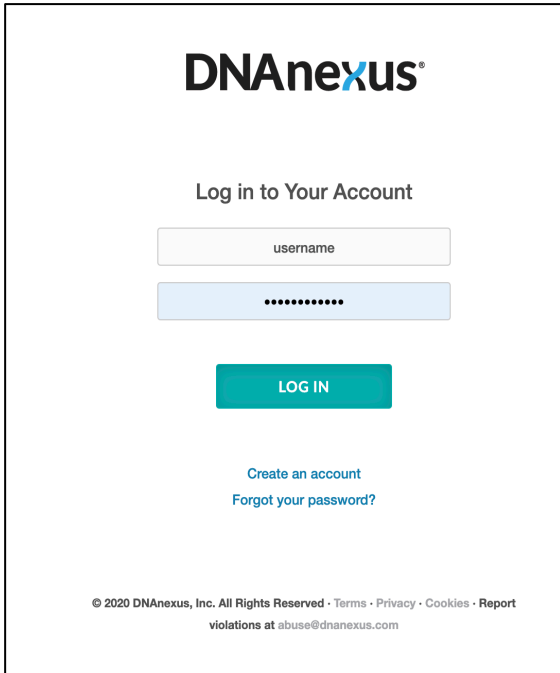
 <https://platform.dnanexus.com/app/sequencerr>



DNAnexus®

Log in to Your Account

username

.....

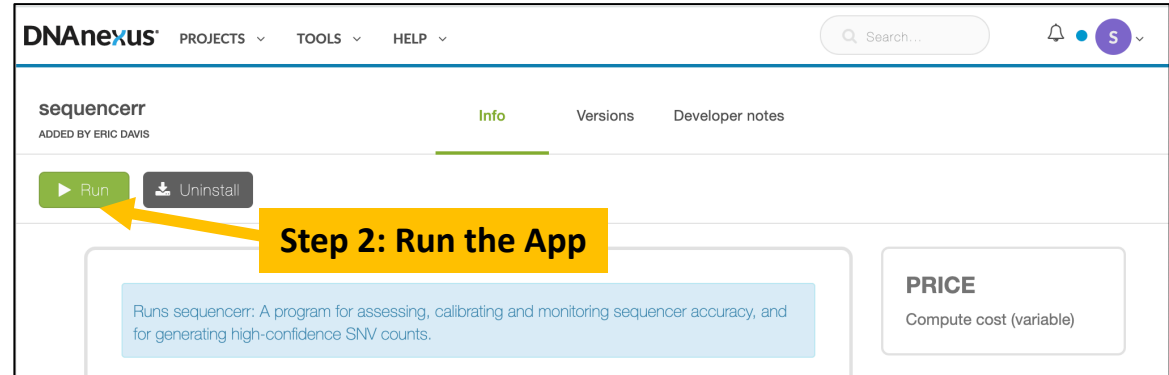
LOG IN

[Create an account](#)
[Forgot your password?](#)

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Step 1: Log In

Open the **SequencErr** App in the internet browser using following URL
<https://platform.dnanexus.com/app/sequencerr>
Enter the username and password to log in



DNAnexus® PROJECTS ▾ TOOLS ▾ HELP ▾

Search...

