"HYDRA: A live demo".   Authors: Gordon W. Slysz, CJ Baker, Benjamin M. Bozsa, Anthony Dang, David C. Schriemer
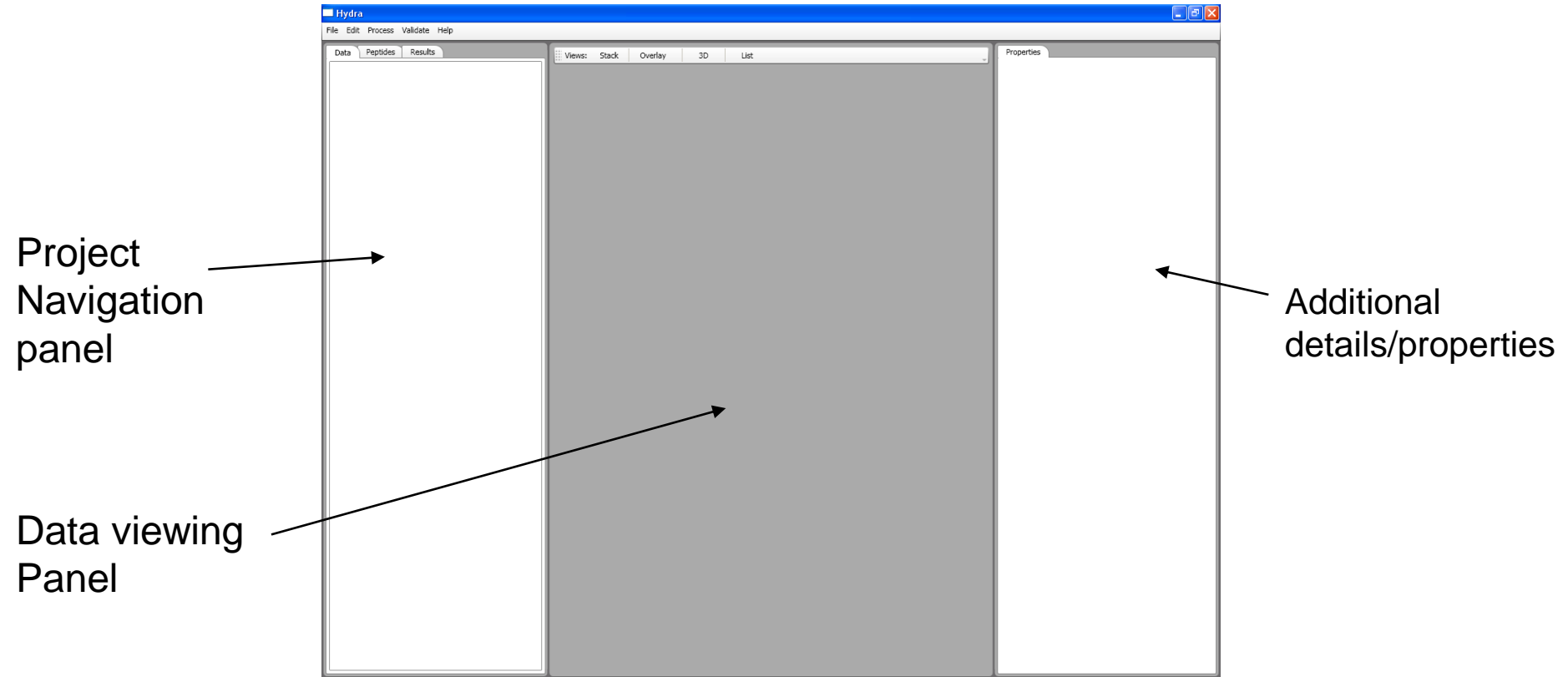
HYDRA

