

What is dpeaqms?

Howsun Jow

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1 Overview

dpeaqms stands for **D**ifferential **P**rotein **E**xpression **A**nalysis using **Q**uantitative **M**ass **S**pectrometry. More specifically it is a statistical tool for the analysis of quantitative proteomic data, obtained from mass spectrometric analyses of isobaric labelled protein samples, for differential protein expression between groups of samples.

A Bayesian statistical approach is used for the analysis carried out in this package and it makes use of the JAGS (Just Another Gibbsian Sampler) software library via the rjags package.

2 Design

The package provides three functions. The first, `dpeaqms.csv2msms`, is a utility function for the conversion of csv files into a data structure that the other functions can interpret. This is an R data frame object with the columns "experiment", "protein", "msmsid", "sample", "group" and "intensity".

The second function, `dpeaqms.mcmc`, is the analysis function. This samples from the posterior distribution of the model parameters using a Markov Chain Monte Carlo (MCMC) algorithm. The output of the function an object of type `mcmc.list` as in the coda package. The third function is another utility function. It extracts the samples from the `mcmc.list` object output `dpeaqms.mcmc` and writes them to tsv files.

The users is under no obligation to make use of the utility functions and can both convert their own data to a compatible data frame object and perform their own analysis on the output of the `dpeaqms` function.

3 References

tbc.