polyxmass
User Manual

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***polyxmass* User Manual**

Revision History

- ⋆ august 2003, corrections here and there; modified the ***polyxcalc*** chapter to reflect the changes in the graphical user interface and the chemical pad's layout configuration file. Corrected a doc bug about Andreas Fink leading the Fink project (which is false);
- ⋆ july 2003, big work on the polyxmassdata chapter that describes the ***polyxmass*** filesystem hierarchy. Also added some notes on the ***polyxmass*** installation on the *Mac OS X* system (thanks Mark Tracy for these notes);
- ⋆ july 2003, continued working on the ***polyxedit*** module's chapter. Removed any proprietary font embedding. Chapter and Section titles now are typeset using freely available fonts (Palatino).
- ⋆ june 2003, started a major overhaul of the document as the ***polyxmass*** software program was entirely rewritten during the last numerous months. The organization of the document will be modified so that the document reflects better the new modularity of the ***polyxmass*** software suite.
- ⋆ july 2002, added the section on the molecular calculator (***polyxcalc***).
- ⋆ july 2002, changed author's address from "University of Bordeaux" to "Present address: Muséum national d'Histoire naturelle" in Paris as I have now moved to the Laboratoire de biophysique.
- ⋆ july 2002, back to the Computer Modern set of fonts in the text of the manual. pdflatex still best way to get to a nice pdf file.
- ⋆ july 2002, added a description of the find/replace procedures.
- ⋆ july 2002, made all the big pictures again better managing their size. The overall size of the document has fallen to 2.2 Mb, while it was of more than 5 Mb.

- ⋆ april 2002, added a description of how to set some values to customize the program in the resources.tex file. New screen dumps allow to describe the process easily.
- ⋆ april 2002, moved general-options.tex to resources.tex.
- ⋆ april 2002, changes related to the fact that the packages are no more relocatable.
- ⋆ april 2002, changes related to the fact that the directory into which the ***polyxmass*** program is installed is from now on `polyxmass` and not `polyxmass`. So some macros were edited in order to produce the correct typographical results. The pxm-macros.tex file is not dynamically regenerated from a pxm-macros.tex.in file upon autotools processing. That allows a very close correlation between the version of the software package and the version elements' rendering throughout all the text.
- ⋆ april 2002, updated the chapter on the ***polyxmass***' filesystem standard to reflect the changes in the program workings (the fact that the ressource files are now in a hidden directory in the user's home directory).
- ⋆ april 2002, added a detailed description, in the options' configuration chapter, of each option available.
- ⋆ april 2002, added a new chapter on the configuration of the options: file general-options.tex.
- ⋆ end of march 2002, added a section on the chemical bridge support.
- ⋆ march 2002, moved file name "config-data.tex" to "filesystem-config.tex" and corresponding chapter title to reflect the real configuration issue that is dealt with in this chapter and to differentiate this configuration issue with the polymer chemistry "configuration" or "definition".
- ⋆ march 2002, added the description of the graphical configuration of the ***polyxmass*** filesystem. Updated relevant parts after the `monomer.dic` file was removed from the configuration files, and its contents are moved to `polymer.dic`.
- ⋆ february 2002, added a section on mass searching, as I have coded it these last days.
- ⋆ february 2002, chopped polyxmass.tex into chapter parts. This is to allow easily producing chapters one apart from the other.
- ⋆ february 2002, added the *PDF* thumbnail support with the wonderful package from Heiko Oberdiek (thumbpdf).
- ⋆ february 2002, changed the organization of the ***polyxmass***-specific chapters into one single chapter, with as many sections as needed to describe all aspects of ***polyxmass***' operation;
- ⋆ january 2002, added the "***polyxmass***' Sequence Editor" chapter;
- ⋆ january 2002, added the "Installing From The ***rpm*** Source Package" section for the sake of completeness;
- ⋆ january 2002, started writing the little (but tough) chapter on the ***polyxmass***' configuration data hierarchy scheme;

- ⋆ january 2002, a wealth of corrections after careful reading of the last version while in Christmas holidays in Viterbo (near Rome);
- ⋆ december 2001, added section on UNIX history... from document by David A. Wheeler: *Secure Programming for GNU/Linux and UNIX HOWTO*;
- ⋆ november 2001, switched from DocBook SGML format to LaTeX format
- ⋆ october 2001, initial writing, DocBook SGML format

To MARIA CECILIA,

*To all the admirable people acting in the "*Free Software Movement*" for a better and cleaner computing world,*

To all the readers who helped me with this manual...

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Preface

This manual is about the ***polyxmass*** mass spectrometric software suite, a computing framework that aims at predicting/analyzing mass spectrometric data on (bio)polymers. As such, this manual is intended for people willing to learn how to install and use this multi-modular software suite.

Mass spectrometry has gained popularity across the past five years or so. Indeed, developments in polymer mass spectrometry have made this technique appropriate to accurately measure masses of polymers as heavy as many hundreds of kDa.

There are a number of utilities –sold by mass spectrometer constructors with their machines, usually as a marketing "plus"– that allow predicting/analyzing mass spectrometric data of polymers. These programs are usually different from a constructor to another. Also, there are as many mass spectrometric data prediction/analysis computer programs as there are different polymer types. You will get a program for oligonucleotides, another one for proteins, maybe there is one program for saccharides, and so on. Thus, the biochemist/massist, for example, who happens to work on different biopolymer types will have to learn the use of a number of different software packages. Also, if the software user does not own a mass spectrometer, chances are he will need to buy all these software packages.

The ***polyxmass*** mass spectrometric computing framework is designed to provide *free* solutions to all these problems. And it does this by:

- ⋆ Allowing *ex nihilo* polymer chemistry definitions (in the ***polyxdef*** module);
- ⋆ Allowing simple yet powerful mass computations to be made in a polymer chemistry definition-specific manner (in the ***polyxcalc*** module);
- ⋆ Allowing the highly sophisticated editing of polymer sequences on a polymer chemistry definition-specific basis along with chemical reaction simulations, finely configured mass spectrometric computations... (in the ***polyxedit*** module);
- ⋆ Allowing customization of the way each monomer will show up graphically during the program operation (in the ***polyxedit*** module);

- ⋆ Allowing polymer sequence editing with immediate visualization of the mass changes elicited by the editing activity (in the ***polyxedit*** module);
- ⋆ Unlimited number of polymer sequences opened at any given time and of any given polymer chemistry definition type (in the ***polyxedit*** module).

This manual will progressively introduce all these functionalities in a timely and clear fashion.

UNIX and *GNU/Linux* Histories

Thanks to the **GNU** Free Documentation License, I borrowed (and cosmetically modified it) the material in this section from a remarkable document by David A. Wheeler: *Secure Programming for GNU/Linux and UNIX HOWTO*. [1] I think that it is important to provide some background to the choice of a development platform when the time comes to document the software that one has taken so much time to code...

UNIX

In 1969-1970, Kenneth Thompson, Dennis Ritchie, and others at **AT&T Bell Labs** began developing a small operating system on a little-used *PDP-7*. The operating system was soon christened *UNIX*, a pun on an earlier operating system project called *MULTICS*. In 1972-1973 the system was rewritten in the programming language C, an unusual step that was visionary: due to this decision, *UNIX* was the first widely-used operating system that could switch from and outlive its original hardware. Other innovations were added to *UNIX* as well, in part due to synergies between **Bell Labs** and the academic community. In 1979, the "seventh edition" (V7) version of *UNIX* was released, the grandfather of all extant *UNIX* systems.

After this point, the history of *UNIX* becomes somewhat convoluted. The academic community, led by Berkeley, developed a variant called the Berkeley Software Distribution (*BSD*), while **AT&T** continued developing *UNIX* under the names "*System III*" and later "*System V*". In the late 1980's through early 1990's the "wars" between these two major strains raged. After many years each variant adopted many of the key features of the other. Commercially, *System V* won the "standards wars" (getting most of its interfaces into the formal standards), and most hardware vendors switched to **AT&T**'s *System V*. However, *System V* ended up incorporating many *BSD* innovations, so the resulting system was more a merger of the two branches. The *BSD* branch did not die, but instead became widely used for research, for PC hardware, and for single-purpose servers (e.g., many web sites use a *BSD* derivative).

The result was many different versions of *UNIX*, all based on the original seventh edition. Most versions of *UNIX* were proprietary and maintained by their respective hardware vendor, for example, **Sun** *Solaris* is a variant of *System V*. Three versions of the *BSD* branch of *UNIX* ended up as open source: *FreeBSD* (concentrating on ease-of-installation for PC-type hardware), *NetBSD* (concentrating on many different CPU architectures), and a variant of *NetBSD*, *OpenBSD* (concentrating on security). More general information about *UNIX* history can be found at `http://www.levenez.com/unix/`.

[1] Get this paper and others at `http://www.dwheeler.com`

Free Software Foundation

In 1984 Richard Stallman's **Free Software Foundation** (**FSF**) began the **GNU** project, a project to create a free version of the *UNIX* operating system. By free, Stallman meant software that could be freely used, read, modified, and redistributed. The **FSF** successfully built a vast number of useful components, including the ***GNU compiler collection*** (***gcc***), an impressive text editor (***GNU Emacs***), and a host of fundamental tools. However, in the 1990's the **FSF** was having trouble developing the operating system kernel; without a kernel the rest of their software would not work.

GNU/Linux

In 1991 Linus Torvalds began developing an operating system kernel, which he named "Linux". This kernel could be combined with the **FSF** material and other components (in particular some of the *BSD* components and Massachusetts Institute of Technology's (**MIT**) ***X Window*** software) to produce a freely-modifiable and very useful operating system. This book will term the kernel itself the "Linux" kernel and an entire combination as "*GNU/Linux*".

In the *GNU/Linux* community, different organizations have combined the available components differently. Each combination is called a "distribution", and the organizations that develop distributions are called "distributors". Common distributions include **Red Hat**, **Mandrake**, **SuSE** and **Debian**. There are differences between the various distributions, but all distributions are based on the same foundation: the Linux kernel and the **GNU** `glibc` libraries. Since both are covered by "copyleft" style licenses, changes to these foundations generally must be made available to all, a unifying force between the *GNU/Linux* distributions at their foundation that does not exist between the *BSD* and **AT&T**-derived *UNIX* systems.

Open Source vs Free Software

Increased interest in software that is freely shared has made it increasingly necessary to define and explain it. A widely used term is "open source software". Eric Raymond wrote several seminal articles examining its various development processes. Another widely-used term is "free software", where the "free" is short for "freedom": the usual explanation is "free speech, not free beer". Neither phrase is perfect. The term "free software" is often confused with programs whose executables are given away at no charge, but whose source code cannot be viewed, modified, or redistributed. Conversely, the term "open source" is sometimes (ab)used to mean software whose source code is visible, but for which there are limitations on use, modification, or redistribution. This book uses the term "open source" for its usual meaning, that is, software which has its source code freely available for use, viewing, modification, and redistribution; a more detailed definition is contained in the Open Source Definition. For information on this definition of free software, and the motivations behind it, can be found at `http://www.fsf.org`.

Those interested in reading advocacy pieces for open source software and free software should see `http://www.opensource.org` and `http://www.fsf.org`. There are other documents in the internet which examine such software, for example, authors have found that the open source software were noticeably more reliable than proprietary software (using their measurement technique, which measured resistance to crashing due to random input).

Typographical conventions

Throughout the book the following typographical conventions are used:

- *emphasized text* is used each time a new term or concept is introduced
- `bash-2.04 $` shows the prompt at which a command should be entered as non-root
- `bash-2.04 #` shows the prompt at which a command should be entered as root
- `this typography` applies to commands that the user enters at the shell prompt
- **`this typography`** applies to options that the user gives to a command at the shell prompt
- ↩ symbolizes pressing the *Enter* key.
- `this typography` applies to an output resulting from entering a command at the shell prompt
- `emacs` is the name of a program
- `libglib` is the name of a library
- ***GNOME***, ***The Gimp*** is the name of a generic software (not a specific executable file)
- `/usr/local/share`, `/usr/bin/polyxmass` are names of a directory or of a file
- `http://www.gnu.org` is a URL (Uniform Resource Locator)

Program Availability, Technicalities

polyxmass has been primarily developed on a *GNU/Linux* system (**RedHat** distribution versions successively 6.0, 7.0, 7.2, 7.3, 8.0, 9.0) using software from the **Free Software Foundation** (**FSF**[2]).

Developing for *GNU/Linux* has been utterly exciting and extremely efficient. My warm thanks do go to all the persons who have engaged themselves (energy and time) in the *Free/true Open Source Movement* by coding, documenting, reviewing... software. The development was mainly centered around the following programs and utilities:

- **GNU** software is central to my developing system:
  - ***GNU Emacs***, a text editor that is an environment *per se*
  - ***Autotools***, an integrated set of programs to make software development easy and portable. Includes ***Autoconf***, ***Automake*** and others...
    (`http://www.gnu.org`, home of the *Free Software Movement*);
  - ***GDK/GTK+***, two libraries for windowing in the X Window graphic environment
    (`http://www.gtk.org`);
  - ***GTK-Doc***, a system for automating the documentation of the source code and making readable developer's documentation in *HTML* format
    (`http://www.gtk.org`);

[2]For an in-depth coverage of the philosophy behind the **FSF**, specifically creating a *free operating system*, you might desire to visit `http://www.gnu.org`

  - ***The Gimp***, a wonderful program for doing graphical illustrations in pixel mode (raster images). Think of it as an excellent free replacement for the ***Photoshop*** program. The "icons" representing each single monomer in the sequence editor were made using ***The Gimp***. It saves in *xpm*, *png*, *jpg* and many other graphic formats
    (`http://www.gimp.org`);
  - ***GNOME***, a graphical environment for the *GNU/Linux* desktop. I used the ***GNOME*** canvas widget to tailor the sequence editor
    (`http://www.gnome.org`);

- Thomas Esser has made a TEX/LATEX environment of exceptional quality. I used it everyday, and typeset this manual using it. Of course, Prof. Donald Knuth is the grand-daddy of all this, having invented TEX and Leslie Lamport is the father of LATEX! ...
  (`http://www.tug.org`; search for ***teTeX***);
- ***Glade*** is a wonderful graphical interface builder (by Damon Chaplin) that I used to design the graphical interface of the program. I used it in conjunction with the `libglade` library (by James Henstridge)
  (`http://glade.gnome.org` and
  `http://www.daa.com.au/~james/software/libglade`);
- **RedHat** is undoubtedly committed to the success of the *Free Software Movement* and happens to be the maker of a popular (my) *GNU/Linux* distribution
  (`http://www.redhat.com`);
- Bernhard Herzog has written a vector drawing package that I used for some illustrations in the ***polyxmass*** package. It is called ***Sketch***
  (`http://sketch.sourceforge.net`);
- Lauris Kaplinski and co-workers have crafted a very powerful program to create and handle scalar vector graphics. This program is called ***Sodipodi***
  (`http://sodipodi.sourceforge.net`);
- Owen Taylor has written a memory profiling tool that I used to detect memory leaks. It is called ***memprof***
  (`otaylor{@}redhat.com`, remove the curly brackets);
- Of course I do forget many software packages that I used for this work. Thanks to their authors and to their maintainers: without their hard work my *GNU/Linux* box would not exist!

Organization Of This Manual

After having rapidly explained the general pattern about installing each of the modules that make the ***polyxmass*** software suite, this manual aims at providing the required concept toolset for understanding what to expect from a computer program project like ***polyxmass***. Thus, the general organization of this book is:

- Installation of ***polyxmass*** modules;
- The basics of polymer chemistry;

- The basics of mass spectrometry;
- Generalities about the ***polyxmass*** software suite;
- The ***polyxdef*** module (definition of a new polymer chemistry);
- The ***polyxcalc*** module (polymer chemistry-aware calculator);
- The ***polyxedit*** module (the main module of the suite, where actual simulations are performed);
- The ***polyxmassdata*** module describing the ***polyxmass***' complex configuration hierarchy;
- Appendices.

polyxmass' Licensing Philosophy

The front matter of this manual contains a Copyright statement. I wish to retain the copyright to ***polyxmass*** and all related writings (source and configuration files, programmer's documentation, user manual...) However, I do not deny others the right to make copies of the work, to redistribute it freely, to modify it according to the **GNU** General Public License for the ***polyxmass*** computer program, and according to the **GNU** Free Documentation License.

The aim of this licensing is to favor spread of knowledge to the widest public possible. Also, it encourages interested hackers[3] to change the code, to improve it and to send patches to the author so that their improvements get in the program to the benefit of the widest public possible. For an in-depth study of the *free software* philosphy I kindly urge the reader to visit `http://www.gnu.org/philosophy`.

Contacting The Author

The ***polyxmass*** program is the fruit of months of work on my part. While I've put a lot of energy into making this program as stable and reliable a piece of software as possible, ***polyxmass*** comes with no warranty of any kind. I hope that ***polyxmass*** will help numerous researchers with their mass spectrometric data prediction/analysis work, which will hopefully ease the creation of *scientific knowledge*.

The general policy for directing questions, comments, feature requests, ***polyxmass*** program and/or ***polyxmass*** documentation bug reports should be self-explanatory by looking at the addresses below:

polyxmass-webmaster@polyxmass.org
polyxmass-maintainer@polyxmass.org
polyxmass-bugs@polyxmass.org
polyxmass-request@polyxmass.org

[3] *Hacker* is a specialized term to design the programmer that codes programs; this term should *not* be mistaken with *cracker* who is a person who uses computer science knowledge to break information systems' security barriers.

To direct any comment(s) to the author through snail mail, use the following address:

D[r] Filippo Rusconi

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2

Installation Overview

The ***polyxmass*** software suite is a multi-modular software framework. It is made of a number of modular packages that depend on each other. The installation of the ***polyxmass*** software suite can be achieved with no pain by following the instructions in this chapter.

The dependencies between the modules of the ***polyxmass*** software framework are "ordered", which means that they require that the modules of the framework be installed on the same system in an ordered manner. We will review this ordered installation procedure below.

Each module of the ***polyxmass*** software suite may be developed independently, which means that it is not required that they have the same version/package number. The dependencies are dealt with at install time, so the best way to make a fresh install of the ***polyxmass*** software suite is to take all the most recent packages from `http://www.polyxmass.org`. If there are no errors (*errare humanum est*) in the dependency system, all the packages should be installed with no difficulty.

Prior to analyzing the installation procedure as a whole, it is necessary to describe the packaging systems that are available for the user to install, in the manner that suits her needs, the individual packages.

Each package comes in a number of different flavors:

- Uncompiled source package
  - *tar.gz* files which need to be compiled using the ***GNU make*** program;
  - *src.rpm* files which need to be compiled using the ***rpm*** tool;
- Binary ready-to-install package

- *i386.rpm* files that are dependent on the computing platform architecture (must be installed using the ***rpm*** tool);
- *noarch.rpm* files that are non-dependent on the computing platform architecture (must be installed using the ***rpm*** tool).

Installing From The ***rpm*** Binary Package

Installing any *rpm* package using the ***rpm*** program[1] is as easy as entering the following command, as root:

```
bash-2.04 # rpm -ivh polyxcalc-1.i386.rpm ↩
```

What this command does is read the `polyxcalc-1.i386.rpm` file contents (this package file probably contains a number of files packed in it) and copy them to their destination directories. The *rpm* file format allows to tell to which directory each file that it contains is to be copied.

Note that when the installation is performed using the ***rpm*** binary package, the installation directory is in the `/usr` standard tree. Once the package is installed, do not move the files from their installation directory, because each ***polyxmass*** module relies on these precise directories to locate the files needed to operate correctly. The binary files (program files, like the `polyxedit` or the `polyxcalc` program files) are installed in the `/usr/bin` directory.

Indeed, it is noteworthy that the package is *not relocatable*, which means that the user is strongly urged not to use the **`--prefix`** option (or the installation will be messed up). The only way to install the software through a ***rpm*** binary package in a customized directory is by recompiling the sources with the *src.rpm* file package. See below for instructions on how to cheat with the ***rpm*** utility.

To see all the files that are provided by a given ***rpm***-based package file, issue the following command:

```
bash-2.04 $ rpm -qpl polyxcalc-1.i386.rpm ↩
```

The output of this command is a list of all the files –along with their destination directories– that would be installed if the package were installed as above.

Installing From The ***rpm*** Source Package

We assume here that the system is a **Red Hat** *GNU/Linux* system, but the directions provided here might also be useful for other ***rpm***-based systems (like **Mandrakesoft**'s or **SuSe**'s?). Installing any ***rpm***-based package file from the *src.rpm* source package[2] is actually simply one more step (the building of the software) than in the previous binary package installation case.

[1] For an in-depth manual on the ***rpm*** packet manager, you might want to read *Maximum RPM*, a book by Ed Bailey, available from `http://www.rpm.org`.

[2] The filename has "src" in it, contrary to the binary package that has the platform name; for **Intel** platforms this is "i386" in most cases.

The *src.rpm* package simply contains two files: the source archive file (in the form of a **GNU** classical *tar.gz* tarball (see next section), and a corresponding ***rpm*** *spec* file. The *tar.gz* tarball is very similar to the one described in detail later, while the *spec* file is a very simple text file that gives the ***rpm*** software directions on how to build a binary *i386.rpm* package out of the *src.rpm* file.

It is important to understand the functioning of the `rpm` program (read its documentation) before using a *src.rpm* package. After installing a *src.rpm* package,[3] the program itself is not available to the user (while with a binary package, the program is immediately available to the user). Apparently nothing happened, but what happened is that the *src.rpm* package's contents are unpacked by the `rpm` program into two different `/usr/src/redhat` subdirectories. In this `/usr/src/redhat` directory, indeed, the `SPECS` subdirectory now contains the *spec* file, and the `SOURCES` subdirectory now contains the *tar.gz* source tarball file. To build a binary package after having installed the ***rpm*** source package, it is necessary to first change directory to the `SPECS` subdirectory and next ask `rpm` to build the package. All these steps are described below with the ***polyxcalc*** module package as an example:

```
bash-2.04 # rpm -ivh polyxcalc-1.src.rpm ↩
bash-2.04 # cd /usr/src/redhat/SPECS ↩
bash-2.04 # rpmbuild -ba polyxcalc.spec ↩
```

The **`-ba`** option tells the `rpmbuild` program to "build all" the package. After a while,[4] the process stops. If the displayed result is 0, then that means that everything went correctly. Further, near the end of the `rpm` output, there must be a line indicating that a *i386.rpm* package file has been written. Change directory (from `/usr/src/redhat/SPECS`) to `/usr/src/redhat/RPMS/i386` and see that the ***rpm*** binary package (in our example that would be the `polyxcalc-1.i386.rpm` file) has been correctly produced. This binary package is nothing but the ***rpm*** *i386.rpm* file package that was described in the previous section. Just install this package as described above for the binary packages.

This newly built package is guaranteed to be compatible with your processor and with your pre-installed programs and shared libraries, since the compilation completed without trouble. Ideally, the process described here should be performed for any ***rpm*** package but, since it is time-consuming, it is only performed on special critical mission software...

Note that there is a shortcut to the procedure described above:

```
bash-2.04 # rpmbuild -rebuild polyxcalc-1.src.rpm
```

It is possible to cheat with the ***rpm*** software so that the installation directory is not the default one. This is done by editing manually the package's *spec* file. It is simply a matter of telling the ***rpmbuild*** program that the *prefix* to be used to construct the installation path is not the default one (`/usr`) but `/opt`, for example. In this case, just add the following line on top of the *spec* file:

```
%define _prefix          /opt
```

if you intended to install the software package in the `/opt` directory. For example, here is how the `polyxcalc.spec` file would read if you intended to install the ***polyxcalc*** package in the `/opt` directory:

```
%define _prefix          /opt
%define name             polyxcalc
```

[3] Using the same command as for a binary package.

[4] Automatic sources unpacking, configuration, building of the program, packaging into a binary package.

Once this slight modification is done, just run:
`bash-2.04 # rpmbuild -ba polyxcalc.spec` ↩

And once the package is recompiled, this time you can install it the usual way:
`bash-2.04 # rpm -ivh polyxcalc-1.i386.rpm` ↩

Installing From The *tar.gz* Sources

Installing a package from the source is as easy as issuing the following commands in the correct order:

```
bash-2.04 $ cp polyxcalc.tar.gz /tmp ↩ copy the package into a safe place
bash-2.04 $ cd /tmp ↩
bash-2.04 $ tar -xvzf polyxcalc.tar.gz ↩ this unpacks the sources into a source tree in
the polyxcalc directory
bash-2.04 $ cd polyxcalc ↩
bash-2.04 $ ./configure ↩
bash-2.04 $ make ↩
bash-2.04 $ su ↩ become root if it is possible
bash-2.04 # make install ↩
```

Unlike with the previous ***rpm***-based installation, it is possible to specify an installation directory to the `./configure` command. Indeed, the user can modify the default installation directory (which is the `/usr/local` tree) by using a qualified **`--prefix`** option to the `./configure` command.

For example, by default (with no qualified **`--prefix`** option), the ***polyxcalc*** module's configuration data and executable files would be installed respectively in these two directories:

- `/usr/local/share/polyxcalc`
- `/usr/local/bin`

To change the installation directory, the user may use the qualified **`--prefix`** option as shown in the following example:

`bash-2.04 $ ./configure --prefix=/usr` ↩

Note that you will need to have root priviledges to be able to install the program in system directories like `/usr` or `/usr/local`.

Interestingly, since version 4.0 of `rpm`, it is possible to build ***rpm*** files with a suitably made source *tar.gz* tarball. This source tarball is nothing than a file containing the source files of the software package along with the corresponding *spec* file (the same we discussed above). The *tar.gz* source tarballs in any of the ***polyxmass*** software suite modules complies with this format, and thus it is possible to build ***rpm***-based files running this very simple command as root, for package ***polyxcalc***, for example:
`bash-2.04 $ rpmbuild -ta polyxcalc.tar.gz` ↩

At the end of the package building process, the two source and binary files are ready in the `/usr/src/redhat` subdirectories (see above).

Installation On A *Mac OS X* System With Fink

The *Mac OS-X* operating system can run **GNU** software when the ***Fink*** porting system is installed (please, visit `http://fink.sourceforge.net` for details on this project). The notes below were kindly provided to me by D^{r} Mark Tracy. If you find errors, they are mine, and I am the only one to be blamed for badly transcribing these notes.

polyxmass was successfully installed on the *Mac OS-X*/***Fink*** platform. For example, version 0.6.0 of the modules of the ***polyxmass*** software suite could be installed using the *info* files provided by D^{r} Mark Tracy. These ***Fink*** *info* files are scripts much like the ***rpm*** *spec* files. The ***Fink*** packaging system relies on the usual *tar.gz* source files, which may be used without modification[5]. However, the case may arise that the *Mac OS-X*/***Fink*** platform requires that the package maintainer changes the code of the source tree for one or more packages in the ***polyxmass*** suite. In this case patches should be applied to the original source tarballs so that these code modifications are recreated when intalling the packages on the *Mac OS-X*/***Fink*** platform. In this case, the *patch* files would be distributed along with the source tarball files and the *info* files. Providing *patch* files for the software to build correctly on any given platform is the task of the package maintainer.

Once you have downloaded all the required files (*info*, *patch*, *tar.gz*), the installation process is as easy as doing the following:

First, since these *info* scripts may not yet be available through the ***Fink*** server, you need to copy them to the right place and go there to continue (run command as superuser):

```
bash-2.04 # cp *.info /sw/fink/10.2/local/main/finkinfo
bash-2.04 # cd /sw/fink/10.2/local/main/finkinfo
```

Note that, in the future, the *info* scripts will be placed in the right directory by the ***Fink*** server. Now, install the packages –in order– by issuing the following commands:[6]

```
bash-2.04 # fink install polyxmassdata ↩
bash-2.04 # fink install libpxmutils0 ↩
bash-2.04 # fink install libpxmchem1 ↩
bash-2.04 # fink install polyxdef ↩
bash-2.04 # fink install polyxcalc ↩
bash-2.04 # fink install polyxedit ↩
```

If the software packager did everything right, ***Fink*** will calculate the dependencies, and ask you if you want to install the dependent packages. When all is finished, open a new X-terminal window to run the software (yes, it has to be new and it has to be X).

This is all is needed to understand how to perform the installation of any package in the ***polyxmass*** mass spectrometric software suite. The next chapters will deal with each module

[5] That's the case for the version 0.6.0 of all the ***polyxmass*** modules.

[6] While the rest of the process happens you can read the user documentation. During the installation of the libraries, ***Fink*** will ask if you want to install the `-shlibs` also: say yes.

separately. The software packages in the ***polyxmass*** software suite should be installed in the following order:

1. `polyxmassdata`
2. `libpxmutils`
3. `libpxmchem`
4. `polyxdef`
5. `polyxcalc`
6. `polyxedit`

Each module is described in its own chapter, with all the details that are required so that the user gets an intimate knowledge of the way the whole ***polyxmass*** mass spectrometric software suite works.

3

Basics in Polymer Chemistry

This chapter will introduce the basics of polymer chemistry. The way this topic is going to be covered is admittedly biased towards mass spectrometry and biological polymers. Moreover, the aim of this chapter is to provide the reader with the specialized words that will later be used to describe and explain the (inner) workings of the ***polyxmass*** program. This manual is not a "crash course" in biochemistry!

Polymers? Where? Everywhere!

Indeed, polymers are everywhere. If you ask somebody to show you something polymeric, he/she will point you at the first plastic object in the vicinity. Right, plastic materials are made of hydrocarbon polymers. But we have many different polymers in our body. Proteins are polymers, complex sugars are polymers, DNA (the so-called "molecule of heredity" is a *huge* polymer. There are polymers in wine, in wood... Where? Everywhere!

The *Oxford Advanced Learner's Dictionary of Current English* gives for *polymer* the following definition: ***natural or artificial compound made up of large molecules which are themselves made from combinations of small simple molecules***.

