


# Overview

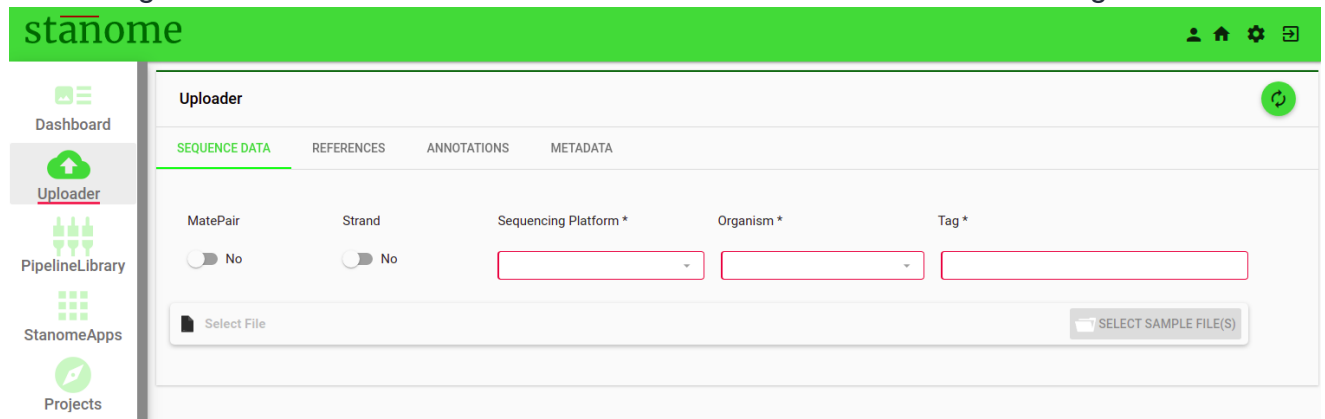
Data upload is the first step in the analysis. Generally, four data types are required:

1. Sequencing data (read files)
2. Reference genomes
3. Annotation files
4. Metadata

Click the  icon in the Utilities menu to access the **Uploader** window. Each data type is uploaded from a separate tab and follows the following three high-level steps:

1. Define the data types with correct tags
2. Verify and check for its existence in users account, format, and name conflicts
3. Upload

Pre-configured references and annotation files are available for the model organisms.



The screenshot shows the Stanome Uploader interface. The top navigation bar is green with the 'stanome' logo and user, home, settings, and help icons. A left sidebar contains navigation options: Dashboard, Uploader (highlighted), PipelineLibrary, StanomeApps, and Projects. The main content area is titled 'Uploader' and has four tabs: SEQUENCE DATA (active), REFERENCES, ANNOTATIONS, and METADATA. Below the tabs, there are five fields: 'MatePair' (toggle set to 'No'), 'Strand' (toggle set to 'No'), 'Sequencing Platform \*' (dropdown menu), 'Organism \*' (dropdown menu), and 'Tag \*' (text input). At the bottom, there is a 'Select File' button and a 'SELECT SAMPLE FILE(S)' button.

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