

Skyline: an open source document editor for creating and analyzing targeted proteomics experiments

Brendan MacLean^{1,*}, Daniela M. Tomazela¹, Nicholas Shulman¹, Matthew Chambers², Gregory L. Finney¹, Barbara Frewen¹, Randall Kern³, David L. Tabb², Daniel C. Liebler⁴ and Michael J. MacCoss¹

¹Department of Genome Sciences, University of Washington, Seattle, WA 98195, ²Department of Biomedical Informatics, Vanderbilt University, Nashville, TN 37232, ³Microsoft Corporation, Redmond, WA 98195 and

⁴Department of Biochemistry, Vanderbilt University, Nashville, TN 37232, USA

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ABSTRACT

Summary: Skyline is a Windows client application for targeted proteomics method creation and quantitative data analysis. It is open source and freely available for academic and commercial use. The Skyline user interface simplifies the development of mass spectrometer methods and the analysis of data from targeted proteomics experiments performed using selected reaction monitoring (SRM). Skyline supports using and creating MS/MS spectral libraries from a wide variety of sources to choose SRM filters and verify results based on previously observed ion trap data. Skyline exports transition lists to and imports the native output files from Agilent, Applied Biosystems, Thermo Fisher Scientific and Waters triple quadrupole instruments, seamlessly connecting mass spectrometer output back to the experimental design document. The fast and compact Skyline file format is easily shared, even for experiments requiring many sample injections. A rich array of graphs displays results and provides powerful tools for inspecting data integrity as data are acquired, helping instrument operators to identify problems early. The Skyline dynamic report designer exports tabular data from the Skyline document model for in-depth analysis with common statistical tools.

Availability: Single-click, self-updating web installation is available at <http://proteome.gs.washington.edu/software/skyline>. This web site also provides access to instructional videos, a support board, an issues list and a link to the source code project.

Contact: brendanx@u.washington.edu

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1 INTRODUCTION

In recent years, the promise of targeted proteomics has gained significant attention. However, the tools for its practice have been either limited and cumbersome or proprietary and specific to a particular instrument vendor (Supplementary Text 1). Skyline was explicitly designed to accelerate targeted proteomics experimentation and foster broad sharing of both methods and results

across instrument platforms (Supplementary Fig. 1). The software is developed under the open source Apache 2.0 License as part of the ProteoWizard project. An official public release is freely available and currently in use in many proteomics labs, both commercial and academic.

2 DESIGN AND IMPLEMENTATION

Skyline uses the MSData component of the ProteoWizard Data Access Library (Kessner *et al.*, 2008) to provide unprecedented import of native output files from Agilent, Applied Biosystems, Thermo Fisher Scientific and Waters triple quadrupole instruments (Supplementary Text 2, Fig. 2). File conversion is unnecessary, although Skyline can also read selected reaction monitoring (SRM) data in XML formats (Supplementary Material). This critical requirement favored the choice of C# and Windows Forms as a development platform, since all of the required vendor libraries existed as Windows-only DLLs, and ProteoWizard already had a common language infrastructure binding.

Other considerations in the choice of C# and Windows Forms included:

- Familiar Windows-based graphical user interface that is intuitive to learn and use.
- High-performance, low-latency, rich data interaction.
- ClickOnce installation, which makes Skyline easy to install from a web site without administrator privileges, as well as self-updating.
- Growing availability of open source and freely available C# software like ZedGraph, NHibernate, SQLite.NET and DigitalRune docking windows.

The development of Skyline as a rich-client application presented the opportunity to build classic, event-driven, document-view software with its unique multilevel undo and redo support (Supplementary Fig. 3). This architecture gives Skyline powerful method editing capabilities that can easily be undone and makes it responsive in displaying large amounts of complex graphical data. We use an immutable tree (Okasaki, 1998) for the document model to maintain these features while performing background processing.

*To whom correspondence should be addressed.

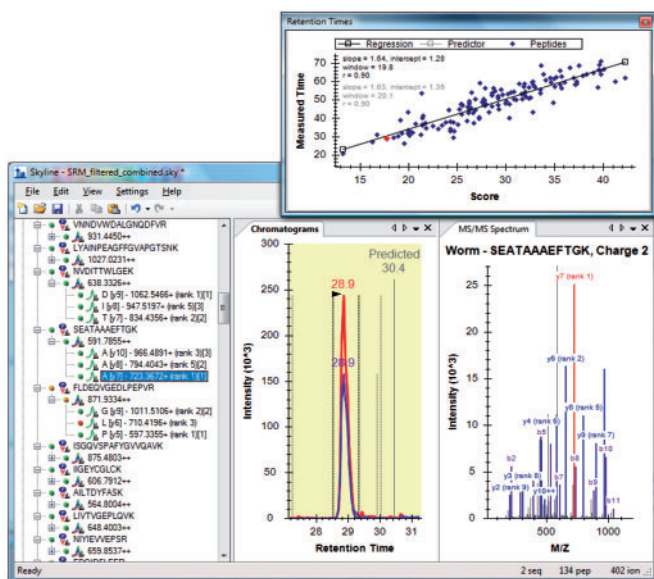


Fig. 1. Skyline user interface with results, retention time prediction and spectral library views.

