm.nih.gov ... An **in-house script** was used to extract the ion types that were matched in all these 2149 spectra. The cumulative number of each ion type matched was determined and these values were normalized to determine the relative frequency of observation of different ion types. ... Cited by 50. Related articles All 8 versions Web of Science: 32. Cite Save

SAINT: probabilistic scoring of affinity purification-mass spectrometry data <u>H Chol</u>, B Larsen, ZY Lin, A Breiktreutz... - Nature ..., 2011 - nature.com ... dataset: To reolicate PP-NSAF 6. we removed 330 contaminants from the dataset

... ustable. To represent PT-NSAF 0, we remove use Constitution and the ustable using the vector magnitude approach. Atter filtering, probabilities were computed using an in-house script following the method presented in ref. 6... Cited by 267 Related articles All 15 versions Web of Science: 182 Cite Save

High-resolution structure determination by continuous-rotation data collection in MicroED

<u>BL Namenga</u>, D Shi, AGW Leslie, T Gonen - Nature Methods, 2014 - nature.com ... MOSFLM. Supplementary Fig. 3: Process flow from raw data to completely processed data set using MOSFLM. The raw data collected on the TEM is first converted to a file compatible with MOSFLM by an **in-house script**. MOSFLM ... Cited by 44 Related articles All 15 versions: Web of Science: 29 Cite Save

Irmu Generation of a predicted protein database from EST data and application to iTRAQ analyses in grape (Vitis vinifera cv. Cabernet Sauvignon) berries at ... J Licker, M Laszczak, <u>D Smith...</u> BMC ..., 2009 - bmcgenomics biomedentral.com ... combined into a second tab delimited file. Duplicate entries among exocarp or mesocarp files were identified using an **in-house script** in the Revinorment with 'Custom ORF ID' as the search string. Then, ratiometric data at each of ... Cited by 49 Related articles All 21 versions Web of Science: 33 Cite Save More

Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic Escherichia coli KG Jeensen, F Scheutz, OLund...Journal of clinical..., 2014 - Am Soc Microbiol ...Briefly, 1,647 (in a later update 5.029) complete bacterial genomes were downloaded from NGBI, and each k-mer (k = 16) with the prefix ATGAC was assued in a database using an in-house script...Another in-house script was used to search the database.... Cleted by 149 Related articles All 12 versions. We bol Science: 79 Cite Save

Cluster failure: Why fMRI inferences for spatial extent have inflated falsepositive rates.

Eklund A¹, Nichols TE², Knutsson H³.

Author information

Erratum in

Correction for Eklund et al., Cluster failure: Why fMRI inferences for spatial extent have inflated false-positive rates. [Proc Natl Acad Sci U S A. 2016]

Abstract

The most widely used task functional magnetic resonance imaging (fMRI) analyses use parametric statistical methods that depend on a variety of assumptions. In this work, we use real resting-state data and a total of 3 million random task group analyses to compute empirical familywise error rates for the fMRI software packages SPM, FSL, and AFNI, as well as a nonparametric permutation method. For a nominal familywise error rate of 5%, the parametric statistical methods are shown to be conservative for voxelwise inference and invalid for clusterwise inference. Our results suggest that the principal cause of the invalid cluster inferences is spatial autocorrelation functions that do not follow the assumed Gaussian shape. By comparison, the nonparametric permutation test is found to produce nominal results for voxelwise as well as clusterwise inference. These findings speak to the need of validating the statistical methods being used in the field of neuroimaging.

Does high public debt consistently stifle economic growth? A critique of Reinhart and Rogoff

Thomas Herndon, Michael Ash, Robert Pollin

Cambridge Journal of Economics, Volume 38, Issue 2, 1 March 2014, Pages 257–279, https://doi.org/10.1093/cje/bet075 Published: 24 December 2013 Article history •

Abstract

We replicate Reinhart and Rogoff (2010A and 2010B) and find that selective exclusion of available data, coding errors and inappropriate weighting of summary statistics lead to serious miscalculations that inaccurately represent the relationship between public debt and GDP growth among 20 advanced economies. Over 1946–2009, countries with public debt/GDP ratios above 90% averaged 2.2% real annual GDP growth, not –0.1% as published. The published results for (i) median GDP growth rates for the 1946–2009 period and (ii) mean and median GDP growth figures over 1790–2009 are all distorted by similar methodological errors, although the magnitudes of the distortions are somewhat smaller than with the mean figures for 1946–2009. Contrary to Reinhart and Rogoff's broader contentions, both mean and median GDP growth when public debt levels exceed 90% of GDP are not dramatically different from when the public debt/GDP ratios are lower. The relationship between public debt and GDP growth.

