

bíogo/ncbi: interfaces to NCBI services for the Go language

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Software Repository: <https://github.com/biogo/ncbi>

Software Archive: <http://dx.doi.org/10.5281/zenodo.582354>

Summary

The National Center for Biotechnology Information makes available BLAST sequence similarity search (Biotechnology Information (US) 2017a) and health science database search through the Entrez service (Biotechnology Information (US) 2005). In addition to an interactive web interface, BLAST and Entrez provide an application programmer interface to allow programmatic use of these services via the BLAST URL API (Biotechnology Information (US) 2017b) and the Entrez EUtilities (Biotechnology Information (US) 2010). The BioPerl suite (Stajich J.E. 2002) provides access to the BLAST API via `Bio::Tools::Run::StandAloneBlastPlus` (Fields C. 2017a) and to Entrez via `Bio::Tools::EUtilities` (Fields C. 2017b). Similarly, Biopython (Cock P.J.A. 2009) provides access via the `NCBIWWW` function in the `Bio.Blast` module and functions in `Bio.Entrez` for EUtilities. Packages within `bíogo/ncbi` provide Go application programmer interfaces to the NCBI BLAST and EUtilities services. The design of `bíogo/ncbi` is light weight, allowing the user to make use of the Go language’s control structures and data types, rather than imposing a library-specific access approach. In addition to allowing remote BLAST searches, BioPerl and Biopython provide mechanisms to parse XML output from local BLAST search via BioPerl’s `Bio::SearchIO` and Biopythons `Bio.Blast` `NCBIXML`. Because of the modular design of `bíogo/ncbi`, XML encoded output from local BLAST searches or remote downloads can be parsed using the Go standard library’s XML package.

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