



YOUSEQ

16S NGS DATA ANALYSIS PIPELINE USER GUIDE

VERSION 1.0

For Research Use Only



YOUSEQ

YouSeq Ltd
8 Moorside Place
Moorside Road
Winchester
SO23 7FX
United Kingdom

+44 333 577 6697
hello@youseq.com

youseq.com

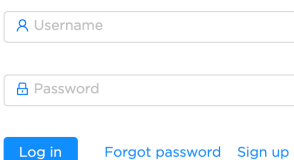
INTENDED USE

The YouSeq NGS data analysis pipeline is designed to generate easy and simple reports from the fastq.gz or bam file data produced by Illumina and Ion torrent sequencers.

The analysis pipeline cleans the data and attempts to assign the reads (or paired reads) to a specific bacterial species. The output of the pipeline is summarized in a sunburst plot along with pdf reports and .csv files. The raw and summarized data can be downloaded and further interrogated in a spreadsheet.

SIGNING UP

1. Go to <https://youseq.basepairtech.com/>
2. Click on 'Sign up':

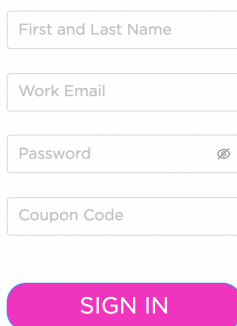


Username

Password

Log in Forgot password Sign up

3. Enter your Name, email address and a memorable password, then click 'sign in':



First and Last Name

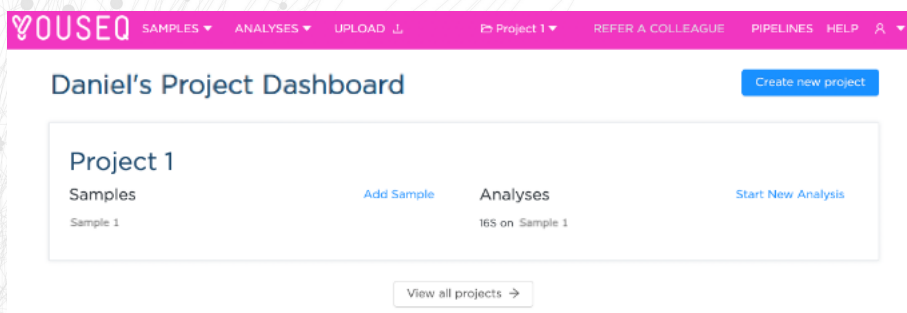
Work Email

Password

Coupon Code

SIGN IN

4. The project dashboard will then open:



YOUSEQ SAMPLES ANALYSES UPLOAD Project 1 REFER A COLLEAGUE PIPELINES HELP

Daniel's Project Dashboard

Create new project

Project 1

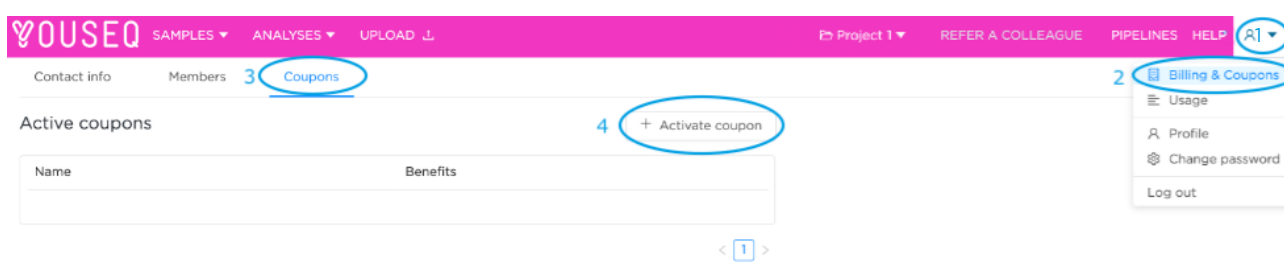
Samples	Add Sample	Analyses	Start New Analysis
Sample 1		16S on Sample 1	