Common problems with research software

- Source code not published/available or even proprietary
- No quality control / automated tests
- Missing documentation
- Discontinued development (e.g. due to end of contract)
- Long-time availability not guaranteed
- Missing citability

https://commons.wikimedia.org/wiki/File:Paris_Tuileries_Garden_Facepalm_statue.jpg - PD

Potential reasons

- Lack of awareness
- Lack of skills
- Lack of time
- Lack of incentives
- Lack of dedicated long-term funding
- No reviewing
- To hinder competitors

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Several iniatives have been launched to address these issues.





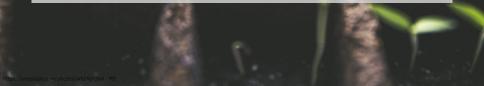
ttps://unsplash.com/photos/vrbZVyX2k4I - Pl

- Software Carpentry (1998)
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- Software Heritage (2016)
- de-RSE (de-rse.org)
- Working group "Digital tool Software and Service" as part of the focus initiative "Digital Information" of the Alliance of Science Organizations in Germany
- Several more ...





https://doi.org/10.5281/zenodo.1172988

Guiding principle

The concept of Good Scientific Practice (GSP) must be also applied to research software.

But what can Good Scientific Practice mean for research software?

FAIR principle should also be applied to software

- Findable
- Accessible
- Interoperable
- Re-usable

Open

• Proper OSI conform licence

Three types of software

- 1. Small tools written for single purpose
- 2. Software applications (as research output)
- 3. Infrastructure and online services

All three levels are relevant and have to be addressed.

Exact needs and possibilities might differ between scientific communities.

Discourse must also happen inside of these communities.

E.g. what exactly means "reproducibility" (bit-identical compilation?) and how long would this needed to be guaranteed?



Raise the awareness for the relevance of research software.



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Introduce standards and mechanisms for quality control of research software.



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Create institutional platforms to publish and archive software/source code/workflows.





Enable citation of such items. e.g. using Citation File Format (CFF - citation-file-format.github.io)



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Make these citations part of the scientific reputation system.





Foster the education of computational skills inside of the scientific community.





Develop new carreer paths like Research Software Engineers, Software Librarians, Data Scientists.



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Raise awareness about and teach legal aspects (i.e. licensing) of software.





Raise awareness about and teach legal aspects (i.e. licensing) of software.

Make open source the default.





Facilitate the transition from single-purpose solutions to application to services.

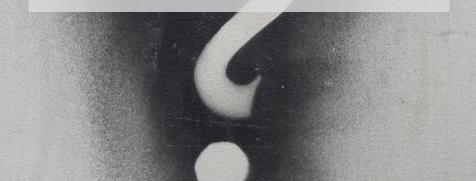




Provide long-term funding to enable sustainable software development.



A lot to do and a lot of open questions.





www.allianzinitiative.de

Matthias Katerbow - Deutsche Forschungsgemeinschaft Michael Goedicke - Deutsche Forschungsgemeinschaft Leander Seige - Deutsche Forschungsgemeinschaft Zeki Mustafa Dogan - Deutsche Forschungsgemeinschaft Dirk Eisengräber-Pabst - Fraunhofer-Gesellschaft Uwe Konrad - Helmholtz-Gemeinschaft Bernadette Fritzsch - Helmholtz-Gemeinschaft Björn Brembs - Hochschulrektorenkonferenz Klaus Wannemacher - Hochschulrektorenkonferenz Thomas Dandekar - Hochschulrektorenkonferenz Georg Feulner - Leibniz-Gemeinschaft Jürgen Fuhrmann - Leibniz-Gemeinschaft Michael Franke - Max-Planck-Gesellschaft Stefan Janosch - Max-Planck-Gesellschaft Johannes Reetz - Max-Planck-Gesellschaft Thomas Rode - Leopoldina

Mathias Bornschein - Bibliotheken der Ressortforschungseinrichtungen des Bundes

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