A polymer is indeed made by covalently linking small simple molecules together. These small simple molecules are called *monomer*s, and it is immediate that a *polymer* is made of a number of monomers. A general term to describe the process that leads to the formation of a polymer is *polymerization*. It should be noted that there are many ways to polymerize monomers together. For example, a polymer might be either linear or branched. A polymer is linear if the monomers that are polymerized can be joined at most two times. The first junction links the monomer to an elongating polymer (thus making it the new end of the elongating polymer which, by the way, is longer than before by one unit) and the second junction links the new elongating polymer's end to another monomer. This process goes on until the reaction is stopped, the point at which the polymer reaches its *finished state*. A branched polymer is a polymer in which at least one monomer is able to contract more than two bonds. It is thus clear that a single monomer linked three times to other monomers will yield a "T-structure", which is nothing but a branched structure.

In the following sections we'll describe a number of different kinds of polymers. Each time, they will be described by initially detailing the structure of their constitutive monomers; next the formation of the polymer is described. At each step we shall try to set forth each polymer characteristics in such a manner as to introduce the way ***polyxmass***' "thinks polymers" and to introduce specialized terminologies.

Once the basic chemistries (of the different polymers) have all been described, we will enter a more complex subject that is of enormous importance to the mass spectrometry specialist: polymer chain disrupting chemistry. We shall see that this terminology actually involves two kinds of chemistries: cleavage on the one hand and fragmentation on the other hand.

While ***polyxmass*** is basically oriented to linear single stranded polymer chemistries, it also can be used to simulate highly complex polymer chemistries. Biological polymers are the main focus of this manual, however all the concepts described here may be applied with no modification (or so slight) to synthetic polymer chemistries.

Well, time has come to make a "biochemical polymers" tour. The reader who feels at home with biopolymers may skip joyfully the next sections. However, the section pertaining to polymer lysis and fragmentation should be of interest even to the expert because they are the opportunity to introduce a "funny" terminology that is not encountered anywhere else (have you ever heard of *"leftrighrules"* or of *"fragrules"*?!).

Various Biopolymer Structures

Biopolymers are amongst the most sophisticated and complex polymers on earth and it certainly is not a mistake to take them as examples of how monomers (be these complex or not) can assemble covalently into life-enabling polymers. In this section we will visit three different polymers encountered in the living world: proteins, nucleic acids and polysaccharides. We shall be concerned with 1) the monomers' structure, 2) the polymerization reaction and 3) the final capping reaction responsible for putting the polymer in its *finished state*.

Proteins

These biopolymers are made of amino acids. There are twenty major amino acids in nature, and each protein is made of a number of these amino acids. The combinations are infinite, providing enormous diversity of proteins to the living world.

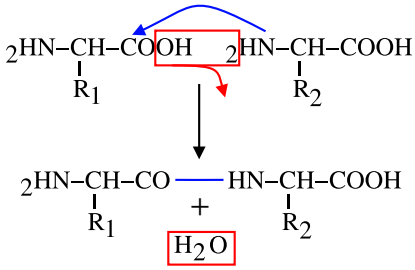

Figure 3.1: **Peptidic bond formation by condensation.** The left end monomer R_1 is condensed to the right end monomer R_2 to yield a peptidic bond. A water molecule is lost during the process.

A protein is a polar polymer: it has a left end and a right end. This means that the polymerization process is something ordered, from left to right.

The Figure 3.1 shows that the chemical reaction at the basis of protein synthesis is a *condensation*. A protein is the result of the condensation of amino acids with each other in an orderly polar fashion. A protein has a left end (called *N terminus; amino terminal end*) and a right end (called *C terminus; carboxyl terminal end*). The left end is an amino group ($_2$HN–) corresponding to the amino group of the non-reacted amino acid. Upon condensation of a new amino acid onto the first one, the carboxyl group of the first amino acid reacts with the amino group of the second amino acid. A water molecule is released, and the formation of a bond between the two amino acids yields a dipeptide. The right end of the dipeptide (and of a polypeptide –*i.e.* of a protein– also, of course) is a carboxyl group (–COOH) corresponding to the un-reacted carboxyl group of the last amino acid to have "polymerized in".

The bond formed by condensation of two amino acids is an amide bond, also called –in protein chemistry– a *peptidic bond*. The elongation of the protein is a simple repetition of the condensation reaction shown in Figure 3.1, granted that the elongation *always* proceeds in the described direction (a new monomer arrives to the right end of the elongating polymer, and elongation is done from left to right).

Now we should point at a protein chemistry-specific terminology issue: we have seen that a protein is a polymer made of a number of monomers, called amino acids. In protein chemistry, there is a subtlety: once a monomer is polymerized into a protein it is no more called a monomer, it is called a *residue*. We could say that a residue is an amino acid less a water molecule.

From what we have seen until now, we could define a protein this way: —"*A protein is a chain of residues linked together in an orderly polar fashion, with the residues being numbered starting from 1 and ending at n, from the first residue on the left end to the last one on the right end*". This definition is still partly inexact, however. Indeed, from what is shown in Figure 3.2, there is still a problem with the extremities of the polymer chain: what about the amino group on the left end of a protein (the amino group sits right onto the first amino acid of the protein), and what about the carboxyl group of the right end of a protein (the carboxyl group sits right onto the last amino acid of the protein)? These two groups are un-reacted, in fact. If we followed the new "residue-based" definition of a protein polymer, we would say that there is a proton in *excess* on the left end and a hydroxyl in *excess* on the right end. However, these two chemical groups are not actually in *excess*, they are called (in ***polyxmass***) the *cappings* or *caps* of the polymer (this terminology is also used in polymer

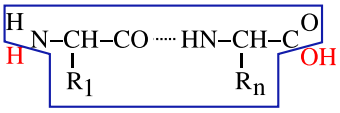

Figure 3.2: **End capping chemistry of the protein polymer.** A protein is made of a chain of residues and of two caps. The left cap is the N-terminal proton and the right cap is the C-terminal hydroxyl. Altogether, the residual chain (enclosed here in the blue polygon) and both red-colored caps (H and OH) do form a complete protein polymer.

science). They ensure that the polymer is in a *finished state*, which means that it cannot be elongated anymore, on whichever end. The proton is the *left cap* of the protein polymer and the hydroxyl is the *right cap* of the protein polymer.

Now comes the question of unambiguously defining the structure of a protein. It is commonly accepted that the simple ordered sequence of each residue code in the protein, from left to right, constitutes an unambiguous description of the protein's *primary structure*. Of course, proteins have three-dimensional structures, but this is of no interest to a program like ***polyxmass***, which is aimed at calculating masses of polymers. To enunciate unambiguously the *sequence* of a protein, you would use a symbology like this:

using the 3-letter code of the amino acids:

Ala Gly Trp Tyr Glu Gly Lys

or, using the 1-letter code of the amino acids:

A G W Y E G K

Alanine is thus the residue 1 and Lysine is the last residue (n = 7).

This primer in protein chemistry should be sufficient for the moment. Let us now go to see how nucleic acids differ from the proteins (and they do no little).

Nucleic Acids

These biopolymers are more complex than the proteins are. This is mainly due to the fact that nucleic acids are composed of monomers that have three different parts, and because those parts differ in DNA and RNA. Nucleic acids are made of *nucleotide*s. A nucleotide is the nucleic acid's brick: *a nucleotide consists of a nitrogenous base combined with a ribose/deoxyribose sugar and with a phosphate group*. There are two different kinds of nucleic acids: deoxyribonucleic acid, also known as DNA (the sugar is a deoxyribose) and ribonucleic acid, also known as RNA (the sugar is a ribose). DNA is most often found in its double stranded form, while RNA is most often found in single strand form. There are four nitrogenous bases for each: Adenine, Thymine, Guanine, Cytosine for DNA; in RNA only one of these bases changes: Thymine is replaced by Uracile.

A nucleic acid is a polar polymer: it has a left end and a right end (same as for proteins, remember?). This means that the polymerization process is something ordered, from left to right (sometimes left is up and right is down in certain vertical representations found mainly in textbooks).

This manual is not to teach biochemistry, which is why I am not going to describe the structure of the monomers in atomic detail. However, since it is important to understand how the polymerization occurs, I drew the Figure 3.3 which shows the polymerization reaction mechanism between a nucleotide and another one, to yield a dinucleotide.

The Figure 3.3 shows that the chemical reaction that is at the basis of nucleic acid

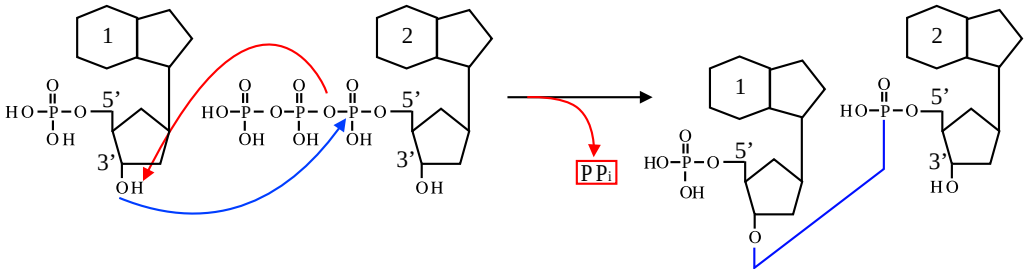

Figure 3.3: **Phosphodiester bond formation by esterification.** The arriving monomer (on the right) has its triphosphate on the 5' carbon of the sugar esterified by nucleophilic attack of the first phosphorus by the alcohol function beared by the 3' carbon of the (deoxy)ribose sugar ring of the left monomer. The bond that is formed is a phosphodiester bond, with release of a pyrophosphate group (P_i). Note that the sugar and nitrogenous bases are schematically represented in this figure.

synthesis is an *esterification*. A nucleic acid has a left end (called *5' end; often this end is phosphorylated*) and a right end (called *3' end; hydroxyl end*). The reaction is the attack of the phosphorus of the new (deoxy)nucleotide triphosphate by the 3'OH of the right end of the elongating nucleotidic chain. Upon esterification, an *inorganic pyrophosphate* (PP_i) is released, and the formation of a phosphodiester bond between the two nucleotides yields a dinucleotide. The elongation of the nucleic acid polymer is a simple repetition of this esterification reaction so that the chain growth is always in the 5'$\Longrightarrow$3' direction. This is achieved in the living cells by what is called the *5'$\Longrightarrow$3' polymerase enzymatic activity*.

The conventional representation of a nucleic acid involves showing the 5' end on the left, and the 3' end on the right, horizontally. Sometimes, to clearly indicate that the left end is phosphorylated, while the right end is not, the ends are indicated as "5'P" and "3'OH".

Figure 3.4 shows a simple way to formalize what a nucleic acid polymer is. The molecule represented on the left is the representation of the "monomer" in the sense that the polymer is made of a number of these monomers (if you put in the presented formula the proper nitrogenous base and the proper sugar –ribose or deoxyribose–, you will get the nucleotide of your choice). We have seen previously that, in the specific case of the protein polymer chemistry, the monomer is called residue once it is polymerized into the polymer chain. In the case of the nucleic acids, there is no such specific term, we just call the monomeric unit a nucleotide. The formula represented on the left of the Figure 3.4 shows the repetitive element in a nucleic acid polymer, exactly the same way as we had shown the residue formula in the protein polymer chemistry section. Indeed, as we had explained earlier with proteins, the formula shown on the right of the Figure 3.4 illustrates that the nucleic acid polymer needs to be set to a *finished state*. The atoms shown in red (outside the boxed repetitive elements) are the nucleic acid *caps*. Thus, we see clearly that in the case of the nucleic acid polymers, the left cap is a hydroxyl and the right cap is a proton. This anecdotically happens to be the exact converse of what we described earlier for proteins.

Now comes the question of unambiguously defining the structure of a nucleic acid. It is commonly accepted that the simple ordered sequence of the named nitrogenous bases in the nucleic acid, from left (5' end) to right (3' end), constitutes an unambiguous description of the nucleic acid sequence. To enunciate the sequence of a gene, you would use a symbology like this:

for a DNA, using the 1-letter code of the nitrogenous bases: A T G C A G T C

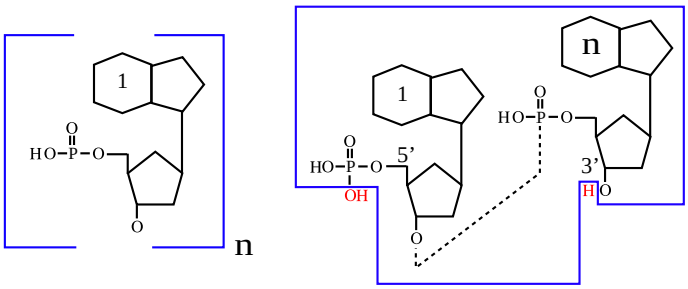

Figure 3.4: **End capping chemistry of the nucleic acid polymer.** A nucleic acid is made of a chain of nucleotides (left formula) and of two caps. The left cap is the hydroxyl group that belongs to the terminal phosphate of the 5' carbon of the sugar. The right cap is the proton that belongs to the hydroxyl group of the 3' carbon of the sugar ring (right formula). Altogether, a finished nucleic acid polymer is made of the nucleotidic chain (enclosed here in the blue polygon), made of the repetitive elements (one of which is shown on the left), and of the two caps (red-colored OH and H, out of the box on the right).

for an RNA, using the 1-letter code of the nitrogenous bases: A U G C A G U C
Adenine is thus the base 1 and Cytosine is the last base (n = 8).

Polysaccharides

These biopolymers are almost certainly amongst the more complex in the living world. This is mainly due to the fact that saccharides are usually heavily modified in living cells. There are a huge variety of chemical modifications occurring on these biopolymers. Furthermore, the ramifications in the polymer structure are more often the normal situation than not. Interestingly these molecules are first thought of as the "fuel" for the cell, which is certainly far from being total non-sense, but it is clear that their structural role is extremely important. Their ability to form complex structures has been exploited in living systems for identification processes. There are a number of complex sugars on the cell walls...

Nonetheless, the general picture is not that complex, if we only think of the way monomers are polymerized together. As far as we are concerned, in fact, the polymerization mechanism is a simple condensation. In this respect, everything looks much like with proteins; some people do use the same terminology: a monomer sugar becomes a residue once polymerized in the saccharidic chain.

There are two main different kinds of sugars: *pentoses* (in C_5) and *hexoses* (in C_6); it should be noted, however, that there is a variety of other common molecules, like *sialic acids*, *heptose*...

A saccharidic polymer is polar: it has a left end and a right end (same as for proteins and nucleic acid, should you remember!). This means that the polymerization process is something ordered, from left to right. The terminology regarding the ends of a saccharidic polymer is rather unexpected at first sight: the left end is said to be the *non-reducing end* while the right end is said to be the *reducing end*. Historically this was observed with monosaccharides (also called *monoses*), which reduced cupric (Cu^{2+}) ions, thus getting oxydized themselves on the carbonyl (when in the open ring aldehydic form).

Figure 3.5 shows the polymerization reaction between a sugar and another one (2 glucose monomers, actually), to yield a maltose disaccharide. The polymerization mechanism is a

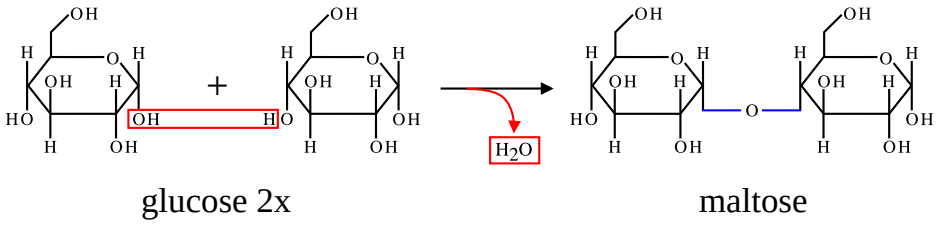

Figure 3.5: **Osidic bond formation by condensation.** The two monomers are subject to condensation with loss of one molecule of water.

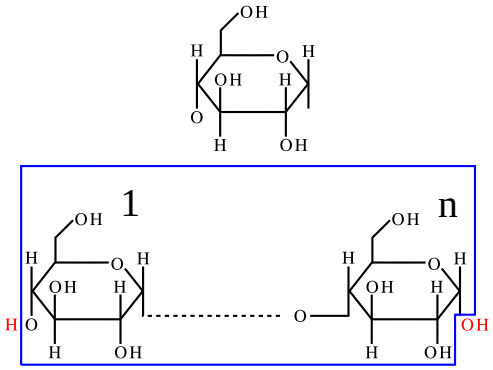

Figure 3.6: **End capping chemistry of the polysaccharidic polymer.** A polysaccharide is made of a chain of osidic residues (blue-boxed formula) and of two caps (red-colored atoms). The left cap is the proton group that belongs to the non-reducing end of the polymer. The right cap is the hydroxyl group that belongs to the reducing end of the polymer.

simple condensation. The elongation of the polysaccharidic polymer is a simple repetition of this condensation reaction so that the chain growth is always in the same orientation, from non-reducing end to reducing end.

The conventional representation of a polysaccharide involves showing the non-reducing end on the left, and the reducing end on the right, horizontally.

Figure 3.6 shows a simple way to formalize what a saccharidic polymer is. The top formula is the representation of the "monomer" in the sense that the polymer is made of a number of these monomers. The bottom formula represents a polysaccharide, with the repetitive elements boxed (there are n monomers polymerized). The atoms shown in red (outside the boxed repetitive elements) are the saccharidic polymer *caps*. Thus, we see clearly that in the case of polysaccharides, the left cap is a proton and the right cap is a hydroxyl. This anecdotically happens to be identical to the protein case and the exact converse of what we described previously for nucleic acids.

Now comes the question of unambiguously defining the structure of a saccharidic polymer. It is commonly accepted that the simple ordered sequence of the named monoses in the saccharidic polymer, from left (non-reducing end) to right (reducing end), constitutes an unambiguous description of the glycan sequence. To enunciate the sequence of a glycan, you would use a symbology like this:

using a 3-letter code:

polymer	name	code	formula	left cap	right cap
protein				H	OH
	Glycine	G	$C_2H_3O_1N_1$		
	Alanine	A	$C_3H_5O_1N_1$		
	Tyrosine	T	$C_9H_9O_2N_1$		
nucleic acid				OH	H
	Adenine	A	$C_{10}H_{12}O_5N_5P_1$		
	Cytosine	C	$C_9H_{12}O_6N_3P_1$		
saccharide				H	OH
	Arabinose	Ara	$C_5H_8O_4$		
	Heptose	Hep	$C_7H_{12}O_8$		
Note: LC=left cap; RC= right cap					

Table 3.1: **Quick comparison of three biopolymers with examples of monomers**

Ara Gal Xyl Glc Hep Man Fru
Arabinose is thus the monose 1 and Fructose is the last monose (n = 7).

Incidentally, this is where the ability of ***polyxmass*** to handle monomer codes of non-limited length comes in handy!

To Sum Up

We have very rapidly made an overview of the three major polymers in the living world. A great many other polymers exist around us.

Table 3.1 on page 22 tries to sum up all the informations gathered so far. Note that the formulae given for the monomers are the "residual" ones. For example, the formula of the glycyl residue corresponds to the formula of the Glycine monomer less one molecule of water.

Many synthetic polymers are much simpler than the ones we have rapidly reviewed, and it should be clear that, if ***polyxmass*** can deal with the complex biopolymers described so far, it certainly will be very proficient with less complex synthetic polymers. Describing the formation of polymers is one thing, but we also have to describe how to disrupt polymers. This is what we shall do in the next section.

Polymer Chain Disrupting Chemistry

As we initially spoke of "polymer chain disrupting chemistry" earlier, we said that this was a complex subject, and that it was of *enormous* importance to the mass spectrometrist. This is why we will treat this subject in a pretty thorough manner.

First of all we should insist on the fact that chemically modifying a polymer does not necessarily mean that the chain structure of the polymer is perturbed. Here, however, we are concerned specifically with the chemical modifications that yield a polymer chain perturbation; *cleavage* and *fragmentation*:

- ⋆ A CLEAVAGE IS A CHEMICAL PROCESS by which a molecule will act directly on the polymer making it fall into at least two separated pieces (the *oligomers*). As a result of the cleavage reaction, groups originating in the cleaving molecule remain attached to the polymer at the precise cleavage location;

- ⋆ A FRAGMENTATION IS A CHEMICAL PROCESS by which the polymer structure is disrupted into separated pieces (the *fragments*) mainly because of energy-dependent electron doublet rearrangements leading to bond breakage.

Here are the details pertaining to each one of these two very different processes:

Polymer Cleavage

We said above that, upon cleavage of a polymer, the cleaving molecule reacts with it, and by doing so directly or indirectly "*dissolves*" an inter-monomer bond. A polymer cleavage always occurs in such a way as to generate a set of *true* polymers (smaller in size than the parent polymer, evidently, which is why they are called *oligomers*). Indeed, let us take the example shown in Figure 3.7, where a tripeptide (a very little protein, containing a methionyl residue at position 2) is submitted either to a water-mediated cleavage (hydrolysis, upper panel) or to a cyanogen bromide-mediated cleavage (lower panel). The two cases presented in this figure are similar in some respects but different in other respects:

- ⋆ in both cases the bond that is cleaved is the inter-monomer bond (in protein chemistry this is a peptidic bond);
- ⋆ in both cases the Oligomer 2 has the same structure;
- ⋆ in the first case the molecule that is responsible for the cleavage is water, while in the second case it is cyanogen bromide;
- ⋆ the structures of the Oligomer 1 species differ when produced using water or cyanogen bromide as the cleaving molecule.

The difference between hydrolysis and cyanogen bromide cleavage is the Oligomer 1 species: the cyanogen bromide cleavage has a side effect of generating a homoserine as the right end monomer of Oligomer 1, while hydrolysis generates a genuine methionine monomer. This is because water reverses in a very symmetrical manner what polymerization did (hydrolysis is the converse of condensation), while cyanogen bromide did some chemical modification onto the generated Oligomer 1 species.

Nonetheless, the reader might have noted that –interestingly– all the four oligomers do effectively have their left cap (a proton) and their right cap (the hydroxyl). This means that in both water and cyanogen bromide-mediated cleavage, all the generated oligomers are indeed true polymers in the sense that: 1) they are a chain of monomers (modified or not) and 2) they are correctly capped (*i.e.* they are polymers in their finished state). This is important because it is the basis on which we shall make the difference between a cleavage process and a fragmentation process.

Thus, the ***polyxmass*** definition of an oligomer might be: *an oligomer is a polymer (of at least one monomer) in its finished state that was generated upon cleavage of a longer polymer.*

When the polymer cleavage reaction precisely reverses the reaction that was performed for the same polymer's synthesis, there is no special difficulty. But when the cleavage reaction modifies the substrate, then this should be carefully modelled. How? To answer this question we might start by comparing the two different Oligomer 1 species that were yielded upon the water-mediated and the cyanogen bromide-mediated cleavage reactions: "the hydrolysis-generated Oligomer 1 is equal to the cyanogen bromide-generated Oligomer 1 +S1 +C1 +H2 -O1"; this is a big difference! The observations we did so far might be worded this way:

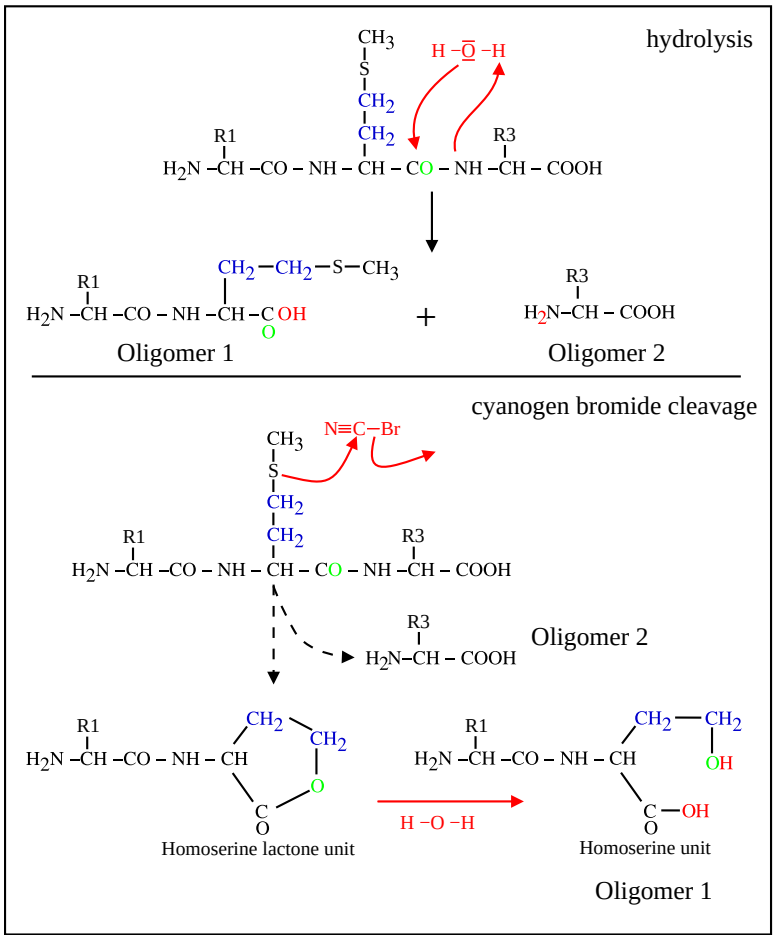

Figure 3.7: **Protein cleavage by water and cyanogen bromide.** A tripeptide (pretty small protein) is cleaved at position 1 either by hydrolysis (top) or by cyanogen bromide (bottom). Cyanogen bromide cleaves specifically on the right of a methionine monomer.

Whenever a protein undergoes a cyanogen bromide-mediated cleavage, the

"-C1H2S1+O1"

chemical reaction should be applied to the resulting oligomers if and only if they have a methionine monomer at their right end. This logical condition is called, in ***polyxmass***' jargon, a *leftrightrule*, and will be described later (see page 52).

Well, this sounds reasonable. But what about the "normal" case, when the cleavage is done using water? Nothing special: the mass of the oligomer is calculated by summing the mass of each monomer in the oligomer (since the monomers are not modified this is easily done) and the masses corresponding to both the left and right caps (these are defined in the polymer chemistry definition; in our present case it would be a proton on the left end, and a hydroxyl on the right end). In this way, the oligomer complies with its definition, which states that it is a faithful polymer made of monomers and that it is in its finished state.

Yes, but then how will ***polyxmass*** manage to calculate the mass of the modified oligomer, like our Oligomer 1 in the case of the cyanogen bromide-mediated cleavage? Simple enough, in a first step it does exactly the same way as for the unmodified oligomer. Next, each oligomer is checked for presence or absence of a methionine residue on its right end. If a methionine is found, the mass corresponding to the "-C1H2S1+O1" chemical reaction is applied. And that's it!

In the previous cyanogen bromide example, the logical condition was involving the identity of the oligomers' right end monomer, but other examples can involve not the right end monomer, but the left end monomer, if some chemical modification was to occur to the monomer sitting right of the cleavage location. In this case the user would have to analyse the situation and provide ***polyxmass*** with the proper chemical reaction by stating something analog to: *if and only if they have a Xyz monomer at their left end* (note the partial analogy with the case described above).

For the moment this is enough polymer cleavage abstraction, as the rest of the description pertaining to the cleavage specification definition is thoroughly detailed at page 52.

Polymer Fragmentation

In a fragmentation process, the bond that is broken is not necessarily the inter-monomer bond. Indeed, fragmentations are oft-times high energy chemical processes that can affect bonds that belong to the monomers' internal structure. This is one of the reasons why fragmentations do differ from cleavages: they are specific of the polymer type in which they occur. Hydrolyzing a protein and an oligosaccharide is just the same process, from a chemical point of view. But fragmenting a protein or an oligosaccharide are truly different processes because the way that the fragmentation happens in the polymer sequence is so much dependent on the nature of each monomer that makes it.

Another peculiarity of the fragmentations, compared with the cleavages that were described above, is the fact that there is no cleaving molecule starting the process. Instead, a fragmentation process is often initiated by an intra molecular electron doublet rearragement that propagates more or less in the polymer structure to eventually break it. Fragmentations are mainly a gas phase process, not some reaction that happens in solution as a result of putting in contact the polymer and some reagent. It is precisely because no cleaving molecule is involved in the fragmentation process that the fragments are not necessarily capped like a normal polymer should be; and this is another really important difference between cleavage and fragmentation.

Let us illustrate these concepts through two examples: proteins and nucleic acids.

Protein Fragmentation

There is a pretty important number of different kinds of fragments that can be generated upon fragmentation of peptides. We are going to detail the most common ones; the user is invited to use the ***polyxmass***' fragmentation-specification grammar to add less frequent (or newly discovered) fragmentation types.

As can be seen from Figure 3.8, the fragmentations do generate fragments of three categories: the ones that include the left end of the precursor polymer (a, b, c), the ones that include the right end of the precursor polymer (x, y, z), and finally the special case in which the fragment is an *internal fragment*, like the immonium ions. When looking at the fragmentations described in the figure it becomes immediately clear why a fragmentation cannot be mistaken for a cleavage: the ionization of the fragment is not necessarily due to the captation of a proton by the fragment. Furthermore, we can also see that a fragmentation is not a cleavage because the fragment that is generated is *absolutely* not necessarily what we call a polymer, in the sense that the fragment might not be capped the same way as the precursor polymer is (in its finished state).

The two observations above should make clear to the reader that calculating masses for fragments is a more difficult process than what was described above for the oligomers. Indeed, while it was simple to calculate the mass of an oligomer (by simply adding the masses of its constitutive monomer units, plus the left and right caps, plus ionization), here there is no chemical formalism generally applicable to all the fragment types. This is why the specification of the fragmentation is left to the user's responsibility.

