Workflow of MSInspector

```
┌─────────────────────────────┐
│   Skyline document file     │
│     (Experiment 1~5)        │
└─────────────────────────────┘
```

Is the value of internal standard preset?

Yes / No

```
┌─────────────────────────────┐     ┌─────────────────────────────┐
│    Skyline document file    │     │  Error report of the missing│
│                             │     │     internal standard       │
└─────────────────────────────┘     └─────────────────────────────┘
```

Extract the data with necessary attributes.

```
┌─────────────────────────────┐
│    Formatted form file      │
└─────────────────────────────┘
```

Detect missing values and unqualified data types.

```
┌─────────────────────────────┐     ┌─────────────────────────────┐
│ Formatted form file without │     │   Error report of miss      │
│ missing values and          │     │   values and unqualified    │
│ unqualified data types      │     │   data types                │
└─────────────────────────────┘     └─────────────────────────────┘
```

Traverse the peptide sequences and run the R script.
Is the running successful?

Yes / No

```
┌─────────────────────────────┐     ┌─────────────────────────────┐
│ Formatted form file without │     │  Error report of the failed │
│ errors to stop R script     │     │   peptides and the reason   │
│ running                     │     │                             │
└─────────────────────────────┘     └─────────────────────────────┘
```

For experiment 1~3, randomly sample 5 peptides to infer the
internal standard. Is the internal standard correct?

Yes / No

```
┌─────────────────────────────┐     ┌─────────────────────────────┐
│ Formatted form file without │     │  Error report of the        │
│ errors                      │     │  incorrect internal         │
│                             │     │  standard                   │
└─────────────────────────────┘     └─────────────────────────────┘
```

Traverse the peptide sequences and run the R script.

```
┌─────────────────────────────┐
│  Corresponding plots and    │
│  tables                     │
└─────────────────────────────┘
```

Evaluate the quality of the plots and tables.
Is the quality of the plots of tables good?

Yes / No

```
┌─────────────────────────────┐     ┌─────────────────────────────┐
│  Approved plots and tables  │     │  Warning report of the      │
│                             │     │  peptide with poor quality  │
│                             │     │  and the reason             │
└─────────────────────────────┘     └─────────────────────────────┘
```

```
┌─────────────────────────────┐
│    QC report (*.HTML)       │
└─────────────────────────────┘
```