sequencerr
ADDED BY ERIC DAVIS

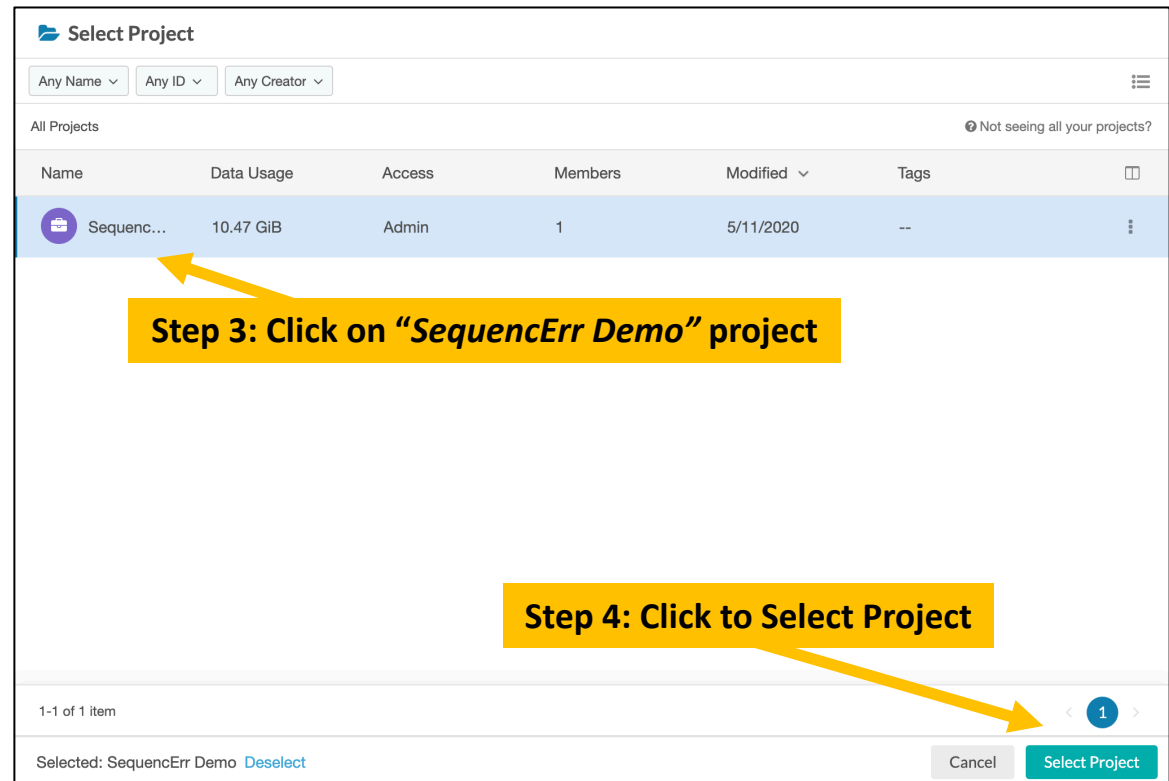
Info Versions Developer notes

Run Uninstall

Step 2: Run the App

Runs sequencerr: A program for assessing, calibrating and monitoring sequencer accuracy, and for generating high-confidence SNV counts.


PRICE
Compute cost (variable)



Select Project

Any Name ▾ Any ID ▾ Any Creator ▾

All Projects Not seeing all your projects?

Name	Data Usage	Access	Members	Modified ▾	Tags	
 Sequenc...	10.47 GiB	Admin	1	5/11/2020	--	

Step 3: Click on "SequencErr Demo" project

1-1 of 1 item

Selected: SequencErr Demo [Deselect](#)

Cancel **Select Project**

Step 4: Click to Select Project



Analysis Settings Analysis Inputs 3 Stage Settings

Execution Name **Step 5: Assign the name (optional)**

sequencerr

Execute in Project

SequencErr Demo (project-FpvqpG89P02g7x7f13QjgQ0b) ...

Execution Output Folder

/ ...



Step 6: Click to choose input BAM file

Analysis Settings Analysis Inputs 3 Stage Settings

sequencerr ▾ Enable Batch ☐ Off

sequencerr ? About this app

* ? bam file name * Select File

* ? bam index file name * Select File



Analysis Settings Analysis Inputs 2 Stage Settings

sequencerr ▾ Enable Batch ☐ Off

sequencerr ? About this app

* ? bam file name * ERR3781296.bam

* ? bam index file name * Select File



Step 7: Click to choose index file



Step 6a: Click on BAM file from the *Input data* folder

Step 6b: Click to Select Data

Select Data

Current Folder and Subfolders ▾ Any Name ▾ Any ID ▾ Any Type ▾ Any Class ▾

Suggested Items All Projects > SequencErr Demo > Input data

SequencErr Demo

SequencErr Demo

counts

Input data

Name ^	Type / Class	Size	Created	Status
ERR3781296.bam /Input data	File	5.37 GiB	5/11/2020	Live
ERR3781296.bam.bai /Input data	File	4.27 MiB	5/11/2020	Live
ERR3790810.bam /Input data	File	5.1 GiB	5/11/2020	Live
ERR3790810.bam.bai /Input data	File	3.6 MiB	5/11/2020	Live

1-4 of 4 items

Selected: SequencErr Demo / Input data / ERR3781296.bam Deselect

Cancel Select Data

Select Data

Current Folder and Subfolders

Any Name

Any ID

Any Type

Any Class

Suggested Items

SequencErr Demo

SequencErr Demo

counts

Input data

All Projects > SequencErr Demo > Input data

Name ^	Type / Class	Size	Created	Status
ERR3781296.bam /Input data	File	5.37 GiB	5/11/2020	Live
ERR3781296.bam.bai /Input data	File	4.27 MiB	5/11/2020	Live
ERR3790810.bam /Input data	File	5.1 GiB	5/11/2020	Live
ERR3790810.bam.bai /Input data	File	3.6 MiB	5/11/2020	Live

1-4 of 4 items

Cancel

Select Data

Step 7a: Click on index file from the *Input data* folder

Step 7b: Click to Select Data



Analysis Settings

Analysis Inputs 1

Stage Settings

sequencerr

Enable Batch

Off

sequencerr

bam file name

ERR3781296.bam

bam index file name

ERR3781296.bam.bai

Step 8: Provide sample id and other optional parameters

sample id

trimming length

5

hard quality cutoff

20

don't report base counts

True (default)