By looking at Figure 3.8, the reader should have noticed that the fragment naming scheme takes into consideration the fact that the fragment bears the left or the right end of the precursor polymer (or none, also). Indeed, the numbering of fragments holding the left end of the precursor polymer sequence begins at the left end, and for fragments that hold the right end at the right end. Thus the third fragment of series *a* –*a3*– would involve monomers [1→3]; and the third fragment of series *y* –*y3*– would involve monomers [6→4] (in the figure these left-to-right and right-to-left directions are symbolized using arrows). Therefore, it should appear to the reader how important –when specifying a fragmentation– it is to clearly indicate from which end of the precursor polymer the fragment is generated (in ***polyxmass*** jargon this is "LE" for left end, "RE" for right end and "NE" for no end). ***polyxmass*** knows what action it should take when it encounters one of these three specifications; for example, if a "LE" specification is found for a given fragmentation specification, ***polyxmass*** adds to the fragment's mass the mass corresponding to the left cap of the precursor polymer.

Now that the stage is set we can start rationalizing fragment specifications, and thus mass calculations.

***a* fragment series** If we take the *a* fragment series, the Figure 3.8 indicates that the fragments include the left end and that their last monomer lacks its carbonyl group (see, on top of Figure 3.8, that the *a1* arrow goes between the CαH and the CO of monomer 1?). So we would say that each fragment of the *a* series should be challenged with the following chemical treatments: 1) addition of the mass corresponding to the left cap (proton), 2) removal of the mass corresponding to the lacking CO group. This way we have the mass of fragment *a1*. If we were interested in the fragment *a4* we would have summed the masses of monomers 1 to 4, added the mass of the left cap, and finally removed the mass of a CO; that's it. The mass calculation is thus mathematically expressed

$$a_i = LC + \sum_{1}^{i} M_i - CO$$

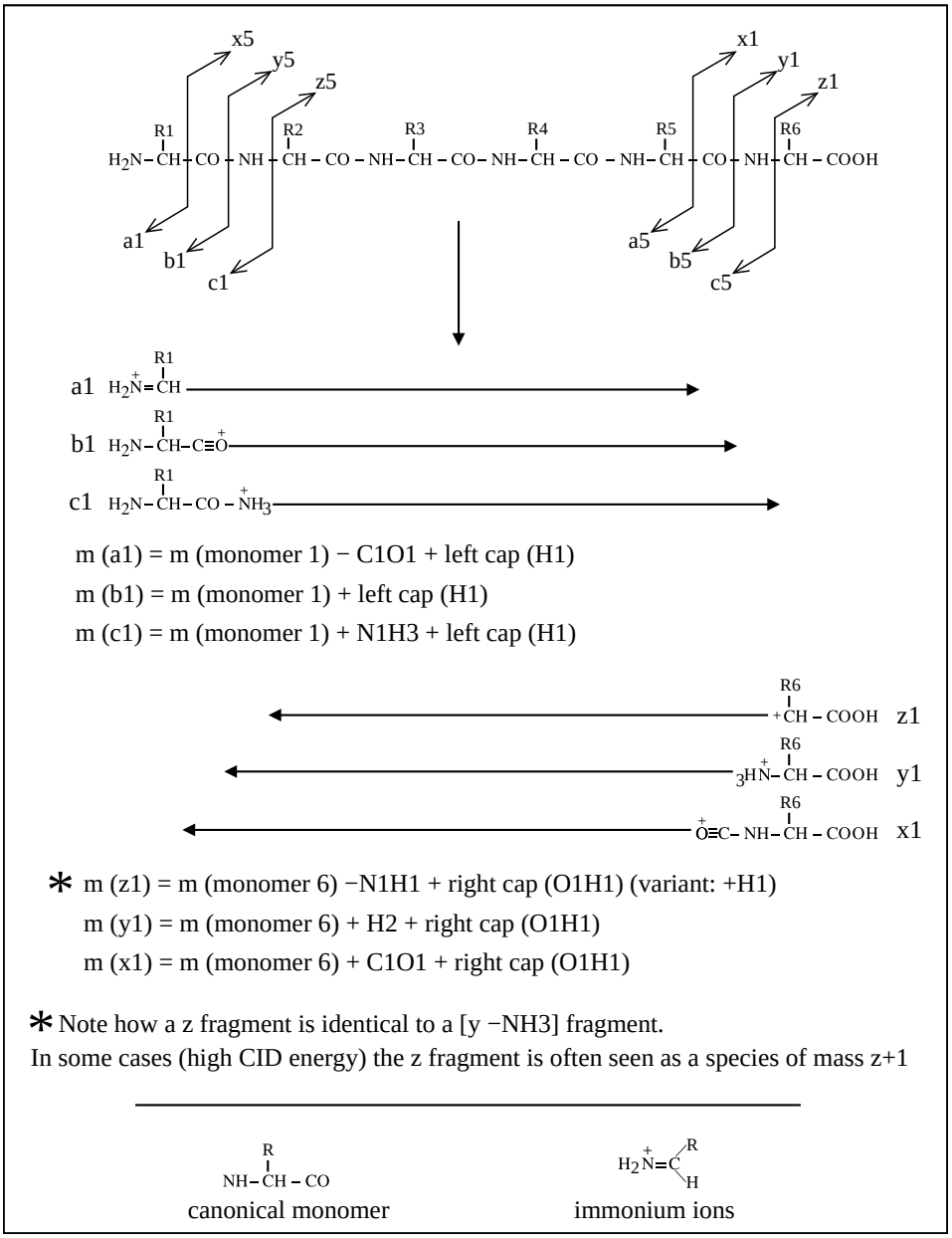

Figure 3.8: **Protein fragmentation patterns most widely encountered.** An hexapeptide is fragmented in the seven most widely encountered manners, such as to generate a, b, c, x, y, z and immonium fragment ions. The figure illustrates the position of the cleavage for each kind of fragment (exemplified using the case of the smallest fragment possible) and the mass calculation method is described for each fragment kind; consider that each fragment bears only *one positive* charge.

***b* fragment series** Similarly, the mass calculation is mathematically expressed

$$b_i = LC + \sum_{1}^{i} M_i$$

***c* fragment series** The mass calculation is mathematically expressed

$$c_i = LC + \sum_{1}^{i} M_i + NH_3$$

***x* fragment series** For this series of fragments we do not add the left cap anymore, but replace it with the right cap, since the fragments hold the right end of the precursor polymer. Note also that the numbering of the monomers using the variable i in the following mathematical expressions goes from right to left (contrary to what happened for the *a, b, c* fragment series. All the fragments that hold the precursor polymer right end are numbered this way, so this applies to fragments *x, y, z*. The mass calculation is mathematically expressed

$$x_i = RC + \sum_{1}^{i} M_i + CO$$

***y* fragment series** The calculation is mathematically expressed

$$y_i = RC + \sum_{1}^{i} M_i - CO$$

***z* fragment series** In low energy CID, the z fragments are expressed this way:

$$z_i = RC + \sum_{1}^{i} M_i - CO$$

which is equivalent to y-NH_3; in high energy CID an additional proton is often measured:

$$z_i = RC + \sum_{1}^{i} M_i - CO + H$$

immonium* fragment series** These fragments are internal fragments in the sense that they do not hold neither of the two precursor polymer's ends. ***polyxmass understands that the user is speaking of this kind of fragment when the "from which end" piece of data –in the fragmentation specification– states "NE" instead of "LE" or "RE" (see page 55). The mass calculation for these fragments does not take into account the monomers surrounding the one for which the calculation is done. The mass for an immonium ion –at position i in the precursor polymer– will be the mass of the monomer at position i, less the mass of a CO, plus the mass of a proton. The mass calculation for these special internal fragments is expressed

$$imm_i = M_i + H - CO$$

Nucleic Acid Fragmentation

The fragmentations that can be obtained with nucleic acid are numerous and it is more complicated than with proteins to describe them fully. The main reason for this is that there are a big number of fragmentation combinations because of the loss of nitrogenous bases from the skeleton. The mechanisms by which this loss happens are fairly complex, and I am not going to detail any of them. Figure 3.9 shows the most common fragmentations (without taking into consideration the potential loss of bases). An example of fragment is given for each fragment series (pretty the same way as we did before for proteins). Note that the fragment representations are aimed at helping the reader to figure out what the product ion is, not taking into account where the negative charge lies on the fragment, since this charge can float around at every de-protonatable group. All the fragments shown bear one and one only negative charge.

The reader might have noticed –at the bottom of the figure– that a provision is made in the case the fragmented molecular species are not 5' end-phosphorylated but 5' end-hydroxylated. Indeed, the canonical monomer is such that, upon polymerization and left capping, the 5' end is phosphorylated. However, oft-times the oligonucleotides are synthesized chemically without the 5' end phosphate group, thus ending in hydroxyl. This special case should be accounted for by applying to all the fragments that bear the left end of the precursor polymer the following chemical reaction: $-HPO_3$. This chemical reaction should be applied *in addition* to the chemical reaction that yields the fragment *per se*.

Exactly as we did for the protein fragments, we are giving below the mathematical expressions used to calculate the mass of different series of nucleic acid fragments; in these calculations we assume that the left end of the precursor polymer is phosphorylated (5' P) and the reader should bear in mind that this precise phosphate might itself be expelled by the fragmentation. The fragment naming scheme consideration that we emitted for protein fragments above (left-to-right or, conversely, right-to-left) applies here also in an identical manner.

***a* fragment series** These fragments most often appear with base loss.

$$a_i = LC + \sum_{1}^{i} M_i - O$$

***b* fragment series**

$$b_i = LC + \sum_{1}^{i} M_i$$

***c* fragment series**

$$c_i = LC + \sum_{1}^{i} M_i - HPO_2$$

***d* fragment series**

$$d_i = LC + \sum_{1}^{i} M_i - HPO_3$$

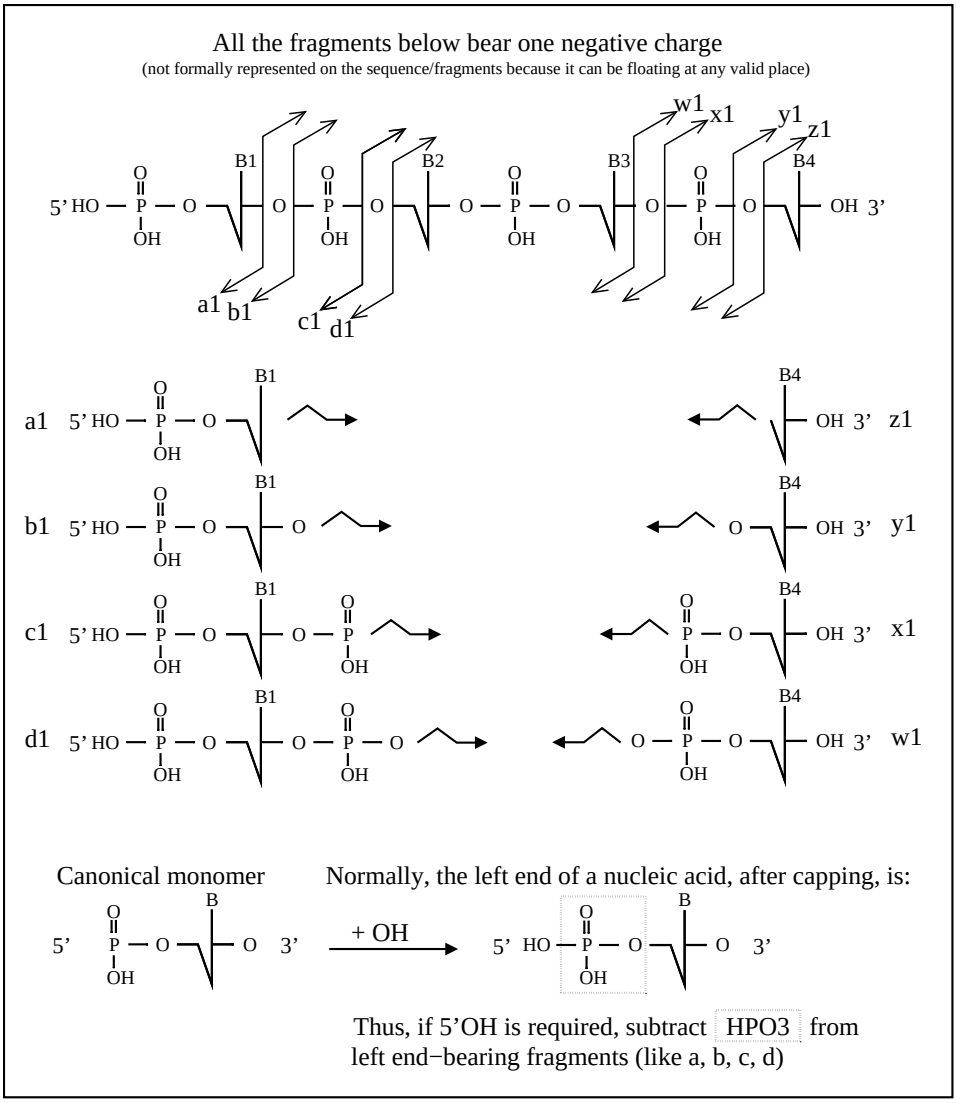

Figure 3.9: **DNA fragmentation patterns most widely encountered.** A short DNA sequence is fragmented in the eight most widely encountered manners, such as to generate a, b, c, d, w, x, y, z fragment ions. The figure illustrates the position of the cleavage for each kind of fragment (exemplified using the case of the smallest fragment possible). and the mass calculation method is described for each fragment kind; considering that each fragment is protonated only once (+1).

***w* fragment series**

$$w_i = RC + \sum_{1}^{i} M_i + O$$

***x* fragment series**

$$x_i = RC + \sum_{1}^{i} M_i$$

***y* fragment series**

$$y_i = RC + \sum_{1}^{i} M_i - HPO_2$$

***z* fragment series**

$$z_i = RC + \sum_{1}^{i} M_i - HPO_3$$

There are also a variety of fragments for which a base is lost. But we cannot describe them all!

More Complex Patterns Of Fragmentation

Before finishing with fragmentations, it is necessary to describe a powerful feature of the fragmentation specification grammar available in ***polyxmass***. This feature was required for the fragmentation of oligosaccharides and also sometimes for proteins. When the fragmentation (the bond breakage reaction itself) occurs at the level of certain monomers, it might be necessary to be able to specify some particular chemistry that would arise on the monomer in question.

We have seen in the cleavage documentation that, upon cleavage of a protein sequence with cyanogen bromide, for example, a particular chemical reaction had to be applied to the oligomers that were generated with a methionine monomer as their right end monomer. Well, in a fragmentation specification it is possible to apply comparable chemical reactions but in a more thorough manner. Indeed, while in the cleavage it was possible to say something like "*apply a given chemical reaction to the oligomer if the right end monomer is Xyz*", in the fragmentation the logical condition can be bound not only to the identity of the currently fragmented monomer, but also (optionally) to the identity of the previous and/or next monomer in the precursor polymer sequence. For example: —"*Apply a given chemical reaction if fragmentation occurs at the level of "Xyz" monomer only if it is preceded by a "Yxz" monomer and followed by a "Zyx" monomer*".

These logical conditions are called *fragrules*. A *fragspecif* can hold as many *fragrules* as necessary. Thus we see that a fragmentation specification is a multi-part specification, with a *fragspecif* optionally integrating *fragrule* objects... All of this is described in great detail at page 55.

To Sum Up

To sum up all what we have seen so far with polymer chain disrupting chemistries:

- ⋆ A polymer sequence gets cleaved into oligomers when a chemical reaction occurs in it at the level of one or more inter-monomer bond(s); monomer-specific chemical reactions can be modelled into the cleavage specification using at most one leftrighrule;
- ⋆ A polymer sequence gets fragmented into fragments when a bond breakage occurs, without the help of any exterior molecule, at any level of the polymer structure, with no limitation to the inter-monomer bond; monomer-specific chemical reactions can be modelled into the fragmentation specification using any number of fragrules;
- ⋆ Oligomers are automatically capped –*on both ends*– using the rules described in the precursor polymer's definition;
- ⋆ Fragments are capped automatically only –*on the end they hold, if any*– using the rules described in the precursor polymer's definition;
- ⋆ Oligomers are automatically ionized (if required by the user) using the rules described in the precursor polymer's definition;
- ⋆ Fragments are never ionized automatically; ionization (gain/loss of a charged group) is necessarily integrated in the fragmentation specification.

4

Basics in Mass Spectrometry

Mass spectrometry has become a "buzz word" in the field of structural biology. While it has been used for long to measure the molecular mass of little molecules, its recent developments have brought it to the center of the analytical arsenal in the field of structural biology (also of "general" polymer science). It is now current procedure to use mass spectrometry to measure the mass of polypeptides, oligonucleotides (even complete transfer RNAs!) and saccharides, amongst other complex biomolecules.

A mass spectrometer is usually described by giving to its three main different "regions" a name suggestive of their function:

- the source, where production of ionized analytes takes place,
- the analyzer, where the ions are electrically/magnetically "tortured",
- the detector, where the ions arrive, are detected and counted.

Before letting Mass Spectrometry in, I would like to state once for all: *mass spectrometry is aware of ionized molecular species only...*

Now, *enter* Mass Spectrometry

Ion Production: The Source

Indeed, mass spectrometry cannot do anything as long as the molecule to analyze (*analyte*) is not in a charged state. The process of creating an ion from an un-charged analyte is called *ionization*. Well, most of the times the ionization is favored by adapting the sample's pH to a value higher/lower than the isoelectric pH of the analyte, which will elicit the appearance of (a) charge(s) onto it. In cases where the analyte cannot be charged by simple pH variations (small molecule that does not bear any ionizable chemical group), the ionization step might require –on the massist's part– use of starker ionization techniques, like electronic impact ionization or chemical ionization. In biopolymer mass spectrometry, the pH strategy is usually considered the right way to proceed. The ionization process might involve complex charge transfer mechanisms (not fully understood yet, at least for certain ionization/desorption methods) which tend to ionize the analyte in a way not predictable by looking at the analyte's chemical structure.

Ion production should not be uncoupled from one important feature of mass spectrometry: solvent evaporation –in case of liquid sample delivery to the mass spectrometer– and sample *desorption* –in case of solid state sample introduction. The general idea is that mass spectrometry works on gas phase ions. This is because it is of crucial importance, for a correct mass measurement to take place, that the analyte be *totally* freed of its chemical immediate environment. That is, it should be "naked" in the gas phase. Equally important is the fact that ions must be capable of travelling long distances without ever encountering any other molecule in their way. This is achieved by pumping very hard in the two regions called "analyzer" and "detector". In this respect, the source is a special region because, depending on the design of the mass spectrometer, it might be partially at the atmospheric pressure during mass spectrometer operation. It is not the aim of this manual to provide insights into mass spectrometer design topics (I just would not be able to enter into the physics details!), but the general principle is that mass spectrometry involves working on gas phase ions. This is why a mass spectrometer is usually built on extremely reliable pumping technology aimed at maintaining for long periods of time (with no sudden interruption, otherwise the detector might suffer seriously) a good vacuum in the conduit in which ions must flow during operation.

The Analyzer

Once an ion has been generated in the gas phase, its mass should be measured. This is a complex physical process. Depending on the mass spectrometer design, the mass measurement is based on more or less complex physical events. Magnetic mass spectrometers are usually thought of as pretty complex devices; this is also the case for the Fourier transform ion cyclotronic resonance devices. An analyzer like the *time of flight* analyzer is much more simple. I will refrain from trying to explain the physics of the mass measurement, just limit myself saying that –at some stage of the mass measurement process– forces are exerted on the ions by electric/magnetic fields (incidentally, this explains why it is so important that an analyte be ionized, otherwise it would not be subject to these fields). The ionized analytes submitted to these forces have their trajectory modified in such a way that the detector should be able to quantify this modification. Roughly, this is the measurement process.

What Is Really Measured?

Prior to entering into some detail, it seems necessary to make a few definitions[1]:

- ⋆ unified mass scale (u): IUPAC & IUPAP (1959-1960) agreed upon scale with 1 u equal to 1/12 the mass of the most abundant form of carbon; the dalton is taken as identical to u (but not accepted as standard nomenclature by IUPAC or IUPAP), it is abbreviaed in Da.
- ⋆ a former unit was "a.m.u." (*i.e.* "atomic mass unit"). It should be considered obsolete, since based on an old 1/16 of ^{16}O standard;
- ⋆ the mass of a molecule (also "molecular mass") is expressed in daltons. The symbol commonly used is "M" (not "m"), as in "M+H" or "M+Na"... Symbol "m" is already employed for ion mass (as in "m/z");
- ⋆ the mass-to-charge ratio ("m/z") of an ion is the ion's mass (in daltons) divided by the number (z) of elementary charges. Hence "m/z" is "mass per charge" and units of "m/z" are "daltons per charge";
- ⋆ nominal mass: the integral sum of the nucleons in an atom (it is also the atomic mass number);
- ⋆ exact (also known as accurate) mass: the sum of the masses of the protons and neutrons plus the nuclear binding energy;

In the previous sections I used to say that a mass spectrometer's task is to measure masses. Well, this is not 100 % exact. A mass spectrometer actually allows to measure something else: it measures the *m to z ratio* of the analyte, which is denoted m/z. What is this "*m to z ratio*" all about? Well, we said above that a mass spectrometer has to exert forces on the ions in order to determine their m/z. Now, let us say that we have an electric field of constant value, E. We also have two ions of identical masses, one bearing one charge (q) and the other one bearing two charges ($2q$) –positive or negative, no matter in this discussion. These two ions, when put in the same electric field E, will "feel" two different forces exerted on them: F_1 and F_2. It is possible to calculate these forces ($F_1 = qE$ and $F_2 = 2qE$). Evidently, the ion that bears two charges is submitted to a force that is twice as intense as the one exerted on the singly charged ion.

What does this mean? It means simply that the numeric result provided by the mass spectrometer is not going to be the same for both ions, since the physics of the mass spectrometer takes into account the charge level on each different analyte. Our two ions weigh exactly the same, but the mass spectrometer simply can not know that; all it knows is how a given ion reacts to the electric field it is put in. And our two ions, evidently, will react differently.

When we say that a mass spectrometer measures a m/z ratio, the z of this ratio represents the sum of all the charges (this is a net charge!) that sit onto the analyte. But what does the m stand for? The molecular mass? No! The m stands for the mass of the whole analyte ion, which is –in a word– the *measured mass*. This is not the molecular mass (which would be M), it is the molecular mass *plus/less* the mass of the chemical entity that brings the charge to the analyte. When ionizing a molecule, what happens is that something brings (or removes) a charge. In biopolymer chemistry, for example, often the ionization is a simple

[1] Interesting posting signed by Ken I. Mitchelhill in the **ABRF** mailing list at `http://www.abrf.org/archives`, and a document published by the California Institute of Technology.

protonation/deprotonation. If it is a protonation, that means that an electronic doublet (on some basic group of the analyte) captures a proton. This brings the mass of a proton to the biopolymer ($\simeq$ 1 Da). Conversely, if it is a deprotonation (loss of a proton by some acidic group, say a carboxylic that becomes a carboxylate) the polymer looses the mass of a proton. Of course, if the ionization involves a single electron transfer the mass difference is going to be so feeble as to be un-measurable on a variety of mass spectrometers.

Let us try to formalize this in a less verbose manner by using a sweet amino acid as an example:

- ⋆ the un-ionized analyte (Glycine) has the following formula: $C_2H_5O_2N_1$;
  the molecular mass is thus $M = 75.033$ Da;
- ⋆ the analyte gets protonated in the mass spectrometer:

  $$C_2H_5O_2N_1 + H \rightharpoonup C_2H_6O_2N_1$$

  the measured mass of the ion is thus $m = 75.033 + 1.00782$ Da and the charge beared by the ion is thus $z = +1$.
- ⋆ the peak value read on the mass spectrum for this analyte will thus be:

  $$\text{value} = \frac{m}{z} = \frac{M + 1.00782}{z} = 76.04$$

  with $z = +1$

We see here that the label on the mass spectrum does not correspond to the nominal molecular mass of the analyte: the ionizing proton is "weighed" with the Glycine molecule.

Imagine now that, by some magic, this same Glycine molecule just gets protonated a second time. Let's do exactly the same type of calculation as above, and try to predict what value will be printed onto the mass spectrum:

- ⋆ the un-ionized analyte (Glycine) has the following formula: $C_2H_5O_2N_1$;
  the molecular mass is thus $M = 75.033$ Da;
- ⋆ the analyte gets protonated in the mass spectrometer *two times*:

  $$C_2H_5O_2N_1 + 2H \rightharpoonup C_2H_7O_2N_1$$

  the molecular mass of the ion is thus $M = 75.033 + 2.01564$ Da and the charge beared by the ion is thus $z = +2$.
- ⋆ the peak value read on the mass spectrum for this analyte will thus be:

  $$\text{value} = \frac{m}{z} = \frac{M + 2.01564}{z} = 38.52$$

  with $z = +2$

Oh! yes!, this time it is absolutely clear that a m/z is not a molecular mass! By the way, if the Glycine happened to be ionized *negatively* the calculation would have been analogous to the one above, but instead of *adding* the mass of the proton(s) we would have *removed* it. It is that simple.

Summing up all this in a few words: an ionization involves one or more charge transfer(s) and in most cases (at least in biopolymer mass spectrometry) also involves matter transfer(s). It is crucial *not* to forget the matter transfer(s) when ionizing an analyte. This means that when an ionization process is described, its description ought to be complete, clearly stating three different pieces of information:

- the charge transfer (net charge that is beared by the analyte after the ionization has completed);
- the matter transfer (optional; usually something like "+H1");
- the ionization level (0 means "no ionization"; usually this would be 1 for a single ionization, but might be as large as 30 if, for example, you were ionizing myoglobin with electrospray ionization (protonation). In this case the m/z value would be computed this way:

$$\text{value} = \frac{m}{z} = \frac{M + 30 \cdot \ 1.00782}{30} = \frac{16959 + 30.2346}{30} = 566.30$$

with $z = +30$

By now, the reader should have grasped the importance of understanding well the ionization formalisms for accurately predicting/analyzing mass spectrometric data!

In the next chapters of this manual we will describe how ***polyxmass*** works and how the user might take advantage of its powerful capabilities. In a first chapter I will introduce some general concepts around the way the program behaves. Next, in the remaining part of this manual, a chapter will be dedicated to each important ***polyxmass*** function or characteristic.

5

polyxmass Generalities

In this chapter, I wish to introduce some general concepts around the ***polyxmass*** program.

General ***polyxmass*** Concepts

The ***polyxmass*** mass spectrometry software suite has been designed to be able to "work" with every polymer on earth. Well, in a certain way this is true... A more faithful account of the ***polyxmass***' capabilities would be: "*The* ***polyxmass*** *software suite works with whatever polymer chemistry the user cares to define; the more accurate the polymer chemistry definition, the more* ***polyxmass*** *will be accurate*". Sounds like much of the responsibility for the proper functioning of the ***polyxmass*** framework is in the hands of the user? That is true! However, with ***polyxmass*** the user has a framework at hand to define polymer chemistries so as to suit his needs.

The main concept that drove the design of the entire ***polyxmass*** framework is *abstraction*. Indeed, for the program to be able to understand a variety of possibly very different polymers, it had to be written using some *abstraction layer* between the way masses are computed and the way the polymer is described "in memory". This abstraction layer is implemented by using a "polymer chemistry definition-driven" set of functionalities. The polymer chemistry definition drives all the mass computations, all the polymer sequence editing, all the polymer chemistry reactions... This is how the ***polyxmass*** software suite makes it possible to handle any polymer type. To implement this abstraction paradigm, the ***polyxmass*** mass spectrometry framework was designed to be modular, as described below.

The ***polyxmass*** mass spectrometry software suite comprises the following packages (not all of them installing actual executable programs):

1. ***libpxmutils*** where housekeeping functions are implemented; this library is not graphical and of little interest to the pure chemist;

2. ***libpxmchem*** where all the chemical intelligence of the ***polyxmass*** software framework lies; this library is not graphical and may be interesting to the chemist so as to understand what a *monomer* or an *oligomer* is, from a programmatic standpoint;

3. ***polyxmassdata*** where all the configuration files are stored, like the different sample polymer chemistry definition files, the little graphics files that are used in the polymer sequence editor to render and display graphically the polymer sequence in a polymer chemistry definition-specific manner...

4. ***polyxdef*** where the user will easily define brand new polymer chemistries, which will produce a *polymer chemistry definition*, later saved in a *polymer chemistry definition file*; this module is an executable graphical user interface file;

5. ***polyxcalc*** where the user will easily perform sophisticated mass calculations either using an available polymer chemistry definition or simply using the predefined set of atoms; this module is an executable graphical user interface file;

6. ***polyxedit*** where the user will easily create/edit polymer sequence files that are of any available polymer chemistry definition, so that mass spectrometric simulations may be performed; this graphical user interface module is the core module for all the user-driven chemical reaction simulations, like modifying a monomer, cleaving the polymer sequence, gas phase fragmenting an oligomer...

The fact that the ***polyxmass*** software suite is able to handle any polymer chemistry is, as we said above, due to its ability to interface a polymer sequence with a polymer chemistry definition. To explain this clearly, imagine a protein sequence that would be this tetrapeptide: "ATGC", which reads as "AlanineThreonineGlycineCysteine". Now imagine a DNA sequence: "ATGC", which reads as "AdenineThymineGuanineCytosine". The two sequences would be entered in a sequence editor by keying in the following key sequence: A T G C. But, of course, you'd expect that the masses for the DNA sequence be much higher than the masses for the protein sequence.

This is where abstraction comes in, and modularity also. In order to let the user perform as flexibly as possible the required computations, she first defines two different polymer chemistries: the first named "protein" and the second named "dna". In each of the polymer chemistry definitions, the user will enter a formula corresponding to each monomer (A,T,G,C). Of course the monomer formula for a Threonine is very different than the one for a Thymine. This is performed in the ***polyxdef*** module (here is modularity). Once a polymer chemistry definition is saved, it may be made available to the system (we'll see how this is done). And when a polymer chemistry definition is made available to the system, any new polymer sequence may be created that abides by this polymer chemistry definition. By having all the polymer chemistry specifications in a polymer defintion file, the ***polyxmass*** mass spectrometry software suite is able to deal with any polymer sequence that complies with the given polymer chemistry definition. This association between a polymer sequence and a polymer defintion is the *abstraction layer* that we mentioned above. Once this is well understood, the originality of the ***polyxmass*** software framework is understood. This is precisely what sets ***polyxmass*** apart from the other mass spectrometry-related software offerings.