View all projects →

APPLYING COUPON CODES

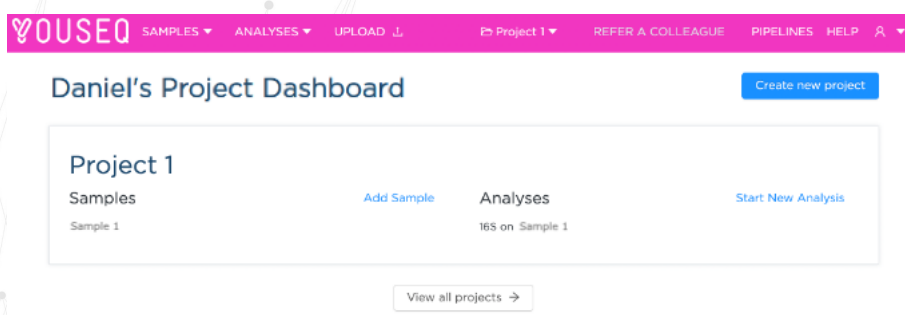
Before analysing the data, a coupon must be activated on your account. Contact us on support@youseq.com, along with the kit serial number, to request a coupon code. The kit serial number can be found on the pouch label.

1. Go to your account menu in the top right corner
2. Click on 'Billing & Coupons'
3. Click on the 'Coupons' tab
4. Click on 'Activate coupon'
5. Enter the provided coupon code and click 'activate'



CREATING A NEW PROJECT

1. Click on the blue "Create New Project" button
2. Enter your Project Name
3. This will create the project overview on the project dashboard:



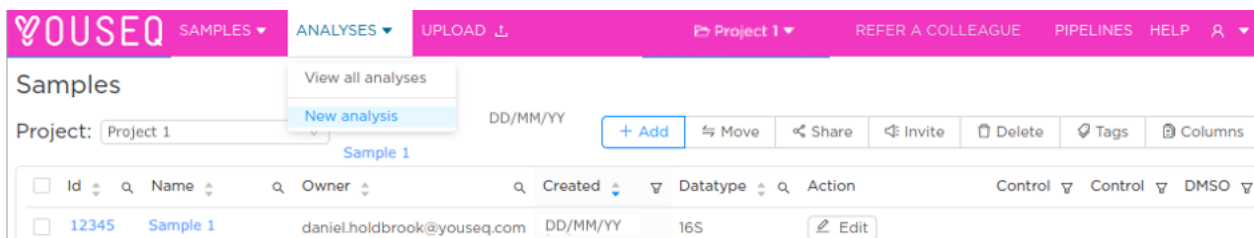
UPLOADING SAMPLE SEQUENCE DATA

From the project dashboard, sample sequence data can be uploaded using the 'Add Sample' button or 'Upload' tab on the top menu bar. This will bring up a pop-up window that allows files to be drag and dropped for uploading. Sequence data can be uploaded from multiple samples at once. This will upload the files to the current project.

