



Biopython Project Update 2017

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and the Biopython Contributors

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What is Biopython?

- ▶ Collection of modules for biological computation in Python
 - ▶ Sequence handling and motifs, parsers, database queries, protein structures, phylogenetics, tool wrappers and more.
- ▶ Started in 1999, first release in 2000
- ▶ Open source and freely available (Biopython license)

In a Nutshell, Biopython...

... has had 11,237 commits made by 192 contributors representing 291,535 lines of code

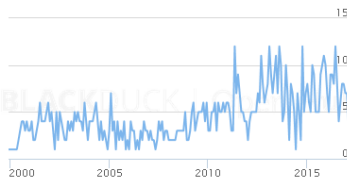
... is mostly written in Python with an average number of source code comments

... has a well established, mature codebase maintained by a very large development team with increasing Y-O-Y commits

... took an estimated 75 years of effort (COCOMO model) starting with its first commit in December, 1999 ending with its most recent commit 3 months ago

Community

Contributors per Month



Source: <https://www.openhub.net/p/biopython>

80 named contributors this year, 51 newcomers with star!

- | | | | |
|---------------------|---------------------------|-----------------------|-----------------------------|
| ▶ Aaron Kitzmiller* | ▶ Chris Warth | ▶ João Rodrigues | ▶ Rodrigo Dorantes-Gilardi* |
| ▶ Aaron Rosenfeld | ▶ Connor T. Skennerton | ▶ Kai Blin | ▶ Sacha Laurent* |
| ▶ Adam Kurkiewicz* | ▶ Emmanuel Noutahi | ▶ Kristian Davidsen* | ▶ Sebastian Bassi |
| ▶ Adam Novak* | ▶ Eric Rasche | ▶ Kurt Graff* | ▶ Sourav Singh* |
| ▶ Adil Iqbal* | ▶ Eric Talevich | ▶ Lenna Peterson | ▶ Spencer Bliven* |
| ▶ Adrian Altenhoff* | ▶ Foen Peng* | ▶ Leonhard Heizinger* | ▶ Stefans Mezulis |
| ▶ Allis Tauri* | ▶ Francesco Gastaldello* | ▶ Marcin Magnus* | ▶ Steve Bond |
| ▶ Andrew Dalke | ▶ Francisco Pina-Martins* | ▶ Markus Piotrowski | ▶ Steve Marshall* |
| ▶ Andrew Guy* | ▶ Francisco | ▶ Mateusz Korycinski* | ▶ Ted Cybulski* |
| ▶ Andrew Sczesnak* | ▶ Pina-Martins* | ▶ Maximilian Greil* | ▶ Tiago Antao |
| ▶ Anthony Bradley* | ▶ François Coste* | ▶ Michał J. Gajda* | ▶ Travis Wrightsman |
| ▶ Ariel Aptekmann* | ▶ Frederic Sapet* | ▶ Michiel de Hoon | ▶ Uri Laserson |
| ▶ Ben Fulton | ▶ Hector Martinez* | ▶ Milind Luthra* | ▶ Uwe Schmitt* |
| ▶ Bernhard Thiel* | ▶ Iddo Friedberg | ▶ morrme* | ▶ Veronika Berman* |
| ▶ Bertrand Caron* | ▶ Jacek Śmietański | ▶ Noam Kremen* | ▶ Vincent Davis |
| ▶ Bertrand Néron | ▶ Jack Twilley* | ▶ Olivier Morelle* | ▶ Wibowo Arindrarto |
| ▶ Blaise Li* | ▶ Jared Andrews* | ▶ Oscar G. Garcia* | ▶ Xiaoyu Zhuo* |
| ▶ Brandon Carter* | ▶ Jeroen Van Goey* | ▶ Owen Solberg | ▶ Zheng Ruan |
| ▶ Brandon Invergo | ▶ Jimmy O'Donnell* | ▶ Patrick Kunzmann* | |
| ▶ Carlos Pena | ▶ John Kern* | ▶ Peter Cock | |
| ▶ Carlos Ríos | ▶ Jordan Willis* | ▶ Rasmus Fonseca* | |
| ▶ Chris Rands | ▶ Joshua Meyers* | ▶ Richard Neher* | |

Biopython 1.68 (released 2016-08-25)

New Features in Biopython 1.68

- ▶ Final Release supporting Python 2.6
- ▶ Added extension to Bio.PDB to allow for parsing of the new MMTF format.
- ▶ Bio.pairwise2 rewritten to address speed and problems with local alignments.
- ▶ SeqGui and xbbtools rewritten using tkinter.
- ▶ Biopython now uses HTTPS instead of HTTP to connect to Entrez and QBLAST API.