Since the different functionalities offered by the ***polyxmass*** framework are well confined in three graphical user interface modules, we'll review each of such modules in the later chapters.

Before going on with the description of the different modules, I would like to introduce some other more chemistry-oriented concepts that are going to be used throughout the ***polyxmass*** framework.

On Formulae And Chemical Reactions

It is all the more frequent for any user who runs any of the ***polyxmass***' modules to make use of formulae or of chemical reactions. These two chemical entities are not identical in ***polyxmass***. While a formula represents a chemical status (a monomer has a given formula, and does not change it), a chemical reaction is something much more dynamic, I should say "active".

This difference is very important in ***polyxmass***. Let's take an example: the Lysyl monomer (we call a protein "residue" a "monomer") has the following formula: $C_6H_{12}N_2O$. If I wish to acetylate this Lysyl monomer, the reaction will read this way: "An acetic acid molecule will condense onto the amine of the Lysyl side chain". This can also read: —*"An acetyl group enters the Lysyl side chain while a hydrogen atom leaves the Lysyl side chain; water is lost in the process"*. If we wanted to put this into a more chemistry-oriented representation, we could write this:

$$R - NH_2 + CH_3COOH \rightleftharpoons R - NH - CO - CH_3 + H_2O$$

That is more briefly stated this other way: "$-H_2O + CH_3COOH$". This is exactly what ***polyxmass*** calls an *"actionformula"* –or, for brevity– an *"actform"*. Simply because there are actions that are associated with formulae; here the H_2O formula is associated with the $-$, which indicates that the water molecule leaves the molecules being reacted, while the CH_3COOH formula is associated with the $+$, which means that the acetic acid molecule enters in to the target molecule. The net formula is thus, as stated earlier: —*"An acetyl group enters the Lysyl side chain while a hydrogen atom leaves the Lysyl side chain; water is lost in the process"*.

The *formula* and *actform* chemical entities are *not* interchangeable in the ***polyxmass*** framework.

The ***polyxmass*** Framework Data Format

All the data in the ***polyxmass*** framework are stored on disk as *XML*-formatted files. *XML* is the *eXtensible Markup Language*. This "language" allows to describe the structure of a document. Have you ever opened an *HTML* file with a text editor? If so, you have certainly seen some markup like `<H1>This is the title</H1>`. The browser that loads this file will understand (because it has been programmed to do so) that the title "This is the title" is to be displayed onto the screen using a bold sans-serif font, for example. Well, let us just say that the *XML* file format is an immensely more powerful equivalent of *HTML*.

There would be a lot... a lot to say about *XML* and *Document Type Definition*s: I'll refrain from entering into the details.

The big advantage of using such *XML* format in ***polyxmass*** is that it is a text format, and not a binary one. This means that any data in the ***polyxmass*** package is human-readable

(even if the *XML* syntax makes it a bit difficult to read data, it is actually possible). Try to read one polymer chemistry definition `.xml` file from the ***polyxmassdata*** package (say, the `protein-sample.xml` file, for example), and you'll see that this is pure text (the same applies for the `.pxm` polymer sequence files in the same package. The advantages of using text file formats, with respect to binary file formats are:

- ⋆ if somebody sends you a file and you do not have the program that made it, you still can extract information from the file, because it is readable by any text editor;
- ⋆ if a text file (such as your most important polymer sequence *XML* file) gets corrupted for some reason (*i.e.* during backup on a bad support, or whatever) you will still be able to extract from the corrupted file all the bits of information that surround the portion that is corrupted, thus minimizing the data loss. This would be impossible with binary files, as they are just totally useless if a single part of them is corrupted;
- ⋆ imagine you would like to write down a simple script that would allow you to find –in a given directory– all the sequence files that contain the "myo" character string in the polymer's name field (in *XML* a field is called *element*). You can do it easily *without* asking anybody for the file format specification –because your sequence files are just text files.

As an example of how simple it is I'll just write a ***bash*** shell script below that I'll save into the `polname-find.sh` file in order to execute it afterwards. That is how the shell script looks like in the `polname-find.sh` file:

```
bash-2.04 $ cat polname-find.sh ↩
```

```
for i in *.pxm
  do grep "<name>.*myo.*</name>" $i ;
  if [ $? == 0 ]
    then
      echo "in file $i"
  fi
  done
```

Now we should make this brand new file executable so we can run it:

```
bash-2.04 $ chmod u+x polname-find.sh ↩
```

Upon execution of this script, the output looks like this:

```
bash-2.04 $ ./polname-find.sh ↩
```

```
<name>myoglobin-horse</name>
in file myoglob-h.pxm
<name>myosin-chicken</name>
in file myos-chck.pxm
<name>myo-fragment1</name>
in file myofrag1.pxm
<name>apomyoglobin-rabbit</name>
in file apomyo-rbt.pxm
```

The script has gone through all the `*.pxm` files and for each file has searched a start tag `<name>` followed by some string containing "myo" followed by the end tag `</name>`. If "myo" is found, the corresponding line is printed to the screen, and the name of the file containing this pattern is printed also.

With a binary file format this would simply have been impossible. This little script lets you screen a big database like a snap. That's the power of *UNIX* and *UNIX*-like operating systems.

Editing the Data in ***polyxmass*** Files

The aim of ***polyxmass*** is to let people use the software the way they like, with no preconception on the way they interact with it. The *XML* files (polymer sequence or polymer chemistry definition files) can be edited using the graphical interface but also using a simple text editor. Figure 5.1 shows two rather different means to the same end: editing a polymer chemistry definition file. The Document Type Definition (DTD) is not shown on the right pane of the figure, since it is at the top of the file being displayed. This DTD will help the user to determine how to edit the file in a safe way, by telling where each element is authorized to be, and so on... You'll need to learn *XML* if you wish to understand the DTD (a sunday afternoon will suffice). Usually, the safer way to do any editing is by using the graphical interface, not because the ***polyxmass*** framework understands the edited data better this way, but because the graphical interface layout (acting like a data correctness censor) just prevents the user from writing badly-formed data directly in the *XML* file.

The example shown in Figure 5.1 can be transposed to the polymer sequence *XML* files in a very same way. Of course all the process that leads to "creating" a new polymer chemistry definition is going to be explained in detail in a later chapter(see chapter 6, page47).

General Polymer Element Naming Policy

Unless otherwise specified, it is *strongly* suggested *not* to insert any non-alphanumeric-non-ASCII character (space, %, #, $...) in the strings that the user enters to identify polymer chemistry definition items. This means that, for example, the user must refrain from using non-alphanumeric-non-ASCII characters for the atom name and symbol, the name, the code or the formula of the monomers or of the modifications, or of the cleavage specifications, or of the fragmentation specifications... It is important not to cripple these polymer data for two main reasons:

- ⋆ so that the program performs smoothly;
- ⋆ so that the results can be easily and clearly displayed when time comes to print all the data.

Graphical Interface Design

For those coming to *UNIX* after having used *MS Windows* (like me), I would like to state some general graphical interface design specificities of the *UNIX* world. The *MS Windows* graphical environment was designed in such a way that the user is very strictly restricted

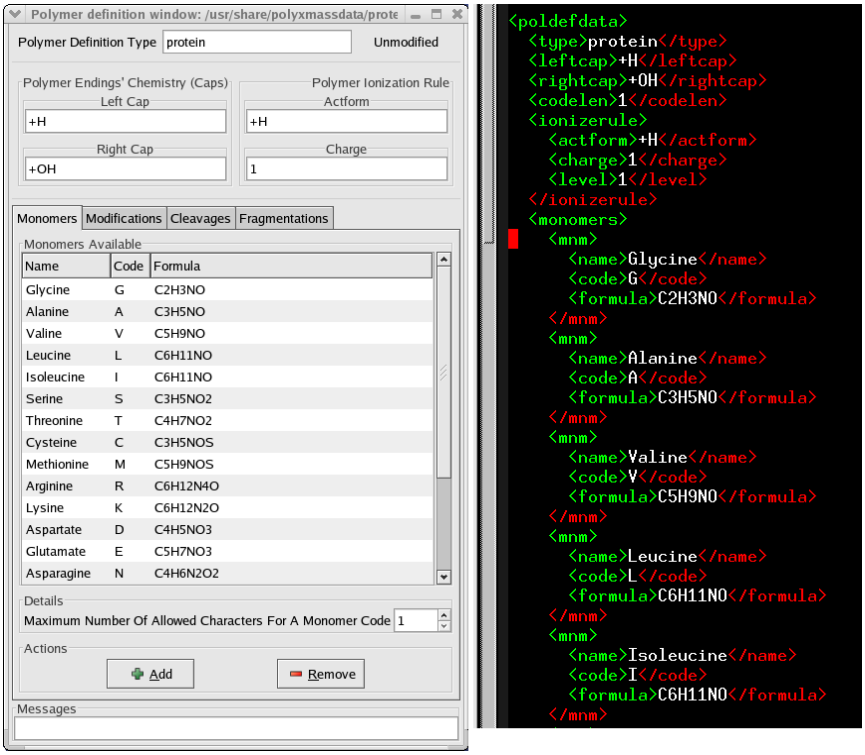

Figure 5.1: **Comparison of a graphical and a text way of editing a polymer chemistry definition file.** The left pane shows the graphical interface that is exposed to the user when defining a polymer. The right pane shows the same *XML* file opened in the `Emacs` editor with the *XML* editing mode switched on.

to a narrow path each time she initiates an action. That policy has often led to arbitrary limitations in the design of software running on the *MS Windows* systems.

This is not going to be exactly the same with a *UNIX* graphical environment: you almost certainly are going to quickly have a great number of windows opened on your desktop; you are the one who knows when to close a results window, not the program designer. When a window is opened, it is not going to be systematically required that it be closed before opening another one. This has a simple reason: imagine that you wanted to compare the oligomers generated by using two different enzymes on the same polymer sequence; you'll need both results windows to be opened at the same time, otherwise how comparison of oligomers could happen? That reasoning is true for a number of situations, and –yes– you'll be responsible for closing the windows you do not need anymore!

This general behaviour is highly desirable, since it indeed allows the user to make comparisons between the data from two different experiments right after having generated the data. But this behaviour introduces a risk: how will it be possible to ascertain that any given set of peptides does come from the cleavage of the first protein using cleaving-agent-1 and not from the cleavage of the first protein using cleaving-agent-2? In other words: how are you going to recognize which results window contains the peptides of the first cleavage, and which other results window contains the peptides obtained from the second cleavage? There is an answer: each time a window is displayed –if there is a risk of ambiguity– it will show the identity of the polymer to which it is related. This identity is nothing else than the *unique* memory address of the polymer to which the window is related.

In any situation where an ambiguity exists about the identity of the data generated on any given polymer sequence, a traceability system is used, as shown in Figure 5.2.

Feedback From ***polyxmass*** To The User

Something very specific to the *UNIX* and *UNIX*-like systems (and that I really like) is the fact that the programs are usually designed to be "verbose" (if the user asks this). The usual means to giving feedback in other systems is to pop up a "dialog" window in which a message is displayed, and the user has to acknowledge in order to close the dialog window. ***polyxmass*** has been implemented with the "console" philosophy in mind: every message that it wishes to "hand out" to the user is sent to the console window from which the program was started.

There are two levels of very important messages: the *CRITICAL* and the *ERROR* level messages. The CRITICAL messages indicate that time has come to make a quick save of all the data, because something bad might happen. ERROR messages cannot even be read in the console window, because they elicit an abortion of the program. These abortions are voluntary on the ***polyxmass***' part, because the error is so bad that it would crash anyway soon or later.

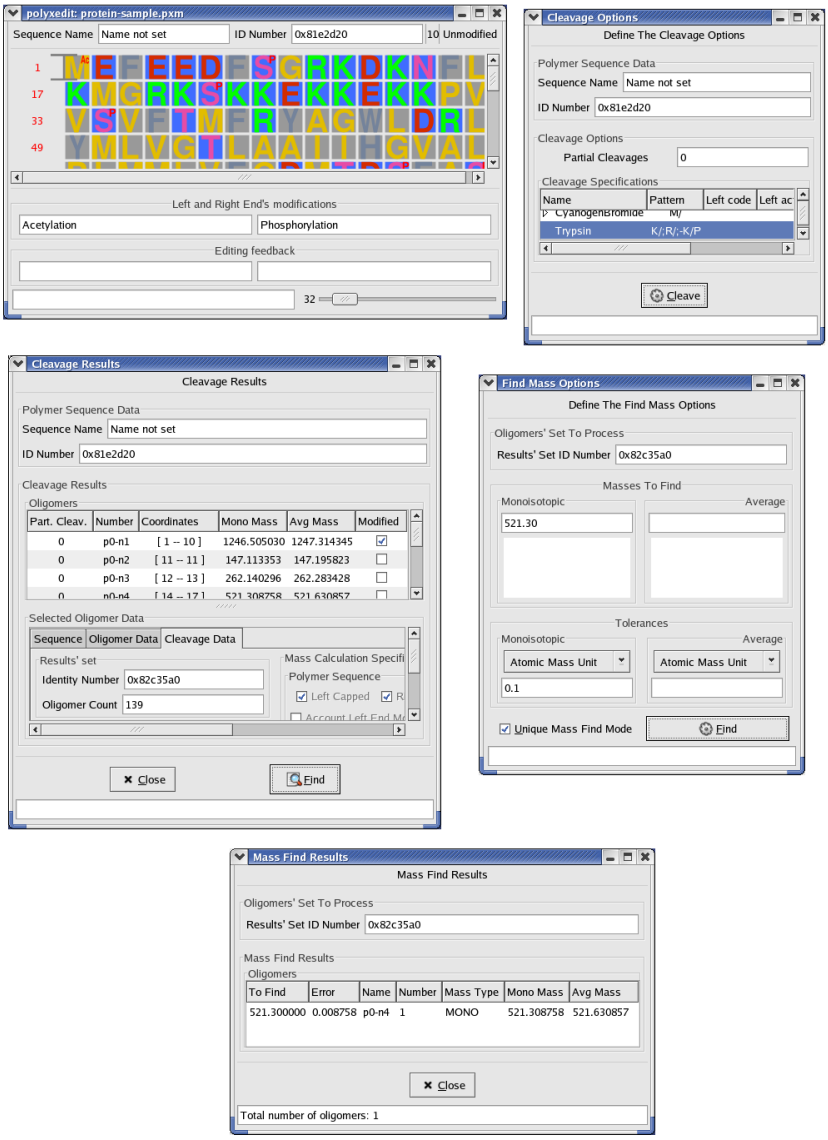

Figure 5.2: **Unambiguous identification of polymer sequences and related data.** When a polymer sequence is loaded/created, it is assigned a numeric value that unambiguously identifies it (for the programmer, this is the pointer to the polymer structure). Each time a window is displayed that contains data pertaining to any given polymer sequence (oligomers generated by cleavage of a given polymer sequence, for example), it is given a reference to the polymer whence the data came, and this reference is the polymer's identity number. This is clearly visible in this Figure, where the sequence has a number 0x81e2d20 and all the related windows display the same number. Note that the cleavage results data have another identifying number (0x82c35a0) that is later used to trace the mass find results data (last bottom window).

6

The polyxdef module: Definition Of Polymer Chemistries

After having completed this chapter you will be able to accomplish the very first steps needed to use the ***polyxmass*** framework's features at best. In order to use the program, indeed, it is required that the polymer on which you would like to experiment be defined according to a number of rules that will be detailed in the remaining sections of this chapter.

polyxdef Invocation

The ***polyxdef*** module is simply called by its name: polyxdef from a command line. The user is invited to launch the following command and to inspect the various options that it accepts:

```
bash-2.04 $ polyxdef --help ↩
```

This command produces the following output:

```
Usage: polyxdef [OPTION...]
  -d, --details     prints the copyright owner and the licensing
                    of the program
  -l, --license     prints the license type of the program
  -v, --version     prints the version of the program

Help options:
  -?, --help        Show this help message
  --usage           Display brief usage message
```

Various Identification And Singular Data

"Identification data" are pieces of information that should be defined in order to describe the polymer (these are non-chemical pieces of information). For example, an identification datum is the polymer chemistry definition type. "Singular data" are pieces of information that are not present in more than one copy in the polymer definition. An example of a singular datum is the string that describes how the elongating polymer sequence should be left- or right-capped so that it gets in its "finished state", after the polymerization has terminated.

Looking at Figure 6.1 while reading the following paragraphs might help. This and subsequent figures illustrate the process by which a polymer chemistry definition "protein" is defined.

As the reader can see, there are a number of identification and singular data to be entered at the top of the polymer chemistry definition window; these are described in the list below:

- ⋆ Polymer Definition Type **protein** String describing the type of the new polymer chemistry definition being elaborated;
- ⋆ Polymer Ending's Chemistry (Caps) Description of the chemical capping reaction that should happen on both the left and the right ends of the polymer sequence, once it is successfully polymerized and should be set to its "finished state". This chemistry is divided into two pieces of information:
  - ✦ Left Cap **+H** String describing the actform that should be applied to the elongating polymer on its left end;
  - ✦ Right Cap **+OH** String describing the actform that should be applied to the elongating polymer on its right end;
- ⋆ Maximum Number of Allowed Characters For A Monomer Code **1** This integer value indicates the maximum number of characters that may be used to describe monomer codes. See below for details about this critical value;

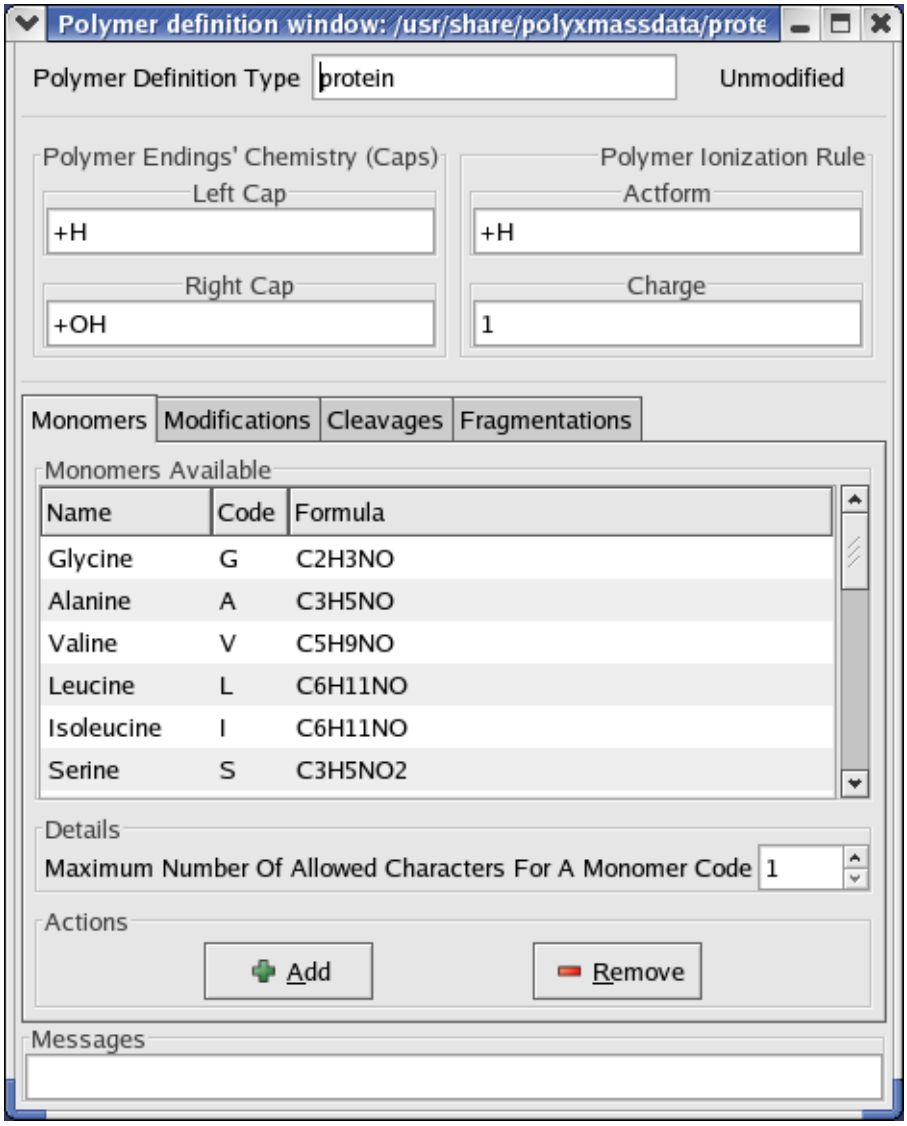

Figure 6.1: **Interface for the definition of the polymer, monomers.** This window shows two different parts, the top half is for the user to enter the polymer identification and singular data, and the bottom part is specialized for the plural data (here showing monomers definition tab). The figure shows how the data should be entered. For example, no double quotes are required when entering strings. Finally, a field is reserved for the number of characters allowed to describe a monomer's code (bottom of the window).

- Polymer Ionization Rule This rule describes the manner in which the polymer sequence should be ionized by default, when the mass is calculated. This rule actually holds two elements:
  - Actform **+H** String describing what chemical reaction should be applied to the polymer in order to ionize it. Here we ask that all the proteins be protonated once by default;
  - Charge **1** Signed numerical value indicating what charge the polymer will hold once the ionization rule's actform has been applied to it. Here, it is asked that the proteins bear one positive charge after that the default mono-protonation mentioned above has taken place.

Now that we have defined the identification and singular data for the polymer, we will go on with another type of data: "plural data". Conversely to what said previously about singular data, plural data are pieces of information that can be present in more than one copy in the polymer chemistry definition. An example of plural data is the data pertaining to the monomers. Of course, if your are working on polystyrene, you will almost certainly have one monomer in your polymer chemistry definition. But what if you work on DNA or proteins? Let us see what plural data are all about.

Various Plural Data

The Monomers

The monomers are the constitutive blocks of the polymer sequence. Their definition should be done with great care, as all the mass calculations are based on the formulae of the defined monomers. Remember that in our ***polyxmass***' jargon, "monomer" stands *not* for the molecule that you bought from the chemicals vendor in order to synthesize the polymer; it stands for this molecule *less* the chemical group(s) that left it when the polymerization occurred. If this sounds strange to you, you definitely should read chapter 3, page 15 for a detailed explanation of the ***polyxmass*** specialized words.

The lower part of Figure 6.1 shows how easy it is to define a new monomer. This is as easy as entering three strings in each column of a row (that may be created by clicking onto the Add button). Note that none of the two Name and Formula strings are limited in size. You could give a monomer a name two gigabytes-long... Of course this would not make much sense.

The case of the Code string is a bit more complicated and depends on the value that is entered in the Maximum Number of Allowed Characters For A Monomer Code field. In our example, this value is **1**, which means that we are allowed to use only one character to describe a monomer's code. Thus, we can see in the figure that all the monomers have a single-character code. It is possible however, to use another value, for example 3. In this case there is a general rule which is enforced in ***polyxdef***: *"The first character of a monomer code must be uppercase, while the remaining characters (if any) must be lowercase"*. That means that in our example of 3-character codes, "A", "Al", "Ala" would be perfectly fine, while "Alan", "AL", "a", "AlA" would be wrong.

The mechanism here is highly sophisticated, contrary to what may look like, because you have to imagine what goes on in the different ***polyxmass*** modules, in particular in the polymer sequence editor (***polyxedit***): how are monomer codes keyed in if "A" and "Ala"

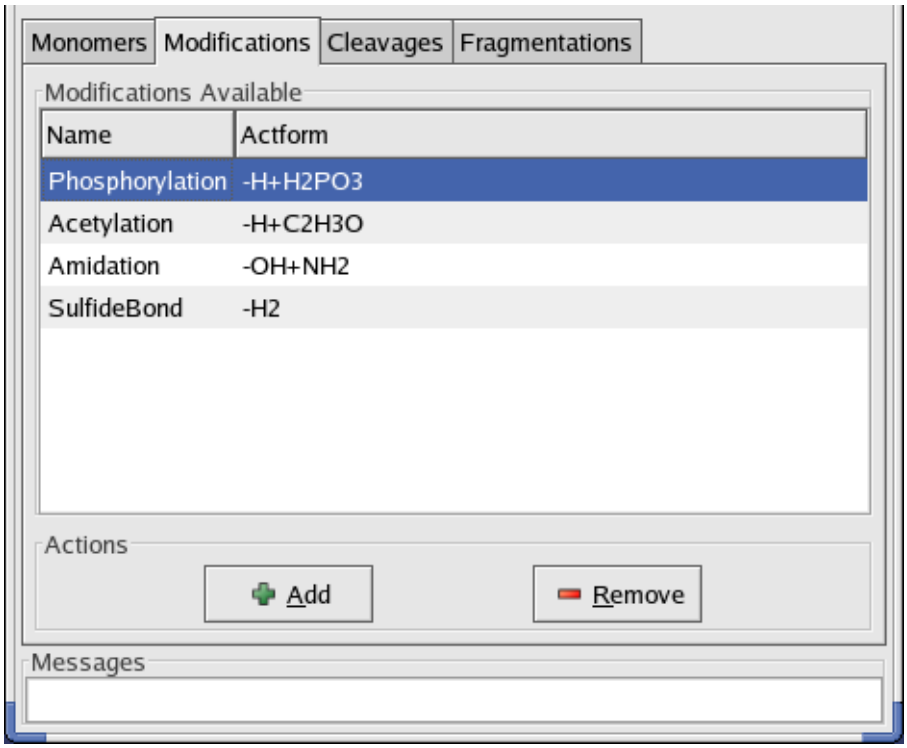

Figure 6.2: **Interface for the definition of the polymer modifications.** This is the same window as for Figure 6.1, but this time the modifications definition tab of it is shown. This figure shows that a modification is simply defined by two strings, a Name string and an Actform string.

are valid monomer codes in a polymer chemistry definition? The magic is described in the chapter about ***polyxedit***.

Not conforming to the instructions above will yield unpredictable results.

The Modifications

Oft-times a polymer will be modified chemically by the user. This is especially true when the user tries to mimick polymer chemical modifications that arise in biochemical processes, in particular regulatory modifications, like protein phosphorylations, for example. Indeed, a biopolymer is modified more often than not. A modification can be a phosphorylation onto a protein residue (on an alcohol function-bearing residue) like a serine, for example, or an acetylation onto a amino function-bearing residue. The ***polyxmass*** mass spectrometry framework gives the user the entire freedom to define any number of modifications. Let us see how; once again, looking at Figure 6.2 will help.

The Figure 6.2 shows, amongst others, how a *Phosphorylation* modification is defined. Most evidently, a modification is defined by a Name string (of unlimited length) and by an Actform string (of unlimited length). The syntax of an actform should by now be somewhat familiar to the reader. In the *phosphorylation* case, it can be read like this: —*"The polymer*

looses a proton and gains H2PO3". When the polymer is modified with this modification, its masses will change by the mass corresponding to this "reaction". Of course, the fact that the actform is written this way is related to the fact that a chemist always thinks in terms of "leaving" and "entering" groups. However, a user might perfectly write "+HPO3" instead of "-H+H2PO3". Both actforms are exactly identical from a molecular mass point of view (and thus also from the ***polyxmass***' point of view).

The Cleavage Specifications

It is common practice –in biopolymer chemistry, at least– to cut a polymer into pieces using molecular scissors like the following:

- proteases, for proteins;
- nucleases, for nucleic acids;
- glycosidases, for saccharides...

For each different polymer type, the molecular scissors are going to be somewhat specific. Indeed, a protease will almost certainly be unable to cleave whatever polysaccharide. The specificity of a cleaving enzyme is thus something that should be described in each polymer chemistry definition, since this specificity is indeed polymer chemistry-specific. Here we show the way that the user can define the cleavage specificity of a molecular scissor. As usual, looking at Figure 6.3 might help in reading the following paragraphs.

By looking at this figure, it should be obvious that defining a cleavage specification gets a little more involved than what we saw earlier for modifications. This is true only for certain chemical reagents that modify the substrate they cleave, which is not that frequent. In the Figure 6.3, the first cleavage specification is "CyanogenBromide" (note that there is no space between *Cyanogen* and *Bromide* in the Name column entry).