False

Step 10: Status of the job available under Monitor tab of the Sequencer Demo project

DNAnexus

PROJECTS

TOOLS

HELP

SequencErr Demo

Settings

Manage

Monitor 1

Visualize

Access: Admin

1

Share

SEARCH SCOPE

Root executions only

recent jobs

NAME

Any

ID

Any

CREATED

Any

STATUS

NAME

EXECUTABLE

LAUNCHED BY

STARTED RUNNING

DURATION

PRICE

WORKER URL

Running

sequencerr

sequencerr (v2.0.7)

SLJude_Reviewer1

05/12/2020 3:06 pm

1m

~ \$0.0027 as of May 12, 3:06 PM

Analysis Settings

Analysis Inputs

Stage Settings

sequencerr

Enable Batch

Off

sequencerr

Version

2.0.7

Instance Type

azure:mem1_ssd1_x2

3.9 GB total memory, 32 GB total storage, x2 cores

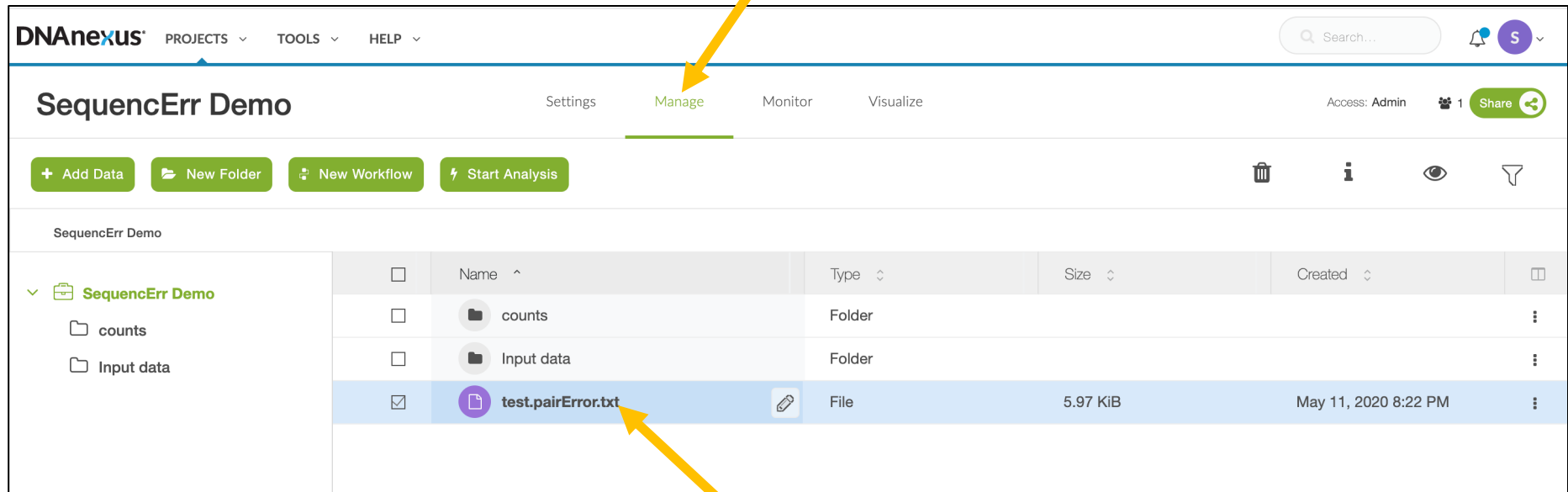
Output Folder

/

Run Analysis

Step 9: Check system configuration and click Run Analysis

Step 11: Output of the analysis will available under Manage tab of the Sequencer Demo project



The screenshot shows the DNAnexus interface for a project named "SequencErr Demo". The top navigation bar includes "PROJECTS", "TOOLS", and "HELP". The project-specific navigation bar shows "Settings", "Manage" (highlighted with a green underline), "Monitor", and "Visualize". Below this, there are buttons for "Add Data", "New Folder", "New Workflow", and "Start Analysis". The main content area displays a file tree on the left with "SequencErr Demo" expanded, showing "counts" and "Input data" folders. A table on the right lists the files and folders:

	<input type="checkbox"/>	Name ^	Type	Size	Created	
	<input type="checkbox"/>	counts	Folder			⋮
	<input type="checkbox"/>	Input data	Folder			⋮
	<input checked="" type="checkbox"/>	test.pairError.txt	File	5.97 KiB	May 11, 2020 8:22 PM	⋮

Two yellow arrows point from the "Step 11" text to the "Manage" tab and the "test.pairError.txt" file.

Step 12: Locate output files of the analysis using directory/file navigation as per input settings