

Towards a Modern BioPerl: BioPerl Update 2010

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The BioPerl project (<http://bioperl.org>, distributed under the Perl Artistic License) is now 15! In this talk, we will present the current state of BioPerl, outlining how BioPerl started, where we are now, and where we intend to go in the near future.

Initially focusing on the present, we will discuss how the BioPerl developers are currently addressing new biological and informatics-based problems, such as use of second-generation sequencing tools like MAQ and BowTie. Furthermore, productive collaborations with other OBF groups will be highlighted, such as the recent publication on FASTQ, ongoing work with BioLib, and the Google Summer of Code. A brief progress report will be given on the BioPerl Google Summer of Code by Jun Yin to refactor the BioPerl alignment architecture.

For the future, we will discuss possible strategies intended to address the current monolithic nature of BioPerl's core, including the possibility of moving towards a more modular design. The use of modern developer and Perl tools with BioPerl will be covered, such as git and GitHub, Moose, and DBIx::Class. Finally, we will give a brief glimpse of BioPerl6; yes, it exists.

BioPerl can now be found on GitHub at <http://github.com/bioperl>.