Let us analyze the data entered by the user in order to fully qualify this cleavage agent (which, conversely to the other ones listed in the Name column of the treeview shown in the figure, is not a protease but a chemical reagent):

- Name **CyanogenBromide** This is merely the name of the cleavage agent;
- Pattern **M/** This tells the ***polyxmass*** framework where to cleave in the polymer sequence when a CyanogenBromide cleavage is asked. The syntax of the cleavage pattern is detailed below;
- Left Code and Left Actform (Empty) This is a special case for those cleavage agents that not only cut a polymer sequence (usually it is a hydrolysis) but that also modify the substrate in such a way that must be taken into account by ***polyxmass*** so that it computes correct molecular masses for the resulting oligomers. These rules are optional. However, if Left Code is filled with something, then it is compulsory that Left Actform be filled with something valid also, and conversely;
- Right Code and Right Actform **M** and **-CH2S+O3**, respecively. Same explanation as above. Here, what we say is that each oligomer resulting from the cleavage of the polymer sequence at a "M" monomer should be modified using the Right Actform actform. Since the cleavage occurs right of "M", it is logical that a "M" is found right of the oligomer that was generated upon a "CyanogenBromide" cleavage. A special case in which a "M" may be found at the right end of an oligomer, without resulting from a

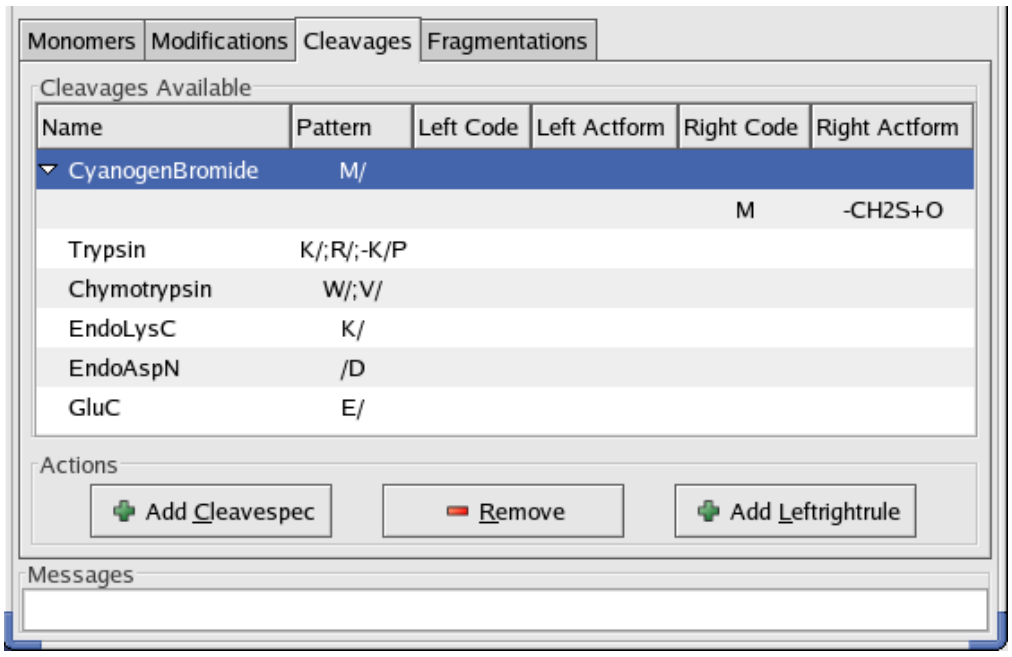

Figure 6.3: **Interface for the definition of the polymer cleavage specifications.** This is the same window as for Figure 6.1, but this time the cleavage specifications definition tab of it is shown. This figure shows that a cleavage specification is defined in a more complex way than previously described for monomers or modifications; see text for further details.

polymer sequence cleavage, is if the "M" was at the right end of the polymer sequence. Of course this case is evaluated and if it is found, the the actform is not applied.

In order to best explicate the cleavage specification pattern syntax I shall provide below some examples:

- ⋆ **Trypsin = K/;R/;-K/P** *"Trypsin cuts right of a K and right of a R. But it does not cut right of a K if this K is immediately followed by a P"*;
- ⋆ **EndoAspN = /D** *"EndoAspN cuts left of a D"*;
- ⋆ **Hypothetical = T/YS; PGT/HYT; /MNOP; -K/MNOP** *"Hypothetical cuts after T if it is followed by YS and also cuts after T if preceded by PG and followed by HYT. Also, Hypothetical cuts prior to M if M is followed by NOP and if M is not preceded by K".*

Please, *do* note that the letters above correspond to monomer codes and *not* to monomer names. If, for example, we were defining a "Trypsin" cleavage specification pattern –in a protein polymer chemistry definition with the standard 3-character monomer codes– we would have defined it this way: "Trypsin = Lys/;Arg/;-Lys/Pro".

Now comes the time to explain in more detail what the Left Code and Left Actform (along with the Right siblings) are for. For this, we shall consider that we have the following polymer sequence (1-character monomers codes):

THIS**M**WILL**M**BECUT**M**ANDTHAT**M**ALSO

If we cleave this polymer using "CyanogenBromide" and if the cleavage is total,[1] we shall get the following oligomers:

THIS**M** WILL**M** BECUT**M** ANDTHAT**M** ALSO

But if there is a partial cleavage, we would *also* get one or more of these oligomers:

THISMWILL**M** BECUTMANDTHAT**M** ALSO WILLMBECUT**M** ANDTHATMALSO

and so on...

Now, the biochemist knows that when a protein is cleaved with cyanogen bromide, the cleavage occurs effectively right of monomer "M" (this we also know already) *and* that the "M" monomer that underwent the cleavage is changed from a methionyl residue to an homoseryl residue (this chemical change involves this actform: "-CH2S+O"). The following two lines of oligomers should definitely "undergo the actform", one time only for each oligomer:

THIS**M**, WILL**M**, BECUT**M**, ANDTHAT**M**

and

THISMWILL**M**, BECUTMANDTHAT**M**, WILLMBECUT**M**

while the two oligomers shown below should not "undergo the actform" because (even if one of them does contain a "M" monomer) the cleavage *did not occur* at a this "M" monomer:

[1] Cleavage occurs at every possible position, right of each monomer "M".

ALSO ANDTHATMALSO

This example should clarify why we clearly indicate –in the cleavage specification for "CyanogenBromide"– that the oligomers resulting from this cleavage should "undergo the '-CH2S+O' actform" *only if they have a "M" as their right end monomer code*.

This would be of crucial importance, if we had a cleavage agent that would cleave not only right of "M" but at some other places: we really would need to specify these rules in a careful way. For example, imagine you had noted –in your many cyanogen bromide experiments– that more often than rarely cyanogen bromide would cleave right of "C" (cysteine) residues, but with no chemical modification of the "C" monomer.[2] In this case, you would be glad that the possibility is given to you to specify that the generated oligomers should "undergo the '-CH2S+O' actform" only if they have a "M" as their right end monomer, so that "C"-terminated oligomers are not chemically modified. You would thus safely define this pattern: "M/;C/"... The logical conditions that the user can set forth for a cleavage reaction are called (in an intuitive manner) *Left Right Rule*s.

Now that we got trained to think in an abstract way with these leftrightrules, we can proceed to yet meatier stuff: the fragmentation specifications. A polymer chemistry definition can hold as many fragmentation specifications as necessary. A fragmentation specification holds a number of pieces of information, amongst which there is a compound datum describing logical conditions similar but more complex than leftrightrules: *fragmentation rules*. Each fragmentation specification might have zero or more (with no limitation) fragmentation rules. We review this complex matter in the next section.

The Fragmentation Specifications

As you might have noticed reading page 25, the fragmentation specification is a tricky business. Figure 6.4 shows examples of protein fragmentation specifications for fragment types *a, b, c, z, y, x, imm*.

Let's concentrate on the fragmentation specification of type *a*. While the first row of this fragmentation specification is effectively valid (for a "protein" polymer chemistry definition, at least), the lower two rows (describing fragmentation rules named *a-fgr-1* and *a-fgr-2*) are fake, only to show the way fully qualified fragmentation specifications can be created.

Let us analyze the data that the user entered to fully qualify this *a* fragmentation specification:

- ⋆ Name **a** This is the name of the fragmentation specification. Fragments obtained with this specification will be named according to the following naming scheme: "a-*i*", with *a* being the fragmentation name and *i* being the position –in the precursor polymer ion– of the monomer at which the fragmentation occurred (see page 25);

- ⋆ End **LE** This is the end of the precursor polymer that is to be found in the fragment. Accepted values are "LE" (left end), "RE" (right end) and "NE" (no end). We have previously seen –for proteins and nucleic acids– that fragments *a, b, c* include the left end ("LE") of the precursor polymer, while "RE" applies to fragmentation specifications that lead to fragments that contain the right end of the precursor polymer (for example, fragments *x, y, z*). Special cases, like proteinaceous immonium ions, do not bear any

[2] This is a purely hypothetical situation that I never observed personally!

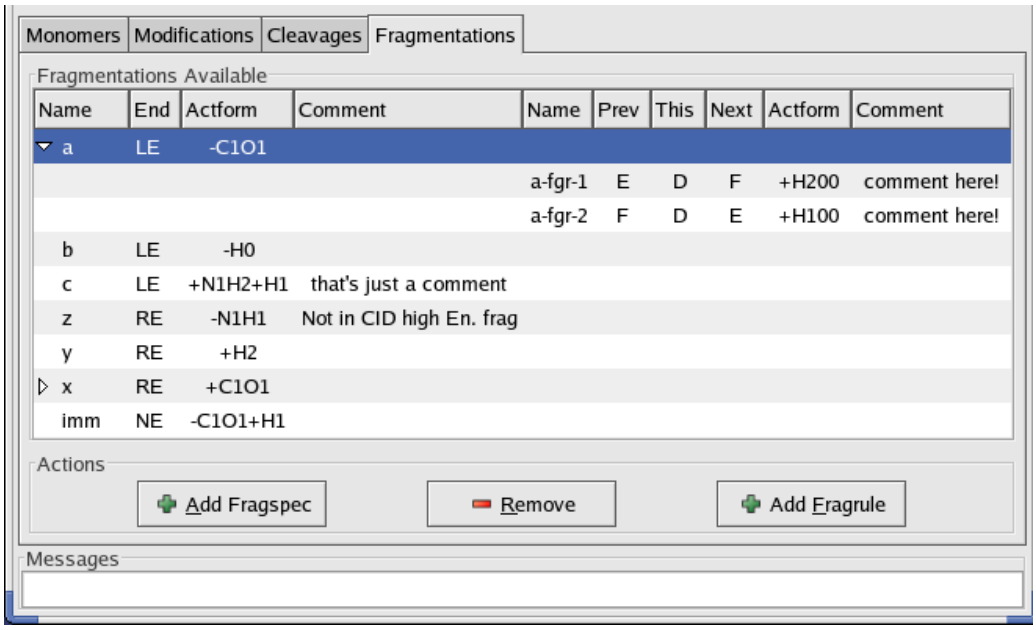

Figure 6.4: **Interface for the definition of the polymer fragmentation specifications.** This is the same window as for Figure 6.1, but this time the fragmentation specifications definition tab of it is shown. This figure shows that a fragmentation specification is defined in a more complex way than previously described for cleavage specifications; see text for further details.

end of the precursor polymer, in which case "NE" (for no end) should be written here instead of "LE").

This End piece of information is important for two reasons: 1) because it tells the fragmentation engine from which end it should iterate (in the precursor polymer sequence) when making all the fragments of a given fragment ion series and 2) because it guides ***polyxmass*** to apply the conventional naming scheme using i with the proper value. Therefore, the smallest fragment of the a series is a-***1*** (note subscript 1), which is the left end monomer of the precursor polymer. The smallest fragment of the x series is x-***1*** (note that subscript is also 1). This time, the x-***1*** fragment, however, corresponds to the right end monomer of the polymer sequence. This is because the numbering of the fragments always starts at the precursor polymer's end that was specified by the End piece of data from the polymer chemistry definition;

- Actform **-C1O1** Optional. This is the chemical reaction that will actually change a monomer chain into the proper fragment. Indeed, the mass calculation of the fragment's mass is performed by summing the mass of the monomers running from the *end* of the precursor polymer up to the position where the fragmentation occurs, plus adding the mass of the end's cap as specified in the polymer chemistry definition. But, for the a fragments, this is not enough, as it does not lead to a correct mass. It is required that the actform "-C1O1" be applied to the monomer chain so that it is of the correct mass (after having added the mass corresponding to the left cap; see below). This actform is optional, because for some fragments (for example, fragments b in the protein polymer chemistry) there is no need for any actform besides adding the masses of the monomers and adding the mass corresponding to the left cap of the polymer chemistry definition. As can be seen on the picture, "-H0" is set as an actform for b fragments. Again, see page 25;

- Comment (Empty) Optional. This is simply a comment, if the user wants to set any. *Ad libitum*.

A fragmentation specification can include zero or more fragmentation rule(s) that help model –in a highly detailed manner– complex fragmentation patterns. Let's see what it takes to define a fragmentation rule:

- Name **a-fgr-1** This is the name of the fragmentation rule. It should be self-explanatory and should somehow provide a hint to the fact that this fragrule belongs to the a fragmentation specification;

- Prev **E** Optional. This is one of the logical conditions that can be set to be verified so that the actform can be applied to the fragment currently generated. In our example, we are saying that if –in the precursor ion sequence– the monomer preceeding the one that is currently fragmented is of code "E", then this condition is verified and the **+H200** actform should be applied to the resulting fragment;

- This **D** Optional. This is an analogous condition as the one above, unless the monomer onto which this condition applies is the monomer being actually fragmented;

- Next **F** Optional. This is similar condition, unless that it applies to the monomer that is one position forward in the precursor ion sequence, with respect to the presently fragmented position;

- ⋆ Actform **+H200** This is the chemical action with which the fragment will actually be challenged if the set of logical conditions above is verified. This actform is the *raison d'être* of the fragmentation rule, so it is compulsory;
- ⋆ comment **comment here!** Optional. *Ad libitum*.

A fragmentation rule is a set of one or more logical conditions that (if verified) determine a user-specified chemical actform to be applied to the fragment that was generated in the first place by fragmenting the precursor polymer using the fragmentation specification to which the fragrule itself belongs. As can be seen in the example figure, the fragmentation specification for fragments *a* (fragmentation specification *a*) contains two fragmentation rules, but it could have contained as many of them as necessary to finely describe experimentally observed fragmentation events...

The following paragraph will explain thoroughly how fragmentation rules modify the way fragments are generated, for a given fragmentation pattern.

We have seen, in our example of a fragmentation specification named *a* (Figure 6.4), that it should generate fragments starting from the left end of the precursor polymer. Now we see that the fragmentation specification includes a fragmentation rule: This is set to "D", which means that this fragmentation rule is evaluated further *only* if the monomer currently fragmented is indeed a "D". If not, the whole fragmentation rule is skipped. If Prev is set to something (for us: "E"), then the fragmentation rule is evaluated further only if the monomer at position [current -1] is a "E". If not, the fragmentation rule is skipped. If Next is set to something (for us: "F"), then the fragmentation rule is evaluated further only if the monomer at position [current +1] is a "F". If not, the fragmentation rule is skipped.

What is called a position **[current +1]** and a position **[current -1]** depends on the kind of fragmentation specification: if the fragmentation specification states that End (seen earlier) is "LE" (or "NE"), then the position [current +1] refers to the position right of the currently fragmented monomer (in the standard left-to-right polar horizontal representation of a polymer); if the fragmentation specification states that End is "RE", then the position [current +1] refers to the position left of the currently fragmented monomer. This has to do with the way the fragmentations are normally described: the fragment numbering scheme starts at the right end of the precursor polymer for "RE" fragments and at the left end of the precursor polymer for "LE" fragments. This is also true here: for a fragment of the series *a*, the fragmentation rule that we have described would effectively be applied to the following sequence:

MYNAMEIS**EDF**FIL

only upon generation of the MYNAMEIS**ED** fragment.

If we were using the same fragmentation rule for a fragment of the series *x* (for which End is "RE"), the fragmentation rule would never have been evaluated. Instead, for the following sequence:

MYNAMEIS**FDE**FIL

it would have, and thus would have generated the fragment **EDF**IL.

Now, what about internal fragment specifications, like the immonium ions' case, where the End is defined to be "NE" in the polymer chemistry definition? ***polyxmass*** evaluates the conditions from left to right; so the conditions are evaluated like for "LE" cases.

Another important thing to figure out: how are the logical conditions tested? The main condition (entered as This) is evaluated first, because this is the simplest evaluation: the value of the This monomer can be compared with the currently fragmented monomer code without depending on the End value. If the monomer context complies with this condition (in our example that would mean that we are actually fragmenting at a "D" monomer), other conditions (if any) are evaluated. Thus, in logic terminology the conditions are *AND*ed one with the other: as soon as a condition is stated it must be verified. If *any* condition is not verified, no fragment is created and the other fragmentation rules are analysed (if any).

If there are more than one fragmentation rule in a fragmentation specification, each fragmentation rule is evaluated separately. If the monomeric context (previous/this/next monomer codes) complies with the logical conditions stated in the evaluated fragmentation rule, a new fragment is generated. When a fragmentation rule is found not to comply with the monomer context, then it is simply skipped (no fragment is generated).

It should be noted that the presence of a fragmentation rule in a fragmentation specification is not exclusive, in the sense that if the fragmentation rule contains never satisfied logical condition(s),[3] a single fragment is indeed generated, which corresponds to the fragmentation specification without taking into account any framentation rule.

The fact that each fragmentation rule –that has logical conditions which are verified in the sequence– yields a new fragment implies that the fragmentation rules are not summative: a fragment is not generated by applying onto it the actform of each validated fragmentation rule in a fragmentation specification. Each fragmentation rule, in a given fragmentation specification, gives rise to a fragment that is a fragment ion resulting from the application of both the actform specified in the fragmentation specification (if any) and the actform specified in the fragmentation rule (this one is compulsory). Next, when another fragmentation rule of the same fragmentation specification is evaluated, a brand new fragment is generated according to the same process as the one just described.

Saving A Polymer Chemistry Definition

Once the polymer chemistry definition is completed, the user can save it to a file. Prior to actually writing to the file, the program checks the syntax validity of the elements that the user has entered in the window. If an error is found in the polymer chemistry definition being worked on, that error is displayed in a window so that the user may identify the problem and fix it. If no error is detected, the program proceeds with writing the polymer chemistry definition to an *XML* file.

The location where the file should be saved, and the manner that it may be made available to the whole ***polyxmass*** framework is to described in another chapter. Indeed, ***polyxmass*** is a very powerful framework, wholly designed to be modular. But this modularity and power have a cost: complexity. A well configured system is the key to a powerful program running smoothly. It is thus very important to grasp the ***polyxmass*** framework configuration data hierarchy so that the program knows at each instant where to find the configuration data required to perform properly both the polymer sequence display and the mass calculations.

But for now go on with the polymer chemistry definition-aware calculator: ***polyxcalc***!

[3] Such as if "this monomer's code" is "Y", "next monomer's code" is "Y" and "previous monomer's code" is "Y" and there is no "YYY" sequence element in the polymer, for example.

7

The polyxcalc module: A Powerful Mass Calculator

After having completed this chapter you will be able to perform sophisticated mass computations in a polymer chemistry-aware manner.

polyxcalc Invocation

The ***polyxcalc*** module is simply called by its name: polyxcalc from a command line. The user is invited to launch the following command and to inspect the various options that it accepts:

```
bash-2.04 $ polyxcalc --help ↩
```

This command produces the following output:

```
Usage: polyxcalc [OPTION...]
  -d, --details          prints the copyright owner and the licensing of the
                         program
  -l, --license          prints the license type of the program
  -v, --version          prints the version of the program
  -t, --type=poltype     the type of the polymer chemistry definition
                         being requested (ie "protein", with no quotes)

Help options:
  -?, --help             Show this help message
  --usage                Display brief usage message
```

polyxcalc Operation: An Easy Task

The way ***polyxcalc*** is operated is very easy. This is partly due to the very self-explanatory graphical user interface of the module, which is illustrated in Figure 7.1.

As the reader can see, there are a number of items that ***polyxcalc*** can handle. We are going to review these one by one:

- ⋆ Initial Masses This is the place where the mass calculator may be seeded so as to start computations on pre-existing molecules of which masses are known already. The user may enter either a Mono Mass or an Avg Mass or both masses. When any of these masses are set and the Result Masses are empty, they are taken into account (***polyxcalc*** considers that the system is seeded with them) in the first mass calculation that is elicited by clicking onto the Apply button. Once the Result Masses are no more empty, these masses are no more taken into account, and instead will be updated to reflect the previous mass calculation results. Thus, each time a calculation is performed, the previous results are stored in the Initial Masses text entry widgets. This way, the user has the ability to always "undo" the last calculation step;

- ⋆ Atom This is a drop-down list widget that contains all the atoms available in the ***polyxmass*** mass spectrometry software framework. The user may select any of these atoms and enter any number (positive or negative) in the related Count text entry widget. Entering a positive value means that the selected chemical entity must be added to the masses, while a negative value will remove this entity from the masses;

- ⋆ Formula/Actform This is a text entry widget where the user may enter as complicated actforms (or a formula) as she wishes. Same as above applies for the Count text entry widget;

- ⋆ Monomers If a polymer chemistry definition file was chosen by clicking onto the New toolbar menu button, this drop-down list widget contains all the monomers listed in the chosen polymer chemistry definition. For example, if the "protein" polymer chemistry definition file had been opened in ***polyxcalc***, then this drop-down list widget would have contained the twenty names of all the naturally-occurring most common monomers (amino-acids). Same as above applies for the Count text entry widget;

- ⋆ Modifications This is exactly the same as for the Monomers drop-down list widget, unless the "chemical elements" listed here are the modifications described in the polymer chemistry definition file, such as "Acetylation" or "Phosphorylation", for example. Same as above applies for the Count text entry widget;

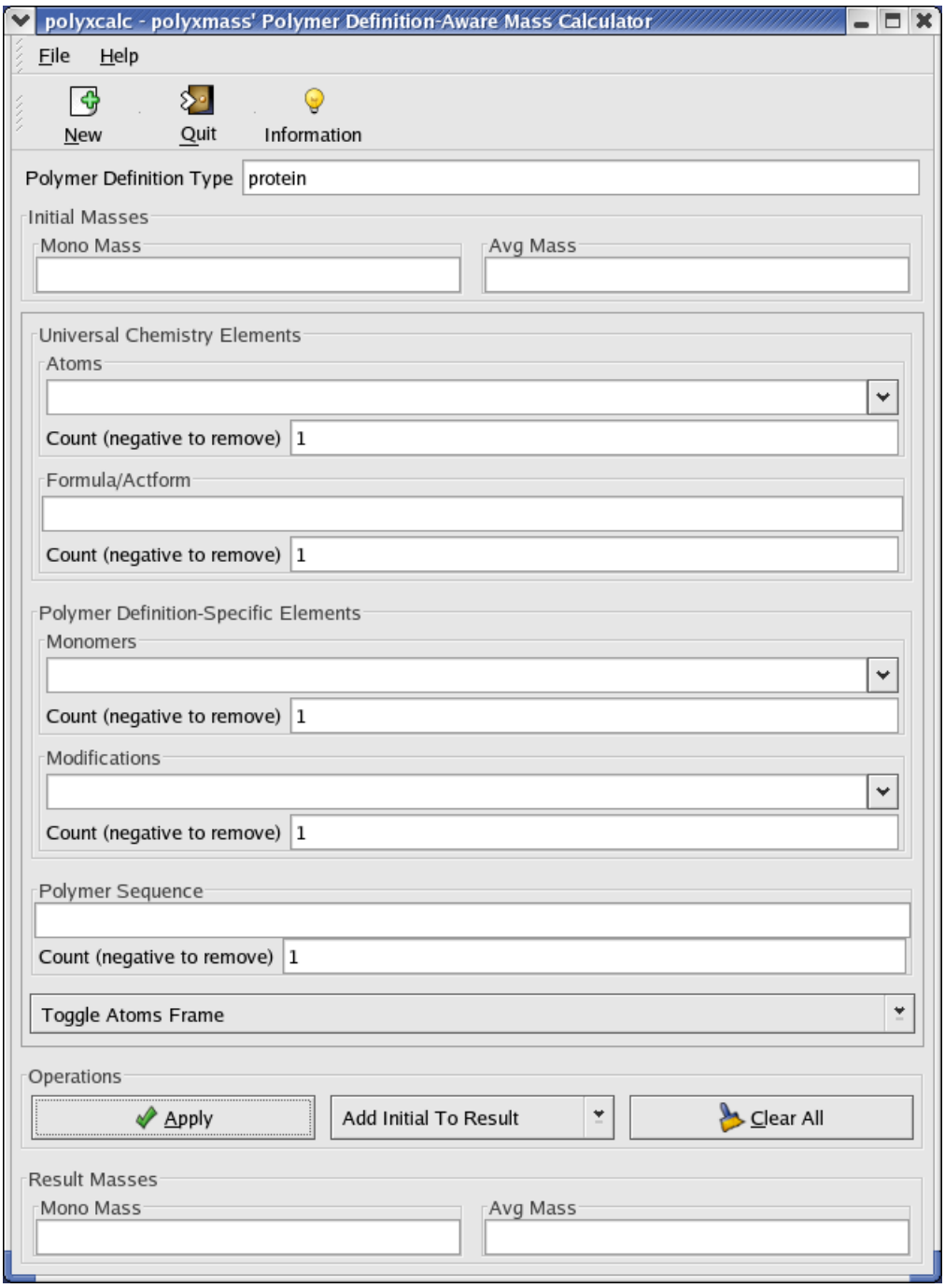

Figure 7.1: **Interface of the *polyxcalc* module.** This figure shows that the ***polyxcalc*** polymer definition-aware module can handle atoms, actforms, monomers, modifications and even polymer sequence for computing masses.

- ⋆ Polymer Sequence This is a text entry widget were the user may enter a polymer sequence complying with the polymer definition currently opened in ***polyxcalc***. A "protein" sequence may be this "MAMISGMSGRKASPTSPINADK", for example, which is the N-terminal end of the chicken gizzard telokin.[1] Same as above applies for the Count text entry widget;

Noteworthy, when ***polyxcalc*** is launched without specifying a polymer chemistry definition, the polymer chemistry definition-specific widgets (monomers, modifications, polymer sequence; all described above) are made insensitive. This is to make sure that the user cannot enter data that would not make sense because the chemistry definition is loaded.

The multi-option menu button widget labeled Toggle Atoms Frame actually contains other similar menu items that unfold when the widget is clicked. The other menu items do exactly the same for all the other items that we have reviewed above: make them either disappear or reappear in a switch-like manner. This is so that the graphical user interface may be simplified if, for example, the user never needs to select individual atoms or modifications...

The Operations frame widget contains three widgets:

- ⋆ Apply This button is the one through which all calculations are elicited. When this button is clicked, all the widgets detailed above are screened and checked for content. If content is found (let's say a Modification entity is found in the corresponding widget), the Count is checked. If this count is non-empty and non-0, the chemical entity is taken into account in the mass calculations;
- ⋆ Multi-Option Menu Button This widget contains the following sub-menu items:
  - ✦ Add Initial To Result When this multi-option menu item is selected, the masses (if any) located in the Initial Masses text entry widgetsare added to the ones located in the Result Masses text entry widgets;
  - ✦ Remove Initial From Result This is a rather similar approach as above, unless the masses in the Initial Masses text entry widgets (if any) are removed from the ones in the Result Masses text entry widgets;
  - ✦ Send Result To Initial This is rather self-explanatory: masses from the Result Masses text entry widgets are sent to the Initial Masses text entry widgets thus overwriting the masses that could have been displayed there;
  - ✦ Clear Initial Masses Self-explanatory;
  - ✦ Clear Result Masses Self-explanatory;
  - ✦ Clear All Chem. Data This will erase all the data that are currently displayed in the chemistry-related widgets that we reviewed above. The Count text entry widgets are also reset to empty;
  - ✦ Cancel Operation This menu item is a "safe-conduit": if the multi-option menu was clicked and no available option needs to be chosen, the user *must* choose this cancellation option, otherwise any other option that gets selected upon releasing the widget will be executed.
- ⋆ Clear All This button simply resets to empty all the mass-related and chemistry-related entry widgets along with all the Count text entry widgets.

The reader may have noticed that, with this interface, any possibly imaginable molecule can be constructed since the "granularity" of the ***polyxcalc*** module is atomic.

[1] If I remember well my PhD experimental work...

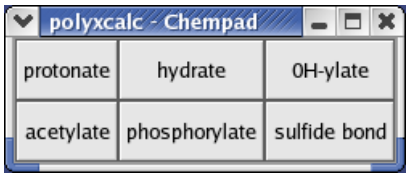

Figure 7.2: **Interface of the chemical pad.** This figure shows that the chemical pad is very similar to what a numerical calculator would display. Here, the user has programmed a number of chemical reactions.

polyxcalc Is A Programmable Calculator

For the scientists who work on molecules that are usually modified in the same usual ways, ***polyxcalc*** features a built-in mechanism by which they can easily program their polymer chemistry-aware calculator. This programming involves the definition of how a *chemical pad* (or *chempad*) may be arranged, exactly the same way as a usual calculator would display its numerical keypad.

An example of such a chemical pad is shown in Figure 7.2, where a "protein" polymer chemistry definition-associated chempad is featured. As shown, the user has programmed a number of chemical reactions that may be applied to the masses in the ***polyxcalc*** main window by simply clicking on their respective item.

The configuration of the Chempad is very easy, as shown in the code below (excerpt taken from file `polyxmassdata/protein/chempad.conf`):

```
#chempad_rows$3
chempad_columns$3

chempadkey=protonate%+H1%adds a proton
chempadkey=hydrate%+H2O1%adds a water molecule
chempadkey=0H-ylate%+O1H1%adds an hydroxyl group
chempadkey=acetylate%-H1+C2H3O1%adds an acetyl group
chempadkey=phosphorylate%-H+H2PO3%add a phosphate group
chempadkey=sulfide bond%-H2%oxydizes with loss of hydrogen
```

What this text file says is very simple:

- That the buttons should be arranged in rows of three columns;
- Follows the description of a number of buttons (chempad keys) to be laid out in the chempad (each line describes one button).

Each button is defined in a line that begins with the text `chempadkey=`. Let's look at one button definition, the "phosphorylate" button. The `phosphorylate` text string after the `=` character is the label that will decorate the button that is being configured. The `-H+H2PO3` text string is the actform that should be applied to the result masses in the ***polyxcalc*** main window when this button is clicked; that's a chemical reaction, in fact. The `add a phosphate group` is a text string that is displayed as a tooltip when the mouse cursor stays for a number of milliseconds over the button.

