Approaches to Package Management – Bioconductor

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“Analysis and comprehension of high-throughput genomic data”

- Established 2002; 1383 packages (core team and contributed).
- Well-respected, cited (20k PubMedCentral full-text citations), used (>350k unique IP addresses / year).

- [https://bioconductor.org](https://bioconductor.org);
  [https://support.bioconductor.org](https://support.bioconductor.org)

- CRAN-style repository. Cloud front content delivery (plus a few mirrors maintained for local purposes).

- Primarily supported through US NIH.
Release cycle

Six-month releases

- ‘Devel’: new packages and features.
- ‘Release’: end-users.

Which $R$? The one end-users see.

- Now: release and devel both on $R$-3.4.
- October: release on $R$-3.4, devel on $R$-devel.

Comments

- Cohesive packages – deep dependency graph.
- Enables change – breakage in devel tolerated.
- *BiocInstaller::biocLite()* to manage repositories seen by *install.packages()*.
- $R$-devel not always exposed to *Bioconductor* packages.
Package management

Version-controlled packages.
▶ All packages under SVN; individual developer accounts.
▶ Versioning scheme $x.y.z$. $y$ even in release, odd in devel. Each commit bumps $z$.
▶ Will discuss GIT in a second…

Comments
▶ Mostly package developer commits, but core team can step in.
▶ Eases incorporation of breaking (ours, CRAN, $R$) changes
Nightly builds

- `R CMD build / check;
- Cross-platform; release & devel.
- SVN snapshot; all packages.
- Successful builds get pushed to public repositories.

Comments

- ‘Continuous integration’, sort of.
- Sometimes ‘impossible’ public repositories
  - A introduces feature that breaks B. A pushed but old B still available.
  - B depends on feature in newest A. A builds and installs (so used by B) but fails check (so not pushed). B builds & checks so pushed.
New packages I

Submission – open and reviewed.

- Maintainer posts a public Github issue.
- Moderated (manual) – is it a legitimate package?
- Built and checked. Usually, maintainers iterate until ‘OK’.
- Assigned reviewer (core team; implementation), plus community input (implementation, science).
- Goal: incremental improvement, rather than absolute standard.
Comments

- Wide range of quality.
- Time consuming and sometimes uninspiring; hard to standardize across reviewers.
- Maybe 80% use roxygen2 (and probably devtools).
- Common issues: Bioconductor interoperability; documentation; R code.
New packages III

Common issues: \( R \) code

- Generally, iteration instead of vectorization (tell-tale sign: use of parallel evaluation).
- Robustness
  - 1:n (vs. seq_len(n)).
  - if (<scalar binary logical>) {} (challenging!)
- ‘Copy-and-append’ \( x = \) numeric(); for (i in 1:n) \( x \leftarrow c(x, i) \)
- Vocabulary apply(x, 2, sum) vs. colSums(x).
- Hoisting constant expressions out of loops.
- Cyclomatic complexity.
Software management

Currently...

- SVN repository
- git / svn ‘bridge’ – sync git repositories with git.
- About 1/2 commits via git / svn bridge.

Migrating to git

- git clone
  https://git.bioconductor.org/packages/BiocGenerics

Challenges

- Cannonical location / distributed support & social environment.
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