Questions and Answers for new Bioconductor package authors

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Before we begin:

- Welcome to the 1st Bioconductor Q&A!
- Please post any questions into the YouTube chat window
- After after a short talk, I will be able to answer them

Major goals for the Bioconductor project:

- Analysis & comprehension of high-throughput genomic data
- Robust software
    - Documented
    - Tested
    - Freely Available
- Reproducible research
- Code reuse and the importance of working together

What is package review for?

- To improve your package

- To ensure that your package helps meet the goals of the project

- To help you to know more about other existing packages/objects

Resources for new package authors:

- Package guidelines (**http://bioconductor.org/developers/package-guidelines/**)

- Primer for new package authors (**http://bioconductor.org/developers/how-to/buildingPackagesForBioc**)

- The support site (**https://support.bioconductor.org/**)

- The bioc-devel mailing list (**https://stat.ethz.ch/mailman/listinfo/bioc-devel**)

What do reviewers look for?

- BiocCheck (**http://www.bioconductor.org/packages/devel /bioc/html/BiocCheck.html**)

- Code reuse

- Good documentation - Everyone must understand vignette.

- Why do people care about how my code looks? (code readability)

Should I publish my academic paper or my package 1st?

- Our svn codebase is public

- Many journals like if your software is already online

- Ultimately: you have to check with the specific journals (It's their policies that matter)

What to do when it's time to submit your package:

- Don't panic - the process is meant to help you.

- Build and check your package (using Bioc 'devel'!)

```
R CMD build MyPkg
R CMD check MyPkg_0.99.0.tar.gz
```

- Put packages into the tracker
  (**https://tracker.bioconductor.org/issue558**)

- Don't create extra issues for new tarballs

Acknowledgments