From a geometrical layout point of view, the user is allowed to set either a number of rows (`chempad_rows$3`, in our example) or a number of columns (`chempad_columns$3`,

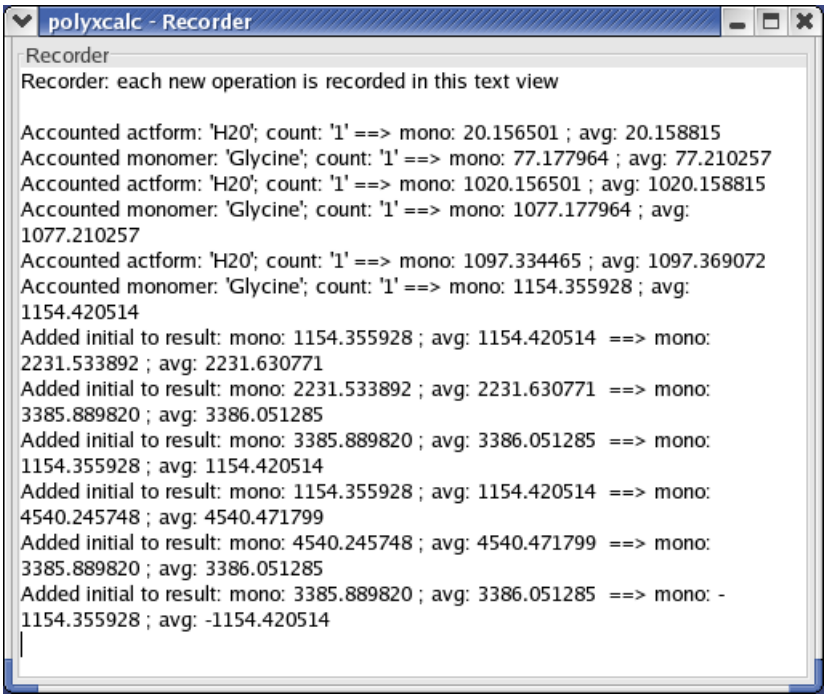

Figure 7.3: **The *polyxcalc* recorder window.** This figure shows that the recorder window is a simple textview widget that records all the mass-significant operations in the ***polyxcalc*** calculator. The text in the recorder may be selected and later used in an electronic logbook or printed.

in the example). The program then chooses the best layout corresponding to the user's requirement.

polyxcalc Is LogBook-Friendly

Each time an action that is chemically relevant –from a mass perspective– is performed, the program dumps the calculations to the ***polyxcalc*** recorder window.

This recorder window is shown in Figure 7.3. The text in the recorder window is editable for the user to customize the ***polyxcalc*** output, and selectable so that pasting to text editors or word processors is easy.

8

The polyxedit module: A Powerful Simulator

After having completed this chapter you will be able to perform sophisticated polymer chemistry simulations on polymer sequences –that can be edited in place– along with automatic mass recalculations.

polyxedit Invocation

The ***polyxedit*** module is simply called by its name: polyxedit from a command line. The user is invited to launch the following command and to inspect the various options that it accepts:

```
bash-2.04 $ polyxedit --help ↩
```

This command produces the following output:

```
Usage: polyxedit [OPTION...]
  -d, --details     prints the copyright owner and the licensing of
                    the program
  -l, --license     prints the license type of the program
  -v, --version     prints the version of the program

Help options:
  -?, --help        Show this help message
  --usage           Display brief usage message
```

If the user passes to the command line strings that do not correspond to any of the options above, then ***polyxedit*** considers them to be filenames of polymer sequences, and thus tries to open these files. If a polymer sequence file could not be found or opened, a warning message is logged to the console.

polyxedit Operation: *In Medias Res*

A typical ***polyxedit*** session looks like what is shown in Figure 8.1 on the facing page.

As the reader can see, there are a number of items that we need to describe and explain. This is the beginning of a journey in the guts of ***polyxedit***... Keep reading the next numerous sections!

polyxedit Main Program Window: The Menu

In this short section we will review the different menus that are currently available in ***polyxedit***. It is most probable that new menu items will be added when new features are added to the program.

As with usual menus, the menus in ***polyxedit*** are hierarchical, and we'll analyse each parent menu along with its submenus (and subsubmenus):

- *File*
  - ⟶*New*... Create a new polymer sequence;
  - ⟶*Open*... Open a polymer sequence;
  - ⟶*Save*... Save a polymer sequence;
  - ⟶*Save As*... Save a polymer sequence with a new name;
  - ⟶*Close*... Not yet implemented;
  - ⟶*Close All*... Not yet implemented;
  - ⟶*Quit*... Quit the program;
- *View*
  - ⟶*Calc. Options*... View/Modify the way calculations are performed, be them mass calculations or elemental composition calculations;
  - ⟶*Mass Display*... Open a window where the mono/avg masses are displayed both of the entire polymer sequence and of the currently selected region;

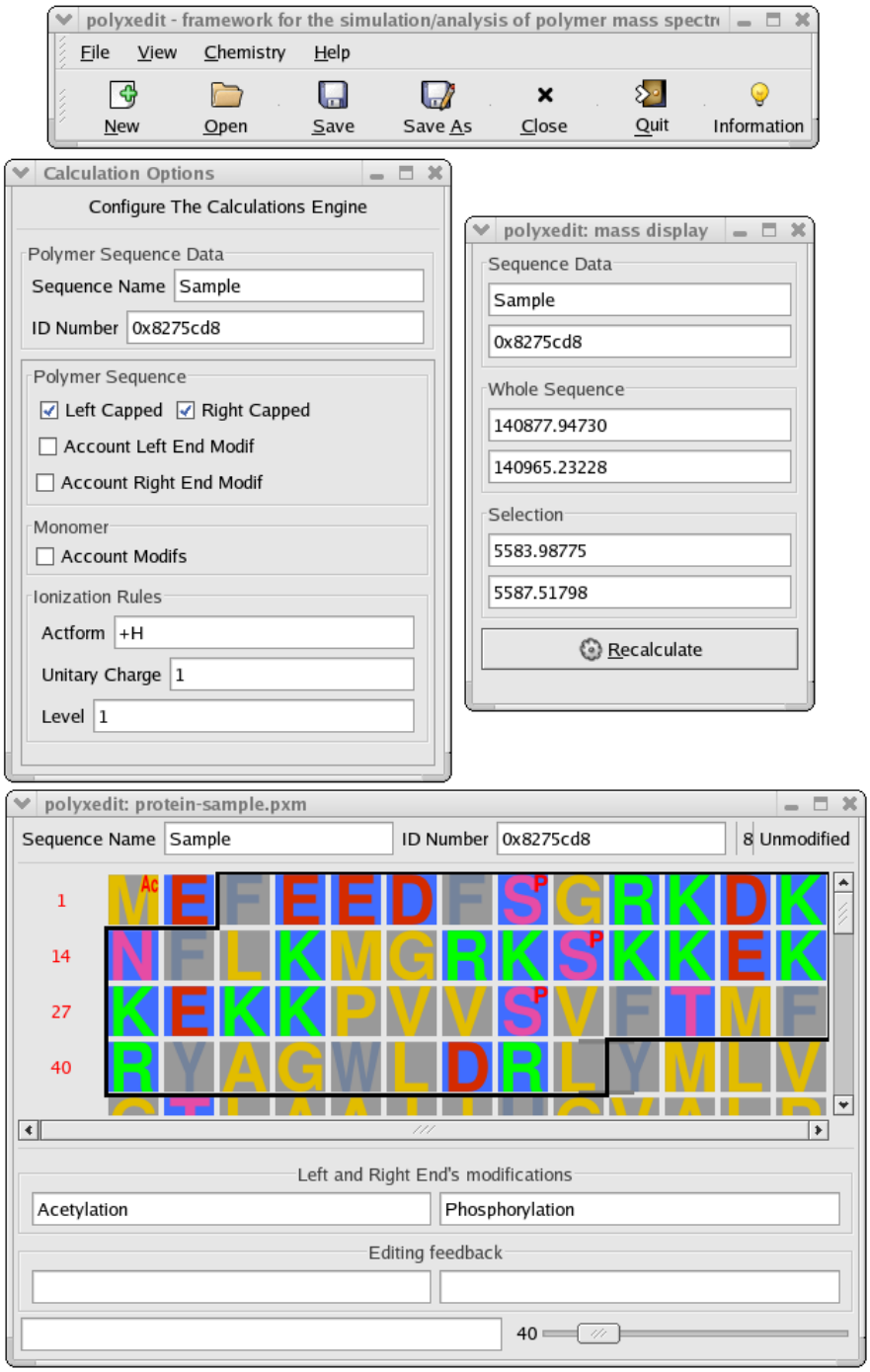

Figure 8.1: **Interface of the *polyxedit* module.** This figure shows that the ***polyxedit***'s minimally useful environment is made of four different windows: the program's main window, with its menu and toolbar, the calculations options window, the masses display window and finally a polymer sequence editor with a sequence loaded in it.

- *Chemistry*
  - ⟶*Modifications*
    - ⟶*Monomer*... Open a window so that a monomer (or any combination of monomers) can be modified or unmodified;
    - ⟶*Polymer*... Open a window so that the polymer sequence can be modified or unmodified either on its left end or its right end (or both);
  - ⟶*Cleave*... Open a window so that a polymer sequence can be cleaved;
  - ⟶*Fragment*... Open a window so that a polymer sequence can be fragmented;
  - ⟶*Compositions*
    - ⟶*Elemental*... Open a window so that options can be set for the program to compute the elemental composition of the polymer sequence or a region of it;
    - ⟶*Monomeric*... Open a window so that options can be set for the program to compute the monomeric composition of the polymer sequence or a region of it;
  - ⟶*Search Masses*... Open a window so that options can be set for the program to search arbitrary oligomers in the polymer sequence that have the same mass as the one(s) searched for.

Displaying Masses

As soon as a polymer sequence is read from disk, the user may want to have masses displayed for it. The *View*⟶*Mass Display* menu will open the polyxedit: mass display window that is shown in Figure 8.1 on the page before. As can be seen, there are three frames in this window, the first dealing with the polymer sequence data, the other two dealing with masses.

The first mass-related frame (Whole Sequence) contains two text entry widgets where masses are displayed. The first text entry contains the *monoisotopic* mass of the whole polymer sequence (for example, of the entire protein). The second text entry widget contains the *average* mass of this same polymer sequence.

The second mass-related frame (Selection) contains two text entry widgets where masses are displayed, exactly as above, unless this time the masses displayed correspond to the currently selected region of the polymer sequence. If no selection is currently made, then the virtual selection is considered to run from the first monomer in the polymer sequence up to the monomer left of the current cursor location.

Try experimenting with an open polymer sequence and move the cursor around in the sequence. See how only the Selection masses do change. Also, try selecting some regions in the text and see how, here also, only the Selection masses do change. Check if, when the entire polymer sequence is selected, the masses displayed in both the Whole Sequence and Selection frames are identical or not.

There is *only one* polyxedit: mass display window in the ***polyxedit*** module, even if more than one polymer sequences are opened. The way masses are displayed for different polymer sequences is simply by updating the mass values in this window when the focus[1] moves from a polymer sequence to another. This system ensure that the masses that are displayed always pertain to the currently "active polymer sequence editor window".

[1]The focus is placed on a polymer sequence editor window when the mouse cursor hits it; as soon as at least one polymer sequence window is open, there is always a "last active polymer sequence window", which is the polymer sequence window that was hit last with the mouse cursor.

Configuring The Calculations

As soon as the user wants to have masses displayed for a given polymer sequence, it is almost certain that she will want to configure the way these masses are computed. The *View⟶Calc. Options* menu will open a window entitled Calculation Options. This window is visible on the Figure 8.1 on page 69. As usual, there is a frame that deals with the name and identity of the polymer sequence for which these options are available.

Another frame, Polymer Sequence contains a number of widgets –mainly checkbuttons– so that the user can configure which chemical entities must be taken into account when masses are computed. The checkbuttons are rather self-explanatory.

Another frame, Monomer will let the user define if the monomer chemical modifications must be taken into account when computing masses.

The last frame, Ionization Rules, will let the user define the way both the whole polymer sequence and the selection must be ionized. The default ionization step is defined in the polymer chemistry definition, but the user can modify it in the text entry widgets made available to her here.

All the configurations that the user will perform in this Calculation Options window will apply to both the whole polymer sequence masses and to the selection masses (see above for the definition of these "whole sequence" and "selection" concepts).

Since it may be of great usefulness that two identical polymer sequences be either ionized differently, or that their masses be computed in different manners, *each polymer sequence window has its own Calculation Options window*. This is shown in Figure 8.2 on the next page: a single polymer sequence file was opened twice as two entirely distinct objects in memory, so that changing either the sequence or the way masses are computed for one of the two polymer sequence editors will be relevant only to the corresponding polymer sequence.

This is clearly visible on the Figure 8.2 on the following page because, while both sequence editor windows display the same Sequence Name text widget's contents, the ID Number text widgets do contain different data: the two polymer sequence objects in memory are different and thus entirely distinct one from the other.

The top polymer sequence has its masses computed by taking into account the monomer modifications, while the bottom polymer sequence has its masses computed by *not* taking into account the monomer modifications. This mechanism gives the user a great flexibility in the manner any comparison may be performed in the way masses are computed, sequence differences are monitored real time, by editing one polymer sequence and not the other, for example...

Editing Polymer Sequences

As we have seen in the ***polyxdef*** module, the user may stipulate that a polymer chemistry definition allows more than one character in order to define the codes of the different monomers of this same polymer chemistry (see section 6 on page 50). Remember that it is not because the number of allowed characters is ***3***, for example, that all your monomer codes must be defined using three characters. ***3*** is the *max* number of characters that you may use. This means that you are perfectly entitled, in this case, to have single-character or bi-character monomer codes in this polymer chemistry definition. Let's start by looking at how the polymer sequence editor window behaves when the user tries to enter multi-character monomer codes. Next, we'll see that whatever the length of a monomer code, if its very first character is unambiguous, the behaviour of the polymer sequence editor is flexible and

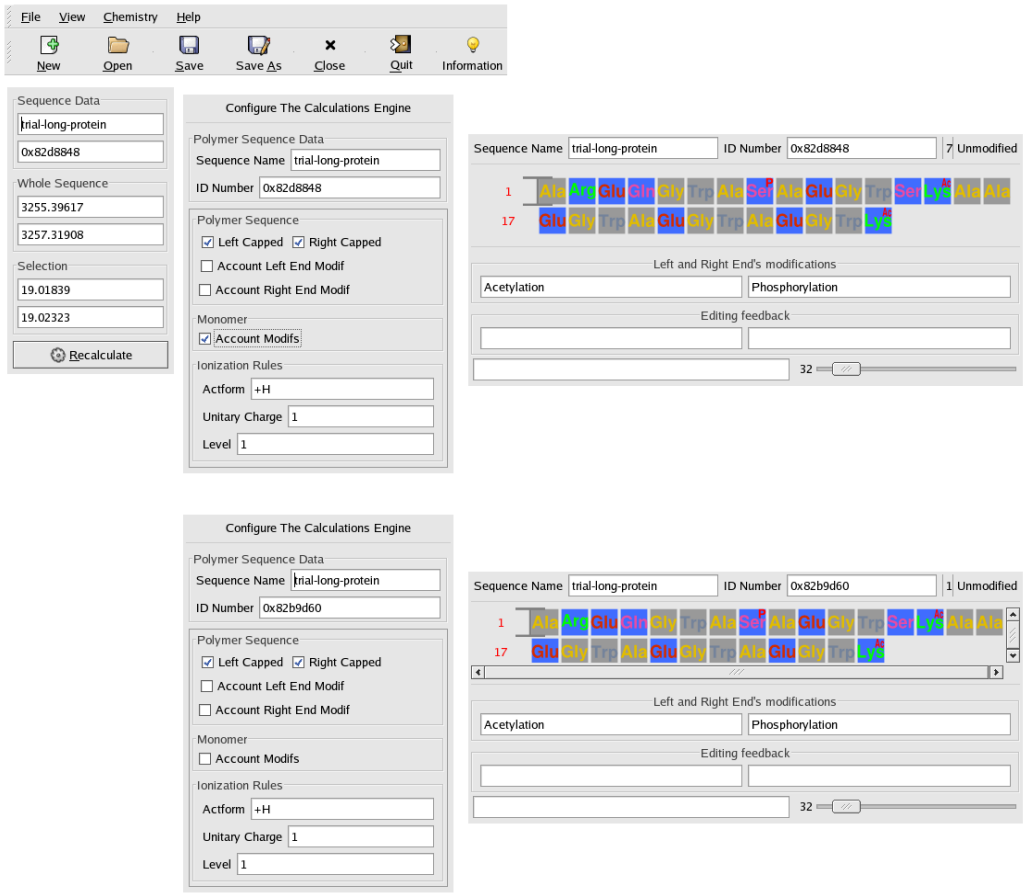

Figure 8.2: **The same polymer sequence opened twice in *polyxedit*.** This figure shows the same polymer sequence being loaded twice in ***polyxedit***. The two polymer sequence editor windows are entirely separated in memory.

powerful.

Multi-Character Monomer Codes

In this section we will describe the editing of a polymer sequence for which monomers can be described using more than one character.

The Figure 8.3 on the following page shows the case of a polymer sequence that is of a polymer chemistry definition that allows three characters to define monomer codes. Let's now assume that the user wants to edit the sequence by insertion –at the cursor point– of a new monomer "Aspartate", of which the user knows only that its code starts with an 'A' (panel 1, Figure 8.3 on the next page).

So, naturally, the user keys-in [A] (panel 2, Figure 8.3 on the following page). To her dismay, nothing happens in the polymer sequence, but she sees an 'A' character now displayed in the left text widget under the label Editing Feedback. The reason why we have this behaviour is due to the fact that we are allowed up to 3 characters to describe a monomer code. If no monomer icon is displayed in the polymer sequence, that may simply mean that more than one monomer code start with an 'A' character: ***polyxedit*** cannot figure out which monomer code the user actually means when keying-in [A].

There is a way, called *completion*, to know which monomer codes –in the current polymer chemistry definition– start with the keyed-in character(s) ('A' for us now). The user can always enter the *completion mode* by using the tabulation [TAB] key. This is what is shown in the small window right of panel 2, Figure 8.3 on the next page. In the current polymer chemistry definition, four monomer codes start with an 'A' character, and these are "Ala", "Arg", "Asp" and "Asn". We could be selecting the right monomer by double-clicking onto the proper list item, which would insert the corresponding monomer icon ("monicon") in the polymer sequence at the cursor location. But, since this is a manual, we are going through another step.

Let's continue editing the polymer sequence and key-in a [s] (we did not forget that we wanted to enter an "Asp" monomer code in the first place, did we?). The result is shown in panel 3, Figure 8.3 on the following page. What we see here, is that this time also, nothing changed in the polymer sequence. What changed is that there is now a "As" character string in the left text widget under the label Editing Feedback. Let's key-in once more the [TAB] key, and we get the small window right of the panel 3, Figure 8.3 on the next page. This time, only two items are listed: "Asp" and "Asn". This is easy to understand: there are only two monomer codes that start with the letters "As" that we have keyed-in so far. At this time, we either select one of the items (we wanted to enter the "Aspartate" monomer, so we'll double-click onto the first item of the list), or we just key-in a last character: [p]. At this point, the monomer is effectively inserted in the polymer sequence, as the seventh monomer, shown in panel 4, Figure 8.3 on the following page.

Unambiguous Single-/Multi-Character Monomer Codes

Let's imagine that we have now a polymer chemistry definition that allows up to 3 characters for the definition of monomer codes, but that we have one monomer code (let's say the one for the "Glutamate" monomer) that is 'E'. This monomer code 'E' is the only one of the polymer chemistry definition that starts (and ends, since it is mono-character) with an 'E'. In this case, when we key-in [E], we'll observe that the monomer code is immediately validated and that its corresponding monomer icon is also immediately inserted in the polymer sequence.

Figure 8.3: **Multi-character code sequence editing in *polyxedit*.** This figure shows the process by which it is made possible to edit polymer sequences with a code set that allows more than one character per code.

Figure 8.4: **Bad code character in *polyxedit* sequence editor.** This figure shows the feedback that the user is provided by the code editing engine, when a bad character code is keyed-in.

This is because, *if there is no ambiguity,* ***polyxedit*** *will immediately validate the code being edited.* This means that you are absolutely free to define *only single-character monomer codes* in your polymer chemistry definition, so that you are not even conscious that the powerful multi-character feature exists! Indeed, in this 1-character monomer code configuration, each time you'll key-in an uppercase character, you'll be inserting its corresponding monomer into the polymer sequence immediately.

Displaying All The Monomer Codes

Equally interesting is the fact that if you key-in the TAB key while no monomer code is being edited (the left text widget under the label Editing Feedback is empty), all the monomer codes defined in your polymer chemistry definition are displayed, exactly as shown in the panel ALL, Figure 8.3 on the preceding page.

Erroneous Monomer Codes

Let's see now what happens when the user keys-in bad characters in the polymer sequence editor window. This is described in the Figure 8.4. If the user enters a lowercase character as the first character of a monomer code, the program immediately complains in the right text widget under the label Editing Feedback. In this case, the monomer code is not put into the left text widget, which means it is simply ignored.

If the user starts keying-in valid monomer character codes, like for example we did earlier with "As", and that she wants to erase these characters because she changed her mind, she *must not* use the BACKSPACE key, because this key will erase the monomer left of the cursor point in the polymer sequence! The way that the user has to remove the characters currently displayed in the left text widget under the label Editing Feedback, is to key-in the Esc key once for each character. For example, let's say I've already keyed-in A and s. In this case the left text widget, under label Editing Feedback, displays these two characters: "As". Now, *I change my mind* and do not want to enter the "Asp" monomer code anymore. I want to enter the "Gly" code. All I have to do is key-in the Esc key once for the 's' character (which disappears) and once more to remove the remaining 'A' character which

disappears also. At this point I can start fresh with the "Gly" monomer code by keying-in sequentially [G], [l] and finally [y].

Chemically Modifying Polymer Sequences

It very much often happens that the (bio) chemist uses chemical reactions to modify the polymer sequence she is working on. Mass spectrometry is then often used to check if the reaction proceeded properly or not. Further, in nature, chemical modifications of biopolymer sequences are very often encountered. For example, protein sequences get often modified as a means to regulate their function (phophorylations, namely). Nucleic acid sequences are very often and extensively modified with modifications such as methylation...

It is thus crucial that ***polyxmass*** be able to model with high precision and flexibility the various chemical reactions that can be either made in the chemistry lab or found in nature. The ***polyxmass*** program provides two different chemical modification processes:

- ⋆ A process by which monomers in the polymer sequence can be individually modified;
- ⋆ A process by which the whole polymer sequence can be modified, either on its left end or on its right end or even on both ends.

We shall review these two processes separately in the two sections below.

Chemical Modification Of Monomers

Modification Of Monomers

There are a number of manners in which monomers can be modified in a polymer sequence. The Figure 8.5 on the next page shows the simplest manner: the user first selects the monomer icon to modify, next calls the *Chemistry*⟶*Modifications*⟶*Monomer* menu and –as a result– is provided with a window where all the modifications currently available in the polymer chemistry definition are listed. Since a monomer icon was initially selected in the editor window, the Selected Monomer target radiobutton is on by default. It is then simply a matter of choosing the right modification from the Available Modifications list and clicking onto the Modify button.

The modified seryl residue is shown in the polymer sequence editor window: a transparent graphics object (a red 'P') was overlaid onto the corresponding seryl monicon.

While the Modification Target(s) frame widget contains radiobuttons the signification of which is rather easy to understand, we want to detail one of these: the Specific Monomer Locations frame. If the user selects the radiobutton inside that specific frame (labelled Positions Should Be Separated With ';'), she also has to write the locations in the text entry widget below it. This text entry widget receives textual strings that should describe what locations on the polymer sequence should be modified. The syntax of the descriptive string allows logical positions to be indicated. The user is invited to experiment, maybe using variations on the themes described below as examples:

- ⋆ **ALL** That would mean that the currently selected modification in the Available modifications list is to be applied to all the monomers in the polymer sequence. This is equal to selecting the radiobutton labelled All Monomers;

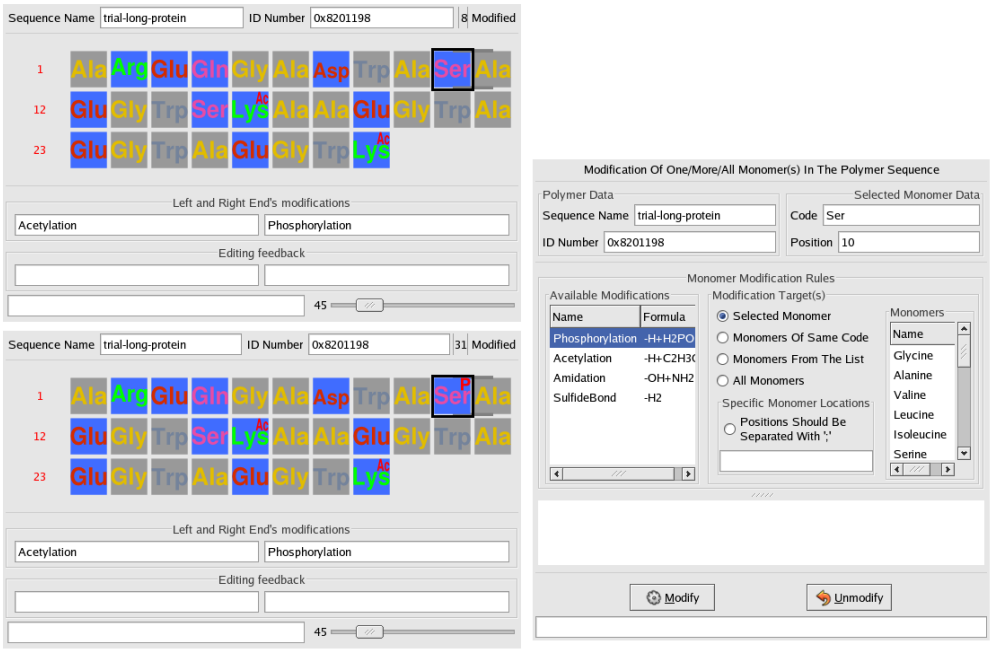

Figure 8.5: **Modification of a monomer in a polymer sequence.** This figure shows the graphical rendering of a phosphorylation of a seryl residue in a protein polymer sequence.

- ⋆ **EVEN** or **even** This will modify all monomers at even positions: 2, 4, 6...
- ⋆ **ODD** or **odd** This will modify all monomers at odd positions: 1, 3, 5...
- ⋆ **EVEN;ODD** is identical to **ALL**;
- ⋆ **[1-10];[20-30,odd]** This will modify all the monomers from position 1 to position 10 inclusive, and all the odd-positioned monomers between position 20 and position 30 inclusive;

The user is responsible for correctly reading the results that are published in the paned textview lying between the upper pane (labelled Monomer Modification Rules) and the two buttons at the bottom of the window. Further, when a modification or un-modification is performed, the count of successful events and of failed events is displayed in the messages' text widget at the very bottom of the window. The messages that are displayed in this widget are not permanent, they last some seconds and disappear. Care should be taken at what is displayed in this messages' text widget.

Attention should be paid to the fact that the user is responsible for applying chemical modifications to monomers that are listed as modifiable with the modification used. For example, if a phosphorylation modification is applied to a monomer that is not listed as phosphorylatable in the relevant configuration file, then the modification is applied to it (which means that –internally– the monomer is modified) but its corresponding monicon is not graphically changed because no graphical rule is associated with the phosphorylation of this monomer (see section 9 on page 92, the file of interest is `monomer-modif.dic`).

It is important to understand that, when a monomer is modified, its previous modification (if any) is overwritten with the new one. The user is invited to experiment a bit with the monomer modification process, so as to be confident of the results that she is going to obtain when real polymer chemistry work is to be modelled in ***polyxmass***.

Un-Modification Of Monomers

If a monomer is modified, then it also should be possible to revert the chemical reaction: to un-modify it. There is, however, a subtlety here, that we ought to put into the limelight: an example will do.

Let's say that all the seryl residues of our protein polymer sequence are phosphorylated.[2] Only seryl residues are phosphorylated in this polymer sequence. We thus see all their corresponding monicons overlaid with a small 'P' on them (see the example above). Other monomers are acetylated, like lysyl residues, for example. What we want to do is un-modify all the phosphorylated seryl monomers in one go. We thus open the monomer modification window, select the monomer code corresponding to the seryl residue in the Monomers list, select the rabiobutton labelled Monomers From The List, we select "Phosphorylation" in the Available Modifications list and finally we click the Unmodify button. All the seryl residues currently phosphorylated are un-modified. This is OK.

Now, let's assume that we had not selected "Phosphorylation" in the list of available modifications, but "Acetylation", for example: no phosphorylated seryl residue would have been un-modified. This is a foolproof feature: if you select a modification name from the list of available modifications, and next click onto the Unmodify button, that means that your un-modifying action has –as targets– monomers that are currently modified with the modification that you selected.

That means that if, in our example, you had selected, as monomer targets to the un-modification, the All Monomers radiobutton, selected the "Phosphorylation" modification and clicked onto the Unmodify button, *only* the phosphorylated monomers[3] would have been un-modified.

Now, if you un-select all the items in the list of available modifications[4], that you select the All Monomers radiobutton and next click onto the Unmodify button, then you'll un-modify absolutely *all* the monomers, because you are not restricting the monomer targets neither by their code, neither by the identity of their potential modification.

The user is encouraged to play with these features... Also of great importance is to understand that the modifications that can be set to the monomers do disappear when the monomer is removed from the polymer sequence. These modifications are *monomer modifications*, they belong to the monomer that is modified. We say that these modifications are *intrinsic*.

Chemical Modification Of The Polymer Sequence

We have seen above that it is possible to modify any monomer in the polymer sequence and that when the modified monomer is removed, the modification associated to it disappears also.

[2] That's protein chemistry stuff.

[3] Whatever they be, because the All Monomers radiobutton was selected.

[4] You may need to maintain the Ctrl key pressed while clicking onto the currently selected item to unselect it.