** note: This was originally presented as a live demo. Here, three Scenerios will represent that which was presented at the HDX-MS Workshop
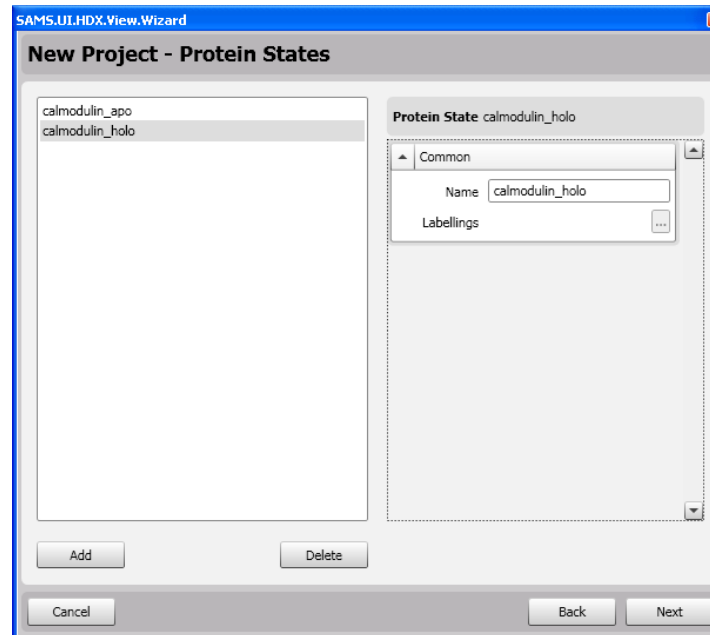
HYDRA's Layout

Project Navigation panel

Data viewing Panel

Additional details/properties

Scenerio 1: Defining the Project

Step 1: Define protein states

Scenerio 1: Defining the Project

Step 2: Define labelling conditions
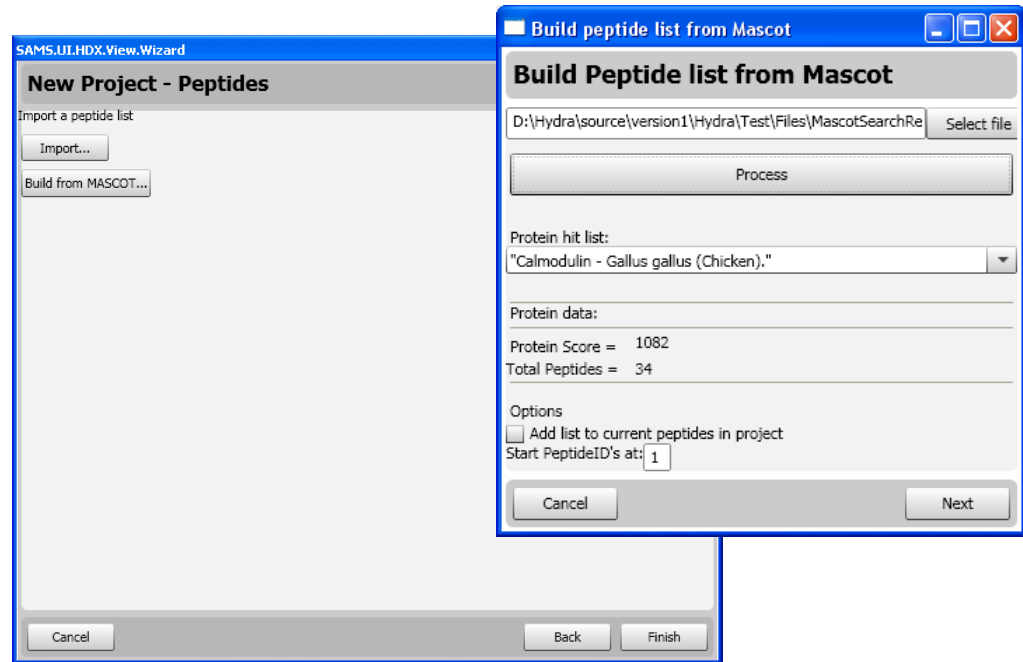
Scenerio 1: Defining the Project

