DAnTE: a statistical tool for quantitative analysis of -omics data

Ashoka D. Polpitiya, Wei-Jun Qian, Navdeep Jaitly, Vladislav A. Petyuk, Joshua N. Adkins, David G. Camp II, Gordon A. Anderson and Richard D. Smith*

Pacific Northwest National Laboratory, Richland, WA 99352, USA

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ABSTRACT
Summary: Data Analysis Tool Extension (DAnTE) is a statistical tool designed to address challenges associated with quantitative bottom-up, shotgun proteomics data. This tool also has been demonstrated for microarray data and can easily be extended to other high-throughput data types. DAnTE features selected normalization methods, missing value imputation algorithms, peptide-to-protein rollup methods, an extensive array of plotting functions and a comprehensive hypothesis-testing scheme that can handle unbalanced data and random effects. The graphical user interface (GUI) is designed to be very intuitive and user friendly.

Availability: DAnTE may be downloaded free of charge at http://omics.pnl.gov/software/

Contact: rds@pnl.gov or proteomics@pnl.gov

Supplementary information: An example dataset with instructions on how to perform a series of analysis steps is available at http://omics.pnl.gov/software/

2 DESCRIPTION
2.1 Dependencies

The graphical user interface (GUI) of DAnTE is implemented using the C# language, and the core algorithms are implemented in the open source R statistical environment (R Development Core Team, 2008). DAnTE runs on a Microsoft WindowsXP platform within a .NET 2.0 framework. The connectivity between R and the C#/DCOM server application (Bairer and Neuwirth, 2007). This unique choice of environments makes DAnTE a very user friendly software tool, even though it cannot integrate into the popular Bioconductor (Gentleman et al., 2004) project.

2.2 Application features

2.2.1 Data loading The input data to DAnTE can be any file that stores tabular data, including flat files (either CSV or tab-delimited text files) and Microsoft Excel files. A unique feature of the data loading mechanism is that it preserves peptide-to-protein mapping information for use later in plotting peptides that belong to a particular protein, as well as in the peptides-to-protein rollup methods. In addition, DAnTE can also process SEQUEST (Eng et al., 1994) results and create spectral count tables.

2.2.2 Factor definitions Factors are used to capture the fixed and random effects in experimental design. For example, the biological condition is a fixed effect factor, while a list of liquid chromatography (LC) columns used to separate the samples can be treated as a random effect. This information is vital in normalization, imputation and hypothesis testing methods in DAnTE. Factors can either be declared once the data is loaded or be loaded from a flat file.

2.2.3 Investigative plots Various statistical plots, including histograms, box plots, correlation diagrams and MA (or R-I: ratio-intensity) plots can be plotted in DAnTE. These plots help the user evaluate reproducibility within the study set and single-out problematic datasets so that they can be excluded from further analysis.

2.2.4 Data normalization As normalization is arguably the most important step in downstream data analysis, DAnTE employs several normalization methods that have been successfully tested for both proteomics data (Callister et al., 2006) and microarray genomics data (Quackenbush, 2002; Smyth et al., 2003).
Among them are a robust linear regression method, lowess method and a quantile normalization method. In addition, global intensity adjustment based on median absolute deviation (MAD) and central tendency adjustment methods are also available.

### 2.2.5 Missing value imputation

Incomplete datasets due to missing values are common with high-throughput proteomics. As imputing these values is a much-debated topic (Troyanskaya *et al*., 2001), DAnTE offers several simple methods, as well as some advanced algorithms to choose from. The simple methods allow the user to fill in missing values with either the dataset mean/median or with a pre-chosen constant. Advanced methods include filling in with a row mean based on a user-defined factor, K-nearest neighbor imputation (KNNimpute), and singular value decomposition-based imputation (SVDimpute).

### 2.2.6 Peptide-to-protein rollup

In most proteomics methods, peptide measurements are rolled up to corresponding protein abundances. Ideally, all peptides from a single protein should have similar abundances that manifest as similar signal intensities; however, in reality many factors, such as digestion efficiency, electrospray ionization efficiency, etc., can affect the identifications and abundances or signal intensities of peptides. In the RRollup method available in DAnTE, peptides that originate from the same protein are first scaled on the basis of a chosen reference peptide in order to bring all peptide profiles across biological conditions to the same level and then averaged to obtain the protein abundance. During scaling, the peptide with the most observations is chosen as the reference peptide and its total abundance across datasets is used as a tiebreaker. In the ZRollup method, a scaling method similar to z-scores (except that medians instead of means from peptide profiles across biological conditions are used) is applied first to peptides that originate from a single protein and then the scaled peptides are averaged to obtain relative protein abundance. In both RRollup and ZRollup methods, outlying peptide values are excluded from protein abundance calculations, using a Grubbs’ outlier test (Grubbs, 1969). In the third QRollup method, peptides are selected on the basis of a user selected abundance cutoff value, and protein abundance is calculated as the average of these selected peptides.

### 2.2.7 Analytical algorithms

DAnTE offers several well-characterized algorithms to further explore patterns in the data. Traditional principal component analysis (Jolliffe, 2002) and associated scores and loadings plots can be useful as an unsupervised way of finding the principal variation in the data. In contrast, the partial least squares method (Wold *et al*., 1984) available in DAnTE can be used as a discrimination procedure whereby the grouping information is assigned using factors. Hierarchical and k-means clustering methods on features/samples are also available as part of the heat map plotting function.

### 2.2.8 Hypothesis testing

A comprehensive ANOVA scheme for unbalanced studies that uses marginal sums of squares (Fox, 1997) and mixed models (Pinheiro and Bates, 2000) is included in DAnTE. The user can also test for interactions among factors in a multi-way analysis of variance (ANOVA). The q-values are also calculated.
along with the p-values in order to control the false discovery rate in multiple testing (Storey, 2002). In addition, DAnTE can check whether the data follows a normal distribution by employing the Shapiro–Wilks test and features two non-parametric hypothesis tests (Wilcoxon rank sum test and Kruskal–Wallis test) when the normality assumption fails to hold.

3 SUMMARY

DAnTE is designed as a complete downstream analysis tool that incorporates a host of algorithms for large-scale bottom-up proteomics data. This tool features an interactive GUI interface and harnesses the power of R statistical environment; its uniqueness lies in its ability to handle incomplete data and to roll peptides up to proteins. Though designed specifically for analyzing proteomics data, DAnTE performs equally well on genomics microarray data.

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REFERENCES


