Release Notes for SeqSense Analysis Solution

Version 2.1

June 2023

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Introduction

SeqSense Analysis Solution is a purpose-built workflow for analyzing and visualizing the next-generation sequencing (NGS) data. SeqSense uses a bioinformatics pipeline that is optimized for mapping, aligning, counting, and normalizing reads generated from libraries containing both short and long RNA. Using SeqSense, you can analyze and visualize NGS data from your FASTQ sample files. You can run the SeqSense analysis pipeline using the SEQuoia Complete Stranded RNA Library Prep Kit and the SEQuoia Express Stranded RNA Library Kit.

General Information and Resources

Supported Browsers

SeqSense is supported on the latest versions of Google Chrome and Apple Safari.

Documentation

The following documents are accessible from SeqSense Analysis Solution, Version 2.1:

- SeqSense Analysis Solution Getting Started Guide, Version 2.1
- SeqSense Analysis Solution User Guide, Version 2.1
- SeqSense Analysis Solution Frequently Asked Questions, Version 2.1

Samples Files Available on DropBox

- Click here for SEQuoia Complete.
- Click here for SEQuoia Express.

Additional Reference Genomes

- Reference genomes for SEQuoia Complete
- Additional reference genomes for SEQuoia Express

For more information, see the SeqSense Analysis Solution User Guide.

New Features and Improvements

New Login Requirement

When logging in, version 2.0 required you to enter your user name. Version 2.1 requires you to enter your email address.

Required Prep Kits

To use SeqSense Analysis Solution, you must purchase a SEQuoia Express Stranded RNA Library Prep Kit (Catalog No. 12017265) or SEQuoia Complete Stranded RNA Library Prep Kit (Catalog No. 17005710) from Bio-Rad (https:/www.bio-rad.com).

To purchase the kits, you must create a Bio-Rad website user account. From the landing page, click Log In/Register and follow the prompts. To use SeqSense to analyze your data, you must create a SeqSense user account. From the application landing page, click New User Form and follow the prompts. For more information, see the SeqSense Analysis Solution User Guide.

New Tab for Existing Sample Files

SeqSense now supports saving uploaded data files to the Existing Sample Files tab for reuse in future pipeline runs. The tab contains a list of samples you have recently uploaded.

Important: Experiments and sample files you created in SeqSense Analysis Solution Version 2.0 are not automatically accessible in Version 2.1.

New Spinner Icon

To alert the user that SeqSense is performing tasks in the background, a spinner icon now appears while reports are being retrieved.

New Advisory Messages When Adding Samples

To match the files as sample pairs, text is added to Add Sample Files Upload tab to advise you that sample files must be named using the standard (Illumina) naming convention.

Important: Duplicate sample file names prompt an error message. Check the Existing Sample Files tab before you upload to ensure the names for your new sample files are unique.

SeqSense Support for SEQuoia Complete Stranded RNA Library Kit

The SEQuoia Complete Stranded RNA Library Prep Kit is a high-performance stranded RNA-Seq kit that captures long and short RNAs in a single library, even from limited and low-quality samples.

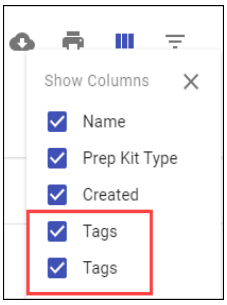
Featuring SEQzyme, a proprietary engineered enzyme that connects cDNA synthesis with adapter addition in a continuous synthesis reaction. The unique enzymatic properties effectively capture all types and sizes of RNA species in a novel enzymatic reaction, significantly improving the diversity and quality of RNA libraries, even from limited or degraded RNA samples. The SEQuoia Complete Stranded RNA Library Prep Kit is available at bio-rad.com.

Additional Instructions For SEQuoia Complete

If you are using the SEQuoia Complete Stranded RNA Library Prep Kit, SeqSense Analysis Solution can process only one sample at a time (R1 or R1+R2). To ensure that reports are generated, upload only one sample for a SEQuoia Complete pipeline run.

Known Issues

- You must begin analyzing the sample files within one hour of uploading them or SeqSense might time out without saving them.
- Experiments and sample files you created using SeqSense Version 2.0 are not automatically accessible in Version 2.1. You must upload the files again and run them using the SeqSense Complete pipeline.
- When you click the View Columns icon on the Samples and Experiments pages, the Tags checkbox is displayed twice in the pop-up and the Tags column can appear twice in the pages. You must clear the second checkbox to display only one Tags column in the Samples page.



- When you click in the Experiment Title field as you create a new experiment, the dropdown list of existing experiment names appears; however, if you select a name from the dropdown list, you receive an error message. You must modify the experiment name before you can continue.
- If you click the browser Back button, you might be returned to the Home page instead of the previous page.
- If you add more than 20 tags to an experiment, an error message appears. You must delete a tag before you can continue.
- When uploading multiple large files, the application might time out. Save your progress frequently to prevent data loss.

Contacting Technical Support

The Bio-Rad Technical Support department in the U.S. is open Monday through Friday, 5:00 AM to 5:00 PM, Pacific Time.

Phone: 1-800-424-6723, option 2
Email: Support@bio-rad.com (U.S./Canada Only)

For technical assistance outside the U.S. and Canada, contact your local technical support office or click the Contact Us link at www.bio-rad.com.

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