The following file types will be accepted: .bam, .fastq, fastq.gz

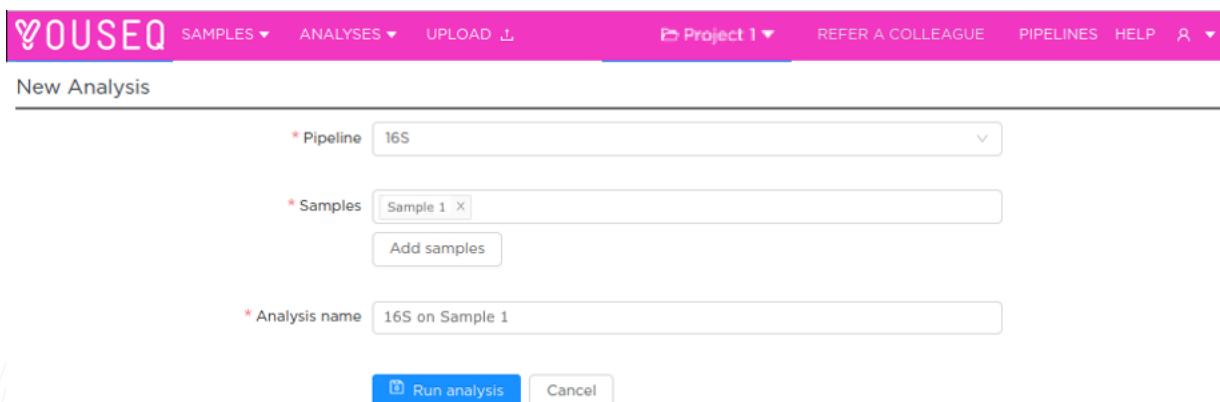
ANALYSING SAMPLE SEQUENCE DATA

1. Hover over the 'Analyses' tab in the top menu bar
2. Click on 'New Analysis':



The screenshot shows the YOUSEQ web interface. The top navigation bar is pink and contains the YOUSEQ logo, 'SAMPLES', 'ANALYSES', 'UPLOAD', 'Project 1', 'REFER A COLLEAGUE', 'PIPELINES', and 'HELP'. Below the navigation bar, the 'Samples' section is visible. A dropdown menu is open under the 'ANALYSES' tab, showing 'View all analyses' and 'New analysis'. The 'Samples' table has columns for 'Id', 'Name', 'Owner', 'Created', 'Datatype', and 'Action'. A sample with ID '12345' and name 'Sample 1' is listed. The 'Action' column for this sample has an 'Edit' button.

3. Click on the dropdown menu in the 'Pipeline' field
4. Select the '16S' pipeline
5. Select a sample, or several samples (each sample will be analysed individually) by clicking on the 'Add samples' button
6. Choose a name for the analysis run (a suggested name will be automatically provided)
7. Click on the blue 'Run analysis' button:



The screenshot shows the 'New Analysis' form in the YOUSEQ web interface. The form has three main fields: 'Pipeline' (set to '16S'), 'Samples' (set to 'Sample 1'), and 'Analysis name' (set to '16S on Sample 1'). There are 'Add samples' and 'Run analysis' buttons. The 'Run analysis' button is blue and has a play icon. There is also a 'Cancel' button.

DOWNLOADING RESULTS

After the samples have been analysed the results can be viewed in a number of formats. The main results page will display the read assignments as a sunburst plot, and as a series of summary tables that contain the top 10 highest occurring assignments at each taxonomic level: Kingdom, Phylum, Class, Order, Family, Genus and Species.

The downloadable PDF report contains a summary of how each read was assigned at each taxonomic level. The raw assignments and summary tables can also be downloaded in csv format.

Option 1: Results can be reviewed online with the interactive sunburst plot: This will be automatically displayed when the analysis window is opened.

YOUSEQ
SAMPLES ▾ ANALYSES ▾ UPLOAD ⬇
Project 1 ▾ REFER A COLLEAGUE PIPELINES HELP 👤 ▾

16S on Sample 1 Edit Share Delete

Completed

[Report](#) | [Info](#) | [Log](#) | [Api response](#)

Sections

- Sunburst
- Table

Download PDF

Search:

