


Overview

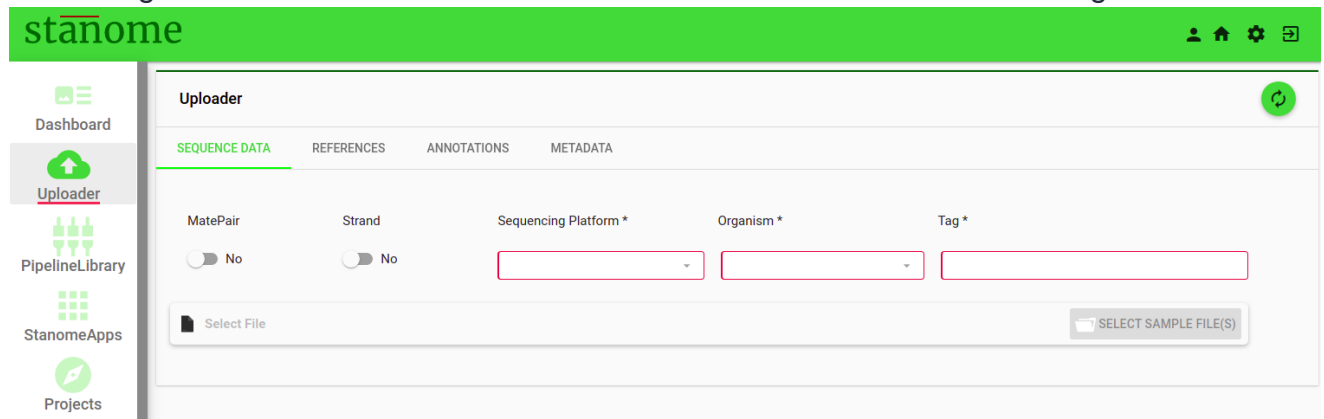
Data upload is the first step in the analysis. Generally, four data types are required:

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 web application interface. At the top is a green header with the 'stanome' logo and navigation icons. A left sidebar contains icons for Dashboard, Uploader (highlighted with a red underline), 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 form fields for '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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