Object Oriented Microarray and Proteomics Analysis (OOMPA)

Kevin R. Coombes

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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.