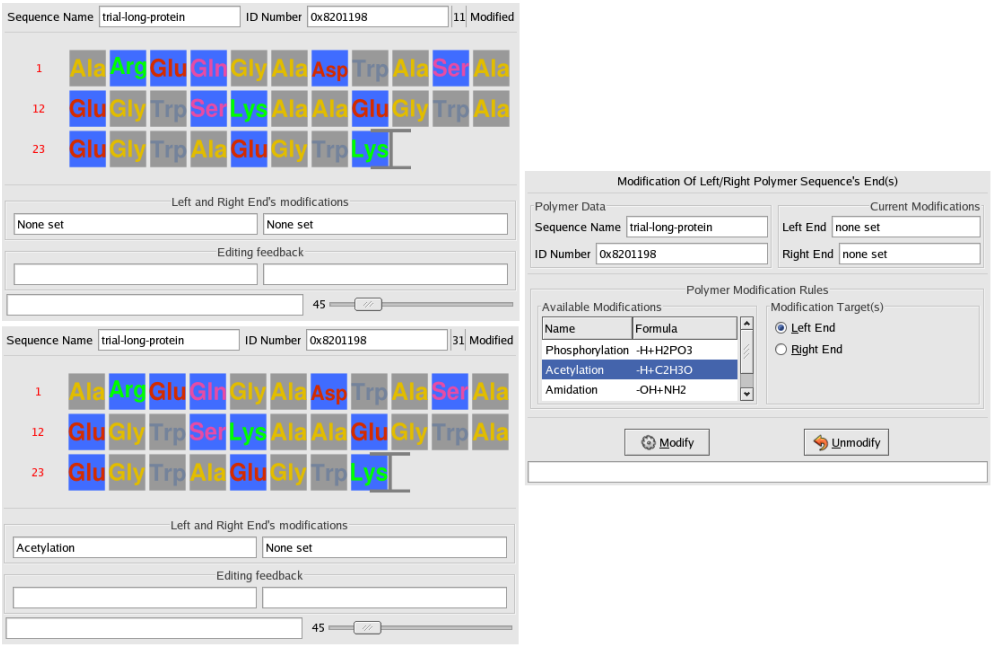

Figure 8.6: **Modification of a monomer in a polymer sequence.** This figure shows how simple it is to permanently modify a polymer sequence on either or both its left/right ends. The permanent modifications currently set to a polymer sequence are conveniently listed in two text widgets located under the polymer sequence rendering area.

The modifications that we describe here are not of this kind. They apply to either the left end of the polymer sequence or its right end. But these modifications do belong to the polymer sequence *per se* and are not removed from it even if the polymer sequence is edited by removing the left end monomer or the right end monomer. We say that these *polymer modifications* are *permanent*.

The way in which a polymer sequence is modified using *polymer modifications* is much easier than the previous *monomer modifications* case. The modification window is opened by choosing the *Chemistry*$\longrightarrow$*Modifications*$\longrightarrow$*Polymer* menu. The Figure 8.6 shows that window.

The modification is absolutely easy to perform, with a clear feedback provided to the user (by listing the permanent modifications in two convenient text widgets located under the polymer sequence graphical rendering area, under label Left and Right Ends' Modifications). In the example (Figure 8.6), the top polymer sequence is not yet modified. By using the window on the right, the polymer sequence is modified on its left end using the "Acetylation" modification. The newly modified polymer sequence is shown in the window below, with the left text widget displaying the name of the left end modification.

The Unmodify button is responsible for the un-modification of the selected polymer sequence end (left/right), so that reverting a modification is perfectly feasible.

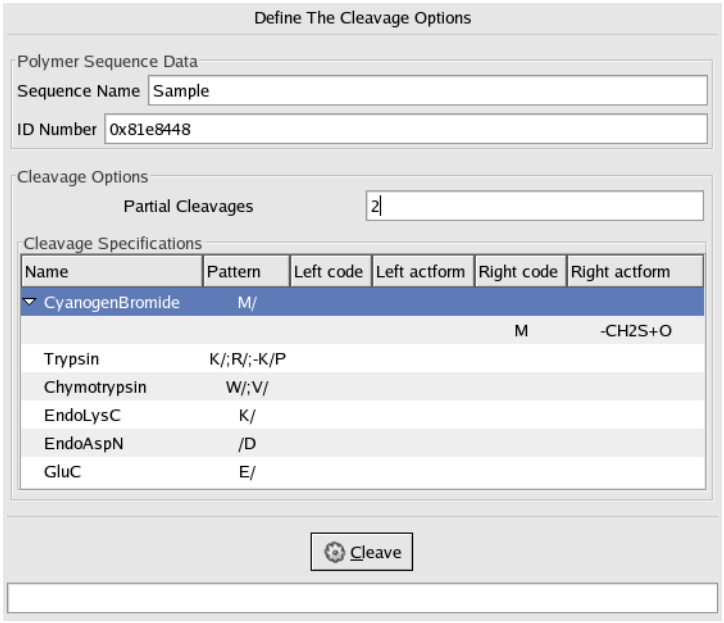

Figure 8.7: **Cleavage options window.** This figure shows the window with which the user is provided when she performs a polymer sequence cleavage. The user can select one cleavage specification and specify what level of partial cleavage the chemical cleavage should perform.

Cleavage Of Polymer Sequences

It happens very often that polymer sequences get cleaved in a sequence-specific manner. These specific cleavages do occur very often in nature, and are made by enzymes that do cleave biopolymer sequences, like the glycosidases (cleaving saccharides), the proteases (cleaving proteins) or the nucleases (cleaving nucleic acids). But the scientist also uses purified enzymes to perform such cleavages in the test tube. ***polyxmass*** must be able to perform thoses cleavages *in silico*. Let's see how a polymer sequence can be cleaved using ***polyxmass***.

It is a matter of having a polymer sequence opened in an editor window and selecting the *Chemistry*$\longrightarrow$*Cleave* menu. The user is provided with a window where a number of cleavage specifications are listed (Figure 8.7). These cleavage specifications are listed by looking into the polymer chemistry definition corresponding to the polymer sequence to be cleaved. The program knows, for example, that the polymer sequence to be cleaved is of the "protein" chemistry type, and thus will list all the cleavage specifications that were defined in the "protein" polymer chemistry definition. The cleavage specifications are available for the user to select one of them to perform the cleavage.

The user selects the cleavage specification of interest and also sets the number of partial cleavages that the cleaving agent may yield. In our example, ***2*** was entered, which means that the cleavage reaction will yield the set of oligomers corresponding to a total cleavage (no missed cleavages=partial cleavages 0) along with the set of oligomers corresponding to 1 missed cleavage and to 2 missed cleavages. The calculating process is extremely rapid, so the user may enter rather high values here.

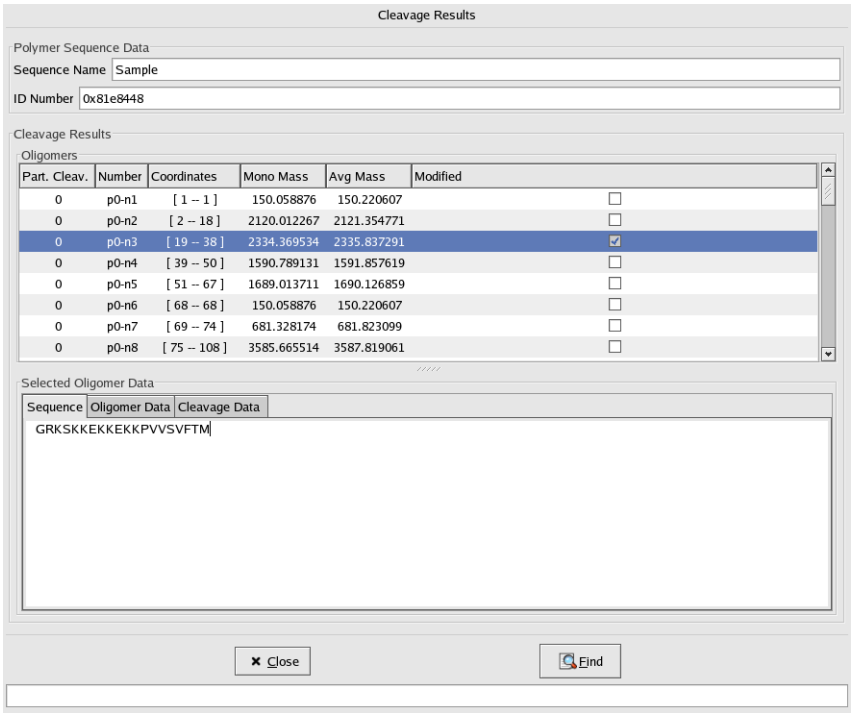

Figure 8.8: **Cleavage-generated oligomers window.** This figure shows the window that is opened so that the oligomers generated upon cleavage of a polymer sequence can be displayed. Other data are also displayed (see text for details).

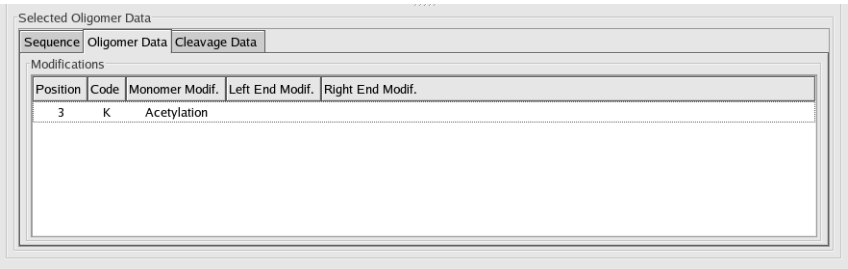

Figure 8.9: **Cleavage-generated oligomers' data.** This figure shows the notebook tab in which data pertaining to a selected oligomer are displayed. In particular, this tab contains a listview where monomer modifications of the selected oligomer (if any) are displayed.

Upon successful termination of the cleavage reaction, the user is provided with a new window (Figure 8.8 on the preceding page) in which all the oligomers that were generated are listed (upper pane). The listview widget on the upper pane sports a number of columns. Each row of this listview widget describes the properties of a single oligomer. The different columns are detailed below:

- ⋆ Part. Cleav. This is the missed cleavage level for which the oligomer was generated;
- ⋆ Number This is the number of the oligomer, so that the user may refer to it simply. The syntax is simple: px-ny means that this oligomer is the oligomer number y from the set of oligomers obtained in the x-missed cleavages series;
- ⋆ Coordinates These are the coordinates of the oligomer as it is occurring in the polymer sequence that was cleaved in the first place. For example, "[19-38]" would mean that the oligomer starts at position 19 and ends at position 38 of the polymer sequence, both values being inclusive;
- ⋆ Mono Mass This is the monoisotopic mass of the oligomer, computed using the options that are set in the Calculation Options window (see section 15 on page 71);
- ⋆ Avg Mass Same as above, but for the average mass;
- ⋆ Modified Indicates if the oligomer contains an intrinsically-modified monomer (it does not mean that the modification's mass was taken into account, it simply says that at least one monomer is modified in the oligomer. See below for details).

The lower pane of the Cleavage Results window contains a number of additional data, displayed in a set of pages belonging to the Selected Oligomer Data notebook widget:

- ⋆ Sequence (Figure 8.8 on the preceding page) This is the sequence that is displayed when an oligomer is selected in the listview displaying the oligomers (in the upper pane);
- ⋆ Oligomer Data (Figure 8.9) This is the place where monomer modifications are listed as soon as an oligomer that contains modified monomers is selected in the listview. Note that each modified monomer in the selected oligomer will show up as a row in this listview.

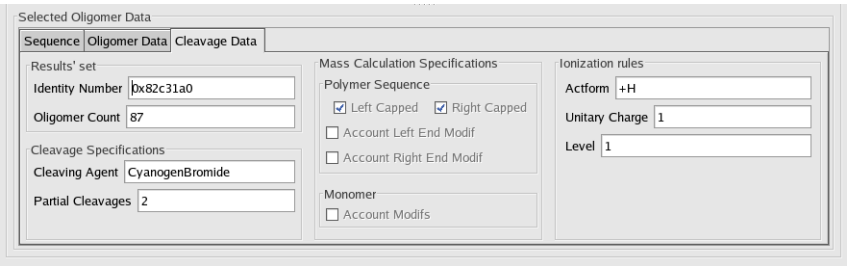

Figure 8.10: **Cleavage specification data.** This figure shows the notebook tab in which data pertaining to the cleavage operation are displayed.

- ⋆ Cleavage Data (Figure 8.10) This is the place where the cleavage operation configuration is reported, so that each cleavage results' displaying window is self-traceable to both the cleavage configuration and the polymer sequence that was cleaved in the first place.

The button labelled Find will allow the user to find masses in the oligomers that were generated upon the cleavage reaction simulation (see section 18 on the next page)

Fragmentation Of Polymer Sequences

It happens very often that polymer sequences need to be fragmented in the gas phase (in the mass spectrometer) so that structure characterizations may be performed. For protein chemistry, this happens very often in order to get sequence information for a given peptide ion selected in the gas phase. ***polyxmass*** must be able to perform those fragmentations *in silico*. Let's see how a polymer sequence can be fragmented using ***polyxmass***.

It is a matter of having a polymer sequence opened in an editor window and selecting the sequence region to be fragmented. Once this is done, the user selects the *Chemistry⟶Fragment* menu. The user is provided with a window where a number of fragmentation specifications are listed (Figure 8.11 on the following page). These fragmentation specifications are listed by looking into the polymer chemistry definition corresponding to the polymer sequence to be fragmented. The program knows, for example, that the polymer sequence to be cleaved is of the "protein" chemistry type, and thus will list all the fragmentation specifications that were defined in the "protein" polymer chemistry definition.

The user selects the fragmentation specification(s) of interest and clicks the Fragment button.

Upon successful termination of the fragmentation reaction, the user is provided with a new window (Figure 8.12 on page 85) in which all the oligomers that were generated are listed (upper pane). The listview widget on the upper pane sports a number of columns. Each row of this listview widget describes the properties of a single oligomer. The different columns are detailed below:

- ⋆ Frag. Spec. This is the name of the fragmentation specification that was used to compute the corresponding fragment;
- ⋆ Name This is the name of the oligomer, so that the user may refer to it simply. The syntax is simple: x-y means that this oligomer is the oligomer number y from the fragmentation specification x;

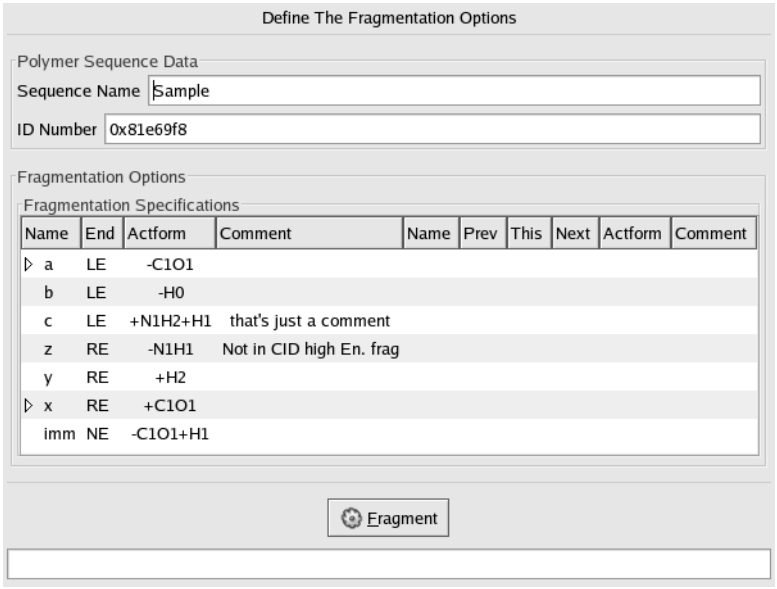

Figure 8.11: **Fragmentation options window.** This figure shows the window with which the user is provided when she performs a polymer sequence fragmentation. The user can select one or more fragmentation specifications (patterns).

- ⋆ Mono Mass This is the monoisotopic mass of the oligomer, computed using the options that are set in the Calculation Options window (see section 15 on page 71);
- ⋆ Avg Mass Same as above, but for the average mass;
- ⋆ Modified Indicates if the oligomer contains an intrinsically-modified monomer (it does not mean that the modification's mass was taken into account, it simply says that at least one monomer is modified in the oligomer. See below for details).

The Sequence, Oligomer Data and Fragmentation Data pages of the notebook in the Selected Oligomer Data frame widget are conceptually identical to the ones described at the section 18 on page 80).

The button labelled Find will allow the user to find masses in the oligomers that were generated upon the fragmentation reaction simulation (see section 18).

Finding Masses In The Results

It is often necessary to make sure that a mass –observed in the real mass spectrum– actually corresponds to an oligomer that was generated during a previous simulation experiment (like a cleaving of the polymer sequence with a given cleavage agent or a fragmentation of a simple mass searching operation –see section 18 on page 88). To allow this, and as shown in Figures 8.8 to 8.12 on pages 81–85, it is possible to ask that masses be found into the oligomers resulting from any previous simulation (cleavage or fragmentation of a polymer sequence or arbitrary mass search operations). Indeed, the button labelled Find will open a window where the user may enter masses to be found.

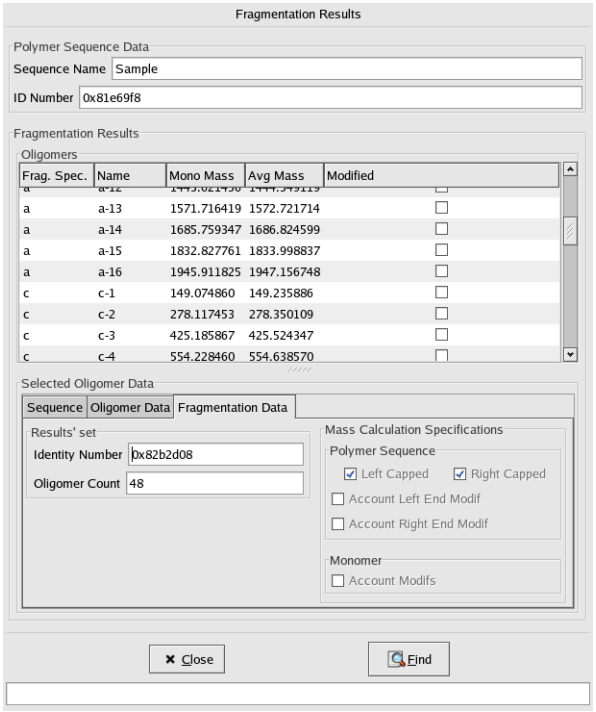

Figure 8.12: **Fragmentation-generated oligomers window.** This figure shows the window that is opened so that the oligomers generated upon fragmentation of a polymer sequence can be displayed.

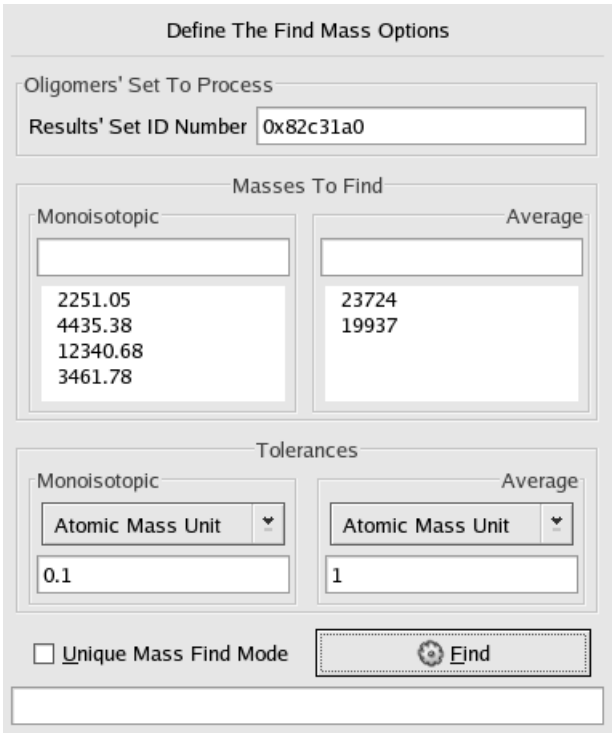

Figure 8.13: **Finding masses in a set of oligomers.** This figure shows how to ask that masses be found in a set of oligomers that result, for example, from the cleavage of a polymer sequence.

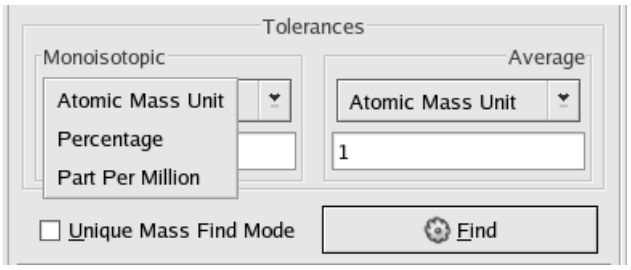

Figure 8.14: **Tolerances available in finding masses.** This figure shows the three different ways that tolerances can be configured.

The Figure 8.13 on the facing page illustrates how easy it is to defines the mass(es) to be found in a set of oligomers, either in the monoisotopic mass list or in the average mass list. There are two ways to actually trigger the mass finding operation:

- ⋆ When the Unique Mass Find Mode checkbutton *is* checked: the user must enter one mass in the single-line text entry widget and hitting the Find button or the ENTER issues the "Find Mass" request. For this to happen properly, it is necessary that only one of the two single-line text entry widgets be filled with a mass (either monoisotopic or average). This is because if there are two masses entered in the widgets, the program would not know which one of the monoisotopic or average masses is to be found in the set of oligomers.

- ⋆ When the Unique Mass Find Mode checkbutton is *not* checked: the user may enter masses in whatever the single- or multi-line widgets (either by keying-in one mass per line or by pasting a preformatted list of masses). In the present case, hitting the ENTER key will trigger the "multi-mass" mass finding operation only if the Find button has the focus. A click onto the Find button will do!

Prior to asking that masses be found, it is required that tolerances be entered for either monoisotopic or average masses (or both if both kinds of masses are of interest) in their respective text entry widget. In the example of Figure 8.13 on the preceding page, the tolerance that is given to the mass finding operation on monoisotopic masses is of ***0.1*** amu, while the one for the average masses is greater (***1*** amu). These values must be understood in a "broad" manner (*i.e.* ± tolerance): for example, if we searched for a mass ***1000*** with a ***0.5*** amu tolerance, we would get all the oligomers having masses ranging $[1000 - 0.5 \rightarrow 1000 + 0.5]$ (which is [999.5–1000.5] *and not [999.75–1000.25]*). The Figure 8.14 shows that there are two other means to define the tolerance with which masses should be found. They all are self-explanatory and should also be understood in the same "broad" manner described above.

The oligomers that were found to comply with the masses to find and with the tolerances defined are displayed in a window similar to the one shown in Figure 8.15 on the next page.

Note that here also the traceability of the data is ensured using unambiguous identity numbers (Results' Set ID Number). This identity number is unique and describes the results window in which the user has asked that masses be found (see Figure 8.13 on the facing page).

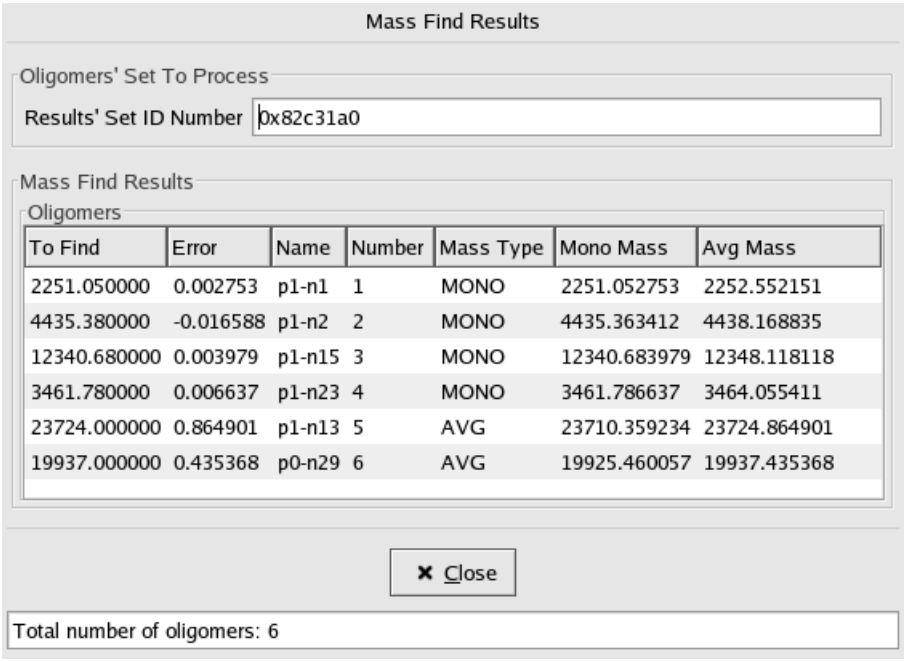

Figure 8.15: **Finding masses in a set of oligomers.** This figure shows oligomers that were found in a set of oligomers after a mass finding operation has been performed.

Searching Masses In The Polymer Sequence

It may happen that the scientist needs to know if some polymer sequence region would have a given mass. ***polyxmass*** allows for mass searching operations in the polymer sequence. This is done by using the menu *Chemistry⟶Search Mass(es)*. The window illustrated in Figure 8.16 on the next page shows up and the user enters masses to search for (see section 18 on page 84 for details on the workings of a very similar window).

Once the masses have been searched, if results are found they are displayed in the window shown in Figure 8.17 on page 90. This window has very similar characteristics to the ones of the previously described results' windows (see section 18 on page 80, for example).

The button labelled Find will allow the user to find masses in the oligomers that were generated upon the mass searching operation (see section 18 on page 84.

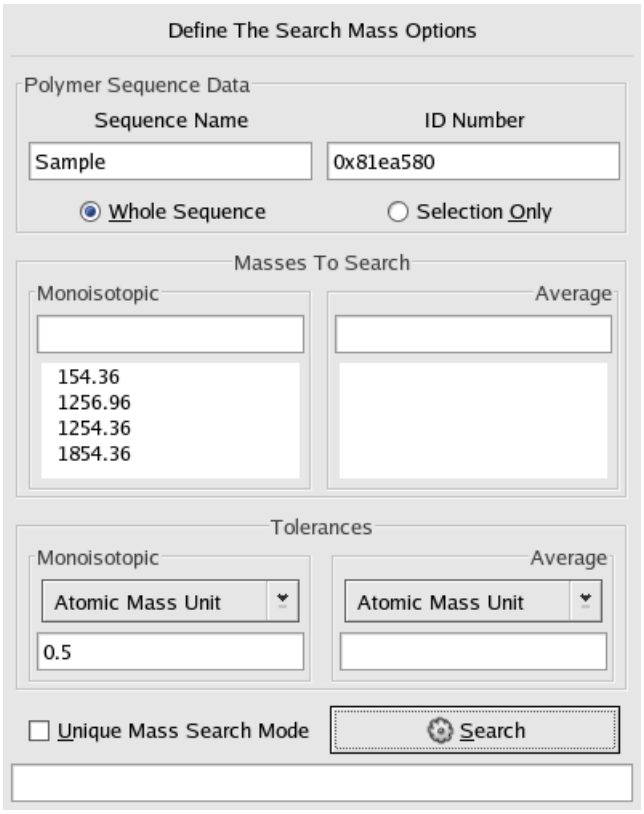

Figure 8.16: **Finding masses in a polymer sequence.** This figure shows how to ask that masses be searched in a polymer sequence.

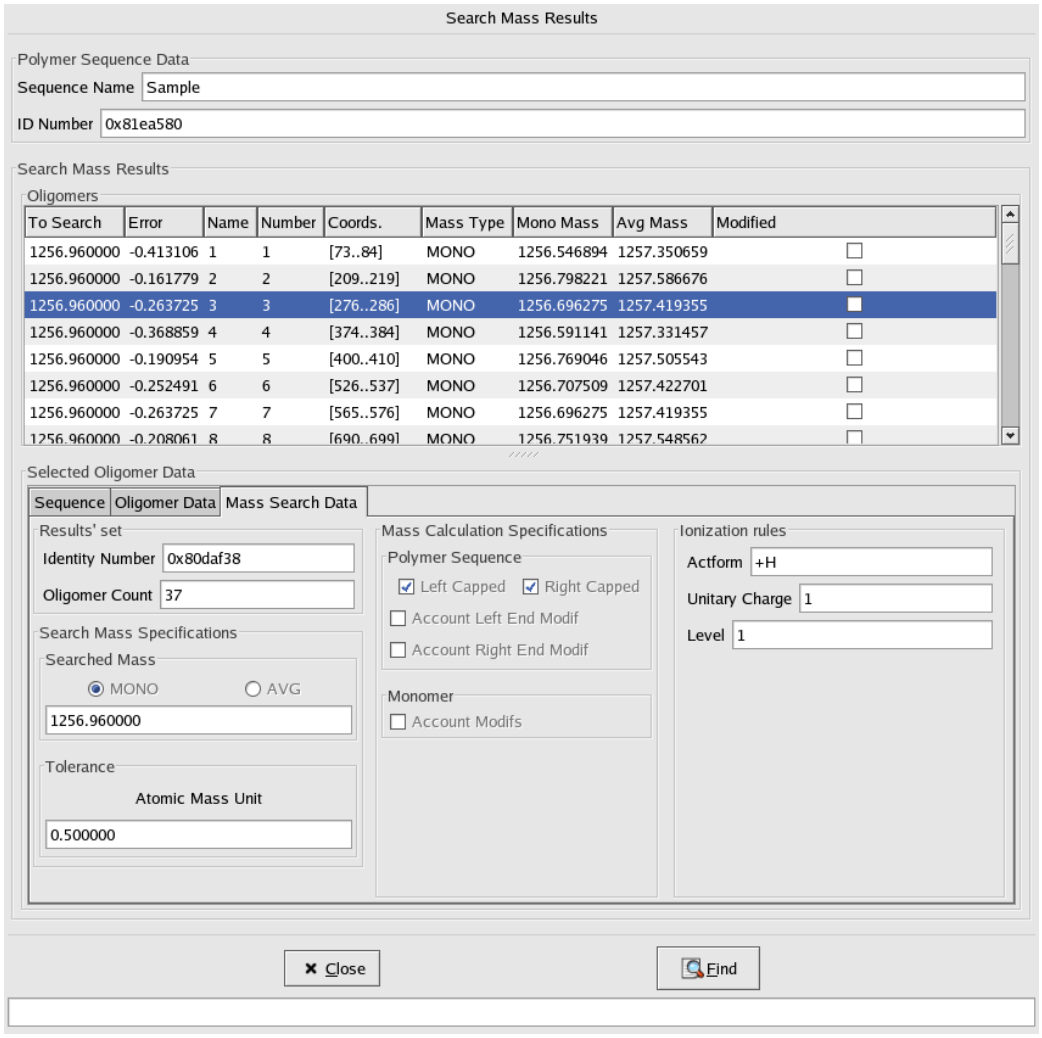

Figure 8.17: **Results window after searching masses in a a polymer sequence.** This figure shows the oligomers that were found upon a mass search operation.