Biopython 1.69 (released 2017-04-06)

Start of re-licensing plan

- ▶ 1.69 marks the start of start of our re-licensing plan, to transition away from liberal *Biopython License Agreement* to the widely used *3-Clause BSD License*.
- ▶ The code base-authorship is being reviewed file-by-file, in order to gradually dual license the entire project.

New features in Biopython 1.69

- ▶ Improved PyPy support, all NumPy and most C code works.
- ▶ Cellosaurus cell line database, cell ontologies and catalogues accessible through the `Bio.ExPASy` module.
- ▶ MAF files supported in `Bio.AlignIO`, including indexing.
- ▶ `Bio.Restriction` updated to REBASE Feb 2017 enzyme list
- ▶ `Bio.PDB` can download PDBx/mmCif (new default), PDB (old default), PDBML/XML, and MMTF protein structures.
- ▶ `Bio.Affy` supports version 4 of Affymetrix CEL format.

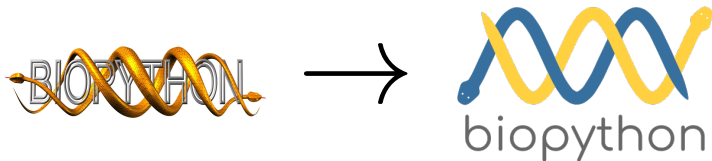
Biopython 1.70 (released 2017-07-10)

New features in Biopython 1.70

- ▶ Module `Bio.AlignIO`
 - ▶ Support for XMFA file format using `Bio.AlignIO.MauveIO`
- ▶ Module `Bio.SearchIO`
 - ▶ Support for new arguments to read and write blast-xml files.
- ▶ Drop support for Python 3.3
- ▶ Deprecate support for Jython.
- ▶ Deprecate `Bio.GA` and `Bio.NeuralNetwork` modules.

New logo for Biopython

- ▶ Version 1.70 marks the transition towards a new logo for Biopython.



- ▶ The new logo was created by Patrick Kunzmann in 2017 and had support from the Python Software Foundation and the Biopython developers community.

Currently supported Python versions

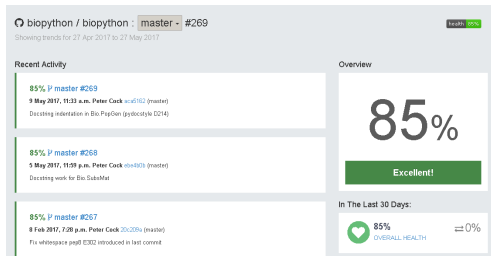
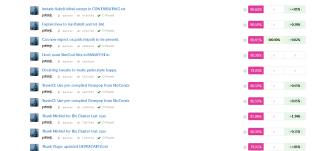
- ▶ Python 2.7
- ▶ Python 3.4
- ▶ Python 3.5
- ▶ Python 3.6
- ▶ PyPy 5.7
- ▶ PyPy3 5.8 beta
- ▶ Jython 2.7 (support is deprecated)

On going work

- ▶ Miscellaneous bug fixes
- ▶ Test suite enhancements and coverage improvements
- ▶ Better [PEP8](#) and [PEP257](#) coding style adherence
- ▶ Automating build process for wheel packages
<http://github.com/biopython/biopython-wheels>

Continuous Integration

- ▶ TravisCI
 - ▶ Linux testing with coverage
 - ▶ Style checks with flake8
 - ▶ Experimenting with Build Stages
- ▶ Appveyor (Windows testing with coverage)
- ▶ Codecov.io (tracking unit test coverage)
- ▶ Quantified Code (metrics and automatic pull requests)
- ▶ Landscape.io (“health score”)

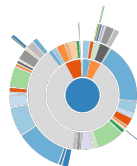


Conclusion

- ▶ Lots of new contributors
- ▶ Lots of new stuff
- ▶ Turn new contributors into recurring ones
- ▶ Biopython 1.71 in the near future

Acknowledgements

- ▶ Peter Cock
- ▶ Biopython Community



Travis CI



O|B|F

Resources!

Website:

- ▶ <http://biopython.org>

Repositories:

- ▶ Main: <http://github.com/biopython/biopython>
- ▶ Website:
<https://github.com/biopython/biopython.github.io>

Mailing lists:

- ▶ General list: biopython@biopython.org
- ▶ Developers list: biopython-dev@biopython.org

Biostars:

- ▶ <https://www.biostars.org/t/biopython/> (“biopython” category)