An introduction to *ADRminer*

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Abstract

This vignette provides an introductory tutorial to the ıADRminer package for the R software. This package implements tools to handle and analyse spontaneous reports. This vignette introduces basic functionalities of the package. It is aimed to show how to load the data into R and use the different automated detection methods implemented in the package.

1 Introduction

2 Getting Started

2.1 Installing ADRminer

Make sure you have a recent version of R ($\geq$ 2.13.0) by typing:

```
> R.version.string
```

ADRminer relies on several packages. In particular, it depends on LBE which is hold on the Bioconductor website. You can install LBE by typing

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("LBE")
```

Then, install adrminer with dependencies using:

```
> install.packages("adrminer", dep=TRUE)
```

2.2 Data Format

For now, ADRminer can handle three types of data input format. The simplest one, when one do not want to introduce individual characteristics, is a three column data file which must contain

1. The drug labels
2. The AE labels
3. The corresponding numbers of Adverse Drug Reactions (ADRs)

This data format is the one which was used for the former version of this package (PhViD).

When one dispose of individual charasteristics such as sex or age of the patients or date recording of the spontaneous reports, ADRminer accepts two different data format. The first one must be made of one file with three mandatory columns

1. The spontaneous report (or observation) identifier
2. The drug labels
3. The AE labels

The subsequent columns represent individual characteristics such as age, gender. It is important to note that with this format, when an SR involve several drug and several AE, it is split into several lines where each line represents one drug AE event combination. Note also that this format leads to duplicate individual characteristics for each drug AE combinations. Here is an example of such data file

```
> library(ADRminer)
> data(sr1)
> head(sr1)
```

```
       id  drugId     aeId sex age     date
369489  1 L01AA01 10029330   2  56 28/03/00
259193  2 B05XB03 10002646   2  78 26/11/98
261691  3 C07AA05 10020955   2  95 07/12/98
257944  4 J01EA01 10018800   1  38 20/11/98
262073  5 N06AA09 10010922   2  67 08/12/98
259654  6 N05AF05 10029282   1  55 28/11/98
```

An alternative to this repetition is to use two different data files as input. The first one one is made of the three mandatory columns described above. The second file contain individual characteristics. Obviously, in order to match both files, the latter must contain in the first column An SR identifier.

One the data file(s) loaded into R (this can be done with the read.table function), the next step is to transform these raw data into objects that ADRminer can handle. Depending on whether one work with aggregated data (first format), or inidividual data (second and third format), this is achieved with two different command lines