1 Introduction

OOMPA is a suite of object-oriented tools for processing and analyzing large biological data sets, such as those arising from mRNA expression microarrays or mass spectrometry proteomics.

This vignette documents the base package, oompaBase. Frankly, it is only here because the BioConductor coding standards require it. The oompaBase package only defines one thing, a class union allowing you to use “numeric” or “NULL” objects in the design of an S4 class. At least as recently as R 1.9, you could not declare a class union and instantiate it in the same package. As a consequence, this base package was created.

End users should never need to invoke this package directly. Developers might want to require it if they have their own need for the class union.

The real action starts with the PreProcess package, which you should read about next.