Step 3: Associate Experiment Runs with Protein State and Labelling Condition
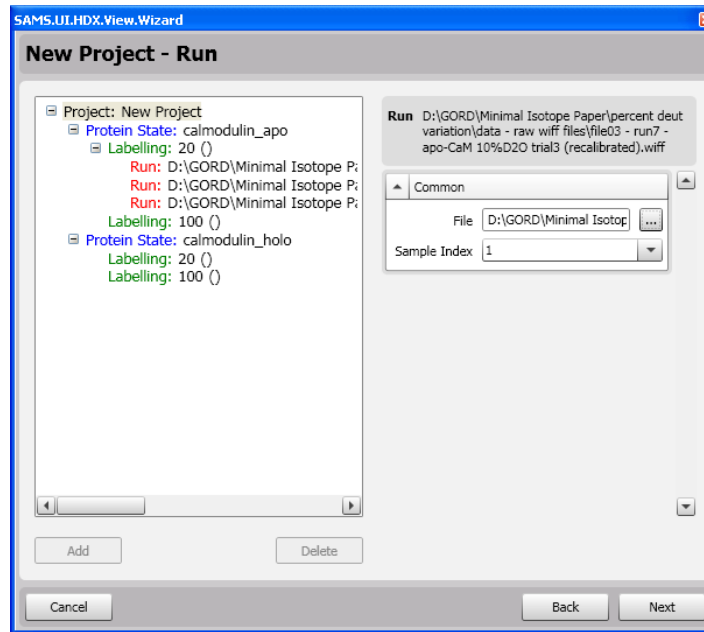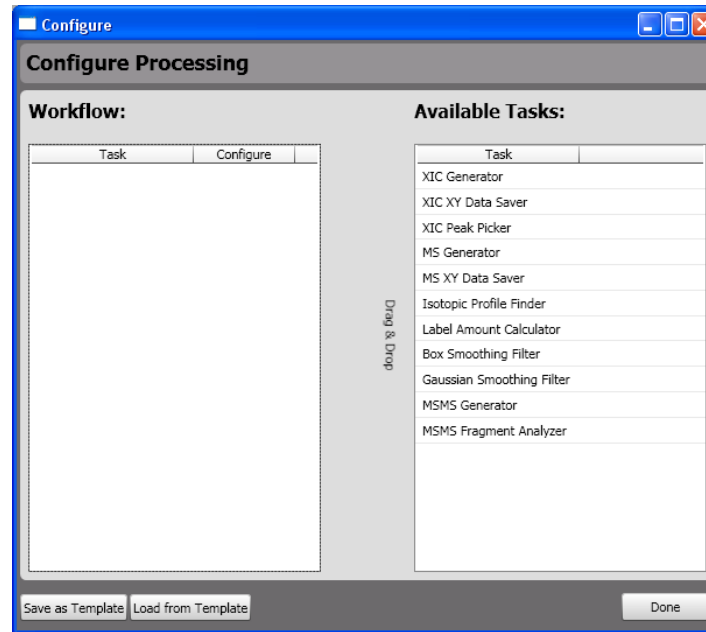
Scenerio 1: Defining the Project

Step 4 (Final step): Generate Peptide list by either importing a previous list or building a list from a MASCOT search result
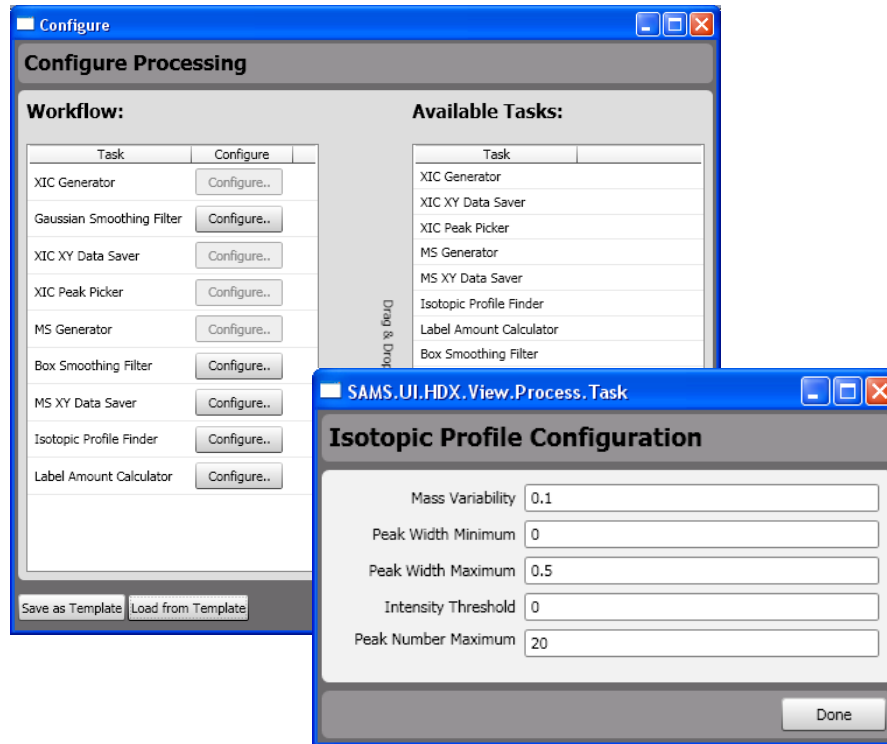
Scenerio 2: Defining the Data Processing Workflow

