chem-bla-ics

# Bioinformatics: Open Source or Open Access??

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b3JnLzEwLjU5MzUwLzV3amc5LTJlNTEy

## Keywords

Opensource, Bioinfo

## Abstract

I have heard that bioinformatics is ahead of chemoinformatics. However, I discoverd that this is not necessarily the case, while preparing for a homology modeling course I gave this week at the CUBIC. Open Access is really no issue there, with open access journals and many open access databases. But it is different when it comes down to open source software.

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Below is a list of bioinformatics programs which are free for academic use, but not open:

- JOY (free after getting license)
- PLATON (free download)
- PROCHECK (free after getting license)
- ProteinPredict (free download)
- SCWRL (free after getting license)
- THREADER (free after getting license)
- WHAT_CHECK (free download)
- WHAT_IF (free after getting license)

And this not even includes the many websites which do not offer the software behind them. And these programs cover several steps in the whole homology modeling process. Open source homology modeling is not possible at this moment :(

But, on the bright side, there are already some open source programs involved too:

- BLAST (public domain)
- GROMACS (GPL)

And protein structure viewers is hardly a problem at all; several open source viewers are available, among which Rasmol, PyMOL and Jmol.

In other words: we might not want to look at bioinformatics too much.