9

The *polyxmassdata* module: The Configuration Data Hierarchy

The ***polyxmass*** software suite is designed to be compatible with any polymer chemistry that the user may want to define. To be that flexible, ***polyxmass*** has to be able to store polymer chemistry definition-related data in a very clearly designed set of data directories and files. This configuration data hierarchy (which relates in some ways to a "filesystem") is what this chapter is all about.

After having read this chapter, the reader will be able to configure the ***polyxmass*** configuration data filesystem hierarchy in such a way that a brand new polymer chemistry

definition is made available to the ***polyxmass*** software suite. The creation of a brand new polymer chemistry definition is typically performed using the ***polyxdef*** module; see chapter 6 on page 47. This chapter will focus on how to register this new polymer chemistry definition with the ***polyxmass*** software suite.

A polymer chemistry definition is only useful to edit any polymer sequence that complies with it (this editing is typically done with the ***polyxedit*** module, see chapter 8 on page 67), if it is associated with graphical files that are used by the sequence editor to render the sequence graphically. This chapter will teach the user to configure the ***polyxmass*** filesystem in such a way that the graphical files can be automatically used by the polymer sequence editor when a given sequence is opened in ***polyxedit***. Further, the chemical modification of a polymer sequence, or chemical reactions simulations can only be performed if the polymer chemistry definition file is correctly integrated in the whole ***polyxmass*** filesystem hierarchy.

What Gets Installed With ***polyxmassdata***

When the user installs the ***polyxmassdata*** package, a number of files get installed in the destination directory that was chosen by the user if the package was installed by a method that allows using an option specifying in which directory the installation should be performed (see the chapter 2 on page 9).

The following listing lists the files that are installed when the ***polyxmassdata*** package is installed (using an un-modified `polyxmassdata` ***rpm*** package), in the `/usr` system directory. This list was slightly edited to remove a number of lines that do not bring more information than what is needed to start figuring out the general architecture of the filesystem hierarchy of the ***polyxmass*** software suite.

- Non polymer-specific configuration files:

  `/usr/etc/polyxmass.d/polyxmassdata.conf`

  `/usr/lib/pkgconfig/polyxmassdata.pc`

  `/usr/share/polyxmassdata/polymer-definition.dtd`

  `/usr/share/polyxmassdata/atoms.xml`

  `/usr/share/polyxmassdata/chempad.conf`

  `/usr/share/polyxmassdata/cursor.svg`

  `/usr/share/polyxmassdata/poldefs-dictionary.dic`

- Polymer-specific configuration files:

  - "protein/peptide" polymer chemistry definition:

    `/usr/share/polyxmassdata/protein.xml`
    `/usr/share/polyxmassdata/peptide.xml`

    `/usr/share/polyxmassdata/protein/monomer-modif.dic`

```
/usr/share/polyxmassdata/protein/alanine-text.svg
/usr/share/polyxmassdata/protein/alanine.png
/usr/share/polyxmassdata/protein/alanine.svg
/usr/share/polyxmassdata/protein/acetyl-text.svg
/usr/share/polyxmassdata/protein/acetyl.png
/usr/share/polyxmassdata/protein/acetyl.svg
/usr/share/polyxmassdata/protein/arginine-text.svg
/usr/share/polyxmassdata/protein/arginine.png
/usr/share/polyxmassdata/protein/arginine.svg
⋮
/usr/share/polyxmassdata/protein/valine-text.svg
/usr/share/polyxmassdata/protein/valine.png
/usr/share/polyxmassdata/protein/valine.svg
```

- "dna" polymer chemistry definition:

```
/usr/share/polyxmassdata/dna.xml

/usr/share/polyxmassdata/dna/monomer-modif.dic

/usr/share/polyxmassdata/dna/adenine-text.svg
/usr/share/polyxmassdata/dna/adenine.png
/usr/share/polyxmassdata/dna/adenine.svg
⋮
/usr/share/polyxmassdata/dna/thymine-text.svg
/usr/share/polyxmassdata/dna/thymine.png
/usr/share/polyxmassdata/dna/thymine.svg
```

- "rna" polymer chemistry definition:

```
/usr/share/polyxmassdata/rna.xml

/usr/share/polyxmassdata/rna/monomer-modif.dic

/usr/share/polyxmassdata/rna/adenine-text.svg
/usr/share/polyxmassdata/rna/adenine.png
/usr/share/polyxmassdata/rna/adenine.svg
⋮
/usr/share/polyxmassdata/rna/methyl-text.svg
/usr/share/polyxmassdata/rna/methyl.png
/usr/share/polyxmassdata/rna/methyl.svg
/usr/share/polyxmassdata/rna/uracile-text.svg
/usr/share/polyxmassdata/rna/uracile.png
/usr/share/polyxmassdata/rna/uracile.svg
```

- "ose/saccharide" polymer chemistry definition:

```
/usr/share/polyxmassdata/ose.xml
/usr/share/polyxmassdata/saccharide.xml

/usr/share/polyxmassdata/saccharide/monomer-modif.dic

/usr/share/polyxmassdata/saccharide/allose-text.svg
/usr/share/polyxmassdata/saccharide/allose.png
/usr/share/polyxmassdata/saccharide/allose.svg
⋮
/usr/share/polyxmassdata/saccharide/xylose-text.svg
/usr/share/polyxmassdata/saccharide/xylose.png
/usr/share/polyxmassdata/saccharide/xylose.svg
/usr/share/polyxmassdata/saccharide/xylulose-text.svg
/usr/share/polyxmassdata/saccharide/xylulose.png
/usr/share/polyxmassdata/saccharide/xylulose.svg
```

⋆ Example polymer sequence files:

```
/usr/share/polyxmassdata/polseqs/dna-sample.pxm
/usr/share/polyxmassdata/polseqs/long-protein-sample.pxm
/usr/share/polyxmassdata/polseqs/ose-sample.pxm
/usr/share/polyxmassdata/polseqs/protein-fragments-sample.pxm
/usr/share/polyxmassdata/polseqs/protein-sample.pxm
/usr/share/polyxmassdata/polseqs/rna-sample.pxm
```

⋆ User manual files:

```
/usr/share/polyxmassdata/userman/*
```

Let's review these files and comment on them:

⋆ The `/usr/etc/polyxmass.d` directory will contain default configuration files for the different graphical modules that comprise the ***polyxmass*** software suite. For example, when the user installs the ***polyxedit*** package, this directory will contain the default configuration file for this package: `polyxedit.conf`. This directory also contains the most crucial configuration file of the whole ***polyxmass*** software suite: `polyxmassdata.conf`, that is described below.

⋆ `/usr/etc/polyxmass.d/polyxmassdata.conf` This file contains one line:

```
polyxmassdata=/usr/share/polyxmassdata
```

This line indicates what is the directory that contains all the ***polyxmass***' filesystem hierarchy, as it is installed by the ***polyxmassdata*** package. In the present case, since the package was installed using an ***rpm*** package, the `/usr` system directory was the target installation directory and all the data were installed in the

directory.[1] This directory is the main ***polyxmass*** configuration and polymer chemistry data files repository. The ***polyxmass***' modules very often query this file in order to know where to search for configuration data (typically to know where to search polymer chemistry definition files).

We will see that the user may duplicate this repository in one of his owned directories in order to modify the configuration and polymer chemistry definition files for her own use. ***polyxmass*** can be made aware of this new user-owned location very easily, by simply editing one or more files.

⋆ `/usr/share/polyxmassdata/atoms.xml` This file contains the definition of all the isotopes of all the chemical elements that a polymer scientist may have to use in her chemistry simulations. Each atom (chemical element) is actually defined using a set of isotopic mass/relative abundance pairs. The monoisotopic mass is by default (and that is the normal chemical situation) the mass of the lightest isotope. The average mass, as used by the ***polyxmass*** simulations, is computed by taking into account all the *isotopic mass/relative abundance* ratios. There is only one file per system that describes the atoms.

⋆ `/usr/share/polyxmassdata/poldefs-dictionary.dic` This file contains a number of lines, like the ones below:

```
protein=protein.xml%protein
long-protein=long-protein.xml%long-protein
dna=dna.xml%dna
rna=rna.xml%rna
saccharide=saccharide.xml%saccharide
ose=ose.xml%saccharide
peptide=peptide.xml%protein
```

Each line is made of 3 parts. The part left of the '=' sign specifies a *polymer chemistry type*, exactly as it may be referenced in a polymer sequence file. The part left the '%' sign specifies in what file the polymer chemistry is defined. The last part of the line is the name of the directory where the polymer chemistry definition-specific files are located. This directory *must itself be located in the directory that is described in the* `polyxmassdata.conf` main configuration file (see above). In our example, that means that the "protein" chemistry-specific files should be located in the `/usr/share/polyxmassdata/protein` directory.

Interestingly, as we can see, two different polymer chemistry definition types ("protein" and "peptide" may point to the same `protein` polymer chemistry-specific directory, while being defined in two different polymer chemistry definition files (respectively `protein.xml` and `peptide.xml`). The same applies for the "saccharide" and "ose" polymer chemistry types.

⋆ The `/usr/share/polyxmassdata/protein.xml` file is the file where the "protein" polymer chemistry is defined. This file is the one that is associated to the "protein"

[1] The `/usr/share` directory is a standard location for data installed by *rpm* packages, while source *tar.gz* packages install their data in `/usr/local/share` by default.

polymer chemistry definition type in the `poldefs-dictionary.dic` file described above. These polymer chemistry definition files are typically produced by using the ***polyxdef*** module.

- The `/usr/share/polyxmassdata/protein/monomer-modif.dic` file is the file where a number of very important polymer chemistry-specific data are stored. This file contains a number of lines like the following (the numbers at the beginning of some lines were added to ease commenting below):

```
1 A=alanine.svg|alanine.png
C=cysteine.svg|cysteine.png
D=aspartate.svg|aspartate.png
4 S,T$Phosphorylation%T%phospho.svg|phospho.png
5 D$Amidation%O%asparagine.svg|asparagine.png
Y$Phosphorylation%T%phospho.svg|phospho.png
7 !$Acetylation%T%acetyl.svg|acetyl.png
E$Amidation%O%glutamine.svg|glutamine.png
```

  The first line tells that the monomer having a code 'A' should be graphically rendered –in the polymer sequence editor– using one of two graphics files: `alanine.svg` or `alanine.png`. Indeed, when graphically rendering a monomer code in a polymer sequence (by creating a "monomer icon", or "monicon"), the ***polyxedit*** polymer sequence editor first tries to read the "scalar vector graphics" file (`alanine.svg`). This graphics format allows rendering the monomer icon at maximum quality whatever the monicon size requested by the user in the polymer sequence editor. If this rendering fails, for some reason, the program falls back to using the other graphics file (a "raster graphics" file). The raster graphics file cannot be resized without loss of image quality (see the chapter 8 on page 67).

  The fourth line indicates that the monomers having code 'S' or 'T' (in protein chemistry, these are seryl and threonyl residues) may be chemically modified using a modification called "Phosphorylation". The way the "Phosphorylation" modification should be rendered graphically is by compositing 'T'ransparently (see the %T%) the `phospho.svg` or the `phospho.png` transparent graphics files onto the monicon of the monomer being modified (see the chapter 8 on page 67).

  The fifth line shows another graphical compositing rule. This time the rule is not 'T'ransparency, but involves an 'O'paque graphical compositing (see the %O%). This line says that when a monomer of code 'D' is modified using an "Amidation" modification, its monomer icon should be *replaced* using a monomer icon rendered *ex novo* by reading either the scalar vector graphics file `asparagine.svg` or –if something is wrong with this file– the raster graphics file `asparagine.png`.

  The seventh line shows the use of the "joker" '!' character. This '!' character stands for *"all the monomer codes of the polymer chemistry definition"*. This line means that any monomer code in the "protein" polymer chemistry definition may be acetylated using the "Acetylation" modification, according to a graphical rendering rule of transparent compositing of the `acetyl.svg` (or the `acetyl.png`) graphics file onto the monomer icon of the modified monomer.

- The `/usr/share/polyxmassdata/protein/alanine.svg` is the file that contains the scalar vector graphics representation of the "Alanine" monomer. This file was

created using the ***Sodipodi*** software (see chapter 1 on page 1, section 1 on page 4), by converting the textual representation of the monomer (that is a 'A' character) to curves prior to saving the file as a *svg*-formatted file.

- The `/usr/share/polyxmassdata/protein/alanine-text.svg` is provided as a convenience to the user. This is the file that was used to produce the previous one. But this file contains a textual representation of the 'A' character. This file is not correctly interpreted by the ***polyxedit*** polymer sequence editor and should only be used as a model.

- The `/usr/share/polyxmassdata/protein/alanine.png` was prepared by exporting the contents of the `alanine.svg` file to a *png*-formatted file (all this from ***Sodipodi***).

  It is noteworthy that in theory, if all the scalar vector graphics files (*svg* files) are correctly interpreted by the polymer sequence editor, the raster vector graphics files (*png* files) should be totally redundant and useless. However, the *png* file-reading libraries are much more robust than the *svg* file-reading libraries (*svg* is a rather recent standard). This is why it is wise to always provide the polymer sequence editor with a fall-back solution in the form of a raster graphics file to be used in case the monicon rendering from the scalar vector graphics file fails.

- A number of files corresponding to a number of different polymer chemistry definitions are shown so that the user may grasp the way these polymer chemistry definitions are organized in the ***polyxmass*** filesystem hierarchy.

- The `/usr/share/polyxmassdata/polseqs/protein-sample.pxm` is an example of a sequence of the polymer chemistry type "protein". There are other polymer sequences of other polymer chemistry types.

- The `/usr/share/polyxmassdata/userman` directory contains a number of files (including the one that I'm typing right now) that are used to compile the user manual file `polyxmass.pdf`. The command to issue so that the documentation file is compiled is (issue this command twice to resolve the cross-references):

```
bash-2.04 $ pdflatex polyxmass.tex ↩
bash-2.04 $ pdflatex polyxmass.tex ↩
```

Other files are both polymer chemistry-specific or not. For example, each polymer chemistry may have a ***polyxcalc*** chemical pad configuration file. There is one `chempad.conf` file that is general (see the listing above). This `chempad.conf` file is located in the main ***polyxmass*** configuration data directory. The user may define one such file for any polymer chemistry definition. In this case each polymer chemistry definition-specific directory (itself located in the ***polyxmass*** main configuration directory, as we have seen above) may have its own `chempad.conf` file. ***polyxcalc*** will thus read the `chempad.conf` file corresponding to the polymer chemistry definition that is currently loaded in the calculator. If no `chempad.conf` file is found in the polymer chemistry definition-specific directory, the default one is read.

Opening A Polymer Sequence: All The Events

In this section we'll review the internal mechanisms that make the ***polyxedit*** module load the proper polymer chemistry definition file when a polymer sequence is loaded. This will enhance the reader's understanding of the reason why the filesystem hierarchy is that complex.

So, let's start the ***polyxedit*** module of the ***polyxmass*** mass spectrometric software suite, and open a file from the ***polyxmassdata*** distribution. We see that the file selection window points directly to the `polseqs` subdirectory of the main ***polyxmass*** data configuration directory. Let's select the `protein-sample.pxm` file, that is a polymer sequence of polymer chemistry *type* "protein". What does the ***polyxedit*** program do in order to know how to render that sequence in the polymer sequence editor? Let's review that mechanics, but first I suggest that you use your favorite text editor (mine is ***Emacs***) to open that same file. You'd see the following (only part of the file is reproduced below):

```
<polseqdata>
  <polseqinfo>
    <type>protein</type>
    <name>Sample</name>
    <code>SP2003</code>
    <author>rusconi</author>
    <date>
      <year>2003</year>
      <month>05</month>
      <day>13</day>
    </date>
  </polseqinfo>
  <polseq>
```

What you see here is that the `protein-sample.pxm` file contains the *type* of the polymer of which it is (`<type>protein</type>`). That *type* is –in our present case– "protein".

What we have done *right now*, the ***polyxedit*** module does exactly the same way: it opens the file, reads it until it finds the `<type></type>` set of *XML* element tags. When it has found them it just reads the contents of the `<type>` element. That is the "protein" string.

By knowing of what polymer chemistry type the polymer sequence being opened is, ***polyxedit*** can continue its work: it will first query the dictionary file responsible for making the correspondence between each available polymer chemistry type and its definition file. That dictionary file is `poldefs-dictionary.dic`, that we have described earlier. ***polyxedit*** will thus search the line that starts with "protein". This line reads as follows:

```
protein=protein.xml%protein
```

What ***polyxedit*** understands here is that the file that contains the polymer chemistry definition of the polymer chemistry type "protein" is `protein.xml` (check the Appendix to see what this file looks like). Now that ***polyxedit*** knows what file contains the "protein" polymer chemistry definition, it has all the chemical "toolset" to compute masses and perform chemical simulations, like cleavages or fragmentations or whatever.

But what about the graphical rendering of the polymer sequence we are asking to open in the ***polyxedit***'s polymer sequence editor window? What the line above tells ***polyxedit***

is that the "protein"-specific files are located in the `protein` directory, itself located in the ***polyxmass*** main data configuration directory. We have briefly described above the contents of this `protein` directory. What ***polyxedit*** now needs to know is what graphics file to use for any given monomer found in the polymer sequence that is described in the `protein-sample.pxm` file. The correspondence between each monomer code (in the polymer chemistry definition) and the graphics file to be used to render it graphically in the polymer sequence editor is made in a dictionary file located in the polymer chemistry-specific directory (`protein`, for us now):

`monomer-modif.dic`

This file contains lines like the ones described above, that I reproduce here for convenience:

```
1 A=alanine.svg|alanine.png
C=cysteine.svg|cysteine.png
D=aspartate.svg|aspartate.png
4 S,T$Phosphorylation%T%phospho.svg|phospho.png
5 D$Amidation%O%asparagine.svg|asparagine.png
Y$Phosphorylation%T%phospho.svg|phospho.png
7 !$Acetylation%T%acetyl.svg|acetyl.png
E$Amidation%O%glutamine.svg|glutamine.png
```

When ***polyxedit*** reads the `protein-sample.pxm` file it will get the sequence of that protein in the form of a "stream" of monomer codes. Each time it gets a new monomer code it will check what graphics file it should use to render this monomer graphically. If a monomer is described as being modified (in the polymer sequence file), it will perform the graphical operation described by the corresponding line (see lines 4–7 above). Of course there are implementation specifics that I do not describe that allow to make a tight memory management.[2]

Now that we know how ***polyxmass*** copes with the flexibility required to handle any polymer chemistry, we can start thinking of ways to configure it in ways that suit the user's needs.

Configurability By The User

Any single bit of information in ***polyxmass*** is modifiable by the user. That is a prerequisite for a powerful program designed in the most exquisite ***GNU*** tradition. When the ***polyxmassdata*** package is installed, it comes with "default" configuration data[3]. These configuration data are simply examples and are not considered ready for publication of scientific work. The user is required to double-check all these example data before considering for publication any result yielded by the ***polyxmass*** software suite.

In the section above, we have seen that all these configuration data are located in the ***polyxmass*** main configuration directory (it was the

`/usr/share/polyxmassdata`

[2] By never loading twice in memory the same graphics file, for example (these files use up a lot of memory).

[3] Here, configuration is intended "at large", since it refers both to filesystem configuration and to all the polymer chemistry files which "configure" the chemistry of a polymer, or to the graphics files that "configure" the way monomers should be rendered graphically in the sequence editor.

directory). That directory is a subdirectory of the `/usr/share` system directory, and the user needs system priviledges to modify files in these directories.

Let's imagine that the user wants to modify some files to suit her "chemical needs". Or that she wants to modify the way some monomers are rendered graphically in the polymer sequence editor. Unfortunately, it may happen that the user cannot have system priviledges, so she cannot modify the files that were installed by the system administrator. The solution is very simple: copy the entire (or part of) ***polyxmass*** main data configuration directory into a location that she owns or can access with modification priviledges. For the sake of our example, let's consider that the user's login is "rusconi" and that his HOME directory is `/home/rusconi`. Let's continue considering that the "rusconi" user wants to duplicate the ***polyxmass*** data configuration filesystem in `/home/rusconi/polyxmassdata` by issuing the following command:

```
bash-2.04 $ cp --rpf /usr/share/polyxmassdata /home/rusconi ↩
```

Once this configuration data duplication is done, it is necessary to let the ***polyxmass*** software suite know that when any of its modules is run it should search for configuration data in her new location and not in the default installation location (described in detail above).

When the ***polyxdef***, ***polyxcalc*** and ***polyxedit*** packages belonging to the ***polyxmass*** software suite are installed, their default configuration is stored in a file that is located in the `/usr/etc/polyxmass.d` directory.[4]

When the user runs any one ***polyxdef***, ***polyxcalc*** or ***polyxedit*** program, the program in question checks the user's home directory (`/home/rusconi`) for a `.polyxmass.d` directory containing the corresponding package's configuration file (for example, the ***polyxedit*** package has a configuration file named `polyxedit.conf`).

If the `.polyxmass.d` directory is not found, it is created and the

```
/usr/etc/polyxmass.d/polyxmassdata.conf
```

file is copied in it. If the package's configuration file is not found it is copied in the user's `.polyxmass.d` directory straight from `/usr/etc/polyxmass.d/`. For example, when the user "rusconi" runs ***polyxedit*** for the first time ever, this program will check the existence of the

```
/home/rusconi/.polyxmass.d/polyxedit.conf
```

file. If this file is not found it is copied straight from the `/usr/etc/polyxmass.d/` directory with its default contents.

Now, how does a user tell ***polyxmass*** that the configuration data are not to be searched for in the default directory, but in one user-customized directory? That is simply done by editing the user's copy of the `polyxmassdata.conf` file.

Indeed, when any program of the ***polyxmass*** software suite is executed, it first checks if there is a user's configuration directory named `.polyxmass.d`. If it finds that directory, the program checks if there is a `polyxmassdata.conf` file in it. If it finds that file, it reads the configuration directory from it. Since this file is copied from the main `/usr/etc/polyxmass.d` directory in the first place, it contains the default data configuration directory, namely the following line:

[4] Assuming that the packages were installed with the **`--prefix=/usr`** option, or with un-modified ***rpm*** packages.

```
polyxmassdata=/usr/share/polyxmassdata
```

But, we know that user "rusconi" wants ***polyxmass*** to search the configuration files not in the default configuration directory, but in `/home/rusconi/polyxmassdata`. To achieve this, user "rusconi" would only have to change the line above to:

```
polyxmassdata=/home/rusconi/polyxmassdata
```

in the `/home/rusconi/.polyxmass.d/polyxmassdata.conf` file.

As a summary, I can list the contents of the `/home/rusconi/.polyxmass.d` directory after having:

- Installed all the ***rpm*** packages in the usual order;
- Run the ***polyxdef***, ***polyxcalc*** and ***polyxedit*** programs one after the other.

Here are the contents of this directory:

```
polyxmassdata.conf
polyxdef.conf
polyxcalc.conf
polyxedit.conf
```

Let's now see the contents of each file in this directory:

- `polyxmassdata.conf`

```
polyxmassdata=/usr/share/polyxmassdata
```

- `polyxdef.conf`

```
<?xml version="1.0" encoding="UTF-8" standalone="yes" ?>

<package_conf>

<package_name>polyxdef</package_name>

<gladedir>/usr/share/polyxdef/glade</gladedir>

</package_conf>
```

- `polyxcalc.conf`

```
<?xml version="1.0" encoding="UTF-8" standalone="yes" ?>

<package_conf>
```

```
<package_name>polyxcalc</package_name>

<gladedir>/usr/share/polyxcalc/glade</gladedir>

</package_conf>
```

⋆ `polyxedit.conf`

```
<?xml version="1.0" encoding="UTF-8" standalone="yes" ?>

<package_conf>

<package_name>polyxedit</package_name>

<gladedir>/usr/share/polyxedit/glade</gladedir>

<numformats>
<numformat_atom>%.10f</numformat_atom>
<numformat_monomer>%.5f</numformat_monomer>
<numformat_oligomer>%.4f</numformat_oligomer>
<numformat_polymer>%.3f</numformat_polymer>
</numformats>

</package_conf>
```

Note that for the last `polyxedit.conf` file, the user may wish to configure a special directory where her polymer sequences are stored. This is performed by adding right after the `<gladedir>/usr/share/polyxedit/glade</gladedir>` line the following line, for example:

`<datadir>/home/rusconi/laboratory/sequences</datadir>`

What this line says it just that the polymer sequences for the user "rusconi" are stored in the directory that is set between the `<datadir></datadir>` tags. When the user will either open, or save, or save..as a polymer sequence, the file selection window will automatically open with this directory preset. This is merely a convenience feature.

If this line is not configured, then the default location where ***polyxmass*** thinks that polymer sequences are stored is the `polseqs` directory that is itself located in the data configuration directory (in our examples it was either

`/usr/share/polyxmassdata/polseqs`

or the

`/home/rusconi/polyxmassdata/polseqs`

depending on wether we refer to the default data configuration directory of the one that user "rusconi" wanted to configure for himself (see above for the whole story).

Appendices

The Protein Chemistry Definition File

```
<?xml version="1.0" standalone="no"?>
<!DOCTYPE poldefdata SYSTEM
                  "/usr/share/polyxmassdata/polymer-definition.dtd">

<poldefdata>
  <type>protein</type>
  <leftcap>+H</leftcap>
  <rightcap>+OH</rightcap>
  <codelen>1</codelen>
  <ionizerule>
    <actform>+H</actform>
    <charge>1</charge>
    <level>1</level>
  </ionizerule>
  <monomers>
    <mnm>
      <name>Glycine</name>
      <code>G</code>
      <formula>C2H3NO</formula>
    </mnm>
    <mnm>
      <name>Alanine</name>
      <code>A</code>
      <formula>C3H5NO</formula>
    </mnm>
    <mnm>
      <name>Valine</name>
      <code>V</code>
      <formula>C5H9NO</formula>
    </mnm>
    <mnm>
      <name>Leucine</name>
      <code>L</code>
      <formula>C6H11NO</formula>
    </mnm>
    <mnm>
      <name>Isoleucine</name>
```

```
    <code>I</code>
    <formula>C6H11NO</formula>
  </mnm>
  <mnm>
    <name>Serine</name>
    <code>S</code>
    <formula>C3H5NO2</formula>
  </mnm>
  <mnm>
    <name>Threonine</name>
    <code>T</code>
    <formula>C4H7NO2</formula>
  </mnm>
  <mnm>
    <name>Cysteine</name>
    <code>C</code>
    <formula>C3H5NOS</formula>
  </mnm>
  <mnm>
    <name>Methionine</name>
    <code>M</code>
    <formula>C5H9NOS</formula>
  </mnm>
  <mnm>
    <name>Arginine</name>
    <code>R</code>
    <formula>C6H12N4O</formula>
  </mnm>
  <mnm>
    <name>Lysine</name>
    <code>K</code>
    <formula>C6H12N2O</formula>
  </mnm>
  <mnm>
    <name>Aspartate</name>
    <code>D</code>
    <formula>C4H5NO3</formula>
  </mnm>
  <mnm>
    <name>Glutamate</name>
    <code>E</code>
    <formula>C5H7NO3</formula>
  </mnm>
  <mnm>
    <name>Asparagine</name>
    <code>N</code>
    <formula>C4H6N2O2</formula>
  </mnm>
  <mnm>
    <name>Glutamine</name>
```

```
      <code>Q</code>
      <formula>C5H8N2O2</formula>
    </mnm>
    <mnm>
      <name>Tryptophan</name>
      <code>W</code>
      <formula>C11H10N2O</formula>
    </mnm>
    <mnm>
      <name>Phenylalanine</name>
      <code>F</code>
      <formula>C9H9N1O</formula>
    </mnm>
    <mnm>
      <name>Tyrosine</name>
      <code>Y</code>
      <formula>C9H9N1O2</formula>
    </mnm>
    <mnm>
      <name>Histidine</name>
      <code>H</code>
      <formula>C6H7N3O</formula>
    </mnm>
    <mnm>
      <name>Proline</name>
      <code>P</code>
      <formula>C5H7N1O1</formula>
    </mnm>
  </monomers>
  <modifs>
    <mdf>
      <name>Phosphorylation</name>
      <actform>-H+H2PO3</actform>
    </mdf>
    <mdf>
      <name>Acetylation</name>
      <actform>-H+C2H3O</actform>
    </mdf>
    <mdf>
      <name>Amidation</name>
      <actform>-OH+NH2</actform>
    </mdf>
    <mdf>
      <name>SulfideBond</name>
      <actform>-H2</actform>
    </mdf>
  </modifs>
  <cleavespecs>
    <cls>
      <name>CyanogenBromide</name>
```

```
      <pattern>M/</pattern>
      <lr-rule>
        <re-mnm-code>M</re-mnm-code>
        <re-actform>-CH2S+O</re-actform>
      </lr-rule>
    </cls>
    <cls>
      <name>Trypsin</name>
      <pattern>K/;R/;-K/P</pattern>
    </cls>
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