by the GMOD site maintainer. The most common scenario is to load the data from a set of GFF files into a mysql database; `Bio::DB::SeqFeature::Store` provides the `bp_seqfeature_load.pl` script for this purpose.
2. **Unpack the SADI for GMOD tarball in the cgi-bin directory.** The tarball will be unpacked into a `SADI` directory tree which will contain the Perl CGI scripts as well as the required Perl modules.
3. **Add database connection parameters to the SADI for GMOD configuration file.** The configuration file will be located in the `SADI` subdirectory of `cgi-bin`.

6 Conclusion

While the majority of existing biological Web services use XML for data exchange, SADI services use RDF/OWL in order to facilitate automatic integration of data across service providers. As such, the SADI for GMOD services will provide a novel tool for conducting analyses across model organism databases, as well as other biological data sources and tools that are published using SADI.

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