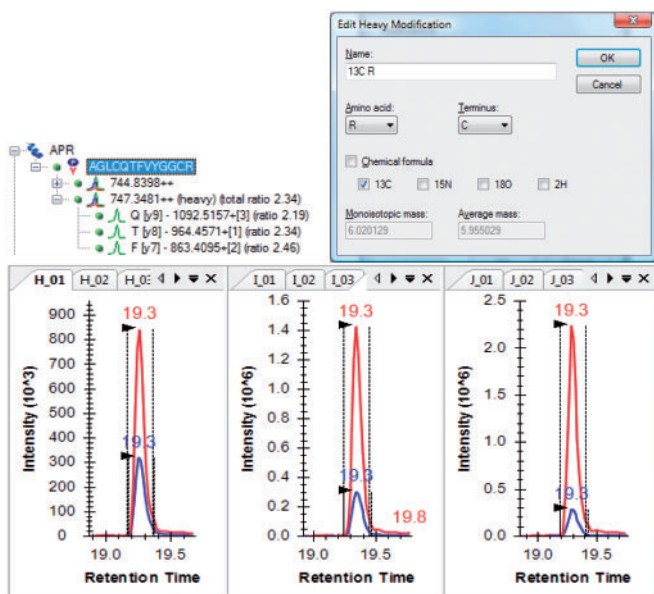


Fig. 2. Skyline support for isotope-labeled internal standards and quantitation.

2.1 Method building

Skyline provides several ways of building and editing SRM methods. Most users establish their Skyline document by pasting protein sequences or lists of peptides, precursors and product ion transitions either into a dialog or directly into the document. Transition lists and results for private and published experiments, including MRMer (Martin *et al.*, 2008) and CPTAC Study 7 (Addona *et al.*, 2009), conducted before Skyline was developed, are easily recreated in Skyline through these mechanisms.

Peptides can also be typed into the document. A background Proteome database, built from the FASTA formatted sequences for an experiment's expected protein matrix, adds further direct editing features like auto-complete from protein description fragments, protein names and peptide sequences (Supplementary Fig. 4). Skyline digests proteins and fragments peptides *in silico* to support direct peptide, precursor and transition picking, as well as automated picking using filters or spectral libraries.

2.2 Spectral library support

Skyline supports reading a variety of public spectral library formats (Supplementary Text). It also builds BiblioSpec libraries (Frewen *et al.*, 2006) (Supplementary Fig. 5) from the peptide search results of many common search engines (Supplementary Text). These custom-built libraries provide full access to library features for peptide spectrum matches acquired in local labs as well as those stored in repositories like PeptideAtlas (Desiere *et al.*, 2006).

Matching spectra are shown in a graph pane with ion peak intensity ranking expressed in both the graph and document tree (Fig. 1). Transitions matching the most intense ions can be automatically selected, as described previously (Prakash *et al.*, 2009), and imported results can be compared with the spectra for verification of ion ratios when no labeled internal standard is present.

2.3 Quantitation

Because of the high sensitivity and specificity of SRM, it has been widely used for quantitative measurements using labeled internal standards. Skyline fully supports these experiments with dialogs for defining static and heavy isotope modifications (Fig. 2) and assigning them broadly or explicitly to individual peptides. After importing result files, Skyline calculates ratios between the unlabeled peptide and the labeled internal standard and provides direct editing of integration boundaries.

2.4 Results analysis

Results analysis in Skyline begins with importing SRM mass spectrometer files in either native or portable format. Skyline caches them in a single high-performance data file which is usually a small fraction of the size of the original files, can be loaded in under a second for experiments with over 50 sample injections and simplifies sharing even complex experiments (Supplementary Fig. 6). During cache creation, the CRAWDAD peak detector (Finney *et al.*, 2008) is used to calculate transition peaks which are then grouped by precursor and stored for quick display in a chromatogram graph pane. With enough screen resolution, Skyline can display useful information in 10 or more graph panes simultaneously and update them all as the selection changes without noticeable latency (Fig. 2). Hydrophobicity scores from SSRCalc (Krohnkin *et al.*, 2004) can be displayed in these graphs to increase confidence in peptide identification using retention time prediction (Fig. 1).

The unique Skyline custom report designer provides complete access to the data contained in the document model, allowing it to be flexibly exported to comma separated value format for further analysis with statistical tools like Excel and R (Supplementary Fig. 7).

3 SUMMARY AND FUTURE DIRECTION

Skyline development continues under the demands of its funding projects with regular public updates and enhancements expected. We hope Skyline will foster broad advances in the use and sharing of targeted proteomics methods and their results.

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REFERENCES

- Addona,T. *et al.* (2009) Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. *Nat. Biotech.*, **27**, 633–641.
- Desiere,F. *et al.* (2006) The PeptideAtlas project. *Nucleic Acids Res.*, **34**, D655–D658.
- Finney,G. *et al.* (2008) Label-free comparative analysis of proteomics mixtures using chromatographic alignment of high-resolution μ LC-MS data. *Anal. Chem.*, **80**, 961–971.
- Frewen,B.E. *et al.* (2006) Analysis of peptide MS/MS spectra from large-scale proteomics experiments using spectrum libraries. *Anal. Chem.*, **78**, 5678–5684.
- Kessner,D. *et al.* (2008) ProteoWizard: open source software for rapid proteomics tools development. *Bioinformatics*, **24**, 2534.
- Krokhin,O.V. *et al.* (2004) An improved model for prediction of retention times of tryptic peptides in ion pair reversed-phase HPLC. *Mol. Cell. Proteomics*, **3**, 908–919.
- Martin,D.B. *et al.* (2008) MRMer: an interactive open-source and cross-platform system for data extraction and visualization of multiple reaction monitoring experiments. *Mol. Cell. Proteomics*, **7**, 2270–2278.
- Okasaki,C. (1998) *Purely Functional Data Structures*. Cambridge University Press, Cambridge, UK, pp. 11–14.
- Prakash,A. *et al.* (2009) Expediting the development of targeted SRM assays: using data from shotgun proteomics to automate method development. *J. Proteome Res.*, **8**, 2733–2739.