k__Bacteria

Count: 3435

Max depth: 7

Font size: 11

Chart size: +

Collapse

Snapshot

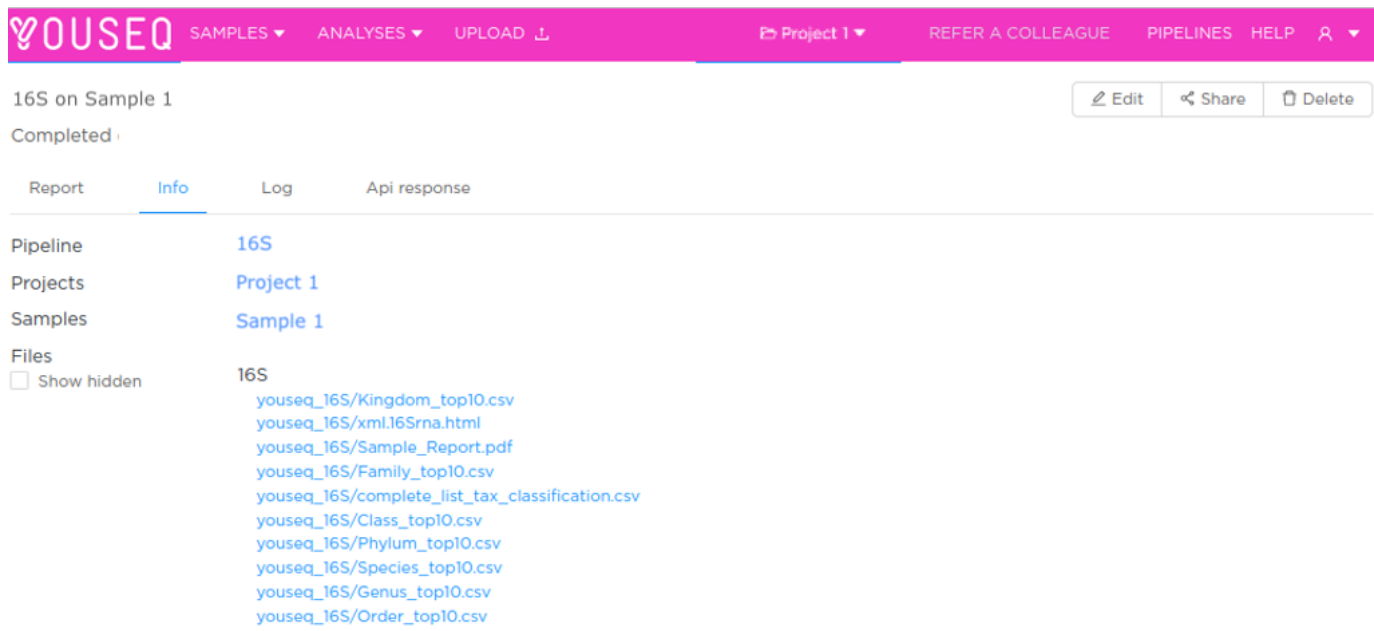
16S rRNA kit

c__BD1-5_unclassified	0.3%
p__SR1_unclassified	0.2%
k__Bacteria_unclassified	0.1%
g__Treponema	0.1%
o__RF39_unclassified	0.03%

16S NGS Data Analysis Pipeline
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Option 2: A PDF report of the data can be downloaded by clicking on the 'Download PDF' button, located above the sunburst plot.

Option 3: A number of reports and file types are produced by the analysis pipeline and can be downloaded by clicking on the 'Info' tab and then the name of file from the 'Files' list. The download will start automatically.



The screenshot shows the YOUSEQ web interface. At the top is a navigation bar with 'YOUSEQ' and menu items: 'SAMPLES', 'ANALYSES', 'UPLOAD', 'Project 1', 'REFER A COLLEAGUE', 'PIPELINES', 'HELP', and a search icon. Below the navigation bar, the main content area displays '16S on Sample 1' with a status of 'Completed'. There are three buttons: 'Edit', 'Share', and 'Delete'. A tabbed interface is shown with 'Report', 'Info' (selected), 'Log', and 'Api response'. Under the 'Info' tab, the following information is displayed:

- Pipeline: 16S
- Projects: Project 1
- Samples: Sample 1
- Files: 16S

There is a checkbox labeled 'Show hidden' next to the 'Files' section. Below it is a list of files:

- youseq_16S/Kingdom_top10.csv
- youseq_16S/xml.16Srna.html
- youseq_16S/Sample_Report.pdf
- youseq_16S/Family_top10.csv
- youseq_16S/complete_list_tax_classification.csv
- youseq_16S/Class_top10.csv
- youseq_16S/Phylum_top10.csv
- youseq_16S/Species_top10.csv
- youseq_16S/Genus_top10.csv
- youseq_16S/Order_top10.csv