PCSS Documentation

Release master

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PCSS is a computational tool for peptide classification using sequence and structure.

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CHAPTER 1

Installation

In the Sali Lab

If you are working in the Sali lab, you don't need to build and install PCSS - it is already set up for you as a module. Just run `module load pcss` to load it.

Dependencies

All dependencies listed below are expected to be found in standard system paths. This may require setting `PATH` and/or `LD_LIBRARY_PATH` environment variables, or modifying the global parameter file. Note that Linux is the only platform on which PCSS has been tested.

- Perl.
- SVMlight.

In the Sali lab, running `module load svm_light` will get all of these dependencies.

Building

Use `make install` to install the library. In most cases you will need to tell `make` where to install (if running on a Linux cluster, PCSS will need to be installed on a network-accessible filesystem), with something like `make PREFIX=/shared/pcss install`. See `Makefile.include` for all make variables that can be configured.

CHAPTER 2

Basic usage

Currently the only practical way to use the PCSS protocol is via the web server.

CHAPTER 3

Indices and tables

- genindex
- modindex
- search