

# Bio::Phylo

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# What it is

- Bio::Phylo is a set of perl5 libraries for handling phylogenetic data:
  - Models nodes, trees, sets of trees; character sequences, matrices, sets of matrices; taxa, sets of taxa.
  - Includes BioPerl-like extensible IO architecture.
  - On <http://www.cpan.org>
  - (Includes ad-hoc methods for biodiversity calculations and treedrawing.)

# Why?

- Historically: small, easy (-er) install
- Test bed for:
  - “best practices”
  - performance optimizations (caching, data models)
  - integration with CIPRES et al.
- “Narrower but deeper” than BioPerl

# How it works

- Bio::Phylo is written in OO perl5, follows “perl best practices”:
  - exception hierarchies,
  - inside-out objects,
  - separate setters and getters
  - UIDs for all objects
  - (additional syntax sugar for array-like operations)

# How it should work

- Bio::Phylo functionality should be exposed to other libraries, hence:
  - Should adopt BioPerl interfaces (already done where possible, but BioPerl doesn't do character matrices that well)
  - Should be able to exchange data “through the wire” (webservices, CORBA, CIPRES)
  - Should have more explicit “bookkeeping” of sets of trees + matrices + taxa (CDAT)

# Relation to other projects

- Bio::Phylo forms the “tree-aware” part of the CIPRES/CORBA stack (see Mark’s talk)
- Bio::Phylo *will* become part of the Bio::CDAT architecture (see Aaron’s talk)
- Bio::Phylo *should* become part (somehow) of BioPerl (see Bio\* bootcamp)