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Definitions

Annotations: Data describing the gene models, pathways, ontologies, and other relevant biological information. Annotations are always associated with a reference genome and are consumed during a command execution through the argument or input variables.

Argument(s): Parameter variables that are defined with a key-value pair (*Example: --Threads 10*). Arguments are used by the tools during command building.

Command: Fundamental unit of a tool that executes a specific job.

Data Store: Stores all data types uploaded into the user's account. The data store is subdivided (sequence data, references, annotations, and metadata) for easy access.

Execution Flow: Displays the list of tools in the execution order

FileList: List of files used by a tool/command

File: A single file used by a tool/command

Metadata: Data that describes an experiment. Metadata is used for data analysis through the options, argument, or input variables.

Merge Step: A step in a pipeline that merges all the input files into a single output file.

My Pipelines: Pipelines shown within a project. Pipelines can be copied from the Pipeline Library into a project.

Hub: Pipelines are grouped into categories (Hub) based on function.

Input(s): Any data files used in a command. These are either uploaded by the user or generated within an executed job.

Jobs: Each execution of a pipeline is designated with a job ID.

Option(s): Command parameters that are defined with a single word (*Example: --ignore*). These are used by the tools while command building.

Output(s): Data files created during pipeline execution.

Pipeline: A set of computational tools, which run either sequentially or parallelly in order to achieve a specific data analysis objective. Tools/commands are designated as steps in a pipeline.

Pipeline Library: The list of pre-configured pipelines available on the platform

Projects: Self-contained mini-workspaces, where sample sets can be analyzed independently without interference from other data, using multiple pipelines.

Reports: Results of a pipeline execution are aggregated into easily understandable formats for quick viewing.

Sample Set: A set of samples (cohort) selected within a project. Sample sets are used for data analysis.

Tool: A bioinformatics software program that solves a specific biological problem. A tool can contain multiple commands (Example: Samtools index, sort)

Frequently Asked Questions

Who can use the Stanome platform?

Anyone who has NGS data to be analyzed can take advantage of the platform. The user does not need hardware resources or computational knowledge of NGS tools to use the Stanome platform.

Which browsers and operating systems do I need to use to access the Stanome platform?

The platform is tested and validated on the latest versions of the Chrome browser and works best on any operating system that supports the Chrome browsers.

How can I contact Stanome's technical support team?

Mail your detailed query to support@stanome.com.

How can I use my own custom reference genome?

Upload custom reference genomes through the **Reference/Annotation files** tab on the **Upload** window. Refer to section 4.2 (Upload Reference and annotation files) for detailed instructions on how to upload custom reference and annotation files.

How can I share my data with only my team members?

The multi-tenancy feature allows data sharing and analysis between group members of a shared account. Group members can request other members to join the group.

Can I download analysis files and how?

Yes, analysis files can be downloaded through the Report section. Refer to section 7.5 (Reports) to learn more about accessing all the intermediate output/analysis files.

Can I get a customized report?

Yes, a customized report with custom plots and tables can be obtained upon request. Contact Stanome technical support team (support@stanome.com) with details of the requirement.

How do I troubleshoot my failed pipeline?

Check your mail with the job status update. Issues related to the input data are described in the mail. Contact Stanome technical support team along with the job ID, if you are still not able to troubleshoot the issue.

Can I build a command that only generates standard output?

Yes, a command could be built using the **Command builder** dialog box within a pipeline. However, its output could be found in the output.log on the “sample deep dive” page described in section 7.4. In order to redirect the output to the next step in the pipeline contact the Stanome technical support team with details of the requirement.

How can I delete the data completely from the platform?

Raw sequence data can be deleted from the **Sequence Data** window (Utilities Menu). Analysis data can be deleted from the **Projects** window.

How long is the data retained?

Unless requested, all the data is purged after 30 days.

Why do I see duplicated pipelines?

Duplicate object names are not allowed on the platform. However, in a multi-tenancy setup, it’s allowed to create pipelines with the same names between shared users. Please use the owner tag to filter user-specific pipelines.

Are Stanome configured pipelines allowed to add to the favorites?

Stanome configured pipelines are accessible for all the users on the platform. These pipelines can’t be added to the favorites but can be copied into your projects.

Why the header line required in the BED files?

The BED file format is adapted from the UCSC https://genome.ucsc.edu/FAQ/FAQformat.html. We certify and validate the BED files against the reference genomes. Though header is not generally required, Stanome uses the header (*track name#*) content for the Genome Browser visualization in Stanome Report.

Quick Start Guide

This is a shorter version of the user guide that helps the users to get familiar with the platform quickly.

Steps to perform your first analysis

Step 1 : Upload samples and other required files through "Uploader". Each file will go through the validation process. Check the DataStore to verify the status of the uploaded files.

Step 2 : Create yours first project using Projects from the left menu.

Step 3 : Inside the project, create a Sample Set from the DataStore.

Step 4: Create a new pipeline or copy a preconfigured pipeline from the PipelineLibrary (My Pipelines).

Step 5: Execute the pipeline by clicking the Initialize Pipeline button. Fill in the required fields and click "Execute Pipeline".

Step 6: Monitor pipeline execution progress through Jobs.

Step 7: After the run completion, Report is ready to reviewed.

Customisation

Adding a New Organism

Click on settings icon  from the right upper corner. Select 

from the left menu bar. Create a new organism by clicking  icon. Fill in the required information and click  icon to save it.