Step 1: Drag and drop Tasks from Available tasks OR load a previously saved Workflow
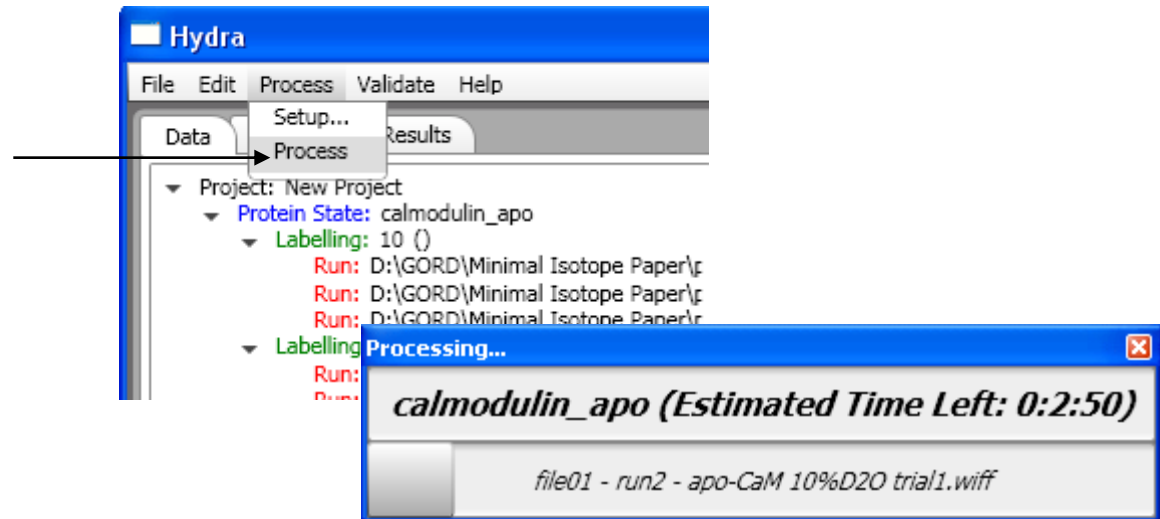
Scenerio 2: Defining the Data Processing Workflow

Step 2: Configure tasks

Scenerio 2: Defining the Data Processing Workflow

Step 3: Perform 'Single-click' to process data

Scenerio 3: Data Viewing

Primary output: Table of Deuterium Incorporation values, showing general Stats of replicates   (Exportable)
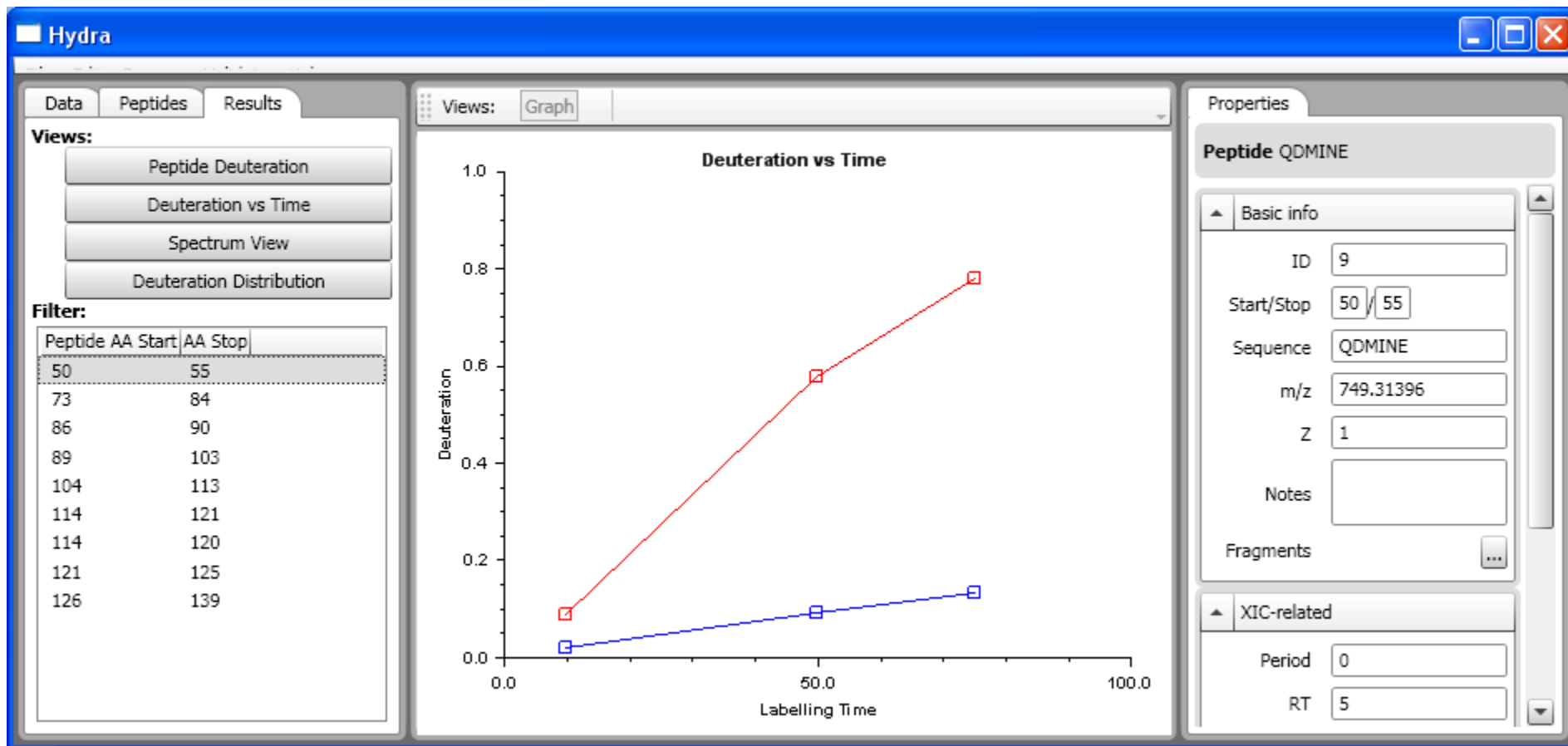
Scenerio 3: Data Viewing

Graphical view of all peptides:
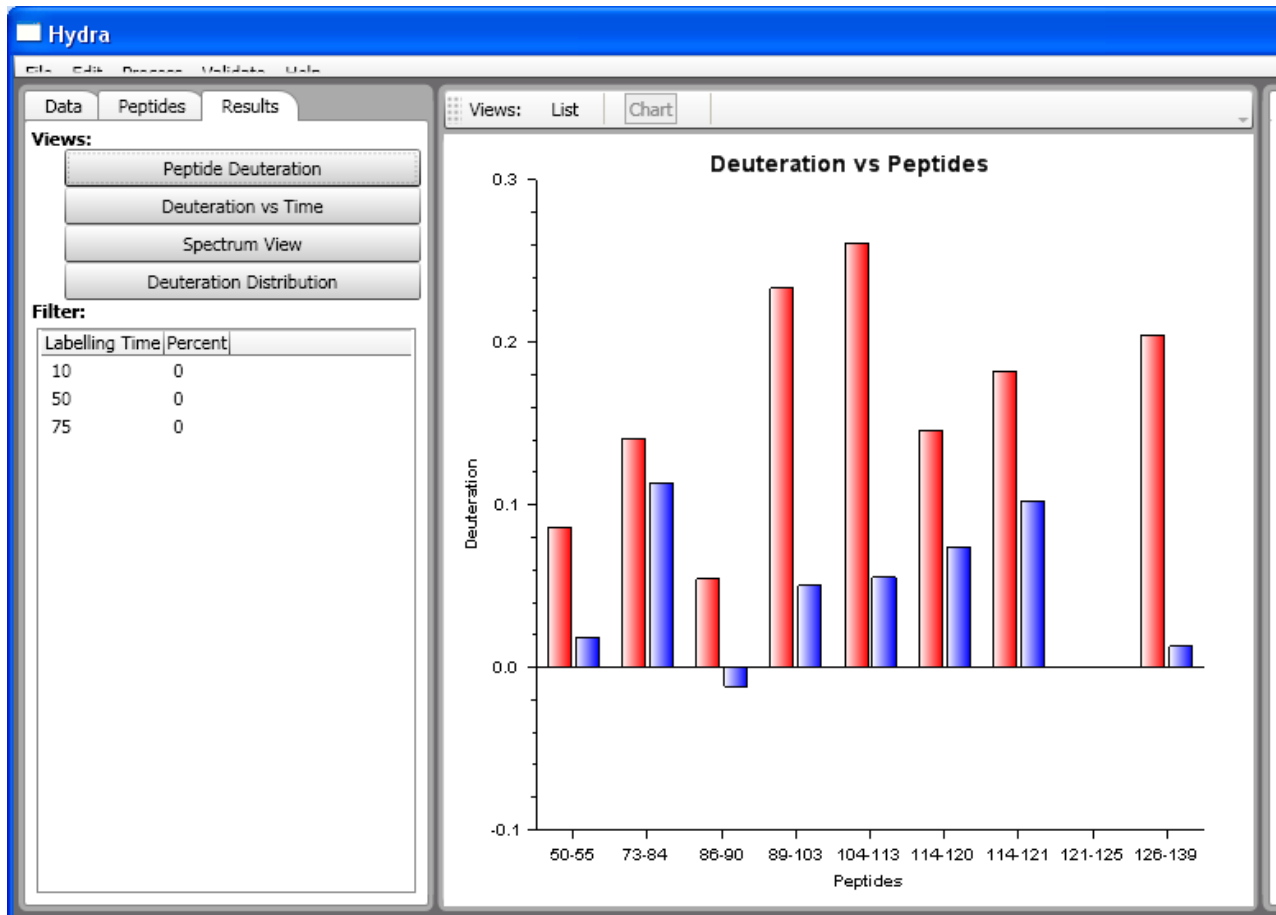
Scenerio 3: Data Viewing

Other views: Kinetic plot

Scenerio 3: Data Viewing

Other views: Spectrum view

Scenerio 3: Data Viewing

Other views: Deuterium Distribution Analysis
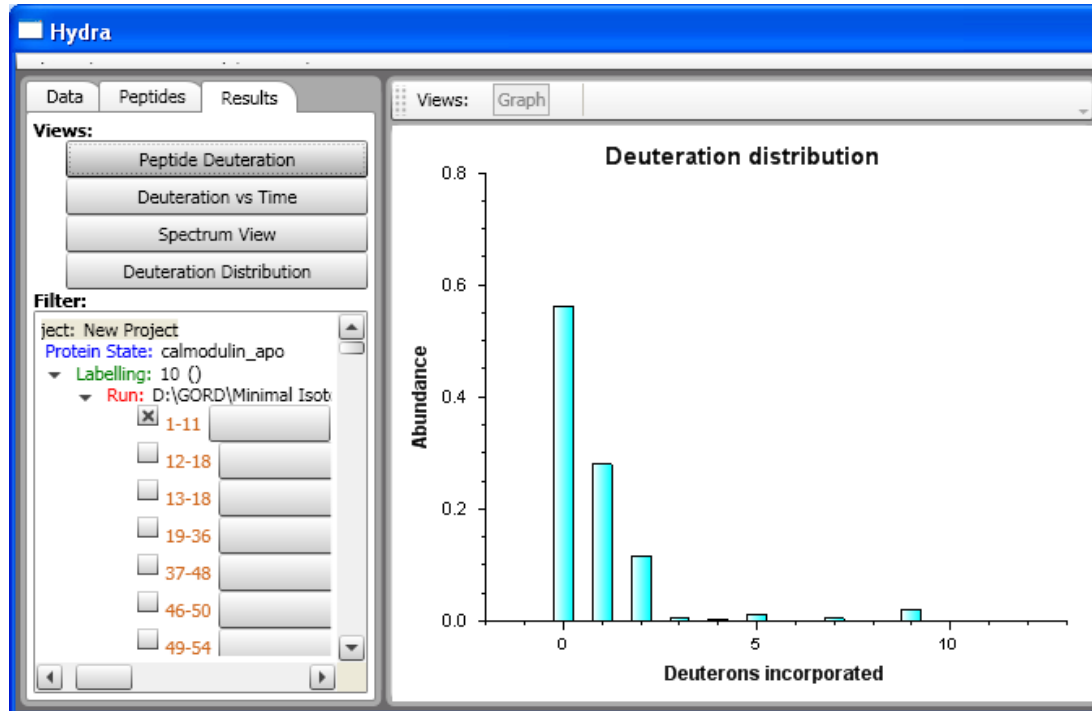
Summary and Key Features

- HYDRA uses step-by-step wizards to walk users through project configuration, and thus requires little training.

- HYDRA provides an automated means of extracting deuterium incorporation data including distribution information.

- Visual tools provide a quick way of validating results.

- Flexibility shown by the ability to adapt or add new data processing workflows.

SOFTWARE AVAILABILITY:
- Requests for HYDRA should be directed to Dr. David Schriemer (dschriem@ucalgary.ca)

Acknowledgements

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Thanks for your interest!