Ten Simple Rules
for the Open Development of Scientific Software

Andreas Prlic, Jim Procter, Hilmar Lapp

Citation: Prlić A, Procter JB (2012) Ten Simple Rules for the Open Development of Scientific Software. PLoS Comput Biol 8(12): e1002802. doi:10.1371/journal.pcbi.1002802
• Rule 1: Don't Reinvent the Wheel

• Rule 2: Code Well

• Rule 3: Be Your Own User

• Rule 4: Be Transparent

• Rule 5: Be Simple
• Rule 6: Don't Be a Perfectionist

• Rule 7: Nurture and Grow Your Community

• Rule 8: Promote Your Project

• Rule 9: Find Sponsors

• Rule 10: Science Counts
Rule 5: Be Simple
Be Simple -
For yourself and everyone else

• Minimise your timesinks

• Infrastructure

• Tests are not enough - use a build system

• PACKAGING

• Tests == examples for you and everyone else
• Documentation == outreach

• love your website

• love your programmer docs

• issues == documentation
Why not start your next grant proposal on

- <insert ovcs here>?
Rule 1: Don’t Reinvent the Wheel
Windows line ending issue fixes
Some fixes from Codefest.
by konstantin 13 hours ago 1 comment

Fixing a bug in SeqIO.PdbIO in parsing pdb-atom sequence
Fixing a problem that SeqIO.PdbIO outputs erroneous amino acid sequence if the ATOM record has mo...
by matsu3shiro 16 days ago 2 comments

MeltingTemp completely rewritten and extended
More or less completely rewritten and largely extended. 1. Three different Tm calculations: one ... 
by MarkusPiotrowski 20 days ago 1 comment

CDAO: removing dependency on librdf
Users of the Bio.Phylo CDAO conversion modules have had problems installing its dependency, the R ... 
by bendmomis 20 days ago

Customizability features added to Phylo.draw
Features added based on https://redmine.open-bio.org/issues/3336. Users now have the ability to i...
by nmsutton a month ago

Samtools Wrapper For BioPython
Added Samtools(http://samtools.sourceforge.net/) wrapper. Need to write Unit Tests.
by saketkc 2 months ago 11 comments

Reorganization of single and triple letter protein codes
This pull request was triggered by the discussion here. Summary of the changes: I've moved the SC...
by bow 4 months ago 2 comments

KEGG KGML parser and graphical visualisation from Leighton
This pull request is mainly as a discussion point for Leighton's (@widdowquinn) KEGG KGML parser ... 
by peterjc 4 months ago 4 comments

Add the ability to parse CEL version 4 files from Affy
Hey, I noticed that Biopython was missing the ability to parse binary CEL files (version 4), so I...
by hammer 4 months ago 8 comments

Change to set_structure. Allows writing of individual (S)MCRAs
The changes discussed in this thread: http://lists.open-bio.org/pipermail/biopython-dev/2013-Feb...
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Open data, open source.
Our data, like our source code, is wide open. As a non-profit, we're around supporting open tools and nurturing Web-native scholarship.
software

**biopython**
(2009) My fork of the official Biopython repository, used for experimental branches etc. [GitHub](https://github.com)

**maf2sam**
(2010) Convert MIRA Assembly Format (MAF) to Sequence Alignment/Map (SAM) format. [GitHub](https://github.com)

**picobio**
(2011) Miscellaneous Bioinformatics scripts etc mostly in Python. [GitHub](https://github.com)

**tarball2git**
(2011) Simple Python script to take a set of versioned tar balls and import them into a git repository. [GitHub](https://github.com)

**screed**
(2010) a short read database. [GitHub](https://github.com)

**longsight**
(2012) Python code for capturing images from a webcam etc. [GitHub](https://github.com)

**backports.lzma**
(2012) Backport of Python 3.3's standard library module lzma for LZMA/XY compressed files. [GitHub](https://github.com)

**split-dist**
(2011) Unofficial repository for Thomas Mailund's tool Split-Dist (sdist). [GitHub](https://github.com)
**Contribution Activity**

- **7 Commits**
  - Pushed 2 commits to phenoscape/phenoscape.github.com Jul 15
  - Pushed 3 commits to datadryad/dryad-data Jul 10
  - Pushed 1 commit to bendmorris/phylocommons Jun 25
  - Pushed 1 commit to phylotastic/phylotastic.github.com Jun 23

- **3 Pull Requests**
  - Merged: Revert NCBI Linkout stats deposition. 8 days ago
    datadryad/dryad-repo · 1 commit · 0 ++ 367 --
  - Merged: Consolidate and streamline status descriptions and voting process. 17 days ago
    OBF/obf-docs · 1 commit · 46 ++ 57 --
  - Closed: Consolidated and streamline status descriptions and voting process. 20 days ago
    OBF/obf-docs · 1 commit · 46 ++ 57 --

