

RightField is an open source desktop tool for embedding ontology term selection in to Excel spreadsheets to create templates. Vanilla Excel spreadsheets are produced and do not contain macros or require special plugins.

The screenshot shows the RightField application window. On the left is an Excel spreadsheet with columns A, B, C, and D. Rows 1-14 contain metadata fields like 'title', 'summary', 'overall design', etc. Rows 15-29 contain sample data with columns for 'Sample name', 'title', 'CEL file', and 'source name'. Rows 30-45 contain protocol information. Some cells in the spreadsheet are highlighted with green overlays. On the right, the 'ONTOLOGY HIERARCHIES' panel shows a tree structure of ontologies. The 'JERMontology' is selected, and the 'AssayType' class is expanded to show subclasses like 'ExperimentalAssayType', 'fluxomics', 'genomics', etc. Below this, the 'VALUE TYPE AND PROPERTY' panel shows 'Subclasses' and 'Include a property' (checked). The 'ALLOWED VALUES' panel lists various biological processes like 'Comparative genomic hybridization', 'DNA sequencing', etc. An 'Apply' button is at the bottom right of the ontology panel.

RightField enables ranges of cells to be marked up so that they can only be selected from specific ontology terms.

It works with OWL and OBO ontologies, RDF Schema and SKOS vocabularies.

Provenance information such as complete term IRIs, the source ontologies they were taken from and ontology version information is embedded within the Excel spreadsheet itself for later use. However, all embedded ontology information is hidden from the spreadsheet user.

Class hierarchies of loaded ontologies in separate tabs

Method of specifying ontology terms
Terms lists are specified by selecting a class from one of the loaded ontologies and then by choosing to derive the terms as the direct/indirect subclasses or instances of the selected class.

Excel workbook with marked up cells

Marked up cells are shown with green overlays. In Excel, values for these cells must come from the specified list of ontology terms.

Term list for selected cells

The values of the selected marked up cells must come from this list of ontology terms. (In this case, these terms represent subclasses of the AssayType from the JERM ontology.)

When a spreadsheet template with embedded terms and marked up cells is opened in Excel, drop down lists allow users to choose values to enter for that cell.

Once filled out a spreadsheet can be saved and processed so that an RDF Graph, which relates back to the original ontology can be produced.

Biologists, who are intimately familiar with Excel, produce semantic annotations as part of their daily workflow, without any need for specialised ontology editing tools, or knowledge of ontologies.

This screenshot shows a close-up of the Excel spreadsheet from the previous image. A dropdown menu is open for the cell containing 'biological replicate' under the 'quality control type' field. The menu lists several options: 'biological replicate', 'biological replicate', 'dye swap quality control', 'peer review quality control', 'real time PCR quality control', 'reverse transcription PCR', 'spike quality control', and 'technical replicate'. The first two options are highlighted in blue. A note at the bottom of the menu says 'Library but they must match the question number (GPLxxxx)'. The spreadsheet background shows the same metadata and sample data as the previous image.