- **12 Issues Reported**
  - Closed: #21 Add link to DeepFin RCN 3 days ago
  - Closed: #7 Why not distribute under CC0? 7 days ago
# biogem | description | by | cite | version | released | stars | issues source | build | total

| # | biogem | description | by | cite | version | released | stars | issues source | build | total |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | bio | Bioinformatics library (...) | BioRuby project | ![cite](https://biogems.info/bio) | 1.4.3.0001 | 7 weeks | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-18 |
| 2 | biodiversity | Parser of scientific names (...) | Dmitry Mozherin | ![cite](https://biogems.info/bio) | 3.1.2 | 3 weeks | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-16 |
| 3 | bio gem | Biogem is a software generator for Ruby in (...) | Raoul J.P. Bonnal, Pjotr Prins | ![cite](https://biogems.info/bio) | 1.3.4 | 15 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 1961 |
| 4 | bio samtools | Binder of samtools for Ruby, on the top (...) | Ricardo Ramirez-Gonzalez, Dan MacLean, Raoul J.P. Bonnal | ![cite](https://biogems.info/bio) | 0.6.0 | 7 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-12 |
| 5 | entrez | Http requests to entrez e-utilities (...) | Jared Ning | ![cite](https://biogems.info/bio) | 0.5.8.1 | 23 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-11 |
| 6 | bio ucs api | The Ruby ucs api: accessing the ucs genome (...) | Hiroyuki Mishima, Jan Aerts | ![cite](https://biogems.info/bio) | 0.5.2 | 7 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-10 |
| 7 | intermine | Webservice client library for intermine data-warehouses (...) | Alex Kalderimis | ![cite](https://biogems.info/bio) | 1.0.400 | 1 week | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-09 |
| 8 | bio gff3 | Gff3 parser for big data (...) | Pjotr Prins | ![cite](https://biogems.info/bio) | 0.9.1 | 11 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-09 |
| 9 | sequenceserver | Blast search made easy! (...) | Anurag Priyam, Ben J Woodcroft, Yannick Wurm | ![cite](https://biogems.info/bio) | 0.8.5 | 11 weeks | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-09 |
| 10 | bio logger | Log4r wrapper with extra features for roles and (...) | Pjotr Prins | ![cite](https://biogems.info/bio) | 1.0.1 | 15 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-09 |
| 11 | bio maf | Maf parser for BioRuby (...) | Clayton Wheeler | ![cite](https://biogems.info/bio) | 1.0.1 | 11 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-08 |
| 12 | bio gadget | Gadgets for bioinformatics (...) | Shintaro Katayama | ![cite](https://biogems.info/bio) | 0.4.8 | 5 weeks | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-07 |
| 13 | bio grid | A biogem to submit jobs on a queue (...) | Francesco Strozzi | ![cite](https://biogems.info/bio) | 0.3.3 | 8 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-07 |
| 14 | bio blastxmlparser | Very fast blast xml parser and library for (...) | Pjotr Prins | ![cite](https://biogems.info/bio) | 1.1.1 | 5 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-06 |
| 15 | bio faster | A fast parser for fastq files (...) | Francesco Strozzi | ![cite](https://biogems.info/bio) | 0.4.5 | 13 months | ![stars](https://biogems.info/bio) | ![issues](https://biogems.info/bio) | ![build](https://biogems.info/bio) | ![total](https://biogems.info/bio) | 2013-07-06 |
Rule 10: Science Counts
• Differences between computer sciences and bio-sciences

• Software is primarily a means to advance our research

• Software for the consumption of others does not get rewarded

• We write open source because we like to interact with other scientists
- “Build it and they will come” does not work
- Maintenance of code that is no longer relevant to your own research is a serious time sink
- If done right, you can publish both the science and the software for the same project
• **Question:**

• **What do you need to do to get**
  • Published
  • Grants
  • Academic Promotions
  • Tenure?
• Software Articles

• http://www.ploscompbiol.org/static/guidelines#software
Call for Papers

First Workshop on Sustainable Software for Science: Practice and Experiences (WSSSPE)

http://wssspe.researchcomputing.org.uk/
(in conjunction with SC13)
Sunday, November 17, 2013, Denver, CO

Progress in scientific research is dependent on the quality and accessibility of software at all levels and it is now critical to address many new challenges related to the development, deployment, and maintenance of reusable software. In addition, it is essential that scientists, researchers, and students are able to learn and adopt a new set of software-related skills and methodologies. Established researchers are already acquiring some of these skills, and in particular a specialized class of software developers is emerging in academic environments who are an integral and embedded part of successful research teams. This workshop will provide a forum for discussion of the challenges, including both positions and experiences. The short papers and discussion will be archived as a basis for continued discussion, and we intend the workshop to feed into the collaborative writing of one or more journal publications.

In practice, scientific software activities are part of an ecosystem where key roles are held by developers, users, and funders. All three groups supply resources to the ecosystem, as well as requirements that bound it. Roughly following the example of NSF’s Vision and Strategy for Software (http://www.nsf.gov/publications/pub_summ.jsp?ods_key=nsf12113), the ecosystem may